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Abstracts



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The role of saltlicks in creation of spatial ‘hot spots’ with relevance for disease transmission among reindeer on Hardangervidda

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Wild reindeer (*Rangifer tarandus tarandus*) faced an outbreak of chronic wasting disease (CWD) in 2016. The disease poses a serious threat to cervid populations in Norway. Mitigation measures, including a nationwide ban on supplemental feeding of cervids and restrictions on artificial mineral licks, aim to curb disease spread. Mineral licks are suspected to be transmission hotspots, with evidence from the USA showing increased prion concentrations around these sites. Additionally, a 2019 footrot outbreak among reindeer on Hardangervidda highlights the urgency of understanding disease transmission dynamics.

This study aims to identify spatial clusters of reindeer, potentially acting as disease transmission hotspots, and determine their correlation with the location of saltlicks. Using GPS data from reindeer on Hardangervidda, the study will:

1. Quantify the proportion of spatial clusters near saltlicks throughout recent years.
2. Analyze the seasonal patterns of spatial clustering under varying weather conditions.

Spatial analysis will be performed on existing GPS data from approximately 170 reindeer, as well as positions of saltlicks on Hardangervidda to identify and quantify clustering patterns.

Use of salt licks by cervids in alpine areas of Norway and its relevance for disease transmission

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Many wild cervids, such as red deer, frequently visit mineral licks when they are available. While most artificial salt licks are primarily placed to supplement nutrients for livestock, little quantitative data exists regarding their use by wild cervids. Since the outbreak of Chronic Wasting Disease (CWD) in 2016 in Norway, understanding species behavior at these sites has become increasingly important, as these sites may facilitate cross-species interactions, potentially contributing to disease transmission.

This thesis aims to explore the use of artificial salt licks by red deer and other cervids in the Nordfjella region, with a particular focus on their role in the spread of CWD. By analyzing footage from camera traps, the study will quantify visitation patterns, including sex-specific behaviors, seasonal variations, and interspecies interactions. The results will provide critical insights into how artificial salt licks may influence disease dynamics and inform more effective wildlife management strategies in Norway.

Red deer space use, population ecology and level of grazing damages to farmland and forests

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In Norway, there has been a large increase in the red deer (*Cervus elaphus* L.) population, especially in the core areas in western Norway. The red deer population is historically high. Consequently, damages to forests and agricultural grassland has increased and with economic consequences for stakeholders. However, there is a limited understanding of spatial and temporal variation in browsing and grazing patterns of economically important tree species and crops. A deeper understanding of red deer population ecology and patterns of space use is a key to predict damages and to mitigate their impact in human-dominated landscapes and forests. The main objective for my PhD is to quantify the severity of grazing and browsing damages on forests and agricultural grassland and to determine spatial risk factors. To achieve this, I will combine data on grazing damages to agricultural grasslands, to economically important tree species, and a large dataset of tracking GPS-marked red deer. In my first paper I used experiment exclosures (n=57) to assess red deer grazing on infields. I found an overall loss of biomass of 132kg per 1000m², and that high terrain ruggedness and a high red deer population density increased biomass losses by red deer. In my second paper I analyzed bark-stripping damage to Norway spruce in 470 stands. Bark-stripping damage to spruce stands increased in stands with a longer distance to road, higher red deer density and higher terrain ruggedness index. Damages decreased with increased distance to agricultural land and higher forest age. In the coming papers of my PhD, I will look at clustering of red deer using GPS-data, timing of habitat change and spatial revisitation to learn more about red deer movement ecology and their impact on human dominated landscapes and forests.

Investigating the role of small mammal dynamics in the ecological transmission cycle of *Borrelia* pathogens causing Lyme disease

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Lyme disease, caused by *Borrelia burgdorferi* s.l. bacteria spread by ticks, is on the rise in Northern ecosystems. Small mammals like rodents are key reservoir hosts for the bacteria, but we still lack knowledge of how their dynamics affect the persistence and prevalence of *Borrelia* in the ecosystem. In my PhD project I will develop and analyze mathematical models to investigate potential effects of small host dynamics on these outcomes. This PhD project will build on an existing seasonal model framework developed by the group, for a stage-structured tick population feeding on a small and a large host, where *Borrelia* is transmitted between the ticks and small hosts. We will extend this framework in three main steps to incorporate more realistic dynamics of small mammal hosts, to 1) include multi-annual cycles depending on four main phases of small mammal population growth, 2) include environmental stochasticity generating uncertainty in small host population numbers, and 3) include multiple host species in order to evaluate the effects of varying synchrony between them.

Through the theoretical model development and analyses of this project, we aim to provide new insights into how the complex interactions between hosts, ticks, and the pathogens drive the ecological dynamics underpinning Lyme disease risk.

The influence of demographic history and number of specimens on hybridization test

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Genomic data is changing our understanding of species and their evolutionary origins, highlighting hybridization as a key driver of speciation, ecological diversification, and adaptive variation. However, interpreting the presence and role of hybridization is not always straightforward. Current methods for detecting hybridization can be influenced by factors such as population structure, ghost lineages, and population size. A particularly important yet often overlooked factor is demographic history—such as bottlenecks or founder events—, which could skew the data providing signals that can be mistaken as hybridization signatures or mask the extent of the hybridization event. In this project we use genomic simulations data to investigate how demographic changes affect hybridization detection in the widely used D -statistics and f_4 -statistics. Specifically, we focus on three aspects 1) Do bottlenecks increase false positive results in D -statistics and f_4 -statistics? 2) Can these tests detect introgression between populations that have experienced bottlenecks? and 3) Does the number of sequenced individuals affect the outcomes of these tests?

