Norsk symposium i biosystematikk

Programme & Abstracts

13–14 October 2026



Dear colleagues,

Welcome to the 3rd Norsk symposium i biosystematikk, 13-14 October 2026 in Tromsø, Norway.

This symposium was organised in collaboration with Artsdatabanken and research school BIOCORE - Biodiversity Collections and Research Education.

BIOCORE builds on the work of the ForBio Research School by continuing its courses and activities, carrying forward its enthusiasm for biodiversity research, and introducing new ideas to enhance the teaching programme.

Sixty-five participants have registered for this 2026 symposium. Participants will hear keynote lectures by Siri Birkeland (*Natural History Museum, University of Oslo*) and Bastian Fromm (*The Arctic University Museum of Norway, UiT*). The programme also includes 19 contributed full talks and 20 contributed speed talks.

Pre-conference workshop on *Red List Species and Their Relevance* will be led by Stine Svalheim Markussen and Ingrid Toresen *(Artsdatabanken)*.

Thank you for helping us make this symposium possible!

Kind regards,
Galina Gusarova, Micah Dunthorn & Stine Svalheim Markussen

BIOCORE
Biodiversity Collections & Research Education

artsdatabanken

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Organizing Committee

Organizers

Galina Gusarova,

Arctic University Museum of Norway
UiT Arctic University of Norway

Co-organizers

Nataliya Budaeva
University Museum of Bergen
University of Bergen

Micah Dunthorn
Natural History Museum
University of Oslo

Stine Svalheim Markussen
Artsdatabanken

Elisabeth Stur
NTNU University Museum
Norwegian University of Science and Technology

Local organising committee in Tromsø:

Shaddai Heidgen
Andreas Altenburger
Yuan Pan
Catherine Mary Troman
Lucas Dane Elliott

Meeting Programme

NB: talks related to an Artsdatabanken Artsprosjektet are marked with an *.

Tuesday, 13 October

Workshop

Session chair:	**Micah Dunthorn** *(Natural History Museum Oslo)*
10:00–12:00	**Stine Svalheim Markussen** *(Artsdatabanken)* **Ingrid Toresen** *(Artsdatabanken)* Workshop on Red List Species and Their Relevance
12:00–13:00	**lunch**

Opening remarks

13:00–13:10	**Welcome address** **Galina Gusarova** *(UiT Arctic University of Norway)* **Inger Alsos** *(UiT Arctic University of Norway)* **Micah Dunthorn** *(Natural History Museum Oslo)* **Stine Svalheim Markussen** *(Artsdatabanken)*

keynote lecture 1

Session chair:	**Galina Gusarova** *(UiT Arctic University of Norway)*
13:10–13:40	**Bastian Fromm** *(UiT Arctic University of Norway)* Understanding animal complexity and biodiversity through non-coding genome evolution

session 1

Session chair:	**Elisabeth Stur** *(NTNU University Museum)*
13:40–13:55	**Maria Skauge Larsen** *(NTNU University Museum)* *Are dark taxa left behind? Evaluating urban biodiversity management through citizen science
13:55–14:10	**Thomas Wetteland Woxen** *(NTNU University Museum)* Exploring the concept of rarity in Dark Taxa
14:10–14:25	**Lucas Geisler** *(NTNU University Museum)* BUGHAVN: An open-source, low-cost insect trap for large-scale biodiversity snapshots and community science
14:25–14:45	**break**

session 2

Session chair:	**Emily Hartop** *(NTNU University Museum)*
14:45–15:00	**Lasse Topstad** *(UiT Arctic University of Norway)* Rapid loss of arctic plant and animal diversity in the Baltic at the onset of Holocene revealed by sedimentary ancient DNA
15:00–15:15	**Jostein Kjærandsen** *(UiT Arctic University of Norway)* MOTU-anchored vouchers: linking barcode clusters, molecular diagnoses, and museum specimens in integrative dark taxonomy
15:15–15:30	**Elisabeth Stur & Torbjørn Ekrem** *(NTNU University Museum)* Key insights from 20 years of DNA barcoding and integrative taxonomy on Chironomidae (Diptera)
15:30–15:50	**FLASH TALKS** **Torbjørn Ekrem** *(NTNU University Museum)* NorBOL: Building the DNA Barcode Reference Library for Norwegian Biodiversity

Isabelle Ewers *(Natural History Museum Oslo)*
Four days & a makeshift lab later: on-site long-read metabarcoding of fish stomach contents

Jorge Andres Varela Camelo *(Natural History Museum Oslo)*
Unravelling diversity and abundance of freshwater fish in Svalbard through molecular-based monitoring

Andreas Altenburger *(UiT Arctic University of Norway)*
*Taxonomy of Arctic sea ice-associated rotifers of the genus *Synchaeta* based on novel 18S and COI sequences and morphological observations

Bastiaan Maarse *(Norsk Botanisk Forening)*
Engaging the youth in plant taxonomy and biodiversity mapping: the Young Botanist Tromsø project (Ung Botaniker Tromsø)

15:50–16:15 **break**

session 3

Session chair: **Teppo Rämä** *(UiT Arctic University of Norway)*

16:15–16:30 **Zofia Maurer** *(University Museum of Bergen)*
*Diversity and biogeographical patterns of bristle worms (Annelida) from Isfjorden, Svalbard

16:30–16:45 **Luis Martell** *(University Museum of Bergen)*
*Connecting parallel systematics: Integrative solutions for hydromedusan life-cycle mysteries in Tiarannidae and Laodiceidae

16:45–17:05 **FLASH TALKS**
Siluni Thiyumila Samarakoon *(University of Oslo)*
The role of phytal copepods in macroalgal invertebrate diets

Selina Tinkhauser *(UiT Arctic University of Norway)*
Retreating glaciers, emerging ecosystems: invertebrate diversity and the refuge potential of glacier forefield ponds and lakes in arctic and alpine environments

Ana Teresa Capucho *(Natural History Museum Oslo)*
*MeioSkag – updates from meiofauna in the Skagerrak

Emer Flanagan *(UiT Arctic University of Norway)*
Exploring Photoreception in an Arctic Cervid (Rangifer Tarandus Tarandus)

Katrine Kongshavn *(University Museum of Bergen)*
*Pieces of the puzzle; Can information on microhabitat aid in resolving cryptic diversity?

