HELSINGIN YLIOPISTO
HELSINGFORS UNIVERSITET
UNIVERSITY OF HELSINKI

LUOVA
DOCTORAL PROGRAMME IN
WILDLIFE BIOLOGY RESEARCH

LUOMUS
FINNISH MUSEUM OF NATURAL HISTORY

Programme and Abstract Book

32nd

Spring Symposium

Infokeskus, Viikki Campus, University of Helsinki
6th – 8th March, 2023

Acknowledgements

Organizing Committee
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Acknowledgements
The 2022 Spring Symposium Organizing Committee
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Pol Capdevila (Keynote speaker)
Kristiina Tambets (Keynote speaker)
Doctoral Programme in Wildlife Biology (LUOVA)
The Finnish Museum of Natural History (LUOMUS)
The Viikki Info Centre Korona
The faculties and the doctoral school
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Logo designer
A big thanks to Zowi Oudendijk, who designed the logo for the 32nd Spring Symposium and won 1st place in the logo competition. We are also grateful for all the competitors who have submitted their logos.

Welcome! Tervetuloa! Bienvenue! 欢迎!

It's a great pleasure to see you all in the 32nd Spring Symposium. Starting from 1992, the Spring Symposium has been organized yearly by PhD students in the Doctoral Programme in Wildlife Biology Research (Finnish acronym LUOVA) of the University of Helsinki.

The symposium provides opportunity for students to listen to talks from three exceptional international keynote speakers across disciplines, as well as to present their own research (talk for PhD and poster for MSc students) and receive invaluable feedback from peers, keynote speakers, colleagues, and supervisors.

The best talk will be awarded with Olli's prize, which is a 1000 € sponsorship for an international conference. There will also be prizes for the runners-up and a prize for the best poster. Most excitingly, by getting rid of any pandemic restrictions, this year we can go back to our tradition - enjoy the Grande Finale at the Finnish Museum of Natural History! And all the winners of prizes will be announced by our keynote speakers on the last evening in the Grande Finale.

In this booklet, you can find all the programme of the symposium, with all abstracts listed chronologically. We hope that you will join as many sessions as you can, and to provide invaluable feedback to the students.

We hope you enjoy the Spring Symposium!

The Organizing Committee,
Deryk, Joséphine, Nora, Thomas, Yuhan.

Contents

Programme

32nd LUOVA Spring Symposium

Location: Viikki campus, Infokeskus Korona, Oppimistori 1054 (Library main auditorium)

Time	Monday, 6th Mar	Tuesday, 7th Mar	Wednesday, 8th Mar
09:00 - 09:15	Morning coffee	Morning coffee	Morning coffee
09:15 - 09:30	Opening words		
	Keynote Talk	**Keynote Talk**	**Keynote Talk**
	Attila Hettyey	**Kristiina Tambets**	**Pol Capdevila**
09:30 - 10:30	Phenotypic plasticity in chemical defences of a vertebrate: Responses to predators, competitors and pathogens	Biological history in our genes – an archaeogenetic view on the origin and spread of our species.	Bringing resilience on board: marrying the theoretical concept with empirical data across ecological systems
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10:45	**Session 1**	**Session 4**	**Session 7**
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11:00 - 11:15	**Thomas Merrien** — A new ancestral range reconstruction model to investigate the role of barriers in shaping global patterns of biodiversity	**Luisa Fernanda Rodriguez Carrillo** — Continuous capture process based on advection-diffusion-reaction models within Joint species movement modelling	**Sonia Repetti** — Winners and Losers: Integrating phenotypic and transcriptomic responses of algae to salinity change
11:15 - 11:30	**Gregory Andreou** — Can plants keep up? Investigating temperature-mediated plasticity in *Arabidopsis thaliana*	**Eva Karin Rohlfer** — Infaunal contribution to seafloor respiration in sedimentary coastal habitats	**Beatriz Cunha Portinha** — Hybridization allows for better reproductive output under a wide range of temperatures: preliminary insights from wood ants
11:30 - 11:45	**Zowi Oudendijk** — Evolution and prevalence of de novo synthesized pyrazines as chemical defence in Arctiinae species	**Teresa Abaurrea** — An increased begging behaviour compensates mite abundance in the Common cuckoo-common redstart system	**Camila Souza Beraldo** — Effect of temperature in the microbiota composition of a parasitoid wasp
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13:45 - 14:00	**Mikael Englund** — Exploring imaging techniques in integrative insect systematics: case study on an undescribed African geometrid moth (Lepidoptera: Geometridae)	**Thais Ferreira-Araújo** — Resolving the mystery of freshwater breeding flounders	**Basile Marteau** — Comparison on the role of vernal pools and lakes on bats activity linked with the emergence of flying insects
14:00 - 14:15	**UH Biological Stations** — Greetings and news from the University of Helsinki's biological stations. Also communicate with people from stations	**Leena Hintsanen** — Core of the protected areas hosts more cold-dwelling species than edge areas	**Jan Häge** — The genomic basis of rapid color change
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17:00 -	End of the day	End of the day	Grande Finale and Awards at Finnish Museum of Natural History (Registration required)
18:00 -		Drinks and dinner with Keynote speakers in Ambra - open to all (You need to pay your own bill)	

Keynote speakers

Attila Hettyey

Attila acquired his PhD degree at Eötvös Loránd University (2000-2005), Budapest, where he worked on sexual selection in anuran amphibians (sperm competition, mate choice, sexual coercion, and reproductive potential) under the supervision of János Török. Around 2010 he started to work on predator detection, inducible defences, and consequences of plastic antipredator responses with the help of Josh Van Buskirk (University of Zurich). In 2012, he acquired a Lendület grant of the Hungarian Academy of Sciences and started his research group at the Plant Protection Institute, Centre for Agricultural Research, Hungary. During the five years of the Lendület-project, he focussed on inducible changes in chemical defences and engaged in ecotoxicology, combining standard ecotoxicological testing procedures with methods of experimental ecology. Since 2017, he has been increasingly involved in research on chytridiomycosis and ranavirosis, including investigating how infection and disease progression depend on temperature, and how these processes depend on the host species and on the strain of the infecting agent. Now his research has been extended to investigating cryptic effects of pesticides on animal personality, immune function and thermal ecology. Most of his projects have focussed on anuran amphibians, but he also participated in experimental studies on other taxa, including slugs, insects, fishes, birds, and mice.

Kristiina Tambets

Kristiina Tambets is a professor of archaeogenomics at the Institute of Genomics, University of Tartu (UT). She defended her PhD (2004) in molecular biology at the Institute of Molecular and Cell Biology, UT on the phylogeographic studies of human mitochondrial DNA in Europe. She continued in Estonian Biocentre as a senior researcher on population genetics. In 2017 she was trained in ancient DNA lab work in LCHES, University of Cambridge. Since 2018 she has worked at the Institute of Genomics UT, where she has been one of the initiators of ancient DNA research in Estonia. She is a member of the council of the Collegium of Transdisciplinary studies of Archaeology, Genetics and Linguistics of UT. In 2020, she was a visiting researcher at the University of Turku, as a member of the interdisciplinary international expert group BEDLAN, studying the coevolution of genes and languages. Currently she is a visiting researcher at the University of Helsinki, in the KINURA team. Her research focuses on the transdisciplinary studies of human demographic history based on modern and ancient genomes. One of her current projects studies the genetic history of the populations of Eastern Europe, and the population structure and health of Estonian medieval population. Her CV could be found here: https://www.etis.ee/CV/Kristiina_Tambets/eng/

Pol Capdevila

Pol started his research at the University of Barcelona, where his PhD focused on understanding the natural dynamics and the resilience of Mediterranean marine species to global change. After his PhD, Pol gained a Ramon Areces Fellowship to do his first postdoc at the Department of Zoology, University of Oxford (2018-2020), where he combined large datasets and modelling tools to better understand what determines the resilience of species. Next, he gained a Research Associate position at the School of Biological Sciences, University of Bristol (2020-2022), where he studied the impacts of multiple stressors on vertebrate populations worldwide. In 2022 he gained a Maria Zambrano Fellowship and a Marie Curie Fellowship to work at the Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Universitat de Barcelona, where he is exploring the impacts of Marine Heatwaves on the resilience of Mediterranean marine populations and communities.

