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Comparative genetic and demographic responses to climate change in three peatland butterflies in the Jura massif

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Climate is a main driver of species distributions, but all species are not equally affected by climate change, and
their differential responses to similar climatic constraints might dramatically affect the local species composition.
In the context of climate warming, a better knowledge of the ability of dispersal-limited and habitat-specialist
species to track climate change at local scale is urgently needed. Comparing the population genetic and demographic
impacts of past climate cycles in multiple co-distributed species with similar ecological requirements
help predicting the community-scale response to climate warming, but such comparative studies remain rare.
Here, we studied the relationship between demographic history and past changes in spatial distribution of three
protected peatland butterfly species (Boloria aquilonaris, Coenonympha tullia, Lycaena helle) in the Jura massif
(France), using a genomic approach (ddRAD sequencing) and species distribution modeling (SDM). We found a
similar and narrow thermal niche among species, and shared demographic histories of post-glacial decline and
recent fragmentation of populations. Each species functions as a single metapopulation at the regional scale, with
a North-South gradient of decreasing genetic diversity that fits the local dynamics of the ice cover over time.
However, we found no correlation between changes in the quantity or the quality of suitable areas and changes in
effective population size over time. This suggests that species ranges moved beyond the Jura massif during the
less favorable climatic periods, and/or that habitat loss and deterioration are major drivers of the current dramatic
decline observed in the three species. Our findings allow better understanding how history events

*Speaker

and
contemporary dynamics shape local biodiversity, providing valuable knowledge to identify appropriate conservation
strategies.

Application of a genomic SNP panel to the conservation of Capercaillie (Tetrao urogallus) in Scotland, UK

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Capercaillie in Scotland are at critically low levels with only 532 estimated to remain, 85% of which are in the Cairngorms National Park. Capercaillie have already been driven to extinction in the UK once before and the birds currently in Scotland are the result of a reintroduction during the 19th century. Using feathers and faecal samples collected from across the Cairngorms National Park and surrounding areas we aim to 1) compare genetic diversity between capercaillie in Scotland with populations in mainland Europe. 2) develop target enrichment sequencing techniques that are applicable to multiple European populations 3) Compare historic museum samples with the present-day population. DNA was extracted from 634 feather samples and 181 faecal samples collected in Scotland, 82 tissue samples collected from 8 European regions, and 75 samples from museums. Target enrichment probes were developed to target 6666 SNPs across the capercaillie genome. Reduced representation genomic libraries were created for the feather, faecal and museum samples. Mitochondrial sequences were also generated for all samples via sanger sequencing. Three genetic clusters were observed within the European genomic dataset, separating, Finland and France with the other 6 regions clustering together, termed the 'northern lineage'. Capercaillie in Scotland exhibit low levels of genetic diversity compared to the majority of mainland European regions sampled. However, no evidence of recent declines in diversity were observed. A fundamental outcome of this work is the generation of a genome wide SNP panel that is applicable to non-invasively collected samples from across Europe.

*Speaker

HydroGen: Integration of DNA-based assessment tools into water quality and biodiversity monitoring with a focus on macroinvertebrates and microbes

Robert Moise * [1], Michael Connell [1], Jens Carlsson [1], Mary Kelly-Quinn [1]

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The project aims to evaluate how DNA-based methods can supplement and support traditional monitoring methods for the Water Framework Directive across a range of biological quality elements and for regulatory targets related to biodiversity in rivers. Traditional surveys often provide inaccurate data due to issues such as morphological identification errors, low probability of detection, and intrusive approaches. This is one of two PhDs in the EPA-funded HydroGen project, under which forty freshwater sites across Ireland will be sampled over the course of four years. Sites cover a gradient from high to low ecological value and include both seasonal and annual sampling routines. In particular, four sites will be sampled seasonally and the remaining thirty-six annually. This comprehensive approach will allow to detect seasonal variations in the distribution of macroinvertebrates and microbes. The research will provide insights into the added value that can be achieved by using genetic tools, including potential new metrics based on DNA data. It is an opportunity to extend the scale and frequency of studies, thus supporting the efforts of monitoring bodies. The combined approach will improve our understanding of the diversity and distribution of species that inhabit Irish freshwaters.

*Speaker

HydroGen: Intergration of DNA-based Assessment Tools into Water Quality and Biodiversity Monitoring with a Focus on Fish and Diatoms.

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This project will assess how environmental (e)DNA and other DNA based methods can supplement and support traditional monitoring methods for the Water Framework Directive (WFD) across a range of biological quality elements and for other regulatory targets related to biodiversity in rivers. Additionally, the research aims to showcase the added value which can be gained from utilising DNA-based (both DNA & eDNA) approaches including potential novel DNA metrics. Additionally, guidance for their integration into existing programmes will be developed. Traditional monitoring methods for assessing fish involve their direct capture usually through electrofishing, whilst diatoms require time-costly morphological identification. These tradiitonal methods can be inadequate and provide subpar data resulting from issues with morphological identification, low detection probabilities, challenges of gear deployment and are often highly invasive. By incorporating DNA based strategies alongside traditional methods many of these pitfalls can be overcome. A total of 40 EPA monitoring river sites across Ireland representing a gradient of river health from poor to high status have been selected, where water as well as phytobenthos samples will be taken. Four sites will be sampled seasonally, with the remaining sampled yearly. The results from the traditional and DNA-based methods will be compared across spatial and temporal scales **Keywords**: Water framework directive, eDNA, freshwater monitoring.

*Speaker

Counting invisible elephants. Developing non-invasive DNA sampling methods for wild elephants

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Earth's remaining elephants are keystone species in their ecosystems, and are a crucial element in maintaining biodiversity and even restoring degraded landscapes. By selectively browsing certain plant species and spreading the seeds of others, elephants play an outsized role in shaping forest ecosystems. Effective conservation and management strategies for wild elephants require accurate information on population numbers and dynamics, inbreeding potential, disease risks, parasite loads and diet. Increasingly there is also a push to be able to obtain such information non-invasively to avoid unnecessary stress to the target animals. This study highlights how eDNA and scat sampling can provide such information, with a specific focus on a population of savannah elephants (*Loxodonta africana*) living in Arabuko Sokoke forest in Kenya. Arabuko Sokoke forest is the largest remaining fragment of East African dry coastal forest and contains an under studied population of elephants with an unknown population number. The very dense nature of the forest makes traditional counting methods impossible, and so this project will use a novel SNP based approach to generate a population size estimate for the elephants living in the forest, using DNA collected non-invasively from scat samples. By individually genotyping every elephant which visits the one remaining waterhole during the dry season, this project will then be able to extrapolate the number of elephants surviving in the forest. Further the project will utilize DNA metabarcoding methods to uncover both the diet of the elephants and what parasites they carry.

*Speaker

Mitochondrial Genetic Diversity and Phylogeny of Orangutans (Pongo sp.)

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Orangutans (*Pongo* sp.) exhibit significant geographic variation in habitat and behavior, offering valuable insights into primate evolution. However, the impact of environmental and anthropogenic factors on their genetic diversity and differentiation remains underexplored. We investigated the mitochondrial genetic diversity and phylogeny of extant orangutans across the islands of Sumatra and Borneo. A total of 142 mitochondrial DNA genomes were analyzed, including 88 newly acquired ones, providing a comprehensive representation of orangutan distribution.

The analysis revealed four Sumatran and five Bornean clusters, with a clearly delineated separation between Bornean and Sumatran populations. The recently identified Sumatran species, *P. tapanuliensis*, forming a reciprocally monophyletic group with Bornean orangutans. Within Borneo, our analyses revealed a mismatch between the three recognised subspecies and the number of genetic clusters, warranting a future close examination of the demographic history of these groups based on autosomal data.

Our results contribute to identifying important taxonomic units that will aid in conservation efforts on preserving dispersal corridors, as well as protecting isolated populations to preserve genetic diversity and ensure the long-term survival of orangutans.

*Speaker

A new high integrity capture system for aerial genomic surveys

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Air is a medium for dispersal of environmental DNA (eDNA) carried in bioaerosols, yet the atmosphere is mostly unexplored as a source of genetic material encompassing all domains of life. We designed and deployed a robust, sterilizable hardware system for airborne nucleic acid capture featuring active filtration of a quantifiable, controllable volume of air and a high-integrity chamber to protect the sample from loss or contamination. We used our hardware system on a light aircraft across multiple height transects over major aerosolization sources to collect air eDNA, coupled with high-throughput amplicon sequencing using multiple metabarcoding markers targeting prokaryotes and eukaryotes to test the hypothesis of large-scale genetic presence of these bioaerosols throughout the planetary boundary layer. Here, we demonstrate that the multi-taxa DNA assemblages inventoried up to 2500 m using our airplane-mounted hardware system are reflective of major aerosolization sources in the survey area. We also pioneer an aerial survey flight grid standardized for atmospheric sampling of genetic material using a light aircraft and limited resources. Our results demonstrate the usefulness of light aircraft in monitoring campaigns. However, our work also underscores the need for improved marker choices and reference databases for species in the air. Overall, this work establishes a foundation for aircraft campaigns to comprehensively and economically inventory bioaerosol emissions and impacts at scale, enabling transformative opportunities in airborne DNA technology and population genomics.

*Speaker

Evaluation of genomic tools to predict individual homozygosity-by-descent for the management of genetic diversity in small populations

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In populations of small effective size, such as those in conservation programs, companion animals or livestock species, inbreeding management is key. In that context, homozygosity-by-descent (HBD) segments are valuable as they allow efficient estimation of the inbreeding coefficient, provide locus-specific information and their length is informative about the "age" of inbreeding. Therefore, our objective was to evaluate tools for predicting HBD in future offspring based on parental genotypes, a problem equivalent to identifying segments identical-by-descent (IBD) among the four parental chromosomes. In total, we evaluated 16 approaches using both simulated and real data, including a sequenced dairy cattle pedigree and genotyped Mexican wolves, a population that faced extinction in the wild. Methods included model-based approaches, mostly hidden Markov models (HMM), that considered up to 15 IBD configurations among the four parental chromosomes (corresponding to the so-called identity states), as well as more computationally efficient rule-based approaches such as those developed to analyze entire biobanks. The accuracy of the methods for predicting genome-wide and locus-specific HBD levels in offspring based on parental genotypes was then evaluated. Comparisons were also done using low-density marker panels or genotyping-by-sequencing data and on small groups of individuals, features typically found in such populations. We found that two HMMs (based on ibd_haplo and ZooRoH) performed consistently well, and that two rule-based approaches (based on phasedibd and ROH) were also efficient for genome-wide predictions. The model-based approaches were particularly efficient when information was reduced (e.g. low marker density, locus-specific estimation). We identified a number of less efficient methods that should not be applied to similar populations. For methods using allele frequencies (AF), performance could drop dramatically when sample AF are used instead of base population AF. In that case, approaches relying on the identification of long IBD segments proved robust. Interestingly, when information is reduced, pedigree-based methods became more competitive for genome-wide predictions.

