UFZ HELMHOLTZ Centre for Environmental Research

ECEM 2023

European Conference on Ecological Modelling

ECOLOGICAL MODELLING FOR TRANSFORMATION

September 4–8, 2023 | Leipzig, Germany

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ECEM 2023
Book of Abstracts

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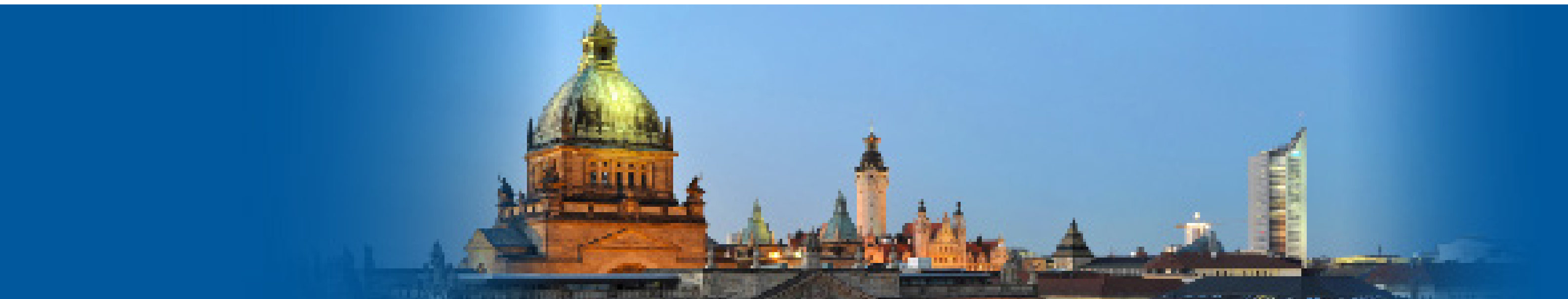

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1. Animal migrations under global changes – threats, implications, and mitigation

Animal migrations under global changes – threats, implications, and mitigation

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No ecological community, no ecosystem exists without migrating organisms. Animal migrations span the globe, involving trillions of individuals from many taxa that uniquely alter nutrient and energy flow, food-web topology and stability, and the structure and dynamics of metacommunities through a variety of transport and trophic effects. As global change is inherently global but spatially and temporally uneven, migratory animals are faced with changes at multiple scales, locations and times, including climatic change, loss and deterioration of habitats through land use change, expansion of human structures and activities, which has already resulted in loss of biodiversity, ecosystem function and the spread of (emerging) infectious diseases.

Understanding and predicting the threats that migratory populations face and their divergent responses to global changes are challenging yet important endeavours to develop successful management plans and conservation measures.

We will shortly introduce models that allow us to predict the complex system change of animal migrations, and present results of ongoing studies that aim to provide a better understanding on how global change processes alter the behavior of migrants. Specifically, we will provide details in how bird systems in a rapidly changing environment have to encounter, respond and adapt differently depending on the species-specific traits, and how the integration of physiological host-pathogen interactions leads to a more informed risk assessment of pathogen spread via migratory birds.

Integrating individual-based models and machine learning for bird migration forecasts and inference about underlying decision rules

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As birds are migrating, they encounter human influences that extend ever more widely and deeper into the lower atmosphere, such as anthropogenic light, aviation, and wind energy infrastructure. To reduce the societal impact of aeroconservation measures, accurate and timely forecasts of bird migration can be used to increase the conservation benefits for the lowest societal costs. Networks of weather radars enable us to continuously monitor the migratory movements of flying animals, and their measurements can thus be used to further our understanding of and to help predict the (mostly nocturnal) migratory movements of billions of birds. In recent years, statistical and machine learning methods fitted with data from weather radars, have been used successfully to forecast bird migration and to reduce associated human-wildlife conflicts.

Here, we present a methodology that builds on previous statistical/ML approaches for bird migration forecasting, but augments it with simulations from individual-based models. We simulate nocturnal migrants using simple decision rules based on wind selectivity and preferred directions, and use their tracks — which can span hundreds of kilometers in a single night — to dynamically sample environmental conditions encountered by these hypothetical migrants. We use these tracks to separate environmental conditions experienced on the stop-over locations, while migrants are in flight and when these birds fly directly over our radars. This approach allows the model to later capture effects of environmental conditions on the stop-over as well as in-flight decisions of these migrants. We use these environmental conditions in a machine-learning workflow using gradient boosting, to predict altitude-specific bird densities for a model to be used eventually for wind energy curtailment in the Netherlands. We train the model on data from Dutch and nearby German and Belgian weather radars. We expect explicitly incorporating conditions encountered by hypothetical migrants at different stages of migration, will result in more accurate predictions of the dynamics of mass movements of nocturnal migrants. We address model performance and compare this approach against models using fixed sites for sampling of environmental conditions. Furthermore, we show how this mixed approach can be used to infer about the underlying decision rules of individual birds shaping pulses of bird migration, both in flight as well as on the stop-over sites.

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2. Modelling species migration and range shifts under global change

Modelling the role of multiple global change drivers on future range shifts in a tropical Biodiversity Hotspot

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Climate change is causing plants to alter their known ranges to track newly suitable habitat. Species extinction risk due to global and local change drivers is highest on geographically isolated islands with high endemism such as Madagascar. For plants like Calophyllum paniculatum (C. paniculatum), they have a double threat, after high mortality rates were discovered within Ranomafana National Park, linked to a newly identified vascular wilt like pathogen [1]. Ranomafana National Park is a tropical evergreen montane rainforest in southeastern Madagascar and covers an area of 416km². C. paniculatum is “vulnerable” on IUCN Red List [2] and is found between elevations of 600 to 1480 m at 5 different site locations within the Park [1,3]. Previous studies that have modelled future range shift responses for endemic plants in Madagascar included land cover and a limited proxy for dispersal capability [4].

We modelled C. paniculatum under multiple future climate, land cover, dispersal, and pathogen-spread scenarios through a combination of correlative and mechanistic approaches to disentangle the driving forces of range shift into the future at national and regional scales. For correlative models, we utilised Maxent, using 7 of the 19 bioclimatic variables [5] that are most significant to plant survival while capturing seasonal variation and extremes [6].We opted to model future climate using a high emission scenario (RCP 8.5) from global climate model CMIP5 to year 2100 [7]. For mechanistic models, we parameterised scenarios using locally collected lemur dispersal data and a population-specific mortality probability from five consecutive years of spatially explicit monitoring of C. paniculatum tree health in Ranomafana National Park [1]. Mean dispersal distance was parameterised from multi-year behavioural observations of three lemur species: Eulemur rufifrons, Eulemur rubriventer and Varecia variegata present in the Park [8,9,10].

Initial results suggest range shift becomes increasingly limited when utilising dispersal parameters from field collected data, as they do not account for less common, long distance dispersal events. With current rates of pathogen spread alone, local populations of C. paniculatum may not be able to sustain themselves within the measured time-period without intervention or support. Localised change drivers such as fragmentation of forest edges, with the additional increased mortality due to pathogen, may have more direct impacts on the plants’ future status than climate alone. Further analysis is required to ascertain the risk posed by localised environmental factors such as the pathogen spread, and to understand what this means for endemism in Madagascar.

CATS: Modelling plant migration in a changing environment

Andreas Gattringer; Johannes Wessely; Karl Hülber; Dietmar Moser; Stefan Dullinger

University of Vienna

The loss of biodiversity is among the most important and widely discussed effects of anthropogenic climate warming. To escape extinction, species may respond to a changing climate by shifting their ranges to track the climate suitable to them. Such range shifts are under the joint control of various processes, including the local dynamics of populations, the mobility of individuals and (trophic) interactions with other species and the magnitude of climatic change.

To be able to predict range shifts of species under changing environments, we developed the high performance software framework CATS. CATS is spatially and temporally explicit, and combines a demographic and a dispersal sub-model. The demographic model is stage-structured, and links environmental conditions to the vital rates driving the demographic processes. These vital rates can be quantified by either the output of species distribution models (SDMs), or by other, external models. Migration is simulated via user-specified, mechanism-agnostic dispersal kernels, which define the spatial probability distribution of seed and propagule transport.

CATS was written in C, with a focus on performance (multi-threaded and optional MPI (Message Passing Interface) support), allowing continental-scale simulations at high spatial resolutions. Its modularity gives flexibility in terms of formulating the demographic and dispersal sub-models, e.g. for simulating species other than plants.

We showcase the capabilities of CATS by simulating the range dynamics of oligophagous butterflies and their host plants in Europe. Thereby, we examined whether range dynamics of host plants restrict migration of the (potentially) more mobile insects under expected climatic conditions of the 21st century.

Impact of climate change on suitable distribution of key tree species in Qinghai-Tibetan plateau based on combined model

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Species distribution, as a product of multiple ecological processes, has been a hotspot of research, especially for impact of climate change on species distribution patterns. Qinghai-Tibet Plateau, as the third pole of the world, its unique environment has created many unique species. However, global warming has had a great impact on the plateau environment and many species are endangered. Therefore, understanding the relationship between species at risk of extinction and their environment and finding out the changes in the geographical distribution of plateau species under climate change scenarios are helpful to the targeted protection and management of species.

In this study, the typical species distribution data of coniferous and broadleaf trees were obtained through field investigation, literature statistics and expert collection. At the same time, a large number of environmental data were collected, including current and future basic climate data, pollen data. soil data and altitude data.

On this basis, the LAVESI model was set up to simulate reproductive process of the tree species with explicit seed dispersal and resulting migration in the complex landscape. Also, the MaxEnt (maximum entropy model) was used to simulate the potential distribution of species in current and future scenarios, and the relationship and mechanism between species distribution based on occurrence data. The differences of the potential distribution area of species was determined by the comparison of future-current scenario results from both individual based spatially-explicit simulation with LAVESI and MaxEnt modelling. Species conservation effects in current and future scenarios were analyzed by overlapping species potential distribution and existing nature reserves. Our study is aiming at answering the following research questions:

(1) Under ancient, current and future conditions, how will the distribution of species perform?

(2) The reproductive success or dynamic range shifts of species from ancient time to the future.

The study will finally allow suggestions to improve the existed protected area system.

Introduction to session: Details matter! – importance of small-scale processes to model high-latitude ecosystem responses

Stefan Kruse; Josias Gloy; Ramesh Glückler; Veronika Döpper; Ulrike Herzschuh

Alfred Wegener Institute Helmholtz Center for Polar and Marine Research

Ongoing latitudinal treeline expanse might cause dramatic losses of tundra areas that have no space for refugia in the north as they are limited by the Arctic Ocean. Limited largely on warmth deficit an increasing forest immigration rate is expected. However, processes that act over larger-scales as well as small-scales can have an important impact on forest migration but are mostly neglected in model studies because of their complicated assessment. We therefore implemented different processes to test their impact on boreal forest and treeline migration responses.

We established an individual-based boreal forests vegetation model LAVESI as a tool to test our hypotheses. Our simulation experiments involve individual based, spatially-explicit seed dispersal and subsequent establishment as well as the interaction with (micro-)topography and biotic factors. Further, we implemented explicit pollination of seeds and variable traits so that these can be passed down to the offspring. This enables populations to adapt to changing conditions and testing the importance of the level of adaptation under changing environments. The data for parameterization was collected on several field campaigns and completed by literature. With novel methods such as ground and UAS-based laser scanning we explore how to extract the necessary spatial information on forest structure for LAVESI. By integrating this information with our field data, we generate validation data that spans landscapes, as opposed to local plots.

Our results let us conclude that the small-scale processes and the increased complexity in the model significantly change the outcome of the modelled impact of global warming on high-latitudinal boreal forest.

Tree migration in complex landscapes

Olalla Díaz-Yáñez; Paloma Julia Martinez; Harald Bugmann

ETH (Zurich)

Tree migration rates and their spatial pattern are strongly influenced by the arrangement of habitat patches in a landscape. Complex landscapes have higher topographical variability, and changes in slope-aspect relationships have an influence on local climatic conditions. Tree migration rates are influenced by the variability in the local climate, due to landscape complexity, and due to overall climate change. However, it is not clear how they influence tree migration rates overall, and how alternative spatial patterns plays a role, such as those caused by different landscape fragmentation levels. In this study, we aim to understand 1) how changes in climate modify tree migration rates for different levels of landscape complexity, and 2) the role of landscape fragmentation in complex topographies. We selected three catchments in Switzerland that are representative of a gradient of landscape complexity defined by the first principal component of different indices of topographic complexity. Tree migration was simulated in an empty landscape for a monospecific initial population of two early and late successional species, respectively: Betula pendula and Pinus sylvestris, vs. Fagus sylvatica and Picea abies. We used the forest landscape model LandClim to simulate tree migration under the influence of different climate scenarios and alternative levels of landscape fragmentation. Recently, LandClim has been updated to an annual time scale with a new formulation for tree dispersal. Alternative formulations for dispersal kernels are tested at the species level. The results are confronted with independent migration estimates based on genetic or pollen reconstructions. We will discuss the computational and ecological challenges of the new model formulation and alternative kernels. We also evaluate the results related to species migration rates with a focus on the effect of different landscape complexities, climate change scenarios and levels of landscape fragmentation.

Simulating landscape-scale treeline dynamics under climate and land-use change to support forest management strategies

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Forests are long-lived ecosystems, very sensible to rapid environmental changes. In mountain areas, the effect of climate warming on the treeline ecotone and the subalpine forest belt can already be observed today. Although rising temperature may improve forest growth and promote an upward shift of the treeline, other environmental constraints, as well as land-use and management activities, may alter these effects. So far, many studies have focused on single effects of climate variability on treeline forest dynamics. Nonetheless, no spatially explicit approach evaluating landscape scale patterns have been used yet. Focusing on a mountain forest landscape in the Central Alps (Stubai Valley, Austria), we aimed at evaluating the effects of climate and land-use change on the treeline ecotone by simulating forest dynamics from the stand to the landscape scale. We applied a process-based forest landscape model (iLand) under different climate scenarios, comparing two land-use scenarios that might affect treeline dynamics, namely business-as-usual and maximum land-use abandonment. Our preliminary results showed a general advance of the treeline but this effect is highly heterogeneous and contingent on multiple environmental factors. The treeline ecotone reached highest elevations under the highest emission scenarios, but its expansion was highly modulated by different land-uses, which strongly influenced forest regeneration patterns across the landscape. Overall, we observed a significant expansion of the forest area in the subalpine belt which was considerably greater under the abandonment scenario and in south-facing slopes. Forest expansion led also to denser stands characterized by smaller diameter, with an increase of Larch (Larix decidua Mill., 1768) at the expanses of other species, especially mountain pine (Pinus mugo Turra, 1764). Although modelling future treeline dynamics remains a challenge due to the complexity of multiple interacting factors acting at different scales, our study highlights the potential of dynamic forest landscape models to project future treeline development. Such modelling approaches also allow exploring future spatial patterns of the upper treeline, guiding decision makers in the context of forest management planning, particularly to alpine ecotone biodiversity, improving conservation strategies and provision of mountain forests' ecosystem services.

Competition and demography rather than dispersal limitation slow down upward shifts of trees' upper elevation limits in the Alps

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Species range limits are expected to be dramatically altered under future climate change and many species are predicted to shift their distribution upslope to track their suitable conditions (i.e. based on their niche). However, there might be large discrepancies between the speed of the upward shift of the climatic niche and the actual migration velocity of the species, especially in long-lived organisms such as trees. In fact, most studies did not find any significant upward shift in the distributional limits of temperate forest trees over the last decades. It, therefore, beckons the questions of why trees are moving upslope much slower than their bioclimatic envelope and what are the implications for ecosystem functioning. We compared the simulations of the upslope displacement of the bioclimatic envelope of 16 tree species inhabiting temperate mountain forests under ongoing and future climate change obtained by correlative species distribution models (SDMs) to those from a dynamic forest model accounting for dispersal, competition and demography. We then partitioned the discrepancy in upslope migration velocity between the SDMs and the dynamic forest model into different components by manipulating dispersal limitation, interspecific competition and demography. Tree species in the dynamic forest model migrated only slowly upslope in contrast to the SDMs. Most of the difference in migration velocity can directly be attributed to the tree's demography (long life cycle), followed by effects of competition and only a marginal contribution of dispersal limitation. Additionally, lower elevation species ("non-treeline") shifted slower upslope than high elevation species ("treeline") indicating a strong effect of inter-specific competition at their leading edge. Forests have a high inertia to climate change because of their longevity and ability to acclimatise to high climatic fluctuations. Lower-elevation tree species (deciduous) only slowly establish in stands at higher elevations where coniferous species dominate and likely profit from facilitation by disturbance events. Therefore, forest ecosystems seem to persist, even if the climate becomes unfavourable until they approach a tipping point at which an extreme event (e.g., drought, storm or insect attack) leads to a large dieback and resource change enabling new suitable species to spread and establish.

Postglacial range formation of temperate forest understorey herbs – insights from a spatiotemporally explicit modelling approach

Johannes Wessely

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Our knowledge of Pleistocene refugia and postglacial recolonisation routes of forest understorey plants is still very limited. The geographical ranges of these species are often rather narrow and show highly idiosyncratic, often fragmented patterns indicating either narrow and species-specific ecological tolerances or strong dispersal limitations. However, the relative roles of these factors are inherently difficult to disentangle. Here, we used spatiotemporally explicit modelling to reconstruct the postglacial range dynamics over the last 17,000 years of five forest understorey herbs of European beech forests. We varied niche requirements, demographic rates and dispersal abilities across plausible ranges and simulated the spread of species from potential Pleistocene refugia identified by phylogeographic analyses. Then we identified the parameter setting allowing for the most accurate reconstruction of its current geographical range. We found a largely homogenous pattern of optimal parameter settings among species. Broad ecological niches must be combined with very low but non-zero rates of long-distance dispersal via chance events and low rates of seed dispersal over moderate distances by standard dispersals vectors. However, long-distance dispersal events, although rare, led to a high variation among replicated simulation runs. Our simulations suggest that small and fragmented ranges of many forest understorey species are best explained by a combination of broad ecological niches and rare medium- and long-distance dispersal events. Stochasticity is thus an important determinant of current species ranges, explaining the idiosyncratic distribution patterns of the study species despite strong similarities in refugia, ecological tolerances and dispersal abilities. We therefore argue, that rare long-distance dispersal events are an important ingredient for modelling range shifts, especially of species with currently rather narrow and fragmented geographical distributions, also influencing future prediction of species ranges under global change.

Estimating species ability to follow climate change – dispersal matters and current environmental envelopes might not be sufficient

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We are facing rapid climate change in the near future, for which we need to generate knowledge on how current vegetation will be responding.

One way to gain insight into how vegetation will be responding to the current climate change is it investigate how it responded to previous climate change.

The last episode of profound climate change has happened over the last 15000 years following the end of the last glacial period.

In this study we are simulating the range shift of the main European tree species with the dynamic vegetation model LPJ-GM, using either explicit seed dispersal or assuming seeds to be present everywhere (free dispersal). The environmental envelopes of the species are fitted to their current range. Analyzing the performance of the simulation compared to pollen data for southern and central Europe, we find that the dispersal limited simulations differ strongly from the free dispersal simulations in periods of rapid climate change and matched pollen data better. However, using environmental envelopes based on current distribution of tree species results in a number of extinction within the simulation over the last 15000 years, hence we are hypothesizing that the current distribution, which represents the realized niche rather than the potential niche needs to be enlarged to be able to evaluate the ability of tree species in following climate change.

Modelling Northern Hemisphere tree migration in the last 50,000 years

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The global vegetation cover underwent strong changes during the past glacial cycle. How much these changes were driven by climatic fluctuations, migration to new climatically suitable areas and interaction with other species is often not clear. We used the newly-implemented model LPJ-GM 2.0 to simulate the change in vegetation cover across the Northern Hemisphere (NH) for the last 50,000 years. The model allows plant species to migrate simultaneously while interacting with each other species by coupling to the dynamic global vegetation model LPJ-GUESS a migration module with two alternative algorithms for the simulation of seed dispersal. Given the large temporal and spatial extents, we applied the simplified migration algorithm FIXSPEED, which avoids the high computational load required to explicitly simulate the dynamics of seed dispersal, and allows the use of coarser spatial (0.5 degrees) and taxonomic (from species to plant functional types) resolutions. We compared the change of vegetation cover between two dispersal scenarios (free dispersal and dispersal limitation) across simulation time and tested their reliability in providing realistic paleo-vegetation reconstructions against Holocene records of European land cover. Our results show that the NH forest cover simulated under the dispersal limitation scenario is consistently lower and its spread slower if compared to a scenario with unrestrained migration, especially in Europe (with estimated migration lags of up to 3,500 years). Comparisons with pollen data indicate that the dispersal limitation scenario manages to reproduce more accurately the Holocene spread of European forests at points of rapid warming. Overall, our study suggests that it is necessary to include migration processes when simulating vegetation range expansion under rapid climate change.

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3. Movement modelling: underlying principles and processes

A piece-wise approach to developing a butterfly movement model

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Modelling insect movement is challenging, many of the common statistical tools used to analyse changing movement patterns are unsuitable as the vast majority of insects cannot carry tracking instrumentation. Nevertheless, understanding how insects move and utilise their environment is important for understanding the impacts of changing habitats and climates. Here, we outline a project where we developed an agent-based movement model for grassland butterflies by breaking down the various components of the movement process. We will discuss the data collection process, and how butterfly movement rates were influenced by factors such as body size, weather conditions, behavioural motivation, and habitat barriers. I will then describe the culmination of the project, a butterfly model that predicted the effect of changing habitat structure of reproductive fitness in an agricultural landscape. Our findings suggest that exploring the relationship between traits and different aspects of the movement process could provide a promising approach for predicting movement for data-poor insect species.

Linking movement and life history traits though dynamic energy budget modelling

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All animals need to take up food from their environment to fuel bodily functions. Movement is an integral part of foraging behavior, thus, influences individual fitness and life history traits. Individual movement behaviors change in response to environmental characteristics, such as temperature, vegetation, or other factors that may limit movement rates and will, thus, have consequences for individual growth and reproduction. In this presentation, we will illustrate some general principles behind body-size scaling of foraging related movement. Moreover, we will provide an example from earthworms and dynamic energy budget (DEB) modeling how environmental factors influence movement and subsequently life history traits.

In earthworms, soil moisture, temperature, and the organic matter content are considered limiting factors of movement: In laboratory experiments, earthworms showed decreased burrowing activity with decreasing moisture levels and even avoidance behavior of these unfavorable moisture conditions. Moreover, the movement activity of earthworms is affected by temperature, which was approximated by the number of casts produced in laboratory experiments. Finally, the organic matter content plays a significant role for the burrowing and movement of earthworms. Integrating changes in earthworm movement and life histories in response to soils characteristics through DEB modelling revealed that the food ingestion via movement is an integral part of the earthworms' energy budgets.

Due the generality of DEB models, the earthworm example can serve as a blueprint on how to integrate the principles of foraging movement and life histories in one process-based model.

Movement modelling for small and medium sized mammals of the agricultural landscape for pesticide risk refinement

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To refine the risk of plant protection products to small and medium sized mammals EFSA (2023) considers the use of spatially explicit population models as a higher tier option. Since spatial behavior directly influences exposure to these products, a realistic simulation of movement is crucial for a realistic simulation of dietary doses, effects and finally the risk.

Since spatial behavior varies considerably between the different food guilts and corresponding focal species, the simulation models need to reflect these differences. This means, movement models need to include all relevant parameters and processes to allow the simulation of realistic spatial behavior of the respective species but need also take the availability of necessary data and computation time into account. Therefore, different kinds of movement models may be reasonable for different species. In the proposed oral presentation, movement models will be outlined for focal species of the small and medium sized mammal used in the risk assessment for plant protection products. These are, common vole (Microtus arvalis), wood mouse (Apodemus sylvaticus), common shrew (Sorex araneus), brown hare (Lepus europaeus) and European rabbit (Oryctolagus cuniculus).

The proposed movement models used for these species can be divided into two different basic types. For the small mammal species (common vole, wood mouse, and common shrew), movement is only implicitly simulated. In these cases the position and size of the home range of each individual is simulated spatially explicit as a model entity. The individual's location in this home range, however, is unknown and it is only assumed to be somewhere in the home range. Contrarily, movement is simulated explicitly for the medium sized mammal species (brown hare and European rabbit). This means, for each day and individual a spatially explicit daily walk is simulated. The corresponding home range emerges, as in field studies, from all locations of several days. These two basic models were adapted for the corresponding species to include all relevant processes, e.g. territoriality, home range abandoning, need for food, shelter and conspecifics, nesting or burrowing, etc. During the presentation, both basic models will be explained together with species-specific adaptions, advantages and challenges. This will also include the discussion of necessary data and methods for model parameterization and calibration, possibilities for model validation and implication for the use in the risk assessment of plant protection products.

How virtual environments help to parameterize learning and decision making in a model for wild chimpanzee movement

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When using movement tracks for individual animals without other attributes like memory capacity or physiological state, it is impossible to uniquely identify the correct driving mechanisms leading to the observed patterns. There are simply too many candidate variables (some of which are unobservable and with unknown spatio-temporal variability) and potential processes which may influence that movement. This is also the case for movement tracks of chimpanzees that have been (and are being) collected in the wild. Here we present results from a study where activities and decisions by captive chimpanzees in an interactive virtual environment help to constrain the options to model wild chimpanzee movement and behaviour. The virtual environment is a type of interactive game that is available to the chimpanzees via touch screens. It presents a forest with fruit-bearing trees that the chimpanzees try to find (when successfully finding a fruit tree, they get a small reward). Some fruit trees occur at predictable locations and others at random. Besides the avatar of the chimpanzee who is playing (the focal individual), there are avatars of other chimpanzees who are individually recognizable and possess different levels of knowledge about fruit tree locations. These avatars can be followed or ignored by the focal individual in his search for fruit. We record if and how fast the focal individual learns where predictable locations for fruit bearing trees can be found, as well as if (and how fast) the focal individual recognizes when it is advantageous to follow other individuals in their search for fruit trees.

We implement the learning processes and parameters obtained in this way in a model to interpret movement tracks of chimpanzees in the wild. When adopting these learning processes, the observed movement patterns can be reproduced with considerably lower requirements for spatio-temporal memory as well as sensory capacities than when excluded. In addition, we expect that this learning process will to some degrees explain the fission-fusion dynamics that is so characteristic for Chimpanzee foraging movements, however this aspect is currently still being investigated.

Anticipating common buzzard population patterns in the afforesting UK landscape

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The coexistence between humans and other animals is typically impacted by landscape change, which affects animal distribution and abundance. Afforestation on grasslands has been increasing across Great Britain in the last 30 years, driven by socio-economic reasons and climate change mitigation. Beyond expected benefits, a key question is what are the consequences of this scale of landscape change for wider biodiversity. Here we explore the impact of such change on the expanding population of common buzzards Buteo buteo, a raptor that has been battling human-induced setbacks for at least the last five centuries. We used Resource-Area-Dependence Analysis on 10-day radio-tracking sessions and the 1990's Land Cover Map of GB to estimate the individual buzzard's resource needs. Secondly, we created an Agent-Based Model in which virtual buzzards with resource needs and territorial behaviours similar to those of wild buzzards colonised the landscape map, as well as three maps depicting an increasingly afforested lowland UK. The model predicted that buzzards in our study area in lowland UK had fully recovered (to 2.2 ind/km2) by 1995. It also anticipated that the conversion of 30%, 60% and 90% of economically-viable meadow (patches > 20 ha) into woodland would reduce buzzard abundance non-linearly by 15%, 38% and 74%, respectively. This counterintuitive result, in which buzzard abundance collapses despite the increase in one of its key resources (trees for roosting and nesting), demonstrates that when dealing with complex systems, such as landscapes or ecosystems, even well-intentioned actions such as afforestation may have undesired consequences. This work also illustrates how animal movement associated to resource-use structures home-ranges and territories within the geographical space of a real landscape, and how that scales to the population. This same empirical ABM approach could allow for cost-effective anticipation of other animals' individual and population patterns in changing landscapes, which may hopefully contribute with the harmonisation of economy, landscape change and biodiversity.

To go or not to go? Modeling the decision-making process behind ungulate partial migration

Ricardo Martinez-Garcia

Center for Advanced Systems Understanding (CASUS) - Helmholtz Zentrum Dresden-Rossendof (HZDR)

Despite the importance of ungulate migrations, we lack a complete understanding of why some ungulates species migrate and some do not. Moreover, at the population level, some migrate and others remain behind as residents, a phenomenon known as partial migration. Even though progress has been made towards understanding long-term fitness benefits of partial migration, the underlying decision-making process that makes some individuals migrate and others remain within one single range remain unknown. In this presentation I will combine empirical data from three different migrant ungulate species and mathematical modeling to address this question. I will first show that, across these three ungulate species, the number of residents is unrelated to total population size, a pattern predicted by no previous modeling framework. Next, I will introduce a new model of ungulate partial migration wherein individuals probabilistically decide to start migrating based on the intensity of environmental and social cues. Within this modeling framework, residents arise for most parameter combinations and the number of residents is largely invariant with total population size. Therefore, this new model explains the ubiquity of residents in migratory ungulate populations and presents novel patterns to be tested with further data collection.

Trait-based patterns in step-selection responses across species

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Environmental change affects the movement patterns of animals, which can result in further consequences for populations, communities, and ecosystems. However, not all species react to their environment in the same way. Previous studies have found relationships between species traits, such as body size and feeding guild, and movement metrics such as home range sizes and mean displacement. However, little is known about these cross-species patterns at finer temporal and spatial scales. Such patterns would allow for the extrapolation of findings in species for which tracking data is readily available onto lesser studied and threatened species. Further, they can inform the development of movement processes within process-based ecosystem models, which often relate ecological processes to species traits. Trait-based approaches may offer an opportunity for more detailed movement mechanisms representing the respective species' ecology. In this project, we explore cross-species patterns by fitting integrated step-selection functions to the tracks of >500 individuals in 39 mammal species. We include environmental and anthropogenic drivers of movement (e.g., NDVI, land cover and human population density) and estimate step-selection responses as well as resource-independent step length distributions. We find some allometric patterns in resource-independent step length distributions. For example , larger animals tend to have longer step lengths, and distribution shapes differ between feeding guilds. However, we could not identify consistent patterns related to species traits in responses to environmental and anthropogenic covariates. These findings suggest that movement at smaller scales is potentially driven by higher degrees of environmental stochasticity, while the allometric relationships observed in previous literature are an emergent property only observed over larger scales.

Continuous capture process based on advection-diffusion-reaction models within Joint species movement modelling

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The Joint species movement modelling framework (JSMM) enables inferring species and community level movement parameters from multi-species data. Within this approach, movement parameters are modelled as function of species traits, phylogenetic relationships, and spatio-temporal covariates. I introduce a continuous capture process (CCP) that extends the JSMM framework for diffusion-advection-reaction models parametrized with low resolution capture-mark-recapture data. The JSMM originally assumed a capture process mimicking a researcher visiting a particular site and attempting to capture marked individuals during an instantaneous time. The novel CCP method is aimed for ecologists that conduct experiments in which traps while open capture individuals on a continuous fashion over a given time period. As application example, I analyzed data corresponding to six species of dung beetles over three study sites to examine how the species traversed riparian buffers connected to a continuous forest within an oil palm plantation in Sabah, Malaysian Borneo. The CCP is one of the new features of the JSMM framework implementation for diffusion-advection models. The user-friendly software aims to be a useful tool for ecologists interested in studying causes and consequences of variation in movement behavior.

A method to evaluate the barrier effect of urban elements: a case study with blackbirds in Munich

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Connectivity maps can aid city planners by identifying areas important for animal movement and thereby preserve urban biodiversity. Faunistic urban connectivity analyses primarily focus on landscape-scale dispersal processes between populations. However, urban dispersal events are rare due to the limited geographic extent of cities. Animal movements instead mostly occur within the home range. The barrier effect of artificial landscape features within the home range can have a significant impact on resource accessibility, and thereby on home range formation and species distribution.

I will present a methodology for creating urban connectivity maps based on the home range scale using the blackbird in Munich as a case study. To (i) identify areas with sufficient resources for blackbird home ranges and (ii) evaluate the resistance of different urban elements, this study uses high-resolution land cover data and various sets of presence-absence data. The resistance of streets and buildings is evaluated using a connectivity approach based on graph and circuit theory. I will show the results of a model selection procedure for different resistance values of urban elements, isolation distances of resource patches, and connectivity metrics.

From the case study, several conclusions can be drawn on the barrier effect of urban elements. Only a few combinations of isolation distances and resistance maps attain a high explanatory power for the movement of blackbirds. They all indicate that buildings and streets are more resistant to movement than vegetation and that higher buildings (over 13 m) have a stronger barrier effect than lower buildings or streets. The models with the highest explanatory power have a relatively high maximum patch isolation distance, suggesting that blackbirds include remote resource patches in their home range. The best models use a least-cost path analysis whereas the explanatory power of the random walk-based models is relatively low. This could imply that blackbirds know their home range well and can optimize their paths for a low energy expenditure within their home range.

The presented methodology can be applied to other cities and birds to depict urban connectivity based on the most frequent animal movements and to better understand the distribution of animals in the city. The resulting connectivity analyses could aid city planners in transitioning to a city that supports free animal movement, promoting urban biodiversity.

A multi-sensor GEE framework to match high-quality remote sensing data with wildlife movement when spatiotemporally scaling behaviour-driven resource selection

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Environmental sensing via Earth Observation Satellites (EOS) has recently started a "Klondike Gold Rush" era for movement ecologists. The main advantage of such a synergy between remotely sensed data and wildlife movement resides in extrapolating (over large extents) resource suitability, which may be referred to as the environmental resources within a habitat that can be potentially selected during wildlife behavioural states (e.g., foraging), and/or phenological periods (e.g., breeding). This information is key to understanding dynamic habitat preferences, even though sensor technology and sensed information are reasonably inadequate for all study cases and functional ecological scales. On this issue, there is a lack of frameworks and tools able to address multiple spatial and temporal scales of data extraction over long time series, while targeting many EOS sensors and associated satellite generations.

We present an original EOS-based framework operational within Google Earth Engine (GEE) to allow for straightforward remote sensing data extraction at multiple spatiotemporal scales and for different sensors, namely Sentinel-2, Landsat and MODIS. This consists of three steps: (1) imageries filtering and calibration; (2) calculation of comparable metrics across sensors; (3) scaling of spatiotemporal remote sensing data from telemetry data (or occurrence). We illustrate the framework reliance through a highly complex case concerning the seasonal distribution of a threatened elusive bird (little bustard; Tetrax tetrax), focusing on telemetry data (>2000 telemetry-based daily observations, between 2017 and 2021) during a cloudy period in winter. A Random Forests variant was used to discriminate significant (top) habitat metrics for each sensor separately, and concomitantly (data fusion).

During cloudy periods, more data was retained from sensors with high site revisitation (MODIS), though missing data from other sensors can be efficiently solved through gap-filling steps described and implemented within the framework. Similar top-performant metrics were selected across sensors, highlighting vegetation and spectral bands, where fine scales were more represented by finer sensors, and coarser sensors by higher ones, reflecting different habitat requirements. This condition was corroborated when considering sensors concomitantly, with Sentinel-2 and MODIS-derived metrics resulting as top performant in explaining species occurrence. Being user-friendly designed and implemented in a widely used cloud platform (GEE), we believe our approach provides a major contribution to effectively extracting high-quality data that can be quickly computed for metrics, converted at any scale, and extracted from ground information such as telemetry. Additionally, the framework was prepared to facilitate comparative research initiatives and data-fusion approaches in ecological research.

5. Reusable building blocks (RBB) for agent-, and individual-based models

Reusable building blocks for agent-based modelling: benefits, challenges, and a strategy for their release

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The development and increasing use of standards for documenting and testing agent-based models (ABMs, e.g. ODD, ODD+D, TRACE protocols) has contributed significantly to increasing transparency and reproducibility, but most ABMs are still developed from scratch. This is not only time-inefficient, but also leads to ad hoc interpretations of some commonly agreed principles of model design, such as the implementation of a particular behavioural theory in a computational code. We argue that reusable building blocks (RBBs) can alleviate this problem. An RBB is a submodel that represents a particular mechanism or process that is relevant across many agent-based models in an application domain, such as plant competition in vegetation models, or reinforcement learning in a behavioural model. RBBs must be distinguished from modules, which represent entire subsystems and include more than one mechanism and process. While linking modules faces the same challenges as integrating different models in general, RBBs are "atomic" enough to be more easily reused in different contexts and thus models. RBBs can serve as a basis for a systematic community effort to develop theories of complex social-ecological systems. We first give a brief overview of how and why building blocks are used in other areas of software development, and the advantages of doing so. We then present examples of existing building blocks from the social sciences and ecology. We discuss the direct benefits to the community as a whole and to individual modellers, and how these benefits can be supported by top-down processes such as the provision of web repositories. Finally, and most importantly, we propose and initiate a strategy for community-based development for the release and use of RBBs.

Developing a Benchmarking Framework for a Ready-to-Use RBB Library for Forest Ecology: pyMANGA

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Computer models are commonly used in forest ecology to simulate how trees adapt to changes, such as those caused by climate change, and how this is ultimately reflected in the response patterns of forest stands. However, the development of models, especially for specific research questions, is often ad-hoc, which can make them error-prone and inefficient. To address this issue, we have developed pyMANGA (PYthon Models for AgeNt-based resource Gathering), a platform that collects model descriptions for the growth of tree-like plants in response to environmental conditions, or competition and facilitation among neighboring trees. pyMANGA is not only a collection of single descriptions, or reusable building blocks (RBB), but a ready-to-use model library, where RBB can be switched on and off, so that a model can be configured in order to meet different research demands. The development of the platform is based on four design objectives: (i) modularity, (ii) transparency (iii) automation and (iv) foster contribution. Modularity is achieved using object-oriented programming (OOP) paradigms, whereas the other objectives are supported by the use of several GitHub services. However, the flexibility needed for the platform to grow is not fully provided from the beginning. One reason, of course, is that we are not skilled programmers. Another is that the reusability of individual functions or BBs was often not recognized during initial implementation. As a result, the continuous expansion of pyMANGA often requires adaptation of existing BBs. To ensure the functionality of the individual RBBs and the whole platform, we have developed a benchmarking framework for pyMANGA. For each RBB, a benchmark following defined design rules needs to be provided. From a technical perspective, this allows to test the functionally of new RBB, i.e., the functioning of interfaces, as well as ensures code functionality after platform updates, i.e., tests whether model output is similar before and after an update. Moreover, those benchmarks are a first test for model consistency, i.e., does the model do what it should do, and they allow users to compare RBBs with other implementations, e.g., in other programming languages. While sharing models with (complex) case studies is common practice, we advocate for presenting RBBs along with simple and easy-to-replicate benchmarks. Here, we present our benchmarking framework and its integration into an automated testing workflow.

Online Model Library of larval fish: a tool to better understand fish recruitment in changing marine ecosystems

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Early-life history of marine fishes is one of the main drivers of the recruitment variability and an important bottleneck in the adaptation of fish populations to changing climate. Individual-based models (IBMs) that simulate the behavior of individual fish and its interactions with the biotic and abiotic environment are widely used in fisheries science to study starvation, predation and dispersal mortality of fish early-life stages (ELSs). In particular, stand-alone or coupled physiological IBMs are a powerful tool to better understand starvation mortality of fish ELSs, the role of suboptimal feeding and larval behavioral or metabolic adaptation to unfavorable feeding conditions. Despite a general trend toward open reproducible science, such models often remain dispersed across various publications and are not easily accessible to the scientific community. To address this issue, we developed an Online Model Library of Larval Fish, which brings together physiological IBMs previously published for various marine fish species. Our library aims to provide a comprehensive access to these models, including their summaries, codes, and quality control measures to ensure their accuracy. Furthermore, our library not only features models but also includes various laboratory and field data available for model calibration, validation and further development. Based on previously published models, we aimed to perform a comprehensive review of existing approaches, identify differences and similarities in methods used to build up the main model components, such as prey field, larval foraging, energy budget and growth allocation. Overall, our Online Model Library of Larval Fish aims to provide a one-stop resource for researchers interested in larval IBMs as a tool to investigate drivers of fish recruitment in marine ecosystems under climate change and various anthropogenic pressures. By consolidating these models and data in one place, we hope to facilitate future research in this critical field and contribute to the sustainable management of fish populations.

Review on process-based predictive models for studying impact of disturbance on marine mammals

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Process-based models (PBMs) are increasingly used to understand and predict the impacts of human disturbance on wildlife populations, including marine mammals. PBMs explicitly model the underlying biological and ecological processes and interactions between individuals and the environment that drive changes in individual and population-level metrics. However, PBMs are often criticized for being developed using ad hoc approaches tailored to specific systems, which makes wider reimplementation and testing challenging. In marine mammal PBMs, the inclusion and implementation of processes relevant to disturbance can vary widely between models. To better understand the current state of process-based model use in marine mammal disturbance modeling, we conducted a review of peer-reviewed and grey literature publications. Based on 245 articles, we synthesized commonalities and differences in the representation of biological mechanisms and disturbances in these models. We identified seven fundamental biological processes that have been commonly implemented in marine mammal PBMs: energetics, movements, behavior and adaptation, evolution and genetics, health and physiology, demographics, and species interactions. Additionally, we identified seven key types of disturbances that these models address: vessel traffic and noise, chemical pollution and toxins, direct takes and collisions, fisheries competition, climate change and extreme events, non-specific behavioral modification or food limitation, and infectious disease. We then discuss alternative processes and approaches which have been employed in marine mammal PBMs, identify which processes are necessary for representing specific disturbance types, pinpoint key data gaps, outline best practices, and discuss pros and cons of using process-based models in studying the effects of anthropogenic activities on marine mammals.

Entity Component System (ECS) – a design for flexible and performant individual-based models (IBMs)

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Development of individual-based models (IBMs) involves challenges from both the modelling as well as the software development perspective. In this contribution, we focus on the latter and propose the use of a concept developed in video game design: the Entity Component System (ECS) design.

ECS is particularly suited for IBMs and offers a wide range of benefits for modellers. IBM concepts like entities, state variables and sub-models are directly represented by the ECS design. This frees modellers from a lot of technical design decisions, and helps guiding them towards a design that makes it easy to compose complex models out of loosely coupled sub-models. ECS offers great flexibility and modularity, which are required for the typically iterative modelling process. Further, it allows for highly performant models due to a memory layout tailored for contemporary computer architecture.

We explain the concept of ECS and demonstrate it using simple example IBMs from the fields of ecology and epidemiology. We detail why ECS is particularly beneficial for IBM developers, and provide an entry point to develop models with ECS, and to find suitable libraries. Further, we elaborate on differences and commonalities between the requirements of modellers and game developers, and derive implications for IBM development using ECS.

Finally, we use different implementations of the example models for a performance comparison. We demonstrate that flexibility and ease of development are not bought at the expense of increased runtime and that, on the contrary, ECS-based models can outperform from scratch model implementations.

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6. Next-generation advances in individual-based modelling

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

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A metacommunity is a collection of communities, sets of potentially interacting individuals, linked by dispersal. Conceptual and mathematical models behind metacommunity theory typically distinguish processes that operate within local communities (e.g.: biotic interactions), from those that operate among local communities (e.g.: dispersal). This dichotomy between local and regional processes has typically restricted theory to communities bounded within single habitat patches. However, local interactions often occur in spatially continuous communities or in local communities that inhabit several discrete patches.

In this study we aim to explore the matches and mismatches between metacommunity theory and empirical studies, focusing on the delimitation of local communities. We first motivate the study with a systematic review to explore how the spatial boundaries of the local communities are defined in empirical studies and to what extent those definitions are compatible with the underlying theoretical assumptions. Second, we use spatially explicit IBMs to exemplify different ways in which communities can be spatially arranged and sample observational data as an empirical ecologist would do in the field. With the simulations, we aim to explore whether the uninformed delineation of local communities influences the metacommunity assembly processes that can be inferred from that system.

The preliminary results suggest a fundamental mismatch between theory and empirical studies, as empirical studies often do not explicitly define the scale of the local communities, or the definitions are inconsistent with the theoretical assumptions. Further, IBMs promise to be a useful tool for expanding metacommunity theory to encompass other types of landscape and community configurations. This is because IBMs are able to integrate local and regional processes in a meaningful and realistic way, with larger-scale processes arising naturally from the specified local processes.

Individual-Based Models to inform elasmobranch conservation in a Mediterranean sub-basin

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Elasmobranchs have been globally facing a strong decline in abundance over the past century. Compared to other fish species, their life history traits (e.g., large size, slow growth, late sexual maturity, low fecundity) and their typical behaviours (e.g., long migrations, aggregations) make them vulnerable to fishing pressure, especially before they have reached the sexual maturity. Management actions are strongly needed to reduce human pressure and support elasmobranch conservation. However, testing their effectiveness in pilot projects can be complicated, especially when comparing different solutions, and effort and time consuming. Ecological models have therefore a crucial role in assessing solutions to improve elasmobranch conservation status and the potential success of different management scenarios. In this study, we propose the use of a single species model approach, Individual-Based Modelling (IBM), as a tool for comparing the effects of different management measures on elasmobranch fish and related fishing activities. In the Northern Adriatic Sea, a sub-basin of the Mediterranean Sea, we built an IBM for smooth-hound sharks (Mustelus spp.), which are commercially valuable species often fished when they are still sexually immature. The model integrates bioenergetic theory, density-dependent functions and intra-specific variability to simulate the main processes of the life cycle of each elasmobranch individual, so compared to traditional population dynamics models this approach can give a better representation of reality when informed by proper data collection. After uncertain parameters have been estimated, the model was used to investigate management scenarios that both favour elasmobranch population growth and sustain the local community which strongly relies on fisheries as a source of income (especially artisanal ones). In particular, we investigated the effect of the enforcement of a minimum retainable size, below which sharks should be released by fishers, on both population size and landings trends. Although this kind of models are complex and require many species-specific information on life history traits, so that model uncertainty must be explored rigorously, they are useful screening tools to systematically identify and select, within a pool of options, promising management actions which aim toward elasmobranch conservation and sustainability of fisheries.

Fish condition as an indicator of stock status: a DEB-IBM approach to support fisheries management

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Standard stock assessment combines field-data and model-based information, and provides backbone of sustainable fisheries decision-making. However, current time-, labour- and money-intensive assessment practice limits its implementation to less than quarter of world fisheries, and provides only limited temporal resolution. Rapid stock assessment based on easy accessible and commonly collected (bio)metrics is therefore recognized as a promising alternative for majority of unassessed stocks, as well as valuable checkpoint during and in-between existing assessments.

The focus of standard stock assessment are populations, often overlooking the individual condition and performance as a main driver dictating population dynamics. Insufficient understanding of the interdependencies between individual-level processes and population-level responses additionally hinders the adoption of individual performance indicators, such as condition index, into current practices. Mechanistic modelling of individual ontogeny, integrated into population models, is acknowledged to be a powerful tool to elucidate the correlation between individual and its population, and can therefore be used to create supporting information for implementation of individual-level information.

To this end, we build a process-based composite model of extensively exploited European pilchard to link the individual condition to the state of its population. We use the Dynamic Energy Budget (DEB) theory to model individual performance as a function of food and constant temperature, and integrate it into the individual-based modelling (IBM) framework to simultaneously track both individual- and population-level statistics. Using the model, we explore the effects of fishing mortality on the statistics in two constant and food-limited environmental carrying capacity scenarios.

Results show that, regardless of the species' environmental carrying capacity, in a food-limited populations, individual condition index will increase with fishing mortality and the reduction of stock size. This directly opposes the traditional definition of a poor stock, implying that very good fish condition could actually indicate reduced stock size and imminent threat of overfishing. We conclude that information obtained from condition index can be used for a rapid estimate of stock size relative to its food-limited carrying capacity, and it can also support fine-tuning of existing fisheries decision-making. We further promote use of DEB-IBM composite modelling as an innovative approach to explore additional feedback mechanisms between individual- and population-level traits, and strengthen confidence in existing, as well as identifying novel, individual-level stock indicators.

Dynamic energy budget individual-based models revisited: integrating individual-scale behaviours

Wissam Barhdadi; Aisling Daly; Jan Baetens; Bernard De Baets

Individual-based models (IBMs) provide valuable insights into ecological systems by capturing complex interactions between individuals. While current IBMs have proven useful, integrating bioenergetic models, such as Dynamic Energy Budget (DEB) models, presents an opportunity for further advancement. Current DEB-IBMs, however, often still rely on patch-averaged functions to describe behaviour, overlooking the underlying micro-scale mechanisms. This limitation can lead to an incomplete understanding of how individual physiology, behaviour, and environmental factors interact to shape population dynamics.

To address this limitation, we present an IBM that incorporates DEB theory, connecting individual physiology and micro-scale processes in spatially heterogeneous environments. Our model emphasizes individual-scale foraging mechanisms, facilitating a more comprehensive understanding of the influence of individual biology, behaviour, and environmental factors on population dynamics.

By simulating a consumer-resource system, we demonstrate our model's ability to account for the influences of individual behaviour, temperature, resource carrying capacity, and individual variability on population dynamics. We further illustrate the model in a case study by comparing simulated population dynamics with both the classical DEB-IBM and experimental data for a laboratory Daphnia magna population. Both the simulation and case study showed how including micro-scale processes mediates the metabolism's impact on population dynamics.

In conclusion, our IBM offers a valuable addition to the ecological modelling toolbox by incorporating metabolic theory and individual-scale processes within spatially heterogeneous environments. By scaling spatial individual behaviours from patch-averaged functions to their underlying mechanisms, life history may emerge from both behaviour, physiology and environment, overcoming the limitations of imposed functional relationships in IBMs.

New approaches in model calibration for studying epigenetic mechanisms of homeostasis in response to environmental stressors

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Identifying how organisms respond to environmental stressors is of central importance as human impacts continue to shift the environmental conditions for countless species. Some mammals are able to mitigate these environmental stressors at the cellular level, but the mechanisms by which cells are able to do this and how these strategies vary among species is not well understood. Our study system consists of genomic data from the cultured cells of 16 mammalian species exposed to different levels of temperature, glucose, and oxygen. These species, including humans, dolphins, bats, and camels, among others, vary in the stringency of organism-level buffering, offering a comparative approach for identifying the mechanistic rules whereby cells achieve robustness in changeable conditions. Here, we present ongoing efforts to effectively calibrate an agent-based model of an animal cell system from detailed genomic sequencing data. We aim to use our calibrated model to identify the epigenetic mechanisms involved in cellular responses to environmental change, which is not possible to directly accomplish through our empirical data from just a few time points that may not capture essential intermediate responses. In the model, agents are regulatory elements and genes that are able to impact the states of each other depending on their own state. We used various model calibration techniques, including genetic algorithms and statistical regression analyses, to numerically identify the impact of genes and regulatory elements on each other. We discuss the relative success of each calibration method as well as the challenges of calibrating models of this kind. Our model calibration process is generalized for any species, any cell type, and any environmental stressor, offering many applications of the model beyond our study. This study will increase our understanding of organism resilience to environmental stressors at the cellular level. By integrating molecular and genetic mechanisms in response to stress, this model can better address how organisms are impacted by and respond to environmental changes.

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7. New methods and applications in trait-based modelling in ecology

How traits control species’ biomass in monoculture and mixture and drive biodiversity-ecosystem functioning relationships

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Humans are driving unprecedented environmental change, causing the loss of species from local ecosystems. Previous studies have shown that the effects of species loss on ecosystem functioning are strongly related to the relative biomass of species in monoculture (i.e. "functioning") vs. in mixed communities (i.e. "dominance") - also known as the 'function-dominance correlation'. Here, we explore which traits control species’ biomass in monoculture and mixture and thereby drive the function-dominance correlation in different systems (grasslands, forests, drylands). To do this, we perform a modeling experiment with six trait-based models of plant community dynamics and classify model traits as either ‘size related’ or ‘resource related’.

We found that size related traits, but not resource related traits, predicted species’ monoculture biomass (function) in five out of the six models. However, in mixture, resource related traits became more important and explained substantial variation in two of the six models. The function dominance correlation was predicted by how consistent the importance of size related traits was from monoculture to mixture. Our model-based analysis shows how generalizable categories of functional traits (size versus resource related) allow predicting the strength and direction of biodiversity-ecosystem functioning relationships across systems, and thereby the potential effects of losing species on ecosystem functioning.

Trait patterns simulated by aDGVM2 can be used for biome classification

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Biomes classification schemes are widely used to map biogeographic patterns of vegetation formations on large spatial scales. Future climate change will influence vegetation dynamics, and vegetation models can be used to assess the susceptibility of biomes to experience biome transitions. However, biome classification is not unique, and various classification schemes and biome maps exist. We, therefore, assessed how the choice of biome classification schemes influences modeled rates of future biome changes. We used the trait-based dynamic vegetation model aDGVM2 to simulate biogeographic patters of multiple traits for Africa, tropical Asia and Australia. Then, we classified vegetation into biomes using (1) a classification scheme based on the cover of different functional types, (2) a cluster analysis based on the cover of different functional types, and (3) a cluster analysis based on trait patterns simulated by the aDGVM2. We compared the resulting biome maps to multiple observation-based biome and land cover maps to asses the performance of different classification approaches. Then, differences in projected biome changes under the RCP8.5 scenario were quantified for the different classification schemes. As expected, biome patterns were strongly related to the scheme used for biome classification. The highest data-model agreement was derived for a cluster analysis using simulated trait patterns. The area projected to undergo biome transitions under climate change varied between 16.5% and 32.1% for different classification schemes. Despite this variability, different schemes consistently showed that grassland and savanna areas are most susceptible to climate change, whereas tropical forests and deserts are stable. Our results demonstrate that traits simulated by aDGVM2 are appropriate for biome classification. We conclude that studies projecting biome transitions under climate change should consider applying different biome classification schemes to avoid biases in such projections caused by biome classification schemes.

Using a trait-based model to identify land use schemes that increase plant diversity while maintaining high yields in grasslands in Germany

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Managed grasslands are often optimised for high biomass and forage production. However, intensively managed grasslands often have a low plant diversity, which reduces their cultural value, habitat provision for other taxa, and potentially the temporal stability of the yield of grasslands. In this study, we aim at identifying different land use schemes (frequency of mowing, grazing intensity, and fertilisation level) to increase plant diversity in grasslands while maintaining a high yield. For this purpose, we develop and analyse a difference equation model to describe the biomass dynamics of virtual plant species on a regional scale, with each species characterised by eco-physiological traits. The model assumes that each field in the landscape is homogeneous and connected to other fields by dispersal. We used trait, biomass, and species data that was collected on a local scale and biomass and species diversity data that was derived by satellite images for the field scale as an input and to calibrate the model for three regions in Germany. In each of these regions, grasslands with different land use intensities are included. This model fills a gap between local-scale individual-based models and large-scale dynamic global vegetation models. In the future, the model is intended to be used as an evaluation tool of measures for a biodiversity-oriented agriculture in grasslands.

Simulating trait shifts of German forests under droughts and climate change - First results of ForestSpectrum

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We here present the first results of the ForestSpectrum project (waldspektrum.de) which aims at quantifying the trait ranges and management options of German forests best suited under future climate conditions (including increased frequencies and intensities of droughts). We present shifts of specific leaf area (SLA), wood density (WD) and rooting depth (D95) simulated with the LPJmL-FIT model and what happens when we test respective most productive trait combinations found with LPJmL-FIT in the 4C forestry model under different management scenarios. We further provide a preliminary attempt of trait to tree species translation and quantify changes in important ecosystem functions and services like biomass, carbon sequestration rates, evapotranspiration, soil moisture and timber harvests. We close with an outlook and discussion of further experiments.

Exploring variations in species traits and indicator values correlating with the invasiveness of plant species

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It is important to comprehend the factors that enhance the invasiveness of plant species to create efficient methods for managing invasive species that pose a threat to biodiversity. Investigating a data set of an index of vascular plant species invasiveness combined with a novel database of plant species indicator values and traits, we find that values of the plant invasiveness index were correlated with values of plant species indicators and traits. We interpreted the consistency of these correlations and suggested that this can be used to develop an early warning system to help target efforts to control invasive vascular plants. We used machine learning modelling to correlate the indicator values of plant species invasiveness with values of plant species indicators and traits and the Shapley variable importance measure for variable importance. Our study provides crucial information for regional and local authorities to implement focused control measures.

Quantifying the effect of competition on functional assembly of moss and lichen communities: A process-based model analysis

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Environmental filtering and competition are two fundamental processes that shape plant community assembly in terms of functional composition. Understanding the impacts of these two processes on functioning and composition of non-vascular vegetation, such as mosses and lichens, is important since the organisms provide essential ecosystem services in many regions around the world. Responses of non-vascular communities to environmental selection pressures have been explored in a range of experimental and modelling studies. However, it is still largely unknown to what extent competition affects the composition of functional traits of non-vascular communities. Moreover, it remains poorly explored which traits that are associated with competition are key for shaping the community functional assembly. Here we applied a process-based model to simulate the trait composition of non-vascular communities at two sites in temperate climate that differ in microclimatic conditions (a shaded and an open site). We also performed a simulation experiment to understand the impacts of competition on the trait distribution at these two sites. Our results reveal that the trait composition is likely a result of weak competition. Furthermore, height seems to be a key trait for competition. However, the results indicate that no single trait can consistently explain the functional composition. The presented simulation provides a new insight into trait-based approaches for non-vascular community ecology. We suggest that competition may not always be essential for predicting the trait composition of non-vascular communities under temperate climatic conditions. Moreover, we suggest to be cautious to associate competition to a single trait while analyzing the community functional assembly.

