

VIRTUAL CONFERENCE

BOOK OF ABSTRACTS



**3rd International Conference
on Community Ecology**

13-14 December 2021 / Budapest, Hungary

ComEc3
3rd International Conference on Community Ecology

13–14 December 2021
Virtually from Budapest, Hungary

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Please be aware that certain changes introduced in the Conference programme after editing has been closed may not be included in this Book of Abstracts due to the publishing deadline.

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Programme of the 3rd International Conference on Community Ecology

Virtually from Budapest, Hungary
13–14 December 2021

CET (GMT+1)	Monday, 13 December		
17:20–18:20	Technical guidelines for session chairs		
18:20–18:30	Opening remarks <i>Ferenc Jordán</i> (Hungary) Conference Chair		
18:30–19:00	Plenary Talk	<i>Alberto Basset</i> (Italy)	An individual based approach to spatial organization of communities
19:00	Welcome Drink		

CET (GMT+1)	Tuesday, 14 December		
	Session I	Chair: Katalin Patonai	Community Ecology
9:00–9:30	Plenary Talk	<i>Vojtěch Novotný</i> (Czech Republic)	How to experiment with complicated food webs from tropical forests?
9:30–9:40	Short Break		
9:40–10:00	Normal Talk	<i>Sándor Bartha</i> (Hungary)	Constraints and freedom in vegetation dynamics – spatial pattern analyses with temporal extension
10:00–10:20	Normal Talk	<i>Balázs Deák</i> (Hungary)	Traits supporting long-term survival of grassland specialist plant species in habitat islands embedded in agricultural landscapes
10:20–10:40	Normal Talk	<i>Emanuele Fanfarillo</i> (Italy)	Factors affecting species richness and composition of Italian arable plant communities across different agricultural landscapes
10:40–11:00	Normal Talk	<i>Simona Maccherini</i> (Italy)	Silvicultural management does not affect biotic communities in conifer plantations in the short-term: A multi-taxon assessment using a BACI approach
11:00–11:20	Normal Talk	<i>Mohd Hafiz Mohd</i> (Malaysia)	Revisiting discrepancies between stochastic agent-based and deterministic models
11:20–13:20	Lunch Break		
12:00–13:00	Virtual Sightseeing Tour – Highlights of the Buda Castle quarter		

	Session II	Chair: Marco Scotti	Biodiversity and Ecosystem Function
13:20–13:50	Plenary talk	<i>Laura Dee</i> (USA)	Putting community ecology to work for conservation
13:50–14:10	Normal Talk	<i>András Abonyi</i> (Austria)	Towards resolving a conflict between diversity and dominance effects on the resource use efficiency of phytoplankton
14:10–14:30	Normal Talk	<i>Veronika Gergócs</i> (Hungary)	Open field mesocosm experiment provides new opportunities to investigate the effects of soil-dwelling mesofauna on soil N-cycling
14:30–14:50	Normal Talk	<i>Marina Gerling</i> (Germany)	Do mycotoxigenic fungi use heterogeneities in arable lands to overwinter?
14:50–15:10	Normal Talk	<i>Michaela Jakubcsiková</i> (Slovakia)	Soil nematode communities structure affected by <i>Fallopia japonica</i> (Houtt.) Ronse Decr. invasion
15:10–15:30	Normal Talk	<i>Laurie A. M. Wojcik</i> (Germany)	Functional diversity increases the robustness of tritrophic plankton food webs to a nutrient pulse
15:30–15:50	Normal Talk	<i>Salmah Yaakop</i> (Malaysia)	Understanding the interaction between <i>Metisa plana</i> , its hyperparasitoids and primary parasitoids from Good Agricultural Practices (GAP) and non-GAP of Malaysian oil palm plantations
15:50–15:55	Speed Talk	<i>Edina Kundrát-Simon</i> (Hungary)	Tree species to explore ecosystem functioning: sensitivity to air pollution based on APTI
15:55–16:30	Break – Show Your Pet		
	Session III	Chair: Ursula Scharler	Ecological Networks
16:30–16:50	Normal Talk	<i>András Hidas</i> (Hungary)	Revealing keystone species with network index can be tricky
16:50–17:10	Normal Talk	<i>Wei-chung Liu</i> (Taiwan)	Measuring functional diversity in food webs
17:10–17:15	Speed Talk	<i>Matteo Loschi</i> (Italy)	Building weighted networks for plankton communities from semi-quantitative data
17:15–17:20	Speed Talk	<i>Katalin Patonai</i> (Hungary)	Application of three modelling frameworks for aquatic ecosystems: a network-based approach
17:20–17:50	Break		
17:30–17:35	Introduction of an Ecology Lab in Hungary (5 min video)		
17:50–18:20	Plenary talk	<i>János Podani</i> (Hungary)	The wonder of the Jaccard coefficient: from alpine floras to bipartite networks
18:20–18:50	Plenary talk	<i>Alexadra Worden</i> (USA)	Microbial communities in the sea
18:50–19:00	Closing Drink - Award		

Opening Remarks

Monday, 13 December

Special issue of Community Ecology

All registered participants of ComEc3 are invited to submit their paper to Community Ecology and, following a standard peer review process, a selection of the finest ones will be published in a special issue of the journal (in 2022).

The deadline for submitting the manuscript is 15 February 2022.

For further information please visit the webpage of Community Ecology: <https://www.springer.com/journal/42974>

Plenary Talk

Monday, 13 December

An individual based approach to spatial organization of communities

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Ecological interactions occur between or among individuals, which occupy or use a same unit of space at a certain interval of time. The spatial unit, being the individual home range or a single patch, represent the interactive arena where individuals can succeed or fail.

Space use behavior of individuals at both patch and home range scale has received attention highlighting large inter-individual variability and individual personality, at the intra-specific level, and body size dependent variability, at the inter-specific and, particularly, when differences in body size among species are large. Individual body size is a main determinant of individual metabolism and energy requirements, with cascading effects, as individual metabolic size, on the individual space use behavioural traits, as well as on other individual traits.