Genetic Load Accumulation Following the Founder Effect in Heliconius Butterflies: A Population Genomics Study on Gorgona Island, Colombia

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Island colonization often results in significant changes to the genetic diversity of populations due to founder effects, genetic drift, and changes of selective pressures. Reduction of population sizes can lead to the accumulation of deleterious mutations that may influence the adaptability of island species. For my MSc's I will be investigating three subspecies of *Heliconius cydno* present on Gorgona island. I will study population size changes to determine population bottlenecks, identify and characterize deleterious mutations (genetic load). To address this, I will employ population genomic tools, including demographic analyses and coalescent-based models, to assess the effects of colonization on genetic diversity.

Changes in trait detection in GWAS through population simulations

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My MSc focuses on simulating population-level data under common scenarios of population split and divergence to test how can we improve the power of GWAS-based approaches. Using SLiM, an evolutionary simulation framework, I will be coding two main scenarios: a single population where a trait arises and is maintained; and a two-population model where the trait evolves in one population and spreads to the second via gene flow.

The goal of this research is to understand how a population's evolutionary histories and the characteristics of the trait influence the detection of genes of interest and to provide recommendations for conducting GWA studies. For this end, the genomic data will be generated while varying population sizes, gene flow ratios, selection coefficients, and the genetic architecture of the trait. This will allow us to ultimately assess the effectiveness of common GWAS methods in detecting these traits with different sample sizes.

Although each scenario is simple, the number of combinations grows rapidly when considering parameters such as selection coefficients, trait complexity, and GWAS methods. Lastly, the inferences from these simulations will be validated against empirical datasets such as *Heliconius*, three-spined stickleback or Darwin's Finches.

Step by step, an adaptive radiation is made: Ecological disparity as a driver of adaptive radiation

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Adaptive radiations occur when a single lineage diversifies to occupy a broad range of ecological niches. However, the way these niches are occupied and the progression through ecological space remain unknown. Two possible hypotheses are proposed: ecological occupation is either random (species occupy environments without a specific pattern) or progressive (species follow a particular environmental gradient and move through different aspects of it). In this study, I collected data from four iconic adaptive radiations: Galápagos finches (Galápagos), *Descurainia* (Macaronesia), *Aeonium* (Macaronesia), and Anoles (West Indies). I analyzed phylogenetic and ecological distances between species and found that correlations between these data sets support the hypothesis of progressive ecological occupation. This suggests that species occupy ecological niches along a niche axis, indicating that adaptive radiations may follow a more structured, progressive pattern.

The Birth of the Brazilian Society for Evolutionary Biology: von Humboldt, Darwin, Wallace, Bates, Müller, Dobzhansky — making amends with History at last

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It is well known that Brazil harbours a considerable portion of Earth's biodiversity. Thus, it is unsurprising that the country was not only able to launch but has also succeeded in sustaining for decades flourishing Scientific Societies devoted to the study of chief biological fields, such as the Sociedade Botânica do Brasil (est. 1950), the Sociedade Brasileira de Genética (est. 1955) and the Sociedade Brasileira de Zoologia (est. 1978). Nonetheless, in contrast to this scenario and against what would be expected, it was not until very recently that we — a group of Brazilian evolutionary biologists based both in Brazil and abroad — commenced working on the creation of the Brazilian Society for Evolutionary Biology (SBBE) seeking to overcome our dissatisfaction with the absence of a national Society solely devoted to the field of Evolutionary Biology in our country. After months of preparation, the foundation of SBBE finally took place on the 24th of September during the first SBBE General Assembly, which more than 100 SBBE Founding Members attended.

Alongside the establishment of SBBE, we have also been working on the I Brazilian Conference on Evolutionary Biology (SBBE24), which will take place in Curitiba — Paraná from the 20th to the 22nd of November 2024 with the great financial support of an SBME Interdisciplinary & Regional Meetings Grant. Although we cannot deny that organising a national event for the first time in a country of continental proportions has been quite a challenge, we consider that SBBE24 is bound to be a success since it will have more than 630 participants distributed in well-balanced proportions amongst categories regarding both career stage and gender. Finally, around 90 institutions will be represented at SBBE24, and SBBE already has good social media engagement.

Although we are rather content with the traction SBBE has gained thus far, we do acknowledge that SBBE has yet to manage to attract supporters evenly across the national territory, and we believe that this disparity has profound historical roots. Therefore, we are already working on solutions that can mitigate this issue and lead SBBE to be a truly national Society as we firmly believe that it is only by reaching every nook and cranny of Brazil that SBBE will be capable of contributing to the advancement of investigations related to Organic Evolution throughout Brazil.

