Abstract book

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FACULTY OF SCIENCE
UNIVERSITY OF OULU

TIETEENTEKIJÄT
Oulun yliopiston akateemiset OYA ry

BIODIVERSE ANTHROPOCENES
UNIVERSITY OF OULU

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Audience Zoom-link: https://oulu.zoom.us/j/67399406891

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MORNING SESSION

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14:20 - 14:40 Coffee break

14:40 - 15:00 Jacob Pavlin *Dendroecological perspective on tree growth patterns across a gradient of shade tolerance in primary temperate forests of Europe*

15:00 - 15:20 Lauralotta Muurinen *Trait responses and long-term diversity changes in herb-rich forests under global change*

15:20 - 16:00 Dr. Tiina Väre *Breastfeeding in 19th century Southwestern Finland according to δ15n and δ13c values in horizontally cut dentin segments of archaeological first permanent molars*

16:00 - 16:20 Closing words and a special talk by **Prof. emeritus, Dr. Esa Hohtola**

Friday, 10.12.2021

WORKSHOP

Introduction to Finnish common bird monitoring data and example analyses using R

Time: **9:00 - 12:00**

Location: **online in Zoom** https://oulu.zoom.us/j/67131707902

Instructor: **Dr. Aleksi Lehikoinen**, Senior curator of Monitoring team, The Helsinki Lab of Ornithology, Finnish Museum of Natural History, University of Helsinki

The workshop will be an introduction to the data types of the breeding bird monitoring schemes of line transects and point counts as well as winter bird surveys. Dr. Lehikoinen will explain how to calculate population trends of species during winter and breeding season and shifts in species center of gravity. Also, brief examples how the data has been used earlier will be given. All the analyses will be conducted in R. No previous experience in R is needed, but basic skills will be useful.

POSTER SESSION, 8-10.12.2021

Posters will be displayed at the Ecology and Genetics research unit coffee room (J-exit, 2nd floor, Linnanmaa campus, University of Oulu) during the three days of the event.

Metsähallitus (Forest and Park Service), Our role in wildlife conservation / monitoring of wildlife

Tuomo Ollila

Metsähallitus, Rovaniemi, Finland

The department of Parks and Wildlife is a part of both Metsähallitus and the Finnish Environmental Administration, and it is responsible for the management of National parks and other conservation areas. The monitoring and conservation of designated animal species such as the Saimaa ringed seal, arctic fox, peregrine falcon, gyrfalcon and lesser white-fronted goose fall under its responsibilities as well. Monitoring of large carnivores, especially wolverines in Lapland, is also one of its key tasks.

Additionally, Metsähallitus carries out surveys, monitoring efforts and conservation actions for several other species and habitats. One of the key tasks is the compilation of golden eagle breeding data, which is utilized in the territory-based compensation system for damages caused to reindeer husbandry by the eagles.

Metsähallitus itself does not conduct research, but it co-operates with universities, research institutes as well as with individual researchers. The collected data is normally available without financial compensation, but access requires a mutual agreement where the purpose of use and other legal aspects are defined.

Step-length parameter in movement analysis: improvement based on the dead reckoning in combination with GPS telemetry

Monika Faltusová[1*], Miloš Ježek [1], Václav Silovský[1], Astrid Olejarz[1], Justine Güldenpfennig[1], and Michaela Másílková[1]

1 Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague, Prague, Czech Republic
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The Global Positioning System and biologging technology can provide a range of precise positions for free-range animals with short, fixed intervals, which makes them suitable for long-term monitoring. Speed and distance traveled provide quantifiable links between behavior and energy and are among the metrics most often estimated from animal tracking data. We focused on the speed of the animals, more precisely, daily distance traveled (DDT). There are several methods to estimate the DDT; however, their accuracy is still debated. We compared the values of this parameter obtained by two different methods (DDT based on GPS telemetry and dead reckoning). We used data for two species (wild boar, red deer) tracked by a GPS collar with high-resolution accelerometer and magnetometer sensors. For the analyzes, we used 45 collared animals with an average tracking period of 325 days. Preliminary results show that the values for the average DDT of deer and boar calculated by these two methods differ significantly. As expected, lower values were obtained through the method based on GPS telemetry, and higher values through the found by dead reckoning. The DDT based on dead reckoning is 1.7 to 2.1 times greater than the DDT based on GPS telemetry with positions recorded at 30-minute intervals depending on gender, age category, and season. With the interval of GPS fixes changed to 1 hour or 2 hours, the dead reckoning DDT values are 2.6 to 3.4 and 4.3 to 7.1 times greater respectively. This is the first study to compare the mentioned methods. Given that animal monitoring has been a critical area of interest for biologists for decades, the study provides a new approach to movement pattern research and can contribute to improving wildlife management.

