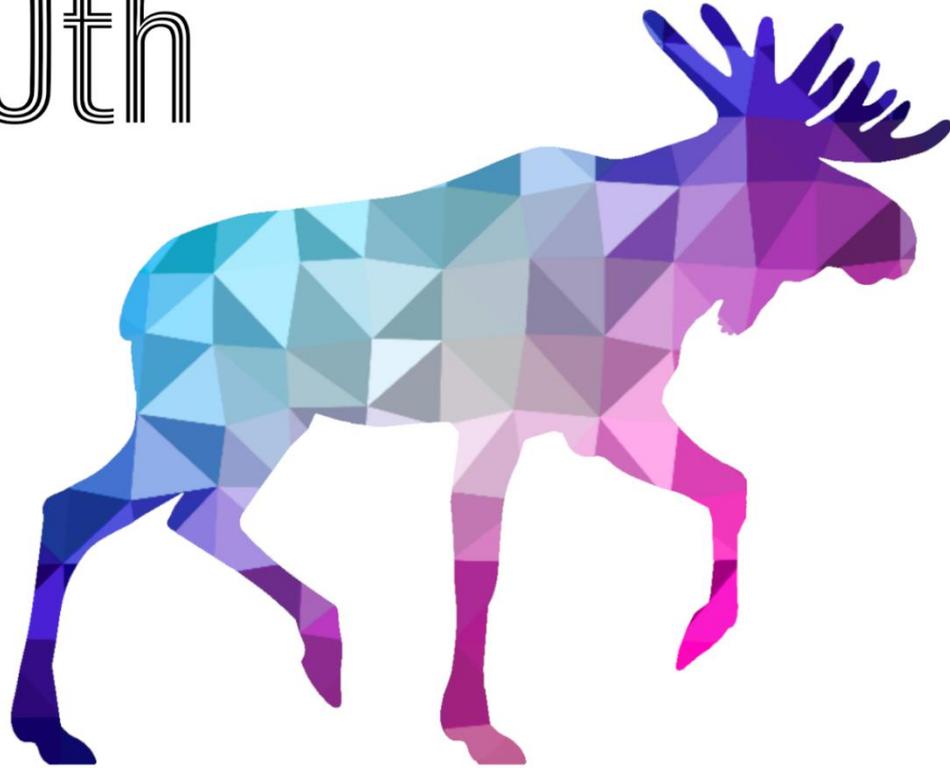


Programme and Abstract Book

30th



SPRING SYMPOSIUM

Online 8-10 March 2021



UNIVERSITY OF HELSINKI

WELCOME

We are honored to welcome you to the 30th Spring Symposium. The annual meeting is organized by – what is nowadays– the Doctoral Programme in Wildlife Biology Research (Finnish acronym LUOVA), University of Helsinki. Every year, the Spring Symposium brings together PhD and MSc students from a range of research fields related to ecology, evolution, systematics, and nature conservation. The Spring Symposium provides the students an opportunity to present their research in a friendly atmosphere and receive invaluable feedback on scientific content and presentation skills from fellow students, colleagues, supervisors and invited external evaluators. The best talk will be awarded with Olli's prize, a sponsorship for attending an international conference.

This year is exceptional for the Spring Symposium as the event is organized remotely for the first time in its history, due to the ongoing COVID-19 restrictions. Despite the new format (or perhaps encouraged by it) we received a flood of registrations, and the programme is now fully packed with enthusiastic presenters for the whole three days. Thank you all for signing up! The new format also brings slight changes to the evaluation system. To avoid online conference fatigue, this year's evaluation duties are distributed to an extended group of people that includes both our international keynote speakers as well as representatives from the University of Helsinki. Still, every presenter will receive feedback for their talk from four evaluators including at least one keynote speaker.

The 30th birthday of the Spring Symposium is also celebrated online with a special event on Monday evening. The Symposium will end in an online prize-giving ceremony and hangout session on Wednesday evening. We hope to see your virtual presence on both occasions!

In this booklet, you can find the programme of the symposium as well as all abstracts listed chronologically. We hope that you will join the poster session and can attend as many talks as possible to provide valuable feedback to the students as well as engaging in lively discussions.

The Organizing Team,

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Clio Hall

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Sonja Saine

Nadja Verspagen

ACKNOWLEDGEMENTS

The organizing team wants to thank:

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Cristina Banks-Leite
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The 29th Spring Symposium organizing team: Katarina, Elena, Antti, Marju, Luisa, Kati and Miisa (for sharing their wisdom)

and all students who contributed to the 30th Spring Symposium

Acronyms for affiliations

DENVI	Doctoral Programme in Interdisciplinary Environmental Sciences, UH
EEB	Master's Programme in Ecology and Evolutionary Biology, UH
EPHB	Doctoral Programme in Environmental Physics, Health and Biology, UEF
GeoDoc	Doctoral Programme in Geosciences, UH
IPS	Master's Programme in Integrative Plant Sciences, UH
LUOMUS	The Finnish Museum of Natural History, UH
LUOVA	Doctoral Programme in Wildlife Biology Research, UH
MMB	Master's Programme in Microbiology and Microbial Biotechnology, UH

CONTENTS

PROGRAMME.....	4
KEYNOTE SPEAKERS.....	7
ABSTRACTS.....	8

MONDAY 8.3.

KEYNOTE 1.....	8
SESSION I.....	8
KEYNOTE 2.....	13
SESSION II.....	14

TUESDAY 9.3.

KEYNOTE 3.....	18
SESSION III.....	19
SESSION IV.....	23

WEDNESDAY 10.3.

KEYNOTE 4.....	27
SESSION V.....	28
SESSION VI.....	32
SESSION VII.....	36

POSTERS.....	39
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PROGRAMME

MONDAY 8.3.

10:00 OPENING

Opening words by the director of LUOVA Mar Cabeza-Jaimejuan

10:10 KEYNOTE 1

Naiara Rodríguez-Ezpeleta Modernizing marine management using innovative genomic

11:10 BREAK

11:20 SESSION I

Wenfei Liao Emergent plants enhance urban wetland biodiversity by providing prey refuges

Ella von Weissenberg Combined effect of salinity and temperature on reproductive success and oxidative stress in brackish-water copepods

Andrew House Sex-specific lipid profiles in the muscle of Atlantic salmon juveniles

Vasco Veiga Branco The age of the cyborg: machine learning in wildlife conservation

12:40 LUNCH

13:30 KEYNOTE 2

Samniqueka Halsey Understanding disease emergence patterns by combining long-term data sets and computational approaches

14:30 BREAK

14:40 SESSION II

Nadja Verspagen An altitudinal cline in the Glanville fritillary butterfly: temperature but not altitude affects performance

Miriam Torres Miralles Contribution of High Nature Value farming systems to sustainable livestock production

Bastien Parisy Interactions between plants and microbes as determinants of Arctic vegetation dynamics

Susu Rytteri Butterflies in changing weather conditions: implications for ecology and conservation

16:00 BREAK

17:00 BIRTHDAY PARTY

Anniversary talk by Spring Symposium veteran Liselotte Sundtröm

LUOVA Pub Quiz

PROGRAMME

TUESDAY 9.3.

10:00 KEYNOTE 3

Cristina Banks-Leite How much habitat do we really need to preserve biodiversity?

11:00 BREAK

11:15 SESSION III

Sirke Piirainen How to validate predictive species distribution models?

Michelle García Arroyo Different tolerance to humans? Alert and flight initiation distances of two bird species

Niko Johansson The role of woodpeckers as dispersal vectors for epiphytic organisms

Federica Manca Investigating ecological networks of macrophytes and associated fauna in the Baltic Sea

12:45 LUNCH

13:45 SESSION IV

Kati Suominen Why citizens giving you sh*t is contributing to understanding bat ecology in Finland

Katarina Meramo The response of functional diversity of bat communities to anthropogenic disturbance in Caatinga ecoregion, northeastern Brazil

Thais Ferreira-Araújo The Lake Pulmanki flounder: ecology, adaptation, and speciation

Andreas Otterbeck Climate induced range shifts explain trends in bird migration passage dates

15:15 BREAK

15:30 POSTER SESSION

Silvija Milosavljević Enhancing heterologous protein production using a directed evolutionary approach

Shengyu Wang Species identification errors in the ecological studies: incidence, consequences and precautions

Nora Bergman Reed warblers at range edge — Genomic effects of a recent range expansion

Carla Coll Costa Evolution of three-spined stickleback across Europe

Lluís Serra Linking Hierarchical Modelling of Species Communities (HMSC) with nestedness and turnover

Skylar Burg The relative role of thermoregulatory plasticity on inflorescence pigmentation and reflectance in *Plantago lanceolata*

Clelia Mulà Variation in disgust response provides differential social information for predators: implication in the evolution of aposematic colorations

Uxue Rezola Insect-associated bacteria interfere with virus transmission in a perennial host plant

Gabriele Retez Habitat selection of four large mammals, in winter season, within the Ceahlau National Park, Romania

Linnea Kivelä Does the wavelength of artificial light influence mate attraction in the common glow-worm (*Lampyrus noctiluca*)?