Network-informed selection of traits for ecosystem research

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Plant functional traits and the trait-based approach have shown great potential to advance our understanding of terrestrial ecosystem process and function. However, despite numerous studies, guidelines for selecting essential traits remain lacking. In this study, we employed network analysis to quantify the dissimilarity of all possible reduced trait networks to the full network and aimed to identify a concise reduced network that accurately represents the full network. Our results show that trait redundancy and network performance gradually increase with network size, accompanied by a consistent decrease in network dissimilarity. Small-size networks with a suitable trait combination exhibit structural similarity to the full network and improved performance. The consistent networks also show an average 25% improvement in minimum network performance. Notably, the best-performing network series not only effectively capture the structural complexities of the full network but also demonstrate high consistency in network metrics across ecoregion gradients. The cost-effective analysis shows that a 14-trait network attains a 78% performance rate with only 41% of the expense. Our results thus identify the main structure of a complex trait space with a core set of essential traits, theoretically advancing our understanding of plant traits and adaptation strategies, and practically informing trait measurements in field research.

EcoMoveR: A species-based ecosystem model at the landscape scale

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Ecosystems are among the most intricate and dynamic entities, describing a vast number of biotic interactions, subjected to often stochastic abiotic factors. Given the large threat anthropogenic impacts and the limited capacity of descriptive approaches to generate reliable projections under novel conditions, the relevance of process-based ecosystem models may become more apparent than ever. Modeling the complex array of ecological interactions and processes in a process-based approach requires, however, compromises regarding resolution, scale and complexity. As such, ecosystem models may have similar restraints, as they are tailored to either specific locations or species, rather than simulating ecosystems in their entirety. Here, we present a mechanistic general ecosystem model named EcoMoveR, aimed at simulating ecosystem processes at a fine-scale resolution, incorporating interactions between animals, vegetation and climate following an agent- based approach. With EcoMoveR. we intent to provide a bridge between global-scale, full-ecosystem models, such as Madingley, and existing single-species local-scale models. By increasing the definition of species-specific (functional) traits, EcoMoveR allows for greater control of modeled groups as well as food-web interactions. In addition, EcoMoveR incorporates animal movements using levy walks parameterized using allometric relationships. Emerging movement patterns determine the usable area (i.e. home range), and subsequently, the usable area dictates the accessible resources.

To showcase the capabilities of EcoMoveR, we developed a case study simulation for the Serengeti. For this particular case study, we relied on a detailed parameterization of mammal species, and modelled the remaining heterotrophs, such as other vertebrates and arthropods, as functional groups. Emerging space use, population density and life history patterns were compared against independent empirical data sources. The simulated relationship between body mass and space use was shallower compared to the empirically obtained relationship, estimating home ranges accurately for smaller-bodied mammals, but were underestimating them for larger-bodied mammals (>100 kg). Overall the population densities of mammals modeled by EcoMoveR were over the full body size range ~1 order of magnitude higher compared to densities obtained from empirical sources for the same species and taxonomic order. Deviations between simulated and empirical data may be partially explained by the high availability of resources estimated from the current vegetation model and the exclusion of human pressures in the current modeling framework. These deviations may provide interesting avenues for subsequent model developments as well as the future study of variation attributed to intra-species variation, environmental variation or human induced pressures.

Hierarchical ordination, a unifying framework for drivers of community processes

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Ordination methods are used by community ecologists to describe and explore the communities they sample by reducing variation down to a small number of dimensions. More recently, Joint Species Distribution Models have been developed to model and predict the distributions of several species simultaneously. Contemporary models for both of these problems are essentially the same, and are called Generalised Linear Latent Variable Models (GLLVMs). Currently, the only way to include predictors for species (i.e., traits) is through the fourth-corner model. Drawing from both ordination and JSDMs, we propose a new modeling framework that incorporates traits, environmental measurements, and potentially spatial coordinates and phylogenetic relationships to study ecological communities. The proposed model that we call "hierarchical ordination" can be seen as a more flexible, and fully model-based, extension of double constrained ordination methods previously proposed for community ecology. Unlike double constrained ordination, hierarchical ordination builds on both the modelling strengths developed from JSDMs and the visualisation and interpretation provided by ordination.

Amazon southeastern presents higher functional richness but lower ability to store carbon with reduced precipitation

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How the rainfall gradient (northwest-northeast) found in Amazon basin determines spatial distribution of functional richness (Fric; a component of functional diversity that expresses the variability of functional trait values found in an ecological unit) and how Fric affects the ability of forest to store carbon under projected reduced rainfall remains unclear. We addressed these questions employing the trait-based model CAETÊ (Carbon and Ecosystem functional Trait Evaluation model) under current and reduced rainfall (-50%) in three quadrats cells along the rainfall gradient: Northwestern (higher precipitation), Central, and Southeastern (lower precipitation) Amazon. CAETÊ represents trait variability through 3,000 plant life strategies (PLSs) comprising unique combinations of six functional traits (carbon allocation and residence time in leaves, wood, and fine roots). Southeastern presented the higher Fric value while Northwestern presented the lowest, distinct from previous taxonomic diversity studies. Reduced precipitation increased Fric in all three regions but at a higher degree in Southeastern due to its higher Fric in previous climatic conditions. Reduced precipitation also led to an increase in the occurrence of PLSs with higher carbon allocation to fine roots at the expense of other pools (especially wood), indicating a change in composition with the selection towards strategies prioritizing water acquisition versus carbon acquisition in water-limited conditions. This change was more pronounced in the southeastern, but also imposed for this region a lower ability to store carbon due to the increase in the root:shoot ratio. Although studies show that higher Fric can increase ecosystem's resilience (persistence of ecosystem functions and properties) and lower vulnerability to tipping points, we show that even in a highly functional rich ecosystem (southeastern), not all ecosystem functions are maintained or maximized (e.g. observed decrease in carbon storage). We show that Fric is fundamental to modulating the amount of carbon stored in different plant compartments and consequently the capacity of Amazon forest to continue to act as a carbon sink. It evidences that heterogeneous spatial distribution of Fric throughout the basin is likely to define a range of resilience and vulnerability to tipping points in different regions of the Amazon under rainfall changes in future scenarios of climate change.

Assessing the tree regeneration niche from inventory data using a dynamic forest model

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The tree regeneration niche is governed by many processes and factors, that are challenging to determine. Besides species distribution ranges along climatic gradients, complex dynamics in forest ecosystems (e.g., competition) are fundamental elements for successful trees regeneration. Consequently, the representation of tree regeneration in dynamic forest models is a notoriously complicated process which often involves many subprocesses. In the ForClim model, regeneration is mainly driven by species traits. However, the tree regeneration module in ForClim (and in most other dynamic forest models) has never been confronted with large-scale data. Therefore, the regeneration niche in ForClim is entirely determined by species trait parameters which are based on ecological knowledge without any constrains by real world observations. Here, we compare two approaches for parameterizing the regeneration niche. One is using a trait-based approach (TBA), where the quantification of the regeneration niche is based on ecological knowledge. The other is an inverse calibration approach (ICA), where we estimate species traits from a large observational dataset of unmanaged European forests. This is done with a simple and complex model variant without and with competition during regeneration, respectively. Specifically, we use Bayesian inference to estimate shade and drought tolerance as well as the temperature requirements for 11 common tree species along with the intensity of regeneration (i.e., the maximum regeneration rate). We find that the species' light niche (i.e., light requirements) is similar between the TBA and ICA for both model variants, while only the complex model led to plausible estimates of the drought niche. The temperature niche as defined in the TBA could not be recovered from the data by either model variant using the ICA. The parameter estimates differed between the complex and the simple model, with the complex model performing better. In both model variants, the calibration strongly changed the parameters that determine regeneration intensity compared to the default.

We conclude that the regeneration niche of the tree species in this large European dataset can be recovered in terms of the stand-level parameters light availability and regeneration intensity, while abiotic drivers (temperature and drought) are more elusive. The higher performance of the ICA underpins the importance of informing dynamic models by real-world observations. Future research should focus on an even larger environmental coverage of observations of demographic processes in unmanaged forests to verify our findings at species range limits under extreme climatic conditions.

Including the collaboration gradient of root traits and mycorrhiza in a Dynamic Vegetation Model

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Plant roots have a large diversity of form and function which are being increasingly researched in order to understand their role in community structure and ecosystem processes. Research concerning root trait diversity has revealed parallels with the leaf economic spectrum, but have also shown a strong relationship between the importance of mycorrhizae and root form in resource acquisition, known as the mycorrhiza collaboration gradient.

In this study we included the variation of root traits and mycorrhiza-mediated nutrient uptake into a trait-based DVM (LPJ-GUESS-NTD) in order to test if the inclusion of the root collaboration gradient improves model fit to observations. We ran the model along a well-studied tropical montane forest elevation gradient, and evaluated if LPJ-GUESS-NTD is capable of reproducing observed patterns of vegetation biomass stocks and productivity as well as plant trait distributions with and without root-mycorrhizal collaboration.

Our results show that simulations including the collaboration gradient implementations are able to accurately represent the biomass gradient across elevations, but underestimate forest productivity. Deactivating mycorrhiza-mediated nutrient uptake significantly reduced biomass values, particularly in the highest elevation site, from 80.1 Mg C/ha +/- 8.14 SD to 16.96 MgC/ha +/- 2.31 SD. Similarly, observed changes in the distribution of root traits towards higher collaboration with mycorrhiza and reducing specific root length with increasing elevation is reproduced by the model only in the scenario where mycorrhiza uptake is active.

We conclude that the mycorrhiza collaboration gradient and its link to root traits is important for understanding ecosystem functioning across elevations in our study area. Incorporating it into dynamic vegetation and ecosystem models has the potential to improve vegetation nutrient interactions in dynamic vegetation and ecosystem models, which are valuable tools for understanding and predicting the carbon cycle and feedbacks from ecosystems on climate.

Small-scale coexistence of three congeneric tree species is driven by trait differentiation and plasticity in a Brazilian flooded white-sand forest

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Trait variation and spatial distribution patterns have been increasingly employed to understand mechanisms structuring diverse communities. In a 1-ha plot of seasonally flooded white-sand forest in southeast Brazil, a previous study employing spatial point pattern analyses found that three Myrcia species show habitat filtering to the same seasonally flooded patches, within which the species do not show evidence of competition. We hypothesize that the coexistence of the three species within such small-scale patches is due to interspecific trait variation resulting from niche differentiation. The interspecific trait variation can be similar to or larger than the variation at the plot scale. The species are widely distributed in different habitats in Brazil, so we also expect intraspecific trait variation between the white-sand forest and other habitats that are not seasonally flooded. We used six environmental variables to characterize flooding and measured 12 traits related to resource acquisition and tolerance in the plot. We also compiled trait values in other habitats from databases and literature. Most traits differed between two or among the three species at the plot scale. The first PCA axis explained 36.7% of the variation, with M. brasiliensis showing higher leaf area (LA), and M. multiflora and M. racemosa showing higher wood density (WD) and allometric coefficient (AC). The three species showed intraspecific trait variation at the plot scale and differed in their traits within seasonally flooded patches. Myrcia brasiliensis and M. multiflora showed lower LA, higher WD, and higher AC within seasonally flooded patches, while M. racemosa showed the opposite association with flooding. The values of traits measured in the white-sand forest were all within the range of the data compiled for other habitats. Interspecific trait variation can promote the coexistence of the three species in the white-sand forest. Furthermore, the two species that show higher similarity at the plot scale differentiate at seasonally flooded patches, suggesting an additional mechanism for avoiding interspecific competition. The intraspecific trait variation at the plot scale is likely explained by plasticity, as natural selection should not be operating due to gene flow among environmental patches. Although the three species showed plasticity at the plot scale, seasonal flooding does not act as a selective pressure differentiating populations of each species between the white-sand forest and other habitats. We suggest that spatial distribution patterns and trait variation at different spatial scales should be combined in more complex models to understand species coexistence in diverse communities.

Model-based Impact Analysis of Climate Change and Land-use Intensification on Trophic Networks

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Before a global change-induced decline in biodiversity can be measured in terms of species numbers, the structure of communities within trophic food webs is affected. While land use is the most important driver of terrestrial biodiversity loss, its impact in combination with climate change, particularly on terrestrial trophic networks, is less well understood. We are investigating the combined effects of climate change (temperature, precipitation) and land-use intensification using a process-based general mechanistic ecosystem model (‘MadingleyR’), that simulates ecosystem dynamics for trait-based functional groups of species (i.e., ectothermic and endothermic herbivores, carnivores, and omnivores) for different regions such as India and Europe.

The results show patterns, widely consistent across the selected regions. In terms of feeding guilds, the greatest effect of climate change and land use is observed for carnivores. Both, land use intensification and climate change, cause a substantial decrease in the biomass of different functional groups, while some functional groups (generalists, omnivores), partially benefit. Land use intensification leads to a shift in body mass distribution and thus to smaller organisms in the food web. In particular, large endotherms are negatively affected by land use intensification, while ectotherms are under pressure from rising temperatures in a changing climate. Arid and tropical regions show a higher response to climate change, with losses of up to -3.4% and -1.85% in total biomass, while areas with low net primary productivity show the most negative response to land use intensification (up to -6.66% in total biomass).

Our results suggest that further land use intensification (i) will have a significant impact on larger organisms and predators, leading to a major restructuring of global food webs, (ii) Ectotherms are particularly vulnerable to rising temperatures, and (iii) particularly regions in tropical or arid climates will experience significant changes in their community composition and will be threatened in their biodiversity.

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8. Integrative approaches to capture natural disturbance impacts in models

Simulating biotic disturbance agents and their interactions in forest landscapes

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The role of different biotic disturbance agents in forest ecosystems is increasing around the globe as they respond strongly to rising temperatures. In addition, global trade and movement have increased the number of introduced pests and pathogens exponentially over the past decades. However, studies simulating vegetation dynamics have so far either ignored biotic disturbance agents or considered only a very limited number of agents. Here, we introduce examples of simulating biotic disturbance agents and their interactions using BITE, a process-based model including the key processes for all biotic agents. BITE (BIotic disTurbance Engine) is coupled with the process-based forest landscape simulation model iLand, which here is responsible for the vegetation dynamics. The aim in developing BITE was to create a general approach for simulating different biotic agents from the tiniest fungal pathogens to large mammals by identifying the common processes in their biology and thus developing a simple and modular modelling framework for wider use. The biomass of agents and hosts is used as a common currency in BITE from which the impacts of different agents on the ecosystem can be derived. Here, we provide examples on the use of BITE in simulating the impacts of a wide variety of agents in different forest ecosystems. In the first example, we simulated a total of 720 different agent trait combinations (e.g. dispersal, population growth, impact) to analyze which are the most harmful to forest ecosystems (forest functioning, landscape structure and composition). The second example illustrates how BITE can be used to study interactions between different sympatric browsing agents in boreal forests. Here, we simulated the dynamics of the most important browsers in Finland and Alaska to compare their browsing patterns and impacts on forests. The modular structure of BITE enables simulations with agents of varying information level for parametrization. Including multiple biotic agents and their interactions is a step forward in vegetation modelling and to better understand the complex dynamics of shifting disturbance regimes in a changing world.

Predisposing and inciting stress factors leading to beech mortality in Switzerland

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Over the last decade, prolonged water deficits combined with persistent and intense hot periods resulted in large mortality pulses in low-elevation forests across Europe. The drivers and processes leading to mortality induced by climatic extremes are being continuously investigated at multiple spatial scales by means of both empirical and dynamic forest models.

Despite cross-scale modelling efforts, most dynamic forest models fail to capture the drought signals leading to tree mortality, especially for the 2018-2019 period. Substantial uncertainty is associated with both abiotic and biotic drivers but most importantly to dynamic processes resulting in mortality events.

We integrated empirical and dynamic modelling approaches to investigate which drivers and processes lead to observed mortality patterns in the years 2018-2019 at selected drought-prone beech sites in Switzerland. In a first step, we compared the performance of a wide range of drought indices in terms of their suitability for capturing stand-level growth responses to drought. Once we selected the best performing index, we tested whether the signal it carries feeds through growth and mortality dynamics in the forest gap model ForClim.

To account for the multiple interactions across biotic and abiotic stressors over short and long term periods we integrated the Decline-Disease theory in our current modelling framework. Accordingly, we postulated a combination of predisposing and inciting factors which include a drought memory as predisposing factor and a drought duration term associated to seasonal soil water deficit in both spring and autumn months as inciting factor. In addition, we developed a novel model feature by enhancing the response of both growth and mortality dynamics to environmental extremes and soil water dynamics. We tested this new modelling framework in low elevation even-aged beech dominated forest sites in Switzerland by reproducing the observed response to drought-induced mortality in the years 2018 and 2019.

We also assessed the associated uncertainty rising by the alternative processes formulations by means of a pattern-oriented modelling approach. Specifically, we tested the new model feature along a climatic gradient of sites in Central Europe where we simulated potential natural vegetation development over time.

We argue that a novel ForClim feature is more suited to capture the mortality responses induced by extreme drought events at both managed beech dominated sites in Switzerland and along a climatic gradient in Central Europe.

A window into the future: Forest reorganization in landscapes with contrasting disturbance regimes

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The forests of the future are being born right now. What they will look like, where they will occur and how similar they will be to our current forests remains unclear. A critical puzzle piece in our understanding of future forests is the reorganization phase, a short window of time after disturbance in which a system either renews itself or transits to a different trajectory. How the reorganization phase plays out depends on the disturbance itself, as well as climate change effects on the disturbance regime and vegetation.

In our study we investigate the drivers, patterns, and impact of reorganization by simulating three landscapes – Shiretoko National Park (JP), Berchtesgaden NP (DE) and Grand Teton NP (US) – using the process-based forest landscape model iLand. We chose these landscapes because they're located along a gradient in climate (cool/wet/oceanic to hot/dry/continental) and disturbance activity (low to high). Yet, all three landscapes are projected to face major climate risks in the coming decades. Each landscape was simulated under reference climate (resampled from 1990-2020) and four climate change scenarios (wet-warm, wet-hot, dry-warm, dry-hot) from 2021 to 2200.

Our objectives were to determine how different disturbance regimes influence forest landscape responses to climate change. We hypothesize that landscapes experiencing high disturbance activity will respond more strongly to climate change than landscapes with low disturbance activity. To capture the unique disturbance regimes of each landscape, we've implemented several different disturbance agents (fire, wind, different species of bark beetles) in iLand.

We furthermore investigate the drivers of post-disturbance forest reorganization across different landscapes. We hypothesize that characteristics of the disturbance (size, severity, type) as well as the environmental conditions under which they happen (environmental harshness, climate change) influence the direction (deviation from baseline with regard to composition and structure) and magnitude of post-disturbance forest reorganization. Comparing across three landscapes by means of process-based modeling we aim to uncover general mechanisms of climate-driven reorganization in forest ecosystems.

Trade-offs and synergies of forest ecosystem services in temperate European forests under disturbance, management and climate scenarios

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Climate change affects both the growing conditions for trees as well as natural disturbance dynamics imposing abrupt changes in forest structure. Forest management practices are increasingly aiming to adapt forests to these changes as well as to support resilient forest ecosystems, while enabling the continuous provisioning a range of different ecosystem services. Moreover, societal demands and perceptions of forests are changing and there is an increasing focus on protecting biodiversity but also on increasing the role of forests for climate change mitigation either through carbon storage in the forest or through the provisioning of wood products that substitute carbon-intensive materials while also maintaining a forest carbon sink. However, those management decisions are not always consistent and imply trade-offs between the provisioning of different ecosystem services. This study uses the process-based forest model 4C to simulate forest growth and development to understand how forests and the ecosystem services they provide are developing under a wide range of future disturbance, management, and climate scenarios. The model is initialised based on forest inventory data from a set of temperate European countries, Germany, France, Poland and Slovenia. The model is then driven by future climate (CMIP6, RCP2.6, 7.0 and 8.5) scenarios as well as management and disturbance scenarios developed in the I-Maestro and further improved in the LEARNFORCLIMATE project in combination and isolation which are further combine with dedicated scenarios of forest protection. Disturbance scenarios describing wind, bark beetle and fire occurrence are based on observations collected in the Database on Forest Disturbances (DFDE) that holds information about the development of disturbance impacts. Based on these simulations trade-offs and synergies between different management objectives under a wide range of future scenarios of disturbance and climate is evaluated. Furthermore, the full-factorial design, crossing all disturbance, management and climate scenarios will allow us to distinguish the importance of disturbances, management and climate on ecosystem service provisioning from each other.

Simulating biotic disturbances with forest landscape models: comparing different approaches in different forest ecosystems

Marco Mina

Eurac Research

The functioning of forest ecosystems is increasingly jeopardized by global change such as climate warming and intensifying natural disturbance regimes. In North America, invasive insects are among the most urgent threats to forests, inflicting damages at multiple spatial scales. Because of climate change, some of these pests are now able to expand their ranges in regions previously unsuitable for them to establish and thrive. Analogously, bark beetle outbreaks (Ips typographus) have been causing extensive damages to conifer forests in Europe, amplified by warmer climate and by a promoted presence of its major host (Norway spruce). Forest landscape models are valuable tools to investigate the complex interdependencies between interacting disturbance agents, management and the structural and compositional diversity of the forest under mutating environmental conditions.

We compared two forest landscape models applied on two different forest ecosystems to evaluate the potential impacts of insect disturbances in interaction with climate change and forest management. The two models - LANDIS-II with PnET-Succession in Eastern North America and iLand in the Italian Alps - were both spatially-explicit, climate-sensitive and process-based, but differed regarding the consideration of interactions between climate and the simulated frequency and magnitude of outbreaks. iLand simulated direct interactions between bark beetle outbreaks and climate, while LANDIS-II considered only indirect interactions (i.e., climate influencing forest structure and composition but not the severity of outbreaks). Both methods showed pros and cons. The first allowed a more direct comparison of the potential impacts of beetle´s damages under diverging climate scenarios, while the second required a more deterministic design to emulate climate-change effects by increasing outbreak intensities according to climate scenarios. However, the first approach required higher calibration efforts, which limited the investigation to one biotic agent, while the second one allowed a relatively rapid parameterization of multiple biotic agents from literature.

Our results showed that bark beetle disturbances will be amplified by climate change in the Italian Alps, with increased beetle development rates in higher elevation. However, without windthrow disturbances as triggering events these outbreaks did not cause major damages across the landscape. In North America, generalist insect pests attacking broadleaves caused the highest damaging potential and management interventions aiming at diversifying forest composition increased landscape susceptibility and outbreak severity. Despite methodological differences and uncertainties behind assumptions and scenario design, models that consider direct or indirect interactions between climate, disturbance and management can provide useful recommendations for resilience-based management under global change.

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9. Digital twins – a new modelling paradigm for ecology?

A digital twin of the crane migration

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We present one of the first ever Digital Twins (DTs) in ecology, a DT of the crane migration above the Benelux: the Crane Radar. DTs are digital counterparts of real-world processes, entities or systems, represented by models that are continuously updated with data for synchronization with their respective twin. DTs have already been successfully applied in engineering across a range of industries, and are now also being developed in the environmental and health sciences. In presenting the Crane Radar we will explain the basic principles behind DTs, and exemplify how these principles can be applied in ecology. We will discuss the key components of the crane radar that make it a DT, and we will explain what makes DTs unique from other types of models in ecology.

The Crane Radar predicts the location of migrating groups of cranes in current time, based on models that predict flight speed and direction, and observations made by volunteers. Every minute the Radar checks for new observations by volunteers on a biodiversity platform, after which it updates its predictions. The Radar checks for each new observation whether these can be linked with existing groups that are already tracked by the Crane Radar. This allows us to put observation data into context, and to follow the movements of individual flocks of cranes, which is one of the main benefits of DTs: linking observations and enriching data with context. The predictions of flight speed and direction are based on expert knowledge of migration routes, statistical models fitted on historical GPS telemetry data, theoretical knowledge about migration ecology and compensation for wind drift, and near-term wind forecast models representing environmental data. These elements show another important characteristic of DTs: their ability to combine expert knowledge, scientific knowledge, data, models and statistics, and a link with other DTs (weather forecasts) in order to capture natural processes in current time. Finally, the Crane Radar explicitly shows uncertainty of its predictions, which gives directions for further research and strategic sampling for increased monitoring precision and uncertainty reduction.

The Crane Radar is primarily designed for birders to increase their chances of seeing the migration, and will not help in answering important conservation questions. Nonetheless it represents a first example of a DT application in ecology that helps us understand the key principles of DTs for ecology. It allows further exploration of the benefits and barriers of the technology in this field.

From Model to Digital Twin: Use Case Blueprints and Challenges in building Digital Twins for Environmental Research and Policy

Merijn de Bakker, Elena Lazovik, Franziska Taubert, Thanasis Trantas, Volker Grimm, Jeroen Broekhuijsen, Otso Ovaskainen

Loss of biodiversity and quality of the natural environment is a prominent natural and societal problem. Both, researchers and policy makers are facing questions on how to better monitor and predict developments in the biodiversity of ecosystems under a changing climate and land use. In order to foster biodiversity conservation, scientists develop predictive mechanistic ecological models which allow, for example, to predict the biomass growth and plant diversity of grasslands exposed to different management intensities or to predict the spatial distributions of the diversity of birds in forests which are affected by climate change and management. In order to be able to react in a timely manner to environmental changes that could severely or even irreversibly disrupt the ecosystem, a Digital Twin offers the possibility to not only monitor changes of the ecosystem in near real-time, but also to digitally predict changes that require action.

The Horizon Europe BioDT project aims to position such mechanistic predictive models of ecological systems in a Digital Twin framework. Thereby, the transition from ecological models towards a Digital Twin is a task facing multiple theoretical and practical challenges. We begin with defining a use case description blueprint. The use-case description plays a crucial role in the defining of the goal(s) of the digital twin. A use-case description and translation of it into Digital Twin terms is the first phase of the design process of DT. It provides a basis for further elaboration of it into concrete building blocks and defining the dependencies between different blocks. By standardizing the use case description template as a blueprint, it becomes a helpful tool for the description, users and functionalities of the digital twin.

We also define the main challenges in the context of (1) data pipelines, (2) model upscaling and parameter calibration (3) simulation traceability and FAIR (Findable, Accessible, Interoperable, and Reusable) principles, (4) infrastructure and deployments and (5) scenario definitions and dashboarding. Also, we provide possible solutions and approaches to these challenges in building Digital Twins for environmental models.

Effective data pipelines are crucial for integrating diverse data sources and ensuring data quality, while model upscaling and parameter calibration enable accurate predictions at larger spatial and temporal scales. Adherence to FAIR principles ensures that generated data and models are accessible and reusable, fostering collaboration and transparency. Robust infrastructure and deployment strategies are vital for the practical implementation of the Digital Twin framework, and scenario definitions and dashboarding facilitate user-friendly visualization and interpretation of model predictions by different stakeholders.

Individual-based remote sensing of trees: towards digital twins of forests

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Individual-based forest models have long been useful tools to study trajectories of forest development over time under various management alternatives and climate scenarios. However, as an initial state for simulations they either require inventory data, which commonly only cover small areas, or require spin-ups from bare ground under coarse assumptions. With ever improving capabilities of individual tree delineation from remote sensing, the vision of running individual-based forest simulations for any desired stand or even wall-to-wall at regional scale is becoming a real possibility. The Thünen Institute and the Federal Agency for Cartography and Geodesy are working together on a digital twin for Germany's forests. Airborne laser scanning point clouds are being clustered into single tree crowns. Plots of the national forest inventory serve as ground truth to link the obtained crown projection areas to measured stems and derive allometric relationships. Machine learning is used to predict tree species based on 3D features of the crowns. The goal will be a digital twin for every tree in Germany with all its important attributes. The digital twin can then serve as data basis for detailed analyses, forest model initialization and parameterization and as a baseline for tracking the fate of every tree into the future.

Monitoring and protecting biodiversity with Digital Twins

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Climate change and land-use change have accelerated rapidly, bringing more extreme events such as droughts, which can push ecosystems into a state where species become rare or even extinct. Therefore, alongside climate change mitigation, biodiversity conservation has become increasingly important. For example, pollination services provided by domesticated bees and wild insects are vital for natural plant communities and agricultural productivity – with wild bees being even more efficient in pollination services than honey bees. Protecting biodiversity (esp. in case of sudden extreme events) requires decisions based on timely and accurate monitoring, often by field observations of the ecosystem. Such monitoring campaigns, however, can lack a lot of information in terms of temporal and spatial coverage as biodiversity is still mostly observed by hand, and they are very costly. Based on the observations that are available, ecological models can help to overcome this limitation by predicting biodiversity attributes to fill the spatial or temporal information gaps. However, when it comes to future scenarios (e.g. climate or land-use change), observations are not yet available and model predictions need to be based on assumptions about expected developments. As time goes on and new observations become available, model results and associated recommendations may be outdated, especially if environmental conditions change suddenly or unexpectedly. Here, we demonstrate the missing information and uncertainties that arise when biodiversity conservation relies on either observations or model results alone, and report on the benefits of combining observations with model predictions in a Digital Twin framework, where both are frequently updated and the model is adjusted as needed.

Development of three prototype digital twins for (near) real-time biodiversity monitoring and conservation

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We present the planned and in-progress development of three pioneering digital twin prototypes for (near) real-time monitoring of biodiversity and conservation issues as part of the Horizon Europe Nature FIRST project. Each prototype will combat a key issue faced by the project field partners including the protection of endangered species, human-wildlife conflict and monitoring biodiversity. Our aim is to demonstrate the potential of digital twins as an integral tool in the conservationist's toolkit, supporting effective evidence-based decision making through the mobilisation of data and expertise.

The first of these digital twins, aimed at tracking sturgeon migration in the Danube Delta, Romania, is currently in development. Poaching and disruptions to their reproductive migration routes have left four of the five extant Danube Delta sturgeon species critically endangered. This digital twin will predict the current location of the sturgeon using a nowcasting model based on expert knowledge and fed with real-time environmental data and field observations. The eventual goal is for this digital twin to also integrate poaching data and send warnings when sturgeon enter high-risk poaching areas, enabling targeted conservation interventions.

The proposal for the second digital twin is to tackle human-bear conflict around Stara Planina, Bulgaria by tracking brown bear (Ursus arctos) movement. Multiple data sources, likely including ranger surveys, camera traps and citizen science data, will be harmonised to provide an overarching view of the issue. This digital twin will produce nowcasts and near-term forecasts of bear location, providing insight into how they navigate human-influenced landscapes and how conflict is triggered in near real-time, which in turn enables conflict prevention interventions in the field.

The final digital twin is proposed to address the challenge of monitoring and reporting biodiversity in the form of indicators such as the essential biodiversity variables developed by GEO BON. Indicators are created through analysing raw data and, due to the difficulty of collecting comprehensive ecological data, often involve extrapolation. Digital twins can not only generate these indicators automatically for up-to-date information, but through comparing new data with extrapolated data, they can critically examine the reliability and uncertainty of these standard techniques.

While these prototypes will just scratch the surface of what digital twins are ultimately capable of, their development will help lay the foundation for future widespread use of this methodology in ecology and conservation.

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10. Combining process-based simulation models and remote sensing data – benefits and limits

Mapping Amazon Forest Productivity by Fusing GEDI Lidar Waveforms with an Individual-Based Forest Model

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The Amazon rainforest plays an important role in the global carbon cycle. However,

due to its structural complexity, current estimates of its carbon dynamics are very imprecise. The aim of this study was to determine the forest productivity and carbon balance of the Amazon, particularly considering the role of canopy height complexity. Recent satellite missions have measured canopy height variability in great detail over large areas. Forest models are able to transform these measurements into carbon dynamics. For this purpose, about 110 million lidar waveforms from NASA’s GEDI mission (footprint diameters of ~25 m each) were analyzed over the entire Amazon ecoregion and then integrated into the forest model FORMIND. With this model–data fusion, we found that the total gross primary productivity (GPP) of the Amazon rainforest was 11.4 Pg C a−1 (average: 21.1 Mg C ha−1 a−1) with lowest values in the Arc of Deforestation region. For old-growth forests, the GPP varied between 15 and 45 Mg C ha−1 a−1. At the same time, we found a correlation

between the canopy height complexity and GPP of old-growth forests. Forest productivity was found to be higher (between 25 and 45 Mg C ha−1 a−1) when canopy height complexity was low and lower (10–25 Mg C ha−1 a−1) when canopy height complexity was high. Furthermore, the net ecosystem exchange (NEE) of the Amazon rainforest was determined. The total carbon balance of the Amazon ecoregion was found to be −0.1 Pg C a−1, with the highest values in the Amazon Basin between both the Rio Negro and Solimões rivers. This model–data fusion reassessed the carbon uptake of the Amazon rainforest based on the latest canopy structure measurements provided by the GEDI mission in combination with a forest model and found a neutral carbon balance. This knowledge may be critical for the determination of global carbon emission limits to mitigate global warming.

Application of the 3D-CMCC-FEM model to assess gross primary productivity in Mediterranean forests at the regional level

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The Mediterranean basin is a well-known drought-prone region, with projections indicating a high warming rate, decrease of precipitation in the summer and a large increase in the frequency and intensity of extreme events such as heat waves and droughts. Nevertheless, data scarcity and short-term monitoring efforts still represent major challenges in studying the effects of climate change on forest dynamics in mediterranean ecosystems.Process-based forest models are versatile tools developed and tested over a wide range of climatic and ecological conditions.

Yet, such models are typically applied at the local scale (i. e., stand level) where high-quality data to initialize the model is often available. Indeed, applying such models in broad geographical areas like in the Mediterranean basin is challenging, given the multitude of ecological, morphological and soil type gradients and climate conditions.

For the first time, the biogeochemical, biophysical, process-based model 3D-CMCC-FEM was run on a regular 1x1 km grid over one of the southernmost regions in Italy (i.e. Basilicata region) where data are extremely scarce . The model was initialized using spatial information derived by the national forest inventory of the year 2005,remote sensing data and regional forest maps. Carbon fluxes and pools have been simulated over the period 2005-2019 and compared to satellite-based datasets. We focus on gross primary productivity as the first proxy to potentially mainly detect drought-induced productivity losses on temperate forests. We show the capability of the model to simulate current forest gross primary productivity (GPP) at species level and to capture most of the large scale forest response to interannual meteorological variability, i.e. summer droughts, when compared to multiple data sources based on remote sensing products. We demonstrate that model trend analyses of spatialized forest growth can be helpful in identifying areas at risk of climate-induced dieback.

A new approach combining the multilayer radiative transfer model with a forest model: Application to boreal forests in Finland

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To better understand forest dynamics under today's changing environmental conditions, it is important to analyze the state of forests. Forest inventories are not available for many regions, so it is important to interpret other information about forests. More and more satellite data (such as RADAR and airborne) are available. There is great potential in analyzing these measurements and gaining an understanding of the condition of forests. In this work, we combine the new generation radiative transfer model mScope with the individual-based forest model Formind to generate reflectance spectra for forests. Combining the two models allows us to account for species diversity at different height layers in the forest. We compare the generated reflectances for forest stands in Finland, in the region of North Karelia, with Sentinel-2 measurements. We investigate which level of forest representation gives the best results. For the majority of the forest stands, we generated good reflectances compared to the measured reflectance. Good correlations were also found for the vegetation indices (especially EVI). This work provides a forward modeling tool for relating forest reflectance to forest characteristics. With this tool it is possible to generate a large set of forest stands with corresponding reflectances. This opens the possibility to understand how reflectance is related to succession and different forest conditions.

Simulating biodiversity based on remote sensing data: Combining airborne LiDAR data with InVEST Habitat Quality Model

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Biodiversity is linked to the provision of many ecosystem services that people depend on for their well-being. However, biodiversity is getting lost at alarming rates due to human-induced changes such as land-use change. Modelling approaches are becoming increasingly important to investigate the long-term effect of land use change scenarios on biodiversity. The focus of most biodiversity-modelling approaches is on species-specific data derived from labor-intensive and time-consuming field work with only plot-wide data availability. Remote sensing has the potential to overcome the limitations of plot-wide data by delivering high spatial resolution data. Such data make it possible to improve existing model parameterizations, and thus, ultimately to better investigate trajectories of biodiversity shaped by human-induced changes.

Here, we present a methodological approach to inform the biodiversity model Habitat Quality from the InVEST model suite with remote sensing data. The InVEST Habitat Quality model is a spatially-explicit, relative ranking model with a static scenario approach. In InVEST, habitat quality is used as a proxy for biodiversity and depends on the proximity and intensity of habitat to human-modified land use impacts that degrade habitats. Thus, the definition of habitat quality is based on habitat integrity. Habitat with high integrity indicates high quality, it is more intact and therefore better able to conserve total biodiversity than habitat with low quality. The degradation effect of impacts on the surrounding habitat is mediated by different parameters, including the relative weighting of each impact, describing the relative destructiveness of impacts to the habitat and the maximum range of each impact. The output of InVEST Habitat Quality is a habitat quality map.

We show how metrics derived from area-wide LiDAR (light detection and ranging) can be used to parameterize the InVEST Habitat Quality model, focussing on metrics that describe habitat structure. More specifically, we retrieve and systematically select LiDAR metrics describing vegetation structural complexity and apply a Principal Component Analysis to get a habitat quality index. Based on the habitat quality index, several statistical analyses such as mean determination and distance matrix were applied to adjust the index to the parameters of the InVEST Habitat Quality model.

The presented methodological approach enables to link remote sensing data to the process-based biophysical model Habitat Quality of the InVEST model suite and to simulate a simple proxy of biodiversity based on area-wide habitat structure data. It improves existing model parameterizations and enables to focus on general trends in biodiversity development.

Coupling GRASSMIND and PROSAIL models to simulate remote sensing signals of grassland communities with different management

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Advancing our understanding of grassland biodiversity by utilizing cost-efficient and comprehensive data acquisition methods is essential for advancing ecological research. A new approach is proposed, which involves coupling two process-based models, the individual grassland model (GRASSMIND) and the 2-D radiative transfer model PROSAIL, to obtain temporally continuous grassland trait information aligned with a variety of management options. The GRASSMIND model allows explicit modification of drivers of grassland dynamics, such as the frequency and timing of cutting and fertilization, daily weather data, and soil attributes. The PROSAIL model simulates grasslands' canopy reflectance based on the underlying leaf biochemical characteristics and canopy architecture, i.e., the optical traits. This approach provides a powerful tool for obtaining area-wide continuous information on relevant grassland biophysical properties, enabling a better understanding of the relationships between biodiversity, grassland management and the remote sensing signal, and abiotic/biotic factors. An extensive plant (optical) trait sampling was performed accompanied by remote sensing measurements in grassland communities with different underlying management for the subsequent model parameterization. Measurements included plant height, LAI, fresh/dry weight, pigment concentrations and hyperspectral observations and grasslands with a substantial gradient in land-use intensity (extensive to intensive) were investigated (GCEF, Dragnet and NutNet sites). By scaling up the collection of grassland biodiversity information through the integration of ground-based and satellite data, we can enhance our understanding of the ecological processes at work and the effects of management practices on biodiversity. The results of the field campaigns including laboratory retrieved plant traits such as chlorophyll and carotenoid concentrations are shown. We also describe the coupling workflow of GRASSMIND-PROSAIL and how we aim to parameterize and validate it.

Combining remote sensing and forest modelling to assess tropical forest fragmentation

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Large areas of tropical forest have been lost to deforestation, resulting in fragmented forest landscapes. However, the dynamics of forest fragmentation are still unknown, especially in the critical forest edges, which are sources of carbon emissions due to increased tree mortality. Using process-based models, we investigated the effects of altered tree mortality on forest dynamics and found a strong decrease in forest biomass at the forest edge. To assess the amount of forest edge area in the tropics, we analysed changes in forest fragmentation across the tropics using high-resolution forest cover maps. We found that forest edge area increased from 27 to 31% of total forest area in just 10 years, with the largest increase in Africa. The number of forest fragments increased by 20 million, with implications for the connectivity of tropical landscapes. Simulations suggest that continued deforestation will further accelerate forest fragmentation. By 2100, 50% of tropical forest area will be at the forest edge, resulting in additional carbon emissions of up to 500 million tonnes of carbon per year. Efforts to limit the fragmentation of the world's tropical forests are therefore important for climate change mitigation.

Towards disentangling geometric and demographic fragmentation effects in biodiversity data using a virtual ecology approach

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While there is consensus on the negative effects of habitat loss and degradation, there has been a decade-long debate on the consequences of habitat fragmentation (per se) on biodiversity. Recently, we suggested a conceptual framework to foster synthesis and a better understanding of fragmentation-biodiversity relationships across spatial and temporal scales. This framework distinguishes geometric and demographic fragmentation effects. Geometric effects exclusively arise from the spatial sampling of non-random species distributions. In contrast, demographic fragmentation effects emerge from changes in species birth, death, or migration rates in and between habitat fragments. We demonstrated the usefulness of the framework by distinguishing these two types of effects in extensive model simulations. However, we are still lacking methods to disentangle geometric vs. demographic fragmentation effects in empirical data derived from remote sensing and/or ground-based biodiversity samples. In this study, we present and test a method for partitioning geometric vs. demographic fragmentation effects, which is based on spatially explicit species rarefaction curves. These curves attempt to isolate geometric fragmentation effects by controlling for different extents and spatial patterns of landscape-scale biodiversity data sets. To assess the power of these methods, we use a virtual ecologist approach. In this approach, we first apply a novel process-based metacommunity model to simulate spatial biodiversity patterns in fragmented landscapes. By systematically varying model parameters such as dispersal distance, environmental autocorrelation, or species sensitivity to habitat edges, we can create model scenarios with known strength of geometric and demographic fragmentation effects. In the second step, we collect virtual samples from the complete simulation data to mimic real empirical data sets. In the third step, we then apply the spatial rarefaction method to the virtual data. Finally, we can compare if and under which settings, the inferred relative importance of geometric and demographic fragmentation effects derived from the virtual data corresponds to the true and known settings of the simulated model scenarios. In general, we argue that assessing and testing empirical methods using virtual data with completely known properties fosters the development of reliable and powerful methods for empirical biodiversity research. In the future, we envision combining remotely sensed land cover data with ground-based biodiversity samples and applying the partitioning method to this real-world data. Disentangling geometric and demographic effects will help to better understand biodiversity changes in fragmented landscapes and will hopefully contribute to improved spatial conservation planning.

Fragmentation of tropical forests and percolation theory

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Remote sensing allows for the quantification of tropical deforestation with high spatial resolution. This in-depth mapping enabled us to achieve substantial advances in the analysis of continental-wide fragmentation of tropical forests. We identified roughly 130 million forest fragments in three continents that show surprisingly similar size distributions which can be described by power laws with an exponent of -2. The principles of percolation theory provide an explanation for the observed patterns.

Based on these results and percolation theory we developed several models for fragmentation dynamics. Simulations suggest that ongoing deforestation will further accelerate forest fragmentation. Trees in the edge area will show increased mortality resulting in additional CO_2-emission. Percolation theory can be used to quantify the amount of forest at the edge (around 20 % – 30% of the forest is located at the edge). Here we also present results for the regional scale (100 km x 100 km). Spatial distribution of forests show fractal structures which strongly influence fragment attributes and connectivity between forest fragments.

Fragmentation of forests should be taken into account when analysing the role of vegetation in the global carbon cycle. Percolation theory allows to understand patterns of forest fragmentation in the tropics.

Masting of the Fagaceae family: improving simulations of the SEIB-DGVM with remote sensing

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In temperate forest ecosystems, acorns and nuts of the Fagaceae family are important food sources for insects, rodents, deer, and boars among others. The seed production of the Fagaceae family is often geographically synchronized and shows irregular patterns: in some years, there is an abundance of nuts, in other years there is scarcity of them. This phenomenon is called masting, and the number of years between mast years, when peak production occurs, varies widely. Climate change affects the intensity and frequency of masting depending on species and location, which not only affects forest recruitment, but also influences the population and behaviour of animals along the food-web, optionally leading to increased human-wildlife conflicts. To better understand the future impacts of climate change, we incorporated masting into a process-based vegetation model, the Spatially Explicit Individual Based Dynamic Global Vegetation Model (SEIB-DGVM). The modified DGVM had a new plant functional type with masting type of reproduction, which could be optimized along three parameters: resource allocation to flower and seed production, threshold limit to start flowering, and cost of nut production in relation to cost of flower production. Traditionally, the model is validated by using ground observations, but data availability is limited to certain locations and time periods. On the other hand, remotely sensed data became readily available in these past decades and cover large areas. Furthermore, it has the potential to detect masting, as the NDVI of forest canopies tends to increase before mast years. Therefore, we examined whether remote sensing could be used to validate the simulations to overcome the limitations posed by missing ground data. Model validation by remote sensing resulted in similar model selection as when validating by ground data, depending on the resolution of the image used and spatial localization of masting species. Combining the DGVM with remote sensing for validation could help to expand the simulations to global scale and increase the prediction accuracy of future simulations using several of the shared socioeconomic pathway’s climate projections.

Why matrix mosquito population models and remote sensing go hand in hand?

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Matrix population models are used in ecology to describe the dynamics of populations over time, taking into account factors such as birth and death rates, growth rates and the effects of environmental conditions. In recent decades, remote sensing technologies have made significant advances in data acquisition, processing and interpretation, providing a holistic view of the system at a wide range of spatial and temporal scales.

In this study, we explored the use of matrix population models in conjunction with remote sensing data to investigate the population dynamics of mosquito species. We implemented age- and stage-structured, climate-dependent matrix population models to describe the population dynamics of mosquito species of two ecological groups - marsh mosquitoes and urban mosquitoes. The two models were parameterised with the life history parameters of *Aedes vexans* and *Culex pipiens*, respectively. Remote sensing data were obtained from Copernicus data services. These included high-resolution maps of climate variables, surface water cover maps, land cover maps, vegetation and habitat type maps, and digital elevation model data for the regions of interest (ROI). Mosquito population dynamics were calculated for each day and grid cell within the ROIs for the period 2000-2022. In addition to the structure of the mosquito population in each quadrant, the dispersal of adults in space was also simulated. The developed models were also used to investigate the impact of mosquito control measures (larvicides, adulticides and combined treatments) on population dynamics. The simulation results were validated and the models were calibrated against field data.

The simulation results showed good compatibility with the field data over the selected period. This approach points to the importance of considering local variations in environmental factors that determine mosquito development, both for mosquito source detection and for temporal optimisation and spatial planning of mosquito control implementation. The combination of matrix population models and remote sensing data promises to provide a better understanding of mosquito population dynamics and mosquito-borne disease transmission at regional or even global scales. Further research in this area could lead to more effective control strategies and a better understanding of the factors driving the spread of these diseases.

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11. Mathematical and data-driven models in ecohydrology

A global analysis platform for understanding how changing hydrology influences riverine fish biodiversity

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River systems harbor a disproportionately large fraction of global biodiversity and are among the most important and most imperiled ecosystems on Earth. Riverine biodiversity is influenced by a tapestry of factors including hydrology, local landuse, topography, and a variety of anthropogenic effects. In particular, understanding how fish biodiversity in rivers around the world is affected by anthropogenically-driven hydrological changes is a key challenge. In this talk, we introduce a modeling and analysis platform for conducting large-scale analyses of fish biodiversity in river systems worldwide. Our approach combines global datasets on river geometry and hydrology, hydrologically-driven dendritic neutral models, and parallelized, GPUaccelerated high-performance computing techniques. We show that our methods reproduce existing results for the Mississippi-Missouri river basin in the US, yet can be easily transferred to other river systems to facilitate novel insights. In particular, we demonstrate the ability of our platform to highlight the effects of changing hydrology on basin-scale biodiversity with a case study on the Mississippi-Missouri system.

Modeling the functioning of multiple stressed riverine ecosystems: Challenges and solutions

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Riverine ecosystems are source of numerous ecosystem services which are crucially important for human well-being. At the same time, they are under increasing pressure from a multitude of (natural or anthropogenic) stressors. Thus, there is a strong need of management interventions to sustain riverine ecosystem services. While a lot of efforts have been already invested in correlative analyses of stressor-response-relationships, a full mechanistic understanding is still missing so far.

In this talk, we present the mechanistic model system MASTIFF which allow cross-scale analyses of the functioning of multiple stressed riverine ecosystems. This model follows a metacommunity approach where local food webs (benthic biofilm + invertebrate grazers) are coupled through drift and dispersal of the invertebrates. MASTIFF accounts for the interplay of local and regional processes, for the land use and its specific stressors along the river, and is ‘next-generation’ in the sense that its key processes are related to ‘first physiological principles’. We will show an example where MASTIFF is used for analyzing the relevance of clear-cutting of riparian vegetation as threat to ‘biocontrol of eutrophication’, one important riverine ecosystem service. This example nicely demonstrates what factors have to be incorporated for mechanistically understanding multiple stressor effects and their propagation across scales. We will come up with a ‘check list’ which unifies a recent literature debate on this topic, and is another proof of the potential of ‘next-generation ecological modeling’ for addressing multifunctionality in landscapes under transition.

Mechanistically delineating the effects of temperature and salinity on stream dissolved oxygen

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Dissolved oxygen (DO) is fundamental for the maintenance of aquatic life and, as such, a key component of water quality models. The concentration of DO is controlled by different processes. Reaeration and photosynthesis act as sources while respiration, degradation of organic matter, nitrification and benthic demand as sinks. Global changes such as temperature increases and salinisation are of worldwide concern. Therefore, it is important to include temperature and salinity in water quality models. However, limitations are inherent in current approaches for simulating effects of these factors in available water quality models. In most of these models the temperature effect on the processes regulating DO is considered with Arrhenius-type equations and salinity is ignored. Thus, the goal of this study is to improve the dissolved oxygen modelling by considering the combined effects of temperature and salinity on the processes regulating its availability.

Preliminary research indicates limited effect of salinity on organic matter degradation at frequently observed salinity levels of freshwaters. The information on the effects of salinity on nitrification and benthic demand are not extensively studied with limited published data. Accordingly, only the effects of temperature were considered in simulating these processes. Mathematical equations considering the effects of temperature and salinity on reaeration and primary production were retrieved from literature and from empirical modelling. These equations were applied to estimate the algae biomass and DO concentration in the Lower Bode River (Saxony-Anhalt, central Germany). Our results indicate that the estimate of saturated oxygen concentration is only sensitive to salinity at high levels (around 10 PSU). The model reflects the long-term trends of DO concentration. However, the large daily variation in both algal biomass and DO concentration could not be explained. Such limited capacity might be related to our approach representing the whole phytoplankton community by one single group. Further efforts are invested to improve the model. For example, various groups of primary producers such as surface-floating phytoplankton, suspended phytoplankton (in water column) and periphyton are distinguished in the model.

Modelling tropical saltmarshes as signature ecosystems for vegetation reliance on spatial and temporal patterns of both water quantity and quality.

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Water – both in terms of quantity and quality – is a defining factor for the shape and composition of an ecosystem. In tropical saltmarshes, water quantity and salinity vary temporally and spatially, defining vegetation patterns and species composition. These ecosystems exist between tidally influenced mangrove forests and precipitation controlled freshwater vegetation; the tidal influence in tropical saltmarshes, while restricted to only a few spring tides each year, prevents the establishment of most freshwater species, and the seasonal tropical rainfall regime includes extended arid periods, preventing the establishment of mangroves. In this unique setting, saltmarsh vegetation structure reflects the temporal and spatial availability of water in the root zone and patterns of dissolved salt. These water-dependent patterns are likely to change in a future with sea level rise and climate change.

To predict the impact of future change, both for existing species in tropical saltmarshes and for potential invading species, we suggest a model that combines (i) water balance modelling, describing water infiltration, evapotranspiration, unsaturated soil water flow and salt transport processes, and (ii) vegetation modelling, including the potential establishment of either different types of saltmarsh vegetation, or invasion from neighbouring vegetation types, and their unique temporal and spatial feedback on water balance.

We present this modelling approach as an extension of our modular framework pyMANGA for the description of feedbacks between vegetation and water availabilty. pyMANGA was first developed for mangrove ecosystems and combines different building blocks for individual based vegetation modelling, above-ground competition, and below-ground processes describing water availability due to porewater salinity resulting from plant water uptake feeding back with soil hydraulic processes. Expanding the model to saltmarshes required the design of new building blocks for unsaturated soil water processes and saltmarsh vegetation in competition with existing mangrove vegetation. Using our extended model, we present preliminary results for our pilot study site in northern Pará, Brasil.

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12. Advances in forest modelling by using new data sources and methods

Carbon sequestration of German forests: An individual based forest model experiment

Anne Holtmann; Rico Fischer; Andreas Huth; Friedrich Bohn; Corinna Rebmann; Samuel Fischer

UFZ - Helmholtz Centre for Environmental Research

Forests play an important role in climate regulation due to carbon sequestration. Climate and land use changes have a major impact on forest growth. However, the impact on carbon dynamics is very uncertain, as information about forest structure and species composition are often missing. Especially for non-even-aged and species-mixed forests a deeper understanding of carbon flux dynamics is lacking. In this study, we integrated field inventory data of German forests into an individual-based forest model to investigate forest carbon dynamics on tree level to reduce uncertainties regarding carbon flux dynamic predictions. We show that it is important to incorporate small-scale information about forest stand structure and species composition into modelling studies to decrease uncertainties of carbon dynamic predictions.

Carbon change affects Carbon cycle of forest cohorts but not homogeneously

Elia Vangi[1]; Elisa Cioccolo[2]; Daniela Dalmonech[1]; Leonardo Bianchini[2]; Alessio Collalti[1]

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Forest age plays a critical role in the distribution of carbon (C) stocks and fluxes in different forest ecosystems, as it is influenced by replacement ecosystem factors such as forest fires, logging, or insects. Large amounts of C stored for decades or centuries can be rapidly released into the atmosphere following a disturbance. Therefore, the net accumulation of C in forest ecosystems fundamentally depends on the age of the forest, which represents the time elapsed since the disturbance. To investigate the impact of forest age on net primary production (NPP) and total carbon woody stocks (tCWS) in a suite of observed and virtual forest stands, we used an already-validated biogeochemical-based forest growth model in three even-aged European forests across a latitudinal gradient, specifically: a European beech stand in Denmark, a Scots pine stand in Finland, and a Norway Spruce stand in Czech Republic. The model was forced by climate outputs of five Earth System Models under four representative climate scenarios (including one "no climate change" scenario as a benchmark) to simulate the effect of climate change on 11 age classes (from 12 to 140 years) of forest stands. We find out, with notable exceptions, that the production peak was for middle-aged class forests (42-70 years old), while carbon pool sizes increased with age with different trends in the three sites, but not linearly. Indeed, preliminary results show significant differences between the three sites and for the three species. Beech forest has an expected behavior under climate change scenarios, increasing NPP as atmospheric CO_2 concentration increases (following the so-called "CO_2 fertilization effect") as much for younger age classes as for older ones. At the same time, Norway spruce seems already at its optimum for climate, so even a small variation in environmental parameters leads to a drastic decrease in productivity and stocks. Finally, the Scots pine has an intermediate behavior. NPP and tCWS decrease with climate change compared with the NCC scenario, but increasing temperatures and atmospheric CO_2 concentration lead to an increase in tCWS up to the RCP 6.0 and then a relative decrease under RCP 8.5. Age trends in C-cycling and stocks are evident in all three sites, showing that a better understanding of how forest age interacts will significantly improve our fundamental knowledge of the terrestrial C-cycle.

Bayesian calibration of silver fir (Abies alba, Miller) parameters in 4C

Martin Gutsch[1]; Mats Mahnken[1]; Kirsten Krüger[2]; Christopher P.O. Reyer[1]

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Forest models are crucial for projecting forest growth under climate change and thus help us to better manage forest resources and safeguarding forests' integrity. Reliable tree species trait representation in process-based forest models is essential to limit the uncertainty associated with model-based projections of tree growth and forest dynamics under changing environmental conditions. Model parameters describe the tree species traits in complex, state-of-the-art forest growth models. Bayesian calibration enables merging prior knowledge about parameters and additional data that can be incorporated in the calibration to produce posterior estimates of parameters to estimate and restrict the uncertainty in model predictions.

In this study we parameterize an ecologically and economically important European tree species, Abies alba, in the process-based forest model 4C (FORESEE - FORESt Ecosystems in a Changing Environment). We investigate the uncertainties associated with predictions of target variables (DBH and tree height) in model projections that result from model parameter uncertainty. For this purpose, we use methods developed in recent years in the field of Bayesian parameterization and evaluation of forest growth models to integrate data from intensive forest monitoring (ICP-level II). First, we compile a parameter set for Abies alba from available literature. Then we use long-term monitoring data on tree growth from 15 ICP Forests level II long-term monitoring sites in five European countries and another data set from a cluster of 33 forest monitoring sites (Poland) to calibrate and validate the parameter set.

Our hypothesis is that the accuracy of predictions of primary variables of interest, such as diameter-at-breast-height and tree height, at the 33 Polish forest sites are improved by incorporating the ICP Forests data in the calibration process in comparison to the non-calibrated literature-based parameter set.

KDE-likelihood: a tool for fitting individual-based models to equilibrium data

Samuel Fischer[1]; Franziska Taubert; Andreas Huth

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Individual-based models are a valuable tool to study the dynamics of forests and estimate their responses to disturbances and environmental changes. However, fitting such models to observational data can be challenging, because their complexity typically hinders direct application of classical statistical tools such as the likelihood. Hence, modellers often examine the parameter space by applying sampling-based methods (e.g. approximate Bayesian computation, ABC), or they consider aggregated results whose distribution may be approximated via the central limit theorem. However, if the considered forests are assumed to be in equilibrium state, reaching these states in simulations requires long runs, making methods such as ABC difficult to apply. At the same time, aggregating results may lead to information loss that could result in identifiability issues corrupting the reliability of the parameter estimates. In this talk, we suggest the kernel-density-estimate-based (KDE-) likelihood as a tool circumventing these issues. The KDE-likelihood allows modellers to exploit the favourable statistical properties of the likelihood function without deriving it in closed form. We showcase the method's advantages in real applications by modelling the distribution of trees in a temperate Chinese forest using the process-based model Formind.