Increased nocturnal activity of wild boars in the Czech Republic during the first COVID-19 lockdown

Astrid Olejarz[1], Monika Faltusová[1], Justine Güldenpfennig[1], Václav Silovský[1], Miloš Ježek[1], Tomasz Podgórski[1]

1 Department of Game management and Wildlife Biology, Faculty Forestry and Wood Sciences, Czech University of Life Sciences Prague, Prague, Czech Republic

The COVID-19 pandemic had a major impact on human mobility. To control the spread of COVID-19, lockdowns have been declared in many countries. The restricted human activity during these lockdowns caused a change in human-wildlife interaction. Over this time, wildlife experienced a decreased human pressure in space and time, also defined as the "Anthropause". However, in the Czech Republic, the COVID-19 lockdown had the opposite effect on wildlife. During the first lockdown, when the state of emergency was declared, human visitation increased in a suburban forest near Prague by a factor of five. In this study, we investigated the effects of the increased human activity during the first lockdown in the suburban forest near Prague on the movement behavior of wild boar. We analyzed the movements of 40 wild boars equipped with GPS devices in the forest "Kostelec and Černými Lesy" in the Czech Republic during the first COVID-19 lockdown and compared them to the same period in 2019 without COVID-19 restrictions. An automatic counter collected daily human activity by counting humans entering the forest on the road. Our analysis shows that wild boars move 42 m more at night per unit of 150 people visiting the forest. We conclude that the recorded high human activity during the first COVID-19 lockdown in the suburban forest affects wild boars' temporal movement and causes increased nocturnal activity.

Application of ground penetrating radar (GPR) in studies of burrow systems of fossorial mammals

Hannah Othen

Czech University of Life Sciences Prague, Prague, Czech Republic

This study will advance ground penetrating radar (GPR- a geophysical technique for detecting near surface features) usage for detecting and describing aspects of burrow systems in fossorial mammals, specifically moles (Talpa europaea). There are three main aims: to propose the best methodology employing GPR to map the mole burrows, to examine the consistency of mole burrows over time in different seasons and to compare the tunnels in locations with and without electromagnetic interference to verify the potential magnetoreception skills of moles. From the preliminary survey it is apparent, that the 750 MHz antenna depicts the length and depth of complex mole tunnels with greater precision than 450 MHz antenna. In summary, this project builds a valuable link between zoology and geophysics, inferring fundamental navigational mechanisms from geophysical responses. The project uniquely moves beyond simple geophysical imaging and gives fundamental zoological and ecological context to the observed data.

How does environment variation shape wildlife microbiota?

Phillip C. Watts

Department of Biological and Environmental Science, University of Jyväskylä, Jyväskylä, Finland
Email: phillip.c.watts@jyu.fi

Animal gastrointestinal tracts house complex communities of microorganisms (predominantly bacteria, fungi, protists and viruses) known as the microbiota. The gut microbiota can have an important impact on the health of their host through impacts on, for example, the host's ability to utilise dietary material, immune function and defense against pathogens. As such, there is much interest in understanding the types of processes that affect the community composition of the gut microbiota. Here, I outline how variation in environment, such as that derived from pollution and changes in land use, can have a notable effect on the composition of the gut microbiota, and thus a potential impact on wildlife health via a concomitant change in the types of services that are delivered to the host. However, despite an accumulating number of studies that find an association between a change in the environment and a change in microbiota composition, it remains challenging to identify either the drivers of the variation in gut microbiota and/or the services that are affected. In particular, there is a need for considerable care when identifying the relevant drivers of variation in gut microbiota in studies of wildlife, that typically are limited in time and space.

Infection and coinfection status and identity of four systemic pathogens are associated with shifts in gut microbiota of wild bank voles

Ilze Brila[1,2], Anton Lavrinienko[2], Eugene Tukalenko[1,2,3], Eva R. Kallio[2,4], Tapio Mappes[2], Phillip C. Watts[2]

1 Ecology and genetics unit, University of Oulu, Oulu, Finland
2 Department of Biological and Environmental Science, University of Jyväskylä, Jyväskylä, Finland
3 National Research Center for Radiation Medicine of the National Academy of Medical Science, Kyiv, Ukraine
4 School of Resource Wisdom, University of Jyväskylä, Jyväskylä, Finland

Gut microbiota, the collection of microorganisms inhabiting the gastrointestinal tract, provides essential services to its hosts and has been shown to affect numerous aspects of host physiology and health. Various pathogens have been shown to associate with shifts in gut microbiota, potentially affecting host-pathogen interactions. However, our understanding of the associations between systemic infections and gut microbiota, especially in wild animals, is limited. Furthermore, though coinfection is common in natural populations, the potential impact of coinfections on gut microbiota are poorly known.

Here we examine whether gut microbiota of wild bank voles (*Myodes glareolus*) is associated with infection status *per se*, coinfection status, and pathogen identity. We used 16S rRNA gene amplicon sequencing to characterize the gut microbiota of 173 bank voles trapped in two locations in Finland (Harjavalta and Kemi-Tornio). We determined the infection status of four pathogens commonly found in bank voles: bacteria *Anaplasma phagocytophilum*, and *Borrelia burgdorferi s.l.*, apicomplexan protozoa *Babesia microti* and *Puumala orthohantavirus*.

We found that shifts in gut microbiota α-diversity associated with pathogen infection were modified by coinfection, and that gut microbiota community composition was associated with both infection and coinfections status, while community dispersion (inter-individual variation) was associated with coinfection status. Furthermore, we identified pathogen specific associations with gut microbiota α-diversity, community composition and dispersion. Thus, we show that systemic pathogen infection is associated with changes in gut microbiota of wild rodents and highlight the need to consider gut microbiota when studying host-pathogen interactions.