Epigenetic potential and distribution propensity in Eurasian Passer sparrows

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Epigenetic potential is defined as the genomic differences in the capacity for epigenetic mechanisms to mediate phenotypic variation (phenotypic plasticity). This can be determined through several means, one of which is by looking at the number of CpG sites appearing in the genome. It has been found that an increased number of CpG sites could allow for more DNA methylation to occur, which can modulate gene expression and as a result, plasticity. This epigenetic potential through number of CpG sites has been linked as a possible driver for range expansions in some species, including the human-commensal house sparrow (*Passer domesticus*). A standing hypothesis is that epigenetic potential may be highly selected for in the early stages of invasions and range expansions, but later this selection decreases as the populations adapt to the new environments, due to the phenotypically plastic genotypes being outcompeted by genotypes possessing genetically canalized traits. Previous studies that have evaluated epigenetic potential via CpG site number in the house sparrow have mainly focused on specific genes or genome regions, but whole genome evaluation for this form of epigenetic potential in this species, has yet to be conducted, nor has it been looked at in comparison to closely related species. Moreover, whole genome comparisons between levels of epigenetic potential in migratory vs non migratory sparrow ecotypes like the Bactrianus (*Passer domesticus bactrianus*) and house sparrows have not been analyzed either. Therefore, to obtain a clearer understanding of selection for epigenetic potential, and perhaps adaptive plasticity, during events like range expansions, invasions and migration, it could be valuable to examine epigenetic potential across many gene regions in the entire genome for these species.

The genomic basis of adaptation to metal contamination in a common human-commensal bird

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Anthropogenic stressors such as environmental metal contamination are often overlooked when compared to other damaging consequences of human activities like climate change. Nevertheless they represent a pressing issue in the fight to preserve biodiversity and ecosystem structure. In this study, we utilize a combination of genomic tools to investigate the adaptive mechanisms of organisms inhabiting heavily polluted areas.

The genomes of 114 individuals of the non-native bird species, *Passer domesticus*, were obtained and sequenced from areas of Australia interested by both historical and ongoing mining activities, resulting in elevated environmental levels of heavy metals (notably Pb and Cr). For comparison, we also sequenced 104 individuals from non-contaminated habitats. By analyzing this genomic data, we computed region-specific genetic differentiation indicators, including nucleotide diversity and fixation index. We then identified genes associated with regions exhibiting particularly high values of these metrics.

Our project's dual aims are: first, to perform a gene ontology enrichment analysis on the identified genes to elucidate their functions and potential adaptive significance; and second, to gain insights into the structure and evolutionary history of the house sparrow metapopulation in Australia. The synthesis of our findings aims to enhance our understanding of how organisms rapidly evolve in response to human-induced environmental pollution.

**The genomic history of anthropogenic adaptation
in *Passer domesticus***

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Anthropogenic adaptation is a potential evolutionary response to human activity. Some species adapt to exploit anthropogenic niches; others adapt to evade the environmental impact of anthropogenic habitat degradation, pollution, and climate change. The house sparrow, *Passer domesticus*, likely first adapted to a human-commensal lifestyle alongside the rise of early human agriculture. Then, in the last 200 years, house sparrows rapidly adapted to serial anthropogenic range expansions and have become the most numerous bird species on the planet. But now, house sparrow populations are in decline – probably due to anthropogenic causes. How did house sparrows originally adapt to the anthropogenic niche? What genomic mechanisms of anthropogenic adaptation mediated their enormous anthropogenic proliferation? And what are their genomic prospects for evolutionary rescue in the face of their ongoing anthropogenic decline? By combining historical and contemporary genomic, ecological, and environmental data from multiple continents, my doctoral thesis project aims to address these questions and thereby unravel the genomic history of anthropogenic adaptation in *Passer domesticus*.

Bird life in the Anthropocene: Understanding convergent adaptation to urbanisation

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The rapid onset of urbanisation is inflicting dramatic change on the natural world, presenting an unparalleled evolutionary challenge. Currently, 46% of the global human population inhabits urban areas and this number is only set to increase. Quantifying how this impacts biodiversity is crucial yet challenging due to the complex dynamics between organisms and these volatile environments. This project aims to identify the ecological, morphological and genetic traits which characterise urban dwellers across the avian tree of life and whether there are convergent signatures of adaptation within these species. Particular focus will be given to the *Passer* genus; these species have repeatedly shown adaptations to urban environments, with the most prolific example being the house sparrow (*Passer domesticus*), which is ubiquitous in human-altered ecosystems. The project consists of three main components:

1. Using big data, particularly occurrence data from the citizen science project eBird, alongside anthropogenic metrics such as light pollution and population density, models of presence/absence and global estimates of urban association will be produced for a range of species. Morphological data from resources such as AVONET and BirdBase will be integrated to identify traits predicting urban tolerance.
2. Comparing urban and rural tree sparrow (*Passer montanus*) populations in Japan, where they exhibit a close association with humans, followed by an analysis of urban and rural tree and house sparrows in Norway.
3. Extending these findings within the *Passer* genus to determine whether there are convergent patterns of adaptation to an urban niche.

Using bioacoustics to monitor the bluethroat

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Climate change is occurring rapidly in the arctic and in alpine regions. This prompts future challenges for the species in these types of habitats, by increasing phenological mismatches and changes in vegetation type. The bluethroat is a common, but declining alpine bird. I will use passive acoustic monitoring and monitoring nests of the bluethroat via camera traps to enhance the data from acoustic monitoring.