Evaluating the accuracy, realism and general applicability of European forest models with ground-based inventory data and tower-based eddy covariance data

Mats Mahnken

Potsdam Institute for Climate Impact Research

Forest models are instrumental for understanding and projecting the impact of climate change on forests. A considerable number of forest models have been developed in the last decades. However, few systematic and comprehensive model comparisons have been performed in Europe that combine an evaluation of modelled carbon and water fluxes and forest structure. New data sources have now established the possibility to make these evaluations. This study evaluates 13 widely used, state-of-the-art, stand-scale forest models against field measurements of forest structure and eddy-covariance data of carbon and water fluxes over multiple decades across an environmental gradient at nine typical European forest stands. Models' performance in three dimensions are tested: accuracy of local predictions (agreement of modelled and observed annual data), realism of environmental responses (agreement of modelled and observed responses of daily gross primary productivity to temperature, radiation and vapour pressure deficit) and general applicability (proportion of European tree species covered). Results indicate that multiple models are available that excel according to the three dimensions of model performance. For the accuracy of local predictions, variables related to forest structure have lower random and systematic errors than annual carbon and water flux variables. Moreover, the multi-model ensemble mean provided overall more realistic daily productivity responses to environmental drivers across all sites than any single individual model. The general applicability of the models is high, as almost all models are currently able to cover Europe's common tree species. This analysis shows that forest models complement each other in their response to environmental drivers and that there are several cases in which individual models outperform the model ensemble. The applied framework provides a first step to capturing essential differences between forest models that go beyond the most commonly used accuracy of predictions. Overall, this study sets a point of reference for future model work aimed at predicting climate impacts and supporting climate mitigation and adaptation measures in forests.

Abstract based on Mahnken, M., Cailleret, M., Collalti, A., Trotta, C., Biondo, C., D’Andrea, E., Dalmonech, D., Marano, G., Mäkelä, A., Minunno, F., Peltoniemi, M., Trotsiuk, V., Nadal-Sala, D., Sabaté, S., Vallet, P., Aussenac, R., Cameron, D. R., Bohn, F. J., Grote, R. … Reyer, C. P. O. (2022). Accuracy, realism and general applicability of European forest models. Global Change Biology, 28, 6921– 6943. https://doi.org/10.1111/gcb.16384

Xylem formation as the basis of adaptive physiological processes in individual-tree-based models - a new perspective for modelling life-history-related drought sensitivity

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Trees are adaptive organisms, challenging to abstract at the individual level for ecological models. To limit model complicatedness, some physiologically relevant traits such as the stem hydraulic conductivity are usually considered to be invariant, both in terms of tree genotype and life history. The work presented here addresses this gap and links data and patterns from wood anatomical studies to opportunities for formulating new physiological tree growth models describing the interplay between environmental conditions, xylem formation, and hydraulic conductivity. Considering the latter as an adaptive trait, tree growth and drought sensitivity become plastic, life-history-dependent features. The continuous, self-regulated build-up of the hydraulic architecture poses both chance and risk to tree fitness, for which a trade-off is being sought: forming larger vessel cells increases the hydraulic conductivity of a tree and can facilitate its growth, but, on the other hand, also increases its drought sensitivity. Tree species or their varieties may be distinguishable by their vessel size distribution and thus, represent different trade-offs that best fulfill the requirements of certain ecological conditions or strategies. In addition, they can also vary in their plasticity, i.e. how strongly individuals can adapt during their lifetime when confronted with environmental conditions that differ significantly from the recent eco-evolutionary history of their genotype. Hence, the presented framework for a new physiological description for modeling tree growth addresses a hitherto poorly acknowledged but potentially very important mechanism for understanding and predicting adaptive responses of trees under climate change. Besides the possibility of supporting the analysis and understanding of the growth responses of individual trees, e.g. as part of dendroecological studies, implementing this approach in existing forest simulation models offers the chance to investigate the adaptive response of whole forests to climate change scenarios. If we better understand how and to which degree individual trees can adapt during their life cycle, the question also is how long does this take to have an effect on forest functioning and how do different adaptation capabilities influence each other in a community context and our predictions of forest dynamics?

High resolution simulations of forest structure project heterogeneous change across the North American Taiga-Tundra Ecotone

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Boreal forests are expected to shift as the result of persistent warming in the northern latitudes, resulting in changes to the structure and function of the high-northern latitudes. However, the rates, patterns and location of these shifts will likely reflect the heterogeneity in the environmental drivers of forest structure, the influence and interaction of which are poorly understood. Predictions of changes in vegetation across the Taiga Tundra Ecotone (TTE) should account for this heterogeneity across multiple scales and incorporate sometimes opposing feedback mechanisms. Ecological modeling has been effective at integrating the effects of the multi-scale controls across boreal forests in this region. Here, we use a Landsat-scale map of the TTE forest structure patterns to identify different types of forest transition zones, target focal sites for forest model simulations within these zones, project future climate using CMIP6-SSP585, and present the simulation results for the focal TTE sites across the North American arctic/boreal domain. Using Canadian National Forest Inventory (NFI) and numerous sites across the Alaskan Brooks Range and Seward Peninsula, we parameterized and ran the spatially-explicit, high resolution forest model SIBBORK-TTE across a large spatial transect of site demographics and analyzed forest structure and composition metrics to understand current and future forest patterns along topographic, soil and climatic gradients at 10 m pixel resolution. Our results provide some insight into the spatial variability in the direction, rate, and magnitude of some shifts in forest structure at the cold edge of the boreal.

A mechanistic permafrost and soil organic layer module to improving long-term projections of boreal forest dynamics

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Boreal forests play a crucial role in storing terrestrial carbon, but climate change and increased fire are undermining their resilience. To make projections about the future of these forests, we need to consider the effects of permafrost and thick soil-surface organic layers (SOLs), which are important controls of boreal forest dynamics and carbon cycling. However, they are often excluded from vegetation models used to simulate future ecosystem trajectories. To address this challenge, we developed a computationally efficient permafrost and SOL module named the Permafrost and Organic LayEr module for Forest Models (POLE-FM). It simulates daily changes in permafrost depth, SOL accumulation, and their effects on boreal forest structure and functions at fine spatial (1 ha) and temporal (daily) resolutions. The module was coupled with an established forest landscape model and tested in interior Alaska at stand (1 ha) and landscape (61,000 ha) scale. The coupled model accurately simulated patterns of snow accumulation and active layer depth (portion of soil column that thaws throughout the year), permafrost presence, moss biomass, and SOL accumulation. Moreover, long-term trajectories of fire activity, tree species composition, and stand structure at the landscape scale aligned with expectations. In this contribution, we introduce the modelling concept and its implementation, and discuss its performance on model evaluations exercises, as well as long-term simulations. Modular and flexible representations of biophysical processes are essential for reducing uncertainty in future projections and supporting environmental decision-making. By incorporating permafrost and SOLs, process-based models can provide opportunities to address important questions about boreal forest resilience, biogeochemical cycling, and feedbacks to regional and global climate.

The dynamics of the Amazon forests - linking vegetation modelling and remote sensing

Andreas Huth[1]; Rico Fischer[2]; Nikolai Knapp[2]; Luise Fischer[2]; Friedrich Bohn[2]; Kostas Papathanassiou[3]; Edna Roedig[2]

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Precise descriptions of forest dynamics are essential for understanding ecosystem responses to climatic and anthropogenic changes. However, relations between forest productivity and forest structure are rarely investigated, in particular for tropical forests.

We developed an approach to simulate forest dynamics of around 410 billion individual trees within 7.8 Mio km² of Amazon rainforest (using the FORMIND forest model). We then integrated remote sensing observations from Lidar (Lidar profiles, forest height) in order to detect different forest states and structures (caused by small-scale to large-scale natural and anthropogenic disturbances). Under current conditions, we identified the Amazon rainforest as a carbon sink, gaining 0.56 Gt C per year. We also estimated other ecosystem functions like gross primary production (GPP) and woody aboveground net primary production (NPP), aboveground biomass, basal area and stem density.

We analysed the information content of Lidar profiles by comparing the obtained results with results based on reduced information. The inclusion of Lidar files in the framework improves estimates of forest attributes by 20 – 43% as compared to an approach using only forest height. The best results we obtained for NPP if full Lidar profiles have been used.

We conclude that forest structure has a substantial impact on productivity and biomass. The inclusion of forest modeling has a high potential to close a missing link between remote sensing measurements and the 3D structure of forests, and may thereby improve continent-wide estimates of biomass and productivity.

Creating virtual forest around the globe: Forest Factory 2.0 and analysing the state space of forests

Hans Henniger, Andreas Huth, Karin Frank, Friedrich J. Bohn

Forests, as one of the most important carbon sinks on earth, are more and more under stress by environmental changes. The dynamics of forests and consequently their functions in general, begin to change. We therefore present a recent model development, called "Forest Factory 2.0", which generates various virtual forest stands for different biomes on earth. This approach allows to generate forests using the architecture and processes of forest models (here we use individual based gap model FORMIND). Using Forest Factory 2.0, we generated 700,000 forest stands in seven different ecoregions. In contrast to the tradition of investigating the development of individual forest stands over time, we used the Forest Factory 2.0 as a tool to gain knowledge about forests by analyzing the state space of forests. We conducted a structural sensitivity analysis to compare the relationships between structural properties and Biomass, productivity, as well as Species evenness of forests. In this study we analyse the state space of forests in different biomes and demonstrate the potential of this approach for theoretical ecoloForests, as one of the most important carbon sinks on earth, are more and more under stress by environmental changes. The dynamics of forests and consequently their functions in general, begin to change. We therefore present a recent model development, called "Forest Factory 2.0", which generates various virtual forest stands for different biomes on earth. This approach allows to generate forests using the architecture and processes of forest models (here we use individual based gap model FORMIND). Using Forest Factory 2.0, we generated 700,000 forest stands in seven different ecoregions. In contrast to the tradition of investigating the development of individual forest stands over time, we used the Forest Factory 2.0 as a tool to gain knowledge about forests by analyzing the state space of forests. We conducted a structural sensitivity analysis to compare the relationships between structural properties and Biomass, productivity, as well as Species evenness of forests. In this study we analyse the state space of forests in different biomes and demonstrate the potential of this approach for theoretical ecology. gy.

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13. Model-based data integration as a basis for FAIR ecological modelling, monitoring, and synthesis

Integration of forest inventory data, forest growth modeling and 3D visualization: a case study from the Elster-Luppe floodplain forests in Leipzig.

Hans Dieter Kasperidus[1]; Timo Hartmann[1]; Christian Hecht[1]; Georg Rieland[1]; Rolf Engelmann[2]; Caroline Seele-Dilbat[3]; Michael Vieweg[1]; Peter Biber[4]; Mathias Scholz[1]

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In this presentation, we will demonstrate how initial forest inventory data from monitoring plots, located in the Elster-Luppe floodplain forest in Leipzig, Germany, can be used in a model-based comprehensive riparian forest ecosystem management approach. Within the framework of the scientific monitoring of the project "Lebendige Luppe", the assessment of the ecological status of floodplain forest stands and their future development is a central task. Therefore, around 60 study plots were established from 2013 to 2016 with the aim of recording the current state of the forest ecosystem as well as identifying and monitoring changes in ecological parameters and ecosystem services that can be expected from the revitalization measures after completion of the project’s implementation phase.

To get a better understanding of the current forest-based parameters and the forest dynamics, the single tree-based forest growth simulator SILVA will be used to test its suitability for modelling mixed stands with different age structures, which are typical in this location. In a next step, results of the growth forecasts will be further processed using the Sketchup 3D visualization tool because SILVA’s 3D-capabilities are limited. In multi-layered and mixed stands, it is necessary to consider the horizontal and vertical stand structure. This is especially important to determine if future forest stand development is a result of the project’s proposed changes in hydrodynamics or is caused by forest management or other environmental conditions. Thus, visualizing the respective tree species composition and their stratification within a plot allows a better understanding of the ecological conditions and indices from the field survey.

The state of the work shows that the combination and integration of forest growth modeling, 3D visualization, and analysis of key characteristics of forest landscapes is useful to gain better comprehension of the current ecological status of the Leipzig floodplain forest based on measured field data and other existing digital data.

Respect your Data! Efficient integrated modelling of species distributions

Bob O'Hara

NTNU Norwegian University of Science and Technology

With the massive expansion of FAIR data we have the opportunity to develop detailed models of the distributions and dynamics of of species and communities. To do this we need to understand how the data was collected, and use that information in the modelling process. I will outline the approach we are taking to developing the tools to do this.

We model each data set on its own terms, decomposing the sources of potential bias coming from how collection sites are chosen, the probabilities of observing each species, and the probability of mis-identification (including incorporating image analysis). These are integrated together, along with a single process model. These models are using fast inferential (Bayesian!) methods, using INLA. This lets us develop models with spatial effects at both the observation and process levels.

I will discuss the challenges and opportunities this presents, and how our model requirements influence the workflows to go from open data to ecological inference. The richness of the models means that good metadata will be important to improve the predictions of where species are, and where they will be in the future.

A reproducible workflow for the field of data integration

Philip Mostert; Wouter Koch; Anne Bruls; Ellen Martin; Ragnhild Bjørkås; Robert O'Hara

Norwegian University of Science and Technology

Integration of data is needed to address many of the current threats to biodiversity. There has been an exponential increase in quantity and type of biodiversity data in recent years, including presence-absence, counts, and presence-only citizen science data. Species Distribution Models (SDMs) are frequently used in ecology to predict current and future ranges of species, and are a common tool used when making conservation prioritisation decisions. Current SDM practice typically underutilizes the large amount of publicly available biodiversity data and does not often follow a set of standard best practices. Integrating data types with open-source tools and reproducible workflows saves time, increases collaboration opportunities, and increases the power of data inference in SDMs. Here, we address the discipline-wide call for open science and standards in SDMs by (1) proposing methods and (2) producing a reproducible workflow to integrate different available data types to increase the power of SDMs. Integration of datasets is done through a state-space point process formulation: which combines a process model, describing the actual distribution of the species, with data-specific observation models, describing the data collection process. We provide an R package and guidance on how to accommodate users' diverse needs and ecological questions with different data types available on the Global Biodiversity Information Facility (GBIF), the largest biodiversity data aggregator in the world. Finally, we provide a case study of the application of our proposed reproducible workflow by creating SDMs for vascular plants in Norway, integrating presence-only and presence-absence species occurrence data, climate, and habitat data.

A novel pipeline for assessing ecological economics models using an artificial landcover generator

Eyal Goldstein[1]; Kerstin Wiegand; Volker Von Gross; Carola Paul

[1] Goettingen University

Ecological economics is a rising field in the study of sustainable living, focusing on valuation of ecosystem services in our economy, and finding tradeoffs between ecosystem and human needs. Among the different focuses of ecological economics is the use of economics tools to support landcover decision making. One important recent development in the field of landcover decision making has been the use of modern portfolio theory in order to optimize land use for a set of needs. While this method is useful for balancing the tradeoffs between ecosystem services, biodiversity, and human welfare, one major drawback is that the results lack spatial representation, which limits the possibility for validation of many ecosystem benefits which depend on spatial processes. In order to overcome this limitation, we have developed a novel pipeline that gives spatial representation to theoretical portfolios and evaluated them using animal movement models. Based on previous research conducted in the Jambi region of Indonesia, we have taken portfolios that have been generated to optimize landcover for different types of needs (ecosystem service, income, etc.), and gave them spatial representation using the EFForTS-LGraf landcover generator. We then assessed these landcovers using the FunCon model, which simulates bird movement and home range accumulation in order to valuate different landscapes for the capability of supporting tropical bird communities. The entire pipeline allowed us to analyze the ecological implication of different portfolios and demonstrated how portfolios optimized for ecological indicators outperform those optimized for economic indicators under low to medium optimization constraints. This novel pipeline is a good example of how to test and validate theoretical land use decision making models, and can be further expanded by integrating other spatially explicit ecological processes.

Extended discussion on trends and perceived needs to foster modern workflows.

While focusing on our research topic, we often lose sight of the bigger picture, which is getting bigger by the day with an ever-increasing amount of openly available data. While more data helps us to answer more traditional (hypothesis-driven) questions better and more efficiently, it also allows us to derive new knowledge from analysing patterns without a straightforward question in mind, which is not, per se, unscientific. Current forms of A.I. are merely sophisticated machine learning algorithms, but the potential is vast. Already today, various problems arise from machine learning and other sophisticated knowledge-testing algorithms that challenge the knowledge or even the meaning we try to find as scientists. We need to discuss which tools to employ or develop in the future to safeguard and quantify the quality of our scientific findings and how to make those solutions appealing for less tech-savvy scientists to use as well.

14. Leveraging animal ecophysiology to enhance model predictability in a changing world

Explicit Consideration of Temperature Improves Predictions of Toxicokinetic–Toxicodynamic Models

Annika Mangold-Döring[1]; Anna Huang[1]; Egbert van Nes[2]; Andreas Focks[3]; Paul van den Brink[1]

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In the face of global climate change, where temperature fluctuations and the frequency of extreme weather events are increasing, it is needed to evaluate the impact of temperature on the ecological risk assessment of chemicals. Current state-of-the-art mechanistic effect models, such as toxicokinetic-toxicodynamic (TK TD) models, do not explicitly consider temperature as a modulating factor. This study implemented the effect of temperature in a widely used modeling framework, the General Unified Threshold model for Survival (GUTS). We tested the model using data from toxicokinetic and toxicity experiments with Gammarus pulex exposed to the insecticides imidacloprid and flupyradifurone. The experiments revealed increased TK rates with increasing temperature and increased toxicity under chronic exposures. Using the widely used Arrhenius equation, we could include the temperature influence into the modeling. By further testing of different model approaches, differences in the temperature scaling of TK and TD model parameters could be identified, urging further investigations of the underlying mechanisms. Finally, our results show that predictions of TK-TD models improve if we include the toxicity modulating effect of temperature explicitly.

Diving deep into temperature-dependent sex determination of loggerhead sea turtles, Caretta caretta: are mothers contributing more than we think?

Rebekka Allgayer[1]; James Gilbert[2]; Justin Travis[1]; Eugenie Yen[2]; Christophe Eizaguirre[2]

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Over 400 species of vertebrates exhibit temperature-dependent sex determination (TSD), thereby inextricably linking their predicted population dynamics with temperature in a changing world. The endangered loggerhead turtle, Caretta caretta, produces more females at higher temperatures and several instances of female-biased populations are already being observed. Many predictive models of sea turtle responses to climate change view the scope of TSD as being restricted to the incubation period of the clutch and calculate the probability of being male based on average temperature experienced by the egg. We present a model in which TSD extends to processes leading up to laying as well as development of the clutch: duration of internal incubation, inter-nesting interval of the females and therefore number of batches laid in a season, weighted daily development during the thermal sensitive period of egg incubation and metabolic heat production based on location within the nest and nest depth. Furthermore, recent evidence suggests that a female's role in mitigating the effect of temperature is not confined to behavioural aspects such as location and depth of nest. We have included two methods of accounting for maternal contribution by proxy, resulting in shifts in thermal response curves and indices of individual feminisation near the pivotal temperatures. Understanding the link between environmental change and demographic rates can inform immediate conservation actions such as nest relocations and headstart programs to balance survival rate with long-term effects on gender bias in the population.

Using Integrative Biophysical and Agent-Based Models to Predict Plethodontid Salamander Behavior

Kira McEntire

Queens University of Charlotte - Charlotte, NC

Many ectotherms use behavior to regulate their body temperature, altering metabolic rates and water loss rates which can influence their activity time, growth, and survival. Such behavioral plasticity can moderate the impact of changing habitats, including climate change. Physiology, described by biophysical models, can act as a mechanism describing behavior, particularly for amphibians. As poikilotherms with permeable skin, amphibian behavior is governed by the need to regulate body temperature and water loss. Agent-based models offer the ability to integrate behavioral mechanisms to describe patterns. Behavior and physiology interact with each other and integrating these model types allows us to explore this interaction and use both as mechanisms. Vegetation can moderate climate and create fine scale variation of microclimate. Plethodontid salamanders often climb on plants at night, which may allow salamanders to adjust their body temperature and associated metabolic and dehydration rates. Integrated biophysical and agent-based models (ABM) suggest extended potential activity time when salamanders climb if the air is cooler than the soil. This phenomenon often happens during cold fronts and temperature inversions on mountain sides. Field observations support this prediction as climbing behavior increases in response to cooler nighttime temperatures. Salamanders do climb plants under other weather conditions, suggesting either imperfect thermoregulation or additional mechanisms at play. Incorporation of energetics into the model support the idea that juveniles and small species are more sensitive to fine-scale climatic differences and often have lower energy reserves than adults. If juveniles prioritize growth over activity time searching for mates, then they may also climb to seek optimal metabolic temperatures. Preliminary models are inconclusive, likely because Plethodontid salamanders have very low metabolic rates. This mechanism may become more important in extreme climates or during certain times of the year. The flexibility of ABMs allows for a shift in priorities for certain behaviors and future models will explore the possibility of shifting priorities in response to season, size, and food availability. Understanding the mechanisms driving this behavior may help us understand how salamanders may be using behavior to moderate the impact of climate variation.

Predicting effects of climate change on aquatic ectotherms using Dynamic Energy Budgets: a (cray)fish case study (or two)

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Climate change-induced temperature rise has a direct effect on all aquatic ectotherms exposed to temperature variations. Often, an increase in temperature can be combined with a reduced food availability resulting from a shift in food webs. We present here two case studies where the effects of such changes in aquatic environments (an increase in temperature and a decrease in food availability) were explored for two distinctly different groups of organisms with a correspondingly different research focus: (i) marine fish relevant in the context of aquaculture and fisheries, and (ii) freshwater crayfish in the context of biodiversity loss. Bridging the gap between the two groups was possible by applying the common principles of physiological energetics, framed as the Dynamic Energy Budget (DEB) theory: DEB models capture dependence of metabolism, and therefore ontogeny, on environmental conditions.

In the first case study, we use DEB models calibrated for true soles (Solea spp). Temperature– in combination with food availability -will affect the timing of spawning, as well as metabolic rates (growth and development, including metamorphosis) and life history traits of freshly spawned sole larvae and later juveniles. This will affect recruitment —the process of small, young fish transitioning to an older, larger life stage --which will, ultimately, affect sole populations. Determining the combined effect of two expected outcomes of climate change on early-life history traits of fish larvae is valuable for anticipating and adjusting fishing pressure and policy, especially for commercial species like soles.

In the second case study, we develop DEB models for two native and two invasive crayfish species, and investigate key elements of ontogeny and metabolism affecting interspecific competition. Crayfish species native to Europe are facing decline and are increasingly endangered by the changing climate and invasions of non-native crayfish. The success of these invasions largely depends on differences in ontogeny between the native species and the invaders and how changes in the environment will affect the ontogeny. We use the DEB models to predict individual growth and reproduction in current and new conditions that are expected to arise from climate change.

Key words: process models; physiological energetics; life history traits; ontogeny; Decapoda; Solea

Energetic consequences of resource fragmentation in a simulated mammal community: Linking movement, metabolism and coexistence

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Biodiversity is threatened by global changes in land-use. Animals must adapt to these changing conditions, ultimately affecting coexistence patterns. Understanding the impact of environmental change on entire communities is key to predicting and conserving biodiversity in the future. However, uncovering the complex mechanisms behind community coexistence remains a challenge. To address this problem, we first attempt to shed light on the effect of environmental change on single individuals by tracking their physiology and metabolism. We use a novel individual-based metabolic modeling approach that also allows us to scale up from individuals to communities. The model simulates the energy dynamics and home-range behavior of each individual in a small mammal community of ten ecologically-similar species. All individuals forage in the landscape to ingest energy, hence, efficiency depends on landscape features and competition. The ingested energy is then allocated to basal maintenance costs as well as growth, locomotion, reproduction, and storage. If individuals of several species are able to balance incoming and outgoing energy under fodder competition they will coexist, but single species may also outcompete others under certain conditions. After thoroughly testing and validating the model using real-world patterns, such as allometric relationships in field metabolic rates and home-range size, we applied it to scenarios of landscape fragmentation and analyzed coexistence. We find a maximum number of coexisting species with medium habitat fragmentation. In fragmented landscapes, individuals must move more and spend more energy on locomotion to locate food resources. This is not necessarily problematic if the species do not compete with each other - it may even increase population size. However, species often share the same food sources, which are usually limited in quantity and distribution, leading to interspecific competition. In this case, and given that species differ in their movement capacity and energetic costs, fragmentation strongly influences the abundance of species in the community. At medium fragmentation, energy income and energetic costs from movement are best balanced among a large number of competing species. We conclude that such energy dynamics are important to understand coexistence under competition, but also vice versa interspecific competition strongly influences energetics and ultimately fragmentation effects. The consequences for biodiversity should be considered in nature conservation, as landscapes can be protected and designed to maximize coexistence.

Species distribution models are improved by incorporating thermal physiology under current and future climate change

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Temperature is a critical limiter of species' geographic ranges because increased thermal stress under abnormally warm or cool conditions can reduce the amount of time animals may allocate for growth, reproduction, and food acquisition. Thus, rising temperatures are increasingly disruptive to wildlife populations, resulting in declines of global biodiversity and losses of ecosystem functioning and stability. Forecasting and mitigating the biological impacts of climate change requires an understanding of how species distributions are shaped by the upper and lower bounds of their thermal tolerances. However, traditional species distribution modeling (SDM) and niche modeling approaches fail to account for lab-derived physiological data, instead relying on correlational relationships between species occurrence points and meso-scale climate data. Here, we estimate thermal limits of species individuals from laboratory-derived thermal performance measurements and define spatially varying 'offset' terms for use in an SDM. Next, we estimate an SDM as a Poisson point process model with spatially varying latent field and physiological offset term. We find that species-level model predictions improve when accounting for thermal physiological limits and that thermal physiology shrinks the species range predictions especially when projecting the species range in future climate conditions compared to models not accounting for the thermal physiology. Arguably, the physiological offsets increase ecological realism of the range predictions and provide a generalizable tool to include physiological limits of individuals into large scale SDMs. With one of six species threatened by increasingly warming temperatures, it is crucial to bridge physiology and macroecology to understand how thermal physiology limits the geographic distributions of species.

Large herbivores in a dynamic global vegetation model: from physiology to carrying capacity

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Dynamic global vegetation models (DGVMs) are able to scale up from plant-physiological processes to local, regional, or global vegetation dynamics. However, DGVMs typically neglect the impact of terrestrial large herbivores or simplify it with a prescribed feeding rate. Why not integrate large herbivores into DGVMs on a level of mechanistic detail similar to plants?

While wild large herbivores do play a role in shaping some ecosystems today, it was clearly greater in the past. Some authors hypothesized that now-extinct Pleistocene megafauna indeed had a transformative impact on the scale of biomes: by creating and maintaining the glacial “mammoth steppe.” But were large herbivores actually numerous enough for such large-scale ecosystem engineering? Could simulation experiments help constrain megafauna carrying capacity of the mammoth steppe?

We expanded a DGVM (i.e., LPJ-GUESS) with a Modular Megafauna Model (MMM) that scales up from physiological processes (feeding, metabolism, reproduction) to population dynamics. With extinct species, parametrization obviously bears great uncertainties. Moreover, the early stage of model development warrants careful evaluation of model concepts. Therefore, I will present results of a global sensitivity/uncertainty analysis. The simulations will also demonstrate the plausible range of megafauna densities in glacial environments.

MMM is open source and follows best software development practices. As a library, it is reusable and can be coupled with other dynamic vegetation models. MMM’s modular nature promotes replacing and expanding model building blocks. This structural flexibility invites future applications beyond paleo-ecology, such as evaluating potentials for megafaunal rewilding or anthropogenic threats to extant wild herbivores.

Combining bioenergetics and movement models to improve understanding of the population consequences of disturbance

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SMRU Consulting

We used individual-based and dynamic bioenergetics models to investigate how movement ecology and the duration of behavioural responses to anthropogenic disturbance might affect the dynamics of a marine mammal population, taking account of uncertainty in the model parameters and heterogeneity in density and individual behaviour. We considered three marine mammal species (harbour porpoise, grey seal and harbour seal) with contrasting life-history traits (capital vs income breeders) and movement behaviour (resident vs highly-mobile) and modelled the potential effects of a series of disturbance events on vital rates that might realistically occur during the construction of an offshore windfarm and that resulted in a temporary decrease in energy assimilation. Offspring mortality was the vital rate that was most affected by these disturbances, particularly when they occurred in the post-weaning period. Predicted effects varied among individuals in a way that depended on their movement behaviour and the likely density of animals in the region of the modelled construction activity. The magnitude of these effects also depended critically on the assumed duration of the reduction in energy assimilation, but no direct estimates of this variable are currently available. Past population consequence of disturbance studies (PCoD) rarely explicitly consider the effects of individual variability in exposure frequency, different disrupted energy intake and/or differences in life histories between species, which may over- or underestimate the effect of disturbance depending on the species and modelled effect. Out approach can show how to fill in this gap.

Bioenergetic modelling of a marine top predator's responses to changes in prey structure

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Determining how animals allocate their energy, and how external factors influence this allocation, is crucial to understand species' life history requirements and response to disturbance. This response is driven in part by individuals' energy balance, which is itself driven by prey characteristics, foraging behavior and the amount of energy required for essential functions. We developed a bioenergetic model to estimate the minimum foraging success rate of a marine top predator, the sperm whale (Physeter macrocephalus), based on their theoretical energetic requirements using foraging data and prey characteristics from animal-borne tags and stomach contents, respectively. We then used this model to simulate two prey structure change scenarios, 1) lower caloric content, (e.g., decreased prey size), and 2) decreased energy availability (e.g., prey distribution). We estimate that sperm whales need a minimum of ~25% foraging success rate to meet their energetic requirements, and that energy intake is more sensitive to changes in caloric content than energy availability. To estimate sperm whale vulnerability to changes in prey structure, we evaluated the level of compensation that would be required for them to continue to meet bioenergetic demands. Considering a minimum foraging success of 25%, whales would need to increase their energy intake by 18% (2-32%) and 45% (21-62%) to compensate for a decrease of 15% and 30% in caloric content, respectively. For a decrease of 30% and 50% in energy availability, whales would need to increase energy intake by 14% (3-28%) and 23% (5-36%) to meet their energetic, respectively. Our model demonstrates how foraging and prey characteristics data can be used to estimate the impact of changing prey structure in upper trophic level predator energetics, which consequently can help inform top-down effects on marine ecosystems. Moreover, we showed the importance of considering different foraging success rates into bioenergetics models, as this parameter can have decisive implications on the estimates of energy acquired by individuals and consequently affect the conclusions that can be drawn about marine top predator's vulnerability to possible environmental fluctuations.

Estimating Energy Balance of Adélie Penguins Using Depth Data and Machine Learning

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In Antarctica, sea ice plays a crucial role in supporting biodiversity across trophic levels. Sea-ice obligate predators, which depend on sea ice, offer a powerful tool for monitoring sea-ice dependent ecosystems. These predators mostly breed on land, making them easily accessible for study, and depend heavily on the quality, distribution, and quantity of marine resources.

Since the 1990s, bio-logging technologies have enabled researchers to access previously unknown aspects of marine predator ecology, including the estimation of energy expenditure, a key parameter in spatial ecology. The quantity of data generated by these devices, coupled with the advances in analytical tools like machine learning or agent-based modelling, provide greater insights into why and how individuals move in response to a changing environment.

We analyzed at-sea behaviour of the most abundant marine predator species in Antarctica, the Adélie penguin (Pygoscelis adeliae) during a breeding season where accelerometry, depth and doubly labelled water data were collected. Using random forest algorithms, we were able to better estimate at-sea behaviour of Adélie penguins solely from depth temporal series data compared to previous methods by transferring accelerometry-based behavioural classifiction information. Combining historical TDR data and long-term monitoring, we aim to better estimate how sea-ice variations affect energy balance (energy intake vs. expense) of Adélie penguins.

15. Modelling variation and evolution of traits within individuals, populations and communities

How are evolving populations responding to perturbations?

Michael Raatz

Max Planck Institute for Evolutionary Biology

Global change exerts multiple stressors on endangered populations. Such populations can adapt to harsh environments by evolving thir fitness-determining traits in an attempt of evolutionary rescue, creating an adaptive trajectory in trait-space. Perturbations during this adaptation process may affect these trajectories, but it is underexplored how and with which consequences. In this contribution, I will use a stochastic modelling approach to first outline the unperturbed adaptation trajectories in a population that is able to evolve in its intrinsic birth and death rates. Then, I will explore how perturbations can alter these trajectories. Specifically, I will compare the effect of different types of perturbations that either reduce population sizes or temporally reduce fitness by transiently altering the traits. Finally, I will discuss the fitness gradients that prescribe the adaptation and show that the geometry of these fitness gradients can help to understand the effect of perturbations. My research shows that tracking the adaptive response of populations and mediating perturbations that might hinder adaptation and increase the extinction risk are essential goals in conservation aims for endangered species.

Using an individual-based model to identify local drivers of post-colonization population demogenetics within ephemeral patches

Tiago Crispim-Mendes Student[1]; Clara Mendes Ferreira[2]; Joana Paupério[3]; João Paulo Silva[3]; Sérgio Godinho[4]; Paulo Célio Alves[3]; António Mira[1]; Xavier Lambin[5]; Pedro Beja[3]; Ricardo Pita[1]

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Species responses to habitat disturbance can be variable and diverse across space and time. Yet, our understanding of how those responses impacting species persistence (e.g. demographic, genetic) in disturbed environments is still limited. This is particularly true for metapopulations consisting of small local populations inhabiting patchy ephemeral habitats. Assessing how patch attributes (e.g. size, quality, connectivity) affect post-colonization demogenetics of local populations in short-lived patches is therefore critical to improve the conservation of metapopulations in dynamic patch networks.

In this study, we developed and implemented an individual-based model to assess the impact of patch size, habitat quality, and connectivity on local populations of Cabrera voles (Microtus cabrerae), a near-threatened species endemic to the Iberian Peninsula, which is often found in highly dynamic agricultural landscapes.

Using available knowledge of species' life-history traits and genetic diversity in natural populations, we employed a pattern-oriented modelling approach to replicate the effects of patch characteristics on the post-colonization demogenetics of local populations, namely on recruitment, migration rates, relatedness, and inbreeding, within habitat patches with a lifespan of up to two years. Global sensitivity analyses were implemented to distinguish and quantify the main and interaction effects among patch attributes over time since colonization, as well as to estimate the strength of linear associations between demogenetic responses and each patch attribute.

Our results showed that patch size, quality, and connectivity had varying impacts on the demogenetic parameters analysed. Shortly after colonization, patch size had the greatest influence on voles' demogenetics, but this influence gradually diminished, as the interaction effect among patch attributes became more important for all responses analysed. The magnitude and direction of the effects of patch attributes on voles' post-colonization migration and local recruitment rates also changed along the simulation time, overall suggesting that large, high-quality and well-connected patches with a lifespan > 1 year should critically contribute to metapopulation persistence in dynamic landscapes.

In conclusion, models like the one we developed can provide a synthesis of a broad range of knowledge on species demogenetic responses to environmental change. Specifically, by taking into account the complex relationships among patch size, quality, and connectivity, conservation efforts at the local scale can be better targeted to enhance metapopulation persistence in disturbed environments.

The relative effects of climate and habitat on changes of moth communities in Finland: insight from site specificities and species traits

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Global changes are widely affecting species and communities across multiple taxa and at different scales. Despite extensive studies on the subject, evaluating the impact of climate and habitat changes is still complex and the interplay between the two is not well understood. Life history traits, species distribution, and habitat characteristics are key components to assess how species can overcome environmental changes as they are interconnected to species' ability to disperse. Using the Finnish moth long-term monitoring dataset, we evaluated how both climatic and habitat information drive moth communities' responses. We used the Hmsc framework (Ovaskainen & Abrego, 2020) and applied recently developed conditional variance partitioning (Schulz et al., 2021) to evaluate the relative importance and uncertainty of environmental drivers across sampling sites and species traits. From predicted responses at the Finland scale, we linked moth diversity variability to changes in climatic conditions and landscape structure. We showed that site characteristics (habitat disturbance), as well as species-host plant affinities explain both moth occurrences and community diversity current distribution. We encourage studies to inform diversity trends and its variability at multiple scales and to look through the scopes of local conditions as well as accounting for species life history characteristics.

Effects of cyclones: influence on the fish community in a tropical estuary

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Uncertainties of climate changes have been leading to frequent catastrophic events all over globe since last decade. The increasing frequency of such extreme events has the potential to alter the fish assemblage pattern in their natural habitat. This study aims to investigate the consequences of extreme cyclonic weathers in Hooghly-Matla estuary in Indian Sunderbans. Between 2017 - 2022, continuous sampling in the study area has been carried out to assess the undercurrents of fish assemblage pattern. Hydrological and abiotic factors data were collected and fish trait data were considered for analyses the interrelationship between fish assemblage and climatic events. Fish population changes in respect to functional traits and diversity. There is steady decline of few native species over the years. This study reveals the ecological effects of tropical cyclone and illustrates its impact associated with abiotic drivers on fish community. Here, we applied a functional approach to explore how environmental factors affect the functional diversities and traits of fish communities in the estuary. A careful assessment of fish community assemblage fluctuation of this area throughout the year revealed that such periodic cyclones have serious consequences on the assemblage of some fish groups (Latidae, Scatophagidae, Terapontidae), whereas few fish groups was no such significant effect (Bagridae, mugiladae). Statistical analysis revealed strong correlation between assemblage composition and abiotic factors. Shifts in the patterns of fish community composition are noted to be closely associated with fluctuation in salinity, total dissolved solids (TDS) and nitrate level that possibly influence the habitat quality.

Plankton community structure, biodiversity, and related ecological services.

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A novel size-structure resolving plankton model is used to explore relationships among nutrient abundance, plankton biodiversity and related ecological services. The model, based on assumptions that fundamental plankton physiological traits scale with organism size and grazing by zooplankton is structured by an optimal predator-prey length ratio, about 100 size-classes are defined for phytoplankton and a similar number matching size-classes for zooplankton. The model is able to mimic overall pattern in plankton size distribution and diversity and provide a coherent reproduction and interpretation of bottom-up and top-down interactions. Results from 10 years of integration show an emergent pattern of plankton size-structure consistent with theoretical and model prediction presented in literatures and reliable estimates of biogeochemical fluxes and Carbon export, especially when embedded in a one-dimensional (water column) framework, with explicit turbulent diffusion mechanism The inclusion of light affinity as an extra trait gives additional realism to the 1D phytoplankton biomass depth profile, and the presence of depth-dependence in phytoplankton growth rate triggers important consequences for size-structure depth distribution.

ECEM 2023 - European Conference on Ecological Modelling
Sept. 4-8, 2023, Leipzig, Germany

16. Modelling climate-biosphere feedbacks

Conserving biodiversity under global change: towards a universal biodiversity projection platform

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Biodiversity and ecosystems are degrading worldwide at an alarming rate. Addressing this crisis and preventing further losses requires accurate predictions about which species and ecosystems are most at risk to ensure efficient use of limited conservation and management resources. Yet, our understanding and predictive capacity of ongoing biodiversity dynamics remains limited. Part of the problem could be the sheer complexity of nature and the human-mediated impacts, but also limited data and limited availability of flexible and easily modified mechanistic models. We reviewed existing biodiversity modelling frameworks and their applications for decision support, and found problematic gaps. Current applications are heavily biased towards correlative models and towards the population and species level. Existing mechanistic models cannot not easily be reconfigured for other species or systems, omit key biological processes, and cannot accommodate feedbacks with Earth system dynamics. To fill these gaps, we envision an adaptable, accessible, and universal biodiversity modelling platform that is able to forecast essential biodiversity variables, from the gene to the ecosystem level. Wider usage of mechanistic biodiversity models should be further facilitated by a toolbox with easier-to-use methods for data integration and model validation, and best practice guidelines. To address these needs and coordinate efforts, a new working group on biodiversity modelling and knowledge-to-action hub are being launched within the Group on Earth Observations Biodiversity Observation Network (GEO BON). In the presentation, we will give a brief summary of current biodiversity modelling approaches and prevailing challenges, and outline our vision for more integrated modelling.

Acclimation of plant nutrient-reuse strategies to global change in a next generation ecosystem model

Gabriela Sophia

Nutrient resorption from senescing leaves is a critical process of plant nutrient cycling that can significantly affect plant nutrient status and growth, making it essential for land surface models in order to predict long-term primary productivity. Most models assume leaf resorption to be a fixed value of 50% for N and P partially because we lack the knowledge of what drives this process, being unknown its implications when simulating nutrient cycling. Based on our own analysis of global patterns of nutrient resorption from trait data, we developed a dynamic scheme of nutrient resorption for nitrogen and phosphorus driven by leaf structure, longevity and environmental factors, implemented in the QUINCY model. We present the implications of this novel scheme for ecosystem functioning and show that we can better predict plant and soil nutrient dynamics at steady state and crucially, under altered climate and CO_2 conditions. Plant internal nutrient cycling has cascading implications for ecosystem nutrient pools and fluxes, being an essential process in ecosystem models, that allows us to improve our predictions of the future and furthers our understanding of nutrient cycling processes.

Modelling the future distribution and biodiversity of European fen habitats under global change

Patrícia Singh[1]; Borja Jiménez-Alfaro[2]; Liene Auniņa[3]; Petra Hájková[1]; Tatiana Ivchenko[4]; Florian Jansen[5]; Tiina Kolari[6]; Paweł Pawlikowski; Tomáš Peterka[1]; Alessandro Petraglia[7]; Teemu Tahvanainen[6]; Michal Hájek[1]

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Along with the historical decline of fens due to anthropogenic impact, climate change is expected to jeopardise fen biodiversity by reducing their geographic extent and altering species composition. Yet, climate change impacts on fen distribution and biodiversity in the future remain unclear. We used 27,555 vegetation plots representing eight fen habitat types widely distributed in Europe to compute Ecosystem Distributional Models. For each fen habitat type, we projected their future potential occupancy area and range shift and evaluated the influence of different climate scenarios and groundwater pH on distribution and biodiversity. Our findings could be helpful for the nature protection authorities across Europe to assess conservational and restoration measures to mitigate potential future biodiversity loss in European fen habitats.

Assessing human pressure on biomass production and the corresponding risk of ecosystem degradation in the dynamic global vegetation model LPJmL

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Biosphere integrity is a key planetary health indicator often missing in model scenario analyses, not least because its complexity makes it hard to compute. We have developed and applied two complementary indicators that assess human pressure on biomass production (based on Human Appropriation of NPP) and the corresponding risk of ecosystem degradation (based on a modified ecosystem change metric Gamma). They are computed from simulations with the dynamic global vegetation model LPJmL and enable mapping of current spatial and temporal patterns of these anthropogenic biosphere modifications and appropriations. Preliminary results indicate that large regions globally show biomass modification and extraction of over 25% of the preindustrial potential natural NPP. These interferences, together with climate change, lead to drastic alterations in key ecosystem variables, suggesting a high risk for ecosystem degradation. We plan to apply our indicators also to future scenario runs based on ISIMIP3b inputs when those are fully released. We expect changes in biosphere integrity especially in regions with increasing land use intensity, deforestation, management, and climate impacts.

PS.: Even though the title of the conference fits absolutely to what we do, I couldn’t find a session that is a perfect fit. Please feel free to shift me to an in your eyes more appropriate session.

The effect of plant trait diversity on the coupled vegetation-climate system

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In ecology, high plant-functional diversity is associated with strong ecosystem resilience and stability. Growing evidence from field observations has shown that increasing functional diversity enhances ecosystem functioning and resistance. Until now, plant ecology studies have focused on the passive response of global ecosystems to climatic changes while the impacts of plant-functional diversity on climate including its feedback are rarely addressed. Notably, state-of-the-art climate models routinely used to study climate-vegetation feedbacks are often criticized for oversimplifying global vegetation processes. The classic plant functional type (PFT) approach used in these models covers only a restricted range of present-day plant features. Such a deficit may result in an under/over-estimate of the effects of potential plant adaptation on climate. Investigating changes in vegetation-climate interaction in a future non-analog climate is thereby limited.

Based on a process-based plant functioning trade-off scheme developed by Kleidon and Mooney (2000), we have set up the new vegetation model JeDi-BACH into the land component of the ICON-Earth System Model (ICON-ESM). The advantage of this new model is to obtain plant distribution as a result of environmental filtering. Plants are represented based on several fundamental functional trade-offs that link plant functions to abiotic and biotic attributes. In such a way, plants dynamically adjust to a changing environment and meanwhile modify climate. Here, we present a series of sensitivity studies investigating the effect of plant trait diversity on the coupled vegetation-climate system in global simulations with prescribed sea surface temperatures and sea ice concentration. We found that with increasing diversity the global vegetation-climate interactions converge and operate towards a state with high water-cycling. This behaviour can be understood by noting that high-diversity ecosystems naturally encompass more resource-optimal strategies and thus tend to exploit environmental resources (e.g., water) more effectively. High-diversity ecosystems thus lead by active regulation to a more robust climate and ecosystem functioning than low-diversity ecosystems. As a result, the global climate tends to be cooler and wetter with increasing diversity. Our results demonstrate the importance of "biodiversity-climate feedbacks" and highlight the role of plant functional diversity in shaping a robust climate.

Kleidon, A. and Mooney, H. A.: A global distribution of biodiversity inferred from climatic constraints: Results from a process-based modelling study, Glob. Chang. Biol., 6(5), 507–523, doi:10.1046/j.1365-2486.2000.00332.x, 2000.

17. Sustaining insect pollination in a changing world using mechanistic simulation

SyrFitSources: An agent-based model for hoverflies in agricultural landscapes

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Hoverflies (Syrphidae) as well as other insects have declined strongly in agricultural landscapes during recent decades. One of the assumed driving factors is land-use change which can affect insect population at multiple spatial and temporals scales. Like bees, the imagines of the syrphid Episyrphus balteatus are important pollinators, while their larvae are known as voracious hunters of aphids, so that they are also important for pest control. To investigate the impacts of land use and land-use change on E. balteatus, we developed a spatially explicit agent-based model (ABM), called SyrFitSources, simulating the effect of the configuration and composition of the food sources for imagines and larvae in agricultural landscapes throughout the year.

In the model, we simplified the landscapes’ habitat patches to spatial agents, and connected them through a habitat network, retaining the principal composition and configuration. This enabled faster computation of E. balteatus’ lifecycle in landscapes with extents of a few square kilometers and for a timespan of one up to many years. We simulated the amount and phenology of floral resources for each habitat type using the FloRes database. For each plant species, the aphid population dynamics was implemented as a logistic difference equation. The growth rate of the aphid colonies is dependent on mean daily air temperature and phenology of the infested plant. For the syrphid imagines we implemented the energy balance and their foraging behaviour considering effects of daily air temperature on the activity probability per day and increasing mortality during aging. The imagines were the only agents able to move between patches. The voracity of larvae was modelled depending on the density of aphid colonies, air temperature and the larvae’s instar. Finally, the mortality of the larvae was dependent on the daily uptake of aphids. The mortality of eggs and pupae was a fixed ratio that was subtracted at the end of each stage.

We validated SyrFitSources with a time series of E. balteatus’ activity gathered with three Malaise traps set up in each of 13 landscapes located in rural sites of Lower Franconia and Lower Bavaria, Germany, in summer 2011. In Lower Bavaria, population densities were higher than in Lower Franconia, and SyrFitSources was able to simulate this difference, which seems to be driven mainly by aphid occurrence and abundance. The model can be used to assess effects of land-use change and of agri-environmental schemes on aphidophagous syrphids.

March to April 'hungry gap' poses an existential threat to bumblebees in a Bumble-BEEHAVE simulation study

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A common management intervention to support declining wild pollinators is 'pollinator planting'. However, despite years of inclusion in conservation initiatives, global pollinator declines continue. In order to improve our understanding of resource availability on bumblebee populations, we apply the agent-based model Bumble-BEEHAVE with two example species, Bombus terrestris and B. pascuorum.

We explore when during the year bumblebee resource demand is highest in the model, and how that relates to seasonal changes in colony composition (numbers of eggs, larvae, pupae, and adults). Imposing a two-week resource gap across the year allows us to determine when forage scarcity is most detrimental. We find that a gap in forage availability during March-April drives a 50-87% drop in queen production for the following year. This is driven by the resource demands of larvae in the colony rather than the number of adult bees and takes place before the peak flight period.

To see whether our findings have real-life implications, we look at the seasonal nectar and pollen flow in example habitats in the UK and find a previously under-appreciated 'hungry gap' for bumblebees during the critical period. We conclude our presentation with suggestions, how to close this identified gap by enhancing early-spring-blooming herbaceous species or trees. In the model, this had significant, positive, long-term effects on colony survival probability and queen production.

How do honeybees respond to landscape structure and other stressors?

Jürgen Groeneveld[1]; Anna Wendt[2]; Jasmin Krebs[3]; Volker Grimm[4]

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Honey bees (Apis mellifera) are exposed to multiple stressors such as pesticides, forage gaps, diseases and management failures. It is therefore a long-standing aim to develop a robust understanding how stressors impact honey bee vitality. However, experimental and monitoring studies are limited in their ability to assess these relationships between stressors and honey bee vitality systematically. Therefore, we use the established honey bee simulation model BEEHAVE in combination with land use classification maps to contribute to the assessment of honey bee vitality in Germany. We have developed script-based workflows in R to create the required input files, to run the simulation experiments and to finally analyse and visualize the simulation results. Our results are in line with previous findings that temporal foraging gaps and inappropriate bee keeping management are severe threads to honey bees and that landscape elements (e.g. semi natural grasslands) that provide resources in absence of mass flowering crops are essential for honey bee population performance. This study is an important step towards a model-based, automatic, easy and free to apply assessment of honey bee vitality.

A Comprehensive Agent-Based Model for Bumblebees with Temperature Feedback

Jordan Chetcuti; Christopher John Topping

Aarhus University

We present a comprehensive agent-based model for bumblebees, designed to simulate colony growth and behaviour in response to environmental factors. Our Animal, Landscape and Man Simulation System (ALMaSS) model, includes temperature feedback and individual energy budgets to capture the full life cycle of bumblebees, from egg to adult. The queen, workers, and gynes in our model incubate juvenile clusters based on their availability and temperature, while the colony's temperature as a whole is regulated by the number of adults in the colony and their fanning behaviour.

Using an individual energy budget that includes fat storage, our model controls the activity, and ability of adults to warm themselves above the background temperature. Bumblebees in our model obtain energy from nectar and pollen, either supplied to the colony daily or foraged within the ALMaSS landscape. Adults then warm the colony and can incubate clusters of juveniles that grow and develop into adults, stabilising temperature and promoting further growth.

Our model is unique in that it includes temperature feedback, which influences the development of eggs, larvae, pupae, and callow adults. We show how colony growth can be altered by different background temperatures and can replicate laboratory studies of temperature on bumblebees. Limiting the food supply reduces the ability of workers to warm the colony, which has a knock-on effect beyond reduced food for growth alone. This is particularly relevant for understanding the impacts of pesticide exposure on bee populations, as reduced foraging ability and warming caused by pesticide exposure could have significant effects on colony growth and survival.

Our Bombus agent-based model offers a powerful tool for investigating the complex interactions between bumblebees and their environment. By incorporating temperature feedback and individual energy budgets, our model provides a detailed and nuanced understanding of the factors that influence colony growth and behaviour. We believe that our model has important practical applications for understanding and mitigating the effects of environmental stressors, including pesticide exposure, on bumblebee populations.

SolBeePop: a trait-based population model of solitary bees in agricultural landscapes

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Solitary bees comprise a large diversity of species, providing pollination services to crops as well as wild plant communities. They are important to consider in the context of conservation of insect diversity, particularly in agricultural landscapes, and ecological risk assessments of pesticides. At the same time, their range of ecological traits, including diverse nesting strategies, phenology, reproductive rates and flower preferences, need to be accounted for assessing potential impacts of stressors to populations. We are presenting a population model for solitary bees in agricultural landscapes, SolBeePop. The model was developed to simulate a variety of species by using species-specific ecological traits as model parameterizations. The model can be used to simulate managed as well as wild populations. We analyzed and applied the model using example species with different traits. Osmia bicornis and Megachile rotundata use existing above-ground cavities for nesting, Nomia melanderi and Eucera (Peponapis) pruinosa are examples for soil-nesting species. In addition, the species differ in their phenology and floral preferences which govern their interactions with the landscape. Input time series to the model are used to capture temporal and spatial variability in foraging and floral resource availability in the environment. Model evaluations conducted include a comprehensive analysis of parameter uncertainty with two of the species as well as model calibration and validation to available semi-field study data with O. bicornis. The interaction between species' traits and population dynamics under density dependence were compared across the four species. SolBeePop is intended as tool for the assessment of population-level outcomes of stressors, including pesticides. Thereby, applying environmental scenarios informed by landscape- and species-specific data allows the simulation of populations of solitary bee species in realistic landscape contexts.

ECEM 2023 - European Conference on Ecological Modelling
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20. Environmental modelling for policy support – how to build bridges between two worlds

Where can ecosystem services be improved in agricultural landscapes? – An opportunity-map approach for Northwest-Saxony, Germany

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The management of agricultural land can significantly influence the provisioning of ecosystem services (ES) and thus also the multifunctionality of agricultural landscapes. In order to facilitate the transformation of agricultural systems towards more multifunctionality and to strengthen the landscape's resilience towards climate change impacts, the influence of agricultural management practices on ES needs to be better understood. In addition, it is often not clear where measures for changes or adjustments in management should ideally be applied. Various results of modelling and measuring exercises exist that have been used to map ecosystem services and identify areas of improvement – opportunity maps are one example. However, most studies mainly examined the potential of improvement for urban ES or for land cover in general but not specifically for agricultural landscapes. Furthermore, the results are oftentimes based on mapping incongruities between supply and demand for ES though the demand for some ES is often difficult to quantify or allocate spatially. Finally, these approaches lack the consideration of agricultural management impacts on ES provisioning. Using the example of the intensively used agricultural landscape of Northwest-Saxony, we therefore present an opportunity-map approach that uses proxies for ES, which are related to and affected by agricultural management. This way, areas can be identified that have a high opportunity to improve ecosystem services provisioning by altering agricultural management. The approach uses so-called opportunity attributes, which individually or jointly influence the considered ES (e.g., water quality, carbon sequestration and protection from soil erosion and drought). In the case of carbon sequestration, attributes could be, for example, the soil organic carbon level and soil texture, the possibility of land use change (e.g., cropland to forest), applicability of certain management practices that promote carbon storage (e.g., appropriate fertilization practices, crop rotations, agroforestry/landscape elements). The selected attributes are scored using a grading system for each individual land cell, which are then summed and, over all land cells, result in a heat map of the respective ES opportunity (no/low to high potential). The values of the attributes are based on geospatial data but also on stakeholder expertise, i.a. for their validation. The opportunity maps can be used to identify (spatial) trade-offs and synergies between individual ES and as a basis for further modelling work. Further, the methodology can be applied to other agricultural landscapes. This makes it a useful method to communicate areas of potential improvement of ES and multifunctionality to decision makers.

A comparison of agri-environment measures’ contributions to habitat suitability for farmland birds across regions, species, and model algorithms

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Agri-environment measures (AEM) are the main tools of the Common Agricultural Policy to counteract the dramatic decline of farmland biodiversity in Europe. However, their effectiveness seems to vary depending on the regional environmental and land-use context and on the target species. Using ensemble species distribution models combining five algorithms, we investigated the effects of five groups of AEM (buffer areas, cover crops, extensive grassland management, fallow land and organic farming) on the occurrences of region-specific sets of farmland bird species in three study regions in the Czech Republic, Germany and Spain. The models were projected to two land-use scenario: the current AEM adoption scenario, and a “no AEM” scenario in which AEM are entirely removed. For both scenarios, we calculated a relative species richness indicator to better synthesize the modelled effects of AEM across the whole farmland bird community. Model uncertainty was estimated for each SDM by calculating the standard deviation across model algorithms. We also assessed how the use of different threshold values for the conversion of continuous SDMs to binary presence/absence maps affected the relative species richness indicator. Across species, we found both positive and negative associations between bird occurrence and different groups of AEM. However, when comparing the current AEM adoption scenario with the “no AEM” scenario, we found an overall increase in the relative species richness indicator in all study regions. Uncertainty layers for individual SDMs identified areas of disagreement between model algorithms, towards which species-specific monitoring should be directed to ground-proof the model outputs. Threshold-related differences in repeated calculations of the multi-species indicator were instead useful in determining which areas are consistent hotspots of high species richness. Sharing this spatially-explicit, region- and species-specific information with local stakeholders can help reaching a better spatial targeting of conservation measures, thus maximising their efficacy.

Functional Connectivity of Ecosystem Services in Agricultural Landscapes: Implications for Management Strategies

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The University of British Columbia

Management actions and strategies aimed at promoting biodiversity can have significant impacts on the functional connectivity of multiple ecosystem services (ES) in agricultural landscapes. This study explores the potential role of functional connectivity in mediating the delivery and provision of ecosystem services in the Canadian prairies, focusing on the disentangling interactions of multiple ES using functional connectivity at a small landscape scale under different management systems. The study applies a process-based approach to map ecosystem services using the Artificial Intelligence for Environment and Sustainability (ARIES) framework as the model hosting platform. The ARIES framework provided a flexible and customizable platform to integrate and analyze data from multiple sources and models, allowing for a comprehensive and holistic assessment of ecosystem services in agricultural landscapes. We developed an ecological network model by using network analysis and spatially explicit and biophysical models to study the connectivity of multiple ES including pollination, agricultural crop production and soil carbon in the study area. We defined ES nodes and links based on the spatial distribution of ES and ecological processes and ES flows. Network metrics such as degree centrality, betweenness centrality, and closeness centrality were used to quantify the connectivity among different ES. Our findings suggest that management actions and strategies can increase the functional connectivity of multiple ES in agricultural landscapes, creating a more diverse and resilient ecosystem. Specifically, we identified several management practices that promote the connectivity of multiple ES, including the restoration of wetlands, conservation tillage, and crop rotation. We also found trade-offs and synergies between different ES under different management scenarios. This study highlights the importance of considering functional connectivity when designing management strategies for agricultural landscapes. By promoting the connectivity of multiple ES, managers can enhance the provision of essential services, such as pollination, pest control, and nutrient cycling, and ultimately contribute to the sustainability of agroecosystems. The results of this study can be used to inform policy and decision-making, emphasizing the role of ES models and maps in supporting sustainable land management practices. Our approach enables the practical implementation of science-based insights to support policy and decision-making processes. By applying ES models, we can enhance our understanding of ecosystem functions, services, and their trade-offs and synergies, which can ultimately contribute to the development of effective management strategies and the achievement of sustainability goals.