*Speaker

Nature, nurture or somewhere in between? What shapes phenotypic traits of Antarctic fur seals pups

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Consistent individual trait variation has been observed in several important phenotypic traits. What used to be considered statistical noise is now recognized as a critical source of adaptive potential. This phenotypic plasticity is most likely shaped by a combination of intrinsic and extrinsic factors. However, which factors that drive the observed variation remains largely unexplored in wild populations. We sampled a total of 100 mum-pup pairs of Antarctic fur seals (*Arctocephalus gazella*) at Bird Island, South Georgia. Here, a unique natural experimental set up in which two adjacent colonies differ almost four-fold in density allowed us to apply a fully crossed, repeated measures study design. We collected a series of phenotypic traits from all pairs at birth and 60 days postpartum across two successive breeding seasons (2018/19 and 2019/20), which differed severely in food availability. The pups were additionally sampled every 20 days. In this poster, we will outline, how we will use mixed models to conduct variance decomposition, in our aim to explain a substantial proportion of the observed variance driven by intrinsic and extrinsic factors in a range of important phenotypic traits. To further investigate these traits, we fit animal models to estimate heritability. With this project, we aim to provide detailed insights into phenotypic trait variation and the key drivers that influence this variation.

*Speaker

On the conservation genetics and genomics of endangered species: what can the inverse instantaneous coalescence rate (IICR) and spatial simulations tell us?

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Genetic and genomic data from endangered species are often used to quantify and date increases or decreases in Ne, or to compare Ne values between populations or species. They are used to make statements about past habitats and their extent. The underlying principle is that genomic data will inform us on past changes in effective population size (Ne), which will themselves inform us on past census sizes and habitat extent. The phrase "demographic history" is even used to represent the changes in Ne. While this simplified representation of the demographic history of species can be seen as a first approximation, there is no clear justification why we should not move beyond this first step today. Data from paleoclimatology, palaeoecology suggest that the demographic history of many species likely involved periods of spatial expansion and contraction together with periods of fragmentation of habitats. This means that populations have been spatially structure in the past and are likely structured today. This is problematic because, when populations are structured, if one ignores that structure during the inferential process, spurious changes in Ne will be detected, quantified and dated, even if the populations never changed in size. In other words, if we wish to understand the evolutionary history of present-day species, including endangered species, we need to shift away from a "unidimensional view" of their history (Ne). We need to develop a more integrated view in which we try to integrate changes in Ne and changes in connectivity. To do that we need to improve our understanding of structured models. In this presentation I will try to clarify the IICR concept where IICR stands for inverse instantaneous coalescence rate. The IICR is equivalent to the coalescent Ne under panmixia but can significantly differ from inferred Ne under structured models. The IICR can be estimated from the genome of a single individual using the PSMC

*Speaker

method. This is convenient for endangered species but, this means that interpreting PSMC curves from endangered species as indicating changes in Ne may be misleading. I will also show some counter-intuitive results from a spatial simulation study. If the evolutionary history of species is important to improve conservation then we may need to go beyond the Ne concept, and identify the cases where it is required.

New opportunities offered by genomics for the conservation of the Asian elephant: from captivity to the wild

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Many species are threatened with extinction, and genetics plays a crucial role in fitness of populations under pressure. Genomic tools offer the unique ability to infer the population structure and genetic health but are often not fully utilized in conservation efforts. Captive populations can play an important role in conservation via research or actual connectivity to the wild population (e.g. genetic rescue), but efforts may fail if no attention is given to their genetic status. In this project we include genomics-derived measures that are relevant for conservation, using the iconic Asian elephant as model. By generating high depth resequenced genomes, we are currently screening the full European captive population of Asian elephants for important genomic parameters and their connection to wild populations. We aim to resolve the current ambiguous subspecies status of Asian elephants in the wild by generating de novo assemblies for each potential subspecies. We screen these subspecies for inbreeding level, genetic diversity, harmful mutations and signs of local adaptation. Our first results suggest the presence of at least three subspecies within the European captive population, with strong genome erosion in animals derived from isolated populations. We also assess genomic compatibility in terms of structural variation and genetic load. These results can be used to guide management decisions of the captive population, and provide more insight into captive breeding for species consisting of a mixed or unknown background. Finally, we plan to evaluate the potential for reintroduction from the captive Asian elephant population, based on the genomic measures.

*Speaker

Using genomic data to estimate mate compatibilities in the endangered endemic Brassica insularis

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Hermaphrodite plants with a homomorphic self-incompatibility (SI) system may suffer from a "mate-finding Allee effect" in small isolated populations, because of a reduction in the proportion of compatible mates due to limited allelic diversity at the SI locus (S-locus). Such phenomenon, sometimes called the "S-Allee effect", has been well recognized but difficult to assess in conservation programs because of the strong methodological limitations associated with genotyping the S-locus. We use a combination of PCR-based and shotgun sequencing methods to efficiently and exhaustively genotype the S-locus in individuals from four populations of the endangered endemic species Brassica insularis with a range of population sizes (N=80-2000). We found that the S-locus allelic diversity is indeed related to population size and varies from 4 to 17 alleles. This leads to a proportion of compatible plants ranging from 0.44 for the smallest and less diverse population to around 0.7 for the other populations. As these perennial plants do not flower every year, this leads to compatibility rate as low as 0.2 in some years. The effect of this reduction in compatible mate availability on fruit-set measured in the field over eleven years will be investigated in order to determine whether a genetic rescue through introduction of new S-locus alleles is appropriate.

*Speaker

Impacts of environmental changes on demographic history and genetic structure of the iconic butterfly Parnassius apollo populations in France: implications for conservation.

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Mountain species are particularly vulnerable to global environmental change. *Parnassius apollo* (Lepidoptera, Papilionidae) is a cold-adapted iconic butterfly that thrives in open and rocky habitats at elevations ranging mainly from 1000 to 3000 meters. Since 2018, seasonal samplings (non letal) have been conducted annually across its distribution range in France, and a total of 333 samples were sequenced (ddRADseq). We investigated the genetic structure of the Apollo French populations using single nucleotide polymorphisms (SNPs) and revealed seven main genetic groups: three in Massif Central (Auvergne, Cevennes, Ardeche), three in the Alps region (Jura, North Alps, South-Alps), and one in the Pyrenees. The absence of a clear genetic sub-structure in the South Alps supports a metapopulation functioning. We found that populations at low altitude (Massif Central) currently dramatically declining have the lowest genetic diversity. Demographical inferences showed different evolutive histories for each population, with mainly population expansions during LIG-LGM (cold period). Then, they started by declining towards the end of the LGM and throughout the Holocene period (warm period), with an earlier decline for populations in the Massif Central. Additional analysis with museum specimens will be performed to quantify changes in genetic diversity over the last decades. Finally, we identified genetic variation associated with climate variables suggesting local adaptation for the French populations, but further lab experimentations will be performed to confirm this pattern. We also identified populations particularly vulnerable to future climate change, and it is crucial to consider whether these populations will be able to adapt or will require assisted gene flow.

*Speaker

SSM and P2GM : Mutualized Genetics Platforms at the MNHN

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The use of genetic data for the study of conservation genomics requires specific skills in molecular biology, as well as dedicated equipment and spaces. The National Museum of Natural History (MNHN) has established two shared structures to meet this need: the Molecular Systematics Service (SSM), located in the Jardin des Plantes and in the Concarneau Marine Station, and the Paleogenomics and Molecular Genetics Platform (P2GM), affiliated with the Ecoanthropology laboratory and situated in the Musée de l'Homme.
Both structures specialize in DNA extraction from various types of biological samples, including, but not limited to, animal and plant tissues, sediments, feces and water filters. DNA can be extracted from recent samples as well as from historical collections and archaeological remains. After extraction, both structures possess the expertise and equipment to produce microsatellites, PCR data, ddPCR, and mutualized NGS sequencing approaches for small projects, and are also opened to projects dealing long-read sequencing.

*Speaker

Understanding the genetic dynamics of Walloon Crested Newt (Triturus cristatus) Populations: Insights for Effective Conservation Strategies

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The crested newt, an amphibian with limited dispersal, could be affected by habitat fragmentation and
associated genetic erosion. As part of the Life BNIP project (Belgian Nature Integrated Project), samplings
were conducted in 2019 and 2023 at the request of the SPW (Public Service of Wallonia). These collections
aimed to obtain crucial information about how crested newt populations are organized, their diversity, and
genetic divergence in Wallonia (Belgium). A total of 444 individuals were analyzed from 40 different sites
across Wallonia. Eight microsatellite markers were used for genotyping, allowing for a thorough genetic
analysis. The objectives were to assess the status of Walloon populations, evaluate gene flow between
populations, estimate the risks of inbreeding, and assess potential disruptions in genetic connections
between Walloon populations to propose effective conservation measures. Our study results suggest that the
genetic structure of the crested newt in Wallonia exhibits heterogeneity across major natural regions. We
propose an initial distinction between two lineages: that of the loamy Hainaut region and the group formed by
the rest of Wallonia. At a more local scale, at least eight genetic groups seem to emerge. The highest genetic
diversity indices and significant gene exchanges are observed in Hainaut. Issues related to inbreeding are
limited to a small portion of the sampled individuals. Gene flow between populations is generally limited,
especially with geographically distant populations. Conversely, gene flow is significant within

*Speaker

sites,
particularly when ponds form a network. These results emphasize the importance of considering genetic
structure and gene flow in the management and conservation of the crested newt. Furthermore, they
highlight the need to continue conservation measures to improve the genetic health of the species in
Wallonia.

All-you-can-eat buffet in cowsheds: The spider-specialized Myotis emarginatus turns into a pest flies' eater

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Determining the dietary spectrum of European insectivorous bats over time is the cornerstone of their conservation, as it will aid our understanding of foraging behavior plasticity in response to plummeting insect populations. Despite the global decline in insects, a restricted number of arthropod pest species thrive. Yet past research has overlooked the potential of European bats to suppress pests harmful to livestock, in spite of their economic relevance. Here we investigated the diet composition, its breeding season variations and pest consumption of an insectivorous bat species (*Myotis emarginatus*), at the northern edge of its range (Wallonia, Belgium). We also explored the prey ecology to gain insight into the hunting strategies and foraging habitats of this bat species. We used DNA metabarcoding to amplify two COI markers within 195 bat droppings collected in June, July and August, thereby identifying 512 prey taxa predominated by Diptera, Araneae and Lepidoptera. Overall, in 97% of the samples we detected at least one of the 58 potential pest taxa. The June samples were marked by a diet rich in orb-weaver spiders, in accordance with the archetypal diet of *M. emarginatus* bats. However, during the highly energy demanding July-August parturition and lactation period, roughly 55% of the dropping samples contained two cattle fly pests (*Stomoxys calcitrans* and *Musca domestica).* Moreover, among the 88 Diptera species preyed upon by *M. emarginatus* in July and August, these flies accounted for around 50% of the taxa occurrences. This plasticity-the switch from a spider-rich to a fly-rich diet-seems providential considering the dramatic ongoing drop in insect populations but this involves ensuring bat-friendly cattle farming. Our results revealed that bats widely consume pest entomofauna, thereby highlighting their potential role as allies of farmers.

