GÖTEBORGS UNIVERSITET

INSTITUTIONEN FÖR BIOLOGI
OCH MILJÖVETENSKAP

Masters' presentations in biology

May 2025

Schedule & abstracts

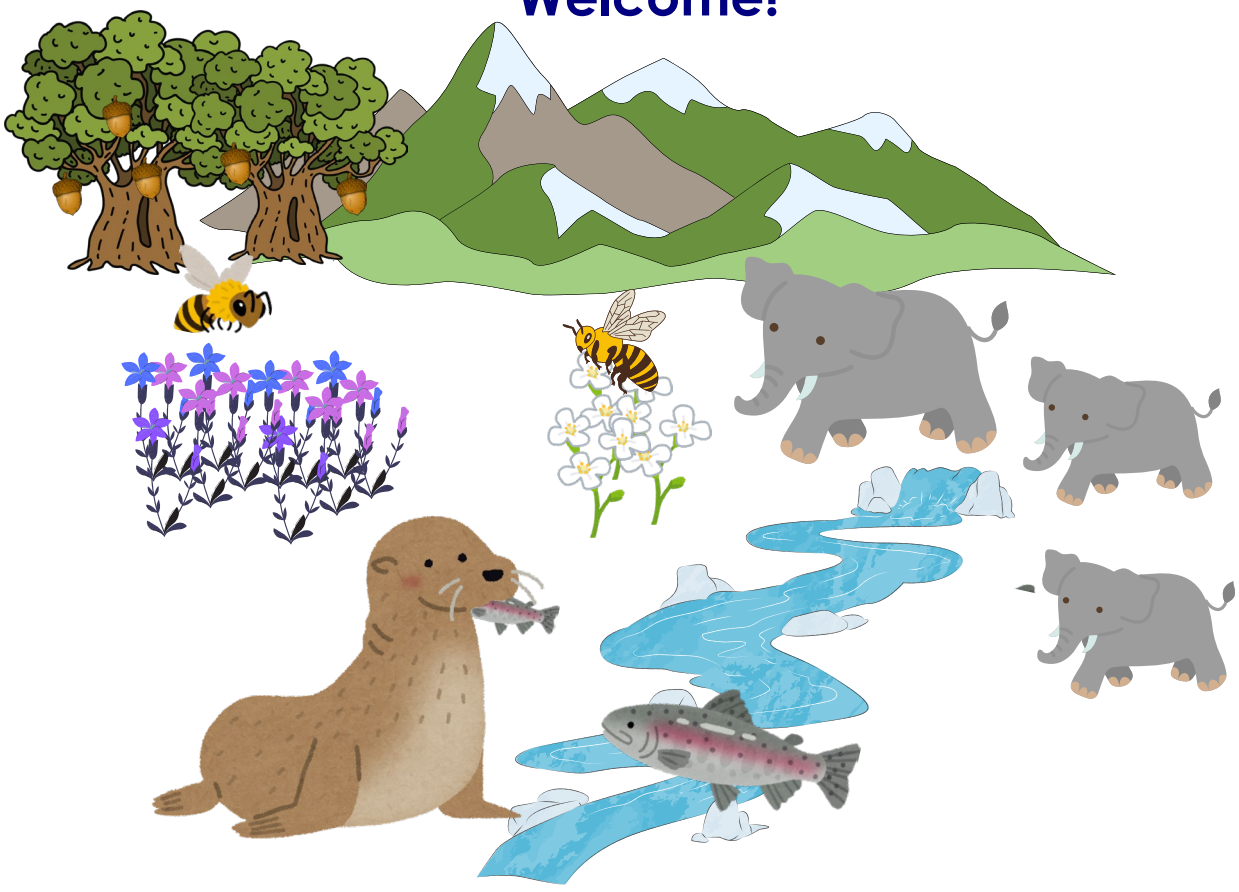
Monday May 26
At Marelden (2125), Natrium 8.30–ca. 16

Tuesday May 27
At Marelden (2125), Natrium 8.30–ca. 17

Wednesday May 28
At Korallrevet (3401), Natrium 8.30–ca. 14

The presentations can also be followed via Zoom.

Welcome!



Schedule

Note! Times below are approximate (except for first presentation each day)

Monday May 26

8.30 **Aamir Faraaz** (Conservation biology, 60 hp)

Testing the resilience of *Apis mellifera mellifera* with other subspecies in Sweden: Nectar sources and mismatches in pollination timing during adverse weather

Opponent: Sebastián Enault de Cambra

Coffee break ca. 9.25

9.45 **Aarati Gyawali** (Conservation biology, 60 hp)

Evaluating the status and potential of honey production in Nepal: insight from pollen analysis and beekeeping practices

Opponent: Bernard Asanbe

10.45 **Neethu Joseph** (Physiology & cell biology, 60 hp)

Genetic regulation of the short-term stomatal CO_2 response in *Arabidopsis thaliana*