Persefone.jl: an adaptable open-source model of agriculture and ecosystems

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The EU’s Common Agricultural Policy (CAP) is a complex system of subsidies and regulations with a huge impact on farmers and biodiversity. Although it aims to both support farmers and safeguard the environment, negative trends continue both socio-economically (e.g. loss of small farming businesses) and ecologically (e.g. bird and butterfly populations decline). One challenge in the further development of the CAP is the multitude of factors and feedbacks in the agricultural system, which can cause unforeseen responses and trade-offs to policy interventions.

To help untangle this complexity, the project CAP4GI is currently developing Persefone.jl, a social-ecological model for “Policy Evaluation for Resilient, Social, and Ecological Farming Operations iN Europe”.

Persefone.jl integrates a regional agent-based model of farms (developed by Lea Kolb) with an individual-based model of various animal species. The two components are linked through a shared dynamic landscape, which is affected by, and affects, both farmers and animals. The model also includes weather inputs and a crop-growth submodel. Thereby, the model can be used to address a wide range of socio-economic, agroecological, and conservation-oriented research questions.

Available as open-source software, Persefone.jl is designed to be easily configurable and readily adaptable to new regions and scenarios. Using the performant Julia programming language allows the model to simulate large numbers of individuals on publicly available remote-sensing maps. Our aim is to make the model as open and usable as possible, in order to enable researchers to offer transparent and rapid policy support.

In this talk, I focus on the ecological submodel of Persefone.jl. I show first results of a study on the biodiversity impacts of the Eco-schemes, as a new set of agri-environmental measures that was introduced in the latest reform of the CAP. I use the model to analyse the likely effects of different Eco-scheme measures on several indicator bird and butterfly species, and explore what degree of uptake by farmers would allow currently-declining populations to stabilise or recover. With this example, I demonstrate how Persefone.jl can be used to assess alternative policy scenarios and to provide relevant and timely input to a fast-moving policy process.

When models become bold - lessons learned from five LULUCF models out of three projects

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Consideo GmbH

When models become bold - lessons learned from five LULUCF models from three projects: The participatory explorative qualitative stakeholder modeling of biomass value webs in Subsaharan Africa, the quantitative system dynamics (SD) modeling of biomass and money flows in Ghana, the holistic view on food security in Africa considering mega trends, the quantitative SD modeling of Germany's land use and its effects on greenhouse gases, and finally the global SD simulation model on the potentials for biotic resources. All models experienced the shift from skepticism to enthusiasm by the participating stakeholders and then to skepticism by the target group. The reasons were silo thinking, psychological fear from uncertainty, and fixed mindsets. The models showed a business as usual scenario that failed to feed the population without major changes. The range of possible changes, however, led to skepticism from both scientists and policy makers. For Subsaharan Africa it was fairly easy to let the stakeholders model the reality of biomass and money flows featuring social and cultural factors that showed that there is little potential for so called value webs. The idea, then, to shift from smallholder to industrial farming using machinery and pesticides and fertilizer was debunked by a quantitative model that showed that the increased income would only benefit a smaller part of the population while for most of the former smallholders access to food would become more difficult. As a consequence we have modeled the bold idea of a shift towards labour intensive agriculture with alternative farming practices that would first feed the population under guaranteed prices and then export the rest branded as fair and sustainable to the world. That would not just mean increased resilience to climate change but also serve as an alternative to all the problems that come with urbanization in developing countries. Well, that idea was too bold. The last model looked at different regions of the world using FAO data (which doesn't add up). It also included the diet, food waste, organic vs. conventional farming, forestry, etc. A change of diet towards healthier legumes would allow for for afforestation and to feed the world through organic farming. First, people do not need a model. Then they find it interesting to include their knowledge. But once we make assumptions about the future they struggle to see the results not as a precise projection but just as hint to a possible development.

Scenarios and monitoring systems: Instruments for exploring and evaluating strategies for the transition towards a sustainable bio-economy

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Bio-economy is regarded a promising route to substitute fossil resources and to make a significant contribution to global climate change mitigation. In addition, responsible political, societal and economic strategies aiming at a bio-economy transition need to consider trade-offs and synergies with other sustainable development goals (SDGs) such as the eradication of hunger, poverty reduction and conservation of biodiversity. In order to conceptualize such strategies and to identify trade-offs between different SDGs, policy makers require information of potential future development under deep uncertainty, e.g. in form of scenarios as well as solid and reliable information on the historic and current status of the bio-economy. This information base covers a broad range of topics including material flows, economic indicators and environmental impacts.

Objective of this presentation is to discuss potentials and challenges of using integrative models for supporting policy-making in the context of bio-economy development. As a working example, we introduce the global modelling framework LandSHIFT. It allows the coupling of a spatially explicit land system model at its core with different economic and environmental modelling approaches. We illustrate two use cases of this framework for policy support: First, a scenario exercise that uses the framework to delineate different pictures and ideas of the future bio-economy and to quantify the consequences on, and by, global land use change; and second, a monitoring system for the German bio-economy developed within the BMBF project SYMOBIO, which is used to calculate environmental footprints as sustainability indicators for water, land, biodiversity and greenhouse gas emissions based on the outcomes of the framework.

Central aspects of our discussion cover questions of (1) engagement of stakeholders in participatory modelling exercises to bridge the gap between policy makers and scientists and (2) transparent communication of modelling results and uncertainties inherent to this type of analysis.

Application of the Carbon Budget Model to assess the contribution of climate-smart forestry for climate change mitigation in forests of the European Alps.

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A climate-smart forestry approach is critical to ensure the sustainability of the forest ecosystem and its ability to act as a carbon sink despite climate change. This study aims to evaluate different climate-smart interventions and their potential to mitigate climate change through a modeling approach.

The Carbon Budget Model from Canadian Forest Service is a landscape-level carbon model, able to simulate carbon flows and a great variety of disturbances with related effects on different pools. It is a powerful model for simulating silvicultural interventions and carbon allocation and requires relatively few input data, mainly related to yield curves and occurrence of disturbances.

It has been widely used in a variety of ecoregions, and it has been recently parametrized for european forests. Nevertheless, it is not fully climate sensitive and it is not able to assess the variations in disturbances regimes and yield curves caused by climate change. To overcome this problem, we coupled it with a process based model (3PG). This second model can be used to modify yield curves depending on future climate scenarios, since it is sensitive to temperature and precipitations. Moreover, we edited the wildfire regimes by statistically modelling the link between burnt-area and expected change in drought indices using data from the period 2000-2020. Both climatic variables and change in the wildfire regime were modeled for climate change scenarios RCP4.5 and RCP8.5.

We applied this framework to the forests of Valtellina and Valcamonica in the Italian Alps and simulated three silvicultural scenarios: i) business as usual, ii) adaptative silviculture and iii) productive silviculture. The alternative scenarios have been co-designed with local stakeholder (forest managers, natural parks managers and wood industry).

The first scenario is based on historical logging interventions, while alternative scenarios are declined in a climate-smart perspective: the adaptative silviculture mainly focuses on fire-prevention interventions and fire-vulnerability reduction. The productive silviculture aims for producing wood adequate for building purposes that could generate emission substitution effects.

Preliminary results show that broadleaves' fitness will increase, and thus their sink. Nevertheless, to avoid C losses it is mandatory to foster fire-prevention interventions since droughts are becoming more frequent in the study areas. With regard to productive management, harvested wood products should be addressed toward long life-span products since this can help to mitigate greenhouse gasses emissions from hard-to-abate sectors like buildings.

A scenario-based analysis for political decision making in Bavaria to enhance biodiversity and climate mitigation

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Ongoing climate and land-use changes are important drivers of upcoming environmental changes at multiple levels. While the amount of global climate change will depend on global political decisions, land-use change can be influenced by regional political decision-making which is easier to achieve due to proximity. To inform and investigate the consequences of today's regional decisions, scenario-based simulations of different models are needed covering different sectors. With that, different future scenarios become comparable, and the consequences can be assessed at a sectoral level.

We apply identical scenarios of local climate change (from three regional climate models each driven by low (RCP2.6) and high (RCP8.5) CO_2 concentrations) and local land-use targets (biodiversity protection, climate mitigation, and climate adaptation) to seven different sectoral models to project spatially explicit impacts for the entire region of Bavaria. The models simulate changes in biotopes, ecosystem carbon storage, crop yields, insects, aquatic and terrestrial plants, land-use preferences, and land-use recommendations, using different methods such as process-based modelling, machine learning, and statistical modelling. We compare the results of the previous decade (2010–2020) with the results for the end of the century (2090–2100) to detect potential changes. We analyse the results by blending the individual changes spatially and summarised for the sectors.

We find different magnitudes of change in the studied sectors depending on the climate model, climate scenario and land-use scenario. Climate mitigation has positive effects on biodiversity and carbon storage, whereas the adaptation scenario results in negative effects for both. Generally, preliminary results show that the land-use scenarios have a greater impact on the studied sectors than climate change. Furthermore, the choice of climate model has in most sectors a larger impact on our outputs than the RCPs. Moreover, we detect spatial differences in the individual responses of the sectors. This helps to identify regions where special protection is crucial for ecosystem functions. For example, our results suggest that the Alpine regions of Bavaria are particularly vulnerable to changes in climate, which could have significant impacts on agriculture and forest productivity, as well as on the biodiversity of high-altitude ecosystems.

Regional political decisions can make a difference on the regional impacts of environmental change on biodiversity and climate mitigation. Therefore, the results of multi-model comparisons provide important information as a basis for decisions towards a sustainable transformation.

Integrating multiple modeling approaches to bridge the gap between modeling and decision-making in management of a marine ecosystem

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Ecological modeling has become a key tool for decision makers from the local to EU level. The models allow scientists and decision makers, alike, to test scenarios and evaluate the impacts of policies and projected environmental change, such as climate change, on the ecosystem in question. The models further allow policy makers to determine whether their policy actions are likely to result in Good Environmental Status. The application of complex models, however, and their use by policy makers is often hindered by issues such as model complexity, uncertainties, and communication of the results and outcomes.

We adopt the concept presented by Uusitalo and colleagues (2022) and merge a number of modeling approaches in order to evaluate the impact of various policy and climate change scenarios on the Israeli marine ecosystem. We further incorporate an efficient visualization approach that also incorporates the uncertainty associated with the models and inputs. The modeling system we constructed included output from climate change models under several climate scenarios, an Ecosim model expanded with Monte Carlo tools, output from an ocean biogeochemical model, and a bio-economic model. Scenario results were visualized using a Bayesian Belief Network (BBN) and marine ecosystem indices developed as part of the EU Ecoscope project. To test and demonstrate the integrated system we ran a number of scenarios that included various drivers spanning multiple domains (geophysics, management, socioeconomics), covering all possible permutations using the Ecosim model. Using Monte Carlo simulations, multiple runs and their corresponding results were then transferred into a BBN. Recreating the various scenarios and resulting outcomes in a BBN allowed us to easily account for, and track, inherent uncertainties and highlight possible management pathways considering multiple stressors

By merging the BBN approach that provides the probabilities of different outcomes along with the marine ecosystem indices, the integrated system offers a means for simultaneous evaluation of environmental and economic goals while also incorporating future projection uncertainty and model uncertainty.

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21. Ecological risk assessment and management – benefits and challenges of ecological modelling

Mechanistic effect models in the environmental risk assessment of chemicals - Possibilities and requirements

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Mechanistic effect models (MEMs) dynamically simulate essential processes in ecological systems, and how these processes are affected by chemicals. Modelled systems can range from (sub)organism over populations and communities up to ecosystems. Recently, MEMs have been increasingly proposed for use in the regulatory environmental risk assessment (ERA) of pesticides. Here, MEMs have been proposed mainly as refinement options, e. g. for assessing the effects of time-variable exposure on organisms or assessing effects on populations. However, MEMs can be very useful explorative tools to address various additional questions, including ranking the effectiveness of alternative risk mitigation measures or to support the interpretation of ecotoxicological studies. Addtionally, in retrospective risk assessments, such models can be used to analyse mechanisms behind effects observed in (semi-) field studies and to support the establishment of appropriate assessment factors in ERA with an improved mechanistic understanding.

This contribution aims to give an overview of potential applications of different types of ecological models in the context of regulatory environmental risk assessment of chemicals. It will draw from the results of a working group of the Society for Environmental Toxicology and Chemistry (SETAC), that focused on model acceptability criteria and scenario development, and developed a number of topics for the regulatory use of mechanistic effect models, including possibilities and requirements for the use of MEMs.

How to Include Temperature in Ecological Risk Assessment

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Temperature is a natural variable, never constant under field conditions. And as global climate change continues, extreme temperature events are expected to increase in frequency. Therefore, prospective environmental risk assessment needs to consider the potential influence of those changing temperature conditions on pesticides' toxicity. For this, the variation of temperature should be considered in mechanistic or process based models like toxicokinetic-toxicodynamic (TKTD) models for chemicals.

There are two different ways to include the influence of temperature on chemical effects. Firstly, temperature can be interpreted as a modulating factor, influencing the TKTD processes of the chemical. Secondly, temperature can be approached as an individual stressor, in addition to the chemical stress. Even though in reality, it might be a combination of both, looking at these two different approaches separately will help to understand the mechanisms of the combined stressors, chemicals and temperature. Temperature has been successfully included in TKTD models as a modulating factor via the Arrhenius equation, however, with limiting applicability regarding temperature conditions outside of the thermal tolerance of the organism.

To explore how to include those extreme (i.e., stressful) temperatures, we developed a module that allows to include temperature as a separate stressor in TKTD models for chemicals. We translated the damage model as used for chemical effects in the General Unified Threshold model of Survival (GUTS), to a damage model for the effects of temperature. We will present the assumptions and mathematical approach of this model and test its performance to predict experimental data. Furthermore, we implemented the new temperature damage model in the mixture GUTS framework to assess the survival of combined exposure to a temperature and a chemical stressor.

A workflow for assessing the quality of model input data - an example from toxicokinetic-toxicodynamic modelling

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In regulatory environmental risk assessment (ERA), standardised workflows support transparency and unbiased risk evaluation. Recent recommendations structure the application of toxicokinetic-toxicodynamic (TKTD) modelling in European ERA of pesticides. TKTD models simulate organismal uptake and elimination of a chemical compound (TK) as well as its effects on the organism (TD). The Reduced General Unified Threshold model of Survival (GUTS-RED) is a TKTD modelling framework that is well established for aquatic risk assessment to simulate effects on survival. In regulatory risk assessment, TKTD models are applied in three steps: calibration based on data from toxicity tests in the laboratory, validation to independent data and prediction under environmental scenarios. Despite a clear understanding of GUTS-RED predictions' sensitivity to model parameters, the influence of input data on the quality of calibration and validation is not systematically explored. We analysed performance of GUTS-RED calibration and validation based on a unique, comprehensive dataset, comprising survival measurements from 59 pesticide toxicity tests. Tests varied in types of compounds, exposure patterns and aquatic animal taxa. We applied a design where all possible combinations of toxicity tests for the same species-compound combination were used for calibration and validation. Calibration and validation quality was assessed by a set of commonly suggested model evaluation metrics. We found that parameter uncertainty was lower when models were calibrated to data that covered the full range of effects (i.e. from high survival to high mortality). In our dataset, increasing the number of toxicity studies used for calibration, further increased parameter precision. Combining tests with differing exposure patterns for model calibration improved model predictions on different types of validation data. Our results provided insights into how input data influence model outcome and which data better inform calibration or validation. Therefore, we derived a stepwise workflow for the assignment of input data to calibration or validation up to a final judgement on the suitability of the dataset for GUTS-RED. The workflow makes traceable how input data is used for model building and for which reasons. Such transparency fosters understanding and trust in model predictions.

Individual-based modelling for risk assessment

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Population models are essential for conducting higher-tier risk assessments (RA) in ecological modelling. Mechanistic modelling principles connect population processes with environmental changes, making population models an obvious choice. However, individual-level models such as Dynamic Energy Budget (DEB) and General Unified Theory of Scaling (GUTS) are currently better described and applied for RA than population models.

This too can be achieved for individual-based models, which derive the properties of a population from the characteristics of the individual organisms. This feature of individual-based models allows for using the results of standard laboratory studies conducted on individuals for the parameterization of more complex models for a higher tier of RA. Thus, population individual-based models can extrapolate observed toxicity at the individual level to the population level.

Individual-based models have established protocols for properly describing, testing, and analysing them, which contributes to their reliability. They can provide insights for the development of an advanced experimental design and analysis of its results, while a validated model can predict results under a broad set of environmental scenarios and exposure profiles. Moreover, individual-based models can consider spatial aspects of the environment.

The modular structure of individual-based models allows for incorporating already tested submodels representing toxicity at the individual level. Promising examples of individual-based models for RA include DEB-IBM and BEEHAVEecotox. These models have the potential for implementation for different groups of organisms for higher tiers of RA.

In conclusion, individual-based models can provide a useful tool for conducting higher-tier risk assessments in ecological modelling. They offer a modular structure, the ability to incorporate already tested submodels, and consideration of spatial aspects of the environment. The development and application of individual-based models for RA have the potential to contribute significantly to the field of ecological modelling.

Using mechanistic effect modelling to evaluate field effect study design for environmental risk assessment

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Mechanistic effect models can benefit environmental risk assessments (ERA) in various ways. Mostly it is used to evaluate risk in realistic scenarios or compare mitigation options. However, it can also be used to evaluate and improve field effect study by comparing different virtual study designs. Field effect studies are among possible higher tier refinement options of ERA of pesticides for small herbivorous mammals focussing on common voles. In these ERAs the crop of interest is usually no primary vole habitat (e.g. winter cereals) and field studies in such crops yield usually only low numbers of individuals, which makes it difficult to detect potential effects. Thus, a common approach is to perform those studies in more favourable habitats for voles as grassland as surrogate ‘crop’. Here, we investigate whether vole field effect studies conducted in grassland are a feasible and protective approach.

This study used the spatially explicit individual-based model for the common vole, eVole, to analyse population dynamics in a landscape consisting of both winter cereal and grassland habitat. The general spatial and temporal population dynamics were observed and effects of pesticide applications in either of the two habitats are investigated.

Our modelling study exemplifies that throughout the year the vole population density was higher and individuals were more homogeneously distributed in grassland compared to cereals, where voles more likely occurred in the field edges. Under pesticide application the vole population in treated grassland habitat was affected at lower application rates compared to treated cereals. Moreover, applications in grass led generally to larger magnitudes and longer durations of potential effects.

The results underpin the assumption that field effect studies conducted in grassland, a habitat closer to vole’s primary habitat, are sufficiently protective to cover the assessment of risks in secondary habitats like yearly field crops. First, in grassland, voles are present all year round at higher densities than in cereals, which allows capturing more voles to better detect effects. Second, the effects themselves are larger for treatments applied in grassland compared to cereals as (i) voles are more frequently affected in grassland due to their higher densities and (ii) because the high interception in cereals, particularly at later BBCH stages, results in overall lower exposition to treatments. Overall, this study underlines the potential of ecological modelling to support ERA not only directly providing additional evidence for the ERA process, but also for evaluating, planning and designing higher tier field options.

Modelling the Fate of Pesticides in ALMaSS: A Multi-Compartment Approach for Risk Assessment

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Pesticide use is common in agriculture, but it can have significant impacts on non-target organisms, such as bees. Accurately assessing these risks requires models that can simulate the fate of pesticides in different environmental compartments. We present a new pesticide fate model within the Animal, Landscape and Man Simulation System (ALMaSS) agent-based model that can predict pesticide exposure in a virtual landscape. Our model considers up to six different compartments (soil, plant canopy, pollen, nectar, inside the plant, and seed coating) and includes transfers between them, such as rain wash-off. It also allows for different application methods and considers drift caused by wind.

We will discuss the importance of modelling pesticides in multiple compartments and showcase the impact this can have on risk assessment. We will also highlight the improved accuracy and flexibility of our model and discuss various use cases.

Our new framework for pesticide risk assessment highlights the importance of detailed information on the fate of pesticides and their impact on non-target organisms. We will demonstrate how our model represents a significant improvement over previous models and how it can be utilised by multiple current and future ALMaSS species in a consistent, reusable manner. This presentation will appeal to those interested in the application of modelling techniques to solve real-world problems and those seeking to improve pesticide risk assessment.

Assessing the abundance variability of beneficial terrestrial arthropod species

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Different arthropods species take different roles in anthropogenic agricultural environments. While some are considered pest species, others fulfil essential Ecosystem Services, like pollination and pest control. Assessing potential declines of population sizes of such beneficial arthropods due to e.g. pesticides proofs difficult due to highly variable abundances. Abundances can change significantly between years and within seasons due to various factors, like weather and (sub-)annual life cycles. Thus, data series covering multiple years and seasons are required to extract such Normal Operating Ranges (NOR) for the species abundance. Such data are only sparsely available for most ecosystem service providing arthropods, making an assessment of NOR based on data alone unfeasible. Combining data-derived results with (mechanistic) modelling approaches can fill data gaps and enable consideration of longer timeseries and e.g. changing weather patterns.

Data availability is thus checked for a number of beneficial species in diverse habitats, including perennial orchards and different arable crops. The extracted data is used to estimate abundance variability in agricultural environments. Furthermore, existing arthropod models are assessed for their potential and applicability to generate population dynamics and abundances that are suitable for NOR calculation. Evaluation includes presence of external and internal stochasticity (e.g. based on weather, death mechanisms) and influences of landscape structure and composition on population modelling results.

As an exemple, a predatory beetle species is simulated in an individual-based landscape modelling platform (ALMaSS), that incorporates many of the proposed modelling aspects. Modelling results are then compared to data-derived species abundances to highlight benefits of a combined approach to assess arthropod population abundances. Knowledge about the NOR of a species enables the detection of stressor induced population declines. Thus, such combined data- and model-derived approaches can support management decisions related to risk assessment and policy making by aiding the definition and implementation of specific protection goals for beneficial species or families.

Uncertainty quantification for model-based decision support for ecological risk assessment

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Decision making in ecological risk assessment and management is challenging, because available evidence is typically far from complete. Mathematical models can help to fill these gaps. Different types of models can be used in this context, from theory-based mechanistic models to data-driven empirical models and machine learning algorithms. However, all models are an abstraction and simplification of reality and we rely on data to calibrate them and/or to assess their applicability to reality. In the scope of ecological risk assessment, the best we can do is to integrate all possible sources of information, from theory, literature, dedicated experiments, field data and expert knowledge. However, all these sources come with limitations, regarding accuracy and transferability to the specific application. Still, the process of integrating information from different sources makes a valuable contribution to synthesizing knowledge.

To assess how well we understand the system and to quantify our certainty about the model predictions to support risk assessment, a comprehensive uncertainty analysis is crucial. Uncertainty can arise in all steps of the model-based decision support process: at the problem structuring phase to define the scope of the decision, at the model building phase, where decisions about input and output variables and the parameterization have to be made, during calibration and assessment of the results, as well as in the phase of deciding about the application cases of the model to make predictions for unseen situations. In this contribution, we will discuss different sources of uncertainty and methods to address them illustrated with practical examples. We are typically concerned about uncertainty from model structure, input, output, and parameters. Dealing with these sources of uncertainty in a comprehensive way already poses several conceptual and practical challenges, a reason why it is rarely achieved. However, these sources of uncertainty just cover the so-called "known" or quantifiable "unknowns". In reality, this is potentially just the tip of the iceberg. In addition, we should acknowledge deeper sources of uncertainty, for example uncertainty in the definition of the decision scope, changing boundary conditions due to climate or land use changes and the co-occurrence of multiple stressors, or ambiguity about the formulation of scenarios for projections to unseen situations. In this contribution, we want to raise awareness about the issue and discuss how far we can go to achieve a comprehensive uncertainty analysis, how to prioritize efforts, and how to assess the robustness of conclusions from model-based decision support.

Modelling the establishment potential and economic impact of plant pests in Germany

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Julius Kühn-Institute - Institute for National and International Plant Health

Quarantine plant pests pose a great economic and ecological risk to native crops, which can be further exacerbated by climate change. However, it has been challenging to estimate the expected damage caused by these pests and long-term risks posed by climate change, which has often resulted in insufficient consideration in phytosanitary pest risk analyses (PRA). To predict the establishment and spread potential of quarantine pests as well as the expected damage due to crop failures and/or plant health measures, a combination of various models can be useful. The ecoclimatic model MoPSi ('Model for Plant Pest Spread Simulations') can provide information on the possible spatial distribution and spread dynamics of the pest as well as on the growth potential in different areas. By combining the ecoclimatic model MoPSi and economic cost-benefit analyses of damages and phytosanitary measures (PM) (MoPSi-Econ), it will be possible to estimate the impact of new plant pests under different climatic conditions and assess various environmental and management scenarios. Hostplant data as well as a damage database that quantifies crop loss, and a cost database for various PMs, are the basis for the calculations in MoPSi-Econ. By linking the expected damage caused by pests and the expected costs and damage mitigation from PMs, different eradication and containment measures, as well as unlimited spread scenarios, can be compared economically. The impairment of ecosystem services, which depends on the severity of pest infestation, distribution and affected host plants, will also be considered in the model. The costs and damage mitigation of different management options, such as chemical agents, physical barriers (e.g. nets), beneficial insects, and clearing, will also be compared in the final model. For this purpose, different infestation, damage and cost classes are used, which contribute to bridging data gaps and standardizing input data and thus to a simplified parameterization and faster modelling results. The results of the model are presented graphically in the form of risk maps and damage/cost maps. These can be used in PRAs to provide a more accurate assessment of economic and ecological risks posed by plant pests. In addition, information on identified high-risk areas can support the planning of survey activities. Furthermore, the model output can serve as a decision support tool for plant breeders and producers.

Multi-agent modelling to simulate the boosted sterile insect technique for fruit fly management

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The sterile insect technique (SIT) was successfully applied to eradicate many type of insect pests and disease vectors. It involves the mass rearing and release of sterile males that do not produce offspring when mated with wild females. An innovative version of this technique, called boosted SIT, proposed to use sterile males as biocide vectors to trigger an epizootic in the wild population.

We built a multi-agent model to simulate boosted SIT for the control of the oriental fruit fly, Bactrocera dorsalis, with the entomopathogenic fungus Metarizhium anisopliae. This fruit fly, by laying its eggs in the fruit, is a major obstacle to the sustainable intensification of mango production in sub-Saharan Africa. In addition, as a quarantine pest, it impacts the mango export industry. The proposed multi-agent model simulates the spatio-temporal dynamics of the fly population in three different landscape contexts (intensive and monovarietal orchards, little diversified or very diversified), the releases of contaminated or non-contaminated sterile males, the transmission of the pathogen within the wild fly population as a result of interactions between individuals (courtship, mating) and the losses in mango production due to the flies.

The model was validated with field data. After showing that the boosted SIT was able to reduce the density of wild flies and fruit infestation in the orchards, simulations were carried out to i) explore the release conditions under which boosted SIT is optimized, and ii) determine the effects of the structure of the three landscapes and early harvest on boosted SIT.

The results showed that the best fruit protection strategy with boosted SIT is its implementation when the fly population is low, to have multiple releases made at 15-day intervals, and to use a high ratio of sterile/wild males. The monovarietal landscape had a higher proportion of saved fruits, especially when releases are made in all orchards in the landscape and early fruit harvest is considered. In terms of optimizing the benefit to cost ratio, it is preferable to release as few sterile males as possible.

However, in comparison with classical SIT, our results showed a lower performance for boosted SIT in the mango-Bactrocera-Metarhizium context. Further studies are needed on some important parameters such as the choice of entomopathogen to improve it. The results provided by the model encourage the implementation of pilot trials to test the effect of boosted SIT on B. dorsalis under field conditions.

Exploring the success of the Boosted Sterile Insect Technique with a theoretical agent-based model

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The environmentally friendly methods of the Sterile Insect Technique (SIT) has proven to be effective in many situations of crop protection of pests or control of vector populations. SIT consists of releasing sterile male insects into the environment to compete with wild males for females and prevent them from reproducing. Unfortunately, this method is often limited by the number of sterile males to be produced. A new approach, called boosted SIT, combining the SIT principle with contamination of wild females by sterile males coated with biocide pathogens has been proposed to improve insect population control. We developed an agent-based model to represent different insect life history strategies as well as characteristics of infectious agent used, in order to determine situations in which boosted SIT reduces the required number of sterile males to be released in comparison with classical SIT. Using this agent-based model, we explored the population dynamics of 5 typical insect species, 3 pests and 2 vectors. We were able to identify situations where a boosted SIT was the most interesting as well as the parameters determining the benefits of the technique. Two parameters were decisive: a low rate of multiplication of the insects as well as a high horizontal transmission of the pathogen outside of reproduction events. These results stress the needs of preliminary in-silico exploration before the deployment of novel pest or vector control solutions that are dependent on the life history and behaviours of the targeted species.

Evaluating the risk of biological invasion by alien plants in India: Ensemble machine learning models revealed management insights

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Biological invasions represent one of the major environmental challenges for the conservation of global biodiversity and the continuation of ecosystem services and have a serious impact on human and animal health and economic development. Pant et al. (2021) and Prajapati et al. (2022) have created a comprehensive database, named, Indian Alien Flora Information (ILORA) (https://ilora2020.wixsite.com/ilora2020) which contains data for 14 variables related to ecology, biogeography, introduction pathway, socio-economy, and distribution of 1747 alien vascular plant species from 22 national and global sources. The data set is expected to assist a wide range of stakeholders involved in India's scientific research, policy formulation, and decision-making related to Invasive Alien Plant Species (IAPS). In recent years, several modelling tools have been used to predict the consequences of climate change on the spatial distribution of animal species, weeds, and crops in India. However, most of the studies are confined to one or to a limited number of species. In this talk, we shall discuss how the ILORA database will be useful in implementing policy regulations with the aid of data science applications. In particular, the identification of the species which are expected to show significant range expansion in India is an important task that will provide management insights. We identified the factors which have significant contributions to the observed climatic niche dynamics for the invasive species by employing an ensemble machine learning approach. We observed that the number of naturalized ranges, native ranges, number of uses, and plant height appeared to be the important factors. This study may be useful to prioritize species and areas of management actions.

An individual-based model to support conservation decisions of a critically endangered grassland bird

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The intensification of agriculture and the increasing frequency of extreme meteorological events due to climate change have led to a widespread decline in biodiversity, highlighting the urgent need for effective wildlife conservation and risk management. In Europe, several threatened grassland bird species, including the little bustard (Tetrax tetrax), have experienced alarming declines. The Extremadura region (Spain) is particularly important for the conservation of the species, but a thorough understanding of the little bustard's distribution over the yearly cycle is needed to accurately determine long-term trends and identify critically important areas aiming for long-term conservation.

In this study, we developed an individual-based model (IBM) aiming for a holistic understanding of the species distribution and population dynamics through the yearly cycle, designed to attain a high-resolution management tool for the species' whole area of occurrence in Extremadura. For this end, we first modelled the species habitat suitability considering the 3 stages of the species phenology (winter, breeding, and post-breeding). We used a 12-year GPS telemetry dataset from 91 tagged individuals in Extremadura and high-resolution remotely sensed environmental metrics (MODIS) to generate phenological "multi-state" species distribution models (SDMs) at a 250m resolution. At a second stage, we used the SDMs as the spatial basis for the development of a spatially explicit IBM. The IBM was developed with a pattern-oriented modelling strategy, simulating realistically demographic individual-level processes over the species' annual cycle, including survival, reproduction, spatial organisation, and migration.

SDMs allowed for the identification of the key environmental factors influencing the species occurrence at different phenological stages. These factors were mainly associated with the habitat's structural characteristics, rainfall rates, and average air temperatures, making the species vulnerable to both land use shifts and climate change. Overall, we found that matching high-resolution remote-sensed data with GPS tracking data resulted in accurate habitat suitability predictions throughout the yearly cycle.

The IBM, combining detailed information on habitat suitability and the species' demographic behaviour, allowed us to understand and monitor the population's response to habitat changes over time. This will help in defining conservation areas for management planning, testing the implementation of measures, and anticipating their effects.

By integrating SDMs and IBMs, this study provides a prime example of how combining various modelling techniques can aid in ecological risk assessment and management, and contribute to the development of decision-support tools for conservation.

Habitat modelling of vascular plants of the hardwood floodplain forest of the Leipzig Northwest Floodplain in the "Lebendige Luppe" project

Frank Masurowski

In addition to restore a near-natural watercourse typical of a floodplain, the “Lebendige Luppe” project aims to reactivate the hydrodynamics typical of a floodplain through regular flood events every one to five years in large areas of the floodplain forest.

A coupled groundwater-surface water model will be used to describe the effects of the new hydrological situation on the floodplain forest. In the project “Lebendige Luppe”, statistical habitat modelling will be used to describe and quantify selected abiotic environmental variables in the context of different species groups. Another aspect of the habitat modelling applied is the assessment of the revitalisation measures carried out on the new river courses and the direct flooding, as well as the associated changes in groundwater conditions. Basically, habitat modelling is used to describe the statistical relationship between the occurrence of some species and their habitats, with the groundwater surface model being the most important factor in describing the future hydrological situation in the floodplain habitat in the area of the Lebendige Luppe.

The habitat modelling is based on an input data set collected from a total of 60 permanent monitoring plots (PMP) in the project area. The PMP, were established using a stratified random design within the FFH habitat type Hardwood Floodplain Forest, with the pre-selection of potential sites carried out in the GIS and finally by experts in the field. The main input data are the status quo of the herbaceous vegetation on the PMP and the survey of abiotic environmental variables. In a first step, data collected over several years are used to describe the status quo and its short-term dynamics. The abiotic environmental variables collected have been examined for their explanatory power in relation to the current vegetation, and sensitive species will be identified whose occurrence is particularly well explained by individual or groups of environmental parameters.

In a second step, the results of the coupled groundwater and surface water modelling have been used to analyse, to quantify and to evaluate the occurrence of the "sensitive" species derived in the first step, first for the status quo and in the near future for the scenarios for the entire project area. The resulting predictions of the responses of the hardwood floodplain forest to the changing abiotic environmental variables of groundwater flow distance will be implemented using spatio-temporal Bayesian modelling. The model results will be used to evaluate the effects of the planned measures.

ECEM 2023 - European Conference on Ecological Modelling
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22. Functional responses: from theory to practice

New perspectives on multi-species functional responses

Daniel Stouffer

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Functional responses relate a consumer's feeding rates to variation in its abiotic and biotic environment, providing insight into consumer behaviour and fitness, and underpinning population and food-web dynamics. Largely owing to their experimental intractability, theoretical developments for multi-resource functional responses have lagged behind their single-resource counterparts. In this talk, I will describe a recently-developed approach to quantify non-independence in resource-specific consumption rates for consumers that are simultaneously able to feed on two distinct resources.Through a combination of theory and analysis of a large collection of empirical datasets, I will show how this approach provides a new lens through which to view variation in consumer feeding rates and disentangle the biological underpinnings of species interactions in multi-species contexts. I will then outline ongoing approaches to generalise this framework beyond just a pair of resources, and the challenges to doing so successfully. I will finish by explaining how this approach, and its inherent linkages to the theory of chemical reaction kinetics, can also provide more general insights into consumer-resource modelling and the question of essential vs substitutable resources.

The implicit Assumptions of Functional Responses

Gian Marco Palamara [1]; Jose A. Capitan[2]; David Alonso [3]

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Research on consumer-resource dynamics is vast and has been addressed in both theoretical and empirical studies. A primary goal in this research agenda is to understand how mascroscopic descriptions of trophic interactions relate to the individual processes that define the consumer-resource interaction in the first place. Despite decades of studies, there is still no clear agreement on the functional forms of the per capita consumption rate of consumers (generally called “functional responses”) not only in community food webs models, but also in simple predator-prey equations. In this talk I will present a modelling approach based on the theory of continuous time Markov processes to describe individual feeding interactions, emphasizing their stochastic nature. Within this framework, we revisit the derivation of two of the most famous classical functional responses, the Holling Type II FR and the Beddington-DeAngelis FR suggesting extensions of them in multi-resource contexts. More importantly, we highlight the common assumptions underlying all these derivations. These implicit assumptions should not be overlooked when using simple models to analyze both experiments and natural consumer-resource interactions, and their food web extensions.

A functional response model accounting for information flow and decision-making

Jingyi Li; Emilio Berti; Ulrich Brose

Accurately quantifying consumer-resource interactions is essential for correctly understanding and predicting community dynamics, stability and ecosystem functioning. The functional response, which describes how the consumer's feeding rate responds to changes in resource density, has long been used to quantify consumer-resource interactions. Generally, three types of functions have been used to quantify the functional response, describing linear, quadratic and sigmoid relationships respectively. Importantly, foraging consists of a sequence of events, including but not limited to search, detection, pursuit and attack. According to this foraging sequence, the likelihood of successfully completing each step is determined by species traits, environmental conditions, and the time required to complete each step. However, in commonly used functional responses, these probabilities and related uncertainties in successfully completing the foraging sequence have often been underlooked. In addition, the few models currently available that incorporate how information regulates trophic interactions cannot be easily applied to empirical studies due to data requirements that are hard to meet even for simple experimental set-ups. Here, we have revisited the derivation of the functional response according to the foraging sequence and developed a new functional response framework that can account for such uncertainties and that can be fitted to existing data. With this, we aim to provide a unified mechanism for the various functional response relationships observed in nature.

In ecological communities, every individual receives sensory inputs that are translated into information, which is then processed to detect potential prey and/or avoid predation by perceiving and analyzing cues in surroundings. Intuitively, stronger cues increase the amount of information received and lower the uncertainty in the predation sequence. Therefore, these cues can regulate individual behaviour, interactions between consumers and resources and, ultimately, the dynamics of the community. To include such probabilistic processes that originate from information constraints and to overcome the problems for empirical data analysis, we developed a functional response framework based on the flow of information and the decision-making process involved in the predation sequence. In particular, we explicitly modelled the probability of successful detection and identification of prey items and integrated these into the predation sequence. We show that this model, which is grounded in theory and based on ecological realistic assumptions of how animals perceive and process information from the environment, can accurately approximate the functional response observed in nature. As such, our model provides a unified explanation of the various functional responses observed under natural conditions.

Design and analysis of feeding experiments for multi-species functional responses

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Multi-species functional responses (MSFR) describe feeding rates of generalist consumers that interact with multiple resource species. They are the backbone of dynamic foodweb models which predict biomass changes of communities over time.

However, empirical support for their specific usage and parametrization is thin. Multi-species feeding experiments are extremely rare. Besides logistical challenges, their statistical analysis is non-trivial. One of the problems is prey depletion over the course of the experiment, which has to be accounted for correctly. Statistically, this can be resolved by numerically simulating differential equations that generate predictions (using a population dynamics model) and fitting them to data, to estimate model parameters like attack rates, handling times and prey preferences. This method has been proven valuable for single species functional responses, and I show its extension to MSFR. Additionally, the question of experimental design is important for MSFR, i.e. which combinations of the amount of available prey should be tested in feeding trials.

I perform an extensive simulation study, in which several classes of MSFR models, experimental designs, and sample sizes are crossed. Here, I 1. simulate realistic feeding trial data with known parameters using a stochastic algorithm, 2. fit population dynamic MSFR models, and 3. evaluate the accuracy of estimated model parameters. Overall, I observe good performances and the investigated MSFR are identifiable from the data. I find that sample size is more important than experimental design. Importantly, for systems with more than 2 prey species, analyzing the combination of all 2-species mixtures is sufficient to estimate all model parameters accurately. Trials with more than 2 prey species are not required, which simplifies the logistics of such experiments.

I propose a framework for estimating MSFR from data by combining dynamical prediction models with Bayesian inference. This study offers guidelines for empiricists who want to perform MSFR experiments. It will open new possibilities for testing hypotheses on topics like prey preference and switching, optimal and adaptive foraging, and foodweb stability.

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23. Like a boomerang: How feedback loops affect ecosystem stability and species coexistence

Competition across scales: Insights into the feedback structure of competition networks from an individual-based model

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In a system of two competing species, stability is determined by the balance of negative, self-dampening feedback, caused by intraspecific competition and positive, self-reinforcing feedback caused by interspecific competition. In diverse networks of competitive interactions, the interplay of positive and negative feedbacks is much more complex and closely linked to network structure. Analysing feedback loop strengths can therefore provide important insights into the relationship between the structure and stability of ecosystems. In a first analysis of empirical competition networks, we used observations of interference competition for space between bryozoan colonies to construct what we call “energy-loss webs”. We showed that the instability of these networks can be predicted by the strongest positive 2-link feedback loop. However, as the network approach aggregates the properties of all individuals into population properties and all interactions between individuals into interactions between populations, the biological interpretation of these results is challenging.

To better understand how the structure of our network models depends on interactions between individuals and how the balance of positive and negative feedbacks develops during community assembly, we then introduce an individual based model of bryozoan colonies competing for space. By adapting the rules that describe colonisation, colony growth and competition, this model allows us to control network structure via a competition-colonisation trade-off. From the simulated data, we construct network models to analyse the effect of this trade-off on feedback structure. This across-level approach enables us to identify the forces determining network structure and stability over time. We found that networks were generally unstable, with a strong initial increase in instability, followed by a slower decrease until competitive exclusion is reached. This pattern is explained by the destabilising effect of strong positive 2-link loops which is then counteracted by self-regulation and increasingly asymmetric pairwise interactions.

Paradoxical effects of nutrient enrichment on the pelagic ecosystem of the northern Adriatic Sea

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According to a bottom-up perspective on marine ecosystems, pelagic fish stocks should benefit from nutrient enrichment, which can promote higher fish biomass through increased planktonic productivity. Here we show that, in the case of the northern Adriatic Sea ecosystem (Mediterranean Sea), this is not always the case and that the biomass of different pelagic fish stocks may benefit or be negatively impacted by nutrient enrichment, depending on species traits such as individual size. In the northern Adriatic Sea, the heavy exploitation of fish and invertebrate communities by fisheries was matched by a strong cultural eutrophication in the second half of the past century, while now this basin is experiencing oligotrophication. By combining the analysis of long-term hydroclimatic, biological and fishery times series with modelling of the propagation of eutrophication and oligotrophication signals through the pelagic food web, we show that increased nutrient inputs have the potential to trigger self-reinforcing feedbacks which can promote large changes in the relative abundance of small-sized and medium-sized pelagic fish species. These changes can include predator-prey reversals and, ultimately, shifts between alternative stable states in the pelagic fish community. Fish size with its relationship to diet and growth rate appears to be a primary factor determing if a pelagic stock responds positively or negatively to nutrient enrichment. We show, remarkably, that a bottom-up pressure such as nutrient enrichment can trigger unexpected top-down dynamics in the pelagic food web, highlighting the importance for an integrated management of eutrophication and pelagic fisheries whose need is particularly clear in view of the oligotrophication recently taking place in this coastal ecosystem.

Time-dependent higher-order interactions

Thomas Van Giel; Jan Baetens; Aisling Daly; Bernard De Baets

Ghent University

Traditionally, community ecologists have studied pairwise interactions between species as the basis of how ecological communities can coexist. More recently, higher-order interactions (HOIs) have attracted scientific attention in different domains, especially in ecological community modelling. HOIs are interactions that look beyond the pairwise aspect, allowing for a third species to modify the original pairwise interaction.

In current theoretical research into HOIs, only the equilibrium behaviour of fully connected HOI-ecosystems is typically studied. While this has its own merits, it does not show the intricacies of HOIs, and exactly how HOIs can affect an ecosystem. Also, in real world ecological networks, there are usually only few HOIs present. The work we present here focuses instead on the effects of individual HOIs, and on the transient behaviour they induce. Ecologically, these HOIs can have a direct effect on the original interaction, but also indirectly via environmental modification. Both the modifying species and the environmental modifiers can be changed to act over slower or faster timescales than the species abundances, and thus the effect of the speed of the HOI onset in an ecosystem should be investigated. For the analysis of these time-dependent HOIs, we have developed a new mathematical model that for certain parameterisations can be reduced to a commonly used HOI model.

We show that many factors influence the effects of the HOI, and that the combination of different HOI speeds can completely change population dynamics and system outcomes. Depending on the original interaction of the HOI, modifying species and strength of the HOI, modifying species have the ability to induce oscillations in an otherwise stable system, or stabilise an otherwise oscillating system. For different modifier speeds, it is possible to transition from an oscillating system to a stable system, back to oscillating, or vice versa, without changing any other parameter settings in the model. Depending on the speed, these modifiers can act as an extra species, creating or destroying feedback loops in ecosystems where this would be impossible with conventional models. The significant impact that modifier speed can have on ecological stability, transient behaviour and feedback loops highlights the importance of this previously ignored parameter, and how it can provide more insight into the impacts of transient behaviours caused by a HOI on both short- and long-term behaviours of ecological systems.

Feedback between different dispersal strategies and self-organised pattern formation supports consumer coexistence in metacommunities

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Models explaining coexistence of species in metacommunities often evoke environmental heterogeneity in patch quality to enable regional (across patches) coexistence via habitat partitioning and local (within-patch) coexistence via source-sink dynamics. Here we study coexistence of two consumer species in a small meta-food web on two patches with identical environmental conditions by accounting for within-patch population dynamics and between-patch dispersal dynamics. Coexistence due to habitat partitioning is not possible because one consumer is the superior competitor for the shared food resource in both patches. However, we show that when static heterogeneous biomass distributions emerge via self-organised pattern formation, coexistence is possible if the superior competitor exports more biomass from the favourable (source) to the unfavourable (sink) habitat than the inferior competitor. When spatio-temporal biomass patterns emerge (here in the form of anti-phase oscillations between the patches), coexistence is possible if a higher dispersal rate enables the inferior competitor to anticipate changes in resource availability. In both cases, the ability to plastically reduce the emigration rate out of a patch with favourable growth conditions further widens the conditions under which the inferior competitor can persist in the system. Strikingly, if the competitors have very different dispersal rates and therefore differ in their ability to induce pattern formation, a novel coexistence mechanism emerges, where the temporarily dominant competitor modifies the spatio-temporal variation in the resource biomass in a way that favours the recovery of the currently rare competitor. Such a feedback loop is not possible if environmental differences between the patches are determined by an external factor. Self-organised pattern formation thus provides a generic mechanisms for supporting diversity in metacommunities without requiring particular environmental conditions.

Metacommunity size and connectance affect local diversity enhancement from self-organized pattern formation

Louica Philipp; Toni Klauschies; habil. Christian Guill

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Habitat destruction and fragmentation are major threats to biodiversity worldwide. In fragmented landscapes, separate communities in local habitats are still connected to each other via dispersal. In such metacommunities, species assembly and diversity are shaped by both local interactions and regional processes including species dispersal, which in turn depends on the species' movement abilities and the overall number and connectedness of the habitat patches. Understanding how these different biotic and abiotic processes separately and jointly affect the diversity of metacommunities is crucial for effective landscape management that counteracts further anthropogenic disturbance.

One important driver of biodiversity in metacommunities is spatial heterogeneity of the environment, which can emerge in a self-organized manner as (Turing) pattern formation in the resource concentrations and the species biomass densities. These patterns generally result from scale-dependent positive and negative feedback loops, where for example consumers locally facilitate their own growth by accumulating resources (nutrients, water), but also deplete that very resource in their surroundings, thereby causing competition and decreased growth over longer distances. Recently it was shown that this mechanism can enhance the local diversity within simple metacommunities.

Building on this study, we explored how metacommunity size (number of patches) and connectance (number of dispersal links) affects the potential of self-organized pattern formation to enhance functional diversity in a generic food-web model.

We found that local diversity can be enhanced through pattern formation in metacommunities of all tested sizes - small to large - and connectance levels – sparsely to fully connected. Higher connectance levels did however enable stronger enhancement of local diversity, as did a larger size of the metacommunities. Fragmentation processes that reduce the size and connectance of metacommunities might therefore negatively affect local diversity through weakening the effect of self-organized pattern formation.

Eco-evolutionary feedbacks within communities

Lynn Govaert

Unprecedented environmental changes induce strong selection pressures on species. Studies have shown both ecological and rapid evolutionary responses of species to these ongoing environmental changes. Increasing evidence that ecological and evolutionary processes can occur at similar temporal and spatial scales and might thus frequently interact has raised the concern that these processes should not be studied in isolation from each other, but instead should be integrated if we attempt to better understand species responses to environmental change. Even more so, because species are embedded within communities, environmental change does not act on single species, but acts simultaneously on all species within the community, giving rise to potentially complex eco-evolutionary dynamics in communities. Since species may also evolve at different speeds, this may have consequences for how competitive interactions further alters population dynamics. However, how such eco-evolutionary feedbacks play out in communities is still understudied. In addition, a coherent framework to address and study eco-evolutionary dynamics within communities is still lacking, despite the many theoretical and conceptual advances made during the last decades. Following a synthesis by M. Vellend which showed that community ecology could be organized along analogous processes of evolutionary biology (i.e., selection, migration, drift and diversification), we argue that by explicitly considering interactions between these processes of evolutionary biology and community ecology, it may facilitate our understanding of eco-evolutionary dynamics in multi-species communities. Focusing on interactions between processes of evolutionary biology and community ecology may enable explorations of the full range of eco-evolutionary community dynamics, may provide a way forward to reveal generalities and formulate hypotheses about eco-evolutionary community dynamics and guide the design of novel experiments and theoretical models that explicitly take these interactions into account.

Evolutionary community assembly with varying niche width: exploring the conditions for coexistence and emergence of generalists and specialists

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Species and populations in nature fall along a specialist-generalist continuum, be it in habitat preference, resource use, or seasonal activity. However, with few exceptions, traditional works on niche packing and diversification have mostly focused solely on the position of species along an axis, assuming constant niche widths. On the other hand, evolution of generalism has been modelled given a fixed, discrete set of resources. We try to synthesize these approaches by explicitly considering co-evolution of both niche positions and widths, and its impact on packing, coexistence, and properties of the resulting communities.

We first derive a Lotka-Volterra competition model from an explicit resource-consumer model. We then study evolution of niche positions and widths in a community governed by these dynamics, under an Adaptive Dynamics framework. Notably, we observe that even under perfectly symmetric resource scenarios, evolution can lead to branching and differentiation of niche widths resulting in the emergence of generalist and specialist phenotypes.

We then proceed to compare the effect of evolving niche widths on the properties of the final communities. To this end, we contrast communities issued from coevolutionary and diversification processes (Evolutionary Stable Communities) with non-evolutionary assemblages. We also explore how our results are conditioned by the role of resource availability and the trade-off shape (cost of generalism-specialization).

Eco-evolutionary dynamics and tipping points: when evolution creates or modulates feedbacks

Nicolas Loeuille

Sorbonne Université

An important issue in the context of current perturbations (global changes) is to understand under which conditions abrupt transitions can occur in ecological communities. The occurrence of such tipping points is currently strongly debated. At the same time, multiple observations point to the possibility of rapid evolution in the face of such changes. It is therefore crucial to better understand how such evolutionary dynamics can facilitate or reduce these potential abrupt transitions. I will discuss here two aspects of this question: (1) under what conditions does evolution generate systems with strong positive ecological feedback loops, which are de facto prone to tipping points; (2) how such tipping points may emerge not from ecological dynamics, but from eco-evolutionary dynamics.

Eco-evolutionary dynamics in 2-species mutualistic systems: One-sided population decline triggers joint interaction disinvestment

Franz Weyerer[1]; Avril Weinbach[2]; Christiane Zarfl[1]; Korinna Theresa Allhoff[2]

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The interplay between ecological and evolutionary dynamics can create feedback loops that reinforce the impact of external disturbances and thus threaten species' coexistence in a changing world. In the case of two mutualistic interaction partners, such as plants and their pollinators, a decreasing abundance of one interaction partner (such as insect decline) might force the other to invest more energy into being independent (e.g. via selfing or clonal reproduction) and less into the interaction (e.g. via reduced flower or nectar production). This disinvestment reduces the waste of energy at the cost of accelerating the initial partner decline, up to its potential extinction. When considering one-sided population decline, we ask under which conditions such self-reinforcing feedback occurs in mutualistic systems. We furthermore ask whether it can be counteracted by self-dampening feedback if the co-evolution of both interaction partners is taken into account. We address these questions using a mathematical model, based on the framework of adaptive dynamics. In line with previous studies, we find that the described pattern of accelerated population decline occurs for a wide range of parameter values. In our model, this was due to a concave allocation trade-off between independent growth and interaction investment. When both partners are co-evolving, the undisturbed population disinvests first, forcing the declining population to disinvest as well, in favour of other energy sources. A decelerated decline can occur if the adaptation of the undisturbed partner is too slow compared to the environmental change, reducing the speed of its disinvestment, or if the initial investment into the interaction was very high. Our results thus suggest that if actions are taken to save endangered populations, the evolution of the target species, and their interaction partner, but also the type and strength of their interaction should be considered.

Spatial dynamics affect eco-evolutionary feedback within a mutualistic metacommunity - and vice versa!

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The response of a given ecosystem to external disturbances strongly depends on eco-evolutionary dynamics at play within the system. For instance, declining pollinator abundances can trigger an adaptive re-adjustment of energy allocation within an interacting plant population. A decreased investment into the interaction (e.g. reduced flower or nectar production in favor of increased selfing or cloning) can then reinforce the initial partner decline, up to its potential extinction. We hypothesize that the strength of such self-reinforcing eco-evolutionary feedback depends on the characteristics of the spatial landscape in which the interacting partners are embedded. To test this idea, we use a mathematical model, combining concepts from the framework of adaptive dynamics with metacommunity theory. More precisely, we consider a set of patches, mimicking for example an urban landscape of habitat islands within a hostile matrix. Each of these patches contains a mutualistic 2-player system and is coupled to other patches via migration. We vary the connectivity between the patches, as well as the level of heterogeneity in patch quality. We find that both connectivity and heterogeneity have a positive impact on species persistence. This result is consistent with insights from previous, nonevolutionary metacommunities. However, the relative importance of connectivity and heterogeneity depends on whether or not the evolution of the undisturbed interaction partner is taken into account. Without evolution the relative effect of heterogeneity dominates over the effect of connectivity, while the opposite is true when evolution is switched on. This can be explained by the fact that habitat quality and source-sink dynamics affect local evolutionary dynamics - and vice versa. Our results thus suggest that conservation measures should not only consider target species in their respective spatial landscapes but also the interplay between spatial dynamics and potential multi-species eco-evolutionary dynamics.

Plant-soil feedbakcs generated by nitrification modulation by plants impact ecosystem structure, functionning, and resilience

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Plants release root exudates that shape the microbial communities in their rhizosphere, which can, in turn, modify plant growth, survival, and reproduction. In particular, some plants can block or boost the metabolism of nitrifying communities, thereby modulating the rate of transformation of ammonium into nitrate. When combined with plant preference for these two forms of inorganic nitrogen, this creates a plant-soil feedback loop that affects ecosystem properties such as productivity, leaching, and overall resilience. We have used a general model to demonstrate that the modulation of nitrification can maximize plant biomass by minimizing nitrogen losses. Our prediction is that the modulation strategy that achieves the highest biomass should match the plant's preferred form of nitrogen, thus generating a strong positive feedback. For instance, based on a parameterization derived from the Lamto savanna (Ivory Coast), we have found that productivity is greatest for plants that slightly prefer ammonium and inhibit nitrification. However, the drawback of such feedback is that a highly productive savanna can abruptly shift to a lowly productive state in response to a perturbation such as overgrazing, exhibiting a tipping point response. Our comparison with other parameter sets, such as the Pawnee short-grass prairie (USA), an intensively cultivated field, and a hypothetical parameter set, indicates that strategies yielding the highest biomass may be counter-intuitive (i.e., preferring nitrate but inhibiting nitrification), suggesting that the strength of the feedback depends more on environmental parameters such as deposition, leaching rates, and baseline nitrification rates rather than plant preference. Lastly, we emphasize that while contrasted nitrogen preferences offer the possibility of coexistence through niche partitioning, the modulation of nitrification can be viewed as a niche construction process that adds an extra dimension to coexistence conditions.

Multi-species grassland dynamics – how resources allocation affect interspecific competition outcomes

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European permanent grasslands represent a backbone for dairy and meet production, and are hotspots of biodiversity, providing important ecosystem services to society. Understanding how the form of land use and climate variability affect the botanical composition of these grasslands is therefore essential for adequate management adaptations to target sustainable development goals. It is also a key requirement for gauging climate change effects on forage quality, an aspect often overlooked in impact assessments. However, an explicit dynamics of species richness is only rarely included into grasslands models. Here, we present results of the DynaGraM modelling approach to understand short- and long-term changes in grassland biodiversity in response to various forms of land use and climatic variations. We question through this model which feedbacks and mechanisms lead to competitive exclusion or contrariwise to plant coexistence. DynaGraM is a process-based model for simulating seasonal aboveground vegetation dynamics of semi-natural grasslands for plant communities containing any number of species. It has been shown to be capable to reproduce the composition of permanent grasslands in the French Jura Mountains, inferred from floristic relevés.