Using a multi-omics approach to investigate the cycling of arsenic and antimony in Northern peatland soils

Stefan Lambert

University of Oulu, Oulu, Finland

High levels of toxic metals such as arsenic and antimony can be observed in peatlands and have different sources of origin. One of these possible sources are contaminated surface waters derived from mining operations. In Finland, peatlands are often used as passive mine wastewater treatments, which can result in an increase in toxic metalloid concentration.

Previous studies in peatlands in Finnish Lapland indicated that microbial transformations of arsenic and antimony play an important role in contaminant removal. However, the studies also revealed many gaps in our understanding of microbial cycling and the genetic pathways behind the observed transformations of arsenic and antimony. Furthermore, it is still uncertain how arsenic- and antimony-metabolizing microbial communities have adapted to face extreme conditions of high toxic metal concentrations and the low temperatures of the Northern climate. Consequently, these peatlands with high arsenic concentrations constitute an ideal site to better understand the microbial community composition in extreme conditions.

Part of this project aims to (i) compare microbial communities and arsenic/antimony-cycle genes in peatlands with different lengths of exposure to arsenic and antimony in high concentrations by metagenomics and –transcriptomics, (ii) resolve pathways in the cycling of arsenic and antimony in peatlands that are so far not sufficiently understood.

Assessment of microbial and physicochemical risks affecting the quality of potable water supplied by shallow groundwater wells in Finland

Kevin J Lyons[1], Anna-Maria Hokajärvi[2], Jenni Ikonen[2], Ari Kauppinen[2]*, Ilkka T Miettinen[2], Tarja Pitkänen[2,3], Pekka M Rossi[1], Katharina Kujala[1]

1 Water, Energy and Environmental Engineering Research Unit, University of Oulu, Oulu, Finland
2 Finnish Institute for Health and Welfare, Expert Microbiology Unit, Kuopio, Finland
3 Faculty of Veterinary Medicine, Department of Food Hygiene and Environmental Health, University of Helsinki, Helsinki, Finland
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Surface water intrusion and certain kinds of land use can threaten the use of groundwater for potable water supply. In our study, water samples were taken from 28 groundwater wells situated in shallow aquifers used as sources of potable water in Finland. The aim of the study was to reveal links between microbial, physicochemical, and environmental variables that might prove useful in predicting and preventing contamination events. Water samples were assessed for physicochemical water quality, microbial indicators, stable water isotopes ($\delta 18O$ and $\delta 2H$) and bacterial community composition (using 16S rRNA gene amplicon sequencing at the DNA and cDNA levels). High levels of turbidity, heterotrophs, iron, and total nitrogen compromised water quality in some wells, with values up to 2.98 NTU, 16,000 CFU/mL, 2,300 µg/L and 8.1 mg/L respectively. Coliforms were detected in fourteen wells, and general faecal indicator *Bacteroidales* bacteria (GenBac3) in ten wells. Bacterial communities were largely dominated by *Patescibacteria* (43.5%) at the DNA level, and *Gammaproteobacteria* (31.9%) at the cDNA level. Stable water isotope analysis revealed indications of surface water intrusion in five wells, and d-excess values were positively correlated with alpha diversity metrics of DNA-based bacterial communities ($p < 0.05$), suggesting that surface water intrusion is associated with increased bacterial community diversity in these groundwater wells.

Enrichment of Hormone-Degrading Microorganism with Potential Bioengineering Applications in Small-Scale Wastewater Treatment Systems

Katharina Kujala[1], Laura Heisel[2], Johannes Holert[2], Bodo Philipp[2]

1 Water, Energy and Environmental Engineering Research Unit, University of Oulu, Oulu, Finland
2 Institute of Molecular Microbiology and Biotechnology, University of Münster, Münster, Germany

In remote areas in northern Europe, wastewater treatment is decentralized, and wastewaters are often treated directly at the source with onsite treatment system. While package plants, one typical treatment solution, work well in removing BOD, nitrogen and phosphorus from wastewater they often do not effectively remove emerging organic micropollutants like pharmaceuticals or steroid hormones. Microorganisms capable of degrading such micropollutants could potentially be used in bioengineered treatment systems, e.g., in additional units designed for micropollutant removal. The present study aimed to enrich androgen- and estrogen-degrading microorganisms, as these hormones are amongst the most frequently occurring micropollutants. Potential degraders were enriched from municipal wastewater in flow-through reactors supplemented with low concentrations of testosterone, estradiol or ethinylestradiol. Artificial wastewater supplemented with each hormone individually was used for initial enrichment with successive transfers of actively degrading microbial communities to fresh medium. Hormone degradation occurred for all tested hormones and was stable over transfers, but degradation of testosterone was considerably faster than of estradiol or ethinylestradiol. Following the initial enrichment, the system's complexity was increased to approach real-life conditions, e.g., by increasing reactor size, addition of alternative carbon sources and/or real (sterilized) wastewater and by supplementing a mixture of all three hormones. It was observed that alternative carbon sources like acetate or ethanol slowed hormone degradation while addition of real wastewater did not. The microbial communities in the reactors were analysed by 16S rRNA gene amplicon sequencing and differed based on the hormone(s) supplemented. Communities in testosterone-supplemented reactors were dominated by *Comamonas* and *Pseudomonas*, in estradiol- and ethinylestradiol supplemented reactors by *Acidovorax, Pseudomonas* and *Agrobacterium* and in reactors supplemented with the hormone mix by *Comamonas, Pseudomonas* and *Stenotrophomonas.*

The combined results indicate that (i) microbes can remove steroid hormones from wastewater, (ii) alternative carbon sources might hinder the degradation process, (iii) *Comamonas, Pseudomonas* and *Acidovorax* dominate the degrader communities, and (iv) additional research and careful planning is needed for the implementation of bioengineered systems for the removal of micropollutants in onsite treatment systems.