*Speaker

Genetic integrity and susceptibility to pathogens in lions (Panthera leo) from West & Central Africa

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The African lion (*Panthera leo*), once panmictic and widely distributed, is now found in isolated pockets, making it an ideal model to study the effects of habitat fragmentation and reduced population sizes on genetic diversity and disease susceptibility. Lions in West and Central Africa (WCA) are a genetically distinct subspecies and the population in West Africa is listed as regionally Critically Endangered, with less than 400 individuals remaining. This study aims to assess the genetic integrity and disease susceptibility of these populations to ultimately suggest management recommendations.
We will investigate neutral genetic diversity using the latest SNP panels developed for lions, and examine disease susceptibility and adaptive potential by genotyping immune system genes, i.e. Toll-like receptor (TLR) and Major Histocompatibility Complex (MHC) class I and II genes, using Next Generation Sequencing. We will test whether these immune genes are under balancing selection, which could help maintain genetic diversity. Additionally, we will describe bacteria and parasite communities from faecal samples through long read sequencing and metabarcoding.

The presence or absence of balancing selection on immune genes could have significant consequences for the long-term survival of these endangered lion populations. The abundance and diversity of pathogens found in the lion samples will provide further insights into their health status and disease susceptibility, possibly influenced by genetic diversity, increased human encroachment and climate change.
These findings will help inform conservation decisions, such as whether genetic rescue might be necessary to boost diversity and resilience.

*Speaker

Low-coverage whole genome sequencing for powerful and cost-effective population assignment

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Genetic assignment of individuals to their population of origin is an important tool in ecology, evolution, and conservation, used to track spatial distribution patterns, examine rates and directionality of dispersal, and estimate proportions of different populations represented in mixtures. With increasingly efficient sequencing and genotyping technology, it has become possible to develop targeted marker panels that often can distinguish even weakly differentiated populations with high accuracy. Unfortunately, marker panel development can be a costly and time-consuming investment. Recently, a promising new method was introduced to use genotype likelihoods inferred from low-coverage whole genome sequencing (lcWGS) data - rather than a pre-selected set of genotyped markers - for highly accurate population assignment. Initial evaluation suggests that sequencing depth as low as 0.01x can be sufficient for accurate assignment, leading to potential for more affordable and scalable processing of large samples batches than with traditional genotyping-based methods. We here apply this method to evaluate its performance for assignment of an anadromous fish, the American shad, to their native rivers along the east coast of North America. We present a side-by-side comparison of assignment power, accuracy, and cost of implementation for traditional marker-based vs. lcWGS-based assignment to evaluate the potential for circumventing marker panel development in future population assignment efforts.

*Speaker

Pangolin conservation genomics: providing the foundation for informed management and geographic traceability of their illicit trade

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Pangolins form a unique group of scaly mammals that are being trafficked at record numbers for their meat and supposed medicinal properties. The limited genomic resources currently available for the eight, currently described, species hamper global conservation endeavors for sustaining and protecting their rapidly declining populations. To aid these endeavors, we provide a detailed conservation genomic assessment of pangolins, at both a species and population level. First, using whole-genome sequencing, we assess the evolutionary and demographic history of the eight extant pangolin species and suggest a new species to science. We also produce a suite of resources, from key SNPs to reference genomes, for future conservation genetic interventions. Second, applying these resources, we developed probes for targeted sequencing, which

*Speaker

we employed on a hybrid sample set of both museum and newly collected field samples across the geographical ranges of the three most traded pangolin species. This has led to an unprecedented assessment of population delineation, dynamics and fitness for each species, with direct implications for the management of key populations. These data along with the exhaustive sampling efforts form the basis for a global pangolin DNA register, which we used to test the efficacy of tracing the global and local trade of the three key species. Amassed, these outcomes provide a foundation on which conservation researchers and practitioners can build to better understand historical changes in pangolin species and populations, designate conservation management units, and develop versatile DNA-based 'toolkits' for tracing the illicit pangolin trade.

Conservation of Endemic Terrestrial Invertebrates in the Galápagos Islands, a Systematic Perspective

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Despite making up just 5.3% of the planet's surface, oceanic islands are home to 20% of all terrestrial species and 50% of all presently threatened species. As herbivores, decomposers, predators, parasites, and pollinators, terrestrial invertebrates-which comprise insects, arachnids, snails, and segmented worms-are hyper-diverse lineages and valuable bioindicators. Here, we address the conservation strategies for endemic invertebrates based on information gathered during a biodiversity survey conducted at Barrington Island, Santa Fe in Spanish, an uninhabited island spanning 24 square kilometers located in the heart of the Galápagos Archipelago.The data obtained provide a foundation for future monitoring, research on interspecific interactions, and other factors influencing species distributions. Most importantly, this information offers an alternative viewpoint on the conservation of endemic species on oceanic islands, which is highly valuable given the current global decline in terrestrial invertebrate populations.

*Speaker

How genomics informs the conservation status and management of Asia's ancient wolf lineages

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Asia contains most of the global genetic diversity and many endangered populations of gray wolves (*Canis lupus*), some of which have been extirpated. All three main lineages of wolves occur in southern Asia, including the Indian and Himalayan lineages, which are the most ancestral and endemic to the region. Conservation is hampered by insufficient knowledge of their range boundaries, genetic diversity, and genetic load. To address these questions, we sequenced hundreds of wolf samples from across Asia. We identify secondary contact zones that define the distribution of the Indian and Himalayan lineages. We found that Indian and Himalayan wolves had among the lowest genetic diversity, whereas adjacent Holarctic wolves had some of the highest, likely due to admixed lineage ancestries. Inbreeding signatures of both long-term and recent declines in the last 300 years were detected in these two lineages. Our results directly inform current efforts to revise their taxonomy and assign an IUCN Red List status, which is crucial information to guide conservation efforts. Inclusion of scientists in Pakistan and India has been essential to the research as well as dissemination of our findings to governmental bodies and the public.

*Speaker

Challenges in estimating the effective population size of the critically endangered Western Chimpanzee in Guinea-Bissau, West-Africa

Maria Joana Ferreira Da Silva * [1,2,3], Filipa Borges [1,2,4,5,6,7], Federica Gerini [1,2,8], Francisco Silva [4,5], Germán Hernández-Alonso [9], Tiago Maié [7], Rui Sá [10], Catarina Casanova [10], Isa Pais [3,4,5,11], Mafalda Costa [3], Ivo Colmonero-Costeira [1,2,3,12], Carlos Fernandes [13,14,15], Tania Minhós [4,5], Michael W Bruford [3]

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The Western Chimpanzee (*Pan troglodytes verus*) is one of the most threatened subspecies of the Pan genus. The taxon has been classified by IUCN as Critically Endangered in 2016. The distribution ranges from south-eastern Senegal and Guinea-Bissau (GB) on the NW edge to the Niger River on the SE edge. Chimpanzees were once considered extinct in GB, but their presence has been confirmed in at least four protected areas, located south of the Corubal River. Here, chimpanzees are threatened by logging and shifting land occupation for agriculture and by

*Speaker

poaching to supply the national and international trade of exotic pets. The coastal areas of GB and Republic of Guinea, an area which includes the populations of Cufada Lagoons Natural Park (CLNP) and Cantanhez National Park (CNP) in GB, are highlighted as particularly threatened. Recently, leprosy was detected in several individuals in CNP. Past country-wide surveys dating from the 1990s estimated a small population size (of between 600 and 1000 individuals), and it is thought that the population has been decreasing in the past 20 to 30 years. Here, we use assessments of genetic variation and population structure and several methods to estimate the effective population size (*Ne*) and infer the demographic trajectory of the populations using genetic data (N=143 unique genotypes, 10 microsatellite loci, MSVAR) and five whole genomes (coverage of 20x, PSMC). We found evidence for a mild demographic bottleneck for the overall population and a demographic bottleneck for CNP and CLNP of one order of magnitude. The inference of the demographic history using PSMC suggested that the highest *Ne* does not exceed 50 000 individuals. Both methods used to reconstruct the demographic history (whole genomes, PSMC and microsatellite loci, MSVAR) agreed with the time and the type of the last demographic change (*i.e.*, bottleneck at _˜50 kYa). Our work suggests a small population size for CNP and CLNP (of less than 1,000 individuals) and that these populations require immediate management actions to ensure the conservation of the subspecies in the country. @font-face {font-family:"Cambria Math"; panose-1:2 4 5 3 5 4 6 3 2 4; mso-font-charset:0; mso-generic-font-family:roman; mso-font-pitch:variable; mso-font-signature:-536870145 1107305727 0 0 415 0;}@font-face {font-family:Aptos; panose-1:2 11 0 4 2 2 2 2 2 4; mso-font-charset:0; mso-generic-font-family:swiss; mso-font-pitch:variable; mso-font-signature:536871559 3 0 0 415 0;}p.MsoNormal, li.MsoNormal, div.MsoNormal {mso-style-unhide:no; mso-style-qformat:yes; mso-style-parent:""; margin:0cm; mso-pagination:widow-orphan; font-size:12.0pt; font-family:"Aptos",sans-serif; mso-ascii-font-family:Aptos; mso-ascii-theme-font:minor-latin; mso-fareast-font-family:Aptos; mso-fareast-theme-font:minor-latin; mso-hansi-font-family:Aptos; mso-hansi-theme-font:minor-latin; mso-bidi-font-family:"Times New Roman"; mso-bidi-theme-font:minor-bidi; mso-font-kerning:1.0pt; mso-ligatures:standardcontextual; mso-ansi-language:EN-GB; mso-fareast-language:EN-US;}.MsoChpDefault {mso-style-type:export-only; mso-default-props:yes; mso-ascii-font-family:Aptos; mso-ascii-theme-font:minor-latin; mso-fareast-font-family:Aptos; mso-fareast-theme-font:minor-latin; mso-hansi-font-family:Aptos; mso-hansi-theme-font:minor-latin; mso-bidi-font-family:"Times New Roman"; mso-bidi-theme-font:minor-bidi; mso-fareast-language:EN-US;}.MsoPapDefault {mso-style-type:export-only; margin-bottom:8.0pt; line-height:115%;}div.WordSection1 {page:WordSection1;}

Little evidence of inbreeding depression for birth mass, survival and growth in Antarctic fur seal pups

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Inbreeding depression, the loss of offspring fitness due to consanguineous mating, is generally detrimental for individual performance and population viability. We therefore investigated inbreeding effects in a declining population of Antarctic fur seals (*Arctocephalus gazella*) at Bird Island, South Georgia. Here, localised warming has reduced the availability of the seal's staple diet, Antarctic krill, leading to a temporal increase in the strength of selection against inbred offspring, which are increasingly failing to recruit into the adult breeding population. However, it remains unclear whether selection operates before or after nutritional independence at weaning. We therefore used microsatellite data from 885 pups and their mothers, and SNP array data from 98 mother-offspring pairs, to quantify the effects of individual and maternal inbreeding on three important neonatal fitness traits: birth mass, survival and growth. We did not find any clear or consistent effects of offspring or maternal inbreeding on any of these traits. This suggests that selection filters inbred individuals out of the population as juveniles during the time window between weaning and recruitment. Our study brings into focus a poorly understood life-history stage and emphasises the importance of understanding the ecology and threats facing juvenile pinnipeds.