Opponent: Andrea Sartorius

Lunch break ca. 11.45

12.30 **Malin Landgren** (Conservation biology, 60 hp)

Arctic plant phenology and abundance: Understanding temperature-sensitivity and warming impacts

Opponent: Deborah Van Putten

13.30 **Aura Mateus** (Conservation biology, 45 hp)

Reproductive investment and life history strategies in Amazonian tree species

Opponent: Linnea Erikson

Coffee break ca. 14.20

14.40 **Linnéa Wallgren** (Evolutionary and behavioural ecology, 60 hp)

An ecological study comparing pollen collected from different honeybee subspecies and hybrid in Norway

Opponent: Lynn Kleinjan

Tuesday May 27

8.30 **Deborah Van Putten** (Evolutionary and behavioural ecology, 60 hp)

Environmental variation and genetic effects on life-history traits: can adaptation be constrained?

Opponent: Linnéa Wallgren

Coffee break ca. 9.25

9.45 **Mitch Olson** (Conservation biology, 60 hp)

Can different capture methods target different behavioral and morphological characteristics? An experimental study using the invasive brook trout

Opponent: Hans Meinhard Í Eyðansstovu

10.45 **Sebastián Enault de Cambra** (Conservation biology, 45 hp)

Meteorological and geomorphological influence on harbor seal haul-out distribution behavior using drone imagery

Opponent: Gagandeep Kaur

Lunch break ca. 11.45

12.30 **Malin Schött** (Conservation biology, 60 hp)

Exploring the diet of harbour seals (*Phoca vitulina*): Overall diet and inter-individual variation in prey preferences and feeding tactics

Opponent: Mitch Olson

13.30 **Lina Anderberg** (Conservation biology, 60 hp)

Restoration of a semi-natural grassland: the impact of clear-cutting and management by grazing on plant diversity and composition

Opponent: Aura Mateus

Coffee break ca. 14.25

14.45 **Bernard Asanbe** (Conservation biology, 60 hp)

Assessing patterns of extinction risk among mammal species in Nigeria: A comparative analysis of human impact

Opponent: Malin Landgren

15.45 **Lynn Kleinjan** (Conservation biology, 60 hp)

Environmental and social determinants of elephant walking speed in conflict-prone areas

Opponent: Aarati Gyawali

Wednesday May 28

8.30 **Andrea Sartorius** (Physiology & cell biology, 45 hp)

Leaf minimum conductance and bark water vapor conductance in 14 deciduous tree species

Opponent: Neethu Joseph

Coffee break ca. 9.20

9.40 **Hans Meinhard Í Eyðansstovu** (Biodiversity and systematics, 60 hp)

Phylogeny and biogeography of genus Gentianella Inferred from target enrichment sequencing

Opponent: Lina Anderberg

10.40 **Gagandeep Kaur** (Physiology & cell biology, 60 hp)

The impact of fasting and refeeding on intestinal fluid transport and cortisol levels in salmonids

Opponent: Malin Schött

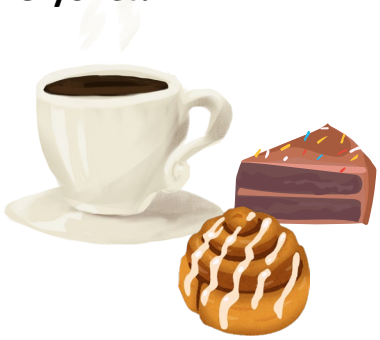
Lunch break ca. 11.40

12.30 **Linnea Erikson** (Conservation biology, 60 hp)

Oak regeneration in conservation-thinned mixed forests in Sweden: A two-decade study on exclosures

Opponent: Aamir Faraaz

Ca. 13.30 **Fika for everyone!!**



Abstracts

Testing the resilience of *Apis mellifera mellifera* with other subspecies in Sweden: Nectar sources and mismatches in pollination timing during adverse weather

Aamir Faraaz (Conservation biology, 60 hp)

Supervisor: Åslög Dahl, Department of Biological and Environmental Sciences, GU
Examiner: Anne Bjorkman

The European honey bee (*Apis mellifera mellifera*) is one of several honey producing *Apis* species and is considered to be the most economically important globally, for pollination services as well as for honey production. It plays a vital role in maintaining biodiversity by providing essential pollination services to numerous wild plants and crops. Its role as a pollinator supports the reproduction of both cultivated and wild plants, which, in turn, contributes to the stability and resilience of ecosystems. This research aims to investigate the resilience of *Apis mellifera mellifera* with other subspecies such as *buckfast*, *carnica* and *ligustica* also what difference nectar sources are used by these subspecies and how adverse weather effect bees foraging in honey yield. Samples were collected from various parts of North and central regions of Sweden such as Södertälje, Arboga, Västerås, Östervåla. Pollens were then observed from 16 different slides to see the abundance of different flora, around 33 different types of pollen were found. Brassicacae and *Trifoilum repens* family were found to be the most abundant and *mellifera* showed a little more resilience as compared to other subspecies its foraging diversity was also higher than other. An astonishing result was seen in *carnica* species when in the early summer it was found that they forage at much higher density as compared to late summer showing less resilience as compared to other species. The reason could be that mellifera is adapted to this climate as compared to *buckfast* which is a hybrid species and *carnica* which is from the Balkan region. This study helps us to identify the different subspecies behaviour in cold climates and can help us to strategize for crop pollination stability, biodiversity support and bee conservation efforts particularly in Sweden