Mebin George Varghese Spatio-temporal dynamics and genetic variation in a butterfly metapopulation

Miina Suutari Do bats show antipredatory behavior when under threat?

Alma Seppälä Inhibition of rhinovirus infections

PROGRAMME

WEDNESDAY 10.3.

10:00 KEYNOTE 4

Øystein Opedal Using plant-pollinator interactions to understand evolution

11:00 BREAK

11:15 SESSION V

Antti Miettinen Using genetic stock identification to preserve the diversity of northern Baltic salmon

Sunandan Das Cranial osteology of *Hypoptophis* (*Atractaspidae*: Serpentes) sheds light on fossorial adaptation and fang evolution in *Atractaspidae*

Saara Mäkelin Temporal variation in elemental stoichiometry of benthic macrofauna

Tuuli Rissanen Species diversity in relation to major biogeographic gradients in Fennoscandia

12:45 LUNCH

13:45 SESSION VI

Purabi Deshpande Decreasing snow depth drives the habitat selection of overwintering birds in Finland

Sonja Aarnio Variation in species composition in coastal diatom metacommunity

Miisa Virta The dramatic population growth of the Eurasian Lynx (*Lynx lynx*) in Finland and its impact on zoonotic *Toxocara cati* abundance and intensity

Anna Haukka Would you buy a beautiful bird? – causes and consequences of global wild bird trade

15:15 BREAK

15:20 SESSION VII

Fernanda Ito dos Santos Research plan: Genetic structure of cave bats in the Brazilian Northeast

Janne Koskinen Turnover is the new black – drivers of fungivore communities

Pekka Hurskainen Land use and land cover mapping in heterogeneous landscapes of Eastern Africa using machine learning and multi-source spatial data

18:00 AWARDS GALA

KEYNOTE SPEAKERS

Dr. Naiara Rodríguez-Ezpeleta

Naiara Rodríguez-Ezpeleta is Senior Researcher at AZTI, Marine and Food Research Technological Center, Spain, where she leads the team Eco-Evolutionary Genomics Applied to Marine Management. She currently leads several projects related to the use of genomic tools for improving marine management.



Dr. Samniqueka Halsey

Samniqueka Halsey is currently an Assistant Professor of Ecosystem Health in the School of Natural Resources. Her research stresses the importance of using long-term data sets, GIS, and remote sensing. Most of her work involves using modeling approaches to delineate how spatial and temporal changes in ecological interactions influence a focal species.



Dr. Cristina Banks-Leite

Cristina Banks-Leite is a senior lecturer/associate professor at Imperial College London. She works at the interface of community ecology and landscape ecology, and her main goal is to unveil the causes and consequences of species turnover and species extinction in human-modified landscapes.



Dr. Øystein Opedal

Øystein Opedal is an Associate Senior Lecturer at Lund University. He's widely interested in evolutionary ecology and evolutionary genetics, with specific focus on understanding how plants and their communities of interactors (pollinators, seed predators, herbivores) respond to environmental change.



Modernizing marine management using innovative genomic tools

Naiara Rodríguez-Ezpeleta

Marine Research, AZTI Basque Research and Technology Alliance (BRTA)

Recent advances in the application of genomics to underexplored environments and/or to the study of non-model organisms have led to a paradigm shift in the field of marine ecosystem and resource management. Major changes have arisen from the application of metabarcoding to the study of macrofauna, and from the application of population genomics to the study of organisms for which no prior genomic information is available. Yet, before these techniques can be routinely applied to monitor marine ecosystems and resources, and thus be used for taking management decisions, they need to be benchmarked, calibrated, and standardized. I will present several case studies on the application of genomics for marine management that illustrate the promises and challenges of this fast-moving field. Ultimately, our results will assist the implementation of this technique within policies such as the Water and Marine Strategy Framework Directives, the Ballast Water Management Convention, or the Common Fisheries Policy.

Emergent plants enhance urban wetland biodiversity by providing prey refuges

Wenfei Liao, LUOVA

Aquatic plants are used as a tool to enhance wetland biodiversity, because their species richness has positive correlation with aquatic invertebrate species richness and has been considered as spatial prey refugia for invertebrates. Yet, little is known about the effects of aquatic plant cover, i.e. the quantity of prey refugia, on invertebrate assemblages in predator-prey dynamics. Here we use diving beetles (*Dytiscidae*), an indicator taxon of wetland biodiversity, to investigate how emergent plant quantity affects invertebrate assemblages in ponds with and without predatory fish. In addition, we investigated the relationship between emergent plant cover and water depth, to give reliable management advice for biodiversity conservation. Our results showed different patterns at the pond level and the microhabitat level: At the pond level, dytiscid presence was positively correlated with increasing emergent plant cover, both with and without fish, revealing the importance of prey refuge quantity for prey species. At the microhabitat level, dytiscid species richness and abundance responded positively to increasing plant cover in ponds with fish, but there was no such relationship in ponds without fish. The different patterns at the microhabitat level indicate that prey species utilise microhabitats with and without prey refugia differently under different predation pressure. We discovered that emergent plant cover is negatively associated with water depth, suggesting shallow waters are needed to support emergent plants. We suggest providing variations in water depth and emergent plant cover to retain high habitat heterogeneity for freshwater biodiversity conservation.

Combined effect of salinity and temperature on reproductive success and oxidative stress in brackish-water copepods

Ella von Weissenberg, LUOVA

Climate-induced warming and increased river inflows due to more precipitation are forcing the Baltic Sea ecosystems to change in a near future. Many brackish-water organisms are experiencing osmotic stress, and temperature is due to change their osmotic tolerance windows. The aim was to study the combined effect of salinity and temperature on reproductive success and oxidative status in zooplankton, using a key copepod species *Acartia* sp. The response of the organism to warming depends on its natural temperature and salinity optima, and we expect that low salinity, especially together with warming, will have a negative impact on reproductive success and oxidative status of *Acartia* sp. Field monitoring was conducted along a natural salinity gradient in summer 2020 at Tvärminne Zoological Station in southwest Finland. Copepods from the three stations were experimentally exposed to ambient or +3 °C temperature. Egg production and hatching success were measured, and oxidative stress biomarkers (lipid peroxidation, catalase, glutathione and glutathione-s-transferase) are measured from the females. Our preliminary results suggest that the highest egg production was reached at the most saline sampling site. Warming accelerated hatching in the laboratory study, but we found no effect of elevated temperature on egg hatching success.

Sex-specific lipid profiles in the muscle of Atlantic salmon juveniles

Andrew House, LUOVA

Energy allocation in juvenile fish can have important implications for future life-history progression. Inherited and environmental factors determine when and where individuals allocate energy, and timely and sufficient energy reserves are crucial for reaching key life stages involved in the timing of maturation and sea migration. In Atlantic salmon, lipid reserves are predominantly found in the viscera and myosepta in the muscle and have been shown to play a key role in determining the timing of maturity. This life-history trait is tightly linked to fitness in many species and can be different between males and females, however, the details of relative energy allocation in juveniles of different sexes is not well understood. Therefore, the aim of this study was to investigate the effects of sex, genetics and environment during juvenile development of salmon on the amount and composition of their lipid reserves. To do so, juvenile salmon were fed one of two different lipid food contents during their first summer and autumn under common-garden conditions. Muscle lipid composition and concentrations were determined by thin layer chromatography. The muscle lipid class concentrations covaried negatively with body length and males showed higher concentrations than females for phosphatidylcholine, cholesterol, sphingomyelin, and triacylglycerol. This sex-specific difference in major lipid classes presents a new scope for understanding the regulation of lipids during juvenile development and gives direction for understand how lipids may interact and influence major life-history traits in Atlantic salmon.