Eirik Aasmo Finne *(UiT Arctic University of Norway)*
Glacial fungal metacommunities and their drivers

Ella Thoen (*University of Oslo)*
*Mortierellaceae in Norway: a highly abundant but neglected fungal family

18:00 Visit to the Polar Museum; led by **Andreas Altenburger**
Søndre Tollbodgate 11B, 9008 Tromsø

19:00 **dinner**
FINT kafé
Skippergata 1c, 9008 Tromsø

Wednesday, 14 October

keynote lecture 2

Session chair: **Nataliya Budaeva** *(University Museum of Bergen)*

09:00–09:30 **Siri Birkeland** *(Natural History Museum Oslo)*
How repeatable is evolution at the edge of the world? Convergence across genomes, phylogenies and populations

session 4

Session chair: **Andreas Altenburger** *(UiT Arctic University of Norway)*

09:30–09:45 **Yuan Pan** *(UiT Arctic University of Norway)*
Betula species delimited by kmer distribution

09:45–10:00 **Kristian Hassel** *(NTNU University Museum)*
*The alpine bryophytes of the Scandinavian Peninsula

10:00–10:15 **Hyeonsik Yoon** *(NTNU University Museum)*
Generation time under clonal reproduction: module founding in the peat moss Sphagnum

10:15–10:35 **FLASH TALKS**

Hans Meinhard í Eyðansstovu *(NTNU University Museum)*
Exploring evolutionary relationships in *Barbarea* (Brassicaceae) using whole-genome data

Joseph Njogu *(Natural History Museum Oslo)*
Phylogenomics and evolutionary relationships of selected Kenyan shrubby aloes: resolving species boundaries using dd-RAD-seq

Lazia Shina Nagujja *(Natural History Museum Oslo)*
Disentangling the phylogeny of the *Chlorophytum gallabatense* complex: a molecular phylogenetic approach

Thea Ramona Olsen *(University of Oslo)*
Taxonomic assessment of *Chlamydomonas* sp. strains RCC7876

(WAP 05) and RCC7886 (WAP 30) from the West Antarctic Peninsula

César Herrero González *(Natural History Museum Oslo)*
Convergent signatures of plant adaptation to the Arctic: comparative genomic, phenotypic and epigenetic studies

10:35–11:15 **break**

session 5

Session chair: **Ella Thoen** (*University of Oslo)*

11:15–11:30 **Irene Zanandrea** *(Natural History Museum Oslo)*
Rapid, unbiased and precise phenotyping using the ALPHA3D pipeline

11:30–11:45 **Rodrigo Salvador** *(Finnish Museum of Natural History)*
Copse snails: phylogeography, taxonomy, behavioural ecology, and adaptations to the Arctic

11:45–12:00 **Mari Eilertsen *(University Museum of Bergen)***
Biodiversity of chemosynthesis-based ecosystems in the Arctic deep sea

12:00–12:15 **FLASH TALKS**

Emily Hartop *(NTNU University Museum)*
De oído: a case of taxonomic murder in Madrid

Franz Goecke (*Norwegian University of Life Sciences)*
*Untangling Norway's freshwater filamentous green algae

Anna Seniczak *(University of Inland Norway)*
*Introduction to the Artsdatabanken project: Mites of Unexplored and Cryptic Habitats (MUCH)

12:15–13:30 **lunch**

session 6

Session chair:	**Torbjørn Ekrem** *(NTNU University Museum)*
13:30–13:45	**Torsten Struck** *(Natural History Museum Oslo)* Promises and challenges of macrosynteny as a phylogenetic marker considering robusticity
13:45–14:00	**Nataliya Budaeva** *(University Museum of Bergen)* *Current knowledge of the diversity of the Arctic annelids
14:00–14:15	**Teppo Rämä** *(UiT Arctic University of Norway)* *Fungi in aquatic environments in Norway
14:15–14:30	**Arve Elvebakk** *(UiT Arctic University of Norway)* From biodiversity to global-scale lichen biosystematics
14:30–14:45	**Magnus Vandbakk** *(UiT Arctic University of Norway)* Aquatic hyphomycete communities from headwaters to the sea in the Målselv catchment
14:45–15:00	**Closing remarks and talk prises**

Invited Talks

Understanding animal complexity and biodiversity through non-coding genome evolution

Bastian Fromm

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What makes animals complex, and how does this complexity relate to biodiversity? Beyond protein-coding genes, non-coding regulatory sequences provide a powerful perspective on the evolution of animal form and function. My talk explores microRNAs as conserved regulators, evolutionary markers, and indicators of changes in organismal complexity. Drawing on several different comparative analyses across animal lineages, I examine how gains, losses, and modifications of microRNA repertoires illuminate major evolutionary transitions, including morphological simplification in parasites. I also discuss how curated annotations and comparative genomic tools reveal patterns obscured by incomplete or inaccurate datasets. Finally, ancient and environmental RNA extend these approaches through time and into ecosystems, opening new opportunities to connect genomic evolution with the history, diversity, and functional biology of living animals.

How repeatable is evolution at the edge of the world?
Convergence across genomes, phylogenies and populations

Siri Birkeland

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Understanding the evolutionary history of organisms depends on our ability to distinguish similarities that reflect common ancestry from those that have evolved independently. Convergent evolution therefore presents both an opportunity and a challenge for biosystematics: repeated adaptations can reveal how natural selection shapes biological diversity, but convergence can also obscure phylogenetic relationships and complicate the interpretation of comparative data. I use Arctic plants as a natural system for asking how often evolution arrives at similar solutions under similar environmental conditions, and at what level this repeatability can be detected. The strong and repeated selection pressures imposed by Arctic environments provide an opportunity to identify genomic signatures of adaptation and explore their genetic basis. In comparisons of Arctic Brassicaceae, I found little evidence that adaptation repeatedly targets the same genes or mutations. Instead, independently evolving Arctic lineages showed convergent signals at the level of functional pathways. Comparative transcriptomic analyses similarly revealed a mixture of shared and lineage-specific responses to cold, suggesting that even closely related species can reach similar adaptive phenotypes through different molecular routes. More recent comparative genomic work across distantly related Arctic plants has revealed stronger evidence for shared signatures of selection, including repeated signals in genes associated with membrane function, protein folding, metabolism, and oxidative stress. Together, these studies illustrate how the apparent repeatability of evolution depends on the evolutionary scale and the level of biological organization being considered. I will first consider how phylogenetic context is essential for identifying convergence, and how convergent evolution can itself complicate the reconstruction of evolutionary relationships. I will then use my work on Arctic plants to explore how comparative genomic and transcriptomic approaches can reveal different degrees and forms of evolutionary repeatability, ultimately asking: how predictable is the history - and future - of life?

Contributed Talks

(speaker underlined)

Taxonomy of Arctic sea ice-associated rotifers of the genus *Synchaeta* based on novel 18S and COI sequences and morphological observations

Miriam Marquardt[1], Bodil A. Bluhm[1], Rolf Gradinger[1] and Andreas Altenburger[1,2]

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[2] The Arctic University Museum of Norway, UiT - The Arctic University of Norway, Tromsø, Norway

Presenting author e-mail: andreas.altenburger@uit.no

The microscale brine channels in sea ice create a unique habitat for cold-adapted organisms, including invertebrates like rotifers, nematodes, and harpacticoid copepods, collectively known as sympagic (i.e. ice-associated) meiofauna (>20 µm). Despite their role in the sea ice food web as grazers, aspects related to their function and biodiversity remain poorly studied at the species level. Arctic sea ice rotifers, though commonly occurring across the Arctic seas, have mostly been examined microscopically, with few studies identifying them beyond the phylum level. To address this taxonomic knowledge gap, we investigated the genetic diversity of 41 sympagic rotifer individuals collected in the Barents Sea and Central Arctic Ocean basins between 2019 and 2025. Using general invertebrate/eukaryotic primers targeting the COI and 18S rRNA genes, we performed PCRs and Sanger sequencing on Chelex-extracted DNA of these specimens. We found four previously unknown COI lineages of the genus *Synchaeta*. Morphological observations tentatively associate these four novel lineages with the known ice-associated taxa *S. hyperborea*, *S. tamara*, *Synchaeta* sp. and *S. glacialis* or *S. cecilia*. *Synchaeta* is a common Arctic marine genus that has previously been recorded in sea ice from the Laptev, Greenland and Barents Sea, and Frobisher Bay (Canada). This study highlights that integrative approaches combining morphological and molecular methods are required to improve biodiversity inventories of Arctic sea ice, as large gaps remain in reference sequence databases.