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Evaluating the status and potential of honey production in Nepal: insight from pollen analysis and beekeeping practices

Aarati Gyawali (Conservation biology, 60 hp)

Supervisor: Åslög Dahl, Department of Biological and Environmental Sciences, GU
Examiner: Anne Bjorkman

Honey production is essential for sustaining rural livelihoods and preserving ecological balance in Nepal. Although it is significant, studies focusing on the authenticity and plant composition of Nepalese honey are still scarce. This research investigates the existing conditions and future possibilities of honey production nationwide, concentrating on pollen analysis to gain insights into bee foraging behaviours' and the quality of honey from various ecological regions. Nepal's landscape features a broad elevation spectrum from the subtropical Terai lowlands to the temperate hilly areas, providing diverse ecosystems. Samples of honey were gathered from various sites in Nepal and transported to Sweden for laboratory testing. Pollen grains were obtained from each sample, mounted on microscope slides, and classified to assess the variety

and prevalence of floral sources, in addition to checking for potential adulteration. Statistical and floristic evaluations were performed to investigate the connection between geographic origin and pollen diversity. More than 70 distinct types of pollen were recognized, featuring some uncommon and previously unrecorded species. The Brassicaceae family was identified as the predominant nectar source, highlighting its significance in both wild and cultivated honey production systems. Honey sourced from hilly areas exhibited greater pollen diversity and was deemed more genuine, whereas samples from the Terai indicated the possibility of sugar feeding in beekeeping, raising concerns about honey purity in that region. This study shows the value of melissopalynology in determining the plant and geographic sources of honey. The results provide important perspectives on both traditional and contemporary beekeeping practices in Nepal and emphasize the necessity for better quality control, conservation initiatives, and region-specific beekeeping strategies

***Keywords**: honey production, melissopalynology, Nepal, pollen analysis, beekeeping practices, Brassicaceae, honey adulteration, biodiversity, sustainable apiculture*

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Genetic regulation of the short-term stomatal CO_2 response in *Arabidopsis thaliana*

Neethu Joseph (Physiology & cell biology, 60 hp)

Supervisor: Mats Andersson & Karin Johansson, Department of Biological and Environmental Sciences, GU
Examiner: Henrik Aronsson

Plants respond to various environmental stimuli, including elevated CO_2, by partially closing their stomal pores. This partial closure reduces water loss through transpiration while allowing photosynthesis to continue. Understanding how plants regulate this response is important for improving water use efficiency, especially in the context of climate change. However, the signaling pathways that control stomatal closure in response to CO_2 are complex, and many components are still unknown. The aim of this study was to investigate the genetic basis of CO_2-induced stomatal closure in *Arabidopsis thaliana* using a MAGIC (Multiparent Advanced Generation Inter-Cross) population based on 19 founder lines. Gas exchange measurements were taken in 206 RILs, and quantitative trait locus (QTL) mapping was used to identify the genome regions linked to stomatal response to elevated CO_2 and related traits. A significant QTL was found on chromosome 1 associated with the percentage reduction in stomatal conductance in response to elevated CO_2. Further analysis of the genes in this region revealed 15 potential candidates. Additionally, a QTL on the same chromosome was linked to the speed of the response when CO_2 concentrations increased from 420 to 800 ppm. This study provides a foundation for exploring these QTLs and candidate genes, with the potential to improve plant adaptation to increased CO_2 and enhance water-use efficiency in future climates.

Keywords: stomatal conductance, CO_2, Arabidopsis thaliana, MAGIC RILs, quantitative trait loci

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Arctic plant phenology and abundance: Understanding temperature-sensitivity and warming impacts

Malin Landgren (Conservation biology, 60 hp)

Supervisor: Anne Bjorkman & Katrín Björnsdóttir, Department of Biological and Environmental Sciences, GU
Examiner: Henrik Nilsson