Opportunistic citizen science data reveal shifts in the breeding distribution of a common alpine bird across the Fennoscandian peninsula

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The threat of climate change is particularly acute for species in arctic and alpine habitats, where changes are more extreme and happening more rapidly. While species are generally expected to shift their ranges northward and upslope in response to changing climates, actual measured shifts in species distributions have been mixed and sometimes unexpected. We tested whether the occupancy dynamics of a common and iconic montane bird, the bluethroat (*Luscinia svecica*), conform to expectations under climate change. Specifically, we leveraged opportunistic citizen science data from across the Fennoscandian peninsula over the last 45 years to test the hypothesis that the breeding distribution of bluethroats has shifted towards higher latitudes and higher elevations. We analyzed over 900,000 observations of bluethroat and 12 background species (to establish non-detection), using spatio-temporal occupancy modeling in a Bayesian framework. We found that the occupancy of bluethroats has declined significantly over the past four decades and, surprisingly, that this decline is particularly striking at higher latitudes. Our work demonstrates that even common and globally stable species are at risk of breeding habitat loss under the looming threat of climate change.

How far back in time do we need to go? Modelling the dependence of current species on past land use and climate change

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Previous studies have demonstrated legacy effects of current species distributions to past environmental conditions, but the temporal extent of such time lag dynamics remains unknown. In this study, we have developed a non-equilibrium Species Distribution Model (SDM) quantifying the temporal extent that must be taken into account to capture 95 % of the effect that a given time series of past environmental conditions has on the current distribution of a species. We applied this approach on the distribution of 92 European forest birds in response to past trajectories of change in forest cover and climate. We found that non-equilibrium SDMs outperformed traditional SDMs for 95 % of the species. Non-equilibrium SDMs suggest unprecedented long-lasting effects of past global change (average time lag extent ranged from 9 years to 231 years). This framework can help to relax the equilibrium hypothesis of traditional SDMs and to improve future predictions of biodiversity redistribution in response to global change.

Impacts of human exploitation on marine life from past to present: A genomic analysis of sea cows

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Sirenians, a taxon of large, herbivorous marine mammals, remain chronically understudied despite their cultural, historical and economic importance. Populations are slowly declining and conservation efforts are urgently needed if we want to protect the genetic diversity of remaining populations and species. Throughout my PhD, I have been investigating the long-term impacts of human exploitation on *Sirenia* using ancient and historic DNA. I have compiled the largest assemblage of historic sirenians from natural history collections to date and successfully generated whole genome and mitogenome data from >100 specimens. I will present the key findings from our recently published mitogenomic dataset ‘Population structure of *Dugong dugon* across the Indo-Pacific revealed by historical mitogenomes’. Additionally, I will discuss my current work in assessing what contributes to successful sequencing of natural history specimens used in aDNA research, and further plans to obtain a better understanding of population substructure and biodiversity among manatees (*Trichechus sp.*) using whole genome data integrated with bulk stable isotope and historical records data.

Dispersal of antibiotic resistance genes and mobile genetic elements in the human infant gut

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Human infants are more or less sterile before birth¹ and their skin and gastrointestinal tract starts to be colonized during birth by microbes from their mother and the environment². This colonization process of a new ecological niche goes through developmental phases and starts to stabilize at one year of age before it fully matures at around 3 years^{2,3}. Even though the microbiota of infants is more similar to their own mothers than other adults, infants carry a higher proportion of antibiotic resistance genes (ARG) than their mothers⁴. In addition, ARGs can potentially be transferred from a commensal to a pathogen in the gut via plasmids, phages, or transposons, together called mobile genetic elements (MGEs). Infants also have a higher abundance of MGEs compared to their mothers⁵. However, it is not known if ARGs actually transfer more often from species to species in the infant's gut compared to adults. Here we look at the dynamics of ARGs and MGEs in the first year of life. We get a detailed insight into ARG and bacterial dynamics, linking ARGs to MGEs, factors effecting ARG and MGE diversity and abundance in infants, and possibly a short peek into the world of plasmids.

1. Kennedy, K. M. *et al.* Questioning the fetal microbiome illustrates pitfalls of low-biomass microbial studies. *Nature* **613**, 639–649 (2023).
2. Milani, C. *et al.* The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. *Microbiol. Mol. Biol. Rev. MMBR* **81**, e00036-17 (2017).
3. de Muinck, E. J. & Trosvik, P. Individuality and convergence of the infant gut microbiota during the first year of life. *Nat. Commun.* **9**, 2233 (2018).
4. Pärnänen, K. *et al.* Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. *Nat. Commun.* **9**, 3891 (2018).
5. Vatanen, T. *et al.* Mobile genetic elements from the maternal microbiome shape infant gut microbial assembly and metabolism. *Cell* **185**, 4921-4936.e15 (2022).

Investigating the venom in the lesser weever fish

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Venom has evolved on numerous occasions among animals. This is also the case in fish, where venom has emerged on at least 19 separate occasions to in most cases serve as biochemical defence against predators. Among these, the best-known species found in Norway is the greater weever fish, *Trachinus draco*, which venomous dorsal and opercular spines cause painful envenomations. However, the lesser fever fish, *Echiichtys vipera*, which causes an even more painful sting, has recently been found in Norway around the south coast and appears to become more common —perhaps as a result of warming climate. However, nothing is known about the venom of this species.