Current knowledge of the diversity of the Arctic annelids

Nataliya Budaeva[1], Tom Alvestad[1], Jon Anders Kongsrud[1], Nicolas Straube[1], Torkild Bakken[2], Martha Everett[1], Zofia Anna Maurer[1], Eva Charlotte Samson[1]

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Annelids are among the most species-rich and ecologically important groups of the Arctic benthos, yet their diversity remains incompletely documented and taxonomically unresolved. We synthesize current knowledge based on the three-year mapping project MAnDAriN, which recorded 293 annelid taxa representing 188 genera. Of these, 199 taxa (68%) were identified to species level. Among them, 172 species have no taxonomic concerns noted, while 21 are recognized or suspected species complexes, indicating that several nominal species probably conceal multiple lineages. About 30% of the taxa could be identified only to genus or family level, showing that the Arctic annelid fauna is far from completely known. This was most evident in Cirratulidae, Paraonidae and Spionidae, three highly diverse and taxonomically challenging families of annelids. DNA barcoding produced 820 barcodes grouped into 188 BINs, covering a large proportion of the recorded morphological diversity. Nevertheless, integrative taxonomy combining morphology and DNA barcoding, together with targeted revisions of the most problematic families and genera, is needed before the true diversity and distribution of Arctic annelids can be assessed.

Unravelling diversity and abundance of freshwater fish in Svalbard through molecular-based monitoring

Jorge Andres Varela Camelo, Hugo J. de Boer, Quentin Mauvisseau

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Arctic freshwater ecosystems are undergoing rapid environmental changes, yet fish diversity, abundance and seasonal dynamics often remain poorly characterized. Conventional fish monitoring is often invasive and logistically demanding, particularly in remote Arctic environments. However, environmental DNA (eDNA) and environmental RNA (eRNA) provide complementary, non-invasive approaches for detecting aquatic organisms and assessing biological communities. My MSc project investigates the use of molecular-based monitoring to characterize freshwater fish diversity and abundance across seasons in Svalbard, with Arctic charr (*Salvelinus alpinus*) as a focal species. Around 90 water samples, including controls, were collected across spring, summer, autumn and winter from freshwater systems included in ongoing monitoring programmes. Samples were filtered on site and both eDNA and eRNA was processed later in laboratory using species-specific droplet digital PCR (ddPCR). We investigated how Arctic charr eDNA and eRNA detection and quantification varied across seasons and compared these results against independent abundance and biomass estimates obtained through conventional fish surveys. In parallel, metabarcoding analysis using COI and 12S primer sets will be used to characterize broader fish and invertebrate communities. This component aims to detect additional fish taxa, including potentially unrecorded or invasive species, investigate seasonal shifts in community composition, and provide ecological and dietary context for Arctic charr. By combining targeted ddPCR with community-level metabarcoding, the project evaluates molecular monitoring at complementary taxonomic scales. Comparing eDNA and eRNA across strong seasonal contrasts will further assess their reliability, repeatability and potential differences in temporal resolution. Ultimately, this work aims to determine how molecular approaches can complement conventional surveys and contribute to routine biodiversity monitoring in remote Arctic freshwater ecosystems.

MeioSkag – updates from meiofauna in the Skagerrak

Ana Teresa Capucho[1], Alexander Kieneke[2], Christopher Laumer[3], Katrine Worsaae[4], Torsten H. Struck[1]

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[3]Life Sciences Department, Natural History Museum, London, United Kingdom
[4]Department of Biology, University of Copenhagen, Copenhagen, Denmark

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Thousands of tiny animals live between the grains of sediment in beaches and at the bottom of the ocean. They are called meiofauna and include an extremely diverse, yet often overlooked, part of marine ecosystems. Despite their importance and abundance, the knowledge about their taxonomy, distribution and ecology is very poor. In Norway particularly, meiofauna records are sparse and often only down to the phylum level. Therefore, the Artsdatabanken project MeioSkag is trying to fix this knowledge gap by targeting meiofaunal species in the Skagerrak, specifically from the phyla Gastrotricha, Platyhelminthes, Annelida and Gnathostomulida. We are halfway through the project and in this talk, I will present some preliminary results. We have collected sediment samples from the supratidal, intertidal and subtidal zones, covering nine different locations in the Oslofjord. We have now registered over 150 specimens, including at least two new species to Norway, but we are still working on the identification. After doing a major literature review, we found out that we can expect many more species than previously thought, since many records were not databased. We started molecular lab work and genome skimming, as we are planning to design new primers to get the CO1 barcode for all the collected specimens. We began with only 40 specimens, as we are still developing the best methods to do this.
Another important part of our project is outreach, and we have participated in several science dissemination activities. We also helped to develop a standard operating procedure for collecting small-sized marine animals for genomic research.

Biodiversity of chemosynthesis-based ecosystems in the Arctic deep sea

Mari Heggernes Eilertsen[1,2], Brenda Lisbeth Esteban Vazquez[1,2], Christian Ludvig Nilsson[1,2], Kristoffer Franzen Nilssen[1,2], Selma Berg Eriksen[1,2], Jon Anders Kongsrud[3]

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Chemosynthesis-based ecosystems (CBEs) - hydrothermal vents, cold seeps, and organic falls - host highly specialized biological communities in the deep sea. Exploration efforts in the last two decades have revealed numerous previously unknown Arctic CBEs, but the characterization of the biodiversity of these systems is still in the early stages. Arctic CBEs support a distinctive fauna dominated by small-bodied organisms, including extensive "worm forests" dominated by the slender siboglinid tubeworms in the genera *Sclerolinum* and *Oligobrachia*. These tubeworms act as foundation species, engineering structurally complex biogenic habitats that host highly diverse macrofaunal assemblages at both vents and seeps, yet the taxonomic composition of these communities has only recently begun to be resolved. The deep basins of the Nordic Seas and the Central Arctic Ocean are isolated from the Atlantic and Pacific by shallow sills, and this geographic isolation is reflected in a high degree of regional endemism among the deep-sea fauna, including within CBEs. As a result, Arctic CBEs harbour a fauna of considerable novelty, including several taxonomic groups that are rare or absent from CBEs at lower latitudes. This presentation synthesizes recent findings on the biodiversity of Arctic CBEs from the WormFEST (RCN, FRIPRO) and NorCBE (NBIC) projects. Environmental gradients appear to shape community composition and may act as drivers of regional diversification. A notable example is provided by gastropods of the family Rissoidae, among the most abundant taxa recorded in Arctic CBEs, which comprise several closely related species with distinct distributions and habitat preferences, suggestive of regional diversification. Together, these findings contribute to a growing recognition of the Arctic deep sea as a centre of biodiversity that is more diverse, and more distinctive, than previously appreciated, underscoring the value of chemosynthesis-based ecosystems as reservoirs of undescribed and biogeographically significant taxa.