The Arctic is warming four times faster than the global average, driving major changes in tundra ecosystems. One key response is shifts in plant phenology, the timing of life events like flowering. These shifts can cause trophic mismatches, affecting insects, birds, mammals, and human societies. Plants that adjust their phenology with warming are considered temperature sensitive. Understanding plant phenology is key to predicting how tundra vegetation may change in the future. With this in mind, our study aims to understand the relationship between temperature sensitivity of plant phenology and abundance change, both experimentally and over time with natural warming. We used an experimental setup in Greenland, Disko Island, with warming chambers (open top chambers, OTC), creating a 1.5–3°C warmer and more humid environment, and monitored plant phenology in both OTCs and control plots. Previously recorded abundance data from the same site was used to see how experimental warming affected abundance, along with a 30-years old dataset to explore changes over time with natural climate warming. Our results showed that flowering time advanced with warming, indicating that most species were temperature sensitive. *Betula nana* and *Bistorta vivipara* were most sensitive, flowering 7 and 15 days earlier, respectively, under experimental warming. We found no strong overall trend of increased abundance under experimental warming; over time the trend was more positive but still modest. *B. nana* consistently increased under both experimental and natural warming, while *B. vivipara* showed a continuous decline. Overall, we found that temperature sensitivity alone did not predict abundance changes. This suggests that other environmental factors (e.g. microclimate variation, soil conditions, and species interactions) likely play important roles. Our study also highlights species-specific responses, with shrubs like *B. nana* would likely expand, while species like *B. vivipara* may struggle in a warmer Arctic.

Keywords: Plant phenology, temperature-sensitive, warming experiment, OTC, abundance change & Disko Island.

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Reproductive investment and life history strategies in Amazonian tree species

Aura Ximena Mateus (Conservation biology, 45 hp)

Supervisor: Daniel Zuleta, Department of Biological and Environmental Sciences, GU
Examiner: Anne Bjorkman

Understanding how reproductive traits influence tree species survival is essential for decoding life-history strategies and predicting forest responses to disturbances, climate change and other global drivers. Reproductive traits like seed mass reflect a species' position on the fast–slow continuum and influence key demographic trade-offs. Small seeds favor dispersal and colonization, while large seeds enhance seedling survival but come with energetic costs that may limit reproduction through a seed size–number trade-off. Here, data from 156 species in

the Amacayacu Forest Dynamics Plot (northwestern Amazon) were used to test the relationship between seed mass and survival. The hypothesis was that this reproductive trait would be positively associated with survival rates. Specifically, it was predicted that species with larger seeds would show higher survival, measured using two metrics: maximum survival probability across the species' lifespan (K) and early-life survival probability (S10). It was also expected that the strength of this relationship would vary with dispersal mode. Size-dependent survival parameters (K and S10) were estimated using Bayesian hierarchical models, and associations with seed mass and dispersal modes were tested using linear mixed-effects models. Seed mass was positively associated with survival in woody trees, consistent with life-history theory and the fast–slow continuum. However, a negative relationship was observed for palms, likely reflecting differences in structural and reproductive strategies. While some dispersal modes differed in seed size, with synzoochorous species having larger seeds, no differences in survival were found across dispersal modes. Although early-life survival (S10) is explained by larger seeds providing more reserves for seedling establishment under stress, the link with adult survival (K) likely reflects correlations with other traits—such as slow growth, high wood density, structural investment, and shade tolerance—that enhance long-term survival. These results highlight seed mass as a key reproductive trait for explaining demographic variation and support trait-based approaches in tropical forest ecology.

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An ecological study comparing pollen collected from different honeybee subspecies and hybrid in Norway

Linnéa Wallgren (Evolutionary and behavioural ecology, 60 hp)

Supervisor: Åslög Dahl, Department of Biological and Environmental Sciences, GU
Examiner: Lotta Kvarnemo

The native honeybee *Apis mellifera mellifera* is an important insect pollinator, was nearly extinct in beekeeping during the late 20th century. It was outcompeted by its southern relatives by beekeepers' preferences and has declined in population size during the last 50 years but is making a recovery. Honeybees perform an important ecosystem service, the pollination, to for example agricultural crops but it also plays an essential part economically. The monetary value of honeybee pollination in Sweden is estimated to range from 189 to 325 million SEK, and the honey production 117 to 135 million SEK. In all of Europe, this value is estimated to be 30 – 50 larger than the Swedish values. The native honeybee *Apis mellifera mellifera* has resided in Sweden for around 8000 years, whereas the subspecies *Apis mellifera carnica* and the hybrid Buckfast are historically recently introduced. In this study, the aim has been to explore the ecological adaptation to the Scandinavian flora in the imported subspecies *Apis mellifera carnica* and hybrid *Buckfast* in comparison to the native honeybee *Apis mellifera mellifera*. The pollen grains, already collected from two sample sites located on two different altitudes in Norway, have been identified and classified via light microscopy and photography. The data has then been analyzed in Excel and in R Studio. Results have indicated a slight difference in pollination preferences among the compared subspecies and hybrid. This could potentially maybe lead to an impact on the local ecosystems, requiring further studies and to be followed by possible biodiversity securitization of the native honeybee *Apis mellifera mellifera.*

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Environmental variation and genetic effects on life-history traits: can adaptation be constrained?