In my project, I aim to describe the genomic and proteomic aspects of the venom of *E. vipera*, and compare the composition of venom located in the to different spines. I will also compare the venom to that of *T. draco*, to test the hypothesis that defensive venoms evolve slowly.

In the starting phase I will go to Mandal to hopefully catch a specimen of the lesser weever fish. This will be done together with contacts that have already caught the fish. The specimen will then be brought back to UIO with dry shipping.

Final plans will be developed.

Genomic and transcriptomic analysis of pseudoscorpion venom

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Pseudoscorpions are a diverse group of small arachnids with over 4000 species. Most of them have venom in either one or two of their chelal fingers, a unique characteristic that sets them apart from their cousins, the scorpions. Despite the significance of venom use in prey hunting, studies on pseudoscorpion venom are rare, with just a few research on its composition, proteomics and transcriptomic analysis. On this project, the aim is to comprehensively study the role of a pseudoscorpion venom through a genomic and transcriptomic lens, which involves the possible identification of the genes and precursors responsible for venom compounds.

Why is the blood of the eel toxic?

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The goal will be, with the use of protein isolation, tissue and proteotranscriptomics, and activity assays, to identify the toxin's activity and function.

Then, with the use of a comparison of comparative genomics and molecular evolution, try to elucidate its origin.

Its role will also try to be identified.

Lacewing venom: Detailed insights into the venom system of a neglected group of venomous insects

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Venom has independently evolved across many lineages, but only a few of these have been studied in detail. This is especially true for insects—one of the most species-rich groups of eukaryotes. One of the unexplored venomous lineages is the insect order Neuroptera, which are ubiquitous and include iconic species such as antlions and lacewings. While adults are non-venomous, neuropteran larvae are ferocious predators that have evolved pincer-like mouthparts from which they administer paralyzing and liquefying venom to tackle and ingest prey. Here, we present the first detailed insight into the venom system of Neuroptera through the widely distributed and agriculturally important common green lacewing (*Chrysoperla carnea*; Stephens, 1836). Using high-quality genomes from a male and female, long-read-based reference transcriptomes from their offspring across each life stage, and venom proteomics, we provide a comprehensive description of a neuropteran venom, including toxin gene families, paralogs, alternative splice variants, and allelic variation. While many of the toxin families comprise proteins convergently recruited into the venoms of other venomous lineages, we find few examples of large toxin gene family expansions, which is surprising given their prevalence in other venomous lineages. Further, we show that the only previously characterised toxin described from Neuroptera (a bacterially derived chaperonin) is not a significant venom component. Instead, the most abundant toxin is an insecticidal toxin (Tc) like protein secreted via a non-canonical secretory pathway, obtained by horizontal gene transfer (HGT), and likely facilitated by an endosymbiont—further highlighting horizontal gene transfer as a source of functional innovation in venomous animals. Our results provide new insights into the uncharted arsenals of venomous insect lineages, contrasting the canonical mechanisms of venom evolution and highlight the importance of studying neglected taxa for understanding mechanisms involved in the evolution of molecular novelties.

Genome of the green-head ant, *Rhytidoponera metallica*, reveals mechanisms of toxin evolution in a genetically hyperdiverse eusocial species

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Ant venoms have emerged as rich sources of extremely diverse peptide toxins, contrasting previously widespread misconceptions that they are primarily acid-based. While this diversity makes ant toxins attractive as pharmacological tools, the eusocial lifestyle of ants also provides opportunities for studying how venom evolution may be affected by selection at different levels of biological complexity. Here, I will present some of our recent work on the composition and function of ant venoms and their toxins, with a focus on the genetically hyperdiverse Australian green-head ant, *Rhytidoponera metallica*, which colonies contain some of the highest-known intra-colony genetic variance for a eusocial animal. I will also present our most recent findings on the genomic architecture and evolutionary mechanisms that underlie the surprisingly complex toxin arsenal of this species. To achieve this, we generated a high-quality genome assembly from a single worker and generated complete maps of toxin paralogues and their allelic variants from transcriptomic and proteomic data. Contrary to previous suggestions that gene duplication plays a minor role in the evolution of venom in stinging hymenopterans, we find evidence of a large toxin-gene family expansion with surprisingly high diversity among functionally distinct alleles. Allelic variation is maintained in a regime of strong positive selection, suggesting that alleles may diverge into different functions and increase the skill-pool effect of the colony. Although it represents an extreme case of genetically diverse colonies, *R. metallica* provides insights into how selection at both individual and colony levels contribute to driving the evolution of adaptive traits in eusocial animals.