NorBOL: Building the DNA Barcode Reference Library for Norwegian Biodiversity

Torbjørn Ekrem[1], Inger Greve Alsos[2], Hugo de Boer[3], Aino Hosia[4], Aina Mærk Aspaas[1], Katrine Kongshavn[4], Gunnhild Marthinsen[3], Marie Kristine Føreid Merkel[2]

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The Norwegian Barcode of Life Network (NorBOL) has served as Norway's national DNA barcoding infrastructure since 2014, supporting the documentation and identification of the country's biodiversity. DNA barcode reference libraries provide an important link between traditional biosystematics and molecular approaches to species identification, but their value depends on the taxonomic coverage and reliability of the underlying reference material. We synthesised barcode data generated through NorBOL and its partner institutions, including the four Norwegian university museums. Barcode coverage was assessed relative to the estimated Norwegian species pool, and representation across major taxonomic groups was evaluated. Approximately 206,000 DNA barcode records from Norway are currently available in the Barcode of Life Data Systems (BOLD), representing around 23,000 species, nearly one third of the estimated Norwegian species diversity. However, only approximately 86,300 sequences are associated with morphologically identified specimens. Coverage varies considerably among taxonomic groups, with relatively strong representation in liverworts, some marine invertebrates and selected insect families, while major gaps remain in nematodes, protists, and several insect and fungal groups. These gaps reflect, among other factors, challenges associated with specimen identification and the availability of taxonomic expertise and reference material. The NorBOL experience demonstrates both the potential and the limitations of DNA barcoding as a tool for documenting biodiversity. Continued collaboration between molecular and traditional biosystematics is essential for expanding reliable reference libraries, resolving taxonomically challenging groups, and making barcode data more useful for biodiversity research, species identification and environmental monitoring. The planned development of NorBOL into a broader national infrastructure for molecular biodiversity research will further strengthen this integration.

From biodiversity to global-scale lichen biosystematics

Arve Elvebakk

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In the 80s, Norwegian botanists mostly focused on biodiversity of a given area, often with a vegetation approach and much time devoted to identification of species including bryophytes and lichens. My studies were on Svalbard and other parts of the Arctic, first with coarse-scale bioclimatic studies, later using plants as temperature indicators locally. During an attempt to extend this method to an area in southernmost Chile, I realized that some exciting lichens there could not be identified, simply because they had not been described. This was my start on biosystematics on South American Pannariaceae lichens, and I had no idea then that starting on this clade would expand to studies on all the seven continents. More than 30 species have now been described with coauthors, and with Soon Gyu Hong from Korea as a key partner on phylogeny we have now described five new genera. *Xanthopsoroma* is a very distinct and isolated austral genus, whereas *Gibbosporina* is instead palaeotropical and estimated to be 75 Ma old. *Psoroma* includes a number of ancestral species from tree trunks in austral Gondwanaland forests, however, the genus adapted to terricolous cold habitats in Antarctica after its isolation at 34 Ma and subsequent cooling. From there, the genus radiated and migrated northwards to cold habitats of many new areas, including mountains of New Zealand and Australia and the Northern Hemisphere. We have described 9 *Psoroma* species and are now describing and studying many more, several new ones from Norway. The well-known *Psoroma hypnorum* will be shown to have a very surprising evolution. The genus *Pannaria* includes many undescribed species and probably evolved in Zelandia where it has its diversity centre with at least one more undescribed genus. I have felt it as dramatic leaving the tradition of exploring the wide biodiversity of an area to instead focus on a small group and follow it anywhere. I have witnessed molecular methods from emerging to becoming universal. However, will future biosystematics find the time needed to be experienced enough to identify samples related to types well enough to supply reliable names on forthcoming sequences?

Four days & a makeshift lab later: on-site long-read metabarcoding of fish stomach contents

Isabelle Ewers[1], Micah Dunthorn[1], Quentin Mauvisseau[1], Denise Rui Ying Ong[2], Adriana Lopes dos Santos[2], Daniel Vaulot[2,3], Jonathan Stuart Ready[4], Jonata de Arruda Francisco[4]

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Long-read metabarcoding of fish stomach contents can be a useful approach to infer their diets and their parasites. Conventional metabarcoding approaches typically require dedicated laboratory infrastructure and time-consuming workflows. We tested a fully portable, off-grid long-read metabarcoding pipeline in a field trial, targeting the 18S rRNA gene region in stomach contents from 39 individuals representing eleven local fish species from northern Brazil. All laboratory steps including DNA extraction, amplification of the rRNA operon, library preparation, and sequencing, as well as bioinformatics, and statistical analyses were performed on-site in non-laboratory conditions using compact, portable equipment and a MinION sequencer. Sequencing generated 1751 OTUs, of which 1597 OTUs contained 18S sequences, of which 1116 OTUs were retained after taxonomic assignment and filtering. While most OTUs were assigned to metazoans, consistent with the feeding ecology of the sampled fish, some fungi and several protistan groups were detected as well. These results demonstrate the feasibility of on-site long-read metabarcoding for rapid dietary and biodiversity assessments, extending molecular workflows beyond conventional laboratory settings into remote, resource-limited environments.

Exploring evolutionary relationships in *Barbarea* (Brassicaceae) using whole-genome data

Hans Meinhard í Eyðansstovu[1], Kristine Bakke Westergaard[1], Michael D. Martin[1], Simone Fior[2]

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I will present preliminary results from my PhD project, which aims to investigate the evolutionary and demographic history of *Barbarea vulgaris* as an alien plant in the Arctic. *Barbarea vulgaris* is native to central and eastern Europe but has been introduced multiple times across the North Atlantic, where it has established populations in North America, Greenland, Iceland and Svalbard. This provides an opportunity to investigate the history and evolution of plant invasions in an Arctic context. However, the genus *Barbarea* is taxonomically challenging and defining species boundaries has been difficult. The first step is therefore to identify the evolutionary lineages that exist within the genus and determine whether these correspond to the current taxonomic classification.

Glacial fungal metacommunities and their drivers

Eirik Aasmo Finne[1], Kristel Panksep[2,3], Red Calore[4], Victoria Prins, The MoSTFun project consortium, Teppo Rämä[1]

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Glacial and periglacial ecosystems, including ice, snow, cryoconite holes, and nearby lakes and rivers, are extreme environments that host unique fungal communities. These habitats differ markedly in their ecological, physiological, and chemical properties, which in turn shape fungal metacommunities. Ice and snow are characterized by fluctuating water availability, low temperatures, and high UV exposure. Cryoconite holes are melt-holes formed when sediments accumulate on ice and offer relatively stable microenvironments. In contrast, periglacial lakes and rivers have extreme sedimentation rates and high turbidity limiting photosynthesis. Understanding fungal communities within these environments, and how they change between habitats, is critical for elucidating the ecological dynamics of glacial ecosystems under changing climatic conditions. We conducted a two-year study to investigate the drivers of fungal diversity and community structure across Arctic and sub-Arctic glacial habitats in Northern Europe. Snow, ice, water, and sediment were collected from multiple sites to capture microbial biomass, and the sampling was repeated five times during the spring-to-winter seasons. Comprehensive metadata, including physiogeochemical parameters, were recorded to assess environmental drivers. Fungal communities were characterized by amplicon sequencing the full ITS region using PacBio. Preliminary analysis suggests a difference in fungal communities between the supraglacial and the periglacial habitats. The supraglacial communities seem to be more dependent on autochthonous primary production and include yeasts and zoosporic taxa known for being saprotrophic and parasitic on snow algae, while a more mixed community with several plant pathogens showed up in the periglacial samples. A seasonally linked change in communities was also more apparent in the supraglacial samples, possibly associated with the shift in condition between snowmelt, ice-melt and later the refreezing of the glacial surface. We will present results on the fungal metacommunities of these glacial and periglacial habitats, their geochemical properties, and environmental correlations. This study highlights the importance of fungi as key components of cryospheric biodiversity and their role in biogeochemical cycling in extreme environments.