Abstracts

Day 1 (Monday, 6th March)

Keynote talk: Attila Hettyey

Department of Evolutionary Ecology, Plant Protection Institute, Centre for Agricultural Research, Eötvös Loránd Research Network, Herman Ottó út 15, 1022 Budapest, Hungary.
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Phenotypic plasticity in chemical defences of a vertebrate: Responses to predators, competitors and pathogens

Phenotypic plasticity is a core concept of evolutionary biology and there is ample evidence for adjustments to environmental conditions in a large diversity of traits. Environment-induced changes in chemical defences forms the basis of a large and diverse research field in plants but we know startlingly little about such plasticity in animals. Using the common toad (Bufo bufo), a species that is known to produce bufadienolide toxins, we tested whether tadpoles adjust their chemical defences to the presence and abundance of predators, competitors or pathogens. We performed correlative studies on natural populations and conducted a row of outdoor mesocosm and laboratory-based experiments. In the surveys we performed on natural populations toxin content of B. bufo tadpoles correlated positively with competitor density, but was not related to predator density. Also, toxin production seemed to be associated with the bacterial community structure of the aquatic habitat. Our experimental investigations provided evidence that B. bufo tadpoles can respond to chemical cues of predation risk by producing a higher number of bufadienolide compounds and larger total bufadienolide quantities. We also demonstrated that besides predators, competitors can also induce changes in toxin production, as B. bufo tadpoles contained larger quantities of bufadienolides at higher tadpole densities. In a study investigating how inducible chemical defences are adjusted when both predators and competitors are present, we found that B. bufo tadpoles can adjust their toxin production to predation risk and conspecific density simultaneously, and that at high tadpole densities the presence of predators does not induce an additional enhancement of chemical defences. In a study involving experimental infection with a potent fungal pathogen of amphibians, Batrachochytrium dendrobatidis, we did not observe pathogen-induced enhancement of chemical defences, but rather long-term negative effects on toxin production, which may compromise defences against microbes, predators and competitors. These results suggest that amphibians, and most likely many other animals, including vertebrates, may be able to adjust the synthesis of their defensive toxins in response to several types of threats.

Session 1 (Morning)

Purabi Deshpande (LUOVA)

Apples and oranges... and other fruits. Do frugivorous birds in Helsinki help the spread of alien plant species?

Alien plants introduced into cities can spread, potentially becoming harmful invasives. Seed dispersers like frugivorous birds play a role in this spread, but it is unclear how they interact with alien and native plants in cities. At higher latitudes, the risk of aliens escaping into the wild is imminent due to warmer climates and extended autumn bird migrations. Here we use Helsinki as a case study to investigate whether urban gardens provide birds with a fruit resource (in terms of abundance and plant origin) that differs from forest fragments, whether birds preferentially consume fruits of particular origin, and which seeds are likely to be dispersed. We find alien plants are present in forests, fruits are more abundant in gardens and native fruits are more abundant than alien fruits. More birds were detected in gardens and, despite the high number of alien plants in gardens, birds consumed more native fruits. In faecal samples, we find that contrary to our expectations, here is no difference in the origin of the seeds dispersed, and fewer seeds are dispersed during the end of the season. Indicating that the risk of alien plants spreading through birds is quite poor.

Thomas Merrien (LUOVA)

A new ancestral range reconstruction model to investigate the role of barriers in shaping global patterns of biodiversity

How did Biodiversity arise? What are the mechanisms behind the patterns of diversity we can see? All interactions between individuals and their environment can shape the evolution of life; the quest of evolutionary biologists being, then, to unravel how the different interactions and mechanisms are shaping the tree of life. Biogeography is a great way to summarize information about evolution as it allows to compile data about the environmental conditions of individuals, population, species, etc. Indeed, through biogeographic data you can find out what climate are species dealing with, or what other species they are interacting with. Using comparative phylogenetics, my aim is to develop a new model of explicit ancestral range reconstruction inspired by the previous Landscape Based Geographical (LBG) model (Bouckaert et al. 2012). I will assume that range evolution (i.e., species dispersion) is a diffusion process evolving along a phylogeny and across the geographical landscape. The simplest possible model assumes that the dispersal rate is constant over time and geographical landscape. Other flavors of the model can relax the constant-rate assumption by allowing rates to vary across geographical landscape and time. This flexibility enables testing different hypotheses for how spatial barriers and niche dependence affect range evolution over spatio-temporal scales. One of the aims of my PhD will then be to demonstrate the functionality of our model by testing how different geographical barriers and their dynamics affects dung beetles (Scarabaeinae) and lemurs (Lemuroidea) in Madagascar.

Gregory Andreou (DPPS)

Can plants keep up? Investigating temperature-mediated plasticity in *Arabidopsis thaliana*

As global temperatures rise, there is a growing concern as to how this will affect Earth's current inhabitants. Although seemingly static, plants sense unfavourable change in their environments and adapt. The accelerated increase in global temperatures may present a challenge to plants if they struggle to match the pace by adaptation through natural selection, as it is slow as requires many generations. However, adaptation can also occur at a much smaller timescale over a single individual's lifespan. This is termed phenotypic plasticity (PP) and describes intracellular changes within an individual that leads to the activation of several genes responding to environmental stimuli. Currently, there are only a few temperature-mediated plasticity (TMP) genes described in the model plant *Arabidopsis thaliana* and I wish to detail more. The main aim of my research is to identify genetic, molecular and environmental factors that control TMP in plants. In addition, I wish to reveal cellular, metabolic and hormonal links with PP. Intuitively, plasticity is beneficial by providing flexibility for adaptation, however, some traits are known to provide an advantage when they are canalised. To this, I will be assessing trends in fitness and PP that could aid in improving crop productivity, especially those closely related to *Arabidopsis* such as cabbage and rapeseed. Lastly, there is growing interest in how alternative splicing (AS) and the spliceosome affects PP. Alternative splicing in plants is known to be affected by temperature and allows the plant to diversify the range of mRNAs from a single gene. This is also an exciting area of research.

Zowi Oudendijk (LUOVA)

Evolution and prevalence of de novo synthesized pyrazines as chemical defence in Arctiinae species

Pyrazines are volatile, nitrogen containing heterocyclic compounds widely distributed in plants, insects, fungi, and bacteria and they act as an odour signal to repel predators. In insects, pyrazines are known to be used for a wide range of functions, such as mating attractants and aggression stimulants. However, recently more attention is being paid to their role as a defensive chemical. Aposematic and polyphagous insects can obtain methylalkylpyrazines through sequestration from the host plant or de novo synthesis by the organism itself. Studies on de novo synthesis of defensive compounds within insects are well known among beetles and other insects, while in moths and butterflies (Lepidoptera) this is yet to be explored. A well-studied model species, the wood tiger moth (*Arctia plantaginis*) was found to carry two unique defensive chemicals; sequestered pyrrolizidine alkaloids from their diet and de novo synthesized methoxypyrazines that they emit from their specialized cervical glands as neck fluid when they are provoked. For my doctoral research, I will examine whether other Arctiinae species and close relatives of *A. plantaginis* release neck fluid when provoked, whether it contains pyrazines, and if these are de novo synthesized. From this research, we will gain understanding of when this trait evolved, and its diversity and importance as a chemical defence across Arctiinae and other insects.