Metabolic theory has given a unifying view of ecological implications of body size relating with a single theoretical body individual level responses to population and community patterns; the latter include size range, size abundance and size distribution patterns.

The scaling up process of metabolic theory, from individual to population and community levels has been mainly developed with a spatially explicit approach. Here, I discuss the implications of the body size dependency of individual space-use at higher levels of the ecological hierarchy behaviour. This spatially explicit scaling up approach has aspects dealing with body size mediated coexistence relationships, community organisation and realised body size patterns and aspects accounting for community spatial organisation and spatial extent.

Session I – Community Ecology

Tuesday, 14 December

Constraints and freedom in vegetation dynamics – spatial pattern analyses with temporal extension

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Keywords: community assembly, diversity, grasslands, null models, old field succession, self-organization, spatiotemporal patterns

In contrast to the development of standardized methods, most studies have found weak assembly rules in plant communities. Evidence about small, often non-significant deviations from null models suggest stochastic models of community organization. Community assembly is considered stochastic when species are combined randomly at fine scale within the community and the diversity of combinations are constrained only by coarser scale parameters (total abundance, size of species pool and relative abundance of species). However, it was rarely studied how these coarser scale constraints develop and change in space and time. We argue that constraints included into present stochastic null models may result from deterministic assembly processes. Consequently, our view about the magnitude and role of stochasticity in plant community would change considerably if spatial analyses would be extended to spatiotemporal analyses.

Long-term observations of grassland community patterns were performed in Hungary, in steppe meadows and in open sand grasslands (at five sites in protected areas and in slightly degraded stands). Spontaneously regenerating old fields (adjacent to the grasslands) were also monitored at three sites. Spatial patterns of species were detected annually with a specific sampling protocol (combining high spatial resolution with reasonably high spatial extent). The resolution (5 cm × 5 cm) was fitted to the size of the individuals (or ramets). The spatial extent was up to 52 m while the temporal extent varied between 11 and 25 years. We mapped the presence of plant individuals (ramets) in transects and grids. Data were analyzed by variography and information theory models. The base-line spatial data were re-sampled with different resolutions (computerized sampling) that enable us to fit our analyses to the changing natural characteristics scales of field patterns. We used spatially explicit individual-based simulations (with contrasting parameters) for representing types of community models and fitting field data to modeled patterns.

Considerable spatiotemporal contingencies were found in old field succession with medium-scale patchiness (with ca. 5–15 m patch sizes in space and 3–5 years temporal patch-sizes). Our results provide evidence that medium-scale constraints used in null models may develop as dynamic self-organized structures emerging from fine-scale biotic interactions. The overall spatial dependence of species varied between communities. The highest spatial dependence appeared in mid-successional communities. In contrast, low spatial dependence was found in the meadow steppe community, probably due to emergent neutrality. Transient communities showed divergent trajectories in the coenostate space while mature communities expressed less variability with convergent trajectories. Simulations with spatially explicit individual based models demonstrated how the effects of small interactions, appearing as “insignificant” deviation from stochastic references in snapshot analyses, accumulated over time and become significant after 10–20 years.

Traits supporting long-term survival of grassland specialist plant species in habitat islands embedded in agricultural landscapes

Balázs Deák^{1*}, *Zoltán Rádai*¹, *Zoltán Bátori*², *András Kelemen*^{1,2}, *Katalin Lukács*¹, *Réka Kiss*¹, *István Elek Maák*², *Orsolya Valkó*¹

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Keywords: habitat island, refuge site, verge, functional traits, phylogenetics, conservation, environmental heterogeneity, steppe

In transformed landscapes, grassland biodiversity is often restricted to habitat fragments that are inadequate for arable use or for urban development. In continental parts of Eurasia, the more than half million ancient burial mounds (called “kurgans”) built by nomadic tribes of the steppes are amongst the most widespread landmarks that function as habitat islands and provide refuge for dry grassland species in agricultural landscapes. In our study by using plant functional groups and functional traits, we aimed to reveal the ecological and evolutionary processes shaping the structure and the composition of assemblages of grassland specialist plant species on kurgans that are embedded in the agricultural landscapes of East-Hungary. As a comparison, we also studied the vegetation of roadside verges and pristine extensive grasslands in the same region. We found that despite their small size, due to the lack of human disturbances and high microhabitat diversity kurgans can maintain a high species richness and percentage cover of specialists, especially when compared to verges. We revealed that assemblages of specialist plants on kurgans are characterized by traits typical to island-like habitats such as self-compatibility, large seed mass and tall stature. Kurgans and extensive grasslands were characterized by higher functional diversity (both at the level of single traits and multi-trait based functional dispersion) which is probably due to the higher level of environmental heterogeneity compared to the homogeneous environment in verges.

Acknowledgments

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Factors affecting species richness and composition of Italian arable plant communities across different agricultural landscapes

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Keywords: biodiversity drivers, land use, segetal plants, weed communities

Arable plants are of great conservation and ecological interest due to their support to biodiversity and provision of ecosystem services. In springs of 2018 and 2019, we surveyed arable plant communities in winter cereal and legume crops of mainland Italy using 149 plots of 1×16 m size (one per field, Fig. 1a), oriented along seed-drill lines and positioned in the inner part of the field. We collected sets of agronomic, spatial, environmental, and landscape variables to check their explanatory ability on patterns of species richness and composition of the surveyed communities. Land use was visually interpreted using recent satellite images in a GIS environment, by using a buffer circle of 400 m radius around the field centre. Landscape patches were classified according to seven land use categories.

We used Redundancy analyses (RDA) to assess the effect of the variables on the richness and composition of the surveyed communities. We assessed the significance of RDAs by means of anova tests. Variation partitioning was carried out to highlight the relative contribution of each set of variables to the overall variation in species richness and composition, removing non-significant variables. The analyses were performed in the package *vegan* of R-project.