Searching for pollutant recycler microbes in mining waste

Francisca Prieto Fernández

Water Resources and Environmental Engineering research unit, University of Oulu, Oulu, Finland

Mining operations generate considerable amounts of waste materials, creating contaminated sites in the vicinity of the industrial installations. Tailings are one example of mine waste, and its storage represents an environmental challenge. On the one hand, tailings have an impact on the environment due to the potential release of metals and metalloids (e.g antimony) to natural ecosystems. On the other hand, mine waste might still contain small amounts of valuable metals (e.g copper) that were not extracted in the first place. This PhD thesis work aims to find biological tools to solve current environmental issues of mining industry. The main goal is to identify, isolate and characterize microorganisms from sites contaminated by mining activities such as tailings. In this way, it will provide alternative solutions for the removal of priority pollutants (bioremediation) and the extraction of mineral raw materials (biomining).

Feralisation as a model for evolution in the chicken

Dominic Wright

University of Linköping, Linköping, Sweden

Feralisation is the complex evolutionary process that occurs when a domestic population is returned to the wild. Feralisation thus involves the sudden return of both natural and sexual selection, which domestic populations to a large extent are sheltered from. The feral chickens on the Hawaiian islands provide a unique opportunity to identify genes under selection in the wild and contrast those to genes selected during domestication.

To study both the genetic and phenotypic effects of feralisation, we have sampled chickens from a variety of different Hawaiian Islands, as well as Bermuda (another feral island population of chickens), and assayed them for comb mass, bone allocation, plumage iridescence and behaviour. We have Whole Genome Sequenced over 500 birds and identified selective sweeps in common between the different feral populations. In addition, we have used Genome Wide Association Studies (GWAS) and expression (eQTL) GWAS to identify candidate genes exposed to sexual and natural selection.

Feralisation in many ways can be thought of as the reverse of domestication. Ever since Darwin the study of domestication has been of instrumental value for our understanding of evolution. Surprisingly, however, almost nothing is known about feralisation, although it promises to provide an invaluable tool for understanding the targets of selection in the wild. Feralisation offers the exciting possibility of identifying causal genes and their underlying polymorphisms that are responsible for traits that respond to both natural and sexual selection in a natural environment.

Comparison of utility of target enrichment and ddRAD in species delimitation: A test in admixing parapatric *Melitaea* butterflies

Mukta Joshi[1], Marianne Espeland[2], Vlad Dincă[1], Roger Vila[3], Mohadeseh Tahami[4], Lars Dietz[2], Christoph Mayer[2], Sebastian Martin[2], Leonardo Dapporto[5], Marko Mutanen[1]

1 Ecology and genetics unit, University of Oulu, Oulu, Finland
2 Leibniz Institute for the Analysis of Biodiversity Change (LIB), Zoological Research Museum Alexander Koenig, Bonn, Germany
3 Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Barcelona, Spain
4 Department of Biological and Environmental Sciences, University of Jyväskylä, Jyväskylä, Finland
5 ZEN Lab, Dipartimento di Biologia, dell' Università di Firenze, Sesto Fiorentino, Italy

Parapatrically distributed taxa pose a challenge for species delimitation due to the presence of gene flow and inherent arbitrariness of exactly defining the species boundaries in such systems. We tackled the problem of species delimitation in parapatric species pair of *Melitaea* butterflies, *Melitaea athalia* and *Melitaea celadussa*, using two popular genomic methods – double digest Restriction Site Associated DNA sequencing (ddRAD) and target enrichment (TE). The former is mainly applied at shallow and the latter at both deep as well as shallow phylogenetic scales. We conducted a test of phylogenetic, population genetics and species delimitation methods and compared the results obtained from these two approaches. We recovered consistent phylogenetic relationships across the datasets, both demonstrating the presence of a genetically distinct Balkan lineage and paraphyly of *Melitaea athalia* with respect to *Melitaea celadussa.* The same relationships were also reflected in species tree analysis using ASTRAL. Population genetic STRUCTURE analysis supported presence of two species in case of ddRAD but three species in case of TE, while the Bayes Factor delimitation analysis found both two and three species scenarios equally decisive in both datasets. As the results obtained from the two methods were largely congruent, we discuss some practical considerations and possible benefits of target enrichment over RAD sequencing.

Bacteria in streams: do network position and season matter?