Exploring Photoreception in an Arctic Cervid
(Rangifer tarandus tarandus)

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Life on Earth evolved alongside predictable circadian and seasonal light cycles generated by the Earth's rotation and orbit around the sun. Photoreception, the ability to detect environmental light information, enhances an organism's fitness by facilitating both visual and non-visual biological functions. Visual functions include navigation, resource acquisition, predator detection and social interactions, while non-visual functions include the entrainment of endogenous biological rhythms to environmental cycles. Photoreception via opsin proteins is highly conserved across the tree of life, with extreme and dynamic light environments being associated with increased opsin diversification. Polar regions are examples of extremely dynamic terrestrial light environments which experience dramatic annual variation in photoperiod due to the tilt of the Earth's axis, ranging from continuous darkness during Polar night to continuous daylight in Polar day. Whether such conditions promote novel evolution of photosensitive opsin proteins in endemic polar species is unclear. In this study, photoreception in the Eurasian reindeer (*Rangifer tarandus tarandus*) was explored using a combination of bioinformatic and experimental approaches. A local basic alignment search (BLAST) revealed that reindeer possess a typical cervid opsin repertoire. The spectral sensitivity of each reindeer opsin was predicted based on the presence/absence of known mammalian spectral tuning sites and our predictions were confirmed by performing heterologous action spectroscopy on opsin-expressing HEK cell cultures. Molecular evolutionary analyses revealed no reindeer-specific signatures of positive selection within opsin coding sequences, although evidence of divergent selection acting on the short-wave-sensitive opsin was detected across Cervidae. Our results suggest that reindeer opsins are serendipitously well-suited to the Arctic light environment due to their cervid ancestry, and do not display evidence of novel Arctic adaptation.

BUGHAVN: An open-source, low-cost insect trap for large-scale biodiversity snapshots and community science

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The taxonomic impediment remains a major challenge to documenting insect diversity, with the availability of specimens often limiting the scale of taxonomic and biodiversity research. Although advances in DNA barcoding and high-throughput taxonomic workflows increasingly allow large numbers of specimens to be processed, obtaining sufficiently large and geographically distributed samples remains a fundamental bottleneck. Community science offers an opportunity to overcome this limitation by distributing sampling across many participants and locations, but this requires sampling equipment that is affordable, robust, and simple to deploy. We present BUGHAVN, an open-source, low-cost insect trap developed to facilitate large-scale insect sampling by both professional researchers and community scientists. BUGHAVN follows the principle of passive interception sampling used by Malaise traps but is constructed primarily from inexpensive, readily available materials, reducing both financial and logistical barriers to large-scale deployment. Its open-source design allows it to be reproduced, modified, and adapted to different sampling contexts. The potential of this approach was explored through the Mass Experiment, a large-scale community science initiative in Denmark in which participants contributed insect samples using standardised sampling protocols. By distributing sampling across a large number of participants, community science can generate extensive spatial and temporal coverage that would be difficult to achieve through conventional research teams alone. Such distributed sampling can provide biosystematic projects with substantially larger and more geographically representative specimen collections, creating opportunities for morphological identification, DNA barcoding, species delimitation, and the discovery of poorly known taxa. We present the design of BUGHAVN and discuss its application in large-scale biodiversity sampling, with particular emphasis on the role of community science in expanding the scale and geographic coverage of biosystematic research. BUGHAVN demonstrates how reducing the practical barriers to specimen collection can complement advances in modern taxonomy and help address the taxonomic impediment.

Untangling Norway's freshwater filamentous green algae

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Freshwater algae are often overlooked but ecologically important organisms. These algae grow as tangled masses of filaments that, from one species to the other, look much the same in the field. In this project, we embark on a comprehensive survey of the biodiversity of filamentous green algae across all major Norwegian river types. We combine extensive field sampling with detailed morphological characterization of freshly collected material, followed by laboratory cultivation, and integrate these observations with molecular analyses on the algal cultures and ecological modelling. Our goals are robust and accurate species identification and the discovery of previously unnoticed patterns of diversity and distribution. Together, these approaches will significantly advance the understanding of Norway's freshwater algal biodiversity and lay an important foundation for conservation of this group.
Last summer, we completed the first round of sampling across several sites throughout Southern Norway, providing an exciting first glimpse into the diversity of freshwater filamentous green algae across Norway. The collected material has now been carefully characterized, and *in vitro* cultivation efforts are well underway. So far, we have established a diverse collection of cultures and field samples representing *Klebsormidium, Mougeotia, Rhizoclonium, Spirogyra, Vaucheria,* and *Zygnema*. These cultures are now ready for sequencing and are being closely monitored in cultivation. Because vegetative filaments of many of these genera are nearly identical, species identification has traditionally relied on sexual structures (zygospores, oogonia) that are rare in the field but can be induced in culture. Combining molecular data with morphological observations - especially reproductive traits - will be crucial for resolving species identities and revealing the hidden diversity within this group.

Convergent signatures of plant adaptation to the Arctic: comparative genomic, phenotypic and epigenetic studies

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Arctic plants manage to survive under some of the most extreme environmental conditions on Earth. They face low temperatures, large seasonal changes in light and short growing seasons, but somehow, distantly related plant lineages have independently colonized and adapted to these harsh environments. This raises a fundamental evolutionary question: have Arctic plants repeatedly evolved similar solutions to the same environmental challenges? My PhD investigates the genomic and epigenomic basis of Arctic plant adaptation, aiming to determine whether convergent evolutionary patterns can be detected across independent Arctic lineages at three different biological levels: the molecular, species and population levels. At the molecular level, the evolution of the CBF cold-response pathway will be studied to determine whether genes in Arctic species show convergent evolutionary patterns relative to their closest temperate relatives. At the species level, common-garden experiments with *Draba nivalis* and *Cochlearia groenlandica* will assess how contrasting temperature and light conditions modulate phenotypic responses and DNA methylation, exploring the role of plasticity and epigenetic variation in Arctic adaptation. At the population level, comparative population genomics across distantly related Arctic plants will be used to test whether adaptation along environmental gradients repeatedly involves the same genes, genomic regions or biological pathways. By investigating convergent evolution across these three biological levels, this project aims to clarify how repeatable Arctic adaptation is and improve our understanding of convergent evolution in Arctic plants.