The variables had a higher explanatory power on richness (46% of explained variation) than composition (27%). Some agronomic variables (crop species and amount of fertilizers per hectare, the latter used as a proxy of agricultural intensity) explained differences in species composition, but not in species richness. Some landscape variables (type of rural area, landscape complexity – measured through the Shannon index and the total number of patches – and abundance of different land use types) did not significantly affect community composition. On the contrary, species richness was positively related to the abundance of woody elements (shrublands, hedges, forests, isolated trees) in the landscape (Fig. 1b).

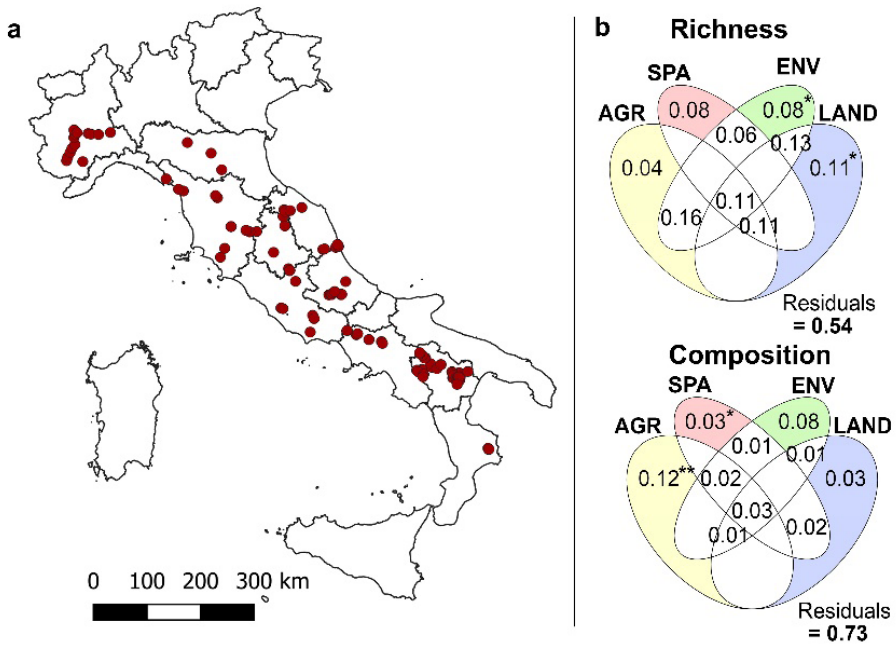


Fig. 1. a) Distribution of the plots in Italy; b) Venn diagrams showing the proportion of explained variation by the selected groups of variables on species richness and composition; * = $P \leq 0.05$; ** = $P \leq 0.01$

Silvicultural management does not affect biotic communities in conifer plantations in the short-term: A multi-taxon assessment using a BACI approach

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Keywords: biodiversity monitoring, Black pine forest, surrogate, thinning

Biodiversity maintenance is a key strategy for sustainable forestry in both above-ground and below-ground biotic communities. However, few studies applied continuous monitoring to analyse the responses of different taxonomic groups to silvicultural treatments. We studied the short-term effects of three silvicultural treatments (no thinning, thinning from below, and selective thinning) on taxonomic richness and composition in two *Pinus nigra* J.F. Arnold plantations in Tuscany (Italy). We conducted a 1 year before–3 years after control-impact (BACI) experiment with a complete randomized design and analysed the responses of five different taxonomic groups (bacteria, nematodes, microarthropods, mushrooms and vascular plants (overstorey and understorey), along with the patterns of different structural variables. The silvicultural treatments induced a sudden decrease of many parameters such as number of trees per hectare, basal area, and standing volume, with a direct impact on the Photosynthetic Active Radiation on the ground. Despite this, biological communities showed a high resistance to the tree thinning intensities. Indeed, none of the thinning treatments significantly affected the different communities in the short-term, neither regarding taxonomic richness nor composition. The different taxonomic groups showed a similar, low or null, sensitivity to forest management, and thus a high congruence in their responses.

Revisiting discrepancies between stochastic agent-based and deterministic models

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Keywords: stochastic and deterministic models, logistic growth, abiotic environments, spatial dispersal process

Predicting which species will present (or absent) across geographical regions, and where, remains one of the important issues in ecology. From a methodical viewpoint, one of the concerns in examining species presence-absence across an environmental gradient is about the robustness of model-based predictions, which are given by distinct modelling frameworks used. Generally, different complexities and ecological factors are incorporated into such models e.g., abiotic environments, spatial dispersal process and stochasticity. Motivated by these ecological issues, we revisit a single-species logistic growth problem by employing stochastic agent-based model (ABM) and deterministic system, and extend these frameworks to incorporate the effects of spatially-changing environments. We observe that our ABM, which is formulated using random walk theory and birth-death process, demonstrate important qualitative behaviours that are consistent with the underlying theories of stochastic process. The results of ABM with large population sizes also agree with those of the deterministic equation. However, some discrepancies are observed when the population size is small. The ABM densities seem to underestimate the deterministic solutions, which illustrate the effects of stochasticity on small populations with some individuals may go extinct simply by chance. To quantify the underestimation of ABM as opposed to deterministic predictions, we employ certain probabilistic techniques: while the means of quasistationary probabilities distribution appear to give a counterintuitive prediction particularly near the edge of species ranges, the expected values given by state probabilities distribution are in agreement with the ABM densities observed for small population sizes across spatial locations. These salient observations depict emergent behaviours of stochastic ABM, which can contribute to additional insights on the dynamics of ecological species. It also shows how such small-scale interactions coupled with local dispersal and spatial phenomena occurring at a microscopic-level can affect macroscopic-level dynamics. As such, comparing and contrasting the dynamics of different models can help in understanding the generality of ecological results, and may offer important insights into the robustness of model-based predictions of species presence-absence.