The repeated evolution of spider venom double-knot neurotoxins

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Bivalent peptides, characterised by two functional domains connected by a short linker, represents a class of molecules with high potency and selectivity toward their molecular targets. Bivalency is prevalent in various spider venoms, particularly among cysteine-rich neurotoxins, yet the evolutionary processes driving the transition from single- to multi-domain peptides remain poorly understood. Here, we show that bivalent toxins featuring the inhibitor cystine knot (ICK) motif—termed double-knot neurotoxins—have independently evolved in Mygalomorph spiders, including the funnel-web spider *Hadronyche infensa* (Hi1a) and Chinese bird spider *Cyriopagopus schmidtii* (DkTx). Through *de novo* transcriptome assembly of 46 available Mygalomorph spiders in the Sequence Read Archive, in addition to characterising the venom proteomes and venom gland transcriptomes of 13 newly sampled Mygalomorph species, we show that the double-knot structure of Hi1a is likely of ancient origin, appearing across multiple families, while DkTx is confined to a small subgroup of the Theraphosidae family. We demonstrate recurrent loss and re-emergence of the bivalent architecture in Hi1a, suggesting structural instability of the gene encoding Hi1a. Furthermore, we created a PacBio HiFi genome assembly of *Hadronyche cerberea*, which uncovered a conserved exon-intron organization in members of the Hi1a-like gene family, with the mature bivalent toxin encoded by a single exon. Our findings suggest that the evolution of bivalent peptides is a recurrent pattern of evolutionary innovation, and raise questions about the general molecular mechanisms involved in generating protein-coding repeats.

**Phenotypic plasticity of the venom of the green lacewing
(Neuroptera, *Chrysoperla carnea*): does the maternal
environment matter?**

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Venom toxins have evolved quickly in macroevolutionary time, but the processes generating variation in venom phenotypes at microevolutionary scales remain elusive. Phenotypic plasticity—the capacity of genotypes to express multiple phenotypes across different environments—can be an important process shaping venom intraspecific variation, but direct evidence is sparse. To fill this gap, we explored whether differences in the maternal environment might elicit changes in the venom composition of the green lacewing *Chrysoperla carnea* (Neuroptera: Chrysopidae). Like other neuropterans, larvae of the green lacewings are voracious predators that use venom to immobilize and liquefy their prey. The short life cycle, high fecundity of females, and their tolerance to manipulation also make *C. carnea* an ideal species to test whether changes in the maternal environment has an effect venom composition of larvae. We collected 19 fertilized females that laid eggs both while in the field and in the laboratory, and raised their offspring under otherwise identical conditions in the laboratory. We milked venom from 108 larvae of known relatedness (55 from field-laid eggs, 53 from lab-laid eggs) and analyzed crude venoms via high-throughput proteotranscriptomics. Overall, we find compositional differences between groups of larvae from different egg origin, suggesting that environmental conditions experienced by dams may affect venom composition of their offspring. Our results highlight the importance of phenotypic plasticity in shaping intraspecific venom variation, and point out to transgenerational effects as an unexplored avenue in venom evolution that deserves more attention.

High-quality reference genome of saithe (*Pollachius virens*) – and comparative analyses

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Earth BioGenome Project (EBP), initiated in 2018, aims to sequence the genomes of all eukaryotic species in a ten-year timeframe. Sequencing and investigating genomes of the species can help understand their evolution and find new approaches to preserve the Earth's biodiversity.

This project will investigate the genome of saithe (*Pollachius virens*) by generating a high-quality reference genome of this species. Saithe is a codfish species occurring in the North Atlantic. A characteristic of saithe is that it has a predominantly pelagic lifestyle. It has an increased blood supply due to its pelagic lifestyle, and a darker flesh color than most other codfishes. Further, the saithe is more migratory than the Atlantic cod. It is worth noting that saithe is one of the main commercial fishery species in Norway.

Wild-caught saithe from the Oslo fjord has been sampled, and the DNA sequenced with PacBio HiFi, Illumina Hi-C, and Oxford Nanopore. The genome has been assembled with an in-house developed pipeline, resulting in a complete set of 20 chromosomes, consistent with existing literature. Currently, the PacBio coverage stands at 40x, which is below our initial expectations, so additional sequencing is underway. Our goal is to enhance the quality to meet EBP requirements, enabling further annotation and comparative analyses.

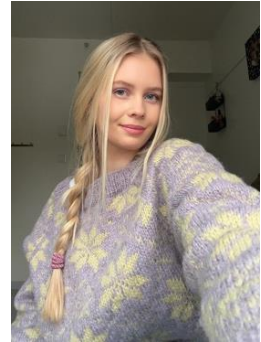
Comparative analysis will be done with available genome assemblies of other closely related codfish species. Potential analyses may be to investigate STR density, MHC copy number, transposons, chromosome structure, and potential inversions.

Population genetic structure of the northern crested newt (*Triturus cristatus*)

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Amphibians are experiencing rapid population declines worldwide, with diseases playing an important role. In Norway, the parasitic fungus *Batrachochytrium dendrobatidis* (Bd) was first detected in 2017, though the long-term effects on the near-threatened northern crested newt (*Triturus cristatus*) is unclear. The aim of this study is to investigate the genetic variation in northern crested newt (*Triturus cristatus*) populations from numerous ponds with or without Bd-infection in Norway.

Samples were collected in the municipalities of Nesodden, Frogn, Ås in southeastern Norway, regions where Bd has been detected earlier, and Innlandet county, where Bd is unlikely to have established itself yet. Water samples, environmental DNA (eDNA), and tissue samples from captured newts were gathered for genetic analysis. Microsatellite markers, which have been effectively applied to *Triturus cristatus* populations, are to be used to assess genetic variability. For the purpose of isolating the newt DNA, the salt extraction method was utilized. eDNA from filtered water samples will be analyzed for Bd presence.