De oído: A Case of Taxonomic Murder in Madrid

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In a museum drawer in Madrid, a small fly has been waiting for almost ninety years. Described by Hermann Schmitz in 1937, *Megaselia introlapsa* was later synonymised with *M. xanthozona*—but the decisive specimen had never been examined. In taxonomy, sometimes the most important evidence is also the evidence that is easiest to overlook. We examined and photographically documented four name-bearing types of *Megaselia* described by Schmitz in 1937 from material held at the Museo Nacional de Ciencias Naturales in Madrid: *M. introlapsa*, *M. pollex*, *M. ruralis*, and *M. ultrabrevis*. For *M. pollex* and *M. ultrabrevis*, lectotypes are designated, fixing the application of their names to specimens preserved in the Madrid collection. The more complicated case was *Megaselia introlapsa*. In 2019, the species was synonymised with *M. xanthozona*, but the Madrid holotype was not examined as part of that assessment. Returning to the specimen revealed a different story. Its male terminalia differ markedly from those of *M. xanthozona*, and the synonymy is therefore rejected. *Megaselia introlapsa* is reinstated as a valid species (*stat. rev.*). We also document the condition, labels, and diagnostic morphology of all four types, providing previously unpublished photographic evidence of these historically important specimens. These images are not intended as complete digital surrogates, but provide an accessible record of critical morphological evidence and allow future researchers to examine features that might otherwise remain hidden in a museum drawer. This case is a reminder of a fundamental principle in systematics: the literature is an interpretation of the evidence, but the name-bearing type is the ultimate source of evidence for a name. When the story does not quite fit, we must return to the specimen itself.

The alpine bryophytes of the Scandinavian Peninsula

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The Scandinavian Peninsula is characterized by the Scandes mountain range running north south. During the last glacial maximum, 29-19 000 years ago, the region was nearly completely covered with ice. Most species must therefore have recolonized the area when the ice retreated. Today the Scandinavian bryophyte flora consists of about 1280 species, and about 20% have their main distribution in the mountains above the tree line. Based on the current distribution patterns for the alpine bryophytes of Scandinavia we explore the importance of different routes of recolonization. What is the contribution of species recolonizing from the south, east, southwest and the Arctic after the retreat of the ice after the last glaciation? What are the signs of long-distance dispersal? Most of the Scandinavian mountain bryophytes have a wide distribution, we find 79%, 77%, 68%, 53% in common with eastern, Arctic, central European and southwestern areas, respectively. Five species are not found in any of the regions and have probably arrived by long distance dispersal. One species is currently considered as a Scandinavian endemic.

MOTU-anchored vouchers: linking barcode clusters, molecular diagnoses, and museum specimens in integrative dark taxonomy

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High-throughput, barcode-first workflows—such as MEGABARCODING, combining HotSHOT extraction with MinION amplicon sequencing—and the dark taxonomy protocol aim to accelerate work on dark taxa: the large number of unnamed barcode clusters, or molecular operational taxonomic units (MOTUs), in reference libraries and metabarcoding datasets. The dark taxonomy workflow shifts the emphasis from lengthy descriptions of new taxa towards robust differential morphological and molecular diagnoses. New software tools increasingly make this workflow operational. IntegraTax supports integrative taxonomic projects by combining DNA data, morphology, and other evidence for species delimitation. It provides cluster-fusion visualizations of genetic distances, interactive specimen annotation, and "instability zones" that identify clusters requiring further validation. UITOTO generates explicit, position-specific nucleotide differences that can be incorporated as molecular diagnoses alongside morphological evidence in differential diagnoses. In parallel, large language models can support auditable quality control of taxonomic treatments—for example, by checking terminology, measurements, internal consistency, and cross-references among diagnoses, descriptions, figures, and tables. Such use should assist, rather than replace, expert taxonomic judgement. I introduce the MOTU-anchored voucher as an operational component of this workflow: a single, curated physical specimen selected to represent a MOTU and anchor its associated species hypothesis. A MOTU-anchored voucher is not proposed as a substitute for a name-bearing type, but as a practical reference linking automated genetic identification to a studied museum specimen. It is selected from the core of a MOTU, as visualized in IntegraTax, among the barcoded material examined in the project. The voucher is deposited in a registered, loan-accessible collection and linked to a UITOTO molecular diagnosis and a searchable lookup FASTA record. MOTU-anchored vouchers provide a transparent and durable connection between morphology, DNA-based identification, and curated collections. They also make explicit—and credit—the taxonomic work required to transform barcode clusters into reliable, reusable reference archives.

Pieces of the puzzle; Can information on microhabitat aid in resolving cryptic diversity?

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What has been perceived as a single known species often consists of several genetic groupings. Such groupings can potentially be unique species, and it is therefore important to clarify the relationship between accepted species names and genetic groups. The NTI project "Species Mapping, Delimitation and Description – Cryptic Norwegian Amphipods (MADAM)" focuses on six marine amphipod families with known mismatches between the number of described species and the genetic diversity. Using well-established methods of integrative taxonomy, we will be analyzing genetic markers, morphology, and ecology to resolve cryptic diversity. We know some amphipod species are closely linked to a specific microhabitat, which is often other invertebrates. In this talk, we will focus on the inclusion of microhabitats to aid in understanding the species. This kind of information is not always available for marine species due to the methods we collect with, but specific habitat information can potentially contribute with resolving cryptic species complexes as part of integrative taxonomy. MADAM is therefore collecting new material with methods specifically suitable for documenting these associations between amphipods and other animal groups. We will share preliminary results from fieldwork ranging from the intertidal to the abyss.

Are dark taxa left behind?
Evaluating urban biodiversity management through citizen science

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Insect diversity is declining globally, leading to increased efforts to locally support biodiversity in urban areas. Urban management measures usually target the more charismatic and well-known insect groups such as bees and butterflies, while hyperdiverse and understudied groups, so-called “dark taxa", receive far less attention. Many dark taxa belong to groups such as flies and midges**.** Despite making up a large proportion of insect diversity and contributing to a wide range of ecological functions, little is known about how well these groups are supported by urban biodiversity management. Similar biases are reflected in public awareness, where familiar and visually appealing species dominate public perception of insect diversity, while the diversity represented by less conspicuous taxa is unknown to most people. Community science therefore presents a unique opportunity not only to monitor ecological responses to management actions, but also to broaden public understanding of insect diversity. This study investigates the effectiveness of biodiversity management in Trondheim, Norway, with a particular focus on dark taxa. Specifically, the study examines whether management efforts designed to support insect diversity mainly benefit well-known groups such as pollinators, or whether they also support dark taxa. Flying insects will be sampled using the BUGHAVN trap – a Malaise trap designed for community science. Sites where management measures targeting insect diversity have been implemented will be compared with urban green spaces made primarily for people, and possibly also natural habitats in the urban periphery. It is expected that management measures have an overall positive effect on insect diversity, but with weaker responses among dark taxa than other groups. The study will contribute to a broader understanding of how urban biodiversity management affects different insect taxa and provide insights into the potential of standardized community science methods for ecological assessments.