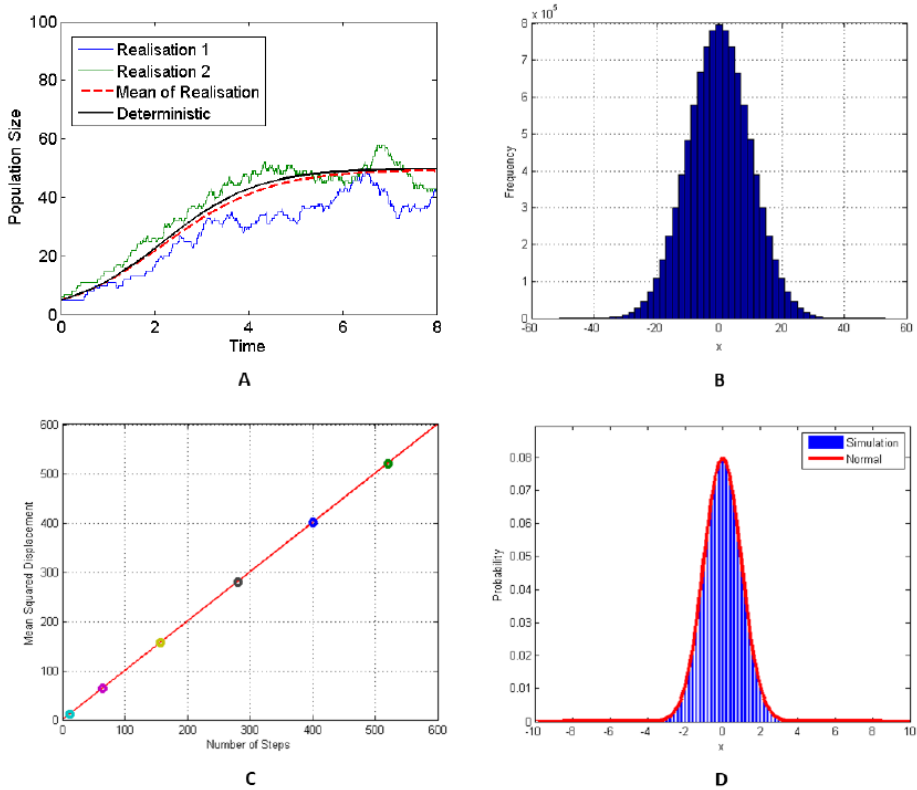


Fig 1. The stochastic simulation for birth-death process and simple random walk theory, which form the principles of our stochastic ABM. (A) The stochastic simulation (over 10 000 realizations) for the birth and density-dependent death process, with $r = 1$, $K = 50$, and initial condition $n_0 = 5$. (B) (respectively, (D)) The frequency (respectively, probability distribution) of stochastic simulation (over 10 million realizations) for simple random walk along one-dimensional lattice with step length of 1 (respectively, 0.1) after 100 time steps, given that the probabilities of moving left and right: $l = r = 0.5$; (C) The stochastic simulation showing mean-squared distances (MSD) equal to different numbers of random steps made by the individual species, which are represented by different colour circles.

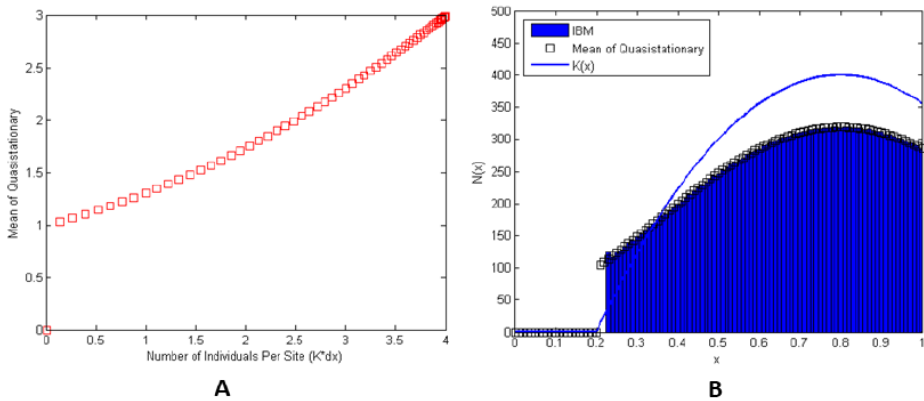


Fig 2. Mean of quasistationary probabilities distribution of the stochastic ABM. (A) Mean of quasistationary distributions (red squares) for distinct number of individuals per site; (B) The mean of quasistationary probabilities (black squares) is fitted on the average density of non-extinct ABM (bar graphs) with deterministic solution and carrying capacity of species (solid curve) is also shown in the diagram. Other parameter values as in Table (1).

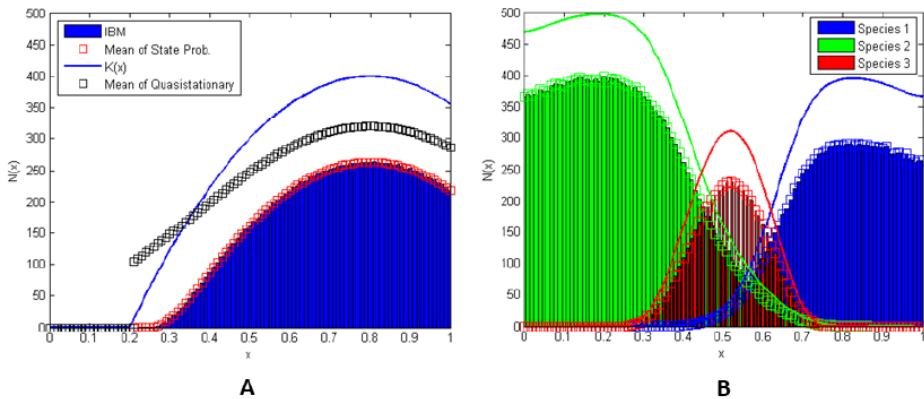


Fig. 3. The spatial distributions of species calculated using our single-species stochastic ABM and a three-species stochastic ABM¹. (A) Comparison of 5000 averaged realizations of single-species ABM (bar graphs), means of state (red squares) and quasistationary (black squares) probabilities. (B) For further illustration of small populations scenario, the results from 5000 averaged realizations of the three-species stochastic ABM (bar graphs), deterministic model (solid curves) and mean of state probabilities (squares) at final time $t = 300$ are also shown, which is based on recent ecological studies¹. Other parameter values as in Table (1).