Jacqueline Malazarte[1], Timo Muotka[1], Jussi Jyväsjärvi[1], Kaisa Lehosmaa[1], Kaisa-Leena Huttunen[1]

1 Ecology and Genetics unit, University of Oulu, Oulu, Finland

Stream networks exhibit longitudinal biodiversity variability from headwater reaches to the lowest downstream location. Microbial studies in stream ecosystems are increasingly relevant due to the functional capabilities of microorganisms that makes them fundamental in regulating the stability of aquatic ecosystems. According to the network positioning concept, the location of a site within the stream network exerts a strong control over local community composition and variability. Our goal in this study was to investigate whether bacterial communities at different positions along the stream network vary differently through time. Sampling was conducted in River Riisijoki (NE Finland) with thirteen sites at different network locations (upstream, midstream, downstream). Bacterial samples were collected at biweekly intervals from late May to October 2018 in different habitat types (benthic biofilm, water column, riparian soil) and were identified using 16S rRNA amplicon sequencing. Water-column (but not biofilm) communities displayed a steep decrease along the network in both taxonomic richness and evenness ($R^2 = 0.77$; $R^2 = 0.79$, respectively), reflecting the loss of soil-derived bacteria as the river widens and aquatic processes are more weakly connected to riparian soils. Bacterial community composition also showed a significant turnover of community composition from headwaters toward downstream sites, being mainly related to variation in stream pH for bacterioplankton and water temperature for biofilm communities. Both water and biofilm communities are dominated by Gammaproteobacteria with shifts in relative abundance that is attributed to the fluctuations of other taxa along the stream network. Riparian soil, on the other hand, is dominated by Alphaproteobacteria, Acidobacteria, and Gammaproteobacteria which are consistently distributed throughout the network. Additionally, biofilm and water-column communities displayed distinct seasonal variation, with closely similar communities in early summer and mid-autumn. In contrast, soil communities were largely aseasonal. Our study emphasizes the combined role of the stream network position and seasonality in shaping the diversity and composition of bacterial communities.

Nest distribution in relation to male leks in ruffs (*Calidris pugnax*)

Hanna Algora[1,2], James D.M. Tolliver[2], Veli-Matti Pakanen[1], Nelli Rönkä[1], Clemens Küpper[2] and Kari Koivula[1]

1 Ecology and genetics unit, University of Oulu, Oulu, Finland
2 Max Planck Institute for Ornithology, Germany

Ruffs *(Calidris pugnax)* provide a textbook example for intensive sexual selection and lekking. Ornamental males compete vigorously in mating arenas (*leks*) to attract visiting females (*reeves*).

Previous studies investigated the origin and maintenance of lekking including the importance of female choice and male-male competition as drivers of lek evolution. One remaining question is whether lekking evolved because males favour to aggregate around other males with high reproductive value (*hotshot hypothesis*), or male aggregations arise in areas of high female density (*hotspot hypothesis*)? Here we investigate the latter, predicting that leks are positioned in places most preferred by females. In our analysis we use spatial information on ruff leks and nests from a large breeding population at Liminganlahti, Finland, monitored over four field seasons. In ruffs, the females provide all parental care, and choice of nest location is crucial for reproductive success and survival. Appropriate nesting location needs to be safe from flooding, provide adequate food sources and protection from predators and male harassment for females and their offspring.

Specifically, we test whether ruff nests are uniformly distributed or whether they clump around certain areas such as leks.

This analysis will shed light on the potential importance of female habitat choice, for the evolution of male mating aggregations.

Settlement decision and reproductive strategy choice in response to conspecific attraction: a case study with Wood warblers *Phylloscopus sibilatrix*

Anna Yu. Kretova

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Birds can copy the breeding-site choices of conspecifics and settle near sites already occupied by others. This behavior is considered to be adaptive because the conspecific presence normally indicates availability of resources on the territory. I have experimentally tested whether the conspecific attraction lead to increase the local wood warbler (*Phylloscopus sibilatrix*) population size if the regional population density is low and whether the type of audio playback song affects the settlement decisions of birds. As shown for the wood warbler, males can distinguish the quality of an individual observed at the site by relying on their song performance (the rate of trill song) to make settlement decision. So I have used two versions of the song with a high and low rate of performance (6 versus 2 trills per minute) to imitate the presence of a 'good quality' and a 'poor quality' males at the treatment sites before the arrival of the first individuals and during the breeding season of 2021.

I found that the population density significantly increased only at the sites of 'good quality' males compared to control sites (no audio playback). However, the wood warbler population at these sites increased only due to the larger number of vagrant male (floaters) appeared at the site for a few days only. The number of resident males who was paired (or keep singing for a long time) did not significantly increased at any territory compared to control sites.

I put forward a hypothesis that floaters pursue a different strategy than resident males. In order to increase their chances to leave offspring, they move through the territory of resident males and copulate with their females. The strategy does not include the formation of a permanent pair with a female or adherence to a permanent territory and aims to leave as many extra-pair offspring in local nests as possible. The strategy may be beneficial where the number of males markedly prevail over females, for example, this is especially noticeable on the northern periphery of the range. I assume that floaters rely on the song activity of local males to find females before they begin to incubate clutches.

Impact of climate change on northern bird populations

Aleksi Lehikoinen

The Helsinki Lab of Ornithology, Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland

Global change puts pressure on individuals, species and communities, forcing them to either adapt, move or go extinct. Climate change has become an increasing driver of species populations leading to changes in species' phenology, population sizes and morphology. In this talk I will present what kind of changes have been observed in northern bird populations during recent decades and how these are linked with ongoing climate change, but also human land use changes. These examples are based on long-term monitoring datasets such as migration counts, line transects, winter bird counts and ringing collected by volunteer birdwatchers.