This study questions the role of a particular mechanism, the allocation of resources by plants into storage organs, on the issue of interspecific competition leading to the competitive exclusion by dominant species often simulated in grassland models. This presentation explores how this allocation affects the issue of plant interspecific competition and promotes, by feedback loops, species coexistence by mitigating the effect of competitive exclusion. We show that this mechanism acts as a buffering effect to environmental variations and management stresses factors. Here, we show that the model predicts highest, resp. lowest vegetation diversity for extensive grazing, resp. extensive mowing. We apply the model to examine how joint stresses factors affects the species composition of pastures. Last, we compared the simulated outcomes to grasslands observations recorded by tele detection in a grassland experiment (Laqueuille, Massif Central, France).

Overall, this model introduces a novel and relatively simple approach to represent competition and adaptation processes in plant community dynamics, thus providing a response to the key challenge of modelling multi-species grasslands. This presentation points out the mechanisms involved in the emergence of coexistence within complex ecosystems.

Livestock management promotes bush encroachment in savanna systems by altering plant–herbivore feedback

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Savannas are characterized by the coexistence of two contrasting plant life-forms: woody and herbaceous vegetation. During the last decades, there has been a global trend of an increase in woody cover and the spread of shrubs and trees into areas that were previously dominated by grasses. This process, termed bush encroachment, is associated with severe losses of ecosystem functions and typically difficult to reverse. It is assumed to be an example of a critical transition between two alternative stable states. Overgrazing due to unsustainable rangeland management has been identified as one of the main causes of this transition, as it can trigger several self-reinforcing feedback loops. However, the dynamic role of grazing within such feedback loops has received less attention. We used a set of coupled differential equations to describe the competition between shrubs and grasses, as well as plant biomass consumption via grazing and browsing. Grazers were assumed to receive a certain level of care from farmers, so that grazer densities emerge dynamically from the combined effect of vegetation abundance and farmer support. We quantified all self-reinforcing and self-dampening feedback loops at play and analyzed their relative importance in shaping system (in-)stability. Bistability, the presence of a grass dominated and a shrub dominated state, emerges for intermediate levels of farmer support due to positive feedback that arises from competition between shrubs and grasses and from herbivory. We furthermore demonstrate that disturbances, such as drought events, trigger abrupt transitions from the grass dominated to the shrub dominated state and that the system becomes more susceptible to disturbances with increasing farmer support. Our results thus highlight the potential of interaction networks in combinations with feedback loop analysis for improving our understanding of critical transitions in general, and bush encroachment in particular.

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24. Integrating analytical modeling and individual-based modeling for complexity reduction, upscaling, and to gain causal understanding

Software-assisted predictability assessment for stochastic hybrid models

Leonardo Aguirre

Eawag, Swiss Federal Institute of Aquatic Science and Technology

While ecological systems are fundamentally comprised of interactions between individuals, the pressing questions are often posed at the macroscopic level where a system may exhibit complex aggregate dynamics and nonlinear response to control actions. Putative mechanisms underlying these emergent dynamics have been explored in theoretical ecology for over a century and lead to mathematical model descriptions in the context of stochastic process theory. However the connection to real ecosystems has often remained at a qualitative stage, in part because mathematically convenient simplifications don't align well with the level of detail required for calibration to realistic scenarios. As a consequence, the eminently important endeavour of predicting ecosystem responses has so far made little use of the more sophisticated stochastic process models. In my talk, I will give insights into an ongoing project that tries to overcome this methodological gap in the context of stochastic hybrid models – a general class of mesoscopic state space models that describe the dynamics of taxa abundances with internal degrees of freedom through a combination of (continuous-time) Markov jump processes and stochastic differential equations. First, I will demonstrate how this model class is versatile enough to capture many prominent examples, ranging from extremely simplified host-parasite interactions, exhibiting quasi-cyclic behaviour, to rather detailed algal bloom community models with inducible defenses. Second, I will outline the progress towards a general software framework, which aims to automatize some classical tasks of dynamical systems analysis by building computational pipelines. Such tasks include the estimation of a model's (quasi-)stationary distribution, state estimation, identifiability/sensitivity analysis and model calibration. Finally, I will show how this framework can be used in order to perform software-assisted predictability assessment for stochastic hybrid models augmented with noisy observables.

Intrinsic growth rates influence stability in the Lotka-Volterra competition

Heike Lischke; Thomas Löffler

Swiss Federal Institute for Forest, Snow and Landscape Research (WSL)

The Lotka Volterra competition model (LVC) incorporates essential features of ecological systems: feedbacks, interactions and nonlinear processes, and is therefore a good candidates to mimic community dynamics, and to transfer theoretical findings. Important parameters of the LVC model are the intrinsic growth rates, which can be assumed to be influenced by environment and its change.

We performed a theoretical analysis of the LVC model, based on eigenvalues of the Jacobian matrix. It showed that the stability of equilibria – in contrast to the composition of equilibria and thus the feasibility - is influenced by relative intrinsic growth rates. Thus, changes in intrinsic growth rates can lead to stability changes. By a numerical study in a space of randomly chosen competition coefficients (between similarly weak/strong competition to very different competition) within each community, we could identify the region of this changeable stability: it is located between an area of always stable equilibria in communities with similar and weak competition and the nonstable area of communities with differing competition strengths. This area of changeable stability shrinks and moves closer to communities with homogenous competition strengths with increasing community size.

Furthermore, we are upscaling the complex forest dynamics model TreeMig (which itself was upscaled from an individual based patch model), by metamodelling to a Lotka-Volterra competition model.

Linking Lotka-Volterra models to the microscale of individuals

Thorsten Wiegand; Samuel Fischer.; Andreas Huth

Helmholtz Centre for Environmental Research GmbH - UFZ

Transporting critical information across scales is one of the major issues in ecology. For example, it is unclear how to transfer the essence of pattern-forming processes operating at the level of individuals (i.e., the “microscale”) into analytical models of community dynamics with “macroscale” state variables such as species abundances. These population models are based on bookkeeping of reproduction and mortality, but their phenomenological parameters are usually not tied to processes and patterns at the microscale. Conversely, individual-based models (IBM) are formulated at the microscale, and macroscale properties emerge from the simulated behavior of individuals, but they lack analytical tractability. We propose here a hybrid modelling approach that takes advantage of the best of these two worlds and apply it to multispecies models of species-rich forests.

To link between scales in forests, we use neighborhood crowding indices to mechanistically describe neighborhood competition for individual trees, and show that estimation of their population averages results in summary functions of spatial point patterns. This approach leads to transfer functions, which express in our example the population-level interaction coefficients α_{ij} as functions of the individual-level interaction coefficients β_{ij} and measures of the emerging spatial patterns. Parameterizing the transfer functions needs to take possible abundance-dependency of the measures of spatial patterns into account. By analyzing the spatial patterns of trees in 21 large forest plots (25 – 50 ha, from the ForestGEO network) we find a general and negative abundance-dependency of conspecific aggregation, with stronger negative abundance-dependency as latitude increases, and individual-based simulations allow us to identify the mechanisms underlying these patterns.

The proposed framework provides analytical expressions that allow to study the role of pattern-generating microscopic mechanisms and processes on macroscale community dynamics and stability. Use of corresponding IBMs allows to check that the hypothesized mechanisms and transfer function approximations work as expected, and they allow for extending the theory into the analytically intractable domain.

SMART Modeling for an Individual-based Ecology in a Changing World

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In the Anthropocene, landscapes are undergoing a multitude of transitions. They are exposed to the ongoing climate change, but also targeted transformations in various sectors of the landscape management. Thus, one grand challenge of the future is the identification of development paths which keep these landscapes multifunctional. This requires a methodology for the provision of 'robust pictures of the future' at a large extent, but a resolution which matches the operational needs of the stakeholder group to be supported. This task requires a new generation of terrestrial environmental models which are (i) Scalable, (ii) Mechanistically sound and account for cross-compartmental effects chains, (iii) of Adjusted complexity, (iv) Robustly predictive, and (v) regionally Transferable. We call this type of models SMART.

This directly leads to the question of whether these is a special modeling strategy which makes the models SMART. We tackled this question by a “transfer of concept” approach as, in hydrology, there exists already a promising SMART modeling strategy. This led to the idea of systematically checking its transferability to ecology. In this talk, we will present some key findings of this transferability check by accounting for the particular importance of individual-level processes in ecology. We will come up with some components of a SMART Modeling Strategy in Individual-based Ecology, address challenges for future work, but also show the potential of the strategy.

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25. Integrating mechanistic modeling and machine learning for environmental problem-solving and supporting transformation

Deep learning for likelihood-free inference in complex computer simulations

Florian Hartig

University of Regensburg

Likelihood-free inference methods such as Approximate Bayesian Computation (ABC) or Synthetic Likelihood (SL) are used to calibrate simulation models whose likelihood function is unknown or intractable. In recent years, deep learning models have emerged as a promising new approach in this field, especially for complex data that cannot be easily reduced to simple summary statistics. In this talk, I will review the principles of likelihood-free inference and discuss the advantages of deep learning models in this area. I will present two recent case studies that illustrate the promise of machine learning and deep learning for model calibration. I will also discuss how deep learning can be combined with ABC to generate statistically valid confidence intervals for model calibration.

Linking non-parametric upscaling of agent-based models to machine learning

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The problem of scaling up from tractable, small-scale observations and experiments to prediction of large-scale patterns is at the core of ecological theory and application, and one of the central problems in ecology. We present a general non-parametric framework to upscale spatially-explicit and agent-based models to predict landscape scale dynamics based on individual-level information, but without simulating the computational demanding interactions among individuals with brute force.

The idea is to design a state space, defined by the important state variables of a small-scale model describing the dynamics of hundreds or thousands of individuals within a patch, and to divide it into a finite number of discrete states. Similarly, the external drivers are divided into a finite number of discrete conditions. For a given time interval, transition probabilities between states are then tallied by monitoring extensive simulation runs of the small-scale model that need to cover the entire range of initial conditions, plausible parameterizations, states and external drivers that may occur for the desired application. If the space of external drivers is not too high, the original small-scale model can be replaced by the transition probability matrices, resulting in Markov chain models. However, in the more general case of a higher dimensional space of external drivers, machine learning, such as deep neural networks, are a promising approach to estimate the transition probabilities in dependence on the environmental variables.

A hierarchical perspective then embeds the upscaled small-scale model into a larger scale model where the dynamics of the states of each patch are driven by the transition probabilities, depending on the environmental variables, and additional larger-scale rules govern possible spatial interactions among patches. This general upscaling approach uses detailed agent-based model simulations to train a meta-model based on states and transition probabilities and therefore accounts for the full complexity of the agent-based model, but views the system only through the filter of the states that reflect what is regarded as important at the large scale.

A hybrid modeling approach for spatiotemporal bird migration forecasts based on weather radar data

Fiona Lippert; Bart Kranstauber; Patrick Forré; E. Emiel van Loon

University of Amsterdam

Operational weather radar networks make it possible to monitor the movements of migrating birds over unprecedented spatial extents. The collected data has become invaluable for developing bird migration forecasts that help evaluate the risk of human-wildlife conflicts, such as collisions with wind turbines or aircraft. Given an accurate migration forecast, stakeholders can develop effective mitigation strategies that minimize both fatalities and economic costs.

Existing bird migration forecasts rely on data-driven models that learn relationships between local environmental conditions and the corresponding migration intensity observed by the radar. While these models typically treat each point in time and space independently, the underlying migration process is inherently spatiotemporal with strong dependencies between locations along the migration route. To resolve this mismatch, we combine a mechanistic metapopulation model, describing movements across the Voronoi tessellation of radar sites, with neural networks that learn the unknown components of the mechanistic model and their relations to environmental conditions from data. The resulting hybrid model is formulated as a recurrent graph neural network, called FluxRGNN, and can be trained end-to-end to match historical radar observations.

We use this approach to make 72-hour forecasts of nocturnal bird migration over Western Europe. Our results show that FluxRGNN, with its spatiotemporal structure, can predict migration intensities more accurately than local regression models. Moreover, the underlying mechanistic model makes it possible to disentangle aerial movements from local take-off and landing dynamics in an unsupervised way. The generated forecasts thus provide a comprehensive picture of the migration process, and can be used, for example, to reason about the spread and accumulation of pathogens like avian influenza.

In principle, our method can be applied to any sparsely observed spatiotemporal system dominated by collective movement or transport processes and has thus broad applications in ecology and environmental science.

Double machine learning for environmental sciences

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Hybrid modeling is a particular case of semi-parametric modeling and an emerging trend in environmental sciences [1]. It refers to the combination of parametric and machine learning models, where non-parametric machine learning models are substituted for portions of the parametric equation to represent complex functions. These models are inferred concurrently with the equation parameters from the available data. Hybrid modeling can describe complex relationships while maintaining scientific interpretability.

We propose the use of Double Machine Learning (DML) as a causally interpretable framework for fitting specific types of hybrid models [2]. DML is a semiparametric modeling tool widely used in the econometric literature for causal effect estimation. DML leverages machine learning algorithms to model non-parametric relationships while retaining important theoretical properties such as unbiasedness and statistical efficiency in parameter estimation. Despite its potential, it has yet to be explored for its applicability in hybrid modeling for geo and environmental sciences.

We demonstrate the applicability of DML in two classical problems from the study of ecosystem carbon fluxes. Both fit into the context of effect estimation of meteorological drivers on carbon fluxes. First, we employ a classical DML methodology to estimate the Q10 parameter, representing temperature sensitivity in ecosystem respiration (RECO). We show that 1) DML yields estimates that are more robust to regularization techniques common in modern ML implementations such as deep neural networks, and 2) it accurately provides confidence intervals for the estimated parameter. Second, we tackle the flux-partitioning problem, which aims at separating the net carbon flux (NEE) into its main contributing gross fluxes, namely, RECO and gross primary production (GPP). We use the light use efficiency (LUE) model to parameterize GPP, and we show that DML can retrieve a complex parametrization for the heterogeneous effect of the light. In our study, we demonstrate that the obtained partitions of the NEE align with traditional methods such as daytime and nighttime approaches. Furthermore, we find a consistent functional relationship between vapor pressure deficit (VPD) and LUE and detect a realistic response of post-rainfall respiration pulses after prolonged dry periods.

Overall, DML offers a promising framework for developing hybrid models with potential widespread application in environmental sciences.

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26. Beyond prediction: application of machine learning to gain new ecological insights

Species distribution models based on ML and DL - can we reliably infer ecological effects?

Maximilian Pichler; Florian Hartig

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Species distribution models (SDMs) increasingly use Machine learning (ML) and deep learning (DL) algorithms to describe the response of species to environmental predictors. The main reason to prefer these models over statistical models such as logistic regression is their superior predictive performance. A concern, however, is that this comes at the cost of explanatory power, in particular because i) ML and DL are more likely to exploit spurious correlations in the data and ii) because explainable AI (xAI) tools that extract effects or response curves from fitted models are often sensitive to feature collinearity.

Here, we show that all of these concerns are justified, but can be alleviated by appropriate methodological choices. First, similar to statistical models, a prerequisite for ML to learn correct causal effects is that feature selection must be based on causal principles, such as conditioning on confounders following Pearl's backdoor adjustment. We also show that this can increase the generalizability of the models, for example when predicting under climate change. Second, appropriate explainable AI (xAI) tools must be used: We propose to use Average Conditional Effects (ACE), which are robust to feature collinearity, to extract effects from ML models. Finally, the choice of ML algorithm is crucial. We show that if the other two conditions are met, neural networks and boosted regression trees are better suited than random forest to reliably separate collinear effects.

We conclude that under the right conditions and with the right tools, predictive ML models can provide more reliable effect estimates (e.g. about the environmental niche). Moreover, as a byproduct, causally constrained ML models often exhibit lower generalization errors, which is relevant when trying to build models for extrapolation, as is done in climate change predictions.

A comparison of machine learning and statistical species distribution models: quantifying overfitting supports model interpretation

Emma Chollet Ramampiandra; Andreas Scheidegger; Jonas Wydler; Nele Schuwirth

Eawag

Species distribution models are commonly used to predict how species respond to environmental conditions. A wide variety of models exist that vary in complexity, which affects their predictive performance and interpretability. To inform environmental management, it is important to use a model with a reasonable level of complexity that captures the true relationship between the response and explanatory variables as good as possible rather than fitting to the noise in the data.

In this study we ask: 1) how much predictive performance can we gain by using increasingly complex models, 2) how does model complexity affect the degree of overfitting, and 3) do the inferred responses differ among models and what can we learn from them?

To address these questions, we applied eight models of varying complexity to predict the probability of occurrence of freshwater macroinvertebrate taxa based on 2729 Swiss monitoring samples, and compared them in terms of predictive performance, overfitting and learned response shapes, during cross-validation and for out-of-domain generalization.

We found that, contrary to our expectations, all models predicted similarly well during cross-validation, while no model performed better than the null model during out-of-domain generalization. We also found that more complex models predicted slightly better than standard statistical models but were prone to overfitting, which impeded the interpretation of the learned response shapes. Thus, in this study, the minor gain in predictive performance from more complex models was outweighed by the overfitting.

Ecological field data that is used as model input or for calibration is typically prone to different sources of variability, from sampling, the measurement process and stochasticity. We therefore call for caution when using complex data-driven models to learn about species responses or to inform environmental management. In such cases, we recommend to compare a range of models regarding their predictive performance, overfitting and response shapes to better understand the robustness of inferred responses.

Exploring spatial autocorrelation and variable importance in machine learning models using patternograms

Jakub Nowosad

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The concept of patternogram is a novel approach to understanding spatial autocorrelation of multiple variables, inspired by the traditional use of semivariograms in geostatistics. Unlike semivariograms, patternograms allow to use any dissimilarity measure and can be applied to points or rasters with many variables/layers.

Patternograms allows for various types of spatial data analysis, including the interpretation of the results of spatial machine learning models. Typically, a response variable and a set of raster layers representing various predictors are required for such analysis. A machine learning model is applied to a subset of available points, and its result is validated on the remaining points. Some machine learning methods allow directly deriving variable importance - the importance of each predictor on the results. Patternograms can be used to show spatial autocorrelations of the given sets of predictors weighted based on their importance. Moreover, patternograms can be created for each predicted range of values or category separately.

The process of creating patternograms involves normalizing the values of the original predictors by scaling their values and then multiplying each predictor's values by its importance. This operation gives larger values for more important variables and smaller values for the less important ones. Finally, patternograms can be created to show the general dissimilarity of the (weighted) predictors with distance, or to show the dissimilarity of the (weighted) predictors with distance for different predicted categories.

The patternogram concept is not specific to any particular machine learning model or data type. It can be applied to any machine learning model that uses spatial data, including regression and classification problems. The goal of patternograms is to help visualize and interpret the results of machine learning models for spatial data. This talk will present the concept of patternogram, its potential applications, and a detailed description of the methodology involved.

Spatio-temporal model and machine learning method reveal patterns and processes of migration under climate change of North Pacific spiny dogfish

Yuki Kanamori[1]; Toshikazu Yano; Hiroshi Okamura; Yuta Yagi

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Climate change has disrupted natural phenological patterns, including migration. Despite extensive studies of phenological shifts in migration by climate change and driving factors of migration, a few issues remain unresolved. The first issue involves the complex effects of driving factors on migration with interactions and nonlinearity. Complex descriptions of the relationship between species and migration-driving factors make it difficult to interpret the results of analyses; therefore, method for an easily interpreting the results is needed. The second issue involves partitioning of the effects of factors into spatial, temporal, and spatio-temporal effects. When data include both temporal and spatial information, the interpretation of the effect of the factor on species occurrence (e.g., regression coefficient) is vague; does the factor affect the variation in species occurrence spatially, temporally or both? Use of the partitioning approach can lead to further understanding of migration, including whether species actively seek out specific conditions or merely react to changes in conditions. Here, to elucidate the migration patterns as well as the driving factors under climate change, we first examined long-term changes in the timing and geographic location of migration by applying a spatio-temporal model to ca. 5-decade time series data of the Pacific spiny dogfish. We then evaluated the spatial, temporal, and spatio-temporal effects of driving factors (sea surface temperature [SST], depth, productivity, and magnetic field) on seasonal occurrence patterns using a machine learning model. We found that the migration area did not change over ca. 5 decades, whereas the migration timing advanced by a month after 2000. The spatial effects of magnetic field and depth were consistently large and the spatial and spatio-temporal effects of SST increased in the migration season, even though temporal effect of SST was always weak. These results suggest that the migration area of spiny dogfish was stable over time because their spatial distribution was determined by geographic features, whereas the migration timing advanced by tracking a suitable SST location which increased steeply after 2000. Therefore, temperature and other factors simultaneously influence migration under climate change, highlighting the importance of considering both biotic and biotic factors.

Tracking shifts of forest ecotones in aerial imagery with deep learning

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Forest ecosystems are sensitive to global change, especially at the ecotones we often expect high sensitivity to changes in climate, disturbance regimes or land use. For instance, the treeline ecotone is expected to move upward in elevation with global warming. With the advent of machine learning, tools like computer vision are at our hands to monitor ecotones over large scales using remote sensing data. We investigated the spatiotemporal development of the ecotones bracketing the subalpine forest belt in a protected forest landscape in the European Alps. Our specific objectives were, first to identify trees and shrubs on historic and recent orthophotos with deep learning under special attention on how to integrate multiple sensor types into one computer vision framework. Second, to map the a) treeline and b) montane-subalpine ecotone based on the computer vision outputs and third to describe spatiotemporal changes in both ecotones.

We base our analysis on historic and recent aerial images of Berchtesgaden National Park covering roughly 210 km² in nine time steps from 1953 to 2020. The images have been obtained by using analog (panchromatic and color infrared) and digital (color infrared, RGB) cameras. We manually interpreted randomly distributed 0.5 ha segments of all time steps to obtain training data for deep learning. The training data contains more than 110,000 annotations of coniferous and broadleaved trees and shrubs, as well as standing dead trees. We tested a set of instance segmentation frameworks and compared individual models for each sensor type with models integrating all sensor types.

We used the inference of the best performing model architecture to generate wall-to-wall tree maps for all time steps. Using structure and composition of the tree maps, we delineated the ecotones and tracked changes over time. As a general trend, we found that subalpine forests gained more crown cover over time. However, we did not find general patterns of ecotones shifting upward in elevation, but were able to identify areas of change and stability.

Assessing long-term changes is critical for better understanding ongoing and future ecological changes. Here we used a unique combination of historic and recent aerial imagery with deep learning to track key ecotones in mountain forests for almost 70 years. Changes in these ecotones can be a challenge to conservation, restoration and management. Our approach can help to address these challenges, e.g., in the combination with habitat modelling.

Model evaluation strategy impacts the interpretation and performance of machine learning models

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Agricultural yields are vulnerable to extreme weather events, such as droughts, floods or heatwaves, but the relationships between growing-season climate conditions and harvested yields are complex and nonlinear. Consequently, extreme crop yield failure may be caused by a combination of weather events that would not individually be considered extreme. For example, co-occurring hot and dry weather conditions can impact crop yields simultaneously. A more complex temporally-compounding example is the phenomenon of 'false spring', which causes damage to crops when all of three conditions are met: abnormally warm temperatures in early spring, sufficient above-freezing days for the plant to enter a vulnerable stage of development, and finally a subsequent frost.

Machine learning techniques are capable of learning such nonlinear relationships from data, and interpretable machine learning methods have been used in recent studies to explore the influence of seasonally-aggregated weather data and/or hand-picked extreme climate indicators on crop yields. However, robust model evaluation on spatiotemporal datasets is challenging, and commonly-used interpretable machine learning methods have been found to return implausible, contradicting or ambiguous results.

We train machine learning models to predict simulated maize yield variability from growing-season climate indices, and assess the impact of model evaluation strategy on the interpretation and performance of the models. By training models to emulate a process-based crop model (LPJmL), we are able to comment on the plausibility of the resulting model 'explanations' and determine the best choice of evaluation strategy. We then employ this methodology to identify meteorological drivers of yield failure from a range of simulated crop model datasets, compare the identified drivers between crop models, and explore interactions between drivers learned by the machine learning models. Ultimately, our goal is to present a robust method for the identification of compound meteorological drivers of crop yield failure.

Disentangling the role of weather drivers and forest structure on large-scale tree mortality with Transformer

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Globally, forests act as a carbon sink and help slow climate change. However, recently there has been an increase in weather-induced tree mortality. The aggregate response of forest to weather drivers also depends on forest structure variables like age, diameter and leaf area index. Forest structure variables are a function of long-term weather, thus making it difficult to disentangle the impact of weather on large-scale tree mortality. Deep learning is known to capture long-term dynamics across multiple variables with different modalities, but typically, they are data-hungry. To this end, we generate a hundred thousand years of weather using a stochastic weather generator AWEGEN. Further, we use FORMIND, a physiological forest model, to simulate forest dynamics. A Transformer model is trained to predict tree mortality using weather data and summarised forest structure variables. The co-attention module helps generate the attention maps for each weather and forest structure variable. Finally, the attention maps are grouped to identify the dominant weather drivers of large-scale tree mortality in a forest with different forest structures.

Mapping joint species distribution model predictions on the known species interactions space to increase causal understanding

Christophe Van Neste; Quentin Groom

Meise Botanic Garden

Species distribution models that ignore the interactions and dependencies between organisms will always be viewed with suspicion, because those interactions and dependencies are so important to the success or failure of an organism to survive and reproduce. In order to provide reliable policy relevant information on biodiversity we have to address the complexity of biological systems and their relationship with the environment and other organisms. Policy decisions on wildlife management, conservation, land use and infrastructure can have unpredictable consequences due to their complexity. GUARDEN is a European Horizon project to safeguard biodiversity by building ecological models and offering its data-driven results to policy and decision makers by virtue of easy to use tools.

By project design we will go beyond predicting and prove our predictions to be easily understandable and data-driven. Part of our team is developing a deep learning framework for species and habitat distribution modeling, while another is responsible for including species interactions data in a dependent task. For this task, our first aim is to test the generated joint species distribution models (SDM) for compatibility with interaction data retrieved from GloBi (www.globalbioticinteractions.org). Within the interaction network we will retrieve all triads (sets of three taxons mutually connected) based on the different interaction types to perform a triad count analysis. Overrepresented triads of interaction types for the species modeled in the GUARDEN case studies will be correlated with the model predictions. We are building a Python package using a neo4j graph database to conduct these studies. At the conference we will present the initial results and a web tool to perform these interaction-triad SDM informed correlations. Furthermore, we will do a qualitative analysis of the GUARDEN case studies data and models to test if the triads can be used for causal understanding. In a next iteration, we aim to predict new triads in the network and quantify how many of them have a similar positive correlation to the results from the SDM models.

Dynamics of collective plant macrophenology from crowd-soruced data

Karin Mora; Jana Wäldchen; Michael Rzanny; Guido Kraemer; Ingolf Kühn; Patrick Mäder; Sophie Wolf; Teja Kattenborn; Miguel Mahecha

Monitoring changes in phenology, i.e. changes in flora states, is key to understanding the impact of climate change on ecosystems and biodiversity. Crowd-sourced data from smartphone applications are gaining in value in many ecological applications and are especially relevant for automated species recognition. However, the potential of crowd-sourced data for studying phenology at macroecological scales has not been deeply explored. We aim to quantify the collective phenology of plant co-occurrences based on citizen science data.

We analyse crowd-sourced German plant observation data collected with the smartphone application Flora Incognita, which identifies plant species native to Central Europe from images in real time using deep learning. We propose that the dynamics of collective flora behaviour is embedded in the temporal co-occurrence observations. To extract this collective phenological dynamics we propose the manifold learning method isometric feature mapping. As this approach is data driven no a priori assumptions are made about how to define collective behaviour. We propose a complexity measure to characterise the dynamics across large spatial scales.

Our results demonstrate that the phenology of macroecological patterns can be effectively detected from crowd-sourced plant observation data. The strong collective flowering in spring and summer allows us to clearly characterise phenological transitions, specifically the faster changes in spring compared to autumn. The emerging complexity measure of collective behaviour is an indicator for linear and nonlinear temporal changes in macroecological patterns in the summer and the rest of the year, respectively.

Despite biases and uncertainties associated with opportunistically collected crowd-sourced data it is possible to derive meaningful indicators for monitoring plant phenology. In the near future multi-year records of such data will be available to explore phenological shifts and how they are impacted by climate change in near real time.

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28. The use of artificial intelligence in ecological modelling

Metamodelling of Ecological Models in the context of Digital Twins

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Ecological models can run into computational challenges when (1) the model is very time consuming to run or (2) the model is relatively fast to run, but requires a large number of model instances to run (e.g. in parameter estimation) or needs to scale to larger areas or time frames. In such sitations, it can be beneficial to use a faster replica of the original model, which is often referred to as metamodelling.

In its most general form, metamodelling is a technique to replace an original complex model with another model. Typically, the metamodel should be capable of capturing the behaviour of the original model and, at the same time, should have benefits over the original model (e.g. computationally faster prediction). In the literature, metamodels are also often referred to as surrogates or emulators, for which usually machine learned models are used, such as a Gaussian Process Regressor, Neural Network or Random Forest.

Fitting a metamodel to the original model comes with several challenges, such as dealing with spatial and temporal dimensions, multi-output problems, stochasticity and efficiently sampling training data from the original model.

When ecological models are used in the context of digital twins, frequent or even near real-time updates of input data can also lead to frequent model –data comparison, recalibration or optimization and updated scenario predictions – each of them potentialy requiring to run a large number of model simulations. In such large-scale contexts, the wall clock time of even a fast model can become a bottleneck. Here, we identify the use and challenges of metamodelling of ecological models in the context of Digital Twins. We illustrate our arguments by means of various use cases from the Horizon Europe BioDT project, including grassland modelling, pollinators and ecosystem services.

Towards a bottom-up assessment of the climate sensitivity of Europe’s forests

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A large number of stand and landscape level forest models exist in Europe, developed and parameterized to capture the diversity of European forests. These models have been used extensively to address questions of forest dynamics under climate change. Studies based on those models paint a nuanced picture of potential climate change effects at the local scale, but for considerations at the continental scale this detailed information remains underutilized. Here, we exploit deep neural networks to harness these models and assess the climate sensitivity of Europe’s forests on the macroscale. Using a community approach, we established a central database of local climate change simulations for Europe covering over 1.1 million forest simulations across 13’500 locations from 16 different forest models. We synthesized these simulations together with auxiliary information of climate and environmental conditions using deep neural networks. Hereby, the networks learn a representation of vegetation dynamics across models and wide ranges of environmental conditions and forcings. Using the trained deep neural networks to predict vegetation dynamics across the full spectrum of climate and environmental conditions within a species’ current distribution range, we investigate the effect of the changing climate on different metrics of competitive strength for ten European tree species. Competitive strength is assessed by the potential of losing dominance in a stand, the change in density and the change in growth potential between current and future climate conditions. We found idiosyncratic species responses to different climate change scenarios. Further, we found that the species show different responses across their distribution range. Specifically, the response at the cold edge often varies from the response at the warm edge of the niche. Together, this study presents a new approach to transfer knowledge based on detailed process-based analysis on the effect of climate change from the local scale to the macroscale.

Scaling connectivity conservation planning with deep reinforcement learning.

Julian Equihua; Ralf Seppelt; Michael Beckmann

Helmholtz Centre for Environmental Research - UFZ

Habitat fragmentation constitutes one of the biggest threats to biodiversity. When natural landscapes get divided by land use, species may be incapable of moving around them to search for resources and to mate, reducing gene flow. A lot of research has been conducted in the theory and practice of estimating the connectedness of landscapes and towards the reversal of fragmentation by restoring corridors or stepping stones (connectivity conservation planning). This has resulted in an ever increasing amount of connectivity indices which have mainly been used for scenario analysis. Some of these indices are highly nonlinear and computationally expensive to calculate making them particularly difficult to target in spatial optimization. Such is the case of the Probability of Connectivity Index (PC), one of the most widely used graph-based indices to analyze structural and functional connectivity. We will show how to model a connectivity planning problem that targets the PC as a markov decision process and solve it using Deep Reinforcement Learning (RL); an artificial intelligence paradigm that has recently excelled in complex decision-making tasks. RL comprises a class of solutions focused on training an artificial agent (with a deep neural network under the hood) to achieve a goal through trial-and-error interaction with a virtual environment. In our setting, the agent moves around a large real world landscape (LULC raster map) and may restore vegetation patches of varying sizes. This happens until a preallocated budget for habitat restoration is spent. In each time step the agent can only partially observe the landscape and receives feedback (a reward) on the local improvement in connectivity measured by the PC. When all the budget is spent the training episode ends, the agent receives the overall improvement in PC as a final reward and a new episode starts. We show that this training loop enables the production of high quality solutions to problems with more habitat patches and more land-use classes with associated restoration costs than those that currently exist in literature.

Combining machine learning and coastal ocean models for spatial predictions of seagrass seasonal growth: an example based on the Arcachon bay's Zostera Noltii meadows.

Héloïse Muller; Etienne Auclair; Aubin Woehrel; Martin Marzloff

Ifremer

Seagrasses form habitats of high ecological and patrimonial value, as they support a rich biodiversity, contribute to water quality, protect coastal areas from erosion, storms and floods and play a role in carbon sequestration and storage. However, in a context of global changes, these underwater meadows are, similarly to other coastal habitats, vulnerable to environmental and anthropogenic stressors. Worldwide, seagrass meadows have been declining at an annual rate of 2 to 5% over the past 60 years (Duarte et al., 2008). In the Arcachon bay in southwestern France, the total surface area of Zostera spp. seagrass beds drastically declined between 1988 and 2008, by 33% for Z. noltei and by 72% for Z. marina meadows, respectively (Plus et al., 2010). It is primordial to understand and predict their ecological dynamics and responses to environmental stressors to inform effective conservation plans. Modeling is one of the means to meet these objectives. Thus, determinist process-based modelling has provided important insights on the drivers of seagrass dynamics and has enable to capture seagrass seasonal growth. However, given the computation time and the complexity of the transposition of this kind of model to other areas and also the lack of knowledge about all the processes that control seagrass dynamics, it is necessary to consider alternative modeling approaches, based in particular on artificial intelligence, to simulate long-term scenarios of seagrass evolution. The aim of this work is to develop an innovative model framework that combines a machine learning local seagrass growth model and a coastal ocean model predicting environmental features. Using this framework on the Z. noltei meadows of the Arcachon bay, the local model was shown to make accurate predictions of seasonal growth while the global framework enabled spatio-temporal predictions in the whole bay using forcing or coupling, two alternative versions of the framework, which highlights a strong potential for making long-term prediction of seagrass dynamics.

Modelling global tree species composition

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The conservation and restoration of forest ecosystems require detailed knowledge of the native plant compositions across the globe. Here, we map the suitable habitat of 10,590 tree species at a resolution of 30-arc seconds, combining geographic dispersal constraints, based on reported native ranges, and species distribution modelling to map ecological suitability based on climatic and pedologic variables. The scale of our models, both spatially and regarding the number of species, allowed us to consider the global composition of tree species at very high granularity. We also assessed the impacts of historical forest cover loss and climate change on tree diversity in forests. Such insights may support management decisions for conservation.

Modelling distributions for a large number of species was facilitated by our implementation of an environmental niche model in Google Earth Engine, a cloud-based platform for geospatial analysis, and its implementation of machine learning algorithms, such as random forests and gradient boosting trees. We attempted to cover the largest number of tree species by compiling multiple databases, cumulating to over 26 million occurrences. To tackle spatial biases typically found in large global occurrence databases, we included smaller databases targeting areas that are generally undersampled. We found that having enough data for each species is key to training accurate distribution models, highlighting the role of increasingly large occurrence databases.

The analysis of global tree composition revealed major biogeographic boundaries complemented with regional environmental gradients determining a local signature of tree lineage assembly globally. Furthermore, we found that historical forest loss has significantly restricted the potential suitable range of tree species in most regions, especially in the Mediterranean and tropical dry forest biomes. In contrast, tropical moist and boreal forest biomes maintain high levels of integration and still harbor extremely large-ranged tree species. Biomes are further projected to differ in their response to climate change, with species in coniferous and boreal forests able to track suitable habitat through latitude or elevation shifts, while tropical dry and Mediterranean ecoregions were predicted to experience the highest species loss.

Our findings highlight the need for preserving the remaining large forest biomes while regenerating degraded forests in a way that provides resilience against climate change. Furthermore, our cloud-based data integration and modelling approach demonstrates the potential of high computing infrastructure to support the documentation of global biodiversity patterns at scales and resolutions unattained before, therefore allowing fine-grained, global analyses such as those presented here.

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29. Ecological Models for the Management of social-ecological Transformations

Aligning agent-based modelling with multi-objective optimization to minimize trade-offs of an agricultural transformation

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In Germany and Europe, especially in productive agricultural landscapes, today's agriculture is oriented towards monofunctional management. This means that food, fodder and biomass are produced in large quantities, but little consideration is given to other ecosystem services (e.g. flood protection, climate regulation or landscape aesthetics) and biodiversity. Accordingly, a transformation of agriculture ("Agrarwende") is being called for by societal and political actors. The aim is to make agricultural landscapes increasingly multifunctional, i.e. maintain or promote the diverse functions of agro-ecosystems and the ecosystem services they provide. In addition, there is the need to adapt to the increasingly noticeable impacts of climate change. However, such a transformation comes along with different trade-offs. Such trade-offs can arise, for example, due to different expectations of societal groups regarding the use of landscapes. A prominent example is the production of cheap food through intensive agriculture on the one hand versus nature conservation and improvement of groundwater quality on the other. We present an inter- and transdisciplinary approach, linking contributions from environmental economics, behavioural science and landscape ecology. Using the example of North-West Saxony, a very productive agricultural landscape in central Germany, we apply an agent-based model as well as multi-objective spatial optimization. Both approaches identify trade-offs that arise due to the application of different agricultural management practices (e.g. tillage, fertilization, crop rotation) and their respective effect on ecosystem services (e.g. agricultural production, water quality, drought protection, carbon sequestration) – but from different perspectives: the agent-based model analyses socio-economic trade-offs based on farmer’s behaviour and different policy instruments while the landscape’s biophysical potential as well as trade-offs between ecosystem services are identified by the optimization algorithm that is coupled with ecological models. Furthermore, the analysis considers different climate scenarios and their impacts on multifunctionality and trade-offs. The results of both approaches are then aligned to determine ‘optimal’ allocations of agricultural management practices such that trade-offs are minimized. These results in combination with further analyses of the agent-based model and a study about society’s ecosystem services preferences allow the identification and development of policy instruments that aim at supporting a successful agricultural transformation. Additionally, the high level of stakeholder integration at the different modelling steps ensures a high degree of societal and practical relevance of the results.

Applying the new developed rubber plant functional type in the Community Land Model (CLM5) to an environmental-friendly ecosystem

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Environmental-friendly ecosystems (EFEs) offer a number of benefits to humans and other organisms, e.g. they show low greenhouse gas emissions, high biodiversity and ecosystem productivity. Land surface models can be used to make predictions about EFEs and look into long-term sustainability of EFEs. This may be of special importance in the tropics, where conversion of forests to tropical woody crops (oil palm and rubber) has been on the rise, especially in Southeast Asia. Here, we use the Community Land Model (CLM5) model that has recently parametrized rubber as a plant functional type and applied it, for the first time, to an EFE, namely a jungle rubber plantation in Jambi, Indonesia. We also compare our jungle rubber model simulations with a model that simulated a monoculture rubber plantation.

Our modeling results generated the following: (i) CLM5 predicted a higher net primary productivity for jungle rubber plantation than monoculture rubber plantation (961 vs 890 g C m-2 yr-1). Similarly, CLM5 predicted a higher transpiration for jungle rubber plantation than monoculture rubber plantation (928 vs 640 mm yr-1). These model predictions are in-line with the ground measurements. (ii) CLM5 predicted a lower latex harvest yield for jungle rubber plantation than monoculture rubber plantation. This prediction, however, was much stronger than measurement (95 % vs 78%). (iii) CLM5 predicted a higher fine root biomass for the EFE jungle rubber plantation than monoculture rubber plantation, suggesting that to reconcile jungle rubber plantation simulations with measurements, some parametric adjustments in carbon allocation to fine roots and latex harvest need would be necessary. Overall, the direction of CLM5's prediction about carbon/water/nitrogen fluxes and states for EFE jungle rubber plantation versus monoculture plantation was in line with the ground measurements. CLM5 predicted that 68% of the jungle rubber plantation is forest trees – this is similar to observation. CLM5 also predicted much reduced soil N leaching for jungle rubber plantation indicating that jungle rubber plantation could act as a potential EFE in the future. The methods used in our study can also be used to study other EFEs such as those that involve biodiversity enrichment experiments.

A modelling tool to explore landscape management strategies to promote pest control and limit beet yellows disease spread

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The ban on the use of neonicotinoids makes it necessary to rethink the prophylaxis of beet crops. In recent years, outbreaks of green peach aphids (Myzus persicae), vectors of beet yellows viruses, have been observed, resulting in significant yield losses. A potentially effective lever to control aphid populations is the management of the agricultural landscape to limit the migration of aphids within fields and their dispersal between fields, and to promote the development and activity of natural enemies involved in pest biological control. The positive effect of landscape heterogeneity on biological control is now clearly accepted (Champlin-Kramer et al. 2011, Véres et al. 2013). However, while this general pattern is established, its translation into landscape management modalities is made difficult by the highly contextual nature of the processes involved (Karp et al. 2019). Landscape effects depend on the functional characteristics of pests and natural enemies (Martin et al. 2019), and can be strongly modulated by agricultural practices carried out locally in the fields (e.g., pesticide effects in Ricci et al. 2019). For highly polyphagous species such as M. persicae, it is necessary to think carefully about the mosaic of plants that make up the landscape, both host crops to pests and non-crop habitats.

We developed a spatially explicit model to explore the potential effects of deploying agroecological infrastructures, diversifying crop rotation or reducing field size in reducing green peach aphid populations and the incidence of beet disease at the landscape level. On existing agricultural landscape (modelled using GIS data), the model simulates aphid population dynamics (growth, movement, biocontrol by natural enemies whose abundance is modulated by the surrounding landscape structure, wintering), and virus transmission between beet plants and aphids. The model operates on a daily time-step and over several years, and integrates climatic conditions and agricultural practices such as the use of pesticides and sowing schedules.

A sensitivity analysis was carried out to determine the most sensitive parameters, which were calibrated using data from a multi-year survey of a monitoring network in France. In a second step, we tested the sensitivity of the model to landscape parameters. Finally, we tested contrasted scenarios of landscape management to identify the most effective ones for reducing disease incidence in the landscape. The outputs of the simulations will be used to discuss with stakeholders the conditions for the deployment of new management methods at the territorial scale.

Using models and multi-objective optimization tools to guide the transformation toward more sustainable agricultural systems

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A redesign of agricultural systems and landscapes is needed in order to halt the decline of farmland biodiversity and biodiversity-related ecosystem services, reduce environmental externalities and increase agriculture's socio-ecological resilience. This redesign should include an increase in agricultural landscapes complexity and a reduction in land use intensity. The implementation of agri-environmental practices (e.g. hedges, field margins, fallow land, reduced tillage, cover crops, etc.) can contribute to both aspects. Having reliable models, capable of representing the link between agro-environmental practices and the supply of various ecosystem services (e.g. food provision, water flow regulation, natural pest control), would play an important role within farmers' decision making process. At the same time, multi-objective optimization tools can help to analyze possible trade-offs among the supply of provisioning and regulating ecosystem services and the conservation of farmland biodiversity. They can support the identification of sustainable allocations for the agro-environmental practices, which allow to navigate trade-offs and maximize the considered objectives.

In our application, we performed a biophysical multi-objective optimization between farmland biodiversity, natural pest control supply (using parasitism of cereal aphids as indicator), water quality regulation and agricultural production. The case study area is the Schwarzer Schöps river basin, located in the East of Germany. Exchanges with an active network of local actors allowed for the identification of locally relevant agro-environmental practices (i.e. hedges, riparian buffers, grassed waterways, retention ponds, cover crops and reduced tillage) and their possible location of implementation within the river basin. The SWAT+ model is applied to assess agricultural production and water quality regulation. Indicators of land-use and management (e.g. share of semi-natural habitat, field size, share of reduced tillage) are instead calculated to predict proxies for farmland biodiversity and natural pest control. We analyzed the shape of the Pareto frontier and performed a spatial frequency analysis of the land use maps resultant from each Pareto solution.

Our presentation will discuss the impact of adopting agro-environmental practices on biodiversity conservation, natural pest control, water quality and agricultural production within the case study area. It will conclude with an outlook on how the identified hotspot areas for the implementation of agri-environmental practices can guide, together with local actors involvement, the redesign of agricultural landscapes toward more sustainable socio-ecological systems.

A GIS modelling approach to analyse landscape structure related capacities for field margin photovoltaics in Lower Saxony (Germany)

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In order to increase the availability of regenerative energy, more photovoltaic installations are one of the current aims in transformation efforts of the energy system. For rural landscapes, conventional approaches of photovoltaic expansions imply a competition of land use for food or for energy production in a mutually exclusive way. In the model presented here, we demonstrate the potential of an alternative application mode that minimises area requirements to gain regenerative energy by using only strips of the agriculturally least productive field margins. A combination of photovoltaic installations along margins with flower strips or self-organised plant succession as undergrowth with minimal management requirements may have a relevant effect to increase rural biodiversity by introducing habitats and connective landscape elements which are beneficial for a considerable variety of wildlife species.

Using remote sensing data and digital landscape models made available by the State Office for Geoinformation and Land Surveying Lower Saxony (Landesamt für Geoinformation und Landesvermessung Niedersachsen) we provide overall capacity calculations for the north-western part of the Federal State of Lower Saxony (Niedersachsen, Germany). With this approach we demonstrate, how to integrate a new landscape element to increase economic sustainability as well as ecological resilience. We differentiate suitability classes for energetic use as well as productivity classes. Furthermore, landscape connectivity aspects with regard to protected areas are analysed and quantified.

The work is part of the transdisciplinary research cluster “Lower Saxony Sustainably New” funded by the Ministry for Science and Culture of Lower Saxony. We employ a living lab approach to study transformation options in a socio-ecological context connecting technological, agronomic, cultural and nature conservation aspects in transdisciplinary research and development (www.vier-n.de).

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30. Modelling change in social-ecological systems – from conceptual reflections to promising case-based examples

Evaluating policy outcomes in complex land-use systems

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To inform the design of policies that effectively contribute towards sustainable development goals, reliable knowledge about both current system dynamics and potential pathways of transition is required. A comprehensive evidence base for policy advice thus needs to capture complex socio-ecological systems, including their biophysical mechanisms and diverse human-nature relationships and interactions. We contribute to the literature on socio-ecological systems modelling by stipulating the use of an existing and already shared terminology in terms of ontology, epistemology and semantics to connect data with theory and models. Here, we add in co-creation as an important element to engage with knowledge-holders from wider society. We present an operationalized conceptual framework for a transdisciplinary, co-productive approach for evaluating outcomes of land-use governance through an integrated policy assessment. The case of Nordic forest policies is then used to elaborate on the role of theory, model integration, and knowledge co-production. We argue that three main components are needed: 1) a comprehensive theory about the structure of the system and causal mechanisms therein, 2) a modular architecture that operationalizes data flows between various models and scales, 3) a procedure to integrate knowledge from multiple stakeholders to inform model set-up and increase relevance and legitimacy. The general idea of such a co-creative modular architecture for integrated policy assessment models can in principle be applied to any land use policy nexus.

Modeling rangelands as complex adaptive socio-ecological systems: An agent-based model of pyric herbivory

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Rangelands cover approximately one third of the earth's land area, at least one billion persons depend on these lands for their livelihoods, and most rangelands have been degraded by inappropriate land use practices. Overgrazing and suppression of fire have facilitated encroachment of woody plants in what formerly were more open grasslands. However, proper management of fire and grazing (pyric herbivory) can mitigate woody plant encroachment. The general ecological relationships involved in pyric herbivory are well understood but the factors that could motivate ranch managers to adapt fire and grazing schemes to changing environmental conditions are not. We describe a spatially explicit agent-based model of pyric herbivory that integrates biophysical and managerial components to simulate shifts in canopy cover of woody plants, forage production, and cattle production resulting from decisions to adjust grazing pressure (cattle stocking rates) and burning schemes (woody plant canopy cover threshold at which to initiate prescribed burns).

We evaluated potential usefulness of the model in simulating pyric herbivory within a complex adaptive systems context by simulating two suites of scenarios on a hypothetical 4000-ha ranch in the semi-arid rangelands of the southern Great Plains of the USA. We designed the first suite to evaluate ability of the model to generate expected patterns of pyric herbivory under fixed grazing pressure and burning schemes. We designed the second suite to explore ability of the model to simulate adaptive management in which managers were allowed to change grazing pressure and burning schemes based on changing ranch conditions (shifts in canopy cover of woody plants, forage production, and cattle production). Preliminary results confirmed ability of the model to generate expected patterns of pyric herbivory under fixed grazing pressure and burning schemes and suggested the model may provide a useful tool for exploring reciprocal feedbacks between biophysical ranch conditions and managerial decisions to alter grazing pressure and burning schemes.

Emerging societal tipping points in social-ecological system models

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Collective action is crucial to embark on sustainable development pathways. Rapid, large-scale transformation is needed to avoid catastrophic tipping points in increasingly intertwined social-ecological systems. However, the question of how collective, cooperative behavior - in which intelligent actors seek ways to improve their welfare in dynamic environments - is unresolved. To make progress in this area, mathematical models are essential. To date, however, there is no modeling framework that can address the elements of collective behavior from intelligent actors in complex biophysical environments in a consistent and understandable manner.

In this talk, I'll present work toward a mathematical modeling framework for this challenge, which integrates equation-based, equilibrium-based, and agent-based modeling into the dynamics of collective reinforcement learning. The agency of multiple actors originates from an established neuro-cognitive learning paradigm, reinforcement learning, which allows the explicit representation of transient, non-linear dynamics while maintaining a connection to equilibrium models in a transparent and understandable way. This approach offers an integrating perspective to investigate the critical leverage points and barriers of emerging abrupt transitions in collective learning towards sustainable outcomes in social-ecological systems.

A data driven approach to model responses of German North Sea fishing fleets to future scenarios

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The southern North Sea is an intensely used ecosystem where fisheries coexist closely with other human uses, many of them restricting the available fishing space. Offshore windfarms (OWF) and dedicated Natura2000 sites will represent the fastest growing human uses in the next two decades, increasing the overlap of spatial fishing restrictions and German fishing grounds from 2% to 20%. This will have strong effects on the fishery sector with regard to spatial dynamics, but also socio-economics and might trigger a transformation of the North Sea fishers as we know it. As part of a broader research project (SeaUseTip), we are developing an agent-based model (ABM) to depict and analyze current and future spatio-temporal dynamics of three German fishing fleets in the southern North Sea catching shrimp, flatfishes and Norway lobster. Our ABM relies on empirical data, e.g. economic, environmental and fisheries-related, and behavioral theories, e.g. habitual behavior, and bounded reality. Every agent (fishing vessel) makes daily decisions about whether and what to fish. Weather, fuel and fish prices, and the actions of their colleagues influence agents' decisions. To combine behavioral theories and enable agents to make dynamic decision, we implemented the Consumat approach, a framework in which agents' decisions vary in complexity and social engagement depending on their satisfaction and uncertainty. Every agent has three satisfactions and two uncertainties representing different behavioral aspects. Using pattern-oriented modelling, we parameterized weightings for these satisfactions and uncertainties for each fleet. We assessed the effect of future fishing restriction by comparing simulated fishing years of one baseline (state 2018) and several future scenarios. Results indicate that fishing effort will concentrate in the remaining open fishing areas and some fishers change their target species from offshore located flatfish to coastal shrimp. Our ABM aims to produce valuable knowledge about potential future spatio-temporal and behavioral changes of German North Sea fishing fleets, which may be used to produce effective marine spatial management. This is necessary for a sustainable human use of the southern North Sea that combines the achievement of renewable energy targets, nature conservation objectives, and the continuation of coastal fishing culture and marine food supply.

Modelling the motivation and acceptance dynamics for implementation of climate change adaptation measures – Realisation of Sponge City measures within different urban residential areas

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Which parameters accelerate and which slow down the implementation of sponge city measures to foster rain water retention? To answer these questions causal loop diagrams were developed including different feedback processes in dependence of the ownership structure of the buildings and their residents. Central variables are found to be consternation of drought and storm rain events, climate change awareness and economic considerations of the building owners and residents as well as the adaptive capacity and the attractiveness of the neighbourhood. The impact of different policies was also considered. Based on these qualitative models we investigated what deeper knowledge we can gain by using quantitative modelling approaches, i.e. using a top-down (System Dynamics) and a bottom-up approach (Agent-based). Because these models consists of a large amount of social or soft variables we discuss how such models may be quantified in top-down and bottom-up models in a reasonable way. To a large extent, the developed model concepts can also be used for other forms of climate adaptation in neighbourhoods.

A game-theoretic systematic of interactions and dynamics in the conservation and management of spatial ecosystem services

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Since many ecosystem services involve spatial scales beyond farm size, their preservation and management in agricultural systems depends on the interaction of the landowners. For the analysis of such interactive land use a dynamic generic land-use model is developed that considers that a landowner’s own payoff depends on the land use on neighbouring land parcels. The landowners’ payoffs are interpreted in a game-theoretic manner which allows for a game-theoretic classification of the different land-use dynamics generated by the model. The model is analysed to determine the proportion, spatial aggregation and temporal turnover of land-use measures. The model results are applied to a number of cases from the literature in which the management of ecosystem services involves a regional scale, including pollinator conservation, pest control, and coordination incentives for the conservation of species in fragmented landscapes.

Modelling changes in traffic-habitat interactions at a global scale

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Whereas the mobility of humans depends on networks of roads, the mobility of animals depends on barrier-free connections between high-quality habitat patches. Yet, road traffic forms an important barrier for animal movement and can be detrimental to the quality of natural habitats. To study this social-ecological interaction and its development over time, it is necessary to understand how road traffic volumes are influenced by socio-economic and demographic conditions and how they subsequently affect the connectedness and quality of habitats. However, in many countries there is a lack of data on traffic volumes, particularly for roads outside of urban areas (i.e. extra-urban roads), where the impacts of traffic on natural habitats are most severe. In this study, we have therefore developed a network-based Random Forest model to predict traffic volume (i.e. Annual Average Daily Traffic; AADT) on extra-urban roads. Making use of socio-economic, demographic and network topological predictor variables, we were able to predict AADT on all extra-urban highways, primary roads and secondary roads across the globe for four time-steps: 1975, 1990, 2000 and 2015. We tested the accuracy of the AADT model with a hold-out validation and by comparing AADT predictions for 1975 to empirical values. We then assessed how the traffic volumes affected the connectivity in protected areas (PAs) and Key Biodiversity Areas (KBAs) to identify social-ecological interactions. We obtained a high accuracy of the traffic volume model. Although we found that absolute traffic volumes were generally lower within PAs and KBAs than outside, in some regions the growth of traffic volumes was higher within these areas than outside. Furthermore, we found that traffic volumes were strongly determined by the social-economic conditions within a country and by the topology of the road network. Findings from this research can be used to develop urban- and transport planning strategies that minimise impacts on natural habitats. In the presentation, we will highlight challenges and solutions of collecting and modelling such social-ecological interactions at a global scale.

Balancing Cost and Benefit: A Theoretical Study of Fungicide Treatment in Multiple Fields

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Fungal diseases in crops result in significant economic losses for farmers. Optimal fungicide treatment coverage can mitigate these losses and maximize net economic gain. In this study, we developed an ODE model for the spread of pathogenic fungi and defined a net economic gain function based on the cost of fungicide treatment and the final harvest. Numerical and analytical computations were performed to study the optimal fungicide coverage. This study extends the concept of economic yield to encompass the scale of regionally cultivated landscapes and incorporates the effect of fungicide resistance on economic yield. Our results demonstrate how the extended economic yield can be evaluated using a simple paradigmatic model of crop disease epidemics. Our study reveals that the law of diminishing returns does not hold with respect to fungicide coverage, and the optimal treatment coverage is achieved at extreme values, either fully treating all the fields or not treating at all. The ratio of relative fungicide cost to relative yield loss plays a major role in determining the optimal treatment coverage. The study also highlights the impact of resistance evolution in pathogenic fungi and its economic consequences for farmers. Our results provide a comprehensive eco-evolutionary and socioeconomic perspective on integrated pest management and sustainability economics.

Social-Ecological Modelling of Bivalve harvesting in the North Adriatic Sea: Insights for Sustainability

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This work presents the findings of a social-ecological study conducted to support the local institution in addressing the depletion of two bivalve resources, particularly smooth venus clams (Callista chione) and clams (Chamelea gallina) in the North Adriatic Sea (Italy). This project aims to enhance the knowledge regarding the state of the resources and the past dynamics of the social-ecological system to support the identification of adaptive protection strategies.

Interviews with experts, both key stakeholders and researchers, and questionnaires were used to examine trends and criticalities in the shellfish sectors, from the perspective of the stakeholders. The bilateral interviews explored the current state of bivalve harvesting activities, while the questionnaires, distributed during a dedicated meeting with fishermen, focused on operators' backgrounds, production dynamics, perceived resource status, and identification of potential threats and early warning signals, as perceived by the operators.

The results show the evolution of dredge fishing practices that were driven by changes in fishing objectives, influenced primarily by resource availability and secondarily by market demand. The perceived impacts of these activities on the resource and the environment were also noted. While species such as clam (Chamelea gallina) and razor shell (Ensis minor) were initially fished, the focus shifted to warty venus clams(Venus verrucosa) and the incidental capture of smooth venus clams (Callista chione) in subsequent years. Additionally, the adopted approach identified weaknesses in the management of the sector, ecological threats, and potential environmental impacts from land use and climate change.