Patrick Heidbreder (LUOVA)

Towards speciation genes and the role of selection in hybridization outcomes

Hybridization between species has recently been recognized to be more common than previously thought and to play a role in a variety of evolutionary processes including speciation and adaptation. Selection for and against interspecific allele combinations shapes the evolution of hybrid genomes through time and is critical to the speciation process. However, the exact sources of selection, whether on phenotype or on intrinsic incompatibilities (i.e. incompatible alleles from the two parental species), and their relative importance remains unclear. The discovery of "speciation genes" (i.e. genes that contribute to reduced gene flow between diverging lineages) provides an approach to resolving which sources of selection are of importance in speciation. Using a system of naturally hybriding wood ants, *Formica aquilonia*, *F. polyctena* and their hybrids, I search for selection against intrinsic incompatibilities and temporally varying selection for loci putatively involved in adaptation. Preliminary exploration of genomic regions under selection has revealed signatures of selection for and against interspecific allele combinations. Temporal covariance has shown positive selection across the genome; work is ongoing to further pinpoint and characterize regions. Selection against interspecific alleles combinations occurs in a smaller number of loci within than between chromosomes, in line with previous research. Coming work will further investigate functional annotation at identified loci. Together this work expands our understanding of the relationship between selection and the evolution of hybrid genomes.

Session 2 (Afternoon)

Ilaria Pia (Domast)

Disentangling processes behind occurrence and abundance of whitefish larvae distribution using fisheries and larvae sampling data

We developed a hierarchical Bayesian model that explicitly considers processes behind occurrence and abundance of sea-spawning whitefish (*Coregonus lavaretus*) larvae distribution along the Finnish coastal region of the Gulf of Bothnia, and used it to predict larvae abundance under current climatic conditions and conditions corresponding to future climate scenarios. This species is sensitive to environmental degradation and increasing water temperatures, and stocks have already depleted in the period of 40 years. Whitefish spawns in late autumn and eggs hatch after ice break-up in spring. Correspondingly, we model both the selection of reproduction area by spawning adults and the overwintering survival of the laid eggs. We estimate the model parameters using data on fisheries catch, larvae sampling and environmental covariates, giving us power to better consider the distinct processes. Our results show that climatic covariates (salinity, temperature and the temporal extent of ice cover) have strong effect on both reproduction areas and recruitment of whitefish. Climate change is predicted to impact negatively both the amount of suitable spawning areas and thus the status of stocks.

Elmo Miettinen (LUOVA)

Living on edges – The roles of border zone and latitude in wild boar home ranges

The Finnish wild boars live in the northernmost edge of the species distribution range. Their population density is highest along the southern parts of the Finnish-Russian border, which is the first passageway to the country for wild boars dispersing north-westwards from Russia. It is important to understand the basics of local wild boar movement capacity to assess conflict risks (e.g., disease transmission and crop damages) and set grounds for further habitat use investigation. Therefore, we analysed the home ranges and movement patterns of 17 wild boars GPS-collared in southeastern Finland. For home range estimations we used minimum convex polygons (100% MCP) and kernel density estimation (95% and 50% KDE). The average home range size of the studied wild boars turned out to be three to five times larger compared to other wild boar studies from more southern latitudes. The individuals living in the border zone showed continuous transboundary movement. Daytime locations were predominantly on the Russian side, while locations on the Finnish side were mainly during nocturnal foraging visits. Preliminary results on foraging sites suggest that crop fields and supplementary feeding sites are actively visited. Due to the large home ranges and active use of human-induced food sources, these results underline the risk of African swine fever transmission. In addition, the study gives an example of the benefits of the restricted border zone for local wildlife.

Mikael Englund (LUOVA)

Exploring imaging techniques in integrative insect systematics: case study on an undescribed African geometrid moth (Lepidoptera: Geometridae)

State-of-the-art imaging techniques are useful in taxonomy, providing unambiguous illustration of structures and diagnoses, often being more informative than written descriptions. Non-destructive imaging techniques are particularly valuable when internal structures of rare species or type specimens need to be examined. We present a case study, demonstrating how integrative approach can be applied in systematics to describe a new species and genus. Our study taxon is a large and conspicuous geometrid moth from South Africa, which we will classify to subfamily Larentiinae. The species has been present in collections at least 129 years but it has not been formally described. Based on DNA barcodes from mitochondrial COIa and several nuclear markers, we determine the taxonomic position of this species through molecular phylogeny. Based on DNA barcode, the genetic distance to nearest available reference species is more than 8%. The presence of the intracellular bacteria Wolbachia was analysed to control for any potential instability of the molecular analysis, and to contribute to the general knowledge of this incompletely understood arthropod endosymbiont. We provide images to illustrate diagnostic characters using microscope and macro photo stacking, as well as scanning electron microscope (SEM). We also compare images of the wing venation and genitalia produced by traditional dissection and slide mounting with images produced without destroying or detaching body parts from the target specimens by Micro-CT x-ray scanning. Finally, we provide a description of the known distribution, habitat, host plant, immature stages, and parasitoids of the new species, *Chloecolora vergetaria* sp. n. Englund & Staude. The new species appears to belong to an isolated lineage being sister to *Scotopterygini* Warren, 1895. We place the new taxon in the tribe *Xanthorhoini sensu* lato and discuss the potential need to reclassify the tribal lineage.

Session 3 (Afternoon)

Paul Bangura (DENVI)

Linking vgll3 genotype and aggressive behaviour in juvenile Atlantic salmon (*Salmo salar*)

Aggressiveness can affect social hierarchies and result in the unequal distribution of resources, with aggressive individuals monopolizing access to food influencing growth. In Atlantic salmon, aggression has been found to have a genetic component, and growth also influences maturation timing. Maturation timing associates with a large-effect locus around vgll3, which is also linked to growth and condition, with vgll3*EE (early maturation) individuals having higher condition factor than vgll3*LL (late maturation). Here, we examine the possibility that aggressiveness may play a role in juvenile vgll3*EE individuals having higher condition factor by having increased food intake due to higher aggression promoting increased food access. This prediction was tested under a social context: aggressiveness and feeding activity in four size-matched individual salmon, two from each genotype, were observed over 95 trials. Contrary to our prediction, vgll3*LL individuals, not vgll3*EE, were more aggressive. Increased aggression of vgll3*LL individuals was independent of their sex and size, and genotypes did not differ in their condition factor nor feeding activity. These results imply that aggressiveness may have an energetic cost impairing growth and condition, especially when food cannot be monopolized. This may have critical implications for individual fitness and aquaculture practices.

Magnus Jonsson (LUOVA)

Populations dynamics of a socially behaving pest insect facing changes to their environment

Climate change is expected to increase the abundance and frequency of outbreaks in forest pest insects in Northern Hemisphere. For example, higher temperatures and longer growth season can result in a faster development, shortened reproductive cycles and hence possibility to produce multiple generations within one growth season. Therefore, to reliably predict how the probability of pest outbreaks changes under varying environmental conditions, we first need to construct realistic population dynamic models that take into account the ecology and life-history traits of forest insects. Using such models, we can then estimate parameters of traits and factors most likely to affect population growth and subsequent outbreak risks. In the following project, I will investigate how insects respond phenotypically and genetically for the changes in environmental conditions and how these responses can shape their population dynamics. As a study system I will use socially behaving Neodiprion sertifer pine sawflies. I will conduct factorial rearing experiments and field predation experiments to estimate how ecological and abiotic conditions shape the fitness of pine sawflies. In addition to experimental data, I will use modelling approach and simulations to test how different ecological (e.g. predation risk), social (sex ratio and group size) and life-history related factors affect population dynamics under different environmental conditions. These models can then be used to predict future outbreak risks in this species and potentially in other invasive species sharing similar life-history strategies.