Table 1 Parameter values.

Symbol	Description	Population Size	
		Large	Small
r	The intrinsic growth rate of species	1	1
K_{max}	Maximum carrying capacity of species	4000	400
x_T	The most favourable location for species	0.8	0.8
w_T	The width of the fundamental niche for species	0.6	0.6
D	Diffusion coefficient	0.001	0.001
Δx	Space step	0.01	0.01
Δt	Time step	0.0001	0.0001
v	Probability of moving left or right	0.001	0.001

Acknowledgments

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Plenary Talk

Tuesday, 14 December

Putting ecological theory to work for conservation

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Keywords: biodiversity conservation, ecosystem services, ecological stability, ecological theory, species losses, food webs

Two grand challenges of our time are climate change and biodiversity loss. This talk focuses on the fundamental question of: to what extent can ecological theory help us understand the consequences of these global changes to inform conservation? I will present two examples investigating this larger question: 1) the consequences of extreme events in boreal forests for ecological stability versus ecosystem services outcomes' and the 2) vulnerability of food webs versus ecosystem services to species losses in coastal food webs. In the first case, commonly used ecological measures fall short of predicting disturbance impacts on forest ecosystem services-- exhibiting low correlations or systematic biases. In the other case, food web robustness is strongly related to ecosystem service robustness in aggregate, but different types of ecosystem services vary in their robustness to species' losses. Together, this work highlights that the complex nature of socioeconomic and ecological systems creates challenges for extrapolating ecological theory to understand threats from global change for conservation goals. Thus, I will outline exciting research avenues for discussion on how ecological theory to contribute to conservation and interdisciplinary research in our inherently socio-environmental systems.

Session II – Biodiversity and Ecosystem Function

Tuesday, 14 December

Towards resolving a conflict between diversity and dominance effects on the resource use efficiency of phytoplankton

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Keywords: BEF, evenness, rare taxa, taxonomic richness

The biodiversity-ecosystem functioning (BEF) theorem proposes that biodiversity enhances community resource use efficiency (RUE) and ecosystem stability. Amounting evidence from empirical datasets suggests that RUE is enhanced by dominance as well. As dominance is associated with competitive exclusion and biodiversity loss, positive dominance-RUE association seems to be in conflict with the well-known BEF relationship. Recent research implies that BEF relationships are not necessarily positive based on realised diversity in field data, and rather, BEF research should focus on local species pool dynamics.

Here we evaluate a large-scale phytoplankton data set from Fennoscandia, covering a natural diversity gradient: from low diversity in Norway to high diversity in Finland. Data suggest that phytoplankton resource use efficiency (RUE) scales positively with richness and dominance (both in the country-level and pooled data sets). Accordingly, low dominance coincides with low taxonomic richness, while towards East or more diverse assemblages, diversity increase comes together with dominance increase. Evaluating the potential effect of the local (pooled richness per lake) and regional (approximated from regionally averaged productivity) species pools in the most extensive Norway dataset, a pattern emerges suggesting that the realised diversity of phytoplankton is associated positively to dispersal (regional processes), while the most efficient assemblages in resource use appear under a smaller-sized local species pool (local processes).

Our finding can be interpreted in multiple ways, (1) community assembly processes (e.g. competition) are directly linked to dispersal, (2) further local conditions such as spatial and temporal environmental heterogeneity at the level of individual habitats affect species coexistence, (3) phytoplankton always contain active (associated with dominance) and non-active (associated with diversity) taxa.

Open field mesocosm experiment provides new opportunities to investigate the effects of soil-dwelling mesofauna on soil N-cycling

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Keywords: soil microarthropods, field mesocosms, nitrate, ammonium leaching, N-cycling, defaunation

Soil microarthropods have significant indirect role in soil N-cycling as they influence decomposing microbes. Soil-dwelling microarthropods have greater role in N cycling processes in N-limited conditions (Filser 2002) but it has not been tested yet. It is difficult to study the hidden life of small sized microarthropods. Their influence on N-cycling is known mainly from laboratory microcosm experiments but these systems mostly provide artificial conditions. We should solve the difficulties of studying the ecological effects of these animals in the field.

We developed an open field mesocosm system with three advantages which together are new for field experiments of soil microarthropods. First, in the mesocosms, abundance of soil mesofauna was kept significantly lower than in the natural communities to investigate the effects of their absence. Second, plants grew in the semi closed systems. Third, a percolation lysimeter was installed under each mesocosm to collect percolated soil water containing leached NO_3^- and NH_4^+ ions. In addition, applied N-fertilisation assured difference in N-sources between mesocosms. Our three-year-long study included several short experiments to test the equipments and detect soil mesofauna, plant biomass and N-content, and in addition, soil and soil water nitrate and ammonium ion content. The experiments were conducted in two locations in Hungary: in a chernozem and a sandy soil. We hypothesized that higher abundance of soil microarthropods cause higher N-ion leaching, mainly in N-limited plots.