The results highlight the importance of stakeholders’ engagement in understanding complex social-ecological systems identifying the relevant variables and processes that influence these interactions. Furthermore, the work underscores the importance of employing social-ecological modelling to develop tools to support scenario analyses to promote the long-term viability of shellfish fisheries.

The road to integrate climate change projections with regional land-use-biodiversity models

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Current approaches to project spatial biodiversity responses to climate change mainly focus on the direct effects of climate on species, while regarding land use and land cover as constant or prescribed by global land-use scenarios. However, local land-use decisions are often affected by climate change and biodiversity on top of socioeconomic and policy drivers. To realistically understand and predict climate impacts on biodiversity, it is therefore necessary to integrate both direct and indirect effects (via climate-driven land-use change) of climate change on biodiversity.

In this perspective, we outline how biodiversity models could be better integrated with regional, climate-driven land-use models. We initially provide a short, non-exhaustive review of empirical and modelling approaches to land-use and land-cover change (LU) and biodiversity (BD) change at regional scales. The reviewed papers form the base for our perspective about integration of LU and BD models and how to further improve upon this integration. We consider a diversity of approaches, with a special emphasis on mechanistic models and on how they assessed climate change effects. We look at current levels of integration and at model properties, such as scales, inputs, and outputs, to identify integration challenges and opportunities.

We find that LU integration in BD models is more frequent than the other way around and has been achieved mostly at four different levels: 1) overlapping LU and BD predictions; reading-in LU predictions into BD models; 3) land-use classes as biodiversity-relevant parameters, which hare calibrated on literature data; 4) simultaneously coupled simulations (i.e. bi-directional effects). Of the integrated LU-BD socio-ecological models, some studies included climate change effects on LU, but the relative contribution of direct vs. indirect effects of climate change on BD remains a key research challenge.

Important research avenues include concerted efforts in harmonising spatial and temporal resolution, in disentangling direct and indirect effects of climate change on biodiversity, in explicitly accounting for bi-directional feedbacks, and in ultimately feeding socio-ecological systems back into climate predictions. These avenues can be navigated by matching models, plugins for format and resolution conversion, and increasing the land-use forecast horizon with adequate uncertainty. Recent developments of coupled models show that such integration is achievable and can lead to novel insights into climate-land use-biodiversity relationships.

Using long-term cross-scale SES modelling to examine trade-offs between climate, food and forest landscape restoration until 2100 in Esmeraldas Province, Ecuador

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The ongoing global environmental changes are characteristic for the Anthropocene and are often referred to as the ‘triple’ challenges of biodiversity loss, mitigating and adapting to climate change, and providing food and other natural resources for a growing human population. These issues are often interrelated and give rise to non-linear, cross-scale dynamics which pose challenges for social-ecological systems (SESs). Such dynamics can for example lead to path dependencies that may be barrier for nature-based solutions such as forest landscape restoration. As the Anthropocene proceeds, sustainability problems are more likely to originate at multiple scales calling for a better understanding of cross-scale dynamics of SESs to improve land governance and environmental management.

Long-term simulations of land use dynamics can support decision processes and policy design to identifying trade-offs and opportunities of sustainable development. Such an approach requires to capture the increasing uncertainty of climate change, population dynamics and settlement processes, as well as bottom-up land use demands for food, fuelwood or timber. This is particularly important for many regions of the Global South were many issues of the Anthropocene come into play and often reinforce each other.

We present a newly developed dynamic and spatially-explicit simulation approach which builds on probabilistic and deterministic functionality. The model is embedded in the PCRaster Python framework and simulates on an annual and hectare basis diverse land use change patterns (incl. cropping systems, agroforestry and forest types). Change dynamics are driven by a long-term SSP2-4.5 scenario storyline, potential forest distribution and natural vegetation according to RCP 4.5, and are further steered by smallholder-driven demands of food, fuel wood and timber. The uncertainty of human behavior in the allocation of land use types is depicted as a probabilistic range relying on a Monte Carlo simulation framework.

We compare a business-as-usual (BAU) setting with a scenario of increasing kcal demands using the province of Esmeraldas in Ecuador as case study (> 1.6 million ha). Scenario outcomes suggests that changing food diet demands in concert with future population and settlement dynamics decreases the potential of forest landscape restoration for Esmeraldas province until 2070 compared to 2060 for the case of BAU. The success rate for future projects of forest landscape restoration will thus rather low until the simulated population peak and until the local demand for food production and settlement areas can be satisfied.

Modelling the trilemma: biodiversity, ecosystem services and socioeconomic returns through a financial compensatory trade-off scheme

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Increasing environmental dynamics implies that biodiversity protection goes beyond protected areas, taking the multifunctional management of landscapes as a critical goal. To foster such a target Payments for Ecosystem Services (PES) have been recognized as an important mechanism to coordinate environmental protection and socioeconomic development. Making more than half of habitable land an effective program trading off agriculture achievements with biodiversity and ecosystem functionality is of paramount importance. Here a dedicated multi-objective optimization model for the management of a socioecological system is introduced. The model questions where and how to manage land use (i.e. what to produce?) for the joint maximization of biodiversity, water and carbon sequestration without jeopardizing economic profits. Quantitative answers to the problem are presented for a case-study region in Southern Portugal, encompassing a landscape historically characterized by a highly sustainable use of a Mediterranean habitat (the Montado) which is nowadays largely pressed by agriculture homogenization and intensification. Scenarios are build based on: (a) proposed PES schemes emerging from the new EU Common Agriculture Policy; (b) the acceptance-profiles of producers in engaging into a sustainable path, through PES, and; (c) the effects of climate change up to 2050 over vertebrate and plant species of EU importance (i.e. listed in Habitats Directive), while considering multiple trade-off policies among the biodiversity and the two ecosystem benefits to maximize. The results herein presented may be used to support a new generation of integrated policies, targeting the sustainable management of the whole landscape for economic profit, biodiversity persistence and long-term environmental functionality.

Large-scale land-based quality of life estimations under climate and socio-economic scenarios

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Understanding human-nature interactions is essential to address global sustainability challenges. Several conceptual frameworks have incorporated bidirectional relationships, and the impact of human activities on nature is often estimated in studies and for policy targets, but natural and human-induced impacts on humans remain poorly integrated from a holistic point of view. Since individuals and communities will focus first on fulfilling their needs, studies that holistically assess Quality of Life (QoL) in the future are required to promote social transformation towards sustainability. One example is in Land System Science: while land use change has been identified as a major driver of impacts that threaten sustainability, land use models have not yet incorporated wellbeing or QoL as future outcomes of such change. In a previous research, we developed the Land System-based framework for estimating the potential provision of Quality of Life, LANDS-QoL, which aims to contribute to filling this modelling gap.

In this study, we use LANDS-QoL combined with ecosystem services and land use data provided by the agent-based land use model CRAFTY-GB and UK-SSP socio-economic indicators to explore changes in quality of life in Great Britain, under six climate and socio-economic (RCP-SSP) scenarios. Quality of life is represented by six dimensions: material, health, security, social relations, freedom, and socio-environmental justice and equity. These dimensions were analysed between 2020 and 2080 for future worlds that simulate weak to strong climate change and societies with weak to strong cohesion, sustainable behaviour, and high to low climate change adaptation and mitigation capacities.

The results revealed that people’s values in the different simulated future worlds determine the levels of QoL in societies and the dimensions that are affected, which is consistent with the SSP-storylines. Inequal, individualistic, and regionally rivalrous societies will prioritise material QoL to the detriment of social relations, whereas in egalitarians societies socio-environmental justice and equity prevails over material aspects. Thus, the six scenarios aggregated positive, negative, and neutral futures for QoL, and the trends of these relationships are consistent over the years. Since LANDS-QoL is mainly built from land-based and socio-economic SSP-indicators, with climate effects mediated through the land system, the climate RCP-scenarios did not show significant impacts on QoL values. The analysis of quality of life under future scenarios through land-use modelling represents an extendable assessment of social and climate change impacts and is a potential support for decision-making about socio-ecological systems.

Predicting Land Use and Environmental Changes in Argentina's Pampas Region Under Varying Price and Climatic Conditions Using an Agent-Based Model

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In this work, we applied an agent-based model (AGRODEVS) previously calibrated and validated for cropping systems in the Pampas region (Argentina) to set environmental thresholds associated with land-use and land-cover change dynamics (LUCC). The main goal was to understand the landscape-level environmental consequences of the simulated LUCC. Firstly, we defined a 625-agent grid to represent the current crop cover and management regime of the most productive agricultural area in Argentina (Pergamino, Buenos Aires). Then, we simulated 45 years under contrasting conditions of prices (three levels), climate (three levels), and technological level (three levels) to assess changes in the regional cover of three land-uses (corn, soybean and the double crop wheat/soybean). Additionally, we evaluated the effects of these LUCC simulations on 1) the use of non-renewable energy, 2) the return of energy invested, 3) the ecotoxicological risk of pesticides, 4) the efficiency in the use of rainwater and 5) the aboveground carbon balance. The results showed that price relationships were the main factor associated with LUCC, placing climate conditions in a subordinate position in the explanation of LUCC. Under conditions of a low Soybeans/Corn price ratio, the cultivation of corn became dominant in the landscape (regardless of the climatic scenario), thus determining relatively low ecotoxicological risk values and high water use efficiencies. Conversely, a high Soybeans/Corn price ratio determined the dominance of the double wheat/soybean crop, resulting in high ecotoxicological risks in the landscape, along with low water use efficiency. For the set of all scenarios, the levels of renewable energy use remained very low, although the aboveground carbon balance almost always met the previously set environmental targets. Beyond the average values, the use of AGRODEVS showed variability in the performance of the agents, exhibiting LUCC trajectories that, coupled with climate, price, and technological level scenarios, were able to avoid trade-offs between LUCC and the appearance of symptoms of deterioration in the environmental variables studied. From future work, it will be possible to detect these desirable trajectories and select them as sustainable in the long term.

Exploring the transformation to more regenerative agricultural systems using empirical case studies and a coupled social-ecological model

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For a long time, conventional agricultural systems have been geared towards maximizing yields, while negative impacts on ecosystems, biodiversity, and human livelihoods have not been at the center of attention. The theme of ecological resilience of agricultural systems in particular becomes more and more relevant in light of increasing climate change impacts, such as a steep rise in the number of droughts.

Due to the social-ecological nature of agricultural systems, strategies for a sustainability transformation have to consider both social and ecological spheres, their interactions and interdependencies, as well as embrace and navigate the complexities arising from them (Rockström et al., 2020). Regenerative agriculture (RA) proposes a systemic approach to agriculture and demands a paradigm shift away from “maximizing yields whilst minimizing (social and ecological) harm” towards “implementing an agricultural system as such that it has positive impacts on people and nature” (Mang & Reed, 2012). Its transformative nature and SES perspective render RA a promising approach to sustainable agriculture.

Social-ecological models of land-use change are important tools to investigate land system transformations. The project presented in this talk combines a qualitative and quantitative approach, including (a) empirical case-based fieldwork in Costa Rica and central Europe in the form of semi-structured interviews and participatory modelling and (b) integrated social-ecological modelling. The project aims to explore the emergent effects of social-ecological interactions and potential leverage points for a systems transformation towards more regenerative agriculture.

The findings show factors influencing the adoption of regenerative farming systems in Costa Rica and Central Europe including context-sensitive dynamics, as well as cross-regional commonalities. Furthermore, the foundations of InSEEDS, a coupled agent-based – dynamic global vegetation model (ABM-DGVM) will be introduced - it uses the copan:CORE modeling framework developed by Donges et al. (2021), which is coupled to the global biosphere model LPJmL.

Finally, research frontiers and challenges of the project are discussed, e.g. regarding (1) the potential of integrating empirical research into large-scale social-ecological modelling, (2) the need for agent diversification, (3) the challenge of representing multi-level interactions.

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Tropical landscape design modulates trade-offs among ecological and socio-economic functions at different spatial and temporal scales

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Land use changes have dramatically transformed many tropical landscapes from forest to agriculturally dominated landscapes. Agricultural land uses, such as rubber and oil palm plantations, increase the socio-economic benefit at the cost of reduced ecological functioning, so called trade-offs. Questions arise on how different landscape designs in terms of fragmentation and connectivity of land cover types as well as different dynamic market prices for rubber and palm oil affect these trade-offs at different spatial (farm- vs landscape-level) and temporal scales (short- vs long-term).

To tackle these knowledge gaps, we developed the integrated ecological-economic land-use change model EFForTS-ABM that follows a combined agent- and grid-based approach. The model simulates the impact of land use change decisions made by smallholder farmers on the economic outcomes from oil palm and rubber plantations as well as ecological functions such as carbon sequestration. EFForTS-ABM is based on socio-economic and ecological field data from the Jambi province in Sumatra (Indonesia). Using EFForTS-ABM we ran model scenarios on different landscape designs (i.e., different landscape fragmentations) and different dynamic crop price scenarios (i.e., constant vs different fluctuations of prices for rubber and palm oil). We then assessed farm-level and landscape-level ecological and socio-economic functions as well as trade-offs among them over the simulation time.

Here, we will demonstrate the challenges in developing EFForTS-ABM and the usefulness of the model to assess the effect of different landscape design and price scenarios on socio-economic and ecological functions as well as trade-offs among them. We expect individual ecological functions to be affected differently by changes in landscape fragmentation, leading to different trade-offs with socio-economic functions. In addition, trade-offs among functions found at the farm-level might be less severe at the landscape-level. Temporal changes of land use and plantation ages driven by crop prices might change trade-offs over time. The results will be an important basis for identifying landscape designs that minimize losses in ecological functions while still allowing for economic benefits.

Semi-empirical modelling meets sensitivity analysis: do droughts impact management decisions in Central European grasslands?

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Climate change is expected to increase the frequency and severity of droughts in central Europe affecting the quantity and quality of grassland yields and thus farmers' income. This may lead to an adaptation of farmers' management behaviour towards less intensive farming in order to increase their resilience to drought. Understanding these dynamics is crucial for designing appropriate policy instruments to conserve grasslands without unintended side effects. Social-ecological models are a suitable tool to investigate this.

A major methodological challenge for modelling in this context is the lack of long-term data to disentangle climate and management effects on yield quantity and quality. Approximate values for these parameters exist as look-up tables for practitioners. However, these values do not take into account climate or site specifics and may be uncertain. This prevents the development and adequate parameterisation of the underlying environmental model that is dedicated to supporting the evaluation of policy instruments for real-world applications.

We develop and apply a guideline on how to build a robust, practice-oriented model for identifying realistic management decision patterns in grasslands under drought conditions when input data are highly uncertain. Therefore, we 1) built a semi-empirical model that returns the farmer's optimal management decision based on either expected utility or prospect value for a given drought scenario. 2) We conducted a global sensitivity analysis (based on Latin Hypercube Sampling) to investigate under which circumstances parameter uncertainty (including the entries in practitioners' look-up tables) has a high impact on the farmer's choice of management decisions and under which it does not, when unrealistic circumstances are excluded.

Our approach of building a semi-empirical grassland model, combined with tools from sensitivity analysis, shows how to assess what data are needed to conduct qualitatively robust explorations of grassland management behaviour, and provides guidance on how to aggregate data and coarse expert knowledge to meet these needs. Our study thus demonstrates how social-ecological modelling can be used to identify appropriate policy instruments, such as payments for ecosystem services or support for drought insurance, that support the transformation processes needed under climate change, even with limited empirical data.

Simulation of spatial crop expansion and its consequences on groundwater resource use in dryland farming systems: how the shift of subsistence to commercial farming can shape landscapes

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During the last decades an increasing world population and rapid urbanization was leading to rising market demands for specialized agricultural produce and associated widespread transformation of rural staple production into market-oriented growth of vegetables, animal feeds, fruits and condiments. In Vietnam, since the 1990s maize production for the animal sector has gained much in importance while in Niger, booming West African onion markets have led to rapidly rising cultivation of onion (Allium cepa L.) and garlic (Allium sativum). We previously developed an explicit spatial dynamic model using farmers' decision rules, food demand, and market orientation at different stages to simulate spatial crop expansion and potential effects on soil degradation in the northern mountains of Vietnam. The model estimated an area of 134 ha, accounting for 18.9% of the total cultivated area, as hotspots for soil degradation under the current intensive maize mono-cropping system during the next 20 years. In applying an adapted model, we want to simulate the effects of spatial crop expansion on groundwater resources in two oasis systems covering a watershed of 820 ha on Mont Bagzam in the Aïr Mountains of Northern Niger. Initial GIS-based remote sensing analyses and field data collection showed an increase in the cultivated onion / garlic area of 55 ha from 2003 to 2022. On this desert mountain plateau at a precipitation to evapotranspiration ratio of 1:10 irrigation highly depends on water harvesting and "mining" of scarce groundwater resources through wells. With the presented work, we aim to (i) apply the spatially explicit dynamic crop expansion model by adapting site-specific parameters for the selected land area on Mont Bagzam, Niger, (ii) simulate crop expansion, and (iii) estimate the additional amount of groundwater needed for irrigation. To this end, a high-resolution digital elevation model was generated and cropping patterns and the location of additional wells were detected by using drone-based surveys. We apply PCRaster, an environmental spatial language, to model the spatial distribution of expanded fields from 2020–2050 and the potential additional amount of groundwater needed for irrigation. The outputs will allow us to explore the role and consequences of local farmers' decisions under three scenarios: (1) current intensive onion production practices versus (2) intercropping and (3) agroforestry systems as more sustainable land use practices in these oasis farming systems.

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31. From dynamic forest models to decision support for forest transformation – How can synergies be achieved?

Strengthening the connection between dynamic model simulations and managing forest risks under climate change

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Ecosystem models are increasingly used to assess the possible consequences of management decisions and policies oriented on biodiversity conservation, climate change adaptation, and implementing bioeconomy principles in forest management. Despite considerable advances in models` complexity, ability to address complex socioecological systems and accommodate emergent understanding of driving environmental forces, the impact of this knowledge on management decisions and forest-related policies remains unclear. The recent global increase in forest disturbance activity made risk management one of Europe's central themes of forestry policy-making. Process-oriented ecosystem models can vitally support these initiatives, for example, by (i) identifying risks emerging from new disturbance interactions, locating future disturbance hotspots, and appraising impacts; and (ii) helping formulate new (and dismantle old) risk management practices that consider changing ecological dynamics, assess these approaches' efficiency and economic performance. In fact, model-based experimentation is often the only way to quantify the efficiency of managing large-scale disturbances, where empirical research is constrained by problematic reproducibility, replicability, and definition of reference (undisturbed) situations. We observe that European forest risk management is often driven by traditional decision-making patterns, only partly reflecting on the ongoing disturbance regime shifts and the availability of model-based projections of future risks and impacts. We suggest that part of the problem stems from the previous severe underestimation of forest risks, which have been observed in recent years across Europe, and from the generally limited ability of models to address complex climate-sensitive disturbance systems. While these issues can be resolved at the technical level by further model development, the major bottleneck seems to be a poor involvement of decision-makers in disturbance research and a lack of trust-building activities between disturbance managers and researchers. We provide insights into this scene based on our experience with the Forest Europe policy process (former Ministerial Conference on the Protection of Forest in Europe) and other initiatives shaping the science-policy interface in forest risk management. We confront the recent development in dynamic forest disturbance modelling with a survey of policy and decision-makers awareness of these tools and their willingness to consider such information in adapting current management practices and policies.

Feasibility of enhancing carbon sequestration and stock capacity in temperate and boreal European forests via changes to management regimes

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Forest management can aid buffering anthropogenic climate change, thus playing a strategic role in the framework of the EU forestry-based carbon mitigation strategy, in particular in Central and Northern Europe. Yet, diversified management strategies can lead to potentially diversified responses in tree carbon sequestration and rarely can multiple options be thoroughly assessed in the forest practice. We questioned the effect of multiple alternative management scenarios, i.e. based on the thinning-clear cut-replanting, on the trees net primary productivity (NPP) and potential carbon woody stocks (pCWS) under future climate change, by means of the biogeochemical forest growth model 3D-CMCC-FEM. The management interventions have been applied to three even-aged European forests which are part of Inter-Sectoral Impact Model Intercomparison Project (ISIMIP, https://www.isimip.org) and PROFOUND database. By applying a “forest-factory” like approach, we systematically explore changes in the system NPP and pCWS space. Our evaluation indicates that the tree capacity to absorb CO2 and stock it in the woody products might have already reached an optimum under business as usual management conditions independently of the climate change scenarios considered and the “CO2 fertilization effect”. In spite of the simplified assumptions in our approach, the consistency of the outcome across sites and conditions, would suggest that over large areas in Europe we might already harvest at the limit of the forest capacity. The methodology applied as well as the findings of our study are of potential interest for both forest practitioners and policy makers which call for more practice-oriented decision support tools and methods.

Simulation-based analysis of trade-offs in ecosystem services in beech forests

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At global scale carbon sequestration by forests is seen as significant contribution to climate change mitigation. The Green Deal of the EU assigns several roles to European forests: increasing the carbon storage in forests, fostering biodiversity, supporting the circular bio-economy with renewable raw material, and strengthening the provision of other ecosystem services. Measures to achieve these goals include, inter alia, setting aside up to 30% of forest area as well as intensification of biomass utilization from forests. The controversial debate about best strategies relies on consistent information about trade-offs in ecosystem services.

The current study analyses the effects of maximizing carbon storage in beech forests in the Biosphere Reserve Vienna Woods on other ecosystem services, in particular timber production, recreational value in the vicinity of the city of Vienna, habitat quality for two flagship bird species, Strix uralensis and Dendrocopus leucotus), and biodiversity (tree species diversity, deadwood).

The analysis is based on two pillars, detailed inventory of a time series of beech stands managed by the Austrian Federal Forests and unmanaged nature reserves, and ecosystem simulation employing PICUS v1.52 and a set of ecosystem service indicators to explore effects of various management alternatives and impacts of climate change on the resilience of ecosystem service provisioning.

Based on identified trade-off relationships among ecosystem services options for a multifunctional forest management will be derived.

Sustainable stem number profiles in Swiss protection forests: What is the role of climate change?

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Within the framework of the Swiss guideline "Sustainability in Protection Forests – NaiS" (German: Nachhaltigkeit im Schutzwald), a profile of forest properties is defined for each natural hazard that must be achieved to ensure the protective function. In the case of rockfall, this profile is determined using the online tool RockforNET. To do this, the stand basal area required for energy destruction has previously been distributed evenly across the stem diameter classes to determine the required number of stems per diameter class. This assumption leads to very high stem numbers, especially in the lower tree size classes, which are often not realistically achievable in forest practice. Also, it is unclear whether the required profile for rockfall protection will be achievable under a changing climate if current best-practice management will be continued in the future.

We used the dynamic forest model ForClim to determine sustainable distributions of stem number and basal area for the four elevational zones of low-montane, upper-montane, high-montane, and subalpine. Both site-specific environmental factors and management regimes were flexibly considered under multiple climate scenarios (historic climate, RCP 4.5, and RCP 8.5).

Parts of the results of the study were implemented in a prototype for an updated rockfall tool in NaiS. Compared to previous estimates, the new stem number distributions are much flatter than in the previous tool. We found that a unimodal basal area distribution is more realistic to achieve for stands at all elevations. We also assessed the extent to which management adjustments would be needed to keep requirement profiles achievable under climate change conditions.

Climate risks of temperate forests of southern South America in the next decades

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The world's forests are facing severe pressures due to climate change and human use. A major source of uncertainty is the extent to which these threats are increasing the risk of forest functionality, particularly in less-studied hotspots of biodiversity and highly exposed to climate change such as temperate forests from southern South America (TFSA). In this region, tree populations are becoming highly influenced by drought because air temperature has increased around 0.25°C per decade (time period 1976–2006) and annual precipitation has decreased by about 40% in the last century (time period 1901–2005). The situation is predicted to worsen, with climate models forecasting further reductions in summer rainfall by up to 23% by 2050. Forests in this region are already showing signs of decay (decreased tree growth and mortality) and human activities have increased the incidence of megafires, with nearly one million hectares of forest burned in the past five years. Therefore, it is highly needed in this region to improve model applications to predict forest sensitivity to global change. This is a necessary task to prescribe future strategies for landscape management aiming at maintaining forest resistance and resilience.

In this work, a forest gap model is applied to predict forest risks associated with climate change on a regional scale in temperate forests of southern South America (35-43°S). The model was calibrated using data on 40 tree species present in the region, and model results were validated using independent information on tree composition from 850 forest inventory plots and the current vegetation maps of the Chilean national forest service. The model's results were then used to describe a valid spatial domain for the model where forest composition agreement between model results and empirical data was >70%. Climate risk maps of TFSA in the valid domain were generated by integrating the results of exposure, vulnerability, and threat into a risk index based on the IPCC framework. Learning from the results, the challenges and opportunities of forest gap models to reduce uncertainties related to climate change impacts on TFSA forest landscapes will be discussed.

To what extent can silviculture foster forest adaptation to climate change? a demo-genetic modelling approach with stress and disturbance regimes

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In managed forests, a classical strategy of adaptation to climate change consists in reducing tree density for short-term benefits on drought stress level, growth and survival, but the long-term evolutionary impacts are poorly considered. An alternative strategy would be to maintain some level of environmental pressure to promote acclimation and genetic adaptation through natural selection. Here, we developed an individual-based demo-genetic modelling approach to study the impacts of silviculture on eco-evolutionary processes in forest tree populations and search for a compromise between short- and long-term objectives.

The model combines growth, competition, regeneration and disturbance regimes, which jointly drive survival and mating success, with genetic variation of quantitative traits related to these processes. The evolutionary rates predicted by the coupled demo-genetic model for two growth-related traits, vigor and sensitivity to drought stress, fit in with the range of empirical estimates found in the literature for wild plant and animal populations.

Using this model to simulate contrasting silvicultural strategies, drought regimes and inter-individual variations, we characterized and quantified the effect of various thinning scenarios on drought impacts and genetic evolution over three generations of trees. We showed that silvicultural interventions partly substitute for natural selection. The more intensive the silviculture, i.e. more frequent, early and intensive thinnings, the lower the adaptive evolution in both vigor and drought sensitivity: compared to the baseline scenario with no management, the most intensive silviculture reduced the evolutionary rate by up to 50%. Intensive silviculture was efficient in the short term in reducing stress and its impacts on stand performances. However, with enough within-stand genetic variation for drought sensitivity, strategies that favored natural selection processes could be more efficient by improving the forest response to stress. As a compromise between short- and long-term benefits, we propose an evolution-oriented strategy consisting in maintaining a period of high density in the juvenile stage to maintain some level of stress exposure and promote natural selection, followed by a classical stress reduction strategy by thinning to reduce the vulnerability in later stages.

This research illustrates the potential of demo-genetic models, here combined with regimes of disturbance impacts, to explore and assess different options of population management across multiple temporal horizons.

Multi-objective forest management – an ecological-economic optimization approach

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How to meet economic objectives of timber harvesting while maintaining the functioning of diverse forest ecosystems? Answering this question requires ecological-economic models that can be easily applied and generalized for uneven-aged mixed-species forests.

Here, we develop a dynamic ecological-economic optimization model, which integrates a state-of-the-art demographic forest model with a continuous cover forestry harvesting model to optimize efficient and sustainable timber harvesting. As a proof-of-concept, we apply the model to a beech-dominated forest in the Hainich National Park, Germany, with the goal of optimizing multiple objectives such as timber yield and the biodiversity value of the forest.

The ecological module is the Perfect Plasticity Approximation (PPA) demographic forest model that simulates forest dynamics based on individual tree growth and survival rates in the understory layer and the canopy layer, respectively, as well as recruitment rates. We used repeated forest inventory data from a 28-ha forest plot to quantify these demographic rates and validated the predictions of the ecological module against the structure of old-growth beech forests in Europe. The economic module includes constant marginal harvesting costs and timber prices to maximize the net present value of timber profits, and can be constrained by the number of retained habitat trees (>70 cm diameter) as an indicator for the biodiversity value of the forest.

The forest model delivered reasonable predictions of the size distribution, basal area, and maximum diameter of old-growth beech forests. When only timber yield was maximized, trees were harvested when they reached 70 cm in diameter, but smaller trees were also harvested with increasing discount rates. This is similar to current management practices in beech forests. There is a trade-off between maximizing timber harvest and biodiversity value. Initially, with a small number of retained habitat tress timber harvest decreases modestly, yet as the number of habitat trees approaches the ecological equilibrium, losses in timber increase sharply until no harvest is possible.

We established a generic ecological-economic modeling framework that reliably represents forest dynamics as well as optimal forest management. The framework can be extended to mixed-species forests and support forest management for diverse ecosystem services.

Is climate change threatening the re-emergence of old-growth forests in Central Europe? A simulation study

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Human land-use has strongly modified the forest ecosystems of Europe for centuries to millennia. As a result, less than 1% of Europe's forest cover today are primary forests. Old forests are particularly valuable because they store large amounts of carbon and are of high value for many forest-dwelling species. As a consequence, conservation efforts aim to increase the share of old-growth forests in Europe. This is frequently done by setting aside areas of formerly managed forests for conservation, e.g. in the form of national parks or strict forest reserves. This approach assumes that old-growth forests will re-emerge with time when management ceases. However, this assumption is challenged by drastic changes in the climate system. In particular, climate change is increasing forest disturbances, which could counteract a development trajectory back to old-growth in protected forests, and rather lead to younger, more open forests. Here, we asked (i) how climate change influences the reemergence of old-growth forests in a national park, (ii) where on the landscape old-growth is most likely to emerge, (iii) what is the scenario-uncertainty in future projections of old-growth, and (iv) how sensitive are results to the old-growth definition used. We focused our analyses on Berchtesgaden National Park, located in the northern front range of the Alps in Germany. Here, centuries of human management have left a strong imprint on forest structure and composition, with forests developing without human influence since the foundation of the national park in 1978. We used the forest landscape and disturbance model iLand to study the re-emergence of old-growth forests. Specifically, we studied three representative concentration pathways until the end of the 21st century, dynamically simulating the impact of wind and bark beetle disturbances. We found that the share of old-growth forest increased in the absence of climate change. Increasing disturbances under climate change led to a reduced share of old-growth forests on the landscape compared to simulations under stationary reference climate. Results varied with different definitions of old-growth, but the general patterns remained robust. Our analyses indicate that the effects of climate change could substantially counteract conservation goals by curtailing the re-emergence of old-growth forests in Europe. Our study also demonstrates how forest landscape simulation modeling can be used to formulate realistic conservation targets in a rapidly changing world.

Biodiversity conservation in the Leipzig Floodplain forest – Using a demographic forest model to support conservation planning

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The Leipzig Floodplain Forest (LFF) is a biodiversity hotspot of national significance. Much of this biodiversity is associated with characteristic hardwood floodplain forest tree species, especially pedunculate oak (Quercus robur) and European ash (Fraxinus excelsior). However, the share of oak and ash has been declining over the last decades due to regulation of the hydrological regime, recurrent droughts, and invasive pests and pathogens. In particular, it is unclear whether the planned revitalization of the hydrological regime (higher groundwater table, more floods) will be sufficient in ensuring the conservation of oak, or whether active oak planting is required.

To answer this question, we apply the Perfect Plasticity Approximation (PPA) forest model. The PPA model is a demographic forest model which simulates changes in forest dynamics according to growth and mortality rates in discrete canopy layers, as well as recruitment rates. We use forest inventory data from the ‘Lebendige Luppe’ project, including approximately 8000 trees growing in either ambient conditions or artificially flooded plots, to quantify demographic rates for eight focal tree species and characterize their dependence on the hydrological conditions. In addition, we take data from small-scale oak plantations (called “femel” in German) with differing sizes to model potential management scenarios.

In the baseline scenario (no revitalization of the hydrological regime, no active management), the basal area of oak trees is projected to decline by half in the next 50 years, indicating that natural regeneration alone is insufficient. Likewise, a scenario where the hydrological regime is revitalized does not ensure sufficient oak recruitment. Therefore, we compare the long-term impacts of different active management scenarios on the tree species composition of the LFF. Our results can support the design of an optimal biodiversity conservation strategy for the LFF.

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Open Topics

Elucidating African swine fever transmission cycle dynamics at the domestic-wildlife interface: Multihost epidemic modelling in Romania

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The global spread of African swine fever (ASF) poses an unprecedented threat to the swine industry. Mathematical modelling has proven useful for quantifying disease transmission and informing control strategies among domestic pigs and wild boars separately. Such models are sufficient for regions where ASF is restricted to a single ecological compartment, however for areas where spillover is suspected—as in Romania where there exists a predominance of low-biosecurity backyard pig holdings—a multihost approach is likely needed. To explain the spatio-temporal infection pattern of ASF in Romania, and to evaluate outcomes from alternative control strategies, a multihost individual-based SIR model was developed and parameterized to the period of initial disease spread: June to December 2018. Two types of domestic pig herds were considered in the model: low-biosecurity backyard farms and high-biosecurity industrial operations. Due to the ubiquity of backyard pig farming, each village was considered to be a single backyard farm with locations represented by village centroids. Industrial farms were also represented by their point coordinates. Wild boar presence was simulated via rasterized CORINE Land Cover data sized to estimated wild boar home-ranges, with wild boar presence modelled as a function of raster cell forest density. For initial parameterization, domestic pig herds iterated through susceptible (S), infectious-undetected (Iu), infectious-detected (Id), and recovered (R) states, while wild boar cells were considered to be perpetually infectious following infection, allowing only S-Iu-Id states. Model fitting was performed through Adaptive Population Monte Carlo, a means of approximate Bayesian computation. A total of 24 models were evaluated, with the observed epidemic dynamics being best explained through frequency-dependent transmission between domestic pig units, density-dependent transmission between wild boar cells and domestic pig units, and 2nd order adjacency spread between wild boar cells. Model outputs estimated that 20% of domestic pig unit infections came from wild boar sources, and 30% of wild boar infections came from domestic pig units. Further, our model estimates that the majority of interhost transmission events occurred during periods of undetected circulation. Alternative control strategy outcomes were evaluated through comparing final epidemic size and relative host contribution, with the biggest decrease in epidemic size occurring through a combination of increasing wild boar surveillance with aggressive local environmental sanitation following initial case detection, and instituting village-wide culling upon ASF case detection in a domestic pig. These results help advance our collective understanding of multi-host pathogen spread to inform animal health policy.

Modelling changing mosquito abundance and distribution in the Netherlands

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We aimed to estimate the future risk of mosquito-borne disease outbreaks in the Netherlands and to determine which areas might be most vulnerable. The prevalence of vector-borne diseases (VBDs) has increased in recent decades and this trend is expected to continue. The Netherlands has experienced introductions of both usutu virus and West Nile virus in recent years. These are both transmitted by Culex pipiens, one of the most common mosquito species in the Netherlands, but knowledge on the distribution and abundance of this species is lacking. Moreover, there is a large knowledge gap regarding how sensitive future distributions are to different climatological and land use scenarios. We conducted field research to investigate the factors most relevant for determining Cx. pipiens abundances. We then used existing mosquito abundance data from field research conducted in both the Netherlands and Belgium to create a statistical model of Cx. pipiens abundance and distribution, accounting for seasonal variation. For this we used a random forest model with a wide range of covariates which we had previously determined to be relevant, including soil properties, weather, land use, water-related properties and human population. ‘Total precipitation in the preceding month’ was the most important covariate, followed by ‘agricultural land area’ and ‘percentage of tree cover’; our model had an R2 value of 0.76. Subsequently, we were interested in how the risk of mosquito-borne disease outbreaks will change in the future. We created One Health scenarios for the Netherlands for 2050, based on the Shared Socio-economic Pathways (SSPs), with a focus on elements relevant for VBD-risk. From these we created land-use maps using the Dyna-CLUE model. These scenarios were used as inputs for our mosquito model to derive future predicted abundances, with weather-based covariates coming from scenarios created by the Dutch meteorological organisation. Combining all this together, we were able to use our model to predict mosquito populations under each of our scenarios. VBDs are complex and their transmission is influenced by many different factors. Hence it is necessary to use a variety of different methodologies to understand them. Using a combination of field research, statistical modelling, socio-economic research and land-use modelling, we have been able to conduct an in-depth study of how mosquitoes are affected by their environment and what changes we might expect in the future.

An exploratory model for ecosystem services in the Venice lagoon

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The Venice lagoon is a complex socio-ecological system, where Ecosystem Services and benefits for people result as emergent properties from the interactions between ecological processes and human activities. Such a complex system is threatened by several drivers of change, including those connected to resource exploitation and ecosystem fruition, along with climate change related drivers. EST (Ecosystem Services Screening Tool) is an exploratory numerical model based on dynamic system theory, aimed at investigating the interactions among the different ecosystem services, the lagoon resources and the social dynamics, and compare possible scenarios of evolution of the whole socio-ecological system. The numerical model considers 13 Ecosystem Services, along with the biophysical component, represented by specific macrohabitats characterizing the lagoon seascape and key faunal groups, and the main groups of actors involved in services fruition. Increase in water temperature and relative sea level rise are provided as external forcings to the model, which also attempts to account for the feedbacks on services produced by the regulation of lagoon high tides, through the closure of mobile gates. EST was implemented in Simile v. 6.1 software environment, as an attempt to improve its applicability for participatory modelling applications. Model development and parameterization is presented, and contrasting tendency scenarios are explored, considering a 50 year time horizon. Scenarios included both changes in climate-related forcings and in governance choices aimed at preserving the biophysical component. Results are discussed in relation to their potential to support territorial planning and strategic environmental assessment processes. Constraints imposed by the availability of input data required by the model are considered, and opportunities and challenges related with the use of complementary information from earth observation and operational modelling discussed.

Multi-model assessment of forest carbon stocks responses to climate change

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Predicting the reactions of forest ecosystems to novel environmental conditions due to the ongoing climate change is challenging because of their longevity and complexity. In this sense, process-based models are helpful tools to improve our understanding of forest dynamics. Nevertheless, since each model is a simplification of reality, multi-model studies are useful to understand the variation in ecosystem responses to changes in environmental conditions.

This work presents the analysis of the development of 14 representative forest ecosystems of Slovakia using two process-based models under changing climatic conditions. Although both models use daily climate data for the specification of climate conditions, they differ in the spatial resolution of simulated ecosystems, and the description of ecosystem processes.

We simulated 50-year-long temporal development of even-aged homogeneous forests of four species: common beech, Norway spruce, Scots pine, and oak under different climate, management and mortality scenarios. We analysed changes in both aboveground and belowground parts of forests, as well as in soil and litter in comparison to the reference climate.

Applied climate scenarios showed that within 50 years we can expect an increase in air temperature at all selected sites, while the average annual precipitation is likely to remain stable. Predictions according to a set of 28 climate scenarios showed that due to climate change we can expect changes in the production and carbon stocks in individual parts of simulated ecosystems compared to the development under the reference climate. Ecosystem changes predicted by both models were largely consistent, e.g. both models predicted an increase in the production of live biomass across sites, species and initial stand ages, which indicates a positive impact of changing climate conditions in the conditions of Slovakia in the next 50 years. Nevertheless, we also revealed several opposite reactions of the models, e.g. in simulated litter carbon stocks. Moreover, the results showed different absolute values of the investigated variables from two different models, which provides us with the valuable information about the variation in ecosystem responses. We revealed that apart from the differences in spatial resolution and description of physiological responses, the reason behind the differences between models is also the set-up of initialization settings for model simulations since this subsequently affects simulated results. The study confirms the importance of multi-model studies not only for predictions of the future development of ecosystems, but also for a better understanding of the behavior of models and ecosystems.

Trapped in Nature's Labyrinth: Exploring Landscape Barriers and Spatial Genetic Connectivity in Red Panda Populations of Eastern Himalaya, Arunachal Pradesh, India

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Landscape barriers can impede the movement and gene flow of species, leading to isolation among sub-populations. Understanding how species navigate these obstacles is crucial for predicting population persistence and implementing effective conservation strategies. In this study, we used landscape genetic techniques to investigate the influence of physical barriers on red panda populations in Arunachal Pradesh, India, within the eastern Himalayan landscape. Our findings revealed fine-scale spatial genetic patterns and contemporary gene-flow among red panda populations, indicating a meta-population structure. The habitat suitability model identified approximately 12,189.75 km² of suitable red panda habitat in Arunachal Pradesh, comprising only 14.5% of the total area, with a mere 443 km² falling within protected areas. Through connectivity models, we identified corridors that connect important habitat blocks, crucial for the species' long-term genetic viability. We also detected significant barriers to gene flow, such as the Sela mountain pass in the western region, the Siang river in the central region, and the Dibang and Lohit rivers, along with the Dihang, Dipher, and Kumjawng passes in the eastern region. The Kameng and Subansiri rivers were found to contribute to the formation of regional habitat blocks in the western part of the landscape. Based on habitat fragmentation analysis and species dispersal analysis, we propose landscape-level and habitat block-level management using geometric reserve design principles. Our recommendations include converting identified core habitats into Conservation Reserves or Community Conservation Areas to preserve landscape connectivity and meta-population dynamics. Furthermore, we emphasize the importance of collaboration with Bhutan to develop a comprehensive monitoring plan for the long-term conservation and management of red pandas in the transboundary eastern Himalayan landscape.

In conclusion, our study reveals landscape impacts on red pandas, identifying key corridors and barriers. We propose targeted conservation measures to maintain landscape connectivity and promote the species' genetic diversity and long-term persistence.

The significance of herbivory in forming the ecosystem of dryland vegetation: tying spiral vegetation patterns and nonlinear nonlocal grazing

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An remarkable feature of dry-land ecosystems is the self-organized vegetation patterns; in addition to being aesthetically pleasing, patterns regulate how these water-stressed systems respond to increasing environmental stress. Although there are many different vegetation patterns, little is understood about the processes that give rise to spiral patterns. These spirals cannot be explained by the well-known models used to explain other vegetative patterns like stripes, rings, and fairy circles. Here, we've chosen a modelling strategy that identifies the interaction of herbivore grazing and vegetation as the cause of spiral formation. We used a grazing term that becomes saturated when fodder is abundant in order to understand the non-linear influence of grazing on the amount of vegetation. It is considered that grazing is dependent on mean vegetation density rather than density at a single site to take into account the impact of the spatial non-homogeneity in vegetation layout. Findings demonstrate how the various types of grazing response fundamentally alter the dynamics of the system. Only in natural grazing situations can the inclusion of non-locality result in spiral-shaped vegetation patterns due to complex eigenvalue induced wave instability; in human-controlled herbivory, no patterning is visible. Overall, our research indicates that one of the primary driving reasons for the creation of spiral patterns is the non-local, non-linear grazing behavior of herbivores.

Posters

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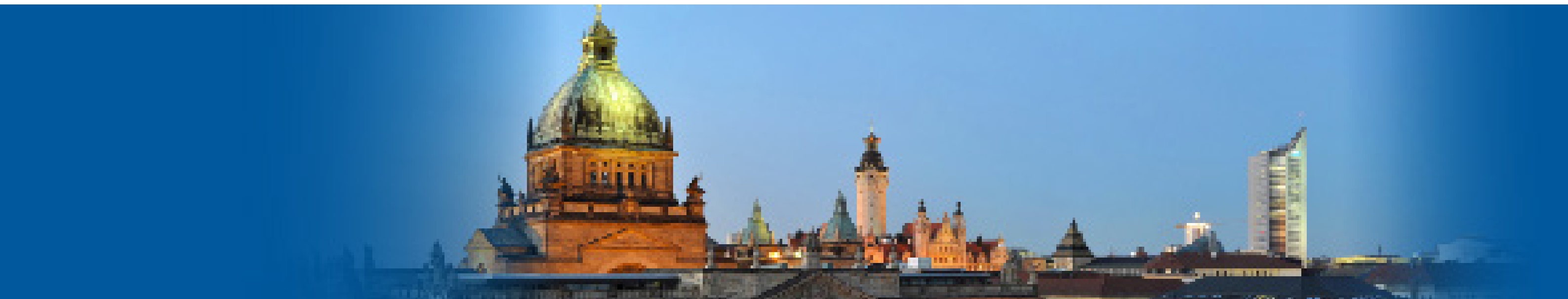

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1. Animal migrations under global changes – threats, implications, and mitigation

Predicting the expansion and redistribution of mosquito species under climate change in Croatia

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Environmental conditions strongly influence the distribution and abundance of mosquito species. As climate change alters these conditions, mosquito populations are likely to shift and expand, with potential implications for human health.

The aim of this study was to predict the impact of climate change on mosquito populations in Croatia through a combination of field studies and modelling studies. Historical data and future time series of environmental variables were obtained from Copernicus Climate Change Service and extracted from RegCM4 Climate Change Adaptation Simulations for Croatia. The potential distribution ranges of the selected mosquito species were predicted by applying a deep learning model trained on data on the global occurrence and ecological niches of the selected species. In addition to species distribution, the timing and duration of mosquito activity in each simulated year in each quadrant of the 5 km x 5 km spatial grid were also assessed. The model was trained using Keras and its inference was applied to each quadrant of the spatial grid. High-performance computing techniques were used to speed up the process.

The results suggest that the increase in temperature and changing precipitation patterns are likely to facilitate the expansion of several mosquito species to new regions. In Croatia, the Mediterranean climate and diverse landscape create an ideal habitat for several mosquito species, including the invasive Aedes albopictus, which is rapidly expanding its range worldwide and is also becoming more common in Croatia. This mosquito species is known to transmit several viruses, including West Nile, Chikungunya and Zika. It could pose a significant public health threat if it becomes established in a country.

In addition to range expansion, climate change is also likely to alter the timing and intensity of mosquito activity. Simulation results suggest that higher temperatures could lead to an earlier and longer breeding season, while changes in precipitation patterns could create more suitable breeding sites for certain species. All this could lead to an increase in mosquito abundance and potentially higher rates of disease transmission.

As part of the project "Adaptation of mosquito population control measures to climate change in Croatia (CADAPT)" (KK.05.1.1.02.0008), funded by the European Regional Development Fund, the results of this study will be used to provide recommendations for adapting mosquito population control measures to climate change.

Predicting geese migration under climate change and habitat alterations

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Changes in routes and timing is a commonly observed response of migratory birds to global change processes. It is, however, difficult to make predictions on these changes given that effects on one location can lead to consequences at distant sites.

We developed a behavioral optimization model within a stochastic dynamic programming framework to test the hypothesis that climate warming and habitat alterations results in temporal and spatial changes of geese migrating from wintering sites in Europe to their breeding sites at higher latitudes.

We investigate past, present and future scenarios using temperature, vegetation growth, and land cover products from the last decades as well as various future projections of these environmental drivers of migration.

From the model output, we compare the magnitude of spatiotemporal changes for different wintering and breeding populations and quantify the need of different geese species to adapt to the changing environments.

Finally, we discuss how the predicted changes affect ecosystem services as well as management and conservation plans of European geese populations and their habitats.

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2. Modelling species migration and range shifts under global change

metaRange: An R package to simulate metabolically constrained and population-based range dynamics

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Context: Mechanistic or process-based models offer greater insights into the future range dynamics for species facing complex threats from climate and land-use changes by focusing on ecological processes and causal relationships. This enables their application to non-equilibrium conditions and the generation of outputs which can be important for conservation such as abundance distributions and migration rates. The two limiting factors in the application of these models to real-

world systems are the computational demand and the data necessary to parameterize them.

Methods: We present a new model as R package, providing a middle ground between complex and calibration heavy individual-based models and correlative species distribution models (SDMs). "metaRange" is a spatially explicit, niche- and population-based mechanistic model that can include a variety of environmental factors and uses the metabolic theory of ecology to couple the local thermal conditions to the metabolic rates of the different populations. The model simulates local population dynamics and dispersal between populations to generate realistic range-wide metapopulation dynamics while using only a limited number of parameters. The model can be informed and calibrated using experimentally measured niche suitability or physiological data, but can also use pre-computed habitat suitability maps (i.e. from correlative SDMs) if such data is not available.

Conclusions: The metaRange R package contributes to a more widespread use of process-based models for the study of range dynamics in applied nature conservation. Its level of abstraction that is focused on populations and the inclusion of metabolic constraints should refine forecasts when predicting future range dynamics compared to correlative models, while providing an easier adoption and using less computational resources compared to complex individual-based models.

Identifying climate change forest refugia in the Berchtesgaden National Park

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Ongoing climate change is altering the geographic distributions of plant species world-wide. In a warming world, terrestrial taxa are predominantly shifting toward colder locations, corresponding to higher latitudes and higher elevations, to track their ancestral climate regimes. Consequently, during the last decades, a progressive decline of cold mountain habitats and their biota has been observed. The vulnerability of mountainous ecosystems urges to adapt current management plans to climate change in order to conserve and protect areas with strong biodiversity potential. In this context, refugia of forest tree species may play a fundamental role to sustain long-term population viability, enabling vegetation communities' persistence, minimizing the potential for deleterious species interactions and avoiding regional species extinctions. Therefore, we are aiming at predicting the location of forest refugia and characterize environmental factors leading to forest refugia occurrence under future climate change in the Berchtesgaden national park, Germany. To achieve this, we used fine-scale spatial datasets combined with a process-based forest landscape and disturbance model, iLand, allowing us to simulate future vegetation dynamics. Our preliminary results show different levels of reorganization of woody species along the altitudinal gradient of these mountainous ecosystems in response to future climate change, from none or few changes to complete reorganization. These research outputs will provide critical information for improving habitats conservation efforts in central European mountains.

Migratory swans individually adjust their autumn migration and winter range to a warming climate

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In response to climate warming, migratory animals can alter their migration so that different events in the annual cycle are better aligned in space and time with suitable environmental conditions. Although such responses have been studied extensively in birds for spring migration and the breeding season, much less is known about the influence of temperature on autumn migration and choice of winter range. We use multi-year GPS tracking data to quantify how daily autumn movement and annual winter distance from the breeding grounds are related to temperature in the Western Palearctic Bewick's swan, a long-lived migratory waterbird whose winter range has shifted more than 350 km closer to the breeding grounds since 1970 due to individuals increasingly "short-stopping" their autumn migration. We show that the movement of individuals is driven by lower temperatures throughout the autumn season and that, as a result, there is large flexibility in their annual winter distance as a response to winter temperature. On average individuals overwinter 118 km closer to the breeding grounds per °C increase in mean December-January temperature. Given the observed temperature increase in the Bewick's swan winter range during the last decades, our results imply that the observed range shift is for a substantial part driven by individual responses to a warming climate. We thus present an example of individual flexibility towards climatic conditions driving the range shift of a migratory species. Our study adds to the understanding of the processes that shape autumn migration decisions, winter ranges and shifts therein, which is crucial to be able to predict how climate change may impact these processes in the future.

TreeMig - A framework to predict spatiotemporal forest dynamicsThe TreeMig Framework for spatio-temporal forest dynamics

Daniel Scherrer; David Böhm; Alain Joss; Achilleas Psomas; Dirk Schmatz; Heike Lischke

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TreeMig is a medium-complexity forest landscape model simulating multi-species forest dynamics and tree species migration from stand-level to continental scales. The core model simulates local dynamics of tree species densities in different height classes by incorporating seed bank dynamics, germination, seedling/sapling survival, growth, competition, mortality (including by disturbances and management) and seed production. Trees interact locally by shading and competition for light. Yearly climate (drought stress index, yearly day degree sum, winter temperature) influences germination, survival and growth. The model is implemented on a spatial grid, with seed dispersal between grid cells.

We developed a new R-package and GUI to simplify preprocessing of input data and postprocessing of results. The package facilitates the inclusion and necessary transformation of input data (e.g. climate data as NetCDF, soil data of water holding capacity, or land use masks) and the adjustment of study-specific parameters, to call the core TreeMig model as well as to provide an overview of the simulation results in a variety of formats. The GUI can be used for the entire pipeline or to derive an R-script which then can be modified for further simulations, e.g. soft coupling with other models. The framework also includes a set of default input data (for Switzerland) and species parameters allowing simulations in any region of Switzerland at different spatiotemporal resolutions, and an extended Tutorial.

An ecological framework to connect the world's ocean: a trait-based guild distribution model to account for ecosystem specificity in range shift mechanisms.

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Marine biodiversity studies need to move away from pattern descriptions and correlative approaches and rather should focus on causality through process-based approaches. This is a more robust way of predicting previously unobserved conditions resulting from the combined effects of human activities and the changing environment on the global ocean ecosystem. In species distribution models that aim to determine the preferred habitat of species, this means considering the relationships between species. Community distribution models based on co-occurring species have gained traction for this reason and because they can determine species relationships without any prior information. However, they are often criticized for their lack of ecological foundations. Additional approaches are therefore required to adequately determine these relationships in a biologically sound manner, and trait-based approaches are among the most promising methods. While most trait-based approaches are often limited to organism size to determine potential predator-prey relationships, the integration of additional traits could greatly improve the estimation of inter-species relationships across a wider taxonomic range. While considering a wide variety of traits could provide information on the functioning of ecological networks by determining biotic relationships more accurately, they could also provide information on the adaptative capacity of species. Finally, traits can characterize socio-ecological linkages and provide knowledges on the sensitivity of the biotic sphere to anthropogenic drivers. Here we aim to present a modelling framework that combines multi-species distribution with a trait-based approach to develop a global, spatial functional guild diversity model. By combining both tools, we intend to predict the potential impact of climate change on ecosystem functioning and the consequences for the functional guilds of the ocean. The resulting information will be useful to determine the role of traits in ecological niche partitioning to better predict which species are most likely to shift in the changing oceans of tomorrow. More importantly, with the changing spatial composition of functional guilds, we hope to understand the community level processes that can hinder or facilitate species range shifts, thus directly accounting for ecosystem specificity in range shift mechanisms, rather than looking at species by themselves. The main objective of the framework will be to provide a new multi-risk assessment method to study the impact of species range shifts on biodiversity. Also, by combining this methodology with spatial maps of human impacts on marine biodiversity in a multi-criteria analysis, we will seek to map hotspots of ecological risk in relation to human activities.

Land-use following a middle-road socio-economic pathway (SSP2) is not enough to recover mammal populations in Southern-Asia.

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Land use is the main direct driver of biodiversity loss and Southern-Asia is, globally, one of the regions under the highest land-use change. Here we estimate how mammals that play a key role in the ecosystem functioning will cope with landscape transformations. We used the a state-of-the-art spatially-explicit agent-based model (RangeShifter) combining local density dependence on fecundity, stage-structured demographics and dispersal to predict the occupancy and abundance for large-body size carnivorous species (Panthera tigris, Panthera pardus) mid-sized and small carnivorous (Cuon alpinus, Felis chaus, Vulpes vulpes and Prionailurus bengalensis) and two Cetartiodactyla species (Sus scrofa and Gazella benetti) in Southern Asia. In addition, we estimated how species-richness changed through time. The model was projected to the period 1850 to 2100 under two socio economic pathways, representing an intermediate scenario (SSP2-4.5) and a fossil-fueled development scenario (SSP5-8.5). We found mixed-response to land-use across species. We estimate the mean total proportion of remaining individuals to be 0.60 (SD = 0.24) under SSP2 and 0.64 (SD = 0.37) under SSP5 compared to baseline land use in 1850. The drop in the total number of occupied cells is of lower magnitude (SSP2: mean = 0.82, SD = 0.27; SSP5: mean = 0.84, SD = 0.32). Mean species richness per cell followed a decline throughout the 20th century (mean = 0.90, SD = 0.15) followed by increase from current time up to 2100 under both scenarios (SSP2: mean = 0.95, SD = 0.18; SSP5: mean = 0.97, SD = 0.22). Our results support biotic homogenization with spread of widespread species and restriction of forest-specialists. We confirm a disproportionate and negative influence of loss of non-disturbed patches, and lower landscape permeability in large mammals, potentially leading to considerable change in mammalian biomass in the ecosystem. These findings suggest that a middle-road socio-economic pathway (SSP2) is not enough to maintain or recover populations compared to pre-disturbance levels.

How null models can help us to evaluate the incorporation of intraspecific variation in ecological niche models. A case study for European beech (*Fagus sylvatica L.*)

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Ecological niche models (ENMs) are vastly applied to predict species range shifts under climate change scenarios. However, classical ENMs assume species homogeneity, disregarding the effects of gene flow limitations and resulting intraspecific variation through local adaptation. Compared to classical ENMs, incorporating intraspecific variation (e.g., by using genetic data) can improve model performance and provide more realistic predictions of climate change impacts. Genetically informed ENMs are still rarely used and may suffer from biased estimates of model performance or overfitting. We use a null model approach that randomises the genetic structure across the species' range to assess the model performance of genetically informed ENMs and provide further information about the meaning of intraspecific variation in ENMs.

We use publicly available range-wide genetic structure and observations from forest inventory plots of European beech (*Fagus sylvatica L.*) to create individual genetically informed models for the distinct genetic groups representing different ecotypes. The obtained individual models are combined into one overall genetically informed model. Model performance is assessed with measures of discriminatory ability, precisely area under the receiver operating characteristic curve (AUC), sensitivity, specificity and TSS statistics. Null models based on randomised sets of spatial points are computed for each of the models. This allows us to estimate null distributions of the performance measures and compare them to the measures of the real model. By doing so, the null models will help us to check if indeed genetic adaptation or rather just statistical artifacts explain the improved habitat suitability found in such approaches. Finally, we compare model performance of the individual models and the overall model against a classical ENM approach. Thus, our approach will allow to quantify the importance of local adaptation for future habitat suitability.