Deborah van Putten (Evolutionary and behavioural ecology, 60 hp)

Supervisor: Luc Bussière, Department of Biological and Environmental Sciences, GU
Examiner: Mats Olsson

To predict how populations will adapt and evolve, it is essential to understand how costly life-history traits genetically covary and trade off in response to variable environments. These trade-offs can limit the response to selection and thus can constrain adaptation in populations. Understanding these genetic trade-offs is especially important for managing pesticide resistance in pest populations. This thesis aims to quantify genetic effects between life-history traits and varying environmental conditions, in *Helicoverpa armigera* moth larvae infected by different doses of a fungal biopesticide. Survival, pupal mass and development rate were measured as response variables. To estimate genetic effects, a half-sibling design was used to partition sire variance from the phenotypic variation. Although the biopesticide did not appear to affect traits on a phenotypic level, including low mortality across all doses, the Bayesian model revealed some evidence for genetic effects. Genetic correlations within development rate were highest for similar doses and lowest for vastly different doses, suggesting gene-by-environment interactions. A positive genetic correlation between pupal mass and development rate was found in the highest dose, while the genetic correlations in the lower doses were closer to 0. This may suggest that certain genetic effects only influence performance under high stress conditions, and that genetic correlations can be masked at low stress environments, due to favorable conditions. Mindful of the limits on power imposed by the number of half-sibling families, my results indicate that genetic effects can change depending on the environment. These findings highlight how environmental variability can potentially constrain adaptation like pesticide resistance. Further research is needed to further investigate the nature of these genetic trade-offs between costly life-history traits and their role in pesticide resistance management.

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Can different capture methods target different behavioral and morphological characteristics? An experimental study using the invasive brook trout

Mitch Olson (Conservation biology, 60 hp)

Supervisor: Johan Höjesjö, Department of Biological and Environmental Sciences, GU
Examiner: Karin Hårding

Invasive species present in aquatic systems can result in numerous adverse ecological effects such as reduced native populations and degraded ecological services. When these effects become too great to ignore management techniques available for invasive fish program vary greatly. Selective manual methods of invasive species removal such as electrofishing and trapping have been shown to be part of successful removal programs but require extensive effort and multiple treatments. Electrofishing requires specialized equipment and training to actively capture invasives whereas trapping uses commonly available traps and after installation is much more passive with fish needing to investigate a new foreign object. Due to the differences between electrofishing and trapping it was theorized by this study that

capture method may select for different behavioral and morphological characteristics in the study species, the invasive brook trout (Salvelinus fontinalis) in a natural Swedish stream. Behavioral differences were theorized that bolder brook trout would be selected for by requiring them to investigate and enter the traps while electrofishing would select for less bold individuals that would remain stationary and be electro fished. Morphological differences could occur as salmonids such as brook trout demonstrate high phenotypical plasticity as potentially part of dietary niche which has been suggested is linked to personality. Behavioral analysis consisted of startle response field boldness testing and group feeding interactions in an artificial stream. Morphological analysis was performed using facial digitization and principal component analysis. Behavioral results showed that capture method does not select for size, weight or induvial or in group boldness of brook trout. Morphological analysis showed that while two facial morphs made up 47% of facial morphological differences there was no significant difference in facial morphology. This study's findings suggest that there is no significant difference in the personality or morphology of the brook trout captured by either method.

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Meteorological and geomorphological influence on harbor seal haul-out distribution behavior using drone imagery

Sebastian Isaac Enault de Cambra (Conservation biology, 60 hp)

Supervisors: Eduardo Infantes & Daire Carroll, Department of Biological and Environmental Sciences, GU
Examiner: Karin Hårding

Harbor seals in Kosterhavet National Park face critical challenges during summer months, as two sensitive life stages (pupping and molting) which are vital for the population's success coincide in time with the increase in tourist activity. This study assessed how topography and meteorological conditions affect seal haul-out site use. Using drone surveys, high-resolution elevation models and slope maps were produced for major haul-out sites. Drone surveys from 2021 to 2023 provided seal counts during key life history stages—pupping and molting—with seal identified manually or using machine learning tools. Subsites within each skerry were defined based on repeated seal presence and classified depending on wind and wave exposure. Statistical analyses provided elevation and slope metrics on the locations seals choose to haul-out, allowing comparison between adults and pups across seasons revealing that pups consistently stay at lower elevations and flatter slopes than adults, with differences observed between adult distributions in pupping season versus molting. Initial linear models showed a preference for sheltered areas depending on wave exposition and for wind when the conditions became harsher. Generalized linear mixed-effects models were fitted showing a small positive influence by temperature and a minor negative effect caused by wind and waves in influencing the haul-out density. Harbor seals only use a little part of the archipelago; therefore, it is necessary to prioritize frequently used haul-out sites during pupping and molting when building conservation plans. Strategically establishing seal sanctuaries could greatly improve the species' long-term resilience in the area. As the seal population is recovering from historical lows because of overhunting, it is vital to continue long-term monitoring. Future studies should address seasonal variability and the potential impacts of human activities such as boat traffic. Incorporating these factors into conservation planning will help ensure that harbor seals remain a stable component of the park's ecosystem.