Norman Göbeler (LUOVA)

Hotfloor: Developing in situ methods to investigate the effects of heatwaves on seafloor community structure and ecosystem functioning

The frequency of marine heatwaves is increasing not only in surface waters, but also in sub-surface layers causing devasting effects to benthic ecosystems. Previously insights into the effects of heatwaves were obtained through opportunistic field observations or manipulative laboratory experiments. Here, we introduce a chamber system ('Hotfloor') capable of inducing elevated water temperatures in benthic habitats in situ over several days, while constantly exchanging the water inside the chambers. The system uses technology normally used in domestic under-floor heating. We conducted a 15-day trial study in July 2021 in a bare-sediment habitat at 2.5 m depth exposing 5 chambers to water temperatures 5°C above ambient temperatures for 6 days and comparing with 5 control chambers. Sediment cores were collected from each chamber to assess the effects of a realistic marine heatwave on natural benthic communities and incubations during light and dark hours were performed to assess changes in ecosystem functioning (solute fluxes). The results indicate that while the benthic community structure remained similar between the treatments, elevated temperatures caused an increase in the magnitude of either efflux or influx of O2, NH4+, PO43- and Si. This study confirms the suitability of the Hotfloor system for examining the impact of temperature on benthic habitats in situ and demonstrates its potential for novel examination of complex habitats and communities, which is essential for our understanding of the ecosystem-level effects of climate change.

Day 2 (Tuesday, 7th March)

Keynote talk: Kristiina Tambets

Biological history in our genes – an archaeogenetic view on the origin and spread of our species.

The history book written into our genes allows a glimpse on very different aspects of the past of the human species. Stories about these remote events unfold with a level of detail that was difficult to even dream of a few decades ago. Where is the cradle of humankind? How has the natural selection and cultural background influenced our current genetic diversity? How does our knowledge about evolution help us to understand the challenges that our species is facing today? To answer these questions from a genetics perspective, we have now a toolbox that combines the state-of-the-art technological methods to isolate biomolecules from both modern and ancient organisms, bioinformatic tools to analyse these biomolecules and our capability to interpret the information hidden into large genomic datasets in a transdisciplinary framework. The biomolecules extracted from human remains allows us, in addition to the analysis of the genomes of modern and ancient people also to study, for example, microorganisms living together with humans. Their palette reflects both the lifestyle changes that have taken place over time, as well as diseases they might have caused. In my lecture I will introduce the development of archaeogenomics and illustrate it with geographically and temporally close and distant examples of the evolutionary history of human. The prospects of joint work of natural sciences and humanities to better understand large migrations and admixture between human groups as well as life trajectories of individuals are discussed.

Session 4 (Morning)

Tanya Troitsky (LUOVA)

When the bat's away, the pathogen will play -The protective role of the skin microbiome during hibernation

Hibernation is an effective strategy for animals to reduce energy costs during seasons with a low abundance of available food. Hibernating animals can remain torpid for months at a time without food or water. However, there are disadvantages to this strategy because the animal has a higher risk of infection due to its lowered immune response. This is the case with bats and white-nose syndrome (WNS), a disease caused by the skin-infecting fungus Pseudogymnoascus destructans (Pd). WNS has killed up to 90% of some hibernating bat populations in North America, yet European bats survive exposure to the pathogen well. Since the fungus originates in Europe, European bats may have developed a tolerance to it with the help of their skin microbiome. The skin of a bat is the first line of defense against pathogens, and it is colonized by a community of symbiotic microbes. These microbes benefit from the survival of their host; thus, it is not surprising that some of them have been found to have antifungal properties that may inhibit Pd. The skin microbiome of European bats may offer a potential solution to the WNS problem in the form of probiotic treatment. However, significant research gaps remain regarding the mechanisms behind the antifungal responses of microbes and the differences between the microbiome composition of unaffected European and infected North American bats. As climate change increases the spread of transmissible diseases, this information is urgently needed to mitigate WNS mortality.

Luisa Fernanda Rodriguez Carrillo (LUOVA)

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

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

Eva Karin Rohlfer (LUOVA)

Infaunal contribution to seafloor respiration in sedimentary coastal habitats

Coastal ecosystems have the potential to act as carbon sinks and benthic macrofauna affects coastal carbon processes both directly and indirectly. Most of the coastal habitats are bare-sediments and quantification of macrofaunal contribution to total seafloor respiration is challenging and cannot be measured directly. Seafloor flux measurements together with infauna community data over a large scale is scarce. In this study, we combine data (n =229) measuring seafloor respiration over environmental gradients in the finnish archipelago together with faunal abundance and biomass data to study the faunal contribution across depth and temporal and spatial scales. We show that faunal respiration is higher in shallow sandy stations (32% of seafloor respiration) compared to muddy stations (9% faunal contribution of seafloor respiration). A seasonal pattern with maximum faunal respiration in late summer was found for shallower stations but not for the deeper station. The faunal contribution to total seafloor respiration was highest in winter as seafloor fluxes were generally lower in shallow habitats. In deeper stations, the faunal respiration was relatively consistent over the year but seafloor fluxes in general were higher in deeper stations. However, highest faunal contribution could be found in August when seafloor respiration fluxes are decreasing and faunal respiration is relatively high. Taxa that were mostly contribution to faunal respiration were Macoma balthica, Mya arenaria, Marenzelleria sp, Hediste diversicolor and Hydrobia. Our results highlight that in shallow coastal areas, infaunal biodiversity in bare-sedimentary habitats influence carbon cycle processes as they are counteracting carbon binding processes and therefore need to be considered in Blue Carbon research.

Teresa Abaurrea (LUOVA)

An increased begging behaviour compensates mite abundance in the Common cuckoo-common redstart system

Nutrition and ectoparasite abundance can determine avian nestling behaviour during development, and thus, in theory, it could also affect nestlings of brood parasites and their hosts. However, knowledge about these interactions in brood parasitism is scarce. Here, we studied the influence of a carotenoid-rich diet on mite abundance, and the effect of mite abundance on the begging behaviour of Common cuckoos (*Cuculus canorus*) and its regular host in Finland, the Common redstart (*Phoenicurus phoenicurus*). To test this, we fed carotenoids to cuckoo and redstart nestlings for a week, sampled mite abundance from nestlings, and recorded begging behaviour. We found that none of the cuckoo nestlings had mites, while 76% of redstart nestlings did, which can indicate that cuckoos have a defence mechanism against mites. In redstart nestlings, we found no differences in mite abundance between carotenoid treated and control groups. Also, nestlings with more mites, begged more, but had slightly lower weight. Our results indicate that, given that a carotenoid rich diet does not contribute to buffering mite effects, redstart nestlings beg more to compensate the costs imposed by these ectoparasites.