The expected outcome of this study is that the presence of fungus *Batrachochytrium dendrobatidis* (Bd) has resulted in a reduction of genetic variation among infected northern crested newt individuals. Understanding the effects of Bd on the northern crested newt population is crucial for conservation efforts. If the fungus poses a threat, it becomes important to come up with strategies to lessen its impact and protect the species.

Which landscape factors affect the distribution of the great crested newt (*Triturus cristatus*) and the smooth newt (*Lissotriton vulgaris*) in Akershus?

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The amphibian populations are decreasing all over the world. In Norway, we have six species of amphibians. Two are the great crested newt (*Triturus cristatus*) and the smooth newt (*Lissotriton vulgaris*). According to Artsdatabanken.no, the smooth newt is rated as least concern (LC), and the great crested newt is near threatened (NT) in Norway. Habitat fragmentation and habitat destruction are some of the reasons why population sizes are decreasing. Understanding which habitat and landscape factors are important for the newts is vital for management. Newts are semi-aquatic, and they alternate between freshwater and land throughout their lifetime.

I will map the distribution (presence/absence) of newts and set this in context to different environmental factors, like urbanization, water quality, and the presence of aquatic predators. To get the data on distribution, ponds were sampled with minnow traps and Environmental DNA (eDNA) was collected from water samples. In May 2024, 70 selected ponds in Ås, Drøbak, and Nesodden in Akershus county were sampled during three weeks. Water samples were taken before traps were set, to analyze water quality and eDNA. Traps were fishing overnight and individual newts were identified and sexed before they were released.

I want to study how habitat characteristics influence the distribution of the great crested newt and smooth newt. I will classify the threat that disturbances, fragmentation, and human activity pose and in addition to other habitat quality criteria. I will do this by studying maps and direct fieldwork in October.

Tracking Holocene ecosystem dynamics from a paleo-archive preserved in a cave in high latitudinal Fennoscandia

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The Holocene is generally considered a stable period in comparison to the preceding Pleistocene. Nonetheless, climate and anthropogenic pressures during the last 10,000 years have shaped the ecosystems we see today. Caves offer a unique opportunity to study past ecosystems, and in their relatively protected environment we often find excellent preservation of organics. Here we present a faunal assemblage excavated in 2023 from Krytjahola, a small cave from the Fauske region in Northern Norway. We combine comparative morphology and ancient DNA bulk-bone metabarcoding to greatly enhance the identification of faunal diversity, especially for birds and fish.

Radiocarbon dating reveals two distinct periods, with 8725–8395 cal. BP covering the Holocene Thermal Maximum and an upper layer dating to 1540–1505 cal. BP. Zooarchaeological analysis of the bone assemblage reveals a diversity of taxa, including mammals, birds and fish. Small mammals are by far the best represented, and are excellent environmental indicators often underrepresented from sites in the region. In addition, the discovery of a feline molar could indicate an early domestic cat in the region or alternatively an expansion of wildcat further north than previously considered. Supplementing the zooarchaeological analyses with ancient DNA analyses of the unidentifiable bone fragments will expand the diversity of taxa we identify and present a more complete overview of past biodiversity. Krytjahola, along with other excavated caves in northern Fennoscandia is contributing to a more detailed and extensive understanding of the spatial and temporal ecosystem dynamics in a region currently facing rapid environmental changes.

Keywords: Ancient DNA, Zooarchaeology, Caves, faunal diversity.

High latitude caves and prehistoric landscapes in Norway: the preliminary findings from Solvikhola and Solsemhola

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Cave deposits provide exceptional preservation conditions for organic remains and archaeological records. From the preserved stratigraphy and excavated remains it is possible to reconstruct biodiversity and even identify macro- and micro-chronological events during the Holocene (last 11,700 years). In the SaveCave project, we are combining methods from multiple disciplines (archaeology, molecular biology, palynology, geology and isotope analysis) to study well-preserved palaeoarchives of Norwegian caves.

To date we have excavated three Nordic caves – Solvikhola, Kryptjahola and Solsemhola, with the aim of contributing to the reconstruction of the Holocene faunal diversity, exploring human impacts on Nordic cave sites and preserving these palaeoarchives for the future. This talk will focus on the preliminary findings deriving from Solvikhola (Fauske, Nordland) excavated in 2023 and introduce the recently excavated site of Solsemhola (Leka, Trøndelag). The excavation in Solvikhola revealed a sediment deposit with seven distinct stratigraphic layers, the earliest layer dating to 7563 ± 31 cal. BP (calibrated years before present), from which organic material (e.g., bone, shell, leaves, charcoal) could be retrieved. This makes it possible to reconstruct arctic faunal diversity over the past 8000 years. Through osteological identification, 24% of the faunal material could be identified to either genus or species level, recording 15 taxa, representing Amphibia, Aves, Mammalia and Pisces. Through bulk-bone metabarcoding we hope to identify additional taxa from the remaining 76% unidentifiable bone fragments to reconstruct the local faunal diversity through time. Moreover, we discovered a hearth from the Nordic Bronze Age at Solvikhola showing great potential to study early human use of cave site and local surroundings. In addition to investigating past biodiversity, our excavations at Solsemhola, a rock art cave site depicting mainly red human stick figures, are also focused on prehistoric human activity. Prior excavations in 1912/13 led by T. Petersen unearthed a rich cultural deposit with artefacts and human/animal bones which, along with our recent excavations, presents us with a unique opportunity to connect rock art production with the archaeological record.