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Exploring the diet of harbour seals (*Phoca vitulina*): Overall diet and inter-individual variation in prey preferences and feeding tactics

Malin Schött (Conservation biology, 60 hp)

Supervisors: Karin Hårding and Fotini Eleftheria Kappa, Department of Biological and Environmental Sciences, GU.
Examiner: Pierre de Wit

Changes in fish species abundance in the marine environment, due to overexploitation, have a direct effect on harbour seals, with recent decline in somatic growth. Providing accurately assessed diet analysis for long-term observations enables early detection of changes in their health. The present study therefore aims to assess both the overall diet of harbour seals and the variation in diet between individual seals, where habitat use or prey preference will be explored. Diet composition was determined by identifying remains of the prey species in scat samples and analyzing their abundance with two different statistical approaches to compare for validity. To assess if there is a variance in diet composition of individual seals, the samples were tested for Local Contribution to Beta Diversity. To further explore individual preferences, two different distances were applied, the Jaccard similarity and the Bray-Curtis dissimilarity. Wrasse, *Trisopterus spp*., haddock/pollack/saithe, flatfish and cod were shown to be the most important prey species when accounting for abundance and haddock/pollack/saithe, wrasse, cod, *Trisopterus spp*. and flatfish when accounting for biomass. The results showed moderate to high variation in diet composition among scat samples, but the variation could not be explained by any specific pattern, such as feeding strategies or prey preference. Prey species from the same species family showed relatively high co-occurrence. The result showed relative consistency with previous studies. Herring, which are thought to be highly important in the diet of harbour seals, showed low abundance in the present study. This could be explained by their migratory patterns or the increased decline in the fish stocks. The variance in species composition between scats can only indicate that harbour seals show individual habitat- or prey species preferences.

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Restoration of a semi-natural grassland: the impact of clear-cutting and management by grazing on plant diversity and composition

Lina Anderberg (Conservation biology, 60 hp)

Supervisors: Anne Bjorkman, Department of Biological and Environmental Sciences, GU & Mats Niklasson, Research & Education, Nordens Ark
Examiner: Sören Faurby

The area of semi-natural grasslands has been greatly reduced during the last century, partly due to afforestation, and many grassland species are now threatened. By restoring afforested former grasslands there is potential for ecological recovery, but follow-up studies are crucial for assessing the development and outcomes. This study investigates vegetation changes 13 years after restoration of a grassland afforested for around 50 years, located on the Swedish west coast. Vascular plant species were surveyed using 2 by 2 meter quadrats in both grazed and ungrazed clear-cuts, and nearby forests were used to infer pre-restoration conditions.

Additionally, historical sources were used for determining forest cover duration to assess temporal effects on diversity. The results show the area has undergone large changes in composition and increases in diversity measures since clear-cut, with a 42% increase in species richness. Grazing did not significantly affect species richness, but species evenness and the richness of grassland indicator species both increased. The duration of forest cover before clear-cutting impacted the species richness positively, while the proportion of indicator species was affected negatively. Diversity did not have a linear relationship to the time since restoration. Species richness, evenness and the presence of grassland indicator species were driven largely by soil conditions. Dissimilarity in composition between both habitat and management types was mainly driven by vegetation height, ground litter cover and the duration of pre-restoration forest cover. These results are important for understanding the mechanisms behind reestablishment of biodiversity in grassland restorations, and could be a valuable insight for future projects in both the planning stage and the evaluation of outcomes and success.

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Assessing patterns of extinction risk among mammal species in Nigeria: A comparative analysis of human impact

Bernard Asanbe (Conservation biology, 60 hp)

Supervisor: Søren Faurby, Department of Biological and Environmental Sciences, GU
Examiner: Pierre de Wit

This study aimed to evaluate how biological traits influence extinction risk among mammal species in Nigeria, and how these traits interact with specific anthropogenic threats such as agriculture, urbanization, and climate change. Focusing on mammal species in Nigeria, we used phylogenetic logistic regression to test the influence of five biological traits: body mass, brain mass, generation time, current geographic range, and historical range contraction, on extinction risk across 9 IUCN threat categories. Standardized models were used to compare trait sensitivity across threats. Brain mass emerged as the most consistent and influential predictor of extinction risk, particularly under threats such as agriculture, biological resource use, and urban development. Species with larger brains, often primates and carnivores, were highly vulnerable. Geographic range size was a strong negative predictor of risk across most models, with range-restricted species more susceptible to habitat loss and fragmentation. Generation time was positively associated with risk under direct human pressures but inversely linked under climate threats. Body mass showed weak and inconsistent effects, which suggests its influence may be secondary to cognitive or spatial traits. The number of species affected was highest under human threats, compared to climate change or pollution. Extinction risk in Nigerian mammals is shaped by intrinsic traits that interact predictably with human pressures. Species with large brains, small ranges, and slow reproduction are at greatest risk. Trait-based models can improve conservation planning by identifying vulnerable species before population declines become critical, especially in regions facing intensive land-use change.