The age of the cyborg: machine learning in wildlife conservation

Vasco Veiga Branco, LUOVA

Wildlife is being threatened at a great and increasing pace. Multiple institutions such as the International Union for Conservation of Nature (IUCN) have over the past decade put out goals and targets in conservation that are unfeasible for the workload conservationists can achieve globally. If we want to succeed in the goal of protecting our wildlife from ourselves, we must also become dual in nature: we must understand and master not only life sciences but innovative technology as well. In my talk I'll briefly explain our current global conservation deficit and how machine learning could help us solve it. As key examples I'll present how machine learning has already been used to infer ecological relationships, models and principles through symbolic regression and briefly explain how the Asterisk workflow and software I'm developing could be used to further automate conservation.

Understanding disease emergence patterns by combining long-term data sets and computational approaches

Samniqueka Halsey

CAFNR Faculty, School of Natural Resources, University of Missouri

Tick-borne diseases are increasing worldwide and have a progressively negative impact on human health. To effectively manage diseases requires enhanced knowledge of the interactions of the tick, its hosts, and the environment. Due to the ongoing expansion of ticks and tick-borne diseases in the United States, there is need to identify the role wildlife hosts play in the establishment and maintenance of tick populations. After quantifying the patterns of both tick and pathogen prevalence relative to wildlife hosts, we developed a spatially explicit individual-based tick interaction model to evaluate vector control strategies. From this, we conclude that effective management efforts should be aimed at multiple stages in the tick's life cycle and enacted for the long term. We then quantified support for three mechanisms (i.e., vector regulation, encounter reduction, and transmission reduction) through which biodiversity–disease relationships occurred using species richness, Shannon H diversity, and host abundance. For each of the dilution effect mechanisms, host abundance was consistently the best-supported predictor of disease risk. Ultimately, understanding the mechanisms through which the wildlife host community influences pathogen transmission cycles in nature will help foster effective control and reduction of disease risk in humans.

An altitudinal cline in the Glanville fritillary butterfly: temperature but not altitude affects performance

Nadja Verspagen, LUOVA

Rising temperatures related to anthropogenic climate change pose many challenges for organisms worldwide. Especially ectothermic organisms, whose body temperature depends on environmental temperature are at risk. This risk increases when organisms are unable to migrate to cooler places, for example due to resource distributions. To gain insight in the survival probabilities of such species, we need to know their potential for genetic adaptation and/or phenotypic plasticity. A useful tool to disentangle these genetic and plastic effects are climatic clines. In this research, we used post-diapause larvae from the Glanville fritillary butterfly (*Melitaea cinxia*), that originate across an altitudinal gradient, and studied how temperature affects a suite of life-history traits. We reared larvae from four altitude groups at four different temperatures, and measured larval growth rate and adult wing loading, a measure relating the wing size to the total body mass of the butterfly. We found that the coldest temperature of 25 °C significantly reduced the growth rate compared to the other three temperatures (28, 31 and 34 °C) and that variation in growth rate is smaller at this temperature. This suggests that 25 °C is a stressful temperature for these larvae. Wing loading is also affected by temperature, but the differences are less pronounced. No effect of altitude was found, implying that no adaptive response to their respective climates is present between the populations studied here. Interestingly, a larger proportion of the variance in larval performance could be explained by differences among families regardless of altitude, which could provide adaptive potential in the light of climate change.

Contribution of High Nature Value farming systems to sustainable livestock production

Miriam Torres Miralles, DENVI

Animal production, and particularly that of livestock, has risen to the key issues in the agricultural sustainability discourse. The study addresses the above through a specific and seldom explored focus – High Nature Value (HNV) farming systems, which are mainly pastoral systems using semi-natural grasslands in production of high-quality animal-based food. The ongoing study aims is to assess the environmental sustainability of production on HNV farms in Finland, based on greenhouse gas emissions, nitrogen balance and land use. We estimated the environmental impact of eleven HNV farms and their alternative state, that is, the same production but without semi-natural grasslands. The HNV farms' impact was comparable to that from the alternative field-based production in terms of their environmental impacts related to production amounts while using semi-natural grasslands minimized use of arable land area, maximized nutrient cycling and maintained unique biodiversity.

Interactions between plants and microbes as determinants of Arctic vegetation dynamics

Bastien Parisy, LUOVA

In terms of rates of change, the climate of the Arctic is predicted to change faster than that of any other region of the globe. It is now a topical question to what extent the different organism groups jointly dictating arctic vegetation structure and dynamics will respond in concert with each other, and what the consequences for arctic vegetation will be. A large-scale expansion of shrubs has been described as a major transition of the whole biome, which may also impact the belowground diversity of other organisms, with effects on soil properties such as nutrients availability and carbon storage ability. While soil microbes have long been recognized as key determinants of plant coexistence where plant fitness is likely affected by changes in the composition of the soil community, the interest in how soil microbe-microbe and soil microbe-plant interactions respond to climate change in the Arctic has rapidly grown. Only few studies have considered complex and species-rich plant communities as found in the field and even fewer were focused on Arctic. Elsewhere, studies in experimental plant communities have shown that increasing plant species richness can lead to increased microbial community richness and functional diversity. Overall, plant community diversity may both alter and obscure the impacts of individual plant species on the characteristics of the soil communities, complicating inferences regarding impacts of plants and environment on soil communities. In summary, our understanding of the diverse relationships among abiotic soil parameters, interactions between soil microbiome and the characteristics of plants communities remains fragmented. During my PhD, I will explore the evidence for how the composition and dynamics of soil communities shape the structure of plant communities in space and in time, and identify key knowledge gaps in our current understanding of plant–microbe interactions of the Arctic.

Butterflies in changing weather conditions: implications for ecology and conservation

Susu Rytteri, LUOVA

Weather conditions are changing due to climate change. These changes together with other anthropogenic stressors may have drastic ecological consequences on insects. We utilised data from two butterfly metapopulations to study the ecological effects of changing weather conditions and their implications for insect conservation. In an experiment, larval winter survival was enhanced by snow cover. However, the individual-level effect of snowy winter conditions was not reflected by metapopulation growth rates in the wild. Instead, metapopulation growth was decreased by growing season drought, which desiccates larval host plants. In the spring, microclimatic variation buffered populations against phenological asynchrony between larvae and their host plants. Larval growth was accelerated by warm microclimates, but survival was highest in cool microclimates. Host plant growth was poor regardless of the microclimate. Flight season weather altered annual dispersal rates of butterflies. Increasing solar radiation and proportion of heat days increased emigration rates and shortened residence times. We simulated the spatial expansion of a translocated butterfly population in the release landscape based on prior knowledge of the habitat-specific dispersal rates in the source population. Dispersal rates were obtained from a movement model parameterised in a hot flight season, and consequently the predicted colonisation rates were overestimated in cool flight seasons. Our work highlights the multiple stressors changing weather conditions pose to insects. Shortening snow cover duration and advancing spring onset may have both direct and trophic interaction mediated adverse effects, which are amplified by stressful weather conditions at other life stages. Warming flight seasons may enhance dispersal with a potential to accelerate range expansions. On the other hand, increasing variation in annual weather conditions may cause range retractions during unfavourable years.

How much habitat do we really need to preserve biodiversity?

Cristina Banks-Leite

Faculty of Natural Sciences, Department of Life Sciences, Imperial College London

The question of “how much habitat is enough” has been in the minds of ecologists, conservationists and politicians for many decades now. Despite the fact that this question has been approached in hundreds of studies and in various ways, we still do not know the answer for most areas of the world. In this talk, I will discuss some of the main methodological and conceptual impediments for reaching a consensus: 1) use of inconsistent measurements of biodiversity and of habitat amount, and 2) lack of consideration for the role of processes occurring at biogeographic scales. I will argue that while species responses to habitat loss are incredibly complex, it is possible to obtain region-specific estimates of how much habitat is enough to preserve biodiversity, and I will show examples of how such estimates have been used to inform conservation policies.

How to validate predictive species distribution models?