*Speaker

Moving from potential to realized applications in conservation genomics: Insights on elements of success from marine threatened species

Lisa Komoroske * [1]

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Genomics-based approaches to support biodiversity conservation have been rapidly expanding, but numerous challenges continue to hinder on the ground conservation efforts. In this talk I will highlight examples of successful applications, and examine key elements that contribute to success (or not) that provide insight on effective integration of genomics in real-world conservation applications. I will discuss several projects from our research group that highlight different aspects and common challenges of implementing genomic-based tools in conservation management, including close-kin mark recapture in elasmobranchs to inform IUCN status assessments, epigenetic assays to quantify climate warming impacts and guide intervention in sea turtles, and coupling gene expression with organismal physiology to derive habitat targets for stress thresholds in endangered fishes. My hope is that sharing the successes (and failures) of this work will facilitate broader discussion around best practices for translating the power of genomic tools into conservation impacts.

*Speaker

Molecular tools for conservation policies: examples and questions

Nicolas Poulet * [1]

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Biodiversity management requires not only comprehensive knowledge but also effective methods and tools to identify species, monitor populations, and enforce environmental policies and regulations. Molecular tools have been a staple in conservation biology research for decades, but their integration into the daily practices of biodiversity managers and decision-makers is still emerging. We will explore several practical cases using genetics and examine the potential of genomics in biodiversity conservation.

*Speaker

Genomics and the rewilding of an African national park

Marc Stalmans * [1]

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Gorongosa National Park, located at the terminus of the Great African Rift Valley in Mozambique, was historically known for its high density of large wildlife. During the protracted civil war following Mozambique's independence in 1975, most herbivores were reduced by 85 to 99%. Large carnivores suffered a similar fate with wild dogs, leopards and spotted hyena being extirpated whilst lions declined by more than 90%. A spectacular recovery has been achieved following nearly 20 years of improved protection and limited wildlife introductions within the framework of an integrated conservation and human development project across an area of more than one million hectares. Gorongosa is characterised by a prodigious biodiversity that is as yet still incompletely documented, a highly productive ecosystem underlain by fertile soils and good rainfall, as well as connectivity to a larger conservation landscape. Some genomic research has already been undertaken on baboons and elephants. The extreme devastation of wildlife populations followed by their rapid recovery that was boosted by limited introductions offers interesting opportunities for genomic research that can address real-world conservation questions. An operational molecular laboratory and supporting systems in Chitengo, the main hub of Gorongosa, provides a logistical base for sample collection and initial processing. Research findings using genomic approaches can inform conservation planning and management, not only in Gorongosa but also in other rewilding projects.

*Speaker

Museomics improves and extends orang-utan mitochondrial phylogeny

Ana Agapito * [1], Viviani Mantovani [1], Samuel Wittwer [1], Irune Ruiz-Gartzia [2], Núria Hermosilla Albala [2], Esther Lizano [2], Logan Kistler [3], Tomàs Marques-Bonet [2], Michael Krützen [1]

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The demographic history of orangutans (genus: *Pongo*) has been shaped by ancient geological events, recent human-driven forest exploitation, and a unique dispersal system with extremely strong female philopatry. Because of the latter, phylogenetic analyses based on mitochondrial (mtDNA) genomes allow for a comprehensive reconstruction of past and present genetic diversity of this genus. Previous work revealed reciprocally monophyletic clusters in Borneo and Sumatra, aligning with the three recognized species. However, previous work was hampered by the lack of samples from areas where orangutans could not be sampled or are now extinct.

In order to complement previous sampling efforts and potentially detect orangutan populations that might have been lost, we created a mitogenome phylogeny using 50 modern mitogenomes from previous studies and sequenced 61 mitogenomes from orangutan's museum specimens. Our analyses revealed a novel monophyletic subclade within Borneo showing a geographic signal. Generally, divergence times were more recent than previous studies, but still within previous estimates.

Our work highlights the utility of museum samples for obtaining a more complete picture of past genetic diversity, especially in organisms that for logistic or political reasons are hard to sample. The advance of ancient DNA techniques also allows to create whole-genome data from museum samples, allowing more complete insights into how orang-utan genetic diversity responded to anthropogenic perturbations while at the same time advancing our understanding of orangutan evolution in the Holocene.

*Speaker

Genomics sheds light on historical and contemporary environmental changes driving conservation challenges of the Maned Sloth in Brazil's Atlantic Forest

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The Maned Sloths, a unique sloth species exclusive to the Atlantic Forest of Brazil, exhibits three isolated populations. Recent integrative taxonomic research suggests the presence of two distinct species within this group: the Northern Maned Sloth (Bradypus torquatus Illiger, 1811), found in Bahia and Sergipe, and the Southern Maned Sloth (Bradypus crinitus Gray, 1850), inhabiting Espírito Santo and Rio de Janeiro. Our study investigates the evolutionary and demographic trajectories of these two Maned Sloth lineages, utilizing whole-genome resequencing data for 10 individuals and an annotated reference genome. Our analysis reveals that the Southern Maned Sloth displays lower genetic diversity, higher inbreeding levels, and a smaller historical population size compared to the Northern Maned Sloth. These disparities likely stem from differing historical environmental and climatic dynamics in the Northern and Southern Atlantic Forests, characterized by greater climate stability and larger Pleistocene refugia areas in the north. However, the Northern population has experienced a recent increase in inbreeding levels (in the last 20 years) and a rapid population decline (over the past century), primarily attributed to recent deforestation associated with tourism enterprises. In addition, the genetic load experienced by the both northern and southern lineages are similar. Together, these results reinforce the independent evolutionary paths of these two lineages and underscore the conservation challenges faced due to historical evolutionary events and contemporary deforestation of the Atlantic Forest.

*Speaker

Inferring the recent demography of a declining narrow endemic Mediterranean plant from identical-by-descent segments

Océane Eychenne * [1], Ophélie Ronce [1], Eric Imbert [1], Pierre-Alexandre Gagnaire [1]

[1] Institut des Sciences de l'Evolution de Montpellier – CNRS-IRD-Université de Montpellier – France

Conservation issues usually require knowledge of the very recent demographic history of populations. However, time-series demographic data are often difficult and expensive to collect. Genetic approaches can infer the recent demographic dynamics by exploiting the recent ancestry information embedded in the population pedigree. We applied this strategy to a declining endemic plant, *Centaurea corymbosa* (Asteraceae), of which only a small, fragmented metapopulation remains in the wild. Our aim was to test whether currently isolated populations were connected by gene flow in the recent past. Using simulations, we show that a recent cessation of gene flow can be detected and dated by comparing the sharing of identical-by-descent (IBD) segments within and between populations over time. To test this empirically, we used haplotagging to obtain phased whole-genome sequences for one hundred individuals from five extant populations. We then detected shared IBD segments between pairs of haplotypes and estimated their age to infer the recent dynamics of connectivity among populations of *Centaurea*. Our study provides insights into future applications of IBD segments in conservation genomics to reconstruct the recent history of genetic connectivity in fragmented metapopulations.

*Speaker

Conservation Population Genomics: how the Site Frequency Spectrum (SFS) helps monitoring recent size variation of any species

Thomas Forest [1], Abdelmajid Omarjee [1], Amaury Lambert [1], Jerome Fuchs [2], Tim Sackton [3], Guillaume Achaz * [4]

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[2] Muséum National dHistoire Naturelle – Museum National d'Histoire Naturelle - MNHN (FRANCE) – France
[3] Harvard University – United States
[4] Centre interdisciplinaire de recherche en biologie – Collège de France, Université Paris-Cité – France

In this presentation, I will explain how "complete" genomes of few dozens of individuals can be used to monitor the variations in population sizes on recent time scale, relevant for conservation purposes, I will focus this presentation on methods basec on the Site Frequency Spectrum (SFS), that is the distribution of variant frequencies that segregate throughtout the genome. I will show how the SFS relates to population size variations and how it can be easily be measured from real data and then used to infer the size variation. I will then describe a new robust method (under developpment) that will overcome most of the previous numerical instabilities and weaknesses of previous softwares. I will illustrate the fundamental limitations of SFS-based methods using simple simulations and then report an ongoing meta-analysis of 35 species of birds, for which we compared systematically predictions from the SFS to the IUCN official trend.

*Speaker

Inference of recent effective population size from high and low coverage DNA data

Romain Fournier [1], Zoi Tsangalidou [1], David Reich [2], Pier Palamara * [3]

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[3] University of Oxford – United Kingdom

Individuals sharing recent ancestors are likely to co-inherit large identical-by-descent (IBD) genomic regions. The distribution of these IBD segments in a population may be used to reconstruct past demographic events such as effective population size variation, but accurate IBD detection is difficult in ancient DNA data and in underrepresented populations with limited reference data. We developed an accurate method for inferring effective population size variation during the past ˜2000 years in both high and low coverage DNA data, called HapNe. HapNe infers recent population size fluctuations using either IBD sharing (HapNe-IBD) or linkage disequilibrium (HapNe-LD), which does not require phasing and can be computed in low coverage data, including data sets with heterogeneous sampling times. HapNe shows improved accuracy in a range of simulated demographic scenarios compared to currently available methods for IBD-based and LD-based inference of recent effective population size, while requiring fewer computational resources. We apply HapNe to several modern populations from the 1,000 Genomes Project, the UK Biobank, the Allen Ancient DNA Resource, and recently published samples from Iron Age Britain, detecting multiple instances of recent effective population size variation across these groups.