Connecting parallel systematics: Integrative solutions for hydromedusan life-cycle mysteries in Tiarannidae and Laodiceidae

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Progress in hydrozoan research is often hindered by incomplete knowledge of jellyfish life cycles, especially in metagenetic hydromedusae. Traditionally, medusa and polyp stages have been studied separately, resulting in parallel systematics where different life stages are classified as distinct species. This practice obscures true species diversity and distribution, complicates ecological and biogeographical analyses, and undermines the reliability of monitoring efforts. To address these challenges, we applied an integrative approach combining morphological, molecular, and life history data to clarify species boundaries and phylogenetic relationships within the hydrozoan families Tiarannidae and Laodiceidae. Based on low-coverage whole genome sequencing complemented with traditional Sanger sequencing, we obtained data for mitochondrial (16S, COI) and nuclear (18S, 28S) genes from material assigned to several species of *Stegopoma* and *Ptychogena*, including type specimens accessed through museomics. Species delimitation methods allowed us to match hydromedusae to their corresponding hydroid stages. Our results reveal that both Arctic *Ptychogena lactea* and Antarctic *Ptychogena antarctica* share a *Stegopoma plicatile*-like polyp, while *Ptychogena hyperborea* is phylogenetically allied with the Hebellidae, outside the Tiarannidae-Laodiceidae clade. Furthermore, combined evidence refutes the hypothesis of *Stegopoma plicatile* as a cosmopolitan species, demonstrating its restriction to the North Atlantic. This study highlights the power of integrative studies in resolving nomenclatural mismatches and improving the accuracy of species diversity, distribution, and ecological understanding in understudied hydromedusae.

Diversity and biogeographical patterns of bristle worms (Annelida) from Isfjorden, Svalbard

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Despite being frequently sampled, Isfjorden fauna remains poorly understood. Exposed to both Atlantic warm-water West Spitsbergen Current and Arctic cold-water East Spitsbergen Current, annelids of Isfjorden exhibit diverse biogeographical patterns. This study is part of Marine Annelid Diversity in Arctic Norway (MAnDAriN) project funded by the Norwegian Biodiversity Information Centre and aims to assess species diversity, taxonomical status and distribution patterns of Annelida found in Isfjorden. We used an integrative taxonomical approach, combining morphological and molecular identification methods, to pick up on the cryptic diversity, increase the general reliability of species ID's and accurately assess distribution ranges. The material was collected in July-August 2024 using a Van Veen grab from 30 stations at 9–266 m depths. COI DNA barcoding was performed on 204 specimens corresponding to 70 genetic lineages, 21 more lineages previously found in Isfjorden were retrieved from BOLD. Only around a third of taxa confirmed with molecular methods had a clear taxonomical status. The remaining taxa were the members of species complexes, potentially new undescribed species, or could not be identified to species level with certainty. Ranges of all species were assessed based on newly obtained and public records with associated molecular data by matching to a BIN in BOLD (>98% similarity). In contrast to previous studies reporting the prevalence of the species with Arcto-Boreal distributions, our data show that half of the annelid species in Isfjorden were restricted to the Arctic region, while less than a third were Arcto-Atlantic, about 10% were Arcto-Pacific and 11% were Arcto-Atlanto-Pacific. This study highlights the importance of molecular data in diversity and biogeography assessments. Moreover, our dataset can serve as a starting reference point for evaluating long-term Arctic faunal shifts due to climate changes.

Engaging the youth in plant taxonomy and biodiversity mapping: the Young Botanist Tromsø project (Ung Botaniker Tromsø)

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Traditional taxonomic knowledge is in decline, highlighting the need to engage new generations with plant diversity. In Tromsø, a youth project seeks to address this challenge by teaching plant taxonomy and engaging the youth in plant biodiversity mappings using Artsdatabanken. The project - Ung Botaniker Tromsø – is part of the broader Ung Botaniker project in the Norwegian Botanical Society (NBF). Through public lectures, keying-evenings, field trips, nature mapping, restaurations and documentary screenings, the project aims to make knowledge of plant diversity accessible, social, and relevant to a new generation. This talk will introduce the approaches taken in the project and invites for discussion on how to create enthusiasm for taxonomy and biodiversity mapping among the youth.

Disentangling the phylogeny of the *Chlorophytum gallabatense* complex: A molecular phylogenetic approach

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Chlorophytum Ker Gawl. is an old world tropical to subtropical genus in family *Asparagaceae* with 216 currently accepted species. Sub-Saharan Africa is the center of diversity of this genus with about 200 species. This is a typical savanna genus, but the species thrive in a wide range of habitats, altitudes and soils. Previously, the African species *Chlorophytum gallabatense* Schweinf. ex Baker, *C. micranthum* Baker, *C. floribundum* Baker and *C. psammophilum* Engl. & Glig were treated as distinct by the local floras (Flora of Tropical East Africa, Flora of Somalia, Flora of Ethiopia and Eritrea, and Flora Zambesiaca). These distinct species were later reduced to varieties of *Chlorophytum gallabatense* by the Flore d' Afrique Centrale. Three varieties are included in the *C. gallabatense* complex namely; *C. gallabatense* var. *gallabatense* (Schweinf. ex Baker) Meerts, *C. gallabatense* var. *micranthum* (Baker) Meerts and *C. gallabatense* var. *floribundum* (Baker) Meerts. The taxon *C. psammophilum* is currently synonymized under *C. gallabatense* var. *gallabatense*. Notably, the current taxonomic circumscription is solely based on morphological and ecological characters. Some recent phylogenetic studies on *Chlorophytum* have shown that the taxa in this species complex are not monophyletic and thus highlighting the need for a comprehensive review of the delimitation. Therefore, we aim to use Sanger sequencing and restriction site-associated DNA sequencing (RADseq) methods to explore the genetic variation within this complex. To maximize distribution coverage of the taxa, the study is making use of both silica-dried leaf samples and herbaria materials from 13 African countries. Sanger sequencing and subsequent phylogenetic analyses of nuclear ITS region and two chloroplast regions (trnL-F and rps16) are currently ongoing. Our findings will hopefully lead to clarification of species boundaries within *Chlorophytum* and thus impact the conservation of the species diversity in the genus.

Phylogenomics and evolutionary relationships of selected Kenyan shrubby aloes: resolving species boundaries using dd-RAD-seq

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Aloe L. represents one of the most species-rich genera in the family Asphodelaceae in the order Asparagales with 594 currently accepted species that are found distributed across Africa, Madagascar, the Arabian Peninsula and adjacent islands. This diversity is pronounced in South Africa, which represents the center of *Aloe* species diversity, with additional high species richness in Eastern Africa. Despite years of taxonomic effort, *Aloe* systematics has been impeded by morphological convergence, reticulate evolution and limited resolution of traditional markers. Recent phylogenomic work has improved the global understanding of the genus but the tropical East African group remains poorly sampled and weakly resolved. Kenyan aloes, majority of which are described as shrubby, form part of the unresolved tropical East African group. Kenya hosts approximately 69 species of aloes of which 21 are red listed by IUCN. A classical problem is seen in the *A. morijensis* S.Carter & Brandam complex. This species was thought to be the diploid progenitor of the shrubby tetraploid aloes found in Kenya such as *A. nyeriensis* Christian, *A. ngobitensis* Reynolds and *A. kedogensis* Reynolds. This suggestion has been disputed by different hypotheses based on classical α-taxonomy and phylogenetic relationship. Nonetheless, previous studies investigating the rare polyploidy within the genus *Aloe* have hypothesised that the tetraploid species are closely related. Within this complex, two species (*A. nyeriensis* and *A. ngobitensis),* lack clarity in their delimitation. This study aims to generate the first high-resolution phylogenomic analysis of shrubby Kenyan aloes using double-digest RAD-seq through comprehensive species sampling to delimit the taxonomic ambiguity within *Aloe nyeriensis* and to provide insights on evolutionary relationships. By clarifying these species boundaries and providing deeper insights into the evolutionary relationships, this research will directly support biodiversity conservation and systematics efforts within Kenya while advancing our understanding of *Aloe* evolution.