Sirke Piirainen, LUOVA

Species distribution models (SDMs) are used to predict how communities change. But how reliable are such predictions? In most studies SDMs have not been validated with independent data, or they have been validated in terms of how well the model fitted to past data is able to predict current distributions. We argue that it would be more appropriate to study how well models predict the change between the past and the current distribution, and that predicting such change is challenging. We applied a joint SDM to model species distributions as a function of environmental and spatial predictors. We trained models with either a full (1975–2016) or a partial dataset (1975–1999) and predicted species occurrence and abundance, either for one time period (2013–2016) or for a change between two time periods (1996–1999 and 2013–2016). To estimate prediction accuracy, we compared predictions to observed values both locally and over regional averages. We then related prediction accuracies to species traits. Prediction accuracy was higher for the full dataset than the partial dataset, and it was higher for predicting the static future distribution than predicting a change in distribution. Regional pooling only marginally improved prediction accuracies. Prediction accuracies were not strongly related to any trait. We showed that current validation methods can lead to overconfidence in model's performance, for two reasons. First, often SDM's prediction capacity has been evaluated without splitting the data to temporally separated training and validation parts, whereas future predictions can be made only using data up to the present. Second, models fitted to past data may predict well the current distribution simply because distributions may have remained stationary, and so even the null prediction of no change can yield high discrimination power. When aiming to predict change, models should be validated based on their capacity to predict where and how the distributions have changed.

Different tolerance to humans? Alert and flight initiation distances of two bird species

Michelle García Arroyo, LUOVA

Birds invest time and resources in escape behaviors, thus changing their foraging strategies, habitat selection, and even reproduction. Flight initiation distance (FID) and the distance at which birds detect a threat, alert distance (AD), have been used as indicators of the ability of birds to detect potential predators. In this study, we compared the two aforementioned measures of risk reaction for the House sparrow and the Orange-breasted bunting, two bird species inhabiting the same urban areas, and assessed if they were related with sex, flock size, and environmental factors. We explored the relationships between environmental factors and ADs and FIDs, finding that both behavioral responses were significantly lower for House sparrows. Although we did not find significant relationships between the assessed variables and bunting ADs and FIDs, we did find House sparrow males to be bolder and a positive relationship with increasing flock size. In general, House sparrows showed to be bolder than Orange-breasted buntings, with differential responses of the sparrow related with sex, flock size, and different environmental factors. Having recorded bolder House sparrow males could be associated with increases in aggressiveness related to the breeding season. These findings add to the lacking behavioral information available for the endemic Orange-breasted bunting and provide insights on the variation of the behavior of House sparrows in small urban areas.

The role of woodpeckers as dispersal vectors for epiphytic organisms

Niko Johansson, LUOVA

Dispersal is a key factor shaping the distributions of species. For many sessile macroscopic organisms with microscopic dispersal propagules, aerial dispersal is often trivially thought to be the main and only dispersal mechanism. However, in many taxa, observed species distributions and gene flow patterns are difficult to explain with aerial dispersal alone. Animal dispersal vectors, especially birds as highly mobile and often migratory animals, have been hypothesized to be important dispersal vectors to various organisms but actual evidence remains scarce. We investigated the role of woodpeckers as dispersal vectors of epiphytic organisms, such as lichens and bryophytes. Fresh specimens of three common Finnish woodpecker species from the collections of the Finnish Museum of Natural History (Luomus) were screened for microscopic propagules attached to bird feet, chest plumage and tail feathers. Sampling was conducted using cotton swabs or direct feather samples, and biological material was extracted using a sonication-vortexing-centrifugation protocol. All specimens studied were found to carry a diverse and abundant assemblage of propagules. Most abundant were various fungal spores, bryophyte fragments and lichen dispersal units. We also identified freshwater diatoms, pollen grains, algal cells, testate amoebae, rotifers, nematodes, and insect scales among other biological material. Our work highlights the potential of woodpeckers as dispersal vectors for a diverse set of epiphytic organisms and showcases the use of natural history collections as data sources for ecology.

Investigating ecological networks of macrophytes and associated fauna in the Baltic Sea

Federica Manca, LUOVA

Understanding how ecological interactions affect ecosystem functioning and diversity is becoming a central issue in ecology and conservation. Ecological network theory offers powerful tools to explore how species interact in complex ecological systems and hence achieve a more holistic view of the mechanisms regulating natural communities. However, the effort in reconstructing ecological networks is unequally distributed, with some systems being disproportionately more studied than others. In this project, I aim at investigating a virtually unexplored system, which is the networks of interactions between aquatic macrophytes and their associated animal species. The research plan will build on a preliminary investigation of potential macrophyte-animal networks reconstructed from literature data. The core of the project will consist in building and exploring a set of macrophyte-animal networks in the area of the Tvärminne archipelago, by sampling individual macrophytes and examining their associated fauna. By combining tools from network analysis and ecological modelling, I will then address the ecosystem importance of macrophyte-animal networks, and specifically, the role of macrophyte-associated invertebrates in the diet of fish species; ultimately, I will explore how future scenarios of climate change will affect the structure of macrophyte-animal networks and, throughout cascading effects, higher trophic levels and hence coastal marine ecosystems as a whole. Overall, the outlined project will ideally provide a novel approach in the study and conservation of macrophyte communities and coastal ecosystem assessment. Additionally, the study of macrophyte-animal interactions in aquatic systems could open up a new field of ecological network research, which might parallel the study of plant-animal networks in the terrestrial environment and increase our understanding of the mechanisms regulating species interactions across different natural systems.

Why citizens giving you sh*t is contributing to understanding bat ecology in Finland

Kati Suominen, LUOVA

Citizen science provides means for people outside academia to contribute to scientific research. Citizen science is a relatively new term, but the practice is old; people have contributed to science throughout history. Citizen science is widely used and increasing in ecology, e.g. in ornithology, where bird watchers provide valuable observation data for scientists. It saves time and money and allows data collection in places that would not otherwise be possible. Often people participating show an interest in the target taxa and gain information they would not acquire without contributing to the project. Bats often utilize human facilities such as attics, cellars, and outdoor buildings etc. for roosting. Citizens are usually aware of the colonies. Hence, people having bats in their buildings were an excellent target volunteer group for a research where we aimed to look for roost sites of different bat species across Finland and determine environmental factors affecting roost selection. Volunteers were approached in the spring by advertising the research via social media. Anybody with knowledge of a bat colony could participate. The project gained a lot of media attention and in total 70 volunteers signed to the first part of the project. Collection kits were mailed to the volunteers who were given the possibility to collect bat droppings every second week throughout the summer on their property. Participants were instructed to collect 20 separate fecal pellets in separate tubes on one day every second week and fill a datasheet of environmental data of the surroundings of the roost. The collection of a dataset this large would not have been possible without the help of the general public. New bat roost locations were identified and GIS analyses are revealing an insight to roost site selection of Finnish bats. This information on bat species roosting are provided to the volunteers who participated to sample collections.

The response of functional diversity of bat communities to anthropogenic disturbance in Caatinga ecoregion, northeastern Brazil

Katarina Meramo, LUOVA

For prioritizing conservation actions, it is vital to understand how ecologically diverse species survive environmental change caused by human activity. Compared to more traditional diversity studies, research based on functional traits provides a deeper understanding of ecosystem functioning and on the structure and dynamics of communities, and helps to proactively react to environmental disturbances as they do not require the occurrence of a disturbance and thus the continuous monitoring and examination of the species diversity. Bats are a species-rich and functionally diverse group, with important roles in ecosystems, and are therefore recognized as a good model group for assessing the impact of environmental change. Bat populations have decreased in several regions, especially in the tropics, and are threatened by increasing human disturbance. The aim of this study is to evaluate the response of functional diversity of bat communities to anthropogenic disturbance. The research was conducted in Catimbau National Park, northeastern Brazil. The acoustic data for bat activity and the environmental data were collected in research sites with varying amounts of disturbance. Functional traits from three sets of data were used: 1) morphological 2) foraging and 3) echolocation. The study will provide not only a new fundamental understanding of the impact of human activity on ecosystem functioning and biodiversity, but essential information for the conservation of bats.