*Speaker

Simulation-based inference of dispersal, densities and population sizes from genetics data under spatial models of isolation by distance

Raphael Leblois * [1], Thimothée Virgoulay [2], François Rousset [3]

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Model-based analysis of neutral genetic data allows to indirectly estimate demographic and historical parameters such as population sizes, migration rates or divergence times because those parameters shape the repartition of genetic variability within and between populations over time. In numerous species, dispersal is spatially-limited (individuals preferentially find geographically close mates) and individuals may be spread over a continuous habitat rather than aggregated into discrete panmictic populations. However, inference methods accounting for localized dispersal still bear a number of limitations in terms of biological complexity of the underlying spatial models and of type of information brought by the analyses (e.g. which parameters can be estimated, as well as their biological interpretation). In this study, we used a new recent simulation-based inference method coupled with a spatial genetic data simulator to infer local demographic parameters of population in a continuous habitat. Our results show that we can estimate with good precision more parameters than with previously available methods, notably by independently inferring population density, dispersal rate and the shape of the dispersal distribution. In contrast to competing studies, we reach these results without assuming that the total population size or the habitat size is known. Instead, these results are possible because the simulations do not require coalescent approximations (such as assuming large population size and small migration rate), and because simulation-based methods can exploit summary statistics for which no simple analytical expectation is known. These results highlight the power of simulation-based inference in population genetics and pave the way for new demogenetic inferences under more realistic spatial population genetic models

*Speaker

A Size-determining Supergene Hampers a Vulnerable Population Recovery

Pierre Lesturgie * [1,2], John Denton [2], Lei Yang [2], Shanon Corrigan [2], Jeff Kneebone [3], Romuald Laso-Jadart [4], Arve Lynghammar [5], Olivier Fedrigo [6], Stefano Mona [1], Gavin Naylor [2]

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[2] University of Florida [Gainesville] – United States
[3] New England Aquarium – United States
[4] Institut de Systématique, Evolution, Biodiversité – Museum National d'Histoire Naturelle, Ecole Pratique des Hautes Etudes, Sorbonne Universite, Centre National de la Recherche Scientifique, Université des Antilles, Centre National de la Recherche Scientifique : UMR7205 – France
[5] The Arctic University of Norway [Tromsø, Norway] – Norway
[6] Colossal Biosciences – United States

Understanding the relationship between census size, recent demography and genetic diversity is central to effective conservation and management of threatened species . Thorny skate (*Amblyraja radiata*) biomass in the northwest Atlantic has declined significantly in the past 50 years, prompting strict conservation measures. Curiously, population recovery has not occurred in the Gulf of Maine. We conducted whole genome sequencing of Thorny skate samples collected from across its range. Genetic diversity was similar in all sampled locations but we discovered a 31 megabase supergene bi-allelic locus associated with a discrete size polymorphism ocurring in the northwest Atlantic. Historical demographic modelling indicates that the (dominant) allele associated with larger size (HB) originally introgressed into the ancestral Thorny skate population in the last 160k years . Off Newfoundland (Canada), where there are signs of population recovery, the supergene genotypes are in Hardy-Weinberg equilibrium. However, in the Gulf of Maine, where population non-recovery is most acute, there was a significant deficit of heterozygotes. This strongly suggests sub-regional effects on fitness associated with the supergene, impeding the recovery in the Gulf of Maine. At the same time, regional migration replenishes genetic variation in the recombining component of the genome preventing speciation between the two morphs. The study highlights a rarely considered role for context-dependent genetic compatibilities in the conservation and management of threatened populations and reconcile census size trajectory and genetic diversity estimates through accurate evolutionary modelling.

*Speaker

Inference of demography and introgression in selfing populations using Approximate Bayesian Computation (ABC)

Lukas Metzger * [1], Neda Rahnamae [2], Juliette De Meaux [2], Aurélien Tellier [1]

[1] Technical University of Munich – Germany
[2] University of Cologne – Germany

Recurrent gene flow between species in modern times, following a period of isolation, can have significant impacts on endangered species. It can potentially augment the availability of advantageous genetic variants while also eroding local adaptation. Yet, determining the extent of contemporary hybridization and the history of gene flow remains challenging. In order to understand the history of gene flow, we focus on the natural gene flow between two endangered plant species, *Arabis nemorensis* and *Arabis sagittata* in a sympatric population. To address this, we develop a unique approach that accounts for the effects of selfing while inferring the age and the selection coefficient of introgressions. The Approximate Bayesian Computation (ABC) method uses a framework based on a transition matrix summarizing the distribution of times to the most recent common ancestor along the genome. We first demonstrate that our method can recover introgression from past changes in demographic history. Second, we incorporate the accuracy of our method and show that we can identify positive and negative selected introgressions by using simulated data. Third, we apply our method to whole genome resequencing data from 37 accessions of *A. nemorensis* and *A. sagittata*, recovering multiple selected introgressions. By determining the history and adaptive potential of introgressions, we can gain further insights into the adaptive capabilities of endangered species undergoing hybridization.

*Speaker

Genetic causes and consequences of sympatric allochronic differentiation in a defoliating insect

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What are the genetic mechanisms implicated in allochronic differentiation and how allochrony may affect the demography and the genetic features of populations is an important question both in evolutionary biology and conservation genetics. In particular, allochronic divergence of populations may reduce effective population size and gene flow and increase inbreeding and genetic load. In the Leiria National Park in Portugal, a population of the pine processionary moth Thaumetopoea pityocampa has undergone allochronic differentiation, resulting in a shifted phenology, a reproductive isolation and a strong genetic differentiation. The objectives of this study are (1) to reconstruct the recent demographic history of the shifted population (SP) compared to unshifted ones, notably to infer the age of the split between these populations and the extent of bottlenecks, (2) to measure the extent of inbreeding and genetic load and its potential purge, and (3) to identify regions potentially involved in the phenological shift and increased genetic differentiation. To achieve these goals, we resequenced individuals and pools of individuals for SP and 7 unshifted portuguese populations. We found a strong genetic differentiation between SP and other populations (Fst ranged from 0.225 to 0.351), and a reduced heterozygosity in SP (on average by 16%). Using msprime and ABCRF, we identified a relatively recent bottleneck in SP and neighboring populations but showed that the split of SP was likely more ancient (_˜3500 generations). Using GONe, we confirmed that the SP population had a relatively small effective size and that most of the Portuguese populations showed a recent decline. Using RZooRoH we found that SP and neighboring populations had relatively high inbreeding compared to other populations, with a 3 times larger fraction of the genomes included in ROH, that were likely generated between 50 to 100 generations ago. We estimated piN/piS and Rxy to evaluate the potential accumulation and purging of deleterious

*Speaker

alleles. Finally, using genome scans, we identified several regions and genes potentially involved in allochrony, the differentiated regions being located on the Z chromosome and leading to its over-differentiation in SP.

Statistical approaches to understanding population structure in genetic variation

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Population structure is a fundamental feature of genetic variation that is crucial to address when carrying out studies in evolutionary biology, conservation genetics, and trait mapping. However, many analytical methods to represent population structure do not incorporate geography directly. Typically, geography must be considered post hoc alongside a visual summary of genetic data. Over the past ten years, an alternative approach we have developed is a spatially explicit method that estimates "effective migration surfaces" to visualize how genetic diversity is geographically structured (the EEMS method). Here, I'll share insights from applications of the EEMS method using examples from multiple species. I'll also highlight possible pitfalls of applying the method and share novel lines of development of the EEMS method, including an extension that allows for long-range migration. These results provide visualizations of genetic diversity that reveal local patterns of differentiation in detail. The fine-scale population structure depicted here is relevant for understanding complex patterns of spatial genetic structure and have application to a diverse range of species.

*Speaker

inferring recent demographic history using the sfs

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In the current context of the sixth major biodiversity crisis on one hand and the drastic reduction in sequencing costs over the last 20 years on the other hand, genomic data represent an additional source of information for developing standardised and automatic methods for reconstructing the demographic history of populations, including on short timescales relevant to conservation biology. The site frequency spectrum (SFS) is a summary statistic widely used to infer scenario parameters of changes in effective population size over time, particularly in the case of genomic data of relatively poor quality. Here we present a tool based on published algorithms that we have redesigned to improve execution speed and thus both scalability and robustness. We illustrate, through simulations, some well-known limitations to the use of SFS in the reconstruction of demographic scenarios, namely the non-identifiability of parameters for piecewise constant demographic models and the number of sampled individuals. Finally, we show that the SFS can be used to infer the recent history of populations, provided that certain methodological and interpretative precautions are taken. This is the case, for example, when population structure mimics the signal of changes in population size. New methodological developments using or not the SFS combined with other statistics could help overcome these difficulties.

*Speaker

A demographic model of structured populations for common chimpanzees (Pan troglodytes)

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Common chimpanzees (*Pan troglodytes*) inhabit tropical forests of Africa and are classified in four sub-species: Western, Nigeria-Cameroon, Central and Eastern chimpanzees. Several genetic studies have shown the existence of population structure, both across the species and within subspecies (Lester et al. 2021, Fontsere et al. 2022). It is increasingly recognised that inferring the past demographic history of species while ignoring population structure can be problematic and lead to spurious signals of change in effective population size (Mazet et al. 2016).

In this study, we used PSMC curves (Pairwise sequentially Markovian coalescent, Li and Durbin 2011) as summary statistics to infer non-stationery n-island models for each subspecies independently using the SNIF method of Arredondo et al. (2021). We found that it was possible to construct a model integrating the four subspecies and that succeeds at explaining the empirical PSMC curves. We also found that this scenario predicts well estimates of genetic diversity and genetic differentiation within each subspecies even though it overestimates genetic differentiation between subspecies.

Future work should be moving towards more complex spatial models that could in particular explain observed patterns of isolation by distance.

*Speaker

How can we infer recent fragmentation using genetic data?

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The increasing availability of genomic data from non-model species presents exciting opportunities to investigate the role of environmental and demographic changes in shaping genetic diversity. This is particularly important for endangered species, aiding conservationists in unraveling the primary drivers impacting genetic loss and connectivity, when demographic surveys are difficult to obtain. Despite ample evidence that past population structure and fragmentation have shaped the genomes of species across various biomes, assessing the impact of very recent demographic or environmental changes (within the last 50 generations) remains challenging. Based on a simulation study, we will demonstrate how several novel summary statistics derived from genotypic and genealogical (ARG-based) data can aid in detecting, dating and quantifying recent changes in connectivity with increased accuracy. We will discuss the challenges of inferring recent fragmentation events and highlight the most promising research space (in terms of sequencing data types and statistical methods) to help characterize recent connectivity changes in endangered species.