Keywords: Extinction risk, brain size, Nigerian mammals, human impact.

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Environmental and social determinants of elephant walking speed in conflict-prone areas

Lynn Kleinjan (Conservation biology, 60 hp)

Supervisor: Søren Faurby, Department of Biological and Environmental Sciences, GU & Kate Evans, Elephants for Africa
Examiner: Luc Bussière

African savannah elephants (*Loxodonta africana*) are keystone species whose movements play a crucial role in shaping ecosystems. Yet, their populations are under increasing pressure from poaching, habitat loss, and rising levels of human-elephant conflict (HEC). Gaining a better understanding of how elephants move, particularly their walking speed, can help improve conservation efforts and reduce conflict. This study explores how time of day, environmental conditions (temperature, rainfall, water availability), and social factors (sex and age class) influence walking speed in elephants living in the Makgadikgadi Pans National Park in Botswana, a high-conflict area known for its large number of male elephants, called bulls. Between June 2014 and April 2017, camera traps were placed along established elephant paths to monitor movement. The data were analysed using linear models and generalized additive models (GAMs). The direction of travel turned out to be the strongest predictor of speed: elephants moved significantly faster when heading toward water or food. Time of day also had a clear influence, with a 24-hour rhythm showing higher speeds at night, likely reflecting both thermoregulatory needs and possible crop-raiding behaviour. Temperature had a non-linear relationship with speed: elephants moved faster as temperatures rose, up to a point, after which their speed dropped, suggesting an optimal temperature range for activity. Interactions between time of day and temperature, as well as between time and direction, pointed to a complex mix of behavioural drivers. Other factors like rainfall, sex, and age had only weak or inconsistent effects. Taken together, these findings, based on a unique ecological and social context, shed light on the movement patterns of elephants and point to the importance of considering time, environment, and social structure when developing conservation strategies and managing coexistence in human-altered landscapes.

Keywords: African savannah elephant - walking speed – movement patterns - conflict mitigation - elephant pathways - human elephant conflict

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Leaf minimum conductance and bark water vapor conductance in 14 deciduous tree species

Andrea Sartorius (Physiology & cell biology, 45 hp)

Supervisor: Lasse Tarvainen, Department of Biological and Environmental Sciences, GU
Examiner: Håkan Pleijel

Different tree species handle drought differently, and different strategies can be used by trees to survive drought. One strategy to avoid desiccation is by resisting water loss. A less studied pathway of water loss in trees is the water that is leaving the leaf through other parts of the leaves than the stomata, called leaf minimal conductance (g_{min}) and through the bark, called bark water vapor conductance (g_{bark}). Although these amounts of water loss are small compared to the tree's total water loss, they have been shown to be more important for tree health than previously known. Therefore, the aim of the study was to study 1. the interspecies

variation in g_{min} and g_{bark} between 14 deciduous tree species commonly used in Swedish cities today and ones that potentially could be planted in the future and 2. how g_{min} and g_{bark} can be linked and if they co-vary with stomatal conductance (g_{sw}) and other leaf properties/morphology. The leaf minimal conductance and the bark water vapor conductance were estimated based on measurements of the weight loss of detached leaves and branch pieces while drying out during well-watered conditions. The stomatal conductance was measured for attached leaves during both well-watered and drought conditions. A significant interspecies difference in the variance of g_{min} ($p < 0,005$) and g_{bark} ($p < 0,005$) was found. Also, low g_{min} corresponded to higher LMA ($p = 0.048$), but no significant relationship between g_{min} and $g_{sw\ control}$ (no drought stress induced) ($p = 0.39$) or between g_{min} and g_{bark} ($p = 30$), LWC ($p = 0.49$) or $g_{sw\ drought}$ (drought-exposed trees) ($p = 0.33$) were found respectively. This can have some interesting implications for the drought tolerance of the studied tree species and for g_{min} and g_{bark} in general.

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Phylogeny and biogeography of genus *Gentianella* Inferred from target enrichment sequencing

Hans Meinhard í Eyðansstovu (Biodiversity and systematics, 60 hp)

Supervisors: George Anthony Verboom, Department of Biological and Environmental Sciences, GU & Kent Kainulainen, Gothenburg Botanical Garden
Examiner: Bengt Oxelman