The Lake Pulmanki flounder: ecology, adaptation, and speciation

Thais Ferreira-Araújo, LUOVA

The goal of this project is to determine whether the flounders in Lake Pulmanki, a small lake in northern Lapland that was disjointed from Norwegian fjords due to isostatic rebound about 4500 years ago, are a new, endemic species that arose with spectacular rapidity following the invasion of a novel habitat. Using a combination of genomic tools, morphological and physiological data I will determine the physiological causes of reproductive isolation between this potential young species and its closest relative (marine *Platichthys flesus* from Norwegian fjords) and investigate their genomic architectures, shedding light on what Darwin called the “Mystery of mysteries”, i.e. how new species arise. Additionally, I will uncover the evolutionary history of the variants involved in the reproductive isolation of the Pulmankijärvi flounders. The recent identification of *Platichthys solemdali* as a new species suggests that high latitude environments can be home to greater biodiversity than commonly thought, and that speciation can occur much faster than generally assumed. Evidence from preliminary genetic analysis and otolith microchemistry suggests that flounders in Pulmankijärvi have gone through a rapid divergence, as they appear to be adapted to reproduce in the lake. There are therefore good grounds to believe the flounders in Pulmankijärvi can be a new, endemic species. A number of complementary approaches involving experiments, genomic and phenotypic analyses as well as otolith microchemistry will be adopted to study these flounders. If the species status will be confirmed, I aim to make formal description of the new vertebrate species to science, as well as reconstruct the evolutionary history of this speciation event.

Climate induced range shifts explain trends in bird migration passage dates

Andreas Otterbeck, LUOVA

During the last decades, climate warming has caused large-scale temporal phenology shifts across many organism taxa, leading e.g. to increasing temporal mismatch in the occurrence of interacting species. However, these phenological changes are considered too slow to compensate for climate change, which may lead to population declines. For birds, studies on spring arrival phenology are mostly based on passage or stopover dates of migrants from bird observatories, without further knowledge of their destinations. Simultaneously, breeding ranges of birds expand northwards, and birds arrive later to northern breeding areas compared to southern ones, to avoid temporal mismatches with their food sources. We propose that studies based on migration passage data underestimate how much spring arrival has advanced locally. If the passing pools of birds show progressively increasing destination latitudes and therefore later arrival schedules, this will cause a bias that opposes trends of true earlier arrival. By reanalyzing published temporal trends in migration phenology of Nordic birds, we show that range shift velocities explain a considerable amount of variation in early spring passage trends. Accounting for this effect suggests that short-distance migrants have during three decades advanced their arrival by five days more than suggested by their passage dates alone. The size of the bias surpasses the overall rate of advancement assigned to birds in the Northern Hemisphere – the most central indicator of organism responses to climate change. Similar biases may be widespread in studies on animal migration phenology, suggesting breeding range shifts may be a key confounding variable.

Using plant-pollinator interactions to understand evolution

Øystein H. Opedal

Department of Biology, Lund University

Pollinator-mediated evolution of flowers has been a classic topic in evolutionary biology since Darwin and before. Plant-pollinator interactions provide excellent systems in which to move towards a predictive understanding of phenotypic evolution. First, the agents of selection driving adaptation (pollinators) are known, and the mechanisms linking phenotypes to fitness (pollination) can be readily hypothesised and experimentally confirmed. Second, floral traits can be readily categorised into functional classes related to distinct functions such as pollinator attraction (advertisements and rewards) and pollen transfer (flower-pollinator fit and ability of self-pollination). For example, showy corollas and distinct fragrances are related to pollinator attraction, while the positions of sexual organs within flowers are important for efficient pollen transfer. This functional understanding allows building fitness functions linking traits to performance (e.g. pollinator visitation, pollen receipt), and in turn fitness (e.g. seed set). Because trait functional classes are general across species, it is possible to derive general patterns of variation in phenotypic selection, evolutionary potential, and constraint. In turn, patterns of selection following different kinds of changes in pollinator communities may also be predictable, such as selection for larger flowers following a change to larger bee pollinators, or selection for smaller, self-pollinating flowers following a pollinator decline. This functional understanding may allow us to forecast the consequences of ongoing pollinator declines and other changes in pollinator communities.

Using genetic stock identification to preserve the diversity of northern Baltic salmon

Antti Miettinen, LUOVA

Atlantic salmon (*Salmo salar*) exhibit a broad range of life history diversity. Salmon vary widely in key life history traits, such as maturation and migration timing, both within and among populations. This variation has been found to have a genetic basis in multiple populations. Furthermore, anadromous salmon return to their natal location to spawn, which frequently results in strong geographical population structuring. Sustainable management of distinct populations and their diversity is essential for maintaining the genetic resilience of salmon stocks. My previous study found genetic differentiation associated with variation in maturation and migration timing within the largest wild Atlantic salmon stock in the Baltic. Therefore, careful temporal management of fisheries could be used to preserve the diversity and sustainability of wild Baltic salmon. To study how fishing at different times and locations affects different populations and their subcomponents, I use genetic stock identification of mixed salmon catches in the northern Baltic. In addition, I use an almost century-old scale archive to study how human activities have altered allele frequencies of genes relevant for fisheries and the ecology of the species. These include genes that have or may have an effect on maturation and migration timing of salmon. The results will help guide fishing pressure away from the rarest genotypes, and thus preserve diverse stocks in the northern Baltic. I will present preliminary results from a genome-wide dataset of multiple northern Baltic salmon populations and hatchery broodstocks. I will discuss how my project will improve our understanding of the effects of fishing on wild salmon populations, and how it will help preserve the biological diversity of the ecologically, culturally and economically important Baltic salmon.

Cranial osteology of *Hypoptophis* (*Atractaspididae*: *Serpentes*) sheds light on fossorial adaptation and fang evolution in *Atractaspididae*

Sunandan Das, LUOVA

Fossoriality evolved multiple times among snakes, including extinct Mesozoic snakes. Accuracy of inference on the palaeoecology of extinct lineages based on anatomical traits is contingent on the availability of comparative anatomical data from extant taxa for which ecological observations can be made directly. *Aparallactinae*, a subfamily of *Atractaspididae*, consists of eight genera of semi-fossorial/fossorial snakes. However, rear-fanged aparallactines never received much attention from morphologists and therefore, knowledge on their anatomy remains scant. We describe the cranial osteology and the inner ear structure of *Hypoptophis wilsonii*, a rare African aparallactine, using micro-computed tomography. The miniaturised skull is adapted for burrowing and feeding on elongated, fossorial squamate prey. Snout bones are modified for digging and have increased points of contact with braincase and palatamaxillary arch, thus reinforcing the skull. The short maxilla has the 'back'-fang positioned quite forward, the relatively anterior position of the fang being produced by near-confluence of the fang-bearing maxillary ectopterygoid and ascending processes. This has implication for fang evolution among atractaspidids and suggests that the peculiar side-swivelling front fang of *fernana* is actually a back-fang brought anterior by complete amalgamation of ectopterygoid and ascending processes. These adaptations appear to be related to predatory habits. The inner ear endocast also shows fossorial adaptations. We have inferred the phylogeny of aparallactines, including *Hypoptophis*. One interesting apomorphy of aparallactines is the split choanal process of palatine bone. Interestingly, even though burrowing has resulted in extensive trait reversal/convergence in snakes, obligate fossoriality has resulted in extreme morphological specialisations which are often unique to a particular lineage and therefore, origin of snakes from an extreme fossorial ancestor is less likely.

Temporal variation in elemental stoichiometry of benthic macrofauna

Saara Mäkelin, LUOVA

Stoichiometric balance between organisms and their habitat is critical for the ecosystem functioning. In coastal habitats, benthic fauna plays an important role in mediating carbon, nitrogen and phosphorus cycles. Benthic fauna stores carbon and nutrients in their body tissues at theoretically homeostatic rates, indicating that the elemental content of their tissue remains stable despite changes in nutrient availability. This suggests that benthic consumers need to be in balance with their resource supply, or alter their stoichiometric traits in consequence of environmental change. By monitoring two sites over a year, we quantified the size and temporal stability of benthic faunal carbon and nutrient pools in coastal soft sediment habitats. Our results show that benthic fauna is not strictly homeostatic, but expresses both inter- and intraspecific variation in C:N:P content ratios. Indeed, we found elemental stoichiometry to be species-specific and varying between life stages. Hence, these aquatic consumers undergo ontogenetic changes in diet and morphology, which influence their stoichiometric characteristics. In addition, faunal C:N:P content ratios showed seasonal variation, indicating that the stoichiometric traits of benthic consumers shift in response to environmental conditions and food sources. Animal tissues generally have higher concentration of carbon and nutrients compared to the surrounding environment, therefore, benthic biomass can function as a significant carbon and nutrient pool. Understanding the animal contribution to the carbon and nutrient cycling is valuable in areas such as the Baltic Sea, where inputs of nutrients and organic matter from land have significantly altered biogeochemical cycles in the coastal zone.