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*Speaker

SelNeTime : a new method inferring demography and selection from genomic time series data.

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Genomic samples collected for a same population at several generations provide direct access to the genetic diversity changes occurring within a specific time period, informing us about both the demographic and adaptive processes acting on the population during that period. A common approach to analyze such data is to model observed allele frequencies using a Hidden Markov model (HMM) ; this approach allows computing the full likelihood of the data, while accounting both for the stochastic evolution of population allele frequencies along time and for the noise arising from sampling a limited number of individuals at each observed generation. Several such HMM methods have been proposed so far, differing mainly in the way they model the transition probabilities of the Markov chain. Following Paris et al (2019), we consider here the Beta with Spikes approximation, which avoids the computational issues associated to the Wright-Fisher model while still including fixation probabilities, in contrast to other standard approximations of this model like the Gaussian or Beta distributions. To enhance the potential of genomic time series data, we present an improved version of Paris et al (2019)'s approach, denoted SelNeTime, whose computation time is drastically reduced and which accurately estimates effective population size in addition to the selection intensity at each locus.

*Speaker

Genetic diversity, population structure, and demographic history of the willow grouse and rock ptarmigan in Sweden

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The willow grouse (*Lagopus lagopus*) and rock ptarmigan (*Lagopus muta*) are birds with a year-round distribution in North America's and northern Eurasia's Arctic and alpine regions, popularly hunted in Sweden. Future scenarios of anthropogenic climate change suggest that both species are likely to experience distribution range contractions related to warmer temperatures. Reductions in population size affect genetic diversity by increasing the strength of genetic drift, the probability of inbreeding, and the potential fixation of deleterious alleles in smaller populations, decreasing species' adaptive potential to environmental changes. Preserving genetic diversity is crucial for biodiversity conservation, and both species have been prioritized for monitoring genetic diversity due to their vulnerability to climate change. This study aims to characterize genetic diversity, infer population structure and effective population size (Ne), and detect inbreeding signals in willow grouse and rock ptarmigan populations using whole-genome sequencing. Genetic diversity and inbreeding will be assessed through observed heterozygosity, genomic nucleotide diversity, inbreeding coefficient, Runs of Homozygosity, and mutation load. Population structure analyses and estimation of Ne through time will be conducted. Our results could identify genetic changes over time that might be related to anthropogenic activities and asses the adaptive potential of the species to future environmental conditions.

*Speaker

Living on the edge – the evolutionary history and uncertain future of peat bog pine (Pinus uliginosa N.)

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Conservation efforts have become more critical than ever, especially considering that current species extinction rates far exceed average background rates. The loss of genetic diversity, resulting from numerous threats, could have particularly severe consequences for forest ecosystems. Evaluating genetic variation and examining demographic, ecological, and evolutionary mechanisms influencing population structure can significantly enhance our predictions and understanding of likely responses among tree species to environmental changes, particularly for threatened species with small and isolated populations, such as peat bog pine (*Pinus uliginosa* N.). The current geographic range of peat bog pine is limited to a few well-known, isolated stands in Central Europe. The accelerated destruction of its primary habitat due to the drying out of bog areas, exacerbated by climatic changes, poses a severe threat to its survival. In this study, we utilized polymorphism data from nuclear, plastid, and mitochondrial genomes obtained from several populations of peat bog pine, as well as reference populations of its close relatives. By analyzing genetic data using population genomics and biological modeling methods, we aimed to: 1) assess the influence of geographic isolation on the contemporary genetic structure of peat bog pine; 2) track the relationship between demographic changes and the level of genetic variation in *P. uliginosa*; and 3) address hypotheses regarding the putative hybrid origin of the species.

*Speaker

Gene flow to the rescue : Using assisted gene flow to save a threatened plant population from extinction

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After the drastic decrease of the population size of *Arenaria grandiflora*'s population in the Parisian region in the late 20st century, a translocation program was implemented in 1999. A preliminary study revealed that the main cause of the population's extinction was the low genetic diversity and the associated low fitness of the last surviving individuals due to inbreeding depression. To save this species from extinction in this region, non-local and local plants were multiplied by *in vitro* culture and introduced in three sites of their natural area. The three translocated populations were funded with the same mixture of 450 individuals, 2/3 being clones of local plants and 1/3 of clones from non-local ones. To evaluate the outcome of the program, yearly monitoring of plant's fitness was performed, coupled with genetic analyses based on microsatellite markers.
First results highlighted that the newly created populations presented an increased genetic diversity compared to the founders, and displayed lower consanguinity due to higher heterozygosity level. These levels of diversity appear to be fairly stable from year to year, which was encouraging for the program's success. Interestingly, fluctuations in fitness were observed between individuals according to their proportion of genome inherited from each founder population.

In order to study this pattern in more details and acquire a better understanding of the complex genetic processes conditioning the success of programs based on assisted gene flow, we are currently resequencing whole genomes from individual sampled from 1999 to nowadays.
By comparing simulations to present-day genotypic data obtained from whole genome sequencing, it will be possible to assess whether natural selection phenomena linked to crossbreeding, such as heterosis or hybrid depression, have influenced the observed patterns of genetic diversity. Finally, we will try to predict the evolution of genetic diversity in the newly established populations.

*Speaker

Predicting species invasiveness with genomic data: is Genomic Offset related to establishment probability ?

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Predicting the risk of establishment and spread of populations outside their native range represents a major challenge in evolutionary biology. Various methods have recently been developed to estimate population (mal)adaptation to a new environment with genomic data via so-called Genomic Offset (GO) statistics. These approaches are particularly promising for studying invasive species, but have still rarely been used in this context. Here, we evaluated the relationship between GO and the establishment probability of a population in a new environment using both in silico and empirical data. First, we designed invasion simulations to evaluate the ability to predict establishment probability of two GO computation methods (Geometric GO and Gradient Forest) under several conditions. Additionally, we aimed to evaluate the interpretability of absolute Geometric GO values, which theoretically represent the adaptive genetic distance between populations from distinct environments. Second, utilizing public real data from the crop pest species Bactrocera tryoni, a fruit fly native from Northern Australia, we computed GO between "source" populations and a diverse range of locations within invaded areas. This practical application of GO within the context of a biological invasion underscores its potential in providing insights and guiding recommendations for future invasion risk assessment. Overall, our results suggest that GO statistics represent good predictors of the establishment probability and may thus inform invasion risk, although the influence of several factors on prediction performance (e.g. propagule pressure or admixture) will need further investigation.

*Speaker

Concept and challenges associated with using the genomic offset metric to inform conservation: an example with seed sourcing in red spruce.

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The current global climatic crisis has begun affecting the entire biosphere, posing a serious threat to the health and persistence of climate-sensitive populations and species. At the same time, recent technological advancements give us access to massive quantities of data pertinent to biodiversity conservation (*e.g.,* genome-scale DNA sequencing, high-resolution climate models) and new sophisticated computational tools that can take advantage of these data to identify conservation risks and opportunities under a changing climate. A key question is how to harness the predictive power of statistical algorithms to generate actionable predictions about which populations will be most heavily impacted by climate change, and how these losses could be mitigated. To address this question, scientists have been developing computational approaches that pair large genomic datasets with high-resolution climate information to estimate the gene-climate relationship and identify populations most vulnerable under a changing climate. During this talk, I will describe how genomic offset can help informing conservation plans aiming at mitigating the negative impact of climate change on natural populations. I will try to illustrate the discussion with the example of red spruce, a North American tree species of high conservation focus.

*Speaker

The burden of mutations: indirect effects of genetic load on fitness through lek attendance

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Deleterious mutations negatively affect fitness, yet empirical evidence of this link is scarce. We address this knowledge gap by modelling the relationship between genetic load and lifetime reproductive success, the gold standard for measuring fitness, using 190 whole genomes and longitudinal life history data in a lekking bird, the black grouse (*Lyrurus tetrix*). Only genetic load inferred through evolutionary conservation (GERP) was negatively associated with lifetime reproductive success, whereas we did not find this link for deleterious mutations inferred through functional effect prediction. GERP-inferred mutations in both hetero- and homozygosity negatively affect reproductive success, suggesting incomplete dominance of ancestral alleles. Moreover, we show that the genomic location of the deleterious mutation impacts the magnitude as well as the direction of the relationship between genetic load and reproductive success, suggesting deleterious mutations should be stratified by gene regions to achieve a more comprehensive understanding of their phenotypic effects. We further demonstrate that genetic load negatively affects fitness through its indirect effects on lek attendance: the trait that explains most variation in annual mating success. Our findings highlight that conservation efforts should not only focus on maximising genetic diversity and minimising inbreeding, but also consider the number of large effect deleterious mutations.

*Speaker

The Role of Population History in Shaping the Mutation Load of Structural Variants Relative to SNPs, in Island versus Continental Lagopus Lineages

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While the importance of specific demographic histories in shaping patterns of mutational load conferred by deleterious single nucleotide polymorphisms (SNPs) has received considerable attention in the recent past, few studies have investigated the corresponding fitness consequences of structural variation in distinct evolutionary lineages. We performed heuristic-based filtering and rapid automated curation of short-read-discovered SVs callsets from 99 re-sequenced individuals across two recently (_˜2 million years) diverged ptarmigan (Lagopus) species. High-confidence SV callsets reveal that the relative proportion of deleterious structural variants is consistently greater in small effective population sizes, but that the relative frequency of deleterious variants differs between populations having experienced temporary bottlenecks versus longer-term low Ne. Despite the Svalbard rock ptarmigan population exhibiting the lowest coalescent Ne (Wattersonś theta) estimate for all populations, it did not carry the highest masked and realised load for both SVs and SNPs. Crucially, these differences in genetic load may reflect differences in the type of bottleneck: the Svalbard population has likely experienced an initial founder event during post-glacial colonisation of the islands, while the Pyrenean rock ptarmigan population likely experienced a longer-term gradual decline exacerbated by recent inbreeding. Our findings demonstrate the importance of considering the nuances of population history, when interpreting the potential effects of small effective population size on mutation load. Furthermore, similar to SNPs, we find that many canonical SV classes (deletions, duplications and inversions) may largely conform to nearly-neutral expectations.

*Speaker

Evolutionary rescue by means of introgression: balancing genetic rescue and swamping

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Theory suggests that the likelihood of evolutionary rescue, where evolution prevents otherwise inevitable extinction, increases with population size and availability of genetic variation. Introgression, which refers to the back-crossing of hybrids with one or both parental lineages, can boost evolutionary rescue by introducing new genetic variation into endangered populations. Although cases of adaptive introgression are known, more often it results in demographic or genetic swamping. We have analyzed a deterministic model, supported by individual-based simulations, to quantify the effects of genetic swamping after a single introduction event of individuals from another population. Our analytical results identify an optimal number of introduced individuals that maximizes the surviving portion of the focal population's genome. Assuming the focal population has declined and exerts little competition, small and early introductions minimize swamping, because the resident population remains large, while larger introductions maximize the probability of rescue. Our analytical results provide insights into the trade-off between genetic swamping and rescue, and also provide tools to guide conservation managers aiming to rescue small and/or inbred populations.