Predicting species distributions from sparse survey data and remotely sensed environmental predictors – a how-to guide for everyone with basic knowledge in R

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Species distribution models (SDMs) are important tools for explaining and predicting the spatial distribution of individual species or communities of species. By predicting species' responses to changing conditions, SDMs can help scientists and stakeholders to identify the most promising transformation processes. SDMs capable of estimating precise community compositions tend to be highly data intensive. However, novel approaches and tools like our recently developed spectre R package allow to predict community compositions (i.e. site-specific presence-absence data) from sparse data. I will present the complete workflow using spectre: estimate α- and β-diversity distributions from field and remotely sensed data (i.e., species presence-absence data, environmental data); identify prediction sites; apply spectre to predict community compositions for prediction sites. The following three questions will be answered. How to generate the algorithm input estimates? How to identify which potential new sites are eligible to make predictions for them? How does uncertainty in input estimates affect the prediction quality? Using bird survey data and environmental predictors collected in Bangalore, India as an example, we predict species distributions under different land-use change scenarios and investigate the sensitivity of the algorithm to uncertainty in estimated α-and β-diversity. At the end of this talk, the listeners will have a sound idea how this modelling approach works and if it is applicable to their data and research interests.

Role of spatiotemporal environmental fluctuations in facilitating range expansion under climate change

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Temperature change can be highly volatile across space and time. Spatial variation (which creates climatic micro-refugia due to topographic complexity of landscapes) and temporal fluctuations (which are increasing with climate change) may facilitate or hinder a species' response capacity to climate change. These can have opposing effects on a population's viability, so a better understanding of this variation, and how spatial and temporal fluctuations interact, is essential to predict which species will be most impacted by current and future climate change and why. We use a single species population dynamics model in discrete time and space to see how spatiotemporal fluctuations impact a species' ability to track a shifting climate along a latitudinal gradient at its colder range margin.

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3. Movement modelling: underlying principles and processes

Modelling the effects of toxicants on behavior - a case study using *Daphnia magna*

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Behavioural ecotoxicology is an emerging field that studies the effects of pollutants and other environmental stressors on the behaviour of organisms. Changes in behavioural elements have been recognized as early warning signals of toxic effects. Daphnia magna is a widely used model organism in ecotoxicology because it is sensitive to various pollutants and has the potential to provide insights into the effects of toxicants on aquatic ecosystems.

In this study, we used a combination of laboratory experiments and mathematical modelling techniques to investigate the effects of fungicides on the movement behaviour of Daphnia magna. First, we conducted experiments to quantify the effects of toxicants on different behavioural elements of Daphnia magna, such as swimming speed, turning rate, and complexity of movement. The movement of Daphnia was simulated with an individual-based model (IBM), which was parameterised based on experimental results. The model was trained with 70% of the experimental data and validated with 30% of the data set.

Our results show that exposure to the toxicants had significant effects on behavioural elements of Daphnia magna that can be quantified. These effects were dose-dependent and were also influenced by the duration of exposure.

The simulation results showed a high correlation with the experimental data.

Using the mathematical model, we were able to predict the effects of the toxicant on the behaviour of Daphnia magna in a virtual aquatic environment. Our results suggest that exposure to the toxicant could significantly reduce the mobility of Daphnia magna, with individuals staying closer to the source of the toxicant and showing reduced movement behaviour. Furthermore, these behavioural changes can be modelled and simulated in in silico experiments with similar toxicants since this study resulted in a versatile framework that can be extended with additional data in order to predict the effects of several other toxicant groups.

Overall, our study highlights the potential of using mathematical modelling techniques to gain insights into the effects of toxicants on the movement behaviour of aquatic organisms. The ability to predict the effects of toxicants on the movement of organisms is of particular importance in ecotoxicology, as it can provide information on the potential effects of pollutants on the overall health and the functioning of aquatic ecosystems.

Life history traits explain variation in spatial population synchrony across European bird species

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Spatial population synchrony is common among populations of the same species and is an important predictor of extinction risk. Despite the potential consequences for metapopulation persistence, we still largely lack understanding of what makes one species more likely to be synchronized than another given the same environmental conditions. Generally, environmental conditions in a shared environment or a species` sensitivity to the environment can explain the extent of synchrony. Populations that are closer together experience more similar fluctuations in their environments than those populations that are further apart and are therefore more synchronized. The relative importance of environmental and demographic stochasticity for population dynamics is strongly linked to species' life history traits, such as pace of life, which may impact population synchrony. For populations that migrate, there may be multiple environmental conditions at different locations driving synchrony. However, the importance of life history and migration tactics in determining patterns of spatial population synchrony have rarely been explored empirically. We therefore hypothesize that increasing generation time, a proxy for pace of life, would decrease spatial population synchrony and that migrants would be less synchronized than resident species.

We used population abundance data on breeding birds from four countries to investigate patterns of spatial population synchrony in growth rate and abundance. We investigated differences in synchrony across a gradient of generation times in resident, short-distance migrant, and long-distance migrant bird species. Species with shorter generation times were more synchronized than species with longer generation times. Short-distance migrants were more synchronized than long-distance migrants and resident birds. Our results provide novel empirical links between spatial population synchrony and species traits known to be of key importance for population dynamics, generation time and migration characteristics. We show how these different mechanisms can be combined to understand species-specific causes of spatial population synchrony. Understanding these specific drivers of spatial population synchrony is important in the face of increasingly severe threats to biodiversity and could be key for successful future conservation outcomes.

Can we infer microbial dispersal mechanisms from the georeferenced genetic sequences?

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One attempt to infer the movement of the modern microbial species' ancestors, as well as to predict the movement of their descendants, is to analyze correlations between physical and genetic distance for samples taken in different locations. However, multiple mechanisms may lead to similar correlations. In addition to a situation where the individuals experience a standard diffusion modeled as a random walk (Louca, ISME, 2022), we suggest a few more options. First, the convection model, where the individuals can be dragged by moving media, such as ocean currents or migrations of hosts. Second, the gene surfing model, where the population as a whole expands to new areas in a manner more reminiscent of directed motion than a random walk (Hallatschek&Nelson, Theoretical Population Biology, 2013). Third, the model with the heterogeneous density of the population, where even in the steady state with the density of the population constant in time there can be a directed flux of individuals from high to low birth rate areas. Finally, the environmental filtering model, where different individuals may prefer different environmental conditions, in which case genetic distance correlates with the difference in climate rather than with the physical distance (Ladau et al., ISME, 2013). We model these mechanisms to see under which conditions they qualitatively reproduce the observed correlations between physical and genetic distance. We show that while the convection model produces genetic trees equivalent to the standard diffusion model, it is not so for the last three models. Namely, for all of them, the descendant of the parent with many descendants is more likely than average to have many descendants as well, either due to location (at the boundary of the expanding population or in the higher birth rate area) or due to better fitness to the environment. We quantify this property using a parameter called local branching index (Neher et al., eLife, 2014) the distribution of which allows us to distinguish trees generated by the last three mechanisms from the standard diffusion model and convection model. We describe our preliminary results on applying these methods to data from georeferenced samples, potentially allowing us to distinguish the role of the different mechanisms in past dispersal. We also speculate that by comparing the speed of the dispersal with the rate of climate change affecting its fitness to the environment (inferred using the environmental filtering model), we can predict the future expansion range of the species.

Critical review of movement representations in ecological models used for chemical risk assessment

Pernille Thorbek; Joachim Kleinmann

BASF SE

Ecological models such as population models are increasingly used for higher tier risk assessments of chemicals like plant protection products (PPPs). In agricultural landscapes, exposure to chemicals is dynamic and varies markedly in time and space. Therefore movement plays a crucial role in determining exposure and hence risk. The models applied to PPP risk assessments cover aquatic habitats, terrestrial habitats and soil as well as many taxonomic groups, e.g. mammals, birds, social insects and other terrestrial arthropods, earthworms, collembola, fish and aquatic invertebrates. Consequently, many different movement patterns have been modelled. The movement algorithms range from simple diffusion, over correlated random work to highly sophisticated adaptive models. In this presentation a critical review of movement models used for PPP risk assessment will be presented including an overview of mode types and pros and cons for use in risk assessments.

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5. Reusable building blocks (RBB) for agent-, and individual-based models

Fish population dynamics into physical-biogeochemical models: preliminary insights

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Small pelagic fish, such as sardines and anchovies, play a vital role in ecosystems and hold significant economic value, particularly in the Adriatic Sea. Small pelagics are quickly influenced by environmental changes, due to their short lifespan, high fecundity, and reliance on plankton; however, few modelling attempts have integrated their population dynamics with physical-biogeochemical models. For this reason, in this preliminary work, we incorporated sardines and anchovies' population dynamic into the Biogeochemical Flux Model for the Adriatic Sea, using a bioenergetic approach. Both species were included as predators of the BFM macrozooplankton group. Sardine and anchovy biomass variation for time unit is described in function of consumption, respiration, egestion, excretion rates and reproduction energetic allocation. Natural and fishing mortality are considered.

Our initial findings reproduced the population trends of these fish species when compared with catch time series data. We will also present and discuss technical and computational challenges we met in coupling physical, biogeochemical, and higher trophic level processes that occur at different spatiotemporal scales. Future steps involve developing a more flexible Agent-based model in 2D, coupled offline with the BFM, while maintaining the bioenergetic approach to account for animal physiology. This comprehensive modelling framework will boost our capacity to investigate sardine and anchovy ecological responses to climate and fishery management scenarios; in addition, it will improve the capability of modelling higher trophic levels, such as marine mammals dynamic, in an urgent need for more effective management and protection all over the Mediterranean Sea.

From combinatorial explosion to transferable predictions: Mechanistic modelling and microbial ecology of multiple stressors.

Milos Bielcik; Mohan Bi; Matthias Rillig

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Microbial ecology has accumulated a wealth of knowledge on the effects of multiple, simultaneously acting global change stressors on soil microbial biodiversity and key microbiome-driven ecosystem functions. However, due to soil properties such as extremely high spatial and biological complexity, opacity, and microscopic scale of ecological processes, the typical empirical approach relies on applying a treatment and measuring response variables at the community or ecosystem level of entire soil microcosms. Although this approach is both practical and environmentally relevant, it is also limited in its ability to provide mechanistic insights into how multiple stressors interact to produce system-level patterns. Because the processes remain black-boxed, researchers face the challenge of combinatorial explosion, in which a variety of stressors can be combined in virtually unlimited ways, and thus the effects of many particular combinations cannot be predicted. Microbial agent-based models (µABM) are well suited to address the challenge of combinatorial explosion because of their ability to simulate mechanisms in a spatially explicit manner, at low organisational levels, and thus enable transferable predictions for soil ecosystems. In order to fully harness abilities of µABMs, it is necessary to identify, develop and combine modular sub-models that simulate relevant microbial processes and classes of stressors with different mechanisms of action, e.g., those that simulate habitat micro-structure, biodegradation of anthropogenic chemicals, biofilm formation, or effects of pesticides and antibiotics. We will present our framework for identification and development of relevant sub-models for multiple stressor research in soil, including a list of physical, chemical, and biological first principles, based on which reusable sub-models should be built. In addition, I will outline examples of existing µABMs in various fields such as biomedicine, biotechnology, or ecotoxicology, that have been identified using this framework and that could serve as a source of sub-models adaptable for multiple stressor research. I will discuss both technical and conceptual opportunities and challenges associated with adapting these existing sub-models.

SwarmSim - Insect swarming simulation package based on IBMs

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SwarmSim is an open-source Python-based simulation package built on individual-based models (IBMs). It uses high-performance computing and artificial intelligence (AI)-based agent behaviour to simulate the swarming behaviour of various insects. With its advanced capabilities, SwarmSim provides researchers with a powerful tool to study the complex behaviour of swarming insects, including haematophagous species such as mosquitoes and horseflies.

Swarming is a collective behaviour observed in many insect species, where individuals form large groups or swarms that move in a coordinated manner. Haematophagous insects in particular have evolved complex swarming behaviour to facilitate their blood feeding habits. This behaviour is crucial for the survival of these species as it allows them to find and feed on their hosts while avoiding predators.

SwarmSim's IBMs are based on the interactions of individual agents, each representing a single insect and the environment in which they operate. The agents in SwarmSim have the ability to interact with each other and their environment and make decisions based on their current state and the behaviour of their neighbours. For this reason, SwarmSim can simulate complex swarm behaviour, including that of haematophagous insects.

A key advantage of SwarmSim is the use of intelligent agents. SwarmSim's agents are designed to learn from their interactions with the environment and other agents, and to adapt their behaviour over time. This makes SwarmSim particularly well suited to the study of complex swarm behaviour, as it allows researchers to investigate how this behaviour might evolve over time.

This research demonstrates how SwarmSim can be used to study swarm behaviour in haematophagous insects such as mosquitoes and horseflies. We use SwarmSim to simulate the interactions between individual agents and the environment, and to study how these insects find and feed on their hosts. We also investigate how this behaviour is influenced by environmental factors such as temperature, humidity and wind speed.

SwarmSim is a powerful tool for studying the complex behaviour of swarming insects, including haematophagous species. With its advanced capabilities, SwarmSim can make an important contribution to understanding these important species and their impact on human health.

6. Next-generation advances in individual-based modelling

Introducing the Formal Model and Model Implementation Documentation with Doxygen (MIDox) Paper Formats for Transparent and Reproducible Modelling

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To address the ongoing issue of inadequate model documentation, the Food and Ecological Systems Modelling Journal is introducing new publication formats to enable modellers to more effectively communicate their models. The recently proposed Formal Model article format (Topping et al., 2022) serves as the first step in model documentation by laying out the theoretical framework, modelling approaches, and externalities of the model before analysis. The Formal Model also makes it easier for reviewers to identify potential problems early in the development process and to provide feedback.

Building on this, we propose a new format called the Model Implementation Documentation with doxygen (MIDox) paper, which focuses on the implementation phase of model development. The MIDox format separates the implementation phase from that of model formulation and evaluation and application articles. By providing detailed documentation of the model's implementation, MIDox enables transparency and reproducibility. The MIDox format will be the second step in our proposed three-step model documentation process. We make the case for why this additional step is necessary and suggest a format for its implementation. The third and final step in the process before analysis is the model validation which runs in parallel with MIDox. These new model documentation formats will allow for improved communication and transparency in ecological modelling, ultimately leading to better research outcomes and faith in models used for policymaking.

A general likelihood-based method for the inferential analysis of agent-space reactant-catalyst-product models.

Niklas Moser; Dmitri Finkelshtein; Sara Hamis; Panu Somervuo; Otso Ovaskainen

While individual-based models (IBMs) have been shown to be suitable for simulating complex system dynamics, the model behaviour is too complicated in most systems to be analysed mathematically. Therefore, the inferential analysis of IBMs faces a fundamental problem: how can we calibrate model parameters with intractable likelihood equations? Most common workarounds use extensive simulations to explore a subset of the full parameter space. In pattern-oriented modelling the simulations are compared to observed patterns of the system according to predefined criteria. However, these approaches are resource-intensive and based on heuristic choices on the criteria and parameter space. Other methods use vague approximations for the exact model characteristics. Some approaches construct a pseudo-likelihood by comparing simulated summary characteristics with observed summary characteristics. For some models a pseudo-likelihood can be constructed by the tractable likelihood of a related simpler model. In frameworks like Approximate Bayesian Computing sampling algorithms are used for updating parameter estimates. The performance of these workarounds heavily depends on the choice of summary characteristics and pseudo-likelihoods as they are a simplification of the true intractable likelihood. In this study we consider a broad range of IBMs in terms of spatio-temporal point process models, the reactant-catalyst-product models (RCP-models) that operate in continuous space and time. Therefore, we apply tools from harmonic analysis to mathematically describe the system of interest by spatial and spatio-temporal moments and cumulants of any order without being constrained by heuristic moment closure methods. We develop a general method for the parameter estimation of RCP-models from observational spatio-temporal co-occurrence data. We derive for the space homogeneous case a Poisson mean-field likelihood and apply a perturbation expansion to include information beyond the mean field. This results in a general likelihood that is rigorously defined and asymptotically exact. Based on the likelihood expression we present a Bayesian parameter estimation framework. We show for both simulation-based case studies (the single-species spatial stochastic logistic model and the host-parasite model) and for empirical data (cancer cell data) the general suitability of this approach for ecological research and beyond.

Automatically Reusing Simulation Experiments in Ecological Modelling and Simulation Studies

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Recreational fishing has been shown to have severe implications for some fish stocks, such as the western Baltic cod. Hence, deeper understanding of angler behavior is required in order to introduce effective policies such as bag limits or seasonal closures. A recent individual-based simulation study aims to explain the factors involved in site choice decisions of recreational fishers using an exploratory modelling approach. The model is revised successively to account for the various data sources and constraints, and a variety of simulation experiments are conducted to explore the diverse cognitive theories.

Transparency and reproducibility concerns have motivated the capturing of provenance using the W3C PROV standard. Provenance, broadly speaking, refers to documenting what products have been used or generated during a study (e.g., research questions, assumptions, requirements, models, experiments, or data) and how they are related by the diverse activities (such as model refinement, calibration, validation, analysis, but also data collection). For the fisheries study this entails, e.g., information about survey data, literature, modelling of angler agents and locations, and analysis scripts needed to explore different behavioral theories. The provenance graph thus tells the story of the entire model development process in a machine-accessible manner.

If provenance is captured not only in retrospect but already during the simulation study, it can be exploited for partly automating the next steps. This would allow for simulation studies to be conducted in a more efficient and less error-prone manner, which is now more crucial than ever as both fast and well-informed management decisions are required.

Therefore, we present an approach for automatically conducting the simulation experiments to come. We define provenance patterns and associate them with semantics, which allows us to interpret the different activities and infer what experiments to generate. For example, once a new behavioral theory was implemented, earlier analyses (such as sensitivity analysis or approximate Bayesian analysis) can be reused and adapted based on meta-information from the provenance graph. This is based on the observation that many analyses are conducted frequently and repeatedly during a simulation study but with different model versions. Another example of this may be the re-validation after major model changes to check if the expectations regarding the simulation output still hold.

Our approach is implemented in the Reuse and Adapt framework for Simulation Experiments (RASE), which can interface with various modelling and simulation tools and was previously applied to a social simulation study of human migration

The mangrove-saltmarsh ecotone: Explaining observed vegetation patterns with a mechanistic modelling approach considering plant-soil-water-feedback

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(Sub)tropical coastal wetlands often consist of mangrove and saltmarsh habitats, where mangroves are usually located in the lower, regularly flooded zones close to the sea, and saltmarsh plants in the upper, dryer and hypersaline zones. The transition between these two habitats, the so called "mangrove-saltmarsh ecotone", is characterised by multiple feedbacks between local abiotic factors and vegetation. We hypothesize that these feedbacks result in characteristic vegetation patterns that are reflected, for example, in the sharpness of transition between the two habitat types. While models exist to describe the dynamics of these two habitat types separately, an integrative approach that accounts for both mangroves and saltmarshes and their interactions with their biotic and abiotic environments does not exist. In the absence of an integrative model, we are missing a mechanistic understanding of ecotone vegetation patterns and their dynamics, including future variability under global change. To address this knowledge gap, we build on the hybrid process-based simulation tool pyMANGA that describes feedbacks between vegetation and subsurface hydrodynamics. This tool has already been successfully used to reproduce the typical zonation of mangrove forests. We extend the pyMANGA simulation to model potential saltmarsh habitat, which requires the description of both saltmarsh plants and the unsaturated soil conditions in which they are often found. Our final model describes the complex interactions between saltmarsh plants, mangrove shrubs, mangrove trees and soil water, simulating the entire mangrove-saltmarsh ecotone. It allows us to systematically investigate the emergence, persistence and temporal shift of different ecotone patterns under changing hydrological conditions. Here, we introduce the model concept and provide a proof of its suitability by presenting a case study of a mangrove-saltmarsh ecotone in north Brazil

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7. New methods and applications in trait-based modelling in ecology

Coupling tree-rings analyses, WUEi and forest modelling to forecast dieback on beech forest along a latitudinal gradient in Italy

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Extreme climatic events such as dry spells accompanied by warmer temperatures can affect forest carbon sink capacity, playing a crucial role to turn forests into a source or sink of carbon, i.e. allowing for a negative or positive feedback to climate change. Nonetheless, the trajectories of carbon sequestration and which forest will be able to survive under extreme climatic conditions are scarcely understood. Here, for the 1965-2017 period, we apply a retrospective analysis of tree-rings, basal area increment (BAI), and water use efficiency (WUEi) to assess forest growth performance and water use strategies (δ13C) in Fagus sylvatica L. along a latitudinal gradient in Italy. In addition, to determine the future tree carbon sink capacity and carbon starvation risk for the period 2015-2100, we perform simulations under future climate scenario by mean of the 3D-CMCC-FEM forest model, a stand-scale process-based model developed to simulate forest ecophysiology and dynamics with a cohort-like approach.

We selected four stands of beech forest along a latitudinal gradient in Italy. The sites were Trentino (TRE), Lazio (LAZ), Matese (MAT) and Calabria (CAL). Sites selection allowed the comparison along precipitation gradients since rainfall decreases from north to south. At all sites, trees showed a BAI decline in the last two decades, and this pattern was more noticeable in the northernmost site. The WUEi, presented a positive trend in TRE, MAT and CAL sites, indicating early stomatal closure during drought and a potential carbon starvation due to reduced photosynthesis rates, whereas in LAZ showed no trend of WUEi, indicating constant transpiration rates under water scarcity, this it might be explained because is the youngest site and is located at a lower elevation. We use these data to compare the forest model simulations trends in BAI and WUEi in the period 2005-2017 in similar sites, for which forest structural characteristics were available and analyzed the future trends in terms of carbon assimilation and growth shaped by forest structures and dynamics and site conditions.

Multi-proxy, retrospective quantifications of tree-rings, BAI, stables isotopes and modelling provide a robust and complementary tool to differentiate dieback causes, and to forecast which stands or trees will show growth decline or, on the contrary, which will be able to survive to forecasted hotter droughts in the future.

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8. Integrative approaches to capture natural disturbance impacts in models

Modelling disturbances in a changing climate: the Eco2Adapt project and a case study from the Swiss Alps

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ETH (Zurich)

The objective of the European project Eco2Adapt is to help stakeholders, forest owners and practitioners to manage forests and to optimise social and environmental resilience, using the concept of nature-based solutions. The project combines interdisciplinary knowledge from scientists and stakeholders in Europe to understand perceptions and provide incentives for adaptive management and policy. The project is based on Living Labs (LLs). These consist in a network of case studies that are situated at the regional scale in climate hotspots in Europe. Data from LLs will be used to refine models to determine temporal social-economic pathways and calculate alternative adaptation strategies for multiple risk analysis and interactions between big bundles of ecosystem services considering a spatial setting. One of the models that will be used in the LLs is LandClim, a spatially explicit forest landscape model developed to assess climatic and management effects on forest dynamics. Moreover, LandClim has different modules to simulate the impacts of natural disturbances, e.g. windstorms or bark beetle outbreaks. One of the Living Lab is situated in the Swiss Alps, in the canton of Grisons. The case study represents the Alpine environment, presenting a wide species range and altitudinal range. Particular attention is dedicated to the protective function of the forest against natural hazards (e.g. rockfall and avalanches) since it is the most particular feature of this Living Lab. Sustainable timber production is a key ecosystem service that would be necessary to investigate as well, especially in the different climate change scenarios. The ultimate goal for the Swiss Living Lab would be to observe how different management practices will affect the sustainable provision of timber and the protective function of forests in future climate scenarios.

Vulnerability assessment to wind damage in a protective forest stand in the Alps.

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The risk of wind damage to European forests is expected to increase due to the changed climate. Therefore, research efforts in forestry have been focussing on the development of analytical and modelling tools to improve the prediction of forests' susceptibility to wind damage, and ultimately to support forest management decisions in increasing wind-resistance in forest stands. Recent catastrophic wind damage to European forests has shown that wind damage risk applies also to montane forests. Some of them are of particular importance for the various ecosystem services they provide, including protection from gravitational hazards and defence against soil erosion. At present, the available forest wind risk models have been tested and used mainly on production or planted forests in different countries, but never in the complexity of mountainous terrains. The aim of this study is to introduce a methodology for the validation of a new parametrization of ForestGALES wind risk model for the alpine environment.

The parameterisation was developed through field test (e.g., pulling tests on trees) and validated based on the observed wind damage caused by the storm Vaia, occurred in northern Italy in October 2018, and the pre-disturbance forest characteristics. The use of this parameterisation can allow the construction of wind vulnerability maps starting from LiDAR data. LiDAR-based mapping vulnerability to natural disturbances, in this case wind, is an innovative tool for forest planning and management as it can produce spatially distributed input data for the model (i.e. crown width, density, dominant height and distance to the gap). The frequency of natural disturbances is expected to increase, as is their severity and forest management need to target interventions to obtain more resistant and resilient forest stands. Management should aim to apply strategies to prevent future damage in a way that ensures continued protective effectiveness, guaranteeing the preservation of local communities and infrastructures.

Effects of insect disturbances on forest biogeochemical cycles using the Quincy Terrestrial Biosphere Model

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Insect outbreaks are major disturbances in forests, causing extensive tree mortality and with the potential to significantly alter forest biogeochemical processes. Current trends of increasing heatwave and droughts frequency and intensity in Europe might increase the occurrence of insect outbreaks. In combination with other disturbances and climate extremes, insect outbreaks reduce the carbon sequestration potential of forests and introduce uncertainties in natural climate mitigation strategies. In this study, we examine the impacts of insect outbreaks on forest biogeochemical cycles by developing a new module for the QUINCY (QUantifying the effects of Interacting Nutrient CYcles on terrestrial biosphere dynamics and their climate feedbacks) terrestrial biosphere model, focusing on two high-impact insect types: bark beetles and defoliators. We prescribed different disturbance rates according to real events and analyse the simulated variations in carbon storage, greenhouse gas emissions, and nutrient cycling (Nitrogen and Phosphorus) resulting from insect disturbances. Our study offers new tools and insights for evaluating the effects of insect outbreaks on forest biogeochemical functions and potential feedbacks with climate.

Modeling the effect of invasive forest pests on carbon stocks with an individual-based forest model

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Biotic damage to forests has been observed to increase globally in response to climate change that relaxes thermal limitations of species distribution, accelerates insects` development, and compromises tree defence. While some ecosystem models can simulate the dynamics of established disturbance agents such as spruce bark beetle, mountain pine beetle, wildfire, and windthrows, capturing the dynamics of emerging organisms is challenging yet potentially crucial for assessing their future impacts and possible disturbance regime shifts. Here we used a Biotic Disturbance Engine (BITE) modular framework embedded within the forest landscape and disturbance model iLand to quantify the potential impacts of one of the most serious new invasive organisms in Europe, the Pine Wood Nematode (PWN). The PWN, native to North American pine forests, has devastated Asian pine stands since the 1960s and was recently accidentally introduced to Portugal and Spain. Projections indicate that this species will cause severe mortality in southern Europe. Further expansion of PWN into central Europe will likely result from a combination of wood transport and climate change, creating climatically favourable conditions for the nematode. We conducted a comprehensive literature review to determine the parameters driving the PWN`s introduction, dispersal, colonization, population dynamics, and impact on vegetation; the building blocks of BITE. We proposed a solution for considering the biology of two involved organisms, the non-native PWN and the native longhorn beetle Monochamus galloprovincialis that acts as a vector. We tested this implementation in a Central European forest landscape (35 000 ha of mixed forests), which can be within reach of the PWN`s climatic envelope between 2030 and 2050, depending on the level of warming. The testing included comparing simulated mortality patterns and mortality rates with areas of current PWN occurrence in Portugal and Spain. Sensitivity to management operations such as salvage removal of infected trees and longhorn beetle population reduction through trapping was also tested, and outputs were confronted with documented observations. We explored an overall impact on the forest in terms of shifts in tree species composition, demography, and landscape carbon. The versatile interface and the modular structure of BITE allow it to be transferable to other dynamic vegetation models, facilitating the collaborative development and testing of different disturbance agent parameterizations. Given the increasing importance of emerging biotic agents and fragmented knowledge of their ecology, population dynamics, and impacts, such efforts are essential for assessing the future impacts of such organisms.

Two sources energy balance model can enhance the ability of crop models to simulate phenology----A case study for silage maize in German

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Understanding how crop phenology responds to warmer temperatures under climate change is crucial. The timing of key phenological stages determines both the duration of radiation capture and potential yield for a given location, as well as, the timing of anthesis when crops are most vulnerable to heat and drought stress. Most previous studies have used the thermal time model to quantify crop phenology response to temperature. However, many of the underlying models perform poorly when applied across environments or production conditions, potentially because they rely on air temperature rather than crop temperature. Air temperature may not accurately reflect the real growth conditions of crops, particularly when soil water deficit or vapor pressure deficit are taken into account. To address this, canopy temperature simulation models are sometimes integrated into crop models to drive temperature sensitive processes. However, most of these models assume a uniform crop canopy which is clearly not applicable when plants are in early vegetative phases and the soil surface can account for the largest share of the energy transfer processes. In this study, we developed a new canopy temperature simulation module based on a two-source energy balance approach. We improved our previous single-source canopy level energy balance model by taking both the canopy source and soil source into consideration, and we applied the Monin-Obukhov Similarity Theory to combine different energy fluxes for calculating canopy temperature. We will use this improved module to drive the crop growth model, SIMPLACE. Additionally, we also simulated the crop growth condition under drought stress owing to the benefit of canopy temperature that can reflect the soil moisture. As previous studies have shown that faster and shorter crop development has a negative impact on global crop yield, our new model can provide a useful tool for assessing crop phenology in a warming future with more drought threats.

Validating simulation result of ecological impact from phenol spilling accident on the Korean river with AQUATOX and EFDC model

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Current ecological risk assessment (ERA) try to expand the target system from the cell to the ecosystem level. However, higher-level risk assessment is highly laborious, expensive, and time-spending. Therefore, the modelling approach is an important part of recent ERA. AQUATOX is one of the ecosystem-level risk assessment models developed by the United States Environmental Protection Agency for simulating various nature disruptions of the aquatic environment. In this study, the AQUATOX model is combined with the EFDC model which is a hydrodynamic model to simulate and validate the phenol spilling scenario in the Korean river. Model simulation is conducted based on a dataset from the Water Environment Information System (WEIS, http://water.nier.go.kr/web) operated by the Korean Ministry of Environment. The chemical accident scenario of phenol is simulated to calculate the change of biomass in the target river system by using AQUATOX-EFDC model coupling and validated by past monitored data from WEIS. Finally, the efficiency expectation of the AQUATOX-FEDC model for biomass change during a chemical accident scenario is evaluated.

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10. Combining process-based simulation models and remote sensing data – benefits and limits

Eddy covariance flux data for supporting local CO2 emissions reduction strategies: integration of direct observations, remote sensing and a machine learning approach

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Under the Paris Agreement, countries are encouraged to preserve and enhance existing carbon sinks, especially forests. In particular, Europe has set the target to reach climate neutrality by 2050. However, recent works highlighted the uncertainty related to the accurate quantification of the land carbon sink and found large discrepancies among the existing methods. Moreover, the definition of climate mitigation policies often occurs at the local level, where details on CO_2 removals from forests and other land uses are traditionally lacking.

In this study, we planned a multidisciplinary approach considering the following methods to improve the quantification of the current regional carbon sink of the Aosta Valley Region (Italy):

i) a data-driven method based on eddy covariance measurements of CO_2 fluxes, MODIS NDVI (250m), daily gridded meteorological variables at 100m spatial resolution, and a land cover map at 250m spatial resolution.

ii) the 3D-CMCC FEM process-based model

iii) Independent data derived from the National Forest Inventory (NFI)

We will discuss the preliminary results of the selected approaches and the potential discrepancies among the different methods by exploring their different advantages and flaws and the role of spatio-temporal variability. Such an assessment of the local carbon budget and its uncertainties could provide a solid base for Climate-smart management of the territory.

Geometric and demographic effects reconcile scale-dependent fragmentation-biodiversity relationships

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Anthropogenic land-use change is recognised as a major driver of biodiversity loss. Typically, land-use change results in the simultaneous loss of habitat, habitat degradation and habitat fragmentation. While previous studies have demonstrated the negative effects of habitat loss and degradation on biodiversity, the effects of habitat fragmentation on biodiversity remain controversial. Results from previous fragmentation studies are mixed, showing positive, negative or neutral effects on biodiversity. One explanation for these seemingly contradictory results is extrapolation from one spatial scale to another, or simply confounding of different spatial scales, despite fragmentation being a landscape-scale phenomenon. In this study, we reconcile these contradictions by explicitly considering fragmentation effects at different spatial scales using a mechanistic simulation model. Using a novel partitioning approach, we distinguish two types of fragmentation effects - geometric and demographic. Geometric effects arise from the spatial distribution of biota prior to fragmentation and the spatial configuration of land-use change, whereas demographic effects are changes in species birth, death and migration rates due to land-use change. To mechanistically demonstrate the interplay between the two types of effects, we developed a dynamic agent-based model. This spatially explicit model simulates fragmented and autocorrelated landscapes using fractional Brownian motion. Demographic processes emerge from the interactions between agents and their environment during dynamic simulations. By simulating different scenarios with varying degrees of fragmentation, while adjusting model parameters to control for geometric and demographic effects, we were able to: (i) demonstrate the scale-dependent relationships between fragmentation and biodiversity, and (ii) show that the effects of fragmentation on biodiversity can range from positive to negative, depending on the interplay between geometric and demographic effects. We are currently developing methodologies to transfer this knowledge from our simulation model to empirical data. We aim to apply these methods to empirical biodiversity data in combination with fragmentation data extracted from land cover maps derived from remote sensing data. Advancing our understanding of the effects of fragmentation on biodiversity in nature is crucial for meaningful conservation efforts and informed policy-making.

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11. Mathematical and data-driven models in ecohydrology

How bio-induced impermeabilization can trigger ecological succession

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Microbial mats are known to alter the hydraulic condition of streams by forming a clogging layer within the benthic zone, which reduces water infiltration. Their presence in ephemeral or intermittent streams may be critical for ecological processes as they can increase spatial and temporal extent of surface ponding. Biofilm growth being itself conditional on water availability, feedback loop mechanisms may trigger regime shifts, even with possible cascading effects on nearby vegetation. Of particular interest is the colonization of abiotic surfaces such as in recently deglaciated outwash plains where the underlying soil permeability is high and biofilms are pioneer communities. Their bio-engineering action is thus essential for ecosystem habitability and ecological succession.

A mechanical description of water exchanges is necessary to better understand such habitability transitions, quantify the bio-engineering potential of microbial biofilms and highlight favorable ecological conditions. Surface ponding dynamics depends on material properties of the mat and underlying soil, as well as on external forcing such as inflow time series and water table movements. We propose a modeling framework that couples surface water, groundwater and bio-clogging. In order to account for water table movements, a novel Green-and-Ampt like description of water infiltration and redistribution for two-layer soils bounded by a shallow water table is presented and tested against solution of the 1D Richards equations. The microbial biofilm dynamics is simply described with a growth/decay model conditioned on surface ponding. This framework is then used to simulate habitability response to complex inflow patterns and water table movements and highlight regime shift potential. The effect of the relative magnitude of biological and hydrological timescales is investigated for different periodic and stochastic intermittency inflows to mimic daily or seasonal patterns.

Because the range of biofilm permeabilities is as large as the diversity of microbial colonies, a field experiment was carried out to target the high-altitude stream conditions of recently degalciated floodplains. Non-destructive measurements of biofilm growth and permeability were taken over a few weeks within a flume monitored under alpine conditions. These results were used as a basis for the simulations.

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12. Advances in forest modelling by using new data sources and methods

Expected enhanced growth in Pyrenean forests under climate change

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In the coming decades climate change could particularly impact mountain forest ecosystems, especially those in the transition between Mediterranean and continental climates, such as those found in the Southwestern Pyrenees. To study the effect of climate change in these forests, long-term study plots in a cool Mediterranean forest (near Aspurz town, 650 masl) and cool continental climate (near Garde town, 1350 masl) were taken as data sources to calibrate the FORECAST Climate model. This model was used to simulate the effect of two levels of climate change, compared to a control scenario without climate change.

To create the RCP 4.5 and RCP 8.5 simulation scenarios we used the forecasts by the Pyrenean Climate Change Observatory (OPCC), recently made available for the mountain chain after an inter-regional effort to homogenize observations and downscaling methods. It is noteworthy that for the Pyrenean region, no significant decrease in rainfall is expected. For CO_2 concentrations, the forecasts of the IPCC´s fifth report were taken. Regarding the type of forest, in each case three different stand compositions were simulated: pure Scots pine stands, pure European beech stands and a 50%:50% mixture of both species (compared to maximum stocking levels of each species).

Our results indicate that, except pine stands in the Mediterranean site, all stand types are expected to have a higher stem biomass production with greater climate change. The main reason is that increased temperatures without increased drought would lengthen the growth period. In particular, in the continental site, the increased temperatures would eliminate cold as a limiting factor for growth, particularly in autumn. In addition, the increase in CO_2 concentrations would have a fertilizing effect, allowing trees to optimize water use by reducing the stomatal opening. In the case of the continental stands, mixed forests could be more productive than the pure ones, something that would not happen at the Mediterranean site. On the other hand, in all cases climate change would cause a reduction in organic matter accumulation in the soil, as the increase in decomposition rates associated with increased temperatures exceeds the increased litterfall inputs due to increased tree growth. This increased organic matter decomposition would also have a fertilizing effect on trees, further increasing stand growth.

As a conclusion, an increase in temperatures and CO_2 concentration without an increase in drought (as predicted for the Pyrenees) could increase the productivity of some forests, especially in cold (usually higher) sites.

Forest Fragmentation in the Tuchola Forest: A Case Study on the Impact of Windstorms

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The Tuchola Forest is a prominent pine forest complex in Northern Poland that has been affected by two severe windstorms in recent years: the August 2017 derecho and the July 2021 tornado. This study employed Forest Area Density (FAD) to evaluate forest fragmentation in the Tuchola Forest post these windstorms. FAD values were determined using the GUIDOS toolbox on designated square neighborhood areas. The data was subsequently categorized into six fragmentation classes ranging from Intact to Rare.

The derecho caused an estimated 80,000 hectares of forest destruction, while the tornado caused an estimated 1,000 hectares of forest destruction. Following the 2017 derecho, there was a significant rise in the Rare, Patchy, Transitional, and Dominant fragmentation classes. Conversely, the Interior class diminished, while the Intact class saw a relative increase. In 2021, post-tornado, the Rare, Patchy, and Transitional classes saw marginal increases, the Dominant class decreased, the Interior class rebounded, and intact landscapes notably augmented. These events precipitated varied shifts in fragmentation dynamics.

Our study found that the two windstorms caused significant changes in forest fragmentation in the Tuchola Forest, with the Rare, Patchy, Transitional, and Dominant classes increasing in size and the Interior class decreasing in size. Promoting connectivity between forest patches are essential to mitigate the heightened vulnerability to windstorm disturbances. Conservation efforts should prioritize the protection and restoration of these fragmented areas.

Modelling demographic processes to understand spatial patterns of alpine treelines and reproduce treeline forms: the STEM

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Alpine treeline ecotones are advancing in response to global warming, but the pace of advancement diverges between different forms of treelines. For example, treelines with an abrupt, step-like transition in tree height from forest to tundra have shown slower expansion than treelines with a slow, gradual transition. As these forms are likely governed by the most limiting processes acting on the tree population (i.e. growth, survival, and biomass loss), and by neighbourhood interactions, the relationships between these processes and the spatial patterns found at treelines, especially transitions in tree height, shape, density or grouping, can provide a key to understand and potentially predict treeline dynamics. To test these relationships, we have developed the Spatial Treeline Ecotone Model (STEM), a spatially explicit agent-based model, in which, in version 1.0, gradients in demographic processes can be imposed directly on the tree population. With the model, we were able to reproduce several different forms of treelines, while others remain elusive. Treelines with smooth, gradual transitions from upright trees to deformed krummholz are difficult to reproduce by the model, highlighting the necessity to better understand how processes interact at these treelines. Similarly, island-type treelines seem to require spatial or temporal variation in demographic rates. In the future development of the model, we will implement more environment-driven demographic rates, hopefully broadening the range of reproducible treeline forms. STEM may also serve other researchers as a tool to test hypotheses on pattern formation at alpine treelines world-wide.

Systematic distributions of interaction strengths across tree-tree networks yield positive diversity-productivity relationships

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Globally, forest biodiversity is being undermined by a wide variety of anthropogenic activities, crippling a wealth of ecosystem functions provided by forests. It is therefore imperative to understand the mechanisms underlying diversity-productivity relationships (DPRs). Tree-tree interactions in diverse communities are fundamental in driving growth rate (a proxy of productivity), potentially shaping the emergent DPRs, yet this relationship remains poorly explored. Here, we used growth data from a large-scale forest biodiversity experiment in subtropical China over 7 years to demonstrate that changes in individual tree productivity were driven by species-specific pairwise interactions, with higher positive net pairwise interaction effects of trees in more diverse neighborhoods. The aggregated pairwise interactions subsequently determined the community DPRs. We employed a novel modelling approach under Bayesian framework and obtained two fully resolved eight-species interaction networks from two independent datasets (no overlapping in tree species). Both interaction networks showed on average inter-specific interactions were positive whilst intra-specific interactions being negative, resulting in positive difference between inter- and intra-specific interactions. We then performed a simulation study in which we shuffled the interaction network following two scenarios: (1) completely random shuffling, (2) constrain the shuffling within inter- and intra-specific interactions. Based on the reshuffled interaction strength, we computed the resultant productivity on both individual and community level. The results from the simulation revealed that the positive differences between inter- and intra-specific interactions were the critical determinant for the emergence of positive DPRs. Surprisingly, the condition for positive DPRs corresponded to the condition for coexistence. Our results thus provide a novel insight into how pairwise tree interactions regulate DPRs, which has implications for identifying the tree mixtures with maximised productivity to guide forest restoration and reforestation efforts.

Exploring the influence of climate and interspecific competition on changes in forest composition in the temperate rainforests of the Valdivian Ecoregion in Chile

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The forest composition is determined by the interaction between abiotic and biotic factors, including climate and interspecific competition for light. These factors directly influence the range of tree species by affecting their demographic processes such as establishment, growth, and mortality rates. There are few studies that assessed simultaneously abiotic and biotic factors role on constrain species ranges for southern South America temperate rainforests tree species. A better understanding of these interactions and their effects on forest composition could help us reduce uncertainties related to the processes that explain past and current forests composition. We assessed the next research questions: i) is the forest composition determined by the interspecific competition for light at low and mid-low elevations? ii) does the biotic control on forest composition change as the altitude increments?; iii) is there a abiotic control dominance on forest composition at high elevations? In this study, we used a dynamic vegetation model (DVM) to analyze the main abiotic and biotic factors that influence the species ranges of 27 tree species in the temperate rainforests of the Valdivian Ecoregion. We predicted the structure and species composition of 27 forests distributed along a longitudinal transect that spans an altitude gradient in south-central Chile (latitude 40.1°S – 41.2°S). Model predictions for species range had a moderate to substantial degree of accuracy for 15 species, and we achieved at least 50% agreement for species composition predictions at stand level in all study sites. Our results suggest that interspecific competition is a major factor constraining species ranges in sites with favorable climatic conditions for establishment and growth, located between the Pacific Ocean and lower altitudes of the western slope of the Andean range. In contrast, abiotic factors, especially minimum temperatures, limit species ranges at high altitudes of the western and eastern slopes of the Andean range. Overall, this research provides valuable insights into the complex interactions between climate and interspecific competition that drive forest composition in the temperate rainforest of the Valdivian Ecoregion. The findings highlight the need for further research on the development and application of DVMs at the regional scale in southern South American temperate rainforests, particularly in the current context of global changes.

Environmental factors affecting the natural regeneration process in a beech forest in the Italian peninsula

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Human population activity is causing changes in both climate and forest lands with negative impacts on these ecosystems, increasing disturbances and reducing the ecosystem services they provide. Indeed, forests contribute to mitigating climate change through carbon uptake and storing it in their biomass. Therefore, to preserve these mechanisms under future climate scenarios, the understanding of the eco-physiological processes, and the dynamics of growth, competition, and mortality as well as regeneration processes as shaped by environmental factors is crucial. Process-Based forest models are an appropriate tool to simulate forest dynamics, under different silvicultural practices and under future scenarios and investigate forest response to the climate change impacts. The 3D-CMCC-FEM is a prognostic stand scale model, designed to simulate carbon, energy, water fluxes, and carbon stocks in temperate and boreal forests, including dynamics such as growth, mortality, and light competition and allowing different management scenarios. The first short-term simulation (10 years) was performed at the Cansiglio beech-dominated forest site in the Italian peninsula, in which the selected monitoring nine plots with three treatments: no-management, shelterwood, and innovative silviculture system, with the last showing the highest net and gross primary productivity, carbon use efficiency and water use efficiency than the others. Furthermore, we present the conceptual model of the new regeneration module and its implementation to determine how environmental drivers such as temperature, light, and water availability can affect the germination process, the establishment rate, and the saplings recruitment. Preliminary results show the good ability of the model to predict the number of seeds per hectare according to observed data and statistical two-sample Kolmogorov-Smirnov test (D value = 0.22, p-value = 0.27) and linear regression (r2 = 0.81) performed. Subsequently will be carried out simulations on a long-time scale (at least 100 years) forcing the model with climate scenarios data both considering the effect or not of CO2 fertilization to investigate the factors that most influence resource allocation for seed production but also increasing mean temperature and water resource that affect growth and mortality of seedling and sapling.

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15. Modelling variation and evolution of traits within individuals, populations and communities

Root-grafted tree networks from an eco-evolutionary perspective – a model-based analysis of the theoretical ecological benefit of cooperative trees

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It is known that some tree species, depending on their location, can form root graft networks. Those can be functional and non-functional. While the latter can increase a tree's mechanical stability, the former represents resource exchange between the trees through hydraulic redistribution. This may be associated with advantages for individual trees involved, the whole network of trees or the dynamics of the entire population, especially in terms of buffering fluctuations in environmental conditions. However, while there are already some empirical observations and simulations of the processes in single trees, our understanding of the benefits of cooperative root graft networks from an eco-evolutionary perspective is still limited. Here, we present a simple individual-based forest stand simulator accounting for differences between grafted and non-grafted trees in mortality and growth. We distinguish between varying affinities to graft and possible share of resources within the network, virtually as genotype traits that are subject to evolutionary selection. In the simulated forest stands, we observed the emerging dynamic size and proportion of root graft networks. As an indicator for the ecologically most rationale combination of those aspects, the fitness of the different populations was assessed by comparing indicators such as basal area and growth increment over multiple generations. To get a more comprehensive picture of how environmental conditions can take an effect, we supplemented the simulation experiments on affinity to graft and effective share of resources with different scenarios for resource availability (low, medium, strong) and varying degrees of seasonal fluctuation (none, medium, strong). With this theoretical, simulation-based work, we want to contribute to a better understanding of the eco-evolutionary processes responsible for the occurrence of root-grafted tree networks and why it can be beneficial that some trees of the same population form root graft networks while others do not.

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16. Modelling climate-biosphere feedbacks

Comparison of estimated reduction in GHG emissions after re-wetting of peatlands depending on the method of estimating emissions and the diversity of vegetation before and after re-wetting

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Re-wetting of drained peatlands leads to an overall reduction in GHG emissions. The general emission factors for drained and rewetted organic soils categorized according to climate zone, land use category and drainage conditions are provided in the IPCC 2013 Supplement to the 2006 IPCC Guidelines for National Greenhouse Gas Inventories: Wetlands. The more detailed approximation of GHG emissions based on vegetation species composition and water level is proposed as GHG Emission Site Types (GESTs) (Couwenberg et al. 2011). I compared the GHG emission reduction results obtained using three modifications of the GEST method (Reichelt 2015, Liu et al. 2020, Jarašius et al. 2022) and the IPCC indices, taking into account the vegetation diversity in a temperate zone fen before and after re-wetting. In the analysis for a non-forested fen, I simulated different percentages of vegetation types on the drained peatland in combination with different percentages of plant communities after re-wetting. I included such vegetation types on the drained peatland: Calthion, Molinion and deeply drained meadow; and such reed and tall sedges communities after re-wetting: Glyceria maxima, Phragmites australis/Typha latifolia, Carex gracilis, C. acutiformis, Phalaris arundinacea. I calculated the reduction in GHG emissions for 2016 theoretical combinations of the above listed vegetation types. The most similar results to the IPCC indices produce GESTs from Reichlet (2015). The most comparable values for the two methods were obtained when Calthion changed to dense Phragmites reeds after re-wetting and when deeply drained meadow changed to Phalaris, C. gracilis or C. acutiformis communities after re-wetting. For other combinations, the differences were greater (from -4 to 6 t CO_2-eq./ha/y), which may suggest a need to refine calculations based on IPCC indicators. Nevertheless, the results based on the generalised IPCC indices are in fact quite close to the results based on Reichelt (2015) GESTs for individual plant communities. Taking this into account, an analysis of potential emission reductions for selected peatlands in NE Poland was carried out for non-forest patches based on IPCC indicators. This research was funded through the 2019-2020 BiodivERsA COFUND call for research proposals on “Biodiversity and Climate Change”, with the national funders: National Science Centre - Poland, FWF Austrian Science Fund, Belgian Science Policy Office, Academy of Finland, Project Management Agency at the German Aerospace Center, The Research Council of Norway (project PRINCESS).

Integrated crop and soil organic matter model for arable cropping systems

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Soil organic matter (SOM) dynamics play a fundamental role in many environmental processes, such as atmospheric greenhouse gas (GHG) emissions from soils and carbon (C) sequestration. In agricultural systems, there is an uncertainty around the effect of climate extremes on SOM transformations, plant growth and nitrate leaching in the current climate and even more so under future climate scenarios. Process-based simulation modelling can help to understand these complex processes and their interactions with crops and climate conditions. Additionally, when based on adequate system understanding, models can be applied to support ecosystem services, such as improved N management in cropping systems and soil organic C sequestration.

Against this background, the overall objective of this project is to develop a process-based, coupled soil C and nitrogen (N) model based on state-of-the-art knowledge and link it with crop growth modules in the SIMPLACE modelling framework. The developed soil model is novel in that it represents organic matter in measurable pools (particulate organic matter versus mineral-associated organic matter), unlike most conventional soil models in agroecosystem models, which use conceptual pools. This enables calibrating the model using measured data on the respective pool sizes, making it more accurate than calibration against total C or N. The soil model also includes the simulation of Δ14C to constrain better the turnover time of slowly cycling soil organic C pools to reduce equifinality during model calibration. The coupled soil-crop model, in multiple soil layers and on a daily basis, simulates C and N fluxes between the atmosphere, crops, and five soil organic C and N pools. It will be calibrated with plant biomass, soil, and weather data collected in the patchCROP experimental site, Tempelberg, Brandenburg, Germany. The patchCROP field experiment is characterized by high spatial heterogeneities of soil properties and is, therefore, suitable for this study, which aims to account for soil heterogeneities in SOM modelling.

The coupled soil-crop model will be an open-source code in the SIMPLACE framework that the scientific community can use for different purposes, for example, to improve the simulation of crop yield, nitrate leaching, and nitrous oxides emissions for different soil characteristics under uncertain weather drivers (temperature, precipitation, etc).

Introducing Animals to a DGVM - How to Implement Herbivory in Vegetation Modelling

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Animals are a key driver for ecosystem functioning (Schmitz et al. 2018, Science, doi:10.1126/science.aar3213) and quantifying their impacts on carbon and nutrient turnover gains more and more interest. So far, the global biogeochemical cycling modelling community does not capture well impacts on vegetation and soil processes arising from the presence of trophic chains in ecosystems. At the same time, ecological models that assess species distributions or interactions between trophic levels do not explore impacts on ecosystem biogeochemical cycles and are often limited in their species representation and their spatial or temporal dimension. We seek to overcome these shortcomings by coupling the animal model Madingley and the dynamic global vegetation model LPJ-GUESS (Krause et al. 2022, Ecol. Modelling, doi:10.1016/j.ecolmodel.2022.110061). We are simultaneously expanding the current Madingley version (Harfoot et al. 2014, PLOS Biol. doi: 10.1371/journal.pbio.1001841; Hoeks et al. 2020, Ecography, doi:10.1111/ecog.05191) with animal C:N stoichiometry, which adds a whole new nutrient cycle to Madingley.

We here present results from the full coupling between the models and analyse how ecosystem composition and leaf biomass impact herbivory, how this resonates to the abundance of omnivores and carnivores, and how these interactions in turn feedback to canopy photosynthesis, productivity and ecosystem carbon cycling. We explore how these feedbacks respond to range of climate change scenarios, assess their role in future ecosystem carbon cycling, explore how presence and abundance of full trophic chains impact ecosystem functioning.

Land-cover and management modulation of ecosystem resistance to drought stress in terrestrial biosphere models

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Drought events are projected to become more severe and frequent across many regions but their impacts depend on ecosystems' ability to maintain functioning during droughts, i.e., resistance. Since plant species have diverse strategies to cope with drought, differences in ecosystem resistance should modulate the magnitude of drought impacts. Human activities such as land use and management, by changing ecosystem composition and structure should, therefore, influence the patterns of drought resistance.

In a previous study (Xiao et al., in review, ESD), we performed a global synthesis of vegetation resistance to drought and heat stress based on remote sensing, and found that forest-crop transition, forest management and crop irrigation play important roles in ecosystem resistance to drought stress under climate change. However, it is not possible to fully disentangle the effect of land use and land cover changes from climate background and CO_2 fertilization effect in observational time series.

Here, we used vegetation carbon simulated by different dynamic global vegetation models (DGVMs) in the TRENDY project to calculate vegetation resistance to drought and heat. We applied a linear autoregressive model using drought, temperature and memory effects as predictors of biomass carbon to characterize ecosystem resistance. Resistance was expressed as the sensitivity of vegetation carbon to drought duration and temperature anomalies. We analyzed how ecosystem resistance varies with land cover across the globe. We then evaluated the model performance in estimating ecosystem resistance to drought and heat by comparing the ecosystem resistance calculated from L-VOD. We contrasted their ecosystem resistance between two simulations: one with changing CO_2 and climate forcing and fixed pre-industrial land-use and management, and another with changing CO_2, climate and land-use/management. Therefore, it can be concluded that the difference is caused by land use and land cover changes instead of climate or CO_2. We find important effects of land-use on drought resistance in Amazon, central Africa and Australia regions, possibly associated with interactive effects with water use efficiency, soil moisture or management. Different vegetation types have divergent water use strategies. The simulated soil moisture can be modulated by different land use types due to changes in evapotranspiration. However, we also observe large differences across models, which could be related to different vegetation dynamics and soil moisture drought simulated.

Xiao, C., Zaehle, S., Yang, H., Wigneron, J.-P., and Bastos, A.: Land-cover and management modulation of ecosystem resistance to drought stress, EGUsphere [preprint], https://doi.org/10.5194/egusphere-2023-304, 2023.

19. Details matter! – importance of small-scale processes to model high-latitude ecosystem responses

Numerical modelling and reconstruction of high-latitude boreal forest dynamics based on current and paleoclimate data

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Boreal forests are exposed to greater temperature rises than the global average, which causes unprecedented changes in their environment. Investigating ongoing changes in the boreal ecosystems could give a better understanding of how their role within the carbon cycle would shift (storage vs source), and how this feeds back to global climate change.

In this study, we used the Larix vegetation simulator (LAVESI) to model the small-scale processes of permafrost-vegetation interactions. LAVESI is a spatially explicit, individual-based model that was created to simulate larch stand structure and dynamics in Siberian forests (Kruse et al., 2016). LAVESI simulates the life cycle of individual trees from seed dispersal to ageing and death. The model works on multiple boreal tree species and is capable of simulating the effect of occasional fires on the forest.

The model was designed to local applications working on individual plots from a single region, but its use in a more general scope is limited. In our work, we prepare a generalized framework for LAVESI, to be able to run the model on multiple sites in Siberia and western Canada. This allows us to examine how the model is applicable in a wider range of areas.

Two climate datasets have been prepared to feed the model, enabling us to compare the responds of different climate time series. Since the climate data goes back 25.000 years, we can run the simulation over a long timescale.

The model is parametrized using parameters collected from multiple forested and non-forested sites in the boreal regions of Russia and Canada. These parameters are then further calibrated via a sensitivity analysis over the working model. Model simulations are validated against available paleoclimatic time series, extracted from pollen data from lake sediments of the investigated regions.

The model results can be used to examine the migration of selected species, and to compare the dynamics of boreal forests in two very distinct areas with different climate history.

References:

Kruse, S. et al.: Treeline dynamics in Siberia under changing climates as inferred from an individual-based model for Larix, Ecol. Model., 338, 101–121, https://doi.org/10.1016/j.ecolmodel.2016.08.003, 2016.

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20. Environmental modelling for policy support – how to build bridges between two worlds

Participatory modelling in the context of African swine fever control in wild boar in Germany

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African swine fever (ASF) is a viral disease that has increasingly become a challenge for the pig industry as well as for wildlife conservationists not only in Germany, where recent outbreaks have been reported. Wild boars are highly susceptible to the disease, serve as reservoirs and thus pose a risk for disease transmission to domestic pigs. Intensive control measures such as carcass search, fencing of affected areas and intensified hunting were implemented to control ASF in wild boar. However, the efforts have not been sufficient to eliminate the disease. In addition, sporadic outbreaks of ASF in domestic pigs and the resulting restrictions challenge pig holdings in close proximity, as e.g. trade restrictions or the obligation to keep pigs indoors affect animal welfare and lead to economic losses. Thus, there is a need for a transformative approach to understand the complexities of ASF control in wild boar and the stakeholders involved.

Systems thinking (ST) is a methodology that provides a holistic view of complex systems and the linkages between the systems' components by developing jointly with affected stakeholder so-called Causal Loop Diagrams (CLDs) and Stock and Flow Diagrams (SFDs). It considers interrelationships among various factors involved in the control of ASF and the diverse actors affected – including veterinary authorities, pig holders, hunters, local forces, etc. – to identify adaptive and sustainable solutions for challenges related to ASF control.