Species diversity in relation to major biogeographic gradients in Fennoscandia

Tuuli Rissanen, GeoDoc

Biodiversity patterns and drivers shaping them on various spatial scales are of fundamental interest in ecological and biogeographic studies. Traditionally, these diversity patterns have been studied along elevation gradients. This has been the case also in Fennoscandia. However, due to its location at the edge of Eurasian continent and the length of the peninsula, there are other strong environmental gradients affecting as climate shifts from southern temperate to northern arctic and from western oceanic to more continental conditions in the east. Along with the heterogeneous elevation conditions of Scandes mountains, these climatic gradients shape the arctic-alpine area and its vegetation. To investigate the vascular plant diversity of the arctic-alpine realm thoroughly, we study it in relation to the presented major biogeographic gradients. In more detail, we use species richness, composition and uniqueness to describe vascular plant diversity. Furthermore, we use latitude, continentality, and elevation in relation to forest line to present the environmental gradients. Thus, we aim to gain a holistic macro-ecological view to understand better the drivers shaping diversity in Fennoscandian tundra.

Decreasing snow depth drives the habitat selection of overwintering birds in Finland

Purabi Deshpande, LUOVA

As anthropogenic effects on climate and land use intensify, species are responding by changing their preferences for different habitats. This leads to range shifts and homogenisation of communities. However, the exact drivers of such change in habitat selection are only beginning to be understood. Here we explore whether long-term declines in snow depth are affecting the abundance of overwintering birds in Finland, using citizen-led monitoring data from 196 transects over a 32-year period, and assess whether species-specific traits explain observed patterns. We find that snow depth is a major driver of habitat selection in overwintering birds, with abundances of birds increasing in farmland habitats as snow depth decreases, when compared to urban or forest habitats. Additionally, we found that the short-distance migrant trait could explain the increase in abundance in farmlands during periods of decreased snow depth. Our results therefore suggest that local snow conditions drive habitat selection by birds in the winter. This can affect bird movements across habitats in the winter, but also influence migratory patterns and range shifts of species.

Variation in species composition in coastal diatom metacommunity

Sonja Aarnio, LUOVA

Different metacommunity perspectives have been developed to describe the relationship between environmental and spatial factors and their relative roles for local communities. However, only little is known about temporal variation in metacommunities and their underlying drivers. We examined temporal variation in the relative roles of environmental and spatial factors for diatom community composition among brackish-watered rock pools on the Baltic Sea coast over a three-month period. The studied communities housed a mixture of freshwater, brackish, and marine species, with a decreasing share of salinity tolerant species along both temporal and spatial gradients. The community composition was explained by both environmental and spatial variables (especially conductivity and distance from the sea) in each month; the joint effect of these factors was consistently larger than the pure effects of either variable group. Community similarity was related to both environmental and spatial distance between the pools even when the other variable group was controlled for. The relative influence of environmental factors increased with time, accounting for the largest share of the variation in species composition and distance decay of similarity in July. Metacommunity organization in the studied rock pools was probably largely explained by a combination of species sorting and mass effect given the small spatial study scale. The found strong distance decay of community similarity indicates spatially highly heterogeneous diatom communities mainly driven by temporally varying conductivity gradient at the marine-freshwater transition zone.

The dramatic population growth of the Eurasian lynx (*Lynx lynx*) in Finland and its impact on zoonotic *Toxocara cati* abundance and intensity

Miisa Virta, LUOVA

The parasite-host dynamics are assumed to follow Lotka-Volterra predator prey model, in which the population size of the parasite follows the changes in population size of the host. We evaluated the effect of the dramatic change in Eurasian lynx (*Lynx lynx*) population size on the presence of a zoonotic nematode *Toxocara cati*. In Finland, the lynx population has grown from 30-40 individuals to 2800 individuals since the species became protected in 1962. The population growth started from South-Eastern Finland, followed by the expansion to throughout the country. In this study, we used *T. cati* collected from the intestines of 2837 legally hunted lynxes in 1999-2015 to evaluate the effect of the change in population size on prevalence and intensity of *T. cati* infections. We identified *T. cati* based on morphology. Further we performed regression analysis on how following factors are associating with the infection: age, sex, lynx density. Results were interesting; we found *T. cati* from 84% examined lynxes. Although the population size increased from 850 to 2800 individuals in years 1999-2015, it did not have an influence on *T. cati* prevalence. Across the years, the overall proportion of lynxes with *T. cati* remained over 75%. Results for parasite aggregation indicated strong aggregation. The age was significant factor, correlating negatively significantly with lynx age and *T. cati* burden and presence. Although, the worm burden decreased with age, interestingly the interaction with sex and age showed significant differences in worm burden between sexes. Older females had significantly increased worm burden, whereas older males, the burden remained lower. Most lynxes had tapeworm co-infection. Feeding habits, immunological changes and breeding behavior may explain why sexes in older age differ with the *T. cati* burden. Results indicate that *T. cati* is common and abundant parasite amongst lynxes even when the lynx density and population is small.

Would you buy a beautiful bird? – causes and consequences of global wild bird trade

Anna Haukka, LUOVA

Birds are one of the species groups heavily targeted for legal and illegal hunting and trapping for trade in many locations globally from Africa to Asia to Europe and South and North America. Hunting and trade occur in different social and ecological contexts under different motivational drivers. Yet, despite the knowledge that that bird numbers are in steep decline and many species are threatened due to unsustainable harvesting, trade remains one of the most understudied issues in conservation science. We use an easy-to-approach community science internet browser application to increase understanding on which birds are most visually attractive to people and thus likely more susceptible to trade. We create a bird attractiveness measure by collecting attractiveness scores of 1-10 hearts on bird photographs. The scores are given to bird species photographs from the Cornell Lab of Ornithology's Macaulay Library database. After understanding which features in the looks of birds make them more attractive to people we combine this new information with other data sets on global wild bird trade. We aim to understand which bird species currently are, and potentially will be most vulnerable to be captured for trade. This information can also help understand the ecological impacts of wild bird trade.

Research plan: genetic structure of cave bats in the Brazilian northeast

Fernanda Ito dos Santos, LUOMUS

Commonly known as bat caves, some caves found in the Neotropical region are characterized by sheltering exceptional bat populations (>> 10,000s individuals). Such high bat density contributes the maintenance of unique microclimate conditions in those caves, usually with high temperatures (> 34°C) and humidity (> 90%). Although known in Central America, the Caribbean and México, in Brazil the current knowledge on such caves is still incipient, but recent studies have shown that they tend to be more frequent than previously thought in the Northeastern part of the country, with some of those caves harboring populations that exceed 200,000 individuals. Systematic monitoring of some of those caves points out that they may experience severe population fluctuations in short periods of time. Such variations suggest the existence of massive bat movements between different roosts: bats from one bat cave leave it for certain periods, and move as a group to another bat cave. This project aims to investigate, in an innovative way for Brazil, the possibility of genetic connectivity among populations of two cave bats species – *Pteronotus gymnonotus* and *P. personatus*, family Mormoopidae – which form exceptionally large populations in nine bat caves 700 km apart in Northeastern Brazil. Thus, with these results, we would fill an important knowledge gap on the living area and the movement capacity of two common and widespread cave-dependent bat species in Brazil. More importantly, the legal understanding of what is considered the influence area of caves would have to be reviewed. Furthermore, studies on bat caves provide important information for the identification of priority areas for biodiversity and cave conservation in Brazil: such caves frequently shelters exceptional large populations – hundreds of thousands of individuals, in some cases – emphasizing their high ecological and conservation relevance.

Turnover is the new black - drivers of fungivore communities

Janne Koskinen, EPHB

What drives fungivore assembly mechanics? Why are the flies where they are? Utilizing DNA metabarcoding, we disentangle the imprints of latitude, fruiting body decay and host identity on the structure of fungus-associated arthropod communities. We show that latitudinal patterns in these insects affect community structures, but not species richness itself.