Sunandan Das (LUOVA)

Phylogenomic systematics of snake superfamily Elapoidea, with discovery of a new family

Ancient, rapid radiation is the underlying cause behind the spectacular diversity of many prominent groups, such as Neoaves, placental mammals and elapoid snakes. Scarce phylogenetic signal on the short branches, obscuring of the already low signal by substitutional saturation on the long descendant branches and above all, pervasive incomplete lineage sorting (ILS) make rapid radiations in the deep past a contumacious challenge for systematists. Snake superfamily Elapoidea, a cosmopolitan, hyper diverse radiation of snakes, including some of the most toxic snakes like the cobras and mambas and also many unusual ones like the fossorial burrowing asps, is a classic example of an early Cenozoic rapid radiation and its phylogeny and classification has been in a state of flux. We have sequenced over 4500 ultraconserved elements (UCE) loci from representatives of every major named and unnamed elapoid subclades. We estimated gene trees from each locus with appropriate substitution model to avoid possible model violation and used the gene trees to infer multispecies coalescent (MSC) phylogenies with multiple algorithms and filtering strategies. The inferred phylogenies are surprisingly congruent and received very high statistical branch support. Even the supermatrix based Maximum Likelihood phylogenies, which are known to get misled by ILS, were also very similar to the MSC phylogenies. Our phylogenies led to the discovery a new family of snakes – Micrelapidae, with type genus Micrelaps. Several micro-CT scans have also been examined for the study which allowed us to place an enigmatic genus *Brachyophis* to the new family on the basis of cranial synapomorphy. The UCE phylogenies and the scans allowed us to revise and stabilise the family and subfamily level classification of the entire Elapoidea superfamily. Finally, we estimated divergence times using the complete UCE dataset and this indeed proved that all major subclades emerged within a short span of time in the Eocene.

Session 5 (Afternoon)

Sami Vikkula (DENVI)

Bayesian meta-analysis model for assessing bioeconomic impacts of oil on fisheries

The first part of my research focuses on developing a Bayesian meta-analysis model of oil impacts on early life stages of fish. Using the methodology of meta-analysis allows me to synthesize oil impacts from existing studies which is, among other things, more cost effective than creating data by conducting new exposure studies. Furthermore, using Bayesian methods to conduct the meta-analysis allows for the accumulation of information as a continuum. The model produces posterior probability distributions of the estimated oil impacts per species and per different oil type from prior knowledge and data. These posteriors can then be used as prior information in a subsequent analysis with the model when there is a need to update the impact estimates with new data. The meta-analysis model and its results can be used together with a population dynamics model to predict population level impacts of oil spill scenarios. The combination of the models could be extended to also predict economic impacts of an oil spill on fisheries. These estimates could work as a basis for calculating a fair compensation for damages to fishermen while still taking uncertainty, which is transparently evident in the posterior distributions, into consideration. The second part of my research concentrates on the ways of how to derive accurate economic impact assessments on fisheries from population level oil impacts.

Eetu Selenius (LUOVA)

How sexual selection contributes to maintaining color polymorphism in the wood tiger moth

Animal coloration is often directly linked to fitness through thermoregulation, crypsis, aposematism etc. As such, it is expected to be under strong stabilizing selection. Color polymorphism, the presence of multiple color morphs within a population, however, is common in nature and requires an evolutionary explanation. In some species color polymorphism could be maintained via opposing selective pressures from natural and sexual selection. We set out to test the role of sexual selection in maintaining the color polymorphism of the aposematic wood tiger moth (*Arctia plantaginis*), where a dominant white (W) allele and a recessive yellow (y) allele code for male hindwing coloration. Females carry these alleles, but do not express them similarly. We tested both the attractiveness of pheromone-calling females and the mating success of males with different color genotypes in the field, semi-field and fully controlled settings. We found that yy females were the most attractive among all genotypes and males approached them earlier. We also found that WW males had a significantly higher mating success compared to the yy males in all settings although offspring of Wy females had the highest survival. These results indicate that color genotypes can create different sex-specific mating advantages across the mating sequence, which could help explain the evolution and maintenance of color polymorphism.

Thais Ferreira-Araújo (LUOVA)

The Northern Flounder: A Hidden and Plastic Population of European Flounder?

The presence of marine flounders in Lake Pulmanki (Pulmankijärvi), connected by the river Tana in the northernmost part of Scandinavia, have sparked debates about its origin for over a half-century. We now know that they are not genetically distinct from the closest fjord (Tanafjord) but instead collectively comprise a genetically distinct flounder population in Northern Europe (Northern flounders). This project aims to determine if spawning is possible in freshwater and with additional sampling along the Norwegian coast, determine the geographic extent of this potentially unique characteristic of the Northern flounder. Current data indicate that the genetic differences between the Northern flounders and North Sea and Baltic populations are comparable to those expected between (closely related) species. This will be contrasted to the alternative hypothesis; that gene flow along the Norwegian coast is generally low across adjacent fjords that also could explain the genetic distinctiveness of the two populations. This project further seeks to reconstruct the phylogenetic history of the flounder across its distribution range and test to what extent this can explain geographic patterns of genomic regions associated with low salinity spawning. Understanding the evolutionary and population demographic history of flounders in Northern Europe is essential to better understand the impacts of fishing on stock dynamics and ecosystems across the northern distribution range as well as how to best preserve genetic variation for future evolvability of species.

Leena Hintsanen (LUOVA)

Core of the protected areas hosts more cold-dwelling species than edge areas

Climate change causes changes in species abundances and composition of ecological communities. Protected areas can mitigate climate-driven population changes. However, protected areas vary in their size and in habitat composition as do areas outside protected areas. The understanding of how the ecological communities are changing in relation to climate change and how such changes may vary spatially depending on land use at the landscape level is still lacking. Here, we evaluated how the temperature niche composition of breeding bird communities changed as the distance to the edge between unprotected and protected areas increased. We also evaluated whether the communities changed more drastically at a certain distance as the climate warmed, as well as the effect of the habitat on the communities. We used long-term community science bird data and land cover data from Canada 1997–2019 to analyse the variation in bird communities' average temperature niches with a linear mixed effect model. For this, we calculated the community temperature index (CTI) that allows quantifying the proportional dominance of warm- or cold-dwelling species in the community in space and time. Our results show that CTI was lowest in the core of protected areas as well as far outside them, compared to the protected area edges. We also found that CTI varied depending on the habitat type, which indicates that boreal needleleaf forest can maintain higher abundances of cold-dwelling species than human-modified habitats such as urban areas. Understanding the dynamics of the buffer zone around protected areas can improve management of entire landscapes and promote climate change adaptation.

Session 6 (Afternoon)

Raphael Ritter (LUOVA)

Maintenance of variation in a cooperative group defense against predators

While the evolutionary problem of the existence of cooperation is solved in principle, it is much less clear why individuals differ in their cooperativeness, i.e., how the benefits and costs of participating are distributed on the individual level and how they are shaped by social and ecological factors. We study this with the haplodiploid pine sawfly *Neodiprion sertifer* (Hymenoptera). The larvae of this species feed and defend in groups of 20-100 individuals. When attacked, they regurgitate a resinous fluid in concert which makes them less profitable for natural enemies. Data from our predation experiments show that contributing to the defense is beneficial as it increases survival, especially in larger groups. Despite this, not all individuals of a group participate in the defense, and we can see both within and among population variation in nature. Furthermore, our ongoing analysis suggests that this variation in cooperativeness can be explained by the associated costs in terms of life-history trade-offs as well as factors concerning the social environment. We also account for the effects of kin selection by quantifying the degree of within-group relatedness. The insights gained from these data sets enable us to understand the mechanisms maintaining variation in cooperativeness in nature.

Ella Sippola (LUOVA)

Going viral – Understanding the diversity of viruses in Nordic bats

Bats provide important ecosystem services but at the same time are often associated with public health concerns due to their potential as reservoirs of certain zoonotic pathogens. Many bat species utilise anthropogenic structures and roost frequently in human-occupied buildings. Several bat species occurring in Finland roost in close proximity to humans, highlighting the importance of uncovering which viruses are associated with bats and their ectoparasites at these northern latitudes. Feces are a potential shedding route of several viruses. As feces can be collected with non-invasive sampling techniques, they serve as excellent material in studying bat-associated viruses. Previous research also indicates that some bat ectoparasites carry microorganisms closely related to those with zoonotic potential, underlining the importance to study viruses associated with ectoparasites as well.   We conducted a virome analysis on ectoparasites and fecal samples collected from five different bat species (*Eptesicus nilssoni*, *Myotis brandtii*, *M.mystacinus*, *Pipistrellus nathusii* and *Plecotus auritus*) in Latvia and Finland. I present the preliminary results on the viral families discovered in both bat ectoparasites and bat feces. With climate change shifting bat species ranges northward and some species migrating long distances to their overwintering areas, understanding the diversity of bat ectoparasites as well as bat-borne and ectoparasite-borne viruses is crucial as they can be expected to undergo changes in the coming years.