In general spring migration and breeding dates of bird species has advanced due to warmer spring temperatures. The phenological responses during autumn show stronger species-specific variation including both advancing and delaying autumn migration dates. Finnish bird populations have shifted their ranges towards north in recent decades during both winter and breeding season. This has lead into decline of northern populations and increases of southern populations and thus influencing the overall bird community. Population changes are however dependent also on habitat type and quality, where also protected areas have an important role. Northern birds show also changes in their morphology where both their coloration and size may be changing.

A bug’s life in dark waters: how stream macroinvertebrates react to a browning world

Joanna Brüsecke

Ecology and genetics unit, University of Oulu, Oulu, Finland

The browning of freshwaters is an ongoing phenomenon that has been observed in many different parts of the world. It is speculated to be caused by several co-occurring trends, such as changes in climate and land-use, and soil recovery from acid deposition. Regardless of the mechanism, browning is resulting from increased input of dissolved organic carbon (DOC), derived from the partial decomposition of terrestrial vegetation. The ecological impacts of browning are increasingly demonstrated in lake ecosystems, but such evidence from fluvial environments remains scarce. To investigate the effects of browning on stream biota, I surveyed stream microbes (bacteria and fungi) and benthic macroinvertebrates in 72 headwater streams, mostly draining in the River Iijoki watershed. These streams make up a gradient of different levels of DOC, ranging from clear waters (2.9 mg L^{-1}) to highly brownified (27mg L^{-1}). In my presentation, I will focus on the patterns observed in benthic biofilm quality and macroinvertebrate communities. Both the total number of macroinvertebrate taxa and the number of disturbance-sensitive EPT taxa significantly decreased with increasing DOC. According to redundancy analysis (RDA), DOC, alongside with water temperature and pH, significantly controlled macroinvertebrate species composition. The Threshold Indicator Taxa Analysis (TITAN) indicated a threshold of community composition change occurring at a range of around 12 mg L-1 DOC to 15 mg L-1, with many DOC-sensitive taxa decreasing, and a few, DOC-tolerant species, increasing. Many boreal streams are currently approaching that DOC-range and future browning can thus be expected to cause marked changes in stream biota.

Dendroecological perspective on tree growth patterns across a gradient of shade tolerance in primary temperate forests of Europe

Jakob Pavlin

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Shade tolerance is a crucial life-history trait affecting forest dynamics and species distributions. Moreover, the concern that disturbance regimes will alter as a consequence of ongoing climate change, affecting tree life histories as well as species distributions, is encouraging seeking further understanding of shade tolerance and associated growth pattern characteristics of tree species comprising native forests of Europe. Studies analyzing lifelong shade tolerance characteristics of European tree species are rare and mostly performed on a relatively small local or regional sample. With the application of dendrochronological techniques on an extensive database of tree core samples collected on permanent inventory plots across the primary forests of the Carpathians and the Balkan peninsula, we aim to analyze the growth pattern characteristics of dominant tree species (spruce (*Picea abies* (L.) H. Karst.), fir (*Abies alba* Mill.), beech (*Fagus sylvatica* L.), and maple (*Acer pseudoplatanus* L.)), associated with different shade tolerance capacities. Generally, beech and fir exhibit a higher potential to grow slow than spruce, while this potential is the lowest for maple. Consequently, a larger proportion of beech and fir trees establish under suppression in comparison to spruce or maple. On average, for beech and fir, a higher number of release events was detected per core in comparison to spruce and maple, indicating a larger capacity of these species to sustain multiple periods of suppression. In contrast, maple exhibits a higher potential to grow fast than spruce and fir and a particularly higher potential than beech, marking the competitive differences between the species under favourable conditions. A series of mixed models revealed that past canopy removing disturbances crucially affect the capacity of trees to grow fast, which implies that disturbance moderates competitive relationships between the focal tree species.

Trait responses and long-term diversity changes in herb-rich forests under global change

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Land use is the foremost cause of global biodiversity decline. It is suggested that responses vary with species traits, but long-term data on the trait-mediated effects of land use on communities are scarce. Here we utilize vascular plant trait data to study how forest understorey communities in Finland have been affected by land-use and canopy dynamics during 4–5 decades. We resurveyed 245 vegetation plots (original 1968, resurvey 2019) in boreal herb-rich forest understories, and used hierarchical Bayesian linear models to relate changes in diversity, species composition, average plant size (height), and leaf economic traits (specific leaf area SLA and leaf dry matter content LDMC) to reindeer abundance, forest management intensity, and changes in climate, canopy cover and composition. Intensively managed forests decreased in species richness and had increased turnover, but management did not affect functional composition. Increased reindeer densities corresponded with increased LDMC, evenness and diversity, and decreased height and SLA. Successional development in the canopy was associated with increased SLA and decreased LDMC and height in the understorey over the study period. Observed changes in climate had no discernible effect on any variable. In addition to direct impacts land-use and canopy changes affected diversity indirectly by altering average plant height. By favouring smaller species and limiting the size of plant individuals, increased shade and grazing pressure increased diversity. In addition, high light availability and reindeer densities favoured slower leaf economic traits. Our results show that functional traits can be highly useful in connecting vegetation changes to the mechanisms that drive them. Our findings also confirm that functional traits are both indicators and mediators of land-use change effects on plant communities, and underline the importance of including functional metrics in biodiversity monitoring programmes.