Killer Whale Master's Project

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Being able to estimate how closely related two individuals are and whether they are inbred is important in several different fields ranging from behavioural, conservation and medical genetics. In the context of studies of social structure, understanding patterns of kinship within and among groups can require reconstructing complex pedigrees consisting of large numbers of individuals. The killer whale (*Orcinus orca*) is a species with philopatric, kin-based societies, which facilitate the social learning of foraging ecology. Killer whales in Norwegian waters represent a complex ecological and social landscape, consisting of groups with diets of herring, or mixed herring and seals. See *Social and genetic connectivity despite ecological variation in a killer whale network** for more details. **Using whole genome sequences, this Masters project will expand upon recent work (Jourdain et al. 2024) to reconstruct expanded pedigrees to first cousins, to better understand kinship among ecologically diverse communities within the complete social network.**

A motivated MSc student with an interest in kinship dynamics, ecology and animal behaviour. You will join a long-term research project on Norwegian killer whales led by Dr Eve Jourdain of UiO/Norwegian Orca Survey (<https://www.norwegianorcasurvey.no>), with lab work and genome analyses supervised by Dr Andrew Foote of CEES at IBV, UiO.

You will learn how to answer evolutionary and socio-ecological driven questions using modern techniques and molecular approaches. You will gain experience in behavioural ecology, socio-ecology, bioinformatics and genomics. There will also be opportunities for fieldwork and gaining experience in studying the whales in the wild. The skills you will gain will provide an important foundation for future applications to PhD positions or to jobs in industry.

* <https://royalsocietypublishing.org/doi/pdf/10.1098/rspb.2024.0524>

Ancient stickleback genomes reveal the dynamics of the early stages of the freshwater adaptation

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Recurrent adaptation of the marine threespine stickleback (*Gasterosteus aculeatus*) populations to freshwater environments is a well-documented case of parallel adaptive evolution, where pre-existing standing genetic variation facilitates rapid adaptation to the new environment. Here, I present the results of analyses of ancient DNA extracted from 13 putative stickleback bone samples found in lake sediments from multiple post-glacial isolation lakes across Norway. The goal was to better understand the chronology and tempo of this parallel evolution. This work is the latest addition to the growing body of work teasing apart this question by combining genotypic data from both modern and ancient sources. Previous work acquired genotype level data from stickleback bone fossils dating to late Pleistocene from two Northern-Norway post-glacial lakes, showing constraints on adaptive process due to small effective population size. My first PhD chapter demonstrated it is possible to extract similarly high resolution genotype level data from sediment cores and track adaptive genotypes of stickleback across marine-freshwater transition. I found that freshwater adaptive alleles rose to high frequency at major effect loci during earliest stages of environmental change. A similar result has been found in contemporary capture-release experiment with modern threespine sticklebacks. My on-going work expands the analyses of subfossil bones to multiple additional lakes with different geological histories while utilizing improved single-stranded library build method to generate more complete genomes. This dataset provides a novel opportunity to explore consistency in the tempo and chronology of freshwater adaptation on the underlying key loci. My hypothesis is that faster isolation from the marine fjord allows less gene flow during intermediate brackish water period reducing the efficacy of selection and the available genotypes for the selection to work on.

Beware of hitchhikers: how do effective population size and recombination rate influence mutation load associated with a selective sweep?

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Selective sweeps occur when beneficial alleles rapidly rise to high frequency in a population, causing linked genetic variation to “hitchhike” and also rise in frequency. This can include deleterious recessive alleles, previously neutrally harbored in homozygous genotypes at low frequency. Modeling studies have found that local effective population size and recombination rate should contribute to the probability of deleterious mutations being swept to high frequency by being linked to beneficial alleles. Sticklebacks provide an excellent system for understanding recurrent evolution. Marine sticklebacks have independently adapted to thousands of freshwater habitats that became available after the last ice age, resulting in the formation of distinct marine and freshwater ecotypes. Upon colonization of new freshwater habitats, selection acts on ancient standing genetic variation present in marine populations, causing freshwater-adaptive alleles to increase rapidly over tens of generations. These divergent genomic regions have been extensively characterized and drive the phenotypic differences between the ecotypes, such as the number of bony plates and body shape.

I will present the preliminary findings of my postdoctoral project, which examines the relationship between adaptation, demographic history, and mutation load. This current research study is focused on the *EDA* haplotype, which plays a key role in repeated freshwater adaptation, drives the reduction of bony plate armor in freshwater populations, and is under strong selection. We find evidence that a core haplotype containing freshwater-adaptive alleles is shared among Norwegian lake populations. However, the flanking regions of this haplotype are highly differentiated between different lake populations, suggesting different haplotypes have hitchhiked with the core *EDA* haplotype. We plan to identify whether variation in recombination rate, effective population size, and coalescence are associated with an increased mutation load in divergent genomic regions.

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