Land use and land cover mapping in heterogeneous landscapes of Eastern Africa using machine learning and multi-source spatial data

Pekka Hurskainen, DENVI

Classifying land use/land cover (LULC) with sufficient accuracy in heterogeneous landscapes is challenging using only satellite imagery. To improve classification accuracy inclusion of features from auxiliary geospatial datasets in classification models is applied since 1980s. However, the method is mostly limited to pixel-based classifications, and the coverage, accuracy and resolution of free and open-access auxiliary datasets have been poor until recent years. We evaluated how recent global coverage open-access geospatial datasets improve object-based LULC classification accuracy compared to using only spectral and texture features from satellite images. We applied feature sets topography, population, soil, canopy cover, distance to watercourses and spectral-temporal metrics from satellite time series on the southern foothills and savanna of Mt. Kilimanjaro, Tanzania. The classification was based on image objects (groups of spectrally similar pixels) derived from segmentation of four satellite images with 8m spatial resolution using 1370 ground reference points for training, validation, and for defining 17 LULC classes. We built six Random Forest classification models with different sets of object features in each. The baseline model having only spectral and texture features was compared with five other models supplemented with auxiliary features. Inclusion of auxiliary features significantly improved classification overall accuracy (OA). The baseline model gave a median OA of 60.7%, but auxiliary features in other models increased median OA between 6.1 and 16.5 percentage points. Applying object-based classification to geospatial information on topography, soil, settlement patterns and vegetation phenology, the discriminatory potential of challenging LULC classes can be significantly improved. We demonstrated this for the first time, and the technique shows good potential for improving LULC mapping across a multitude of fragmented landscapes worldwide.

Enhancing heterologous protein production using a directed evolutionary approach

Silvija Milosavljević, EEB

Transfer RNA (tRNA) has been shown to have numerous conserved post-transcriptional nucleoside modifications, which exemplifies the importance of modifications, but many of them have been also shown to change as a response to stress conditions. Stress, such as temperature or infection by a pathogen, is known to change the presence or abundance of modifications in RNA molecules and thereby affect translation efficacy. Some tRNA modifications were found only during stress conditions and served for stress-related proteins translation which needs to be efficient and optimized for the cells to survive. Identifying such stress conditions and tRNA modifications can be beneficial for the future of protein production. It has been hypothesized that similar might be true for rRNA modifications and therefore affects ribosome activity. There are many yet unsolved questions about translation, especially about post-transcriptional modifications in RNA molecules: how, when and why are they present, how different are they in different organisms and what are their adaptive roles during translation. On the other hand, industry for pharmaceuticals is enormous and the demand is high so enhancing protein production is always necessary. The new knowledge about translation machineries and their dependence on post-transcriptional modifications could identify a novel optimization approach for the benefit of both fundamental research and industry. The aim of this project is to gain insights into the evolutionary aspect of RNA modifications and their potential use to enhance heterologous protein production. More specifically, the aim is to understand how oxidative stress-related modifications in tRNA and rRNA affect the heterologous protein production in a cell-free translation system reconstituted from yeast. Potential importance for understanding the evolution and adaptations in translation machineries and how biotechnology can benefit from new insights, are what makes this project unique.

Species identification errors in the ecological studies: incidence, consequences and precautions

Shengyu Wang, EEB

Many natural scientists study species, but it seems rare for them to critically evaluate whether they have identified their study species correctly. Species misidentification in empirical research can cause significant losses of money, information, and time, and contribute to false results. In my MSc thesis, I will demonstrate the incidence of errors in species identification at different stages in the course of ecological research in Finland and internationally, and ecologists' views about the importance of species error recognition. How do researchers deal with these errors and their methods to ensure the accuracy of species identification will also be summarized and discussed. I ran an online survey targeted to researchers from scientific institutes around the globe (including universities, research societies, and museums) who completed their doctoral degrees in any ecology-related field of science (e.g., community ecology, evolutionary biology, taxonomy). I have received 117 participants from 27 countries with a doctoral background in 25 countries. 53% of the respondents are leading their own research group. The respondents are from various fields of ecological studies and studying a broad spectrum of taxa, providing excellent resources to investigate the patterns and opinions about species misidentification. I will discuss my research questions and results in my Master's thesis as well as in a peer-reviewed article. Eventually, I hope to contribute to improving the accuracy and efficiency of ecological studies in Finland and worldwide.

Reed warblers at range edge — Genomic effects of a recent range expansion

Nora Bergman, EEB

The reed warbler (*Acrocephalus scirpaceus*) is one of the numerous species that have experienced or are going to experience a range shift towards the poles under the current climate change. An expanding range front moves like a wave, in which successive founder effects can cause strong genetic drift and lower allelic diversity at the range front, especially in species with low dispersal capability. This in turn can make local adaptation more difficult and even halt the expansion. Using a fine-resolution RADseq data set, I will study how such a rapid range expansion has genetically affected the mobile and migratory reed warblers in the recently established Finnish population.

Evolution of three-spined stickleback across Europe

Carla Coll Costa, EEB

Three-spined stickleback (*Gasterosteus aculeatus*) is a model organism for studies of natural populations, especially for studies involving parallel evolution. The species range extends the whole northern hemisphere and the geographic history of the species sets the origin of this organism in the Eastern Pacific. Three-spined stickleback has a facility for adapting to new environments, which is reflected by the several colonization events involving bottlenecks during the species history. During Pleistocene glaciations, European three-spined stickleback populations inhabiting high-latitude areas were eradicated, whereas populations residing (or moving to) in the south often persisted in refugia. After the retreat of the ice sheets covering northern Europe, the high-latitude areas became recolonized by migration from south, and hence, the populations existing there today are relatively young. These contrasting histories between high and low latitude populations explain some of the clear differences we see today in both genetic diversity and differentiation among populations from these latitudinal extremes. Population genetic studies of the three-spined sticklebacks have usually been conducted at high-latitude areas where freshwater populations are typically less than 10.000 years old. Few studies have focused on southern populations, where more of the ancestral diversity is likely to reside. Here, I investigate whether south European three-spined stickleback populations have the ancestral polymorphism present in the lineage that colonized the northern Europe after the Pleistocene glaciation.

Linking Hierarchical Modelling of Species Communities (HMSC) with nestedness and turnover

Lluís Serra, EEB

Quantifying the differences among communities is key for understanding how and why biodiversity is distributed in the way it is. Beta diversity can be understood as the interplay between nestedness (ordered colonization-extinction dynamics that leads to species-poor sites being subsets of the biota occurring in species-rich sites) and turnover (variation in species identities among sites). Partitioning beta diversity into its components can provide deeper insights on the processes driving spatial variability in communities and help in defining robust protected area systems. Hierarchical Modelling of Species Communities (HMSC) allows the integration of environmental covariates, species traits and phylogenetic relationships to model species occurrences or abundances. The aim of this research is to unveil the relationship between beta diversity components (nestedness and turnover) and the outputs of HMSC analyses from simulated data.

The relative role of thermoregulatory plasticity on inflorescence pigmentation and reflectance in *Plantago lanceolata*

Skylar Burg, IPS

Phenotypic plasticity, defined as one genotype having the capability to express several phenotypes depending on environmental circumstances, is one of the possible ways through which species can adjust to changing environmental conditions. It has been proposed that this plasticity in spike reflectance allows individuals to acclimate to difference in the temperature of their growing environment: this capacity is known as thermoregulatory plasticity. Studying the confines of thermoregulatory plasticity in relation to inflorescence pigmentation and reflectance is essential to evaluate how species will react to climate change. Better understanding thermoregulatory plasticity in a model organism such as *Plantago lanceolata* could benefit future studies on biodiversity preservation or crop fitness. In this study, I set up a greenhouse experiment to assess if thermoregulatory plasticity has a functional role in floral reflectance and pigmentation in nine *P. lanceolata* populations grown in three different temperature treatments. I conducted a greenhouse experiment followed by spectrophotometry, infra-red temperature readings, and photography to identify how the spectral absorbance properties of flowers differed and if there were differences in anthocyanin content and internal inflorescence temperature between each treatment. I hypothesize that: 1) anthocyanin content is higher in bud scales from plants grown in cooler environments; 2) reflectance of bud scales are higher from plants grown in warmer environments; and 3) there is a positive correlation between infra-red temperature of inflorescences and anthocyanin content. I am currently in the analysis process of my research.