This study presents the most comprehensive phylogenetic study of *Gentianella* using NGS methods to date and aims to: (1) test the Asian origin of *Gentianella* and map its subsequent dispersal history. (2) Assess the monophyly of the Fimbriate Group (Clade C) and establish an area of origin. (3) To infer monophyly of the European species group and its species complexes. To achieve this 60 samples covering the geographic range of *Gentianella* were collected. Target enrichment with the Angiosperm-353 bait set successfully retrieved on average 333 loci per sample from degraded herbarium material. High levels of locus heterozygosity (>80%) and allele divergence (~1.5%) were observed in most samples, indicating hybridization. Phylogenetic inference consistent with the multispecies coalescent model confirmed the polyphyly of *Gentianella s.l.*, monophyly of *Gentianella s.str.* and further subdivided *Gentianella s.str.* into three main clades (Clade A, B, C) with a local posterior probability of 1. However, node support within clades B and C was low. Phasing with HybPhaser was ineffective at increasing support within clades. Consistent with the out-of-Asia pattern observed in other alpinian genera, this study could confirm an Asian origin of *Gentianella*, and subsequent dispersal to North America, where the lineage split into two main clades (B,C), Clade B dispersed to South America and Australasia while Clade C recolonised Eurasia and Europe. Taxonomic implications are discussed based on the polyphyly of the species complexes *G. amarella* and *G. campestris* and the reliability of morphological apomorphies are discussed.

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The impact of fasting and refeeding on intestinal fluid transport and cortisol levels in salmonids

Gagandeep Kaur (Physiology & cell biology, 60 hp)

Supervisor: Henrik Sundh, Department of biological and environmental sciences, GU
Examiner: Lisa Jönsson Bergman

In fish, the intestine plays a central role in nutrient absorption and also contributes significantly to osmoregulatory balance, particularly under fasting or salinity-related stress conditions. This thesis investigated the impact of fasting and subsequent refeeding on intestinal fluid transport capacity, gut mass, plasma ion concentrations, and cortisol levels in seawater-acclimated rainbow trout (*Oncorhynchus mykiss*). The primary aim was to determine how fasting influences fluid absorption in the proximal and distal intestine, and how systemic responses such as ion balance, intestinal mass, and endocrine regulation are affected. Fish were fed on Day 1, followed by fasting periods of 24 to 120 hours, and then refed for 48 hours. Fluid transport was assessed using the non-inverted gut sac method. Plasma concentrations of Na^+, K^+, Ca^{2+}, and Cl^- were measured using a plasma ion analyser, and cortisol levels were quantified using radioimmunoassay (RIA). Fluid transport per intestine (µL/h) increased with fasting and remained elevated after refeeding, particularly in the distal intestine. However, when normalized to surface area (µL/h/cm²), no significant differences were observed, suggesting that tissue-level transport efficiency remained stable. Empty gut mass increased during fasting, especially in the distal region, and did not fully return to baseline following refeeding. Plasma sodium levels decreased significantly during early fasting (24–48h) but recovered by 72h, while potassium showed a transient increase at 48h. Calcium was highly variable, and chloride remained unaffected. Cortisol levels progressively rose with fasting duration, peaking at 120h, and declined after refeeding. Notably, the fed control group showed poor feed intake, which may have limited the reliability of comparisons against truly fed individuals. These findings may suggest that intestinal fluid transport remains functionally responsive during extended fasting, potentially supported by endocrine stress signalling. However, the absence of histological and molecular data limits clear interpretation. Future studies should incorporate freshwater comparisons to further elucidate intestinal adaptations under fasting conditions.

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Oak regeneration in conservation-thinned mixed forests in Sweden: A two-decade study on exclosures

Linnea Erikson (Conservation biology, 60 hp)

Supervisor: Anne Bjorkman, Department of Biological and Environmental Sciences, GU
Examiner: Natalia Corcoll

Oaks (*Quercus robur* and *Quercus petraea*) are keystone species in the northern hemisphere and have a large ecological influence on biodiversity. Oaks are suffering from poor regeneration, and in combination with their strong attractiveness to browsing ungulates, they are prevented from reaching ecological maturity. Their future is threatened. The aim of this study is to investigate if exclosures can aid and enhance regeneration over the long term. In 12 oak-rich mixed forests in Southern Sweden, exclosures and control plots were established in 2001 following conservation-oriented thinning. In 2024, all of the woody species in the plots

were recorded and classified by species and height. The results show no significant difference in oak seedling stem density between exclosures and control plots. This is likely because they fall below typical browsing height and initially rely on acorn reserves, making them less influenced by treatment. Taller oak sapling cohorts were significantly more abundant inside of the exclosures, indicating a long-term positive effect of browsing exclusion. However, total oak stem density declined by 40% compared to measurements taken in 2012, suggesting that competition within exclosures may be suppressing oak survival and performance over time. This study concludes that exclosures do favor oak regeneration. However, their effectiveness may be enhanced by implementing conservation-oriented thinning within exclosures to reduce the competition that is inhibiting the performance of young oaks. Future studies should investigate the combined effect of browsing exclusion and active conservation thinning and monitor abiotic factors that may influence oak regeneration. Given the ecological importance of oaks and the challenges they face in reaching ecological maturity, understanding how to promote their sustained survival and regeneration is critical. This study contributes valuable insights from a rare, decades-long field experiment, providing valuable knowledge to the effectiveness of long-term conservation management of oaks.

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