Nora Bergman (LUOVA)

Conserved genetic diversity and weak founder effects after a rapid range expansion of a long-distance migrant (*Acrocephalus scirpaceus*)

Many species are currently experiencing range shifts, largely reflecting ongoing climate change. However, colonizing new areas can have serious genetic consequences for the shifting population. Repeated founder events are expected to erode genetic variation and reduce adaptive potential, possibly slowing or even halting the expansion. This is especially known to affect less mobile species with low gene flow, but whether highly mobile species are experiencing similar bottlenecks during range shifts is less clear. Here, we investigated the origin and genetic effects of a recent, northward range expansion of the Eurasian reed warbler (*Acrocephalus scirpaceus*). We compared evidence from historical observations, ringing data from range edge (Finland), and genomic RAD-seq data covering the European breeding range. All evidence supported a southwestern expansion origin. Nucleotide diversity was conserved along the expansion axis, but allele frequency clines revealed a weak founder effect. The results suggest that even philopatric species with high enough dispersal capability can escape the genetic costs of rapid range expansions, retaining adaptive potential in newly colonized areas.

Day 3 (Wednesday, 8th March)

Keynote talk: Pol Capdevila

Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Facultat de Biologia, Institut de Recerca de la Biodiversitat (IRBIO), Universitat de Barcelona, Spain

Bringing resilience on board: marrying the theoretical concept with empirical data across ecological systems

The current biodiversity crisis underscores the need to understand the capacity of natural systems to withstand ongoing global change. As such, resilience - the ability of a system to persist after, and recover from, a disturbance - has become a crucial concept in ecology and conservation. We know that ecosystems have the ability to avoid collapse by being resilient, but this capacity has a limit, a tipping point that when surpassed the ecosystem might collapse irreversibly. Quantifying the resilience of natural systems is therefore crucial to developing effective management plans. For instance, several international conservation targets have been set to maintain the resilience of natural systems to ongoing global change. However, ecological research has been hampered by a lack of coherent ways to define and quantify resilience comparatively. Therefore, resilience has often been conceived as a theoretical concept, with no clear means to be used by empiricists and managers. If ecology is to support and inform robust and successful policy, we must rectify this. To address this knowledge gap in this talk I will provide an overview of how ecologists define, quantify, and compare resilience across different study systems. I will also show examples from my own research at the level of populations and communities, and how these have helped us to better understand the resilience of natural systems. Finally, I will provide general guidelines to harmonise resilience research.

Session 7 (Morning)

Ankita Gupta (FoodHealth)

Presence of Porcine Noroviruses in Finnish pigs.

Noroviruses (NoVs) are small, non-enveloped viruses of the Caliciviridae family. They are classified into 10 genogroups (G) based on their major capsid protein (VP1). Genogroup II is commonly identified in both humans and pigs. Porcine noroviruses (PoNoVs) have their own genotypes (GII.11, GII.18 and GII.19). There is not much research done on PoNoVs in Finland. In the current study, a total of 189 fecal samples were collected from pigs from 12 farms located in Finland. RNA was extracted from fecal suspensions, followed by RT (reverse transcription)-qPCR. The genotypes were determined by Sanger sequencing of the PCR fragments amplified by conventional PCR. 50% of the farm was infected by PoNoVs (6 farms out of 12) and the age group of these infected pigs was between 4.5-6 months. One isolate was determined as GII.18. Genotyping of the remaining positive findings will be soon completed. We could demonstrate the presence of PoNoVs in Finnish pigs, as was expected. PoNoV infection was common in growing pigs which is in line with earlier studies.

Sonia Repetti (LUOVA)

Winners and Losers: Integrating phenotypic and transcriptomic responses of algae to salinity change

The Baltic Sea is considered particularly vulnerable to climate change, and many of its organisms, such as algae, live currently at the lower edge of their salinity tolerance range. This places them at risk of mortality due to environmental changes such as predicted freshening in the upper water layer. My PhD project, which began in January 2023, aims to integrate transcriptomic and phenotypic analysis of algae to explore their responses to changing salinity. Strains of *Phaeodactylum tricornutum*, a diatom that stands to be a 'winner' of environmentally driven salinity change due to its ability to adapt to changing conditions, and *Rhodomonas salina*, a so-called potential 'loser' of environmental change in the Baltic Sea due to its preference for higher salinity and recent declines across the Baltic, will both be grown along a salinity gradient and studied to determine changes in phenotypic traits as well as gene expression. Our multidisciplinary project combines genetic, cell biological and ecological perspectives, which will contribute to understanding of short-term and longer term evolutionary responses of algae in order to predict future environmental changes.

Beatriz Cunha Portinha (ILS)

Hybridization allows for better reproductive output under a wide range of temperatures: preliminary insights from wood ants

Hybridization is pervasive across the tree of life and is known to facilitate fast adaptation to changing environments via introgression of genetic variation between species. The global climate is changing intensely and rapidly, forcing species and populations to adapt to new and demanding conditions in short periods of time. In Southern Finland, the mound-building wood *ants Formica polyctena* and *F. aquilonia* are known to hybridize. Previous research indicates these hybridizing ants are well suited to address how hybridization can aid adaptation to increasing temperatures. The parental species are divergently adapted to temperature: *F. polyctena* is warm-adapted and *F. aquilonia* is cold-adapted. Hybrids are as resistant to heat as *F. polyctena* and, in hybrid males, the frequency of *F. polyctena* alleles rises in warmer years, while the frequency of *F. aquilonia* alleles rises in colder years. Thus, temperature is a key selective pressure to which these hybrids can respond quickly. Here, I exposed reduced numbers of hybrid and parental queens to different temperature regimes. I observed the effect of temperature on their reproductive output and on the early development of their offspring. Laboratory conditions were found to require an egg-laying forcing protocol prior to beginning the experiment. An efficient egg-laying forcing protocol was developed here, and will be included in the experimental protocol I will use for the large-scale experiment this Spring. Hybrid queens laid eggs under a wider range of temperatures compared to queens of the parental *F. aquilonia* species, and eggs from both types of queens developed faster at higher temperatures. These results provide important insights into the role of hybridization in fast adaptation to changes in temperature, and into how climate change will affect the reproductive output of queens and the early development of their offspring in wood ants.

Camila Souza Beraldo (LUOVA)

Effect of temperature in the microbiota composition of a parasitoid wasp

Insects' gut harbors diverse microorganisms — this community, also called the gut microbiota — affects their hosts' functional and ecological roles. It has been shown that environmental shifts caused by climate change, such as temperature variation, can disrupt the stability of the gut microbiota of insect hosts, with consequences for host fitness. However, few datasets on restricted systems are available to explore this question further. Thus, we know little about how temperature alters the microbiota of wild insect populations and the consequences of such changes for species' community ecology. Here, we investigate the effect of environmental temperature in the bacterial community of individuals of the parasitoid wasp *Hyposoter horticola*. Insects were reared in two different temperatures (26 and 28 °C) under controlled laboratory settings from larval to adult stages. We compared sequenced amplicons of the bacterial 16S rRNA gene of 39 individuals reared at 26 °C and 79 wasps reared at 28 °C. This study will help us understand how environmental temperature affects the diversity of bacterial symbionts associated with a parasitoid wasp and will bring new insights into the effects of climate change on the microbiota of wild populations.