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Breastfeeding in 19th century Southwestern Finland according to δ15n and δ13c values in horizontally cut dentin segments of archaeological first permanent molars

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We have explored the breastfeeding practices in 19th-century Southwestern Finland, where according to historical documentation, artificial infant feeding was uncommon. We analyzed the δ15N and δ13C values in collagen of sequentially cut dentin segments of archeological first permanent molars (M1; N=4). The method allows studying breastfeeding as the dentin of M1 is formed in sequential order beginning from the top of the crown during infancy and the nitrogen and carbon isotope composition of its collagen reflects the diet of that period. The tissues of infants consuming their mothers' milk express trophic enrichment of both the values in comparison to the maternal tissues. In breastfed infants, this is observed in the M1 dentin segment closest to the occlusal surface that has formed during the first months of life. In dentin segments further from the top of the crown, formed during the period of weaning, both the values gradually deplete near the maternal baseline. Our results imply a markedly similar pattern of values in the M1s of all the subjects: it seems likely that in the 19th-century Southwestern Finland after exclusive breastfeeding during the first few months, weaning was initiated by the half year mark and breastfeeding ceased between the ages of 1.5 and 2 years.

POSTER

Rodent host population dynamics drive zoonotic Lyme Borreliosis and Orthohantavirus infections in humans in Northern Europe

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Zoonotic diseases, caused by pathogens transmitted between other vertebrate animals and humans, pose a major risk to human health. Rodents are important reservoir hosts for many zoonotic pathogens, and rodent population dynamics affect the infection dynamics of rodent-borne diseases, such as diseases caused by hantaviruses. However, the role of rodent population dynamics in determining the infection dynamics of rodent-associated tick-borne diseases, such as Lyme borreliosis (LB), caused by *Borrelia burgdorferi sensu lato* bacteria, have gained limited attention in Northern Europe, despite the multiannual abundance fluctuations, the so-called vole cycles, that characterise rodent population dynamics in the region. Here, we quantify the associations between rodent abundance and LB human cases and Puumala Orthohantavirus (PUUV) infections by using two time series (25-year and 9-year) in Finland. Both bank vole (*Myodes glareolus*) abundance as well as LB and PUUV infection incidence in humans showed approximately 3-year cycles. Without vector transmitted PUUV infections followed the bank vole host abundance fluctuations with two-month time lag, whereas tick-transmitted LB was associated with bank vole abundance *ca.* 12 and 24 months earlier. However, the strength of association between LB incidence and bank vole abundance ca. 12 months before varied over the study years. This study highlights that the human risk to acquire rodent-borne pathogens, as well as rodent-associated tick-borne pathogens is associated with the vole cycles in Northern Fennoscandia, yet with complex time lags.

POSTER

Stress assessment during hunting activities – use of bio-logging data

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Hunting has been part of human culture for three million years. First considered as only food acquisition, it is now part of every wildlife management strategy. Predominantly driven hunts, where a larger group of hunters and baiters with or without hunting dogs work together to reach predefined goals, are good tools to manage population levels. Concentrated on a few days during the winter months, driven hunts aim to decrease hunting pressure and hunting-induced stress, although other approaches state that driven hunts increase stress. Measurement of stress in free-ranging animals remains challenging and often involves shooting/capturing. The continuous development of tracking devices promises alternative methods, with using bio-logging data to determine physical activity and energy expenditure being one of them. We aim to assess the use of multisensory collars attached to free-ranging wildlife species such as wild boar to measure acceleration energy expenditure and movement behaviour in response to hunting events in a suburban forest close to Kostelec nad Černými Lesy in the Czech Republic. Overall dynamic body acceleration (ODBA) and the vector of the dynamic body acceleration (VeDBA) are considered acceptable proxies for energy expenditure. They can be calculated using three-axial acceleration data obtained from bio-loggers attached to the collars. So far, bio-logging data is available from 17 wild boar, with more data constantly incoming. Movement behaviour is defined using daily movement distance, home range and step-selection functions (SSFs). We found that wild boar tend to stay in their initial home range even if they are directly involved in battues, which was also observed in other studies, although the size of the home range increases. Similarly, the daily movement distance increases compared to the pre-hunt period. ODBA and VeDBA are increased only when directly involved in battues. Understanding the different avoidance behaviours, stress, and individual variability could help optimize hunting strategies to maximize the effect with serious consideration of animal welfare.

POSTER

Estimating Cecidomyiidae species richness in Finland using DNA barcodes

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Gall midges *(Cecidomyiidae)* are a hyperdiverse but inadequately studied dipteran family. The current number of described species is approximately 6600, but due to insufficient research, the real number of gall midge species is still regarded as unknown. Based on DNA barcodes, the number of gall midge species in the world is estimated to be as high as 1.8 million. Therefore, it is clear that complementary studies are needed to unravel the true diversity of gall midges. In Finland, no comprehensive inventories of gall midges have been conducted, and the known number of species to date is 384. The purpose of this study was to estimate the expected number of gall midge species occurring in Finland. Gall midges were collected from 8 sites across Finland using Malaise traps during summer 2020. Additional material from 11 sites from Lapland, collected in 2017- 2019, 1 from North Ostrobothnia (2015) and 1 from Northeast Finland (2017) were also included to the study. The standard barcode fragment of the cytochrome oxidase c subunit I (COI) gene was sequenced from 9025 gall midge specimens. Of the analyzed specimens, 7838 successfully returned sequences and formed 1420 operational species units of BINs (Barcode Index Numbers) that are treated as proxy for species in this study. The expected number of gall midge species included in the study material was estimated in R by using model-based extrapolations from rarefaction curves of the abundance data. The material is estimated to include 1.8-fold number of species compared to the analyzed proportion (approximately 1/3). Since the rarefaction curves did not reach the asymptotic, the further extrapolations are held unreliable and the data as insufficient. Therefore, the estimate of the number of gall midge species was not possible to conclude and the expected number of gall midges occurring in the area of Finland still remains unknown. Despite the lack of proper estimates, Finnish gall midge fauna can be stated to be multiple times richer than it is currently known to be. This supports the results of previous studies and estimates of gall midges being one of the most diverse insect families. The study also points out the efficiency of DNA based methods in "dark taxa" research.