The open field mesocosms are promising tools to study the role of soil-dwelling mesofauna in soil ecological processes. We solved the problem to keep the abundance of soil mesofauna lower than in control plots, plants successfully grew in the semi closed systems and in the meantime, soil water samples could be taken from below the mesocosms with percolation lysimeters to detect leached NO_3^- and NH_4^+ . We found differences between the results according to the study years and the two soil types. First year was mainly about testing the mesocosm equipment. In the second year, chernozem soil rather showed those patterns we expected, as the leached N ion concentrations were higher for mesocosms including higher abundance of mites and springtails. The expected patterns were less pronounced in sandy soil. In the third year, both the soil types showed the patterns we expected. However, N-limited plots did not show the more significant role of soil-dwelling microarthropods in N-cycling compared to fertilised plots as added N-fertiliser did not influence the effect of soil microarthropods. This study was simultaneously a field experiment and an equipment innovation. Therefore, mainly in the first two years, the results reflected the problems of the development but in the final year, the patterns can be considered more reliable. Consequently, higher abundance of soil-dwelling mites and springtails cause higher NO_3^- and NH_4^+ even in field conditions, therefore, these animals have important role in soil N-cycling.

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Do mycotoxigenic fungi use heterogeneities in arable lands to overwinter? – A two-year analyses of different *Fusarium* species on herbaceous plants and weeds at the edges of kettle holes in the autumn and winter months

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Keywords: kettle holes, *Fusarium*, overwinter, inoculation

During a field survey in the autumn- and winter months of 2018 and 2019/2020, 9 different kettle holes in winter wheat fields were examined. The study aimed at analysing the abundance and diversity of *Fusarium* species on plants growing permanently at the edges of kettle holes.

Kettle holes, often waterfilled depressions in the landscape, are regarded as hot spots for biodiversity in intensively agriculturally used areas in Europe. Northeast Germany is spotted with up to 40 kettle holes per km².

Beside the ecosystem services provided by them, kettle holes are also suspected to enhance fungal spread and thus increase the infestation risk of adjacent agricultural fields. Kettle holes have various effects on the distribution of diseases through their water flow and temporal flooding as well as through the increased air humidity in their surrounding area. They can influence the biodiversity of all organisms, which are influenced in their development by water or air humidity.

Especially mycotoxigenic fungi like *Fusarium* spp. are significantly influenced by the moisture conditions within a field. In the case of these fungi, different herbaceous plants and grasses at the edges of kettle holes can be considered as a permanent habitat for the development and spore production of *Fusarium*, especially over the autumn and winter months when the fields were not tilled.

Thus, the kettle holes could be a source of inoculation for a long-lasting infection of the neighboring fields and a risk for a higher mycotoxin accumulation of the crops.

At the edge of each kettle hole, 3 different plants were collected and investigated by culture-dependent and culture-independent methods to determine the abundance and the diversity of *Fusarium*. The collected data were analyzed to identify differences in the occurrence and diversity of the *Fusarium* genera influenced by different weather conditions and host plant species.

Preliminary results show that both autumn and winter seasons plants of the genus *Poa*-*ceae* have a *Fusarium* load that is higher than on herbaceous plants. The total fungus load in autumn 2019/winter 2020 was significantly higher than in autumn/winter 2018 due to precipitation.

In 2018, 11 different *Fusarium* species were detected, mainly *F. sporotrichioides*, *F. avenaceum* and *F. equiseti*. In 2019/2020 we determined also 11 species of the *Fusarium* genera, while *F. sporotrichioides*, *F. graminearum* and *F. equiseti* were most frequent.

Soil nematode communities structure affected by *Fallopia japonica* (Houtt.) Ronse Decr. invasion

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Keywords: Nematoda, alien plant invasion, *Fallopia japonica*

The impact of invasive plants on soil ecosystems has attracted world-wide attention in the last decades. Exotic plant invasions often have dramatic impacts on the resident vegetation by modifying its composition and structure (Levine et al. 2003). *Fallopia japonica* is one of the hundred worst invasive species in the world (Lowe et al. 2000), is a globally successful and spreads rapidly after introduction. In this study, we investigated the communities of soil nematodes in the forest habitats invaded and uninvaded by *F. japonica* in urban ruderal part of the Tatra National Park in northern Slovakia. We established ten independent plots and collected soil core samples for characterizing the nematode communities. We collected soil samples for nematode analysis from five plots at a site invaded by *F. japonica* and soil samples from five plots at an uninvaded site containing dominant native plants. We found that *F. japonica* invasion had a negative impact on the native plant communities and on the structure of soil nematode communities during the three years of our study. The impact of *F. japonica* on these communities did not differ among sampling years, indicating a persistent disturbance of the ecosystem and soil food webs in comparison to the uninvaded control plots. Overall nematode abundance and nematode biomass were significantly lower in invaded than uninvaded plots, a weighted faunal analysis characterized the food webs of invaded plots as poorly developed or highly disturbed with prevailed bacterial decomposition pathway.

Acknowledgments

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Functional diversity increases the robustness of tritrophic plankton food webs to a nutrient pulse

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Keywords: functional diversity, trait variation, tritrophic food web, pulse perturbation, nutrient spike, robustness, regime shift

Biodiversity decline causes a loss of functional diversity, which may hamper ecosystems' ability to buffer environmental changes. Previous work studying how functional diversity influences the response of food webs to disturbances have mainly considered systems with at most two functionally diverse trophic levels. We investigated the effects of functional diversity on robustness, i.e. resistance, resilience and elasticity, using the tritrophic plankton food web model developed by Ceulemans et al. (2019)¹. We compared a non-diverse food chain to increasingly more diverse food webs with three adaptive trophic levels. The species fitness differences were balanced through trade-offs between defense/growth rate for prey and selectivity/half-saturation constant for predators. To capture a wide range of dynamical behaviours, we varied the Hill exponent of the intermediate and top functional responses. We found that a more diverse food web was generally more resistant and resilient but its elasticity was context-dependent. Particularly, functional diversity reduced the probability of extinction of an entire trophic level and the probability of a regime shift towards a non-desirable alternative state. Despite the complex influence of the shape and type of the dynamical attractors, the interaction between basal and intermediate species, which was regulated both by the diversity present and by the top trophic level, consistently determined the robustness against a nutrient pulse. Overall, this study confirms a dangerous feedback loop: as functional diversity declines, robustness decreases, thus extinction risk and food webs' vulnerability to future perturbations increase.