Session 8 (Afternoon)

Nadja Verspagen (LUOVA)

Intraspecific variation in thermal plasticity in a temperate butterfly

Temperatures are rising due to climate change, and this especially impacts ectotherms because they are dependent on environmental temperature to maintain function. Changes in temperature for example affect body size, development time, phenology and stress resistance, and the combined effects of this have important implications for species' life histories. Often, research is done at the species level, thereby ignoring often-present differences between populations of the same species. Furthermore, research often focuses on one life stage, whereas different life stages may respond differently to temperature changes.

In my PhD I performed laboratory experiments using different populations of Glanville fritillary butterflies originating across latitudinal and altitudinal gradients to disentangle genetic and plastic responses to high temperatures across life-stages. Phenotypic plasticity can provide a fast response to adverse conditions and may allow species to persist long enough for evolution to occur, but can also be maladaptive in different circumstances. Therefore, knowing the interplay between adaptation and plasticity is important in predicting species' responses to climate change.

We found that larvae from higher latitudes and, to a lesser extent altitude, develop faster than those from lower latitudes and altitudes. Furthermore, we found differences in plasticity in adult resting metabolic rate across altitude, differences in adult lifespan across latitude, but no differences in stress response between southern and northern populations. In this talk, I will give an overview of the results obtained from experiments performed during my PhD, discuss general patterns and provide future directions.

Bijaya Neupane (DENVI)

Ecological Factors Determining Barking Deer Distribution and Habitat Use in the Mid-Hills of Nepal

Barking deer is found in dense tropical and subtropical forests of Asia. It is listed as "least concerned" by the International Union of Conservation of Nature and as "vulnerable" in Nepal, where it is also protected. Due to the habitat loss and fragmentation by human activities, barking deer abundance is decreasing, which may even ultimately lead to its extinction. This in turn might negatively affect local ecosystem such as the abundance of the endangered common leopard, for which barking deer is the main prey species in the mid-hills of Nepal. We therefore need to know factors affecting barking deer abundance and its habitat preferences. To determine these factors, we recorded barking deer either by direct sighting or by any evidence of its indirect presence observed through transect surveys in January and February, 2019. To analyze habitat preference, the presence of barking deer was set to 1 if the barking deer or any sign of its presence were observed "used plots," or to 0 if the barking deer or any sign of its presence were not observed ("habitat availability plot"). We measured main four ecological drivers such as forest management regime, microclimate, disturbance and food resources, which include 11 habitat characteristics in spots where barking deer was present, and in randomly selected spots. We found that elevation, slope, distance from settlement, presence of tree species, depth of leaf litter and percentage cover of leaf litter were most significantly affecting its presence. These results can serve as guidelines for local authorities to prevent decline in abundance of barking deer.

Basile Marteau

Comparison on the role of vernal pools and lakes on bats activity linked with the emergence of flying insects

Vernal pools are small temporary wetlands occurring in forested landscape. They have the particularity of partially or totally drying up over time. This characteristic makes them devoid of large aquatic predators such as fish. Vernal pools are understudied compared to other freshwater ecosystems such as lakes although they are considered as biodiversity hotspots. The aim of this study was to compare the use of temporary wetlands such as vernal pools by bats compared to permanent wetlands such as lakes. The hypothesis was to observe a higher increase of bat activity in vernal pools than in lakes related to the spatial and temporal abundance of the emergence of flying insects. *Myotis spp* activity were in general higher in the lakes than in the vernal pools, while the activity of *Eptesicus nilssonii* increased during the study regardless of the type of habitat. During this study no relationship was found between the emergence of insects and the bat activity. According of these results it seems that vernal pools may have a special importance for bats depending of the bat species.

Jan Häge (LUOVA)

The genomic basis of rapid color change

The ability of animals to rapidly change colors, sometimes within seconds, has fascinated scientists since Aristoteles. While this trait's cellular and subcellular basis has been described, we know surprisingly little about its genetic basis and evolution. In cichlids, a very diverse and species-rich fish family, this ability has been co-opted for a remarkable function: they employ rapid color change (i.e., physiological color change) as a unique way of communicating. By fading and enhancing their dark (melanic) markings on face (eye bar) and body (stripes) within only a few seconds they signal sexual interest to potential mates or aggression towards competitors. However, not all cichlids can perform rapid color change, which begs the question of why and how this ability evolved. As pronounced differences in the ability to rapidly change color exist between closely related species, we are offered a unique possibility to study the mechanistic basis and function of this remarkable trait. My Ph.D. project will combine cutting-edge molecular methods with behavioral experiments, to provide an in-depth understanding of why and how rapid color change evolved. My work will bridge disciplines and demonstrate how genetic changes underly the evolution of color-change communication and social behavior.

Session 9 (Afternoon)

Shraman Kumar Bohra

Molybdenum ABC Proteins of Archaeans as Models of Evolution: An in-silico approach

The diversified nature of ABC transporters is evident from their varying roles in different organisms. In bacteria, these transporters are mediators of antibiotic resistance (ex: DrrAB system in Mycobacterium smegmatis against tetracycline, chloramphenicol etc.), aid in lipoprotein trafficking (LOL system in E. coli) and facilitate the biogenesis of capsular polysaccharides. *Methanococcus maripaludis*, an archaeon that uses H2 and formate to meet energy requirements, is recognized here, given that formic acid production was common in the primordial Earth. Because molybdenum concentration is directly proportional to amino acid production and photosynthesis, indicating early earth oxygenation and molybdenum metabolizing capabilities in LUCA, the molybdenum utilization system is used here. Molybdenum ATP-binding cassette (ABC) transporter proteins are located by navigating the entire genome of this archaeon using Artemis. Nine molybdenum ABC proteins from the genome of *M.maripaludis* have been identified. ModA is used in this study. ProtParam revealed the relative stability index of the ModA to be 37.16. Hence, classified as stable. The average GC content of the DNA encoding this protein is 37.76%. The phylogenetic relationship of *M. maripaludis* is traced using MEGA. The co-expression levels of genes encoding similar proteins are studied using the STRING database. Phylogenetic analysis revealed the clear divergence of methanogens from other Archaeans. STRING analysis revealed striking similarities between ModA of *Methanococcus maripaludis* and ModB of Mycobacterium tuberculosis as well as E. coli. ABC transporter systems probably arose during the early stages of life. They are promising models of evolution because they are ubiquitously present in all forms of life.

Anna Haukka (LUOVA)

The iratebirds citizen science project: A dataset of birds' visual aesthetic attractiveness to humans

Amidst a global biodiversity crisis, shedding light on the factors that make humans like one species or another can inform conservation actions, e.g. by leveraging flagship potential, and help identify threats. A part of how humans perceive other species is due to their aesthetic attractiveness, or lack thereof, to us. We created the iratebirds -citizen science project to understand which bird species are visually more aesthetically attractive to humans. The data are from an internet browser-based questionnaire (iratebirds.app), where people were asked to evaluate their reaction to the appearance of a bird on a linear scale of 1-10 (with hearts as symbols on the scale). The ratings were based on the best-quality photographs from the Cornell Lab of Ornithology's Macaulay Library database which hosts user-submitted photographs of the world's bird species. The final data set covers the raw data as well as modeled visual aesthetic attractiveness scores for 11 319 bird species and subspecies globally, based on 6 212 respondents from tens of home countries. This is the first such attempt to quantify the overall visual aesthetic attractiveness of all the bird species to humans.