POSTER

Hybrid Microbial Electrochemical Technology Constructed Wetland: The future of Nature-Based Wastewater Treatment Solutions?

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Constructed wetlands (CW) are engineered systems that take advantage of naturally occurring processes for the treatment of wastewater. As there are some drawbacks to conventional CW treatment, such as a relatively high area demand, combination with microbial fuel cell (MFC) principles has been suggested to improve CW technology. A hybrid CW–MFC includes the installation of an anode in the anoxic zone, where the metabolic activity of electroactive bacteria allows the consumption of organic compounds and release of electrons to the anode, which is connected via an external circuit to a cathode in the oxic zone, where electrons are used in the reduction of oxygen or nitrate. While many MFC-CW approaches target energy recovery, the potential use for more efficient removal of pollutants such as nitrogen has received less attention. Thus, this starting project will use a combination of laboratory and pilot-scale experiments to (1) identify microbial-driven processes involved in organic matter oxidation, nitrogen cycling and greenhouse gas emissions in bioelectrochemical systems, (2) assess the effect of material properties on microbial community composition and activity, and (3) to elucidate the effect of Artic conditions (e.g., low temperatures, snow and ice cover) on pollutant removal processes.

POSTER

Towards bio-literate Finland: a comprehensive DNA barcode reference library for Arthropods

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To associate specimens identified by molecular characters to other biological knowledge, we need reference sequences annotated by Linnaean taxonomy. We created a comprehensive reference library of DNA barcodes for the arthropods of an entire country (Finland), 2) published this library, and 3) delivered a new identification tool based on this resource. The reference library contains mtDNA COI barcodes for 11,275 (43%) of 26,437 arthropod species known from Finland, including 10,811 (45%) of 23,956 insect species. To quantify the improvement in identification accuracy enabled by the current reference library, we ran 1,000 Finnish insect and spider species through the Barcode of Life Data system (BOLD) identification engine. Of these, 91% were correctly assigned to a unique species when compared to the new reference library alone, 85% were correctly identified when compared to BOLD with the new material included, and 75% with the new material excluded. To capitalize on this resource, we used the new reference material to train a probabilistic taxonomic assignment tool, FinPROTAX, scoring high success. For the full-length barcode region, the accuracy of taxonomic assignments at the level of classes, orders, families, subfamilies, tribes, genera, and species reached 99.9%, 99.9%, 99.8%, 99.7%, 99.4%, 96.8%, and 88.5%, respectively. The FinBOL arthropod reference library and FinPROTAX are available through the Finnish Biodiversity Information Facility (www.laji.fi). Overall, the FinBOL investment represents a massive capacity-transfer from the taxonomic community of Finland to all sectors of society.

POSTER

East or west home is best: Homing behaviour of translocated female red deer

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Homing behaviour has been shown across many taxonomic groups including mammals but not fully described in controlled experiments of free-living large herbivores. Our study is focused on red deer response to homing ability, their spatial navigation and orientation in unknown environment. We tracked 23 individuals of female red deer in two different populations with using GPS telemetry for at least 2 years. We translocated all individuals (one by one) to new localities where the animals have never been before after first year of tracking. The release point was based on animal previous home range. Animals were translocated from 13 to 18 km away from home range centroids. All translocated animals were tagged with Daily Dairy (Wildbyte Technologies, UK) placed on the collars and set up for 10Hz sampling frequency of accelerometer and magnetometer. GPS telemetry were fixed every 30 minutes and support bio-logging data during dead-reckoning. Dead-reckoning analyses provided detailed reconstruction of homing movements and animals' compass heading. Twenty-one individuals return back to their home ranges. Results are showing different magnetic alignment directly after translocation, during homing and inside natural home range. We presume that north-south alignment preferences during stage after relocation are inducting 'head compass' calibration and triggering the process of navigation – homing.

POSTER

Possible Case of Partial Postmortem Fetal Extrusion – Preliminary Observations on the Mummified Remains of a Turn-of-the-19th-century Noblewoman in Finland

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We report a plausible case of partial postmortem fetal extrusion dating to the turn of the 19th century. A fetal skull protruded from the obstetric canal of the partially mummified remains of an adult woman buried in a private burial chapel in Vihti, South Finland. The fetal size implies the mother having died during the early third trimester of her pregnancy. The cause of death was not obvious from the limited external examination of her remains, but the underdeveloped state of the fetal remains renders it unlikely that this case represents a maternal death resulting from dystocia. Rather, the finding should be interpreted as a case of partial postmortem fetal extrusion, a process probably interrupted by decelerated decomposition of the maternal remains before full expulsion of the fetus.