Participatory modelling workshop series were initiated in an ASF-affected and an ASF-unaffected area of Germany. The participating stakeholders developed CLDs and SFDs to visualize and quantify relationships, to illustrate unintended effects of current control measures and to identify potential solutions for the challenges faced by the participating stakeholders.

The workshops highlighted that improving communication channels and collaboration between all affected stakeholders is crucial for an effective response to ASF outbreaks. In addition, the need to increase public awareness on ASF was identified as a relevant factor, as it could lead to better compliance with control measures. Finally, the need of further research to support decision making was highlighted in the workshops.

In conclusion, ASF requires a ST approach to better understand the interconnectivity and diversity of actors involved. By working together with relevant stakeholders, it is possible to develop new, adaptive, sustainable and efficient solutions to control the spread of ASF, and to reduce the impact on animal welfare and economic consequences for the pig producers, in Germany and other countries.

Opportunities and limitations of modelling approaches to evaluate the efficacy of policy instruments within the policy advise process

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The challenges to address the social, environmental and economic challenges triggered by the global climate crisis are tremendous. Policy decisions and processes to solve these problems by developing policy instruments are highly complex. One opportunity to evaluate the efficacy of policy instruments is in modelling the underlying complex and social system by qualitative (e.g. Causal Maps) or quantitative modelling techniques (e.g. System Dynamics, Agent-based Modelling) and testing the impact that such policies might have. However, to implement such modelling approaches in policy advice is challenging and a complex process itself. In this presentation we suggest pathways how qualitative and quantitative modelling approaches can be implemented in the process of the development of policy instruments. Besides the opportunities we also highlight the huge challenges which are connected with the implementation of such modelling approaches in the political practice.

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21. Ecological risk assessment and management – benefits and challenges of ecological modelling

An Integrated Modelling Approach to Optimize Farm Management Resource Allocation Accounting for Weather Variability in Northern Ghana

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Smallholder farmers in Northern Ghana face challenges due to weather variability and market volatility among others, which hinder their ability to invest in sustainable intensification options to increase farm production. Modelling can help understand the relationships between farm productivity, the environment (e.g. soil fertility), and economic aspects, but few models have explored the effects of weather variability on crop management and resource allocation. This study introduces an integrated modelling approach to optimize resource allocation for smallholder mixed crop and livestock farming systems in Northern Ghana. The model combines a process-based crop model, a farm simulation model, and an annual optimization model. To better investigate the effects of weather, the crop model simulations are driven by a large ensemble of weather time series for two scenarios: good and bad weather. The results suggest that farmers could increase their incomes by allocating more land to cash crops like rice, groundnut, and soybeans. The optimized cropping patterns also have a higher probability of increasing farm assets, particularly under bad weather scenarios, compared to the current cropping systems.

Incorporating fossil data into climate change vulnerability assessments

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Climate change represents one of the most concerning anthropogenic threats to biodiversity and ecosystems. Often, the incompleteness of occurrence data used to forecast climate change impact on biodiversity may hamper the reliability of these predictions. In our research, we aim at evaluating whether the inclusion of paleontological records into Species Distribution Models (SDMs) significantly increases the width of sampled climate niche by providing information on species-climate relationships from the past. We collected current and fossil occurrence data for 38 mammal species, along with a set of climate variables covering the last 800 kya and rasterized at ~50 km spatial resolution. In addition, we retrieved 2100 climate variables according to two climate change scenarios (RCP4.5 and RCP8.5). Starting from these data, we calibrated SDMs relying on living occurrences alone ("Only-living" SDMs) and pooling living and fossil occurrences ("Full" SDMs). Models were projected over current time and 2100 under RCP4.5 and RCP8.5 scenarios. Both Only-living and Full SDMs achieved good predictive performances (Only living SDMs mean AUC=0.817; Full SDMs mean AUC=0.820). In addition, we showed that the increase in climate niche width granted by the inclusion of fossil data is significantly correlated with a reduction in range net change predicted by "Full" SDMs with respect of "Only-living" ones ($r=0.10$, $p < 0.01$). Our results provide evidence that including fossil data into SDMs allows a more comprehensive sampling of the climatic niche and leads to overall milder climate change effects predicted on biodiversity.

Individual-based demographic modelling reveals the impacts of electrocution and its mitigation on Bonelli's eagles

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Anthropogenic mortality can have a significant impact on population dynamics and broader ecological processes, particularly for long-lived top predators. Such populations are highly vulnerable due to their low intrinsic population growth rates, small population sizes, and large home ranges. As a result, conservation strategies for the most vulnerable species are critical for effectively reducing or eliminating anthropogenic mortality. Electrocution at power lines is one example of anthropogenic mortality, which can have severe consequences for bird populations, particularly raptors.

In this study, we focus on the Bonelli's eagle, a long-lived and territorial raptor, to investigate the population-level impacts of mortality by electrocution (ME) using an individual-based modelling framework implemented for the southern Portugal region along 50 years. By simulating individual behaviours, including territoriality and aged-structured and spatial-implicit processes, we aim to gain new insights into how distinct levels of ME affects population viability. For this, we combined different percentages of territories affected by ME, with different ME probabilities within territories and across age classes. Specifically, we seek to identify critical thresholds for ME, understand how the population responds when ME targets territorial or non-territorial individuals, and identify critical demographic parameters in the population.

Sensitivity analysis showed that adult survival is the most critical parameter for the population growth rate. Nevertheless, the survival rates of other age classes also played a significant role in determining the population trend, particularly when compared to demographic parameters like the adult fertility. These findings reinforce the idea that the non-breeding segment of the population is highly important for its long-term dynamics and persistence. Our results also suggest that the population can tolerate a certain level of ME, though this varied according to whether effects target territorial or non-territorial individuals. Specifically, when ME impacts only territorial birds, the population can tolerate high ME levels, provided that only a small proportion of territories are affected. In such cases, intermediate and high levels of ME within specific territories produce comparable results in terms of population growth rate. However, if non-territorial birds are subject to intermediate or high levels of ME, then a substantial decline in the population may occur when compared with similar ME values in territorial birds.

Our findings emphasize the importance of considering all population components, including juveniles, floaters, and breeding birds, as well as breeding and pre-adult settlement areas, when assessing and mitigating ME effects, and possibly other anthropogenic sources of mortality.

Merging an agent-based modelling approach of nutritional ecology and a population dynamics model at landscape level for the management of the Senegalese grasshopper

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Locusts are among the most destructive agricultural pests in the world. Oedaleus senegalensis, the Senegalese grasshopper, may cause serious crop damage and food security problems throughout the Sahel region. Contrary to the protein-limitation paradigm which stipulates that low N concentration in plants impairs herbivores fitness, recent studies have shown that the Senegalese grasshopper can maximize its performance by selecting foods with high carbohydrate content relative to protein. Previous studies conducted in experimental plot fields showed that soil amendments, which decrease carbohydrate/protein content within plants had a negative impact on the pest fitness. However, the extent to which soil amendment linked with the nutritional ecology of individuals may shape population dynamics remains unknown. This study aims at testing if we can extrapolate those results supporting a Carb-limitation hypothesis, at a landscape scale and population level of the Senegalese grasshopper. We developed an agent-based model coupling processes extracted from a population dynamics model from the 1990s with an agent-based modelling approach of nutritional ecology representing the individuals' choices of food according to their carbohydrates to protein ratio. The resulting ABM describes the life cycle and the dynamics of Oedaleus senegalensis in a virtual landscape representing habitats and environmental conditions in Senegal. Simulations with the model examined the effect of soil amendments on the population dynamics while considering other sources of seasonal and latitudinal variability, such as predation, climate, vegetation availability and composition. We believe that such model combining population ecology with agricultural land use practices can further provide evidence-based management strategies to support farmers in their decision-making to keep the pest below a density threshold and minimize damage.

A regulatory view on the use of effect models for the environmental risk assessment of plant protection products

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UBA, German Environment Agency

Mechanistic effect models (MEMs) can complement current environmental risk assessment (ERA) methods and approaches rather than replacing them. MEMs can be seen as tools to virtually extend limited real-world experiments by testing our mechanistic understanding of observed effects and by exploring effects beyond the conditions tested. The use of MEMs in the ERA process of plant protection products should contribute to increasing realism without impairing a required level of conservativeness. Fit for purpose MEMs (i.e. appropriately parameterized and validated) could be used to explore and get better risk descriptions, e.g. when considering exposure to multiple chemicals, biotic and abiotic stressors, and their interactions under realistic field conditions. At the individual level, TKTD models may particularly support the assessment of effects at additional observation times and different exposure profiles. Population and community / ecosystem models can particularly support the (meta-) analysis of (semi-) field studies under consideration of varying test conditions, and the ranking of alternative risk mitigation measures by their effectiveness. However, here we present a regulatory view where we generally discourage the use of MEMs in ERA to extrapolate from laboratory tests to the field or from one species to another due to high levels of uncertainty that are difficult to quantify. There are important issues related to MEMs that must be addressed before being used as a tool in ERA, e.g. representativeness, conservativeness, uncertainty and variability, realism, and validation. There are also some challenges related to the development of new ERA methodologies, as set in the legislative framework, e.g. for risk assessors to evaluate MEMs within a tight timeframe and to do so in a harmonized way across MS whereas guidance and expertise are still lacking.

Multi-scale analyses of past climate change impacts on desert locust population dynamics

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The desert locust, Schistocerca gregaria, is a species of grasshopper that display phase polyphenism: an extreme form of density dependent phenotypic plasticity. At high density, gregarious desert locusts create swarms that can cause significant damage to crops and pastures, threatening the food security of human populations from western Africa to India. Dependent on favourable weather conditions to multiply, climate change may have significant impacts on the desert locust, particularly in terms of spatial distribution of phase change from solitarious to gregarious and outbreak events. To determine the effects of climate change on the dynamics of desert locust phase change, we studied the dynamics of the number of signs of gregarization observed between 1985 and 2018 at three different spatial scales.

Our first approach was to look at a global scale across West Africa. We observed an overall decrease in gregarization events. However, this scale, which includes very heterogeneous environments, did not allow us to determine whether this decrease was due to climate change, to preventive management applying high pressure, or to a combination of both. Therefore, we developed a multi-scale approach adding two supplementary scales. The area of interest was divided into a grid of 0.5° cells for a more detailed study of the phenomena. For each cell, a climate analysis was performed for rainfall and temperature, with trends obtained by a harmonic decomposition model on monthly CHELSA data. Analyses of gregarization occurrences showed only a few significant trends of decrease in gregarization events over time in central Algeria and western Mauritania. Among these few significant trends, an even smaller portion corresponded to a climatic environment with an increase in the rainfall trend. To increase the statistical power, these cells were grouped into clusters based on the means and trends of the climate variables. At that scale, there were also trends of decreasing observation of gregarization events, of which only one was significant. For the concerned cluster, we observed that there was no increase in the rainfall trend. Although surprising at first glance these results highlight the important effect of the preventive management, which may counteract the positive effect of climate change on locust proliferation.

Consistent wildlife modelling across Tiers of the European environmental risk assessment

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According to new EFSA wildlife guidance for environmental risk assessments (ERA) of pesticides, the toxicological effects of a substance on the wild rabbit (Oryctolagus cuniculus) must be considered as standard scenario. Following the guidance, toxicodynamic-toxicokinetic (TKTD) models have been proposed as a refinement at Tier 2 of the effect assessment and as highest tier, population modelling is considered a possible refinement option.

A population model should be consistent with the modelling of TKTD-processes at Tier 2. Consistency can be achieved by incorporating the effects on individual reproduction predicted by the TKTD model into the population model to assess potential population level effects or recovery.

The wild rabbit has a great reproductive potential, and several litters per female and year are common. On the other hand, mortality within the first year can be as high as 90%. Therefore, modelling the effects on growth and reproduction using a DEB-TKTD for many individuals could provide information on whether high reproduction could buffer toxicological effects or exacerbate the effects, e.g. by carryover toxicity.

Our DEB-TKTD-IBM for the wild rabbit can be used as a first step of the higher tier effect assessment of ERAs. It is integrated in a modular software environment, which allows modelling the individual’s life cycle. The model follows assumptions and outcomes of lower Tier risk assessment, such as foraging patterns. This ensures consistence among Tiers.

Commonly, population models for application at higher tier consider different environmental and behavioural complexities and their interactions, such as resulting from animal movement and dispersal. Constructing such models requires substantial effort. Model development usually takes years. Further, the complexity often impedes consistency with lower Tier assessments. In contrast, our spatially implicit modelling approach is readily available and based on the underlying risk assessment Tiers. If necessary, its modular approach even allows step-wise additions of additional processes.

Global Sensitivity Analysis of the harmonised Lemna model

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Ecological and effect modelling is becoming more and more important for environmental risk assessment in the framework of pesticide authorization. For instance, the EFSA Scientific Opinion on TKTD modelling (EFSA, 2018) has judged the GUTS model (Jager et al., 2011) for lethal effects and the model for the standard aquatic macrophyte test organism Lemna (Schmitt et al. 2013) as “ready for use”. Nevertheless, national regulatory authorities are still hesitant to accept ecological and effect modelling studies because they do not have sufficient experience with these models.

One way to increase confidence in a model is to perform a Global Sensitivity Analysis (GSA). This is the analysis of how much each of the input factors contributes to the variance of the model output(s). In the case of ecological and effect models, a GSA notably allows to identify and rank the importance of i) toxicokinetic and toxicodynamic parameters, ii) physiological parameters of the organism, iii) environmental driving data (radiation, temperature, nutrient concentrations).

A two-step global sensitivity analysis (GSA) of the refined and harmonized Lemna model (Klein et al., 2022), which is publicly available as an R package (https://cran.r-project.org/web/packages/lemna/), was performed. In a first step a Morris sensitivity screening was conducted. This semi-quantitative global method is very parsimonious and allows to filter out non-influential input factors. In a second step, a true variance-based GSA was carried out with the Sobol' method and a reduced set of input factors.

The GSA was conducted for four different concentration levels and three different exposure regimes: i) constant exposure, ii) two exposure pulses with varying intervals between peaks, and iii) realistic exposure time series as generated with the FOCUS surface water models. Moreover, two different sets of input distributions of TKTD parameters were examined: i) distributions reflecting the parameter range for a specific substance (example: metsulfuron-methyl based on the calibration by Schmitt et al. (2013)); ii) distributions reflecting the whole realistic parameter range (different substances).

The presentation will give a synthesis of the results of the GSA.

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22. Functional responses: from theory to practice

Anthropogenic stressors alter food webs of freshwater fish communities

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Multiple stressors arising from human activities are posing a threat to the biodiversity, functioning, and services of freshwater ecosystems. However, our current understanding of how human intervention impacts freshwater communities across multiple trophic levels is limited. This knowledge gap is particularly problematic when predicting the effects of human impact on the range of emergent ecosystem properties since anthropogenic effects on one trophic level can cascade through the food web.

Our study aimed to investigate the drivers of food web structure and functioning in freshwater fish communities. To accomplish this, we conducted a comprehensive sampling of fish communities in 51 sites of small freshwater ecosystems, including ponds, lakes, and channels. We surveyed these sites along gradients of various human activities, including agricultural practices, highway impact, gravel exploitation, and communal waste disposal, which encompassed both solid waste and wastewaters.

At each study site, we collected data on fish species richness and abundance, as well as the body sizes and stomach contents of each individual fish. Using this data, we constructed food webs and analyzed the effects of intensifying human impact and water properties on the trophic organization of these fish communities.

Our results showed that intensifying human impact caused a shift in the body size distribution of fish species across trophic levels, altered the food web structure of fish communities and their diet specialization. These effects were both direct and indirect manifested through the changes in water properties and via the trophic cascades. Furthermore, we observed that these effects were dependent on the ecosystem type (pond vs. lake vs. channel) and the type of anthropogenic impact.

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23. Like a boomerang: How feedback loops affect ecosystem stability and species coexistence

Top-down and bottom-up coupling effects of subsidies on recipient ecosystems

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A subsidy can directly enter a recipient ecosystem by either being consumed or being recycled to the nutrient pool with both pathways causing multiple indirect and potentially conflicting effects. Subsidy pathways are prone to anthropogenic stressors, which can impact the relative strength of the recycling and direct consumption fluxes. Current studies have mainly focused on a single coupling pathway, limiting our knowledge of subsidy effects on recipient ecosystems. We derive a series of models to predict the relative and interactive effects between consumption and recycling subsidy coupling pathways on the biomass and functions of a recipient ecosystem. We solved the models for analytical equilibria, and compared model predictions with and without each subsidy pathway. Our results show that the direct consumption and recycling coupling pathways of subsidies interact antagonistically, as the feedbacks between both pathways led to lower stocks and functions of the recipient ecosystem than a model which omits these feedbacks. These subsidy effects are consistent for each trophic level of the recipient ecosystem. Our models also predicted that consumption and recycling pathways of subsidies had differential effects on the recipient ecosystem. Recycling coupling pathway always led to equal or higher stocks and functions across recipient ecosystem trophic levels, whereas consumption couplings had alternating positive and negative effects depending on trophic level and characteristic of a trophic cascade. We suggest that future empirical and theoretical research on subsidies should consider various coupling pathways to provide a more mechanistic understanding of the effects of subsidies.

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24. Integrating analytical modeling and individual-based modeling for complexity reduction, upscaling, and to gain causal understanding

Succession in semi-natural habitats - a multi-modelling approach for a spatially explicit landscape model

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Research insitute gaiac

The LandS model is a landscape succession model developed at the Research Institute gaiac using a multi-modeling approach. It simulates vegetation development spatially explicit on a local scale, e.g. in a national park or protected area. In particular, the species composition of the herbaceous vegetation community is simulated together with the early encroachment of shrubs and trees. A key feature of the model is that the herbaceous layer is simulated using differential equations and Ecological Indicator Values (EIVs) derived from phytosociological and empirical scales. It includes EIVs for different environmental factors such as temperature, light, soil moisture, soil pH, and soil nutrients, as well as different land use types such as mowing, grazing, and trampling. This reduction in complexity is paired with individual-based modeling (IBM) of woody vegetation. The IBM approach for trees and shrubs allows for a more realistic representation of the modeled landscape and successional processes. The vegetation sub-models are complemented by stochastic or analytical mechanisms for wildlife disturbance.

The model has been successfully applied as a decision support system (DSS) for nature conservation measures in two different types of semi-natural landscapes. It was first developed for the Eifel National Park to simulate future landscape management scenarios. Later it was extended to simulate natural forest development on windthrow areas after major storm disturbances. Both developments resulted in high acceptance of the modeled scenarios, as they were developed in close cooperation with stakeholders. The model has recently been adapted to be easily applied to other sites by exchanging sets of species without changing the source code. In addition, the model is currently being extended to include additional environmental factors in order to represent the succession of floodplain landscapes.

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26. Beyond prediction: application of machine learning to gain new ecological insights

Factor dissimilarity explains variability of soil functions in response to multiple global change factors

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Soil functions are facing threats from various co-acting anthropogenic disturbances (eg. climate change, chemical contaminations, microplastics etc.). Although previously the soil properties and functions have been found to be directionally driven by the number of factors acting simultaneously, we still know little about the joint impacts of multiple GCFs. Additionally, predicting the effects of simultaneously acting multiple global change factors (GCFs) becomes more challenging as the number of factors increases. Null models have been commonly used for predicting the joint effects of multiple factors, but their predictive ability is limited for high-GCF levels because potential factor interactions are generally overlooked. To better evaluate the risks of multiple GCFs impacts on soil systems, inspired by the factor classification framework based on their effect mechanisms, here, we hypothesise that co-acting GCFs with more diverse effect mechanisms, or higher dissimilarity, have more severe impacts on soil functions. We chose 12 different human influences as factors to make up a factor pool. Dissimilarity indices of co-acting factors in each high-GCF level (2, 5 and 8 factors) were calculated based on the measured responses of soil properties and processes to the single factors from the factor pool. In all multiple factor levels, we found significant correlations between factor dissimilarity indices and the joint effects of GCFs on soil decomposition rate, water stable aggregation, soil pH and soil enzyme activities. To further assess the dominant drivers of soil responses to multiple GCFs, a multiple explanatory variable modelling framework was applied based on a machine learning algorithm. Predictor variables (number of factors, individual factor contributions and factor dissimilarity) were added to the permutation-based random forest models respectively. Result shows that, on the basis of predicting response variations by number of factors and individual factor contributions, adding factor dissimilarity indices as predictor variables increased model explanatory power by 33.4%, 18.0%, 14.8% and 14.4% for the soil responses of decomposition rate, soil N-acetyl-glucosaminidase activity, phosphatase activity and β-glucosidase activity, respectively. Our finding shows that factor dissimilarity plays a unique role in driving soil functions that cannot be explained by mathematically combining the individual factor contributions. This work provides new insights into the impacts of multiple global change factors on soil ecosystems.

Modeling species diversity in streams: comparing three machine learning algorithms

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Understanding the spatial pattern of species diversity in relation to environmental variables and human disturbances is critical for biodiversity conservation and restoration. The distributions of stream fish species are affected by a wide range of ecological processes operating at the levels of the local habitat, watershed, and basin in complex ways. Machine learning is increasingly chosen to disentangle the complex effects of environmental factors on biodiversity. This study compares Random-Forests (RF), Boosted regression tree (BRT), and Lasso regression in modeling the relationships between the species richness of fish and 66 environmental factors (e.g., climate, geology, stream size, topography, and land use in the watershed) across 937 wadeable stream sites in Illinois, USA. The fish samples were collected based on a standard protocol of electrofishing between 1995 and 2010. The environmental data are derived from the database of the Greak-Lakes Gap analysis Project. RF explained the variance best but gave weights to almost all predictors and often equal to those correlated predictors, making the effects of predictors difficult to interpret. Lasso explained the variance less well but dropped about half of the predictors in a biologically meaningful way. BRT is intermediate in both counts. The three algorithms also agreed well on the ranks of top and bottom predictors but differed greatly on moderately important ones. Overall, Lasso regression and BRT appear preferable for inferring the effects of environmental factors on species richness.

Landscape-level soil CNP stoichiometry driver relationships are scale-dependent

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Soil CNP stoichiometry is critical for overall terrestrial nutrient cycling and ecosystem functioning. Different drivers including vegetation influence this stoichiometry in various

landscapes. However, much emphasis has focused on soil CNP stoichiometry driver relationships in individual spatial scales, ignoring the potential effects of different scales on these relationships. Here, we evaluate the scale-dependent (i.e., spatial grain size) effects on the relationships between soil CNP stoichiometry estimates and its main drivers, vegetation, and topography over massive landscape levels. Our findings clearly show that spatial scale has a significant impact on the relationships between soil CNP stoichiometry and its drivers, highlighting the need to account for scale-dependent effects in soil-related processes. By considering multiple spatial scales, we can avoid misinterpretations and make more accurate inferences from our models.

BEyond - Learning from the Biodiversity Exploratories to make predictions beyond them

Marvin Ludwig; Jan Linnenbrink; Maite Lezama Valdes; Lena Neuenkamp; Norbert Hölzel; Hanna Meyer

The understanding and monitoring of spatio-temporal dynamics in biodiversity and ecosystem functioning at the landscape-scale is a major challenge in ecological research. The Biodiversity Exploratories Project makes a significant contribution to this by intensively studying biodiversity patterns and ecological processes on field survey plots in three regions in Germany since 2006. However, for a landscape-scale understanding, spatial predictions of relevant biodiversity indicators are required. For this, machine learning offers great opportunities for predictive mapping, due to the ability to model non-linear and complex relationships between drivers and biodiversity indicators. However, recent research indicates considerable challenges when trained models are applied to make predictions beyond intensively studied areas. Further, complex machine learning models provide little insights into drivers and processes, hence initially do not support a mechanistic understanding of biodiversity patterns.

The BEyond projects aims to overcome these challenges. With a focus on grasslands, we aim at learning from the Biodiversity Exploratories to make spatio-temporal predictions of biodiversity and ecosystem functioning variables on a landscape scale - beyond the experimental plots. We further aim at going beyond predictions and explore what models have learned and why local predictions were made. Here, we present first results of landscape-wide predictions of biodiversity patterns and their explanation. By using an indirect modelling approach combined with explainable AI methods we aim to identify the contributions of potential drivers like terrain, soil, climate, land use and landscape structure to the prediction in order to contribute to a more mechanistic understanding of biodiversity and ecosystem functioning patterns.

An automated rapid assessment of post-disturbance forest resilience

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As a result of climate change disturbances regimes are changing around the globe, challenging the sustainable provisioning of ecosystem services to society. As a consequence, the disturbance resilience of forests (here: their ability to recover important structural and compositional features) is a key process for forest management, yet measuring resilience remains a challenge. Recently big data and machine learning have opened up new avenues for exploration, particularly in areas where data acquisition can be tedious and expensive. Here, we propose a novel system that leverages computer vision and deep neural networks to derive important parameters of resilience from simple photos captured in recently disturbed forest stands. Our approach is geared towards a rapid assessment of resilience that allows swift considerations on the post-disturbance state of the forest without the need for extensive data collection.

Our approach has two components. First, we estimate depth maps, which determine the distance of each pixel in the image from the camera position, using a pre-trained neural network for monocular depth estimation. Secondly, we use a manually labelled dataset of post-disturbance forest images to train a panoptic segmentation model. This model maps each pixel to “thing” and “stuff” classes, such as trees and shrub, respectively. Training data contained 1147 images generated in an extensive field campaign across sites disturbed in the drought years of 2018-2020 in northern Bavaria (Germany), spanning four major forest types. By combining these two models, we estimate various metrics of relevance for forest resilience, such as stem density based on the distance to detected trees, ground vegetation cover, and the canopy complexity of the immediate surrounding.

In this contribution, we introduce our approach, and demonstrate the training procedure based on our data. Furthermore, we present first results based on the computer vision pipeline and derived forest metrics. We conclude that computer vision is a promising approach for generating relevant information for forest resilience from simple images of post-disturbance forests. Our approach holds potential for future application in on-site decision support, helping forest owners to gauge the resilience of individual disturbance patches and determine evidence-based priorities for post-disturbance forest management.

Revealing patterns of global vascular plant co-occurrences with nonlinear dimensionality reduction

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Environmental data sets are becoming more voluminous and complex. For this reason, their optimal representation in low-dimensional space is an important step towards more efficient reduced-order modelling using machine learning (ML) techniques. One of the examples of such data are species distributions of broad spatial and taxonomic coverage published via Global Biodiversity Information Facility (GBIF). The data include information on over 300,000 vascular plant species and inherit noise and biases from compound, mostly opportunistic, data sets. Large number of dimensions (species) and data complexity require application of nonlinear approach. Here we aim to derive plant co-occurrence gradients from the global GBIF dataset using nonlinear dimensionality reduction methods.

We analyse global vascular plant co-occurrences using the Isometric Feature Mapping (Isomap) method, which can be considered a nonlinear extension of multi-dimensional scaling. In this case, instead of linear distances between points in low-dimensional space, Isomap uses so-called “geodesic distances". Similarly to their meaning in geography, geodesic distances are the shortest distances along the underlying nonlinear structure, i.e. manifold. The method requires no a priori assumptions and allows effective representation of high-dimensional data sets.

The following questions are at the centre of this study: (1) what are the limitations and advantages of GBIF records in contrast to curated floristic data sets, i.e. checklists; (2) how the co-occurrence gradients from binary presence-absence data are compared with those derived from relative abundances; (3) what are the most important drivers shaping these gradients.

The study explores the potential of constantly-growing open access biodiversity data for large-scale analysis and cross-validation. As the quality and quantity of opportunistic biodiversity observations will continue to increase, we expect empirical reduced-order models to provide support for advanced interpretation of species distribution drivers in the context of ongoing environmental change.

Integration of UMAP and Random Forest for Improving Our Understanding of Soil-Landscape Relationships

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In Digital Soil Mapping (DSM), predictive models, such as machine learners (ML), have been used to determine the relationship between soil observations and environmental covariates to investigate the spatial and temporal changes in soil classes and properties. A common practice is to acquire and use a large suite of environmental covariates, such as data derived from digital elevation models, remote sensing, and other geospatial information sources which can be highly correlated, thus, making soil modelling and the interpretation of those models to be a complex challenge. For this, it is necessary to reduce the size of environmental covariates by removing redundant informative variables and consequently, not only achieve a robust prediction model but also reduce the risk of over-fitting. To address the issue of having highly correlated environmental covariate data, multiple dimensionality reduction methods have been used in soil-related research. In the current research, we applied three methods for reducing dimensionality: principal component analysis (PCA), t-distributed stochastic neighbor embedding (tSNE), and Uniform Manifold Approximation and Projection (UMAP). An initial suite of 160 environmental covariates was reduced to 10 and used to train a Random Forest (RF) model. The results demonstrated that combining RF machine learning models with UMAP estimates soil classes most accurately (overall accuracy of 0.80) compared to PCA and tSNE. This demonstrates the effectiveness of UMAP in addressing non-linear relationships among predictor environmental covariates for RF model.

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28. The use of artificial intelligence in ecological modelling

kNNDM: k-fold Nearest Neighbour Distance Matching Cross-Validation for map accuracy estimation

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Random and spatial Cross-Validation (CV) methods are commonly used to evaluate machine learning-based spatial prediction models, and the obtained performance values are often interpreted as map accuracy estimates. However, the appropriateness of such approaches is currently the subject of controversy. For the common case where no probability sample for validation purposes is available, in Milà et al. (2022) we proposed the Nearest Neighbour Distance Matching (NNDM) Leave-One-Out (LOO) CV method. This method produces a distribution of geographical Nearest Neighbour Distances (NND) between test and train locations during CV that matches the distribution of NND between prediction and training locations. Hence, it creates predictive conditions during CV that are comparable to what is required when predicting a defined area. Although NNDM LOO CV produced largely reliable map accuracy estimates in our analysis, as a LOO-based method, it cannot be applied to large datasets found in many studies.

To overcome this limitation, we propose a novel k-fold CV strategy for map accuracy estimation inspired by the concepts of NNDM LOO CV: the k-fold NNDM (kNNDM) CV. The kNNDM algorithm tries to find a k-fold configuration such that the Empirical Cumulative Distribution Function (ECDF) of NND between test and train locations during CV is matched to the ECDF of NND between prediction and training locations. In our contribution, we will present the kNNDM CV algorithm and test its performance in a simulation study with different sampling distributions and compare it to other CV methods including NNDM LOO CV as well as other recently proposed CV strategies for map accuracy estimation. In our analysis, we found that kNNDM CV performed similarly to NNDM LOO CV and produced reasonably reliable map accuracy estimates across sampling patterns. Thus, kNNDM provided the advantages of our original NNDM LOO CV strategy while bypassing its sample size limitations. To show how kNNDM can be used in ecological studies, we will also use kNNDM CV to estimate the accuracy of recently published global maps, and compare them to the error estimates stated in the original studies.

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29. Ecological Models for the Management of social-ecological Transformations

Biodiversity-production feedback effects lead to intensification traps in agricultural landscapes

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Intensive agriculture with high reliance on pesticides and fertilizers constitutes a major strategy for ‘feeding the world’. However, such conventional intensification is linked to diminishing returns and can result in ‘intensification traps’ – production declines triggered by negative feedback of biodiversity loss on crop yields at high input levels. We developed a novel framework that functionally integrates biodiversity in crop-yield assessments to evaluate risk and magnitude of intensification traps. Simulations grounded in literature reviews demonstrated that intensification traps emerge in most landscapes (73%), but rarely in major calorie production systems. In trade-off situations, small-loss large-gain trade-offs prevailed allowing for substantial biodiversity gains with production decreases of just 5-10%. However, systematic sensitivity analyses revealed a strong context-dependence and hence, we suggest management safety margins to prevent the double loss of biodiversity and food security linked to intensification traps.

Environmental federalism and agri-environment schemes: is there more to centralization than uniform policies?

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The cost-effectiveness of agri-environment schemes (AES) depends, among other things, on spatial characteristics. In this respect, extensive research has been conducted on how to incentivize habitat connectedness, but far less attention has been given to spatial coordination between regions and how the level of decision-making affects the outcome of AES. In the European Union, there has been a transition towards a more decentralized approach to designing AES. On the one hand, decentralized decision-making entails greater flexibility and allows for the design of AES being tailored to the local conditions. On the other hand, a decentralized approach might result in lack of coordination between regions and consequently in the failure to capitalize on cost-savings opportunities stemming from regional differences in costs and benefits. The present research contributes to filling the research gap by analyzing the design of multiple AES targeting different species through the lens of the environmental federalism literature. For this purpose, a conceptual agent-based ecological-economic modelling procedure has been developed. The model considers two regions, two levels of decision-making, two species and two AES, each targeting one of the two species being considered. Under decentralization, AES are managed purely at the regional level, so the regions do not coordinate but design their AES schemes independently. By contrast, central governments face political constraints that prevent them from providing different jurisdictions with different outputs and are therefore only able to implement uniform policies. In the present context, the central government is constrained to offering the same payment for the same conservation measure in both regions, resulting in only two AES being implemented. Yet, assuming that different AES targeting different species are distinct policies, the central government could implement an AES protecting one species in one region and a different AES protecting the other species in the other region, effectively coordinating the regions and accounting for cost-saving opportunities. We refer to this policy as the “coordination policy”. The expected results include that (i) lack of coordination at the lower level of government could lead to both regions prioritizing the same species, (ii) coordination and specialization under centralized decision-making could lead to higher cost-effectiveness compared to decentralization, and (iii) the results may vary greatly depending on the relative differences in farmers’ opportunity costs between the regions as well as on the combination of species that is being considered.

The spread of *Aedes albopictus* in Spain: linking human mobility and habitat suitability

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Tiger mosquito, *Aedes albopictus*, is an invasive vector of diseases such as Dengue and Chikungunya. The first records in Spain date back to 2004 in Sant Cugat del Vall´es. Since then it has invaded the Spanish Mediterranean coast and is moving inland. Studies have shown that these mosquitoes can travel in vehicles, allowing them to cover long distances. In this work, we explore the colonization process of Aedes albopictus in the last decade with data from the citizen science observatory, Mosquito Alert. We focused on two factors: human movement and habitat suitability. To assess habitat suitability, we computed the Basic reproduction number, R0, from a mosquito mechanistic model that incorporates parameters related to the mosquito life cycle as a function of temperature, rainfall and human density. We combine human mobility, habitat suitability and distance to the invaded regions in a metapopulation model to understand the effect of different dispersal modes in the colonization process. Our findings shed light on the colonization dynamics of Aedes albopictus and provide insights into the interplay between human movement, habitat suitability, and distance to the invaded regions. This research has practical implications for the management and control of invasive species, providing valuable information that can inform strategies aimed at mitigating the impact of these disease vectors on human health and the environment.

Modeling plant community development on a building envelope optimized for promoting plant diversity

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Urbanization is an important cause of biodiversity decline, inducing an increasing disconnect between people and nature. One reason buildings do not support biodiversity in the urban environment is the use of smooth, flat, and impervious surfaces that characterize standard building envelopes. However, vertical building surfaces in cities may be promising intervention zones to support biodiversity, as they represent vast surface areas, are mostly inaccessible to people, and can be modified to offer resources to plant and animal species. Nevertheless, the requirements of envelopes for humans differ from those of other organisms. Thus, the design of multi-species, biodiversity-rich building envelopes necessitates analyzing the tradeoffs between the needs of plants, animals, and humans through multi-objective optimization. In this research, we analyzed these trade-offs using the example of plants growing on a simplified building design. We optimized the size and position of planters and the number and location of windows using the parametric design software environment Rhino/Grasshopper. The objectives were, for humans, to optimize daylighting, maximize energy efficiency by reducing incoming solar radiation, and to reduce the structural load of the planters. For plants, the objectives were to maximize soil available in the planters and create heterogeneous shading conditions for promoting plant diversity. We then compared the suitability of the optimized envelope for a selection of plant species based on their soil depth and shading requirements to a more realistic plant community that could form on the envelope using a modified version of the model of plant community dynamics FATE-HD. The suitability mapping strategy could be used in architectural design, and agreement between the modeled plant occurrences and the suitability mapping will give us more insight into how realistic this proxy will be as a tool to design building envelopes for the promotion of biodiversity.

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30. Modelling change in social-ecological systems – from conceptual reflections to promising case-based examples

Factors to Scale Up Innovative and Sustainable Food Systems: A Flemish Case Study

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There is a need for alternative food practices to be scalable to be able to transform the food system towards sustainability (Morgan 2020; Bonfert 2022). However, such systems are complex and the scalability of sustainable practices remain an issue. Due to the high complexity of agri-food system, agent-based modeling (ABM) arises here as a potentially suitable method in transition modeling.

The objective of this study is to develop an ABM to show the combined effect of different parameters to scale up CSA initiatives: threshold for opportunity window towards sustainability transition, societal pressure, and economic orientation of the farm. The model is built up in NetLogo 6.2.2.

On each step, farms produce vegetal products and sell it to their market (i.e., organic or conventional). Then, they assess the peer pressure originated by neighbor farms that are innovative. Every two years, farms assess their economic performance to compare their revenues with the revenues earned in the last five years. If they have enough pressure from society, if the trend for organic and innovative products is strong enough, if their revenues are sufficient, and if their area is reasonably small, they will scale up and adopt this innovative practice.

The sensitivity analysis revealed the effect of the combination of three key factors in the scaling up of CSA initiatives. For organic farms, having a lower economic orientation always promotes the scaling up, with a maximum of 6% innovative farms in the population, while a strong economic orientation hinders the transition (see Fig. 1). However, a high opportunity window threshold together with low societal pressure lead to a lower upscaling. For conventional farms, we observe similar results with even a higher percentage of upscale (15%), although the scaling up is blocked at high values of opportunity window threshold with low values of societal pressure (see Fig. 2).

In this study, the opportunity threshold clearly marks the transition. Having perception of these windows of opportunity could promote a higher scaling up of innovative practices. In addition, sustainability transitions fostering innovative, environmentally-embedded practices require a more flexible economic orientation of the farms. In conclusion, the studied parameters seem to play a role together to enhance the scaling up of innovative practices. Further research on the role of more parameters, as well as other impacts of a scaling up in the system is needed.

A new conceptual framework that integrates multiple problems at multiple spatial scales for simultaneous solution of the global environmental issues

Reiichiro Ishii

Research Institute for Humanity and Nature

Biodiversity loss and climate change are regarded as the major global environmental issues, but the interactions between them and other environmental issues which varies in type and magnitude from region to region have not been considered before the measures for each of the major issues are planned, determined or implemented.

To achieve simultaneous resolution of Multiple Environmental Issues without inviting externalization (imposing "wrinkles" on the "outside" of the problem or region) , we need enhance the trans-scale integration of the top-down management and bottom-up action planning sharing the advantages from both ends.

For the Global level, so far, the target amount and year of GHG emission are firdltly determined and the share of each country follows without considering the “ripple effects” from the measure of GHG reduction on the ecosysten and human welbeing in each country.

At the Local (country) level, on the other hand, societal constraints for the measures, demand and capability are mostly understood by policy makers but causal interactions among different issues ot the effects beyond the country scales are not mostly incorporated or prioritized.

We here propose a Double PDCA-cycle to connect local action-plans(Bottom-Up) and global evaluation and recommendation (Top-Down):

The first cycle is simulation based for checking the external and global effects of Local Action Plan proposed by each country before implementation

The second cycle is for actual checking and modification based on the observation.

Advantages of this Double PDCA-cyclescheme can be summarized as flollws :

1) Each country can design its Local Action Plan based on the local natural and cultural condition.

2) Appropriate models are used for the evaluation of the globally integrated effects of the action plans proposed by each country.

3) Existing Observation and Assessing mechanisms can be used.

How policy affects farmers and shapes landscapes - concept for an agent-based exploration

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Preserving farmland biodiversity is one objective of the Common Agricultural Policy (CAP) of the European Union. While the policy contains some instruments that support effective measures such as fallow land, landscape elements, and extensive grassland management, uptake of the schemes by farmers has thus far been insufficient. Furthermore, policies target the farm level, whereas effective biodiversity conservation also requires landscape level approaches. As a result, a steeper trend of biodiversity loss is still observed in agricultural landscapes than in other environments.

The CAP4GI project advises on how to change the CAP for the forthcoming reform in 2028. The objective is to base recommendations on a better understanding farmers' behaviour. We use case studies in Baden-Wurttemberg and Thuringia (Germany), stake-holder platforms, and economic-ecological modelling.

Within the project, Persefone.jl is an economic-ecological model model currently developed together with Daniel Vedder using the performant language Julia. Centred around the farm landscape, the model encompasses interactions from policy payments and regulations, farmer decisions, landscape composition and configuration, and the dynamic response of animals. Taking an agent/individual-based approach, it should allow assessing how both farms and biodiversity are influenced by the newest CAP reform, and testing alternative payment schemes that may come into place in 2028.

With the socio-economic part of Persephone.jl, I hope to uncover factors that restrict or facilitate farmers' uptake of biodiversity-friendly schemes. I also aim to identify instances where other subsidies may counteract the efforts made by the CAP's biodiversity schemes.

This poster explains the socio-economic conceptual model. I identify key elements and processes in the CAP, farmers' decision-making processes and management that shape biodiversity landscapes. In doing so, I discuss how to reduce the complexity of the system according to criteria such as a) the spatial extent of impacts, b) extent to which it can be impacted directly by current of reformed CAP regulations and payments, c) availability of data, and d) representation of an appropriate level of heterogeneity among farms.

Model based approach in understanding the socio ecological change impacts on Asian elephant habitats.

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Human-wildlife conflicts incidents are indicative of the impacts of socio-ecological changes on wildlife habitats. Socio-ecological modelling has great potential to enhance understanding of such changes and support with management of such transformations. Natural and anthropogenic disturbances severely impact wide-ranging species such as Asian elephants, which in turn drive negative interactions with people and present livelihood challenges. The goal of this study is to develop a model to investigate the relationship between human-elephant conflict (HEC) and land-use/land-cover change, as well as other socio-ecological variables, in Sri Lanka. In the model, the number of human elephant conflict incidents treated as the dependent variable – a HEC density map was created using 20 years of data on HEC incidents using Kernel density estimation. The independent variables are: landcover change (binary -changed/unchanged) and conversion type), elevation, slope, rainfall, temperature, population density and distance to features such as rivers, reservoirs, paddy, protected areas, towns, and roads. All the layers convert to a raster surface, thus identifying the hotspots of HEC in Sri Lanka and their drivers. Such a large-scale country-wide analysis of HEC has never been performed before. The results can be useful in informing management and conservation strategies not only in Sri Lanka but across the range.

Model-based exploration of leverage points to foster sustainable nitrogen management in German agriculture

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The worldwide increasing usage of nitrogen fertilizer in agriculture imposes major societal threats as in groundwater pollution, biodiversity losses, climate change and health issues.

Thus, there is a need for reducing nitrogen waste and a key entry point to achieve this goal is a change in farmers' behavior.

In order to identify and explore leverage points to foster sustainable nitrogen management in German agriculture an agent-based-model for farmer behavior is supposed to be developed within the scope of the PhD project.

We hypothesize that policy measures which consider beside of economic incentives also further behavioral influence factors and differentiate between various behavioral types of farmers lead to higher adoption of sustainable nitrogen practices, compared to the current policies.

Another hypothesis to be tested is that heterogeneous policy measures lead to less nitrogen losses for whole Germany.

Quantifying nature’s contributions to agriculture - the role of social-ecological factors

Yiyi Zhang; Hugo Thierry; Lael Parrott; Brian Robinson

Social and ecological processes jointly contribute to the production of ecosystem services (ES), especially in agricultural landscapes. For example, crop yields are produced from ecosystem inputs (e.g., wild pollination) and non-ecosystem inputs (e.g., managed bees). These inputs may have different impacts on yield depending on how they are distributed across the landscape and interact with each other as well as other environmental factors. Quantifying to what extent different human communities depend on different parts of the landscape for their agricultural activities can inform more sustainable land-use decisions and agricultural support. We analyze three ES inputs (water supply, feed productivity, pollination) and their contribution to crop water use, livestock production, and crop yield. We identified factors and feedbacks that mediate the effect of these ES inputs and developed statistical models to estimate the relative and conditional contributions of ES inputs in the agricultural region in Saskatchewan, Canada. Our preliminary results show how ES are co-produced and can be partitioned into different types of inputs using publicly available data.

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31. From dynamic forest models to decision support for forest transformation – How can synergies be achieved?

Uncertainty of a future forest

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What is the best alternative when planning for forest adaptation? The answer is a recommendation with uncertainty associated with it. This question hides a multi-factorial problem where one seeks the optimal trade-off among the criteria selected for the evaluation of the alternatives at hand. The criteria become - in the algorithm - parameters that simulate different scenarios and therefore carry their own variability. That is why the ranking of the alternatives in a decision support system should be seen together with its uncertainty and never as a black-or-white suggestion. We propose a comprehensive sensitivity analysis based on Monte Carlo sampling for a typical modeling approach used in forest decision support. In this kind of framework, dynamic forest models are used to estimate the criteria (with their uncertainties), and a multi-criteria decision analysis (MCDA) approach is used to rank the alternatives based on those criteria. Specifically, we assess the impact of the variability of the input criteria and preference weights as well as algorithmic choices such as normalization or aggregation functions on the outcome of an MCDA analysis. By focusing on a probabilistic approach for a forest decision support system, we shed new light on the uncertainties related to different parts within a decision support pipeline. This new awareness can help to provide stakeholders with additional information to assess and quantify the stability of a decision recommendation.

The potential use of a dynamic forest model as decision support in mountain protection forests of Switzerland

Gina Marano, Harald Bugmann

ETH Zürich

Among multiple ecosystem functions provided by mountain forests, protection against natural hazards is a crucial service for the well-being of human communities, particularly in the European Alps with its steep slopes. In Switzerland, forests with a protective function are actively managed to ensure permanent stand stability against natural hazards (e.g., avalanches, rockfall, landslides).

In the context of the framework 'NaiS' (Sustainability and success monitoring in protection forests) , forest practitioners need to determine whether interventions are needed at the stand scale, typically basing their decisions on temporally and spatially limited data and often in the absence of prognostic tools. However, forest dynamics take place over long periods, and the impacts of future trajectories in climate and disturbance regimes pose a serious challenge to silviculture schemes under such uncertain conditions.

Dynamic forest models can support forest practitioners by providing a set of potential scenarios and projections with the associated uncertainty. In this sense, forest models should not be intended as the exact representation of a future reality, rather as a set of equally stochastic and uncertain scenarios.

Using the forest gap model ForClim, we simulated the future development (i.e., the coming 50 years) of multiple stands in the canton of Grisons (Switzerland). ForClim output was provided to forest managers as decision support for implementing the NaiS framework, distinguishing two cases: a) absence of management (as a baseline to assess the necessity of an intervention during this 50-yr time period); under b) imposing disturbance scenarios at the stand level. Both sets of simulations were done in the absence of climate change as well as under a moderate and an extreme scenario of climate change.

This study demonstrates the high potential of using simulation modeling as an integral component of management decisions in real-world forestry.

Trait-based structuring of animal biodiversity identifies five major patterns

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Add-my-Pet (AmP) is an open access online collection of referenced data on animal energetics, Dynamic Energy Budget (DEB) parameters, and DEB implied traits for over 4000 species from all major animal phyla. DEB models aim to quantify the various aspects of energy and mass budgets in dynamic environments throughout ontogeny, i.e. embryo, juvenile, adult. We define a trait in the context of DEB theory as “a parameter or a function of parameters, which quantifies some eco-physiological property of a species''. We followed the workflow that (measured) data was used to estimate parameters, and the parameters are used to quantify the traits. So, traits here are not measured data, but instead model-derived parameters and implied properties. The reliability of parameter values generally increases with data availability, and the various AmP entries differ a lot in data availability. However, in this way we could evaluate all traits for all species.

Trait values for a species are interlinked. Furthermore, the strict application of mass and energy conservation rules in DEB theory contributes to this interlinking, and provides the consistency between traits. Over the ontogeny of the theory and its large-scale application to animal species, including the analysis of patterns in DEB traits from AmP, we identified five major patterns that can be used to structure animal biodiversity.

First: co-variation of parameter values, based on the idea that species share extensive (scaled to size) parameter values, while appropriate ratios of extensive parameters are intensive. Second: metabolism is specified as a mix of supply and demand components, and species are ranked according to the supply-demand spectrum; the position on the spectrum is quantified by a corresponding DEB trait. Third: the altricial-precocial spectrum is quantified by another DEB trait, which enables placing all animals on the spectrum. Fourth, small bodied species have a metabolic route to handle temporary peaks in their food supply by boosting growth and reproduction, dubbed “waste to hurry” strategy. Last, metabolic acceleration structures the animal kingdom, implying the importance of life-cycles. These findings provide a basis for comparing animal taxa and shed light on metabolic constraints and inter-relationships that together with environmental pressures structured animal biodiversity as we know it today. We present how these patterns work in practice and how adaptations modify the expectations.

An short Overview : The Preview of the Marketing of Firewood in the Federal Capital Territory Abuja, Nigeria.

Michael Oke

Michael Adedotun Oke Foundation

The various needs to develop the forestry sector, the need for rethinking the different strategies of the various ways of marketing and distribution of the different firewood products, and engagement in the production of charcoal, chewing sticks, and sculptured wood items. Thus, Nigeria has over six hundred potential timber species, of which less than three hundred are currently being commercially exploited for international trade. But the industry could contribute significantly to local and international trade if the informal enterprises of small wood-based industries were operated with their formal incorporation into the national economy. These enterprises include the various artisans, cabinet makers, and timber converters who are into selling the different kinds of firewood. More studies are needed to supply various prices; information; networking; linkage of sellers; and documentation of the good practices being used in the marketing of firewood. If there are better ways of improving and supporting those who are into different usages, such as domestic and industrial purposes, The various studies were conducted in the two areas of the Federal Capital Territory, Abuja, namely: Gwagwalada and Municipal, and the different ways of marketing the various firewood were observed. From the field survey, it was observed that the firewood was being marketed in an open environment, separated into different sizes and put together. But there is no detailed information about the different prices. This paper thus proposed the need for re-strategizing the mode of marketing the various types of forestry products; ways of displaying; involvement of community sellers and their formation of cooperative societies; and the need for reforestation and forest protection plans.

Keywords : Firewood, marketing , selling, Federal Capital Territory

Modelling how management options for disturbed spruce areas affect reforestation dynamics – a predictive ecology approach for a supra-regional field trial in Thuringia

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The impact of extreme weather events such as droughts, heat waves, storms, and the intensification of bark beetle outbreaks in spruce forests in recent years, has led to a vast loss of spruce trees in Thuringia and other regions in Germany. Different management options for disturbed spruce areas are practiced but have so far been insufficiently supported by research findings. The consortium of the ResEt-Fi project now implemented a supra-regional field trial to test how specific practices for deadwood management affect the ecological conditions and subsequent reforestation dynamics of natural regeneration and planted trees. In order to visualize and understand the observed short-term (3-5 years) and predict longer-term dynamics, the individual-based forest landscape and disturbance model iLand will be used. Despite having a wealth of data support and reliable modelling software, our study faces the challenge of upscaling results from selected, dispersed trial sites to large-scale, continuous landscapes. With this contribution, we want to address the challenges and opportunities of this ambitious multi-region, multi-scale modeling task. It involves the processing and integration of spatial information on forest stands and abiotic site characteristics, required for the setup of distinguished model landscapes mimicking the different regional conditions of the field trial sites. In addition, continuously monitored dynamics of microclimatic conditions and soil water content as well as observations on the composition and growth of tree saplings and competing vegetation, on the decay of standing dead woody debris, and on soil decomposition over multiple time points within a year will be used as input data and patterns to calibrate and validate the model. Whereas many parameterizations can be adopted or better confined from studies using the same model, others will be defined employing a multi-criteria framework of pattern-oriented modelling, which is schematically presented for the framework of this study. To improve the accuracy and reliability of short- to long-term predictions, sensitivity analysis will assess the robustness of model results to parameter uncertainty. Last but not least, we also present how remote sensing data will be used to gradually expand the environmental conditions and temporal scales to thoroughly test our model results at spatial resolutions not covered by other empirical measurements and in additional areas. With this, the prospective modelling approach aims to provide reliable and valuable insights for forest practitioners and stakeholders, providing them with visual and regionally customized information to support decision-making

Tree diversity in future scenarios of climate change and forest management

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One of the most vulnerable forests in Chile is the Coastal Maulino forest, a young forest with a dominance of deciduous species and the presence of endemic species, which is currently only found in remnant patches, since throughout history it has been replaced by plantations of exotic species destined for forestry production. Due to this fragmentation, it is urgent to advance in its conservation and protection through forest management, especially in scenarios of climatic uncertainty. In this research, the ForClim model was used to predict tree diversity in the Cauquenes river basin, under different climate change and forest management scenarios. This was done by simulating the potential, current and future vegetation. The performance of the model in the prediction of the potential vegetation obtained a degree of agreement from moderate to substantial (Kappa >0.56), while the reconstruction of the current vegetation, evaluated through the Jaccard index, obtained values greater than 0.75, comparing with measurements of 67 plots. Finally, the future tree diversity was analyzed in three representative stands: native forest, mixed forest and forest plantation, finding that the most beneficial scenarios for each one were: enrichment with native species, permanent forest cover and total substitution to native forest, respectively. Although the diversity increases, the compositional and structural changes are significant and suggest a latitudinal advance of the evergreen species within the Coastal Maulino forest. It is necessary to continue as well as to analyze and understand the dynamics of forests.

Open Topics

Understanding the habitat distribution of the threatened Eastern waterfan (*Peltigera hydrothyria*) lichen within Atlantic Canada through the creation of a species distribution model and model-derived products

Miranda Frison[1]; Jean R. Haughian[2]; Peter Bush[3]

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The project will focus on creating a regional species distribution model and for Eastern waterfan (*Peltigera hydrothyria*), which is a threatened lichen species within Atlantic Canada. A

landscape-scale model will be used to understand habitat requirements and predict occurrences of this aquatic lichen. Main data sources will include Canada’s National Hydrographic and Road

Networks, ClimateNA, and Global Forest Watch International. MaxEnt software will be utilized to predict species occurrences with a backwards stepwise selection process to determine the most important predictor variables and prevent overfitting. Variable importance will be evaluated using a jackknife test. Model fit will be determined using area under the curve and evaluated with cross-validation. The final model will be compared to a null model and field validated. Habitat suitability maps will be presented to demonstrate the ecological range of Eastern waterfan within Atlantic Canada. Potential impacts to the species due to climate change will be predicted using temperature and greenhouse gas scenarios provided by the Intergovernmental Panel on Climate Change. Additionally, population sizes will be estimated, and land-use planning recommendations will be provided.

Predicting colony level effects from laboratory data using BEEHAVEecotox

V. Roeben, M. Miles, D. Schmehl, T.P. Preuss

Baxer AG

Bees are crucial pollinators and thus an essential part in our food supply. This is also recognized in the BioDT project aiming to create digital twin prototypes for biodiversity research. One of the use cases of BioDT focusses on pollinators with a focus on how different spatial land use practices, climate scenarios, and beekeeping practices affect the vitality and survival of honey bee colonies. However, also plant protection product use can have an impact on colony dynamics. Therefore, we introduce BEEHAVEecotox; an ecotoxicological module that mechanistically links exposure of bees in the field with the hazard profile for individual honeybees, leading to emerging colony effect. It is an addition to the widely used and extensively tested BEEHAVE colony model. The mechanistic link allows the translation of results from standard laboratory studies to relevant processes and parameters for simulating bee colony dynamics. The BEEHAVEecotox model includes 4 submodules: an external exposure module, in-hive fate module, water foraging module, and an effect module. The external exposure module incorporates the concentration of PPPs in the bee-relevant matrices such as nectar, pollen, and water. When foragers forage on these matrices, they receive an oral dose of the PPP, and they can be exposed via contact on the day of application. The water foraging module incorporates the need for water for cooling of the hive and dilution of stored honey, including potential exposure to PPPs. The in-hive fate module simulates the entry and mixing of the PPP into the hive, through nectar, pollen, or water. The effect module covers the mortality due to exposure for the different cohorts. It uses the slopes and LD50 values of standard acute contact, oral, chronic oral, and larvae studies as inputs. The BEEHAVEecotox model was validated against two semi-field studies with a tunnel setup with two PPPs with different modes of action (dimethoate and fenoxycarb). In the presentation the application of BEEHAVEecotox will be highlighted using a case study to underline its potential application in a risk assessment context and how it could support the assessment of multiple stressors within the BioDT framework.

The visual ODD: A standardized visualization of individual-based models, inspired by the Overview, Design concepts and Details protocol

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Agent-based models are widely used not only in ecology but also in social sciences and technology. To increase transparency in model design, the standardized Overview, Design concepts, and Details (ODD) protocol has been designed for describing models. An increasing number of model studies use such ODDs. However, these are often long documents that are not suitable for a quick overview of a model. For this reason, manuscripts, presentations, and posters often include some form of visualization of the model. These can be flowcharts, landscapes, and other various forms of visuals. This variety of visualizations can make it challenging to compare different models and always requires time to first understand the layout of the figures. In addition, these visualizations are usually poorly linked to the sections of the written model description in the form of an ODD. We suggest that a standardized visualization for ODDs is needed to allow for a quick overview of models and simplify the link to the written model description for readers who are more interested in specific elements. We propose such a generalized visual ODD (vODD) that captures the main concepts of a model without going into each detail. The ODD elements have defined positions in the figure to make them easy to find and compare. We show examples and give guidance on how to build such a vODD. We also provide templates that modelers can use to build their own visualization. While we would generally suggest keeping a visualization as simple and clear as possible, we also show examples of how more complex models can be represented in such a visualization. By establishing a generalized visualization of individual-based and potentially also other dynamic models, we aim to improve the rapid comprehension of models and simplify graphical model representations in manuscripts, presentations, and posters.

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