Laura Hiisivuori (DENVI)

Can we recognize emotions of tigers, monkeys and goats?
Co-authors: Anssi Vainio, Emma Vitikainen, Sonja E. Koski OEB, University of Helsinki

Introduction: Human ability to recognize animal emotions appears limited, but as research on emotion recognition is still scarce, the factors influencing it are poorly understood. Studies thus far have mainly tested recognition of domestic animals. We studied people's ability to recognize emotions of three zoo animal species (Barbary macaque, tiger and markhor). We assessed separately recognition of arousal and valence of the emotions to scrutinize emotion recognition in more detail. We hypothesized that recognition is influenced by the species' phylogenetic closeness to humans and that arousal is better recognized than valence.

Methodology: The material consisted of short clips of a tiger, a barbary macaque, and a markhor goat (5 of each, 15 in total) presenting emotions of high, medium and low arousal and of positive, neutral and negative valence. Of these we composed three video collections, each including five clips and each of the three species. The respondents evaluated the arousal and valence in the clips in 7-step Likert scales.

Results: We obtained answers from N=1127 respondents. We found that, as predicted, people recognized better the emotions of Barbary macaques compared to those of tigers and markhors (F=148.9 df=2, p< 0.001). We also found that valence was overall less accurately recognized than arousal (t= 8.91, df= 10941, p< 0.0001), while this also varied among the species. Species also differed in which emotions were better recognized than others.

Conclusions: Recognition of the three species' emotions was overall rather poor, but varied according to the species, valence and degree of arousal. Understanding the factors influencing animal emotion recognition needs more research, as improved recognition isis highly relevant for animal welfare in a wide range of contexts, as well as in improving human-animal relationships.

Laura Pietikäinen (DPPS)

Thermal plasticity of seed germination traits in European plant species

Biodiversity is under threat because of climate change. Our ability to predict the capacity of species to adjust to and persist under rapid environmental change is limited. We lack a coherent understanding of variability in the extent to which different species or even populations can adjust their phenotype according to changes in the environment (i.e. phenotypic plasticity) or adapt through evolutionary adaptation and whether this variability is predictable based on e.g. range size. Thermal plasticity in germination traits such as timing are understudied, known to covary with climatic variation, and can determine a plant's entire lifecycle. As a part of my PhD project, I am investigating thermal plasticity of seed germination traits in European plants of differing range sizes and in populations from the edges vs. core of species distributions. Preliminary results of these germination tests will be presented and their relevance in ex situ conservation and predicting biodiversity responses to climate change will be discussed.

Kaisa Kraft (LUOVA)

Multiplatform detection of filamentous cyanobacteria blooms in the Baltic Sea

Cyanobacteria form harmful blooms with potentially deleterious effects on recreational use, human and animal health, as well as ecosystem functioning. Despite extensive research, open questions still remain concerning the factors driving the bloom dynamics. Emerging high-frequency imaging-in-flow cytometry applications, such as Imaging FlowCytobot (IFCB), provide community composition information at frequencies impossible to attain using conventional monitoring methods. The instruments often operate in an automated mode producing continuous real-time big data. To analyze this data deployment of novel computer vision and machine learning systems is needed. Though producing information on the phytoplankton community in a completely novel manner, imaging-in-flow cytometry applications are yet still costly and rare, and deploying these systems is still an emerging field. Detection of phytoplankton pigments has been a more traditional high-frequency method to follow the community composition but lacks detailed information on the taxonomy. Comparing the imaging-in-flow cytometry applications with the more traditional high-frequency methods, such as fluorometers detecting pigments, can create novel ways to use and interpret previously collected data sets. Chl a fluorescence is usually considered a good proxy to describe the phytoplankton abundance, however, the primary pigment of cyanobacteria is not chl a but phycocyanin. The cyanobacteria biomass produced with an IFCB is compared with chl a and phycocyanin fluorescence as well as turbidity and the possibilities of utilizing these are further discussed.

Poster Titles

Day 1

1 Kasper Mickos
Investigating recent changes in species composition and abundance of littoral fish in SW Finland

2 Martti Levo
Comparing historic and contemporary plant populations to measure realized adaptation to climate change

3 Gabriela Lemoine
Timeline of *Chaenothecopsis consociata* parasitising *Chaenotheca chrysocephala* in Europe.

4 Andreas Lunde
Macrozooplankton communities of Svalbard

5 Pilvi Ahonen
Bird tick infestations: connection between the number of ticks and the species characteristics of birds and the development of tick abundance in recent years.

6 Julian Schach
Phylogeny of the *Cotesia acuminata* species complex parasitizing Melitaeini butterflies

7 Valeria Valanne
The effect of artificial light at night depends on lamp type and foraging guild on urban bats

8 Gloria Murari
Can AI be used for movement tracking in field experiments?

9 Patrick Selänniemi
Protected Area Deforestation in Tropical Countries

10 Karoliina Kinnari
Welfare assessments in Korkeasaari Zoo

11 Sanna Korhonen
Wolbachia infection status of Finnish *Ischnura elegans* damselflies

12 Heidi Myllylä
Considering animal welfare by monitoring shade availability and its use in large herbivores of Korkeasaari Zoo

13 Annina Malmsten
Comparing carbon stocks in urban meadows and parks in Helsinki

14 Lisa Treiber
How to identify a lioness if you only hear her calling?

15 Anssi Vainio
Zoo visitor's ability to interpret animals emotions and which factors affect it?

16 Adam Bloch
Tracking evidence of climate change through pine pollen

17 Katri Alavalkama
Reading an animal's mind - evaluating how people's general ability to feel empathy and their political views affect their interpretation of animal emotional states

18 Pauli Putkiranta
Detecting Spatial Patterns in Tundra Plant Communities Using High-Resolution Multi- and Hyperspectral Imagery

Day 2

1 Ella Ahti
Movement patterns of large carnivores in Sibiloi, Kenya

2 Susan Lindgren
How does artificial light at night affect a freshwater gammarid species?

3 Maria Lehmusvaara
Assessing the accuracy of forest biodiversity models for forest conservation purposes

4 Mihika Sen
Community perceptions of wildlife fencing in Laikipia, Kenya

5 Ronja Saarinen
Information hiding strategies in the common redstart (*Phoenicurus Phoenicurus*)

6 Francisco Silva
Amphibian and reptile diversity in a forest-rice-cashew mosaic in rural Guinea-Bissau

7 Riku Kangasniemi
Specialists in cities - Plant species composition differences on urban grasslands

8 Mirko Pomatti
Different results for the same Animal welfare assessment of different species located in Korkeasaari zoo. Species or assessor dependent?

9 Lola Fernández Multigner
Effects of Habitat Fragmentation per se on the Genetic Diversity of the Glanville Fritillary Butterfly

10 Ari Kaukiainen
Mapping reed beds using existing remote sensing time series data in combination with Corine land cover

11 Rebecca Nygrén
Visual perspective taking in horses

12 Silva Lehtonen
Impact of climate change on the top-down effect of a dominant mesopredator in the Baltic Sea

13 Markus Hiukka

Climate Change, A Butterfly Effect The effect of metapopulation dynamics and environmental change on patterns of genetic diversity in a population of *Melitaea cinxia*

14 Janita Ikonen

Assessing zookeepers' views on animal welfare

15 Marina Rodríguez Vilalta

Recording of small mammal vocalizations as a tool for species and population monitoring

16 Veikko Yrjölä

Comparing functional diversity of arthropods between mango plantation and savanna in Northern Ghana

17 Maria Reiman

Plant biodiversity and ecosystem functioning in a latitudinal gradient of heath forests in Finland

18 Tapani Neuvonen

New insights into the distribution and biology of smoke-flies (Diptera: Platypezidae: Microsaniinae)

19 Nicholas Armeni

How environmental heterogeneity and complexity affect the emergence and resilience of biodiversity in in-silico simulations