*Speaker

Living on a rock with three heterozygous sites per megabase: the genomics of the Aeolian wall lizard

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Small populations give a unique opportunity to investigate the relative roles of drift and selection in evolution. In particular, small populations can show an accumulation of deleterious mutations (the genetic load) due to the strong effects of drift. The Aeolian wall lizard *Podarcis raffonei* is endemic to the Aeolian archipelago, located in the Mediterranean Sea, North of Sicily. The extremely restricted distribution range includes two small islets (La Canna, 940 m2, and Strombolicchio, 3,070 m2). Here, we analysed the genomic variation pattern and the genetic load in these two small populations, and compared them with those observed in the sister species *Podarcis waglerianus* (the Sicilian wall lizard), where the distribution range and the population size are much larger. A newly assembled genome was generated for the Aeolian wall lizard, and whole genomes were resequenced for ten individuals each from La Canna and Strombolicchio and for ten individuals of the sister species. The Aeolian wall lizard shows a uniquely low level of polymorphism, especially for the La Canna population with the lowest value of genome-wide heterozygosity documented in vertebrate species (3.4x10-6, *i.e.* one SNP every 300 kb). Both La Canna and Strombolicchio individuals show exceptionally high levels of inbreeding (FROH=0.99 and 0.67, respectively). Genetic load estimates based on annotation and evolutionary conservation revealed an accumulation of deleterious mutations in homozygosis for the Aeolian wall lizard when compared to the Sicilian wall lizard. Despite the much lower population size and genomic variation in La Canna compared to Strombolicchio, their level of genetic load is comparable, suggesting a maximum level of tolerable genetic load in these isolated populations.

*Speaker

Revising the genetic status and quantifying genetic load of the critically endangered Balkan lynx (Lynx lynx balcanicus)

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The Balkan lynx (Lynx lynx balcanicus), the most endangered Eurasian lynx subspecies, faces a critical threat with fewer than 50 mature individuals surviving in the mountain range of the western Balkans. Recent genomic studies reveal alarming trends, indicating the lowest genetic diversity and highest inbreeding coefficient among all Eurasian lynx populations. This study aims to assess the genetic status of the Balkan lynx using a novel high-quality reference genome of the Eurasian lynx. Through a comprehensive analysis, we will infer genetic diversity, past and present effective population size, and the extent of inbreeding. Additionally, we will quantify the genetic load of this subspecies and explore potential signs of genetic purging by comparing it with Eurasian lynx populations with varying demographic histories. Insights gained from this study will inform conservation strategies, especially in evaluating the need for human-assisted gene flow to prevent extinction. By addressing the genetic health of the Balkan lynx, this study plays a pivotal role in guiding targeted and effective conservation actions for this critically endangered subspecies, while also unraveling the nuanced aspects of its evolutionary history, providing invaluable insights for its long-term survival in human-dominated landscapes.

*Speaker

Population genetics in Wild and Captive Populations of Conservation Concern: Challenges and Opportunities

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Genomic studies of rare and endangered species have focused broadly on describing diversity patterns and resolving phylogenetic relationships, with the overarching goal of informing conservation efforts. To this end, I will discuss work conducted on Ethiopian wolves, a canid species endemic to the Ethiopian Highlands, have been steadily declining in numbers for decades. Currently, out of 35 extant species, it is now one of the world's most endangered canids. Previous conservation efforts have focused on preventing disease, monitoring movements and behavior, and assessing the geographic ranges of sub-populations. We added an essential layer by determining the Ethiopian wolf's demographic and evolutionary history using high-coverage whole-genome sequencing data from 10 Ethiopian wolves from the Bale Mountains. We observe exceptionally low diversity and enrichment of weakly deleterious variants in the Ethiopian wolves in comparison with two North American gray wolf populations and four dog breeds. Switch directions, I will also discuss work in captive populations. Tigers (*Panthera tigris*) have a captive population that vastly outnumber those in the wild, yet the diversity of the captive population remains largely unexplored. We conducted a large-scale genetic study of the _˜140 private (non-zoo) captive tiger population in the United States (U.S.), also known as 'Generic' tigers. We find that the U.S. Generic tiger population has an admixture fingerprint comprising all six extant wild tiger subspecies and a comparable amount of genetic diversity to most wild subspecies. We also observed relatively few private variants, fewer deleterious mutations, and inbreeding coefficients that are similar to wild populations.

*Speaker

The Maintenance of Deleterious Variation in Wild Chinese Rhesus Macaques

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Understanding how deleterious variation is shaped and maintained in natural populations is important in conservation and evolutionary biology, as decreased fitness caused by these deleterious mutations can potentially lead to an increase in extinction risk. In this work, we analyze the whole genomes of 79 wild Chinese rhesus macaques across five subspecies and characterize patterns of deleterious variation with respect to runs of homozygosity (ROH) and signals of recent positive selection. We show that the fraction of deleterious homozygotes occurring in long ROH is significantly higher for deleterious homozygotes than tolerated ones, whereas this trend is not observed for short and medium ROH. This confirms that inbreeding, by generating these long tracts of homozygosity, is the main driver of the high burden of homozygous deleterious alleles in wild macaque populations. Furthermore, we show that small and medium ROH have a lower proportion of homozygous loss-of-function variants compared to tolerated ones, suggesting the purging of these variants through natural selection. Finally, we identify regions putatively experiencing a recent or ongoing sweep and examine the presence of deleterious variants in these regions to find signals of genetic hitchhiking. We found 7 deleterious variants at high frequency in regions under selection containing genes involved with olfaction and other processes. Our results suggest that, whereas some strongly deleterious variants may have been purged by negative selection, some deleterious variation has been maintained in wild Chinese macaques through demographic events and inbreeding, and some has hitchhiked to high frequency, shedding light on how evolutionary processes can shape the distribution of deleterious variation in wild non-human primates.

*Speaker

A comparative analysis of the Antarctic fur seal (Arctocephalus gazella) skin and gut microbiome

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Microbial communities are an indispensable part of all living organisms, supporting their hosts with a wide variety of functions. Microbial genes, which greatly outnumber those of the host, are essential for preventing colonization by pathogens and regulating the immune system, nutrients absorption, food digestion and growth promotion.
A number of intrinsic and extrinsic factors can affect the host microbiome, including age, sex and stress. Understanding such associations allows one to derive essential insights about the resilience of hosts and their ability to adapt to environmental shifts, particularly while studying populations residing in untouched and remote areas where systematic knowledge is often lacking. This also pertains to a wild population of Antarctic fur seals (*Arctocephalus gazella*) breeding on Bird Island, South Georgia, which has seen a decrease in numbers over the last thirty years due to anthropogenic decreases in krill availability.
We used 16S rRNA amplicon sequencing to elucidate the factors that shape the composition and structure of gut and skin microbiota of Antarctic fur seal mum-pup pairs inhabiting two colonies of high and low population density. We focus mainly on age, sex and density, a potential indicator of social stress. This study is one of the few that comparatively explains host-microbe interactions for gut and skin bacterial communities and highlights the importance of using omic tools to inform ecological forecasting.

*Speaker

New opportunities for population wildlife studies using high-throughput STR genotyping of snow tracks eDNA

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Continued advancements in environmental DNA (eDNA) research have made it possible to access intraspecific variation from eDNA samples, expanding the genetic toolbox for the study of natural populations. In the context of wildlife studies of macroorganisms, the ability to analyze intraspecific variation from DNA traces in the environment represents an advancement in non-invasive genetic methods typically based on the collection of biological samples such as scats, hair, or urine. Most eDNA based population studies have so far focused on mitochondrial DNA variation, but recent progress in the field now also enables calling nuclear variants in eDNA samples suitable even for individual genotyping. I will present individual genotyping of eDNA obtained from snow tracks of three large carnivores (brown bear, Eurorasian lynx, and wolf) using high-throughput sequencing of microsatellites (STR). Individual genotypes were obtained for all species (44-71% success rate), but genotyping performance differed among samples and species and was higher for the brown bear (88% locus genotyping success). I will discuss our results in relation to field sampling and laboratory protocols, and highlight the new opportunities offered by high-throughput genotyping of snow track eDNA for wildlife surveys and monitoring, and more broadly to advance eDNA–based individual and population level studies. Species of conservation concern and difficult to study in ecosystems with a snowy season and for which ecological data are lacking will benefit from the additional information acquired through snow track eDNA.

*Speaker

Temporal metagenomics – a new dimensions in species conservation

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Studies of endangered populations and species are at the heart of conservation genomics. However, obtaining samples from rare, cryptic, and protected species is often logistically and ethically challenging. The development of genomic methods for non-invasive samples and the increased use of historical collections is revolutionising the field. Particularly the temporal aspect provided by museum specimens enables researcher to identify and quantify the impact of recent anthropogenic disturbances on wild animals. These studies often highlight the detrimental effects of loss of genetic diversity, increase in inbreeding and deleterious mutations, providing foundation for practical conservation measures. In contrast, little is known about how human-driven environmental changes affect host-associated microbiomes and what consequences this may have for their mammalian host. We use museum collections spanning the last 200 years to study the oral microbiome of wild animal populations, focusing on effects of environmental contamination with human-made products (e.g. antibiotics) and population bottlenecks. We find that the prevalence of oral disease in a Scandinavian brown bear (*Ursus arctos*) population is inversely proportional to host population size. Using dental calculus, the preserved form of the oral microbiome, we show that individuals with dental caries harbour distinct oral microbiomes, which show reduced alpha diversity and are enriched for metabolic pathways involved in sugar and acid metabolism. Diseased microbiomes also show high abundance of several opportunistic oral pathogens. This work adds a new dimension to the population-level effects of human-driven declines by incorporating host-associated microbial communities into the conservation biology framework and highlighting the importance of microorganisms for the ongoing biodiversity crisis.