Acknowledgments

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Understanding the interaction between *Metisa plana*, its hyperparasitoids and primary parasitoids from Good Agricultural Practices (GAP) and non-GAP of Malaysian oil palm plantations

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Keywords: bagworm, biological control agent, golden crop, natural enemy, pest insect

The bagworm species, *Metisa plana* (Lepidoptera: Psychidae) is a major pest of oil palm. The existence of its natural enemies (parasitoids) in the ecosystem is reliant on the presence of their host (*M. plana*) and food supplies. Even though several ecological studies have been conducted on *M. plana*, no detailed information on their food interaction has been known. Relying on their importance as a pest of the Malaysian golden crop, the interaction between the *M. plana*, hyperparasitoids, and primary parasitoids is essential to be studied as the model system for the community ecology, specifically in the oil palm ecosystem. Therefore, in this study, we have listed two main objectives, 1) to obtain the diversity of *M. plana* parasitoids from Good Agricultural Practices (GAP) and Non-GAP plantations, and 2) to investigate the relation between hyperparasitism and primary parasitism. The sampling was conducted from six oil palm plantations throughout Peninsular Malaysia (3 GAP and 3 Non-GAP plantations). As a result, a total of 1199 individuals of the hymenopteran parasitoids belonging to 8 families and 16 species, namely *Dolichogenidea metesae*, *Apanteles alluella*, *Apanteles* sp., *Aulosaphes psychidivorus*, *Paraphylax varius*, *Buysmania oxymora*, *Goryphus bunoh*, *Brachymaria carinata*, *Pediobius anomalus*, *Eupelmus cotoxanthae*, *Eurytoma* sp., *Elamus* sp., *Pediobius imbrues*, *Sympiesis* sp., *Tetrastichus* sp. and *Aphanogmus thylax* were successfully collected by using malaise traps for 12 months durations. Based on the Shannon-Wiener diversity index (H'), the diversity of the parasitoids was significantly higher ($p = 0.0001$, $p \leq 0.05$) in GAP plantations compared to the non-GAP plantation. The data collection presented 32.19% for the hyperparasitoids and 67.81% for the primary parasitoids, respectively. Interestingly, the analysis showed a strong negative correlation between hyperparasitoids and the primary parasitoids ($R = -0.807$, $R^2 = 0.6509$) from the GAP plantation. For the non-GAP, the insecticide application issue was assumed to be the main factor for the non-correlated data. These findings have presented the latest information on the diversity of the *M. plana* parasitoids towards contributing to Integrated Pest Management (IPM) strategy for the success of the parasitoid's rearing program.

Tree species to explore ecosystem functioning: sensitivity to air pollution based on APTI

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Keywords: urbanization, chlorophyll, plants, air pollution

Monitoring air pollution and environmental health are crucial to ensure viable cities. We used the Air Pollution Tolerance Index (APTI) to study the sensitivity of tree species to the air pollution. Black locust (*Robinia pseudoacacia*), silver maple (*Acer saccharinum*), common lime (*Tilia x eurpaea*), plane maple (*Acer platanoides*), common ash (*Fraxinus excelsior*), common birch (*Betula pendula*), western hackberry (*Celtis occidentalis*) and common plane (*Platanus x acerifolia*) leaves were collected near to the city center with a high intensity of vehicular traffic in Debrecen, in Hungary. APTI values were calculated based on the ascorbic acid content, total chlorophyll content, pH of leaf extract and relative water content of the tree leaves. We demonstrated that most tree species were sensitive, except the silver maple and common plane. The silver maple was moderately tolerant, while the common plane was intermediate based on the APTI value. There was a significant difference among species based on leaves for the ascorbic acid content, for the pH of the leaf and for total chlorophyll content of leaves. Ascorbic acid content was the highest in common birch leaves, the pH was the highest on the leaves of black locust and western hackberry. The total chlorophyll content was the highest on the leaves of plane maple. We found that tree leaves are reliable bioindicators of urban air pollution. The APTI values are useful indicators to select pollution tolerant species used for urban greening and/or selecting species for green belt development. Based on the value of APTI the silver maple and common plane species are recommended as pollutants accumulator species, while other studied species with lower APTI values are especially useful as bioindicators of air pollution and as a proxy for urban health.

Session III – Ecological Networks

Tuesday, 14 December

Revealing keystone species with network index can be tricky

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Keywords: network index, eDNA, keystone species, indirect interactions

Network analysis plays an important role in community ecology. Hidden patterns and keystone species can be detected. The usage of environmental DNA (eDNA) becomes more and more common which implies large community datasets. Evaluating this type of data requires state-of-the-art methods. There are many indices to assess a given community by computational methods, however finding the most suitable for one's case can be challenging. Here, we compare different network analysis indices on a marine association network.

Djurhuus et al. (2020) studied the proportional abundance of taxa in a marine setting based on eDNA metabarcoding. They identified six subnetworks representing different communities and their changes with time. The resulting dataset was published including correlation networks, trophic linkages and environmental parameters. We gathered the most widely used network indices and tested against some less known but favorable ones.

Our results reveal keystone species which are in some cases different compared to those listed in the paper. Indices that take account of indirect interactions highlight the role of microbes more significantly. We demonstrate how different indices return different results.

Determining keystone species is of high importance in community ecology. Meaningful interactions among species could stay hidden when investigating with classical statistical methods. Hence, using calculations which consider also indirect connections are advised. We advocate developing new indices and combining existing ones to be able to use them in different scenarios.

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Measuring functional diversity in food webs

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Keywords: functional diversity, food web, network position, role

Biodiversity can be measured from various perspectives. One of them, functional diversity, quantifies the heterogeneity in species traits in an ecosystem. Here we present an index for measuring functional diversity from the network perspective in food webs. Species differ in their network positions in a food web, this then attributes to differences in species' interactors. Functional diversity is then quantified basing on species' interactor profiles. In our study we analyse 92 food webs, and for each quantify its functional diversity from the network perspective. We also quantify several global network properties, and establish their relationship with our proposed measure of functional diversity.