Variation in disgust response provides differential social information for predators: implication in the evolution of aposematic colorations

Clelia Mulà, EEB

Before attacking potential prey, predators need to assess costs and benefits. To acquire information about prey profitability, animals rely on what they learned both by personal experience and by observing others foraging. The latter is named social learning, and the realization of its potential has led to an increase of empirical investigation, to understand to what degree observing the action of others favours the evolution of behavioural patterns. Indeed, different studies demonstrated that several avian species show social avoidance learning, rejecting unpalatable food after observing conspecifics and heterospecifics response. However, in all of these studies there is variation in how observers behave and furthermore there is variation in how potential demonstrators themselves respond to unpalatable food. Therefore, to understand how social avoidance learning can work in nature I investigated how Blue tits (*Cyanistes caeruleus*) select between prey after watching demonstrators that present either a strong or weak disgust response, or act as if the food is palatable. To perform the project, I used the miniature novel world protocol, presenting the birds with novel aposematic (i.e. unpalatable) and cryptic (palatable) prey after a video playback treatment. I tested 45 birds and used 5 different demonstrators, obtaining from each of them 3 different videos: (1) response of palatability to aposematic prey, represented by no beak wiping; (2) response of weak disgust to aposematic prey, represented by 10-20 wipes; (3) Response of strong disgust to aposematic prey, represented by 60-70 wipes. The results suggest that social avoidance learning can help facilitate the initial evolution of aposematic signals. However, in blue tits this process is affected by many factors, some still to investigate. Among these there are interspecific and intraspecific variation, predator cognitive perception, prey toxic chemicals concentration, and most importantly strength of cue.

POSTERS

Insect-associated bacteria interfere with virus transmission in a perennial host plant

Uxue Rezola, IPS

A recent study has shown how a stable introduction of the endosymbiont *Wolbachia* into planthoppers inhibits a plant-virus transmission in laboratory conditions, but if and how this process is carried out in wild communities has not been tested yet. I present a MSc. study that will try to see whether symbiotic bacteria of insects can affect the horizontal transmission of plant virus(es) in semi natural conditions. Particularly, the project will focus on how the presence of endosymbiotic infection in aphids affects the titter of the targeted plant-virus in aphids, and its transmission to *Plantago lanceolata* (host plant) specimens.

Habitat selection of four large mammals, in winter season, within the Ceahlau National Park, Romania

Gabriele Retez, EEB

In order to protect a species efficiently, measures need to be taken not only towards the species itself, but also towards the habitats where it occurs. We assessed the habitat selection of four large mammals (*Ursus arctos*, *Canis lupus*, *Lynx lynx* and *Cervus elaphus*) during a study in the Ceahlau National Park, Romania. We conducted transects and camera-trap surveys during October 2019 – March 2020. We analyzed the presence data using the Ecological Niche Factorial Analysis (ENFA), considering as proxies for habitats ten environmental variables. Subsequently, we ran the Monte-Carlo Test to assess whether the species followed a random distribution or not. Finally, we created habitat suitability models with MADIFA. Our main outcomes showed an avoidance of urban, agricultural and steep areas by the four large mammals' species. The brown bear showed no strong selection, apart from the aspect, reporting a random distribution. In contrast, the Eurasian lynx resulted in a strong selection toward broadleaf forests and open areas. The grey wolf and the red deer presence were correlated, both selecting mixed forests and similar altitudinal values. Besides, the wolf selected open areas, while the red deer avoided them. Even if the National Park has a small surface with few suitable areas for large carnivores, their presence was high. Most of the species were detected closer to the limits. Therefore, future inventories and management actions must be addressed toward suitable areas and must include a buffer zone outside the National Park borders. We want to promote the use of pilot studies to minimize the effort and maximize the efficiency of monitoring plans.

Does the wavelength of artificial light influence mate attraction in the common glow-worm (*Lampyrus noctiluca*)?

Linnea Kivelä, EEB

Light pollution, or artificial light at night (ALAN), is a globally growing environmental problem, with potentially dire consequences for nocturnal organisms. Glow-worms are a group of nocturnal insects experiencing global population declines, possibly in part due to light pollution transforming the night-time environment. In the common glow-worm (*Lampyrus noctiluca*) artificial light has been shown to interfere with the ability of male glow-worms to locate females, which are sedentary and attract flying males by glowing in the night. Previous studies have found that dummy females illuminated with white light managed to attract fewer males than those located further away from artificial light. In my MSc project I investigated whether the wavelength of artificial light influences the effects of light pollution on glow-worm reproduction, as glow-worms might not be able to perceive all wavelengths of light in equal measure. I found that illumination with shorter wavelength (blue and white) artificial light decreased the mate attraction success of dummy females, whereas longer wavelength (yellow and red) light had no apparent effect compared to natural darkness. The results suggest that favoring lights with longer wavelength spectra in lighting planning might help to mitigate the negative effects of light pollution on glow-worms.

Spatio-temporal dynamics and genetic variation in a butterfly metapopulation

Mebin George Varghese, EEB

The Glanville fritillary (*Melitaea cinxia*) butterfly inhabiting the fragmented meadows and pastures in the Åland Islands, Finland, has a classic metapopulation structure: its long-term persistence depends on frequent re-colonization events counter-balancing the extinctions of local populations. The spatial structure and the temporal dynamics of the metapopulation are likely to influence genetic variation within and among local population networks. With high population turnover, disappearing populations accelerate genetic drift, potentially leading to a reduction in neutral genetic diversity. This loss is likely to be counteracted with immigration bringing in new alleles especially in well-connected populations. Dispersal has indeed been shown to be a key mechanism in maintaining genetic variation and adaptive potential in fragmented landscapes. In my MSc-thesis, I am utilizing long-term monitoring and genetic data collected from semi-independent networks from the main Åland region (Saltvik) reflecting well-connected metapopulations and from two isolated island networks Föglö and Sottunga. More specifically, I investigate how a decline in population occupancy and abundance in 2010 impacted genetic diversity (neutral and candidate genes) and whether the responses vary among well and more poorly-connected networks. The preliminary results shall be presented in my poster.

Do bats show antipredatory behavior when under threat?

Miina Suutari, EEB

A successful predation event is mortal to the prey, so animals need practices that enable them to avoid predation – antipredatory responses. Bats are the second largest order of mammals but their antipredatory responses are still poorly understood. Even if bats do not have specialized predators in the temperate zones, they are still predated on. In fact, 11% of bats annual mortality is by avian predators, especially by owls. Roost emergence has been suggested as a particularly dangerous time for bats, as their presence is very predictable in time and space. Since bats are mainly active during the dark, they need to divide their active period between foraging and avoiding predation in a way that maximizes their survival. I studied antipredatory responses of bats in two situations: 1. during roost emergence and 2. during foraging. I collected acoustic data of bats in June, July and August of 2020 from 23 roosts and 11 foraging grounds. All places were recorded between 10-13 nights. The roost emergence data was collected with the help of citizen science to maximize the data. In both tests a controlled predation threat, recording of tawny owl calls, was used. During the roost emergence tawny owl nestling sounds were also played as a possible threat. Music and silence were used as controls. Neither owl calls nor music affect bats when they are foraging. However, bats do alter their emergence time when owl calls are played. They leave on average 23 minutes later when tawny owls are heard. With music or nestling sounds there is no difference in emergence time. These results show that bats do have antipredatory responses. They also suggest that bats may be able to recognize high-risk situations and allocate their behavior accordingly or that they place higher importance on foraging than avoiding predation. Here, further studies are needed.

Inhibition of rhinovirus infections

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Rhinovirus infections cause the common cold, for which there is no cure. The consequences of the disease are mainly seen from absence from school or work, as the disease is usually mild, self-limiting and symptoms disappear in few days, but infections can also lead to severe asthma exacerbations and hospitalizations. Previous work done on rhinoviruses and some other enteroviruses identified two pockets on the virus surface, hydrophobic and interprotomer, where the inhibitors, known as capsid binders, can bind and block virus infection. The hydrophobic pocket in the viral protein VP1, usually occupied by a lipid factor, has been studied for decades and led to a development of a range of compounds displacing the lipid factor and stabilizing the virion. The interprotomer pocket formed by VP1 and VP3 molecules at the interface of two protomers has been recently described as a promising target for development of broad range inhibitors of enteroviruses including rhinoviruses. The aim of my work is to test the most promising interprotomer binding compounds on a set of rhinovirus isolates and perform a structural characterization of rhinovirus-inhibitor complex. Cell-based virus inhibition assays led to the identification of two inhibitors against two rhinovirus isolates. I have established the protocol for rhinovirus purification. Cryo-EM structural characterization of rhinovirus complexed with an inhibitor is in progress. The work also includes computational screening of the known drug-candidates and publicly available drug-like decoys to better understand the requirements for the optimal compound binding.