*Speaker

eDNA reveals disappeared amphibians and fungal pathogen co-occurrences in a biodiversity hotspot

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Since the 1970's, striking amphibian population declines and presumed extinctions have been recorded globally. The chytrid fungus, *Batrachochytrium dendrobatidis* (*Bd*), is one of the key drivers of these declines. We used an environmental DNA metabarcoding approach to survey for 42 threatened amphibian species, along with *Bd* lineages, in 11 localities in the Brazilian Atlantic forest (a biodiversity hotspot) and one adjacent Cerrado grasslands locality. We detected DNA traces of nine of our target species, including two amphibian species that were missing for over 40 years, and two *Bd* lineages detected only in canopy-covered microhabitats with mild temperatures. There was a positive association between the presence of the global panzootic lineage of *Bd* (*Bd*-GPL) and our target amphibian species. Our results shed light on the relationship between threatened amphibian species coping to persist in the presence of enzootic *Bd*, supporting a post-panzootic scenario. Our research also brings novel insights into hosts and pathogens simultaneous surveys, especially when host detection probability is low, making an important contribution to tropical ecology and conservation.

*Speaker

A Predictive Model of Biodiversity Resilience to Inform Conservation Strategy

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Resilience is the ability of an ecosystem to withstand or absorb external stress without undergoing a significant or irrevocable state change (Holling 1973). Given the current stress humans are imposing on global biodiversity both directly, through land use practices, pollution, and ecosystem modifications, and indirectly, through changes in temperature and precipitation regimes as an outcome of global climate change, a more precise and quantifiable understanding of biodiversity resilience is of critical importance. A reliable index of biodiversity resilience will allow us to identify habitats or ecosystems to target for protection or remediation efforts, and to understand whether ecological communities will persist or collapse in response to natural or human-mediated disturbances. Though numerous methods for quantifying resilience have been developed (e.g., Baho et al. 2017; Sæther et al. 2023), quantification of resilience remains challenging, particularly for methods that rely on changes in species abundances, which are highly stochastically variable (Shoemaker et al 2020). Community-scale genetic diversity retains a history of population size changes that average over stochastic population dynamics on short timescales (Overcast et al 2023), and could thus prove a fruitful substrate upon which to calculate resilience. High-throughput biodiversity genetic inventories (e.g., metabarcoding/eDNA) coupled with global remote sensing data allow for characterizing the structure of ecological communities as well as the environmental and human-land-use associated correlates of pristine and disturbed systems (e.g., Lin et al. 2021). Contemporary macrogenetic studies (Miraldo et al. 2016; Theodoridis et al. 2020) offer one route in this direction, using data from global biodiversity genetic databases (e.g., BOLD/Genbank). However, these tend to adopt a primarily descriptive approach for characterizing ecosystem genetic diversity at broad spatial scales and quantify biodiversity genetic structure using simple metrics like average nucleotide diversity. What is needed is an index of biodiversity resilience which can provide actionable insight. Here we will demonstrate such a Biodiversity Resilience Index (BRI), which utilizes community-scale intraspecific genetic diversity as may be obtained from contemporary broad-spectrum eDNA metabarcoding approaches. We will also describe a process-based model of biodiversity resilience which is informed by a holistic understanding of eco-evolutionary dynamics to capture the signatures of biodiversity resilience and community genetic health. We will show how this model can be used to make predictions of BRI under competing management scenarios, to inform conservation strategy.

*Speaker

The role of epigenomics into conservation: Case studies on the European sea bass

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While genomics has led to multiple applications that prove powerful for conservation, this is not yet the case for epigenomics, for which we will highlight the potential to be integrated in conservation studies. We will focus on DNA methylation, as a crucial link connecting the genome with the environment. To exemplify this, we delve into case studies using the European sea bass (*Dicentrarchus labrax*) to demonstrate how: 1) epigenetic biomarkers can be developed and used to infer past (at different time ranges) and even predict future environmental conditions. 2) DNA methylation marks can be used to predict the biological age of fishes using epigenetic clocks, for applications into fisheries management and conservation. We will revise the existing knowledge gaps hindering the widespread adoption of these tools. Additionally, 3) increased temperature as an environmental factor can influence the methylome, ultimately impacting the sexual phenotype of sea bass, which raises concerns on the potential consequences on the sex ratio of wild populations in a warming scenario. Finally, we will briefly discuss its inheritance to the next generation, opening the question on whether DNA methylation acts as one of the mechanisms facilitating adaptation to rapid environmental changes.

*Speaker

Genomic Adaptations Associated with Climate Change and Biological Changes in the unionid mussel Unio delphinus (Spengler, 1793)

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Purifying water, recycling nutrients, provisioning habitats, and providing food resources make freshwater mussels (Mollusca; Bivalvia; Unionida) key components of ecosystems. Unionid mussels are among the most threatened groups of aquatic organisms facing habitat degradation by anthropogenic and biotic pressures, intensified by climate change. Here, we aim to assess genomic changes and responses associated with climatic adaptations by exposing two populations (North and South of Portugal) of *Unio delphinus* (Spengler, 1793), an endemic Iberian freshwater mussel, to different water temperatures. The transcriptome profiling of these populations unveiled clear patterns of differentially expressed genes (DEGs) between Northern and Southern populations subject to an acute increment in temperature (0.3 C/min until the critical thermal maximum is reached) and to chronic maintenance at different temperatures (20, 25, and 30 C for 2 weeks). Furthermore, each population exhibited temperature-dependent DEG profiles. These findings bring insights into the biological processes involved in the adaptation of freshwater mussels to environmental disturbance, highlighting the evolutionary history of these species and opening the way to future management actions for biodiversity conservation.

*Speaker

Exploring eDNA dynamics in waterholes in savanna ecosystems

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During the last two decades the utilization of environmental DNA (eDNA) has evolved into a powerful tool for biodiversity assessments and biomonitoring. Hereby, the amount of DNA shed into the environment and the persistence time of eDNA in the respective substrate are of decisive importance for the inferences drawn from eDNA-based data. Most of the eDNA-based research has focused on aquatic systems in temperate systems and within these, on fishes. For these, the eDNA dynamics such as eDNA shedding and degradation are best understood. However, eDNA might also be a great tool for biomonitoring of other systems, such as for monitoring terrestrial wildlife in African savannas. In these dry habitats, terrestrial wildlife must regularly visit waterholes for drinking. While drinking or bathing in these waterholes, animals shed their DNA into the water which might be used to for eDNA-based monitoring. However, currently little is known about how much DNA is shed from terrestrial mammals into the water while interacting with it and how fast this DNA degrades in such waterbodies to a point that it is not detectable anymore. In the presented project we are assessing these eDNA dynamics in South African waterholes. If eDNA-based approaches prove to be effective, they could be applied on a large scale for wildlife monitoring in these ecosystems.

*Speaker

Buffer or exacerbator? The role of DNA methylation in inbreeding depression in a wild vertebrate

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Inbreeding depression occurs when the offspring of closely related parents have reduced fitness. A major challenge in conservation and evolutionary ecology is to understand the mechanisms underlying inbreeding depression. DNA methylation, an epigenetic mechanism, is hypothesized to play a major role in the regulation of inbreeding effects as this biochemical mechanism can alter gene expression without changing the nucleotide sequence of the genome. Consequently, it is considered to be a central mechanism modulating the expression of phenotypic traits. However, the exact role of DNA methylation in regulating inbreeding depression remains unclear. On the one hand, inbreeding might disrupt genome-wide methylation patterns, causing maladaptive gene expression and thereby reinforcing inbreeding depression. On the other hand, DNA methylation could potentially buffer the detrimental effects of inbreeding by adaptive modulation of gene expression patterns. To investigate these scenarios, we need to link genetic and epigenetic variation to data on gene expression and individual fitness. To evaluate the feasibility of such an approach, I analyzed DNA methylation, inferred using epiGBS2, from a dataset comprising whole blood and flipper plug samples from two hundred Antarctic fur seals (*Arctocephalus gazella*, mother-offspring pairs) sampled from two adjacent colonies at South Georgia. I explored the performance of epiGBS2, which to date only has published records on plants and birds, assessed tissue-specificity of DNA methylation and explored the sources of between-individual variation in DNA methylation. Finally, I assessed the association between DNA methylation and multilocus standardized heterozygosity. This study will increase our understanding of how the genome and the epigenome interact to react to inbreeding in a natural population. This is crucial for understanding the viability of wild populations in an era of global environmental change and species declines.

*Speaker

Study of the impact of environmental changes on the bacterial microbiota of wild boar involving health risks

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1

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European wild boar (*Sus scrofa*) populations have risen sharply as a result of climate change or inappropriate hunting management. As a result of this population explosion, the species has been forced to colonise new highly anthropised areas, leading to much more frequent contact with domestic species and humans. However ungulates (including wild boar) are the animals that host the most pathogens transmissible to humans. Wild boars can host or be affected by numerous zoonotic diseases (brucellosis, tuberculosis, salmonellosis, yersiniosis, etc.). Better knowledge of the circulation of these pathogens among wild boar populations is therefore essential to prevent future threats to public health and that of domestic animals. Little is also known about the risk of an increase in the prevalence of these pathogens as a result of the changes to which wild boar are exposed: change of habitat (and hence diet), increase in densities, increase in contact with humans and domestic animals, etc. Nothing is also known about the relationship between these factors and the diversity of the bacterial microbiota of wild boar, which is so important for the health of individuals. The aim of our study is to gain a better understanding of the circulation of bacterial communities (commensal and pathogenic) in ten selected areas of Belgium, with contrasting characteristics (wild boar population densities, proximity to livestock, different habitats, etc.) by : 1) developing a non-invasive detection method for pathogenic bacteria 2) studying the impact of environmental changes on the bacterial diversity of wild boar

*Speaker

Esox flaviae, population genomics revealed entangled origin and differentiation of the Italian populations

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In 2011, Esox flaviae, commonly known as the Southern pike, was identified as a distinct species from the Northern pike (Esox lucius) (Lucentini et al. 2011). It is classified as endangered on the IUCN Red List due to the threat of hybridization with the exotic species E. lucius, which was introduced for angling purposes. It is crucial to understand the population structure and dynamics of E. flaviae to protect it from local extinction, loss of genetic diversity, and loss of local adaptation. There have been few efforts to investigate the structure and substructure of this new species (Gandolfi et al. 2017). In this study, the genomes of 62 pikes, including 50 E. flaviae from six locations and 12 E. lucius from two locations outside Italy, were examined to detect genome-wide hybridization between and admixture among populations. The goal is to analyze the population's structure and dynamics at a higher resolution and to evaluate the consistency of phylogenetic relationships across chromosomes. The phylogenetic-based approach employed indicates variable relationships among populations through the chromosomes, suggesting admixture among the Po population and other populations studied. ABBA-BABA indicates admixture events that were not evident in the initial structure analysis, with the Po population being the most affected by these events. Such mixing, likely caused by human-mediated translocation for angling, complicates conservation efforts. This study lays the foundation for determining conservation units (CUs) and developing informed management plans for these populations. Preserving the adaptive potential of a species or population is crucial for its ability to adapt to changing environments

*Speaker

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- Berthelsen Ane Liv
- Bertola Laura
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