Building weighted networks for plankton communities from semi-quantitative data

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Keywords: semi-quantitative data, plankton networks, iterative approach, ecological models

Quantitative weighted network models are valuable approaches widely used for understanding properties of the system, including health and good environmental status of marine ecosystems. Although plankton community data in terms of composition and abundance are widely available additional semi-quantitative ecological information are needed to build weighted networks for plankton communities (D'Alelio et al. 2016a). The goal of this study is the definition of an approach for developing quantitative networks from semi-quantitative data of plankton communities. The approach is based on a controlled interactive process that is used to develop synthetic networks that are then tested for realism using simple and general emerging properties by node and by the whole network as validating tests.

We used realistic data of the plankton community that consist of biomass values, realistic ranges of the production rate per unit of biomass as well as rates of mixotrophy (from 0 to 1, with 1 = total phototrophy and 0 = total heterotrophy) specific for all taxa of the plankton community. For each consumer realistic range for consumption per unit of biomass and unassimilated rate were given (D'Alelio et al. 2016b). Furthermore, semi-quantitative indications of the strength of interactions between each taxa were defined (improbable/weak link, likely/important link, very likely and strong link). An iterative MCMC approach was used by extracting independent and random values for parameters from their range, through a uniform distribution, and assigning random quantitative values of diet proportions (between 0 and 1) constrained by semi-quantitative strengths. Synthetic models were tested for their respect of energy conservation principles and physiological realism i.e., maximum gross food conversion efficiency, positive emerging respiration and natural mortality for each living functional group.

A large group of valid models (ensemble of 1000 networks) were obtained for each site using the process considering opportunity for some imports to occur or not. Whole network indicators we applied to valid models, e.g., the community primary production and respiration rate (Odum 1969), ascendancy and overhead (Costanza and Mageau 1999). Preliminary results on plankton community networks for a coastal lagoon case study indicate a system, far from its climax, with great potential for further development. The procedure developed could be applied to several marine sites possibly linked to capabilities of the system to provide services.

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Application of three modelling frameworks for aquatic ecosystems: a network-based approach

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Keywords: aquatic ecosystem, Ecopath, loop analysis, STELLA

Freshwater ecosystems are under multiple anthropogenic stressors (1) and it is crucial to find methods to better describe, manage, and sustain aquatic ecosystems. Ecosystem modelling has become an important tool in integrating trophic relationships (e.g. food webs), assessing important nodes using network analysis, and making predictions via simulations. Fortunately, several modelling techniques exist, but the question is which approach is relevant and applicable when?

In this study, we compare three modelling frameworks (Ecopath with Ecosm (EwE), loop analysis in R, and STELLA software) using a case study of a small aquatic network (<16 nodes). We approach this topic from a methodological aspect by describing the data requirements and by comparing the applicability and limitations of each modelling approach. When data are limiting, loop analysis can provide qualitative predictions, while the other two methods provide quantitative results, yet rely on more data. Each modelling framework has its specific focus, but some functionalities and outcomes can be compared (e.g. mixed trophic impact vs loop analysis). Various other considerations will be compared in detail by discussing the results of our preliminary models.

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Plenary Talks

Tuesday, 14 December

The wonder of the Jaccard coefficient: from alpine floras to bipartite networks

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Keywords: a, b, c

$$S = a / (a+b+c) = 1 - (2\min\{b,c\} + |b-c|) / (a+b+c)$$

Microbial communities in the sea

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Photosynthetic microbes in the oceans rival terrestrial plants for their contributions to global photosynthesis and carbon dioxide uptake. Yet the physical interactions between different microbial cells that determine their fate(s) are typically not known, in large part because such interactions cannot be captured effectively in laboratory experiments, and many marine microbes still remain uncultured. Interactions between community members influence not just community structure but also biogeochemical processes and cycling in nature. Here we will discuss recent advances in elucidating cell-to-cell and cell-to-virus interactions, their potential functional significance from a biochemical perspective, and their broader ecological importance with respect to future plankton trajectories.

Side Events

Virtual Sightseeing Tour – Highlights of the Buda Castle quarter

14 December, 12:00–13:00

Have a glance at the exciting main sites of the Buda Castle district!

During this live virtual tour of the Buda Castle we walk you through the key sites of the Buda Castle hill neighbourhood. We start at the Fisherman’s bastion taking in the views of Pest. After that we walk by the iconic Matthias church and the statue to the Holy Trinity before walking down the medieval streets of the castle’s residential area to reach the Alexander Palace which currently serves as the Presidential Palace. During the walk we can cover various topics about Hungary too, like the country’s history, Hungarian gastronomy, and so on.

Tour organized by Behind Budapest (<https://behindbudapest.hu/en>)

Your tourist guide will be Ádám. (<https://behindbudapest.hu/en/tourist-guides/>)

Introduction of an Ecology Lab in Hungary

14 December, 17:30–17:35

Lendület Seed Ecology Research Group

Seeds play a crucial role in vegetation dynamics and ecosystem functioning by allowing persistence, recruitment and mobility in plant populations and facilitating meta-population dynamics. The ‘Lendület’ Seed Ecology Research Group is interested in studying the ecological aspects of seed dispersal in space and time and uses the results for developing a conceptual framework on seed-based ecosystem engineering in order to maximise the diversity and resilience of communities. We use grasslands as model system, as they are diverse and dynamic habitats where recruitment by seed is a major driver of vegetation dynamics. In a series of observational and experimental studies at multiple spatial scales we evaluate the role of seed bank, seed dispersal and seedling establishment in community assembly, and their utilization in restoration ecology and diversity conservation. We hope that our results will give new dimensions to seed-based conservation and restoration science by developing new tools, such as activating deeply buried seeds, designing seed mixtures that maximise resilience or using animal perturbations as establishment gaps.

If you are interested in our research, please visit our [research blog](#) or [facebook page](#).