Taxonomic assessment of *Chlamydomonas* sp. strains RCC7876 (WAP 05) and RCC7886 (WAP 30) from the West Antarctic Peninsula.

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Chlamydomonas is a diverse genus of unicellular green algae found in a wide range of aquatic and terrestrial environments, including Antarctica. Distinguishing closely related species can be difficult because morphological characters may overlap. Combining morphological, ultrastructural, and molecular data can therefore help clarify species boundaries. In this study, two green algal strains isolated from open waters along the West Antarctic Peninsula were compared with *Chlamydomonas* p*riscuii*, a related strain from the permanently ice-covered Lake Bonney in the McMurdo Dry Valleys, Antarctica. We examined whether the open-water strains belong to the same species as the Lake Bonney strain. Cell morphology and ultrastructure were investigated using light microscopy, scanning electron microscopy (SEM), and transmission electron microscopy (TEM). Molecular analyses were based on the internal transcribed spacer (ITS) region of ribosomal DNA. Phylogenetic analyses included the two West Antarctic Peninsula strains, the Lake Bonney strain, and several closely related green algal taxa. ITS2 secondary structures were compared to identify nucleotide substitutions and compensatory base changes (CBCs). Phylogenetic analyses showed that the two West Antarctic Peninsula strains were closely related to the Lake Bonney strain. To investigate whether these closely related strains belong to the same species, the ITS2 region was examined in more detail. Comparisons of ITS2 secondary structures focused on nucleotide substitutions and compensatory base changes (CBCs), which can provide evidence of species-level differentiation among closely related taxa. No clear CBCs were detected between the two West Antarctic Peninsula strains, although several substitutions occurred on one side of paired positions, corresponding to hemi-CBCs. In contrast, one CBC was detected between the Lake Bonney strain and both West Antarctic Peninsula strains. This difference in ITS2 secondary structure, together with the phylogenetic, morphological, and ultrastructural data, supports the interpretation that the open-water strains may represent a species distinct from the Lake Bonney strain.

Betula species delimited by kmer distribution

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Betula L. (birches) are among the most ecologically significant plant genera in arctic environments, serving as key indicators of past vegetation and climate dynamics. However, species-level identification of them from sedaDNA (even modern DNA) remains a major challenge due to their hybridization nature and rapid evolution. Our explanation for the palaeoenvironmental reconstruction can largely depend on the species-level presence of certain taxa. Take *Betula* for example, *B. nana* and *B. pubescens* represent distinct ecological niches: *B. nana* is characteristic of open tundra and alpine environments, while *B. pubescens* is associated with boreal forest and warmer, more humid conditions below/on the treeline. To address this problem, we develop an assembly-free, k-mer-based framework to increase the taxonomic resolution. We extracted k-mer signatures directly from modern reference specimens sequenced at 15x genome skimming depth, without requiring genome assembly or high-quality reference sequences. Pairwise k-mer distances are used to construct phylogenetic trees that successfully resolve species boundaries. The high resolution obtained on modern samples demonstrates accurate and reproducible species discrimination, providing a robust reference framework for ancient specimen analysis. The compatibility between kmer-based methods and the nature of museum specimens or aDNA fragments (short!) provides a better approach to study the past ecosystems and populations.

Fungi in aquatic environments in Norway

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Fungi are an integral and underappreciated part of biota in aquatic ecosystems, including marine habitats, freshwater lakes and rivers, as well as frozen habitats such as sea ice and glaciers. This talk gives an overview of the study on aquatic fungi in Norway, and to some extent also in other Nordic countries. A summary of results from morphological, culturing-based and DNA metabarcoding studies is presented to highlight known total richness and diversity, as well as the better documented groups and habitats of aquatic fungi. Major gaps of knowledge in the distribution and ecology of these organisms are identified and ideas how to address them are presented.

Copse snails: phylogeography, taxonomy, behavioural ecology, and adaptations to the Arctic

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The Copse snail, *Arianta arbustorum* (Linnaeus, 1758), is widely distributed across Europe, reaching from the Pyrenees in the south to the Arctic circle in northern Norway, and from the British Isles in the west to Russia in the east. We conducted a phylogeographic study covering nearly all its distribution and including all recognised subspecies. *Arianta canigonensis* was supported as a separate Pyrenean/Alpine species, with six subspecies. Only three subspecies were retained within *A. arbustorum*: the nominate *A. a. arbustorum* (whose type locality was restricted to Sweden) and the Alpine *A. a. stenzii* and *A. a. styriaca*. The other subspecific taxa are synonyms of nominate *arbustorum*. Our analysis showed the existence of a monophyletic Baltic/Nordic clade representing a recent expansion front of the Copse snail towards northern latitudes, as well as introductions to Canada from the Netherlands and to Iceland from Scandinavia. In addition, we assembled and annotated the full genome of a Nordic representative, as we aim to turn the Copse snail into a model species for evolutionary ecology and are currently conducting comparative behavioural and physiological studies. So far, we have evaluated whether arctic and southern snail populations show phenotypic differences in their behavioural response to light that could explain how these nocturnal animals cope with the "midnight sun season". Arctic snails were more active during the light phase and less active during the dark phase than southern snails, suggesting that the former are more flexible in their behaviour and can more readily take advantage of ideal conditions of humidity during polar days. Such behavioural flexibility may have contributed to the successful colonisation of new and challenging environments by land snails, including human-modified habitats. Further experiments on this species are currently ongoing, and we expect these to provide additional insights into its behavioural and physiological adaptations.

The Role of Phytal Copepods in Macroalgal Invertebrate Diets

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Macroalgal habitats are inhabited by diverse communities of motile invertebrates, yet the trophic relationships remain poorly understood. Within these habitats, phytal copepods, predominantly Harpacticoida, amphipods, isopods, and halacarid water mites likely play a central ecological role for energy transfer to higher trophic levels. Although direct evidence is limited, amphipods and halacarid water mites may be potential predators of phytal copepods, whereas isopods feed primarily on algae. Therefore, the diets and trophic interactions of these phytal invertebrates are investigated, focusing on the consumption of harpacticoid copepods and the importance of this prey within the diets of these predators. Samples were collected from eight sites along the Norwegian coast covering different types of macroalgae including *Fucus serratus*, *Fucus vesiculosus*, *Vertebrata lanosa*, and *Ulva* spp.. Amphipods and isopods were directly isolated in the field, while halacarid water mites were isolated from fixed samples under a stereomicroscope. To analyse their dietary composition and uncover these trophic interactions, DNA metabarcoding of the 18S rDNA and mitochondrial COI regions are employed. Metabarcoding will be combined with feeding experiments to validate the predator-prey interactions. Together, these approaches provide an insight into the dietary composition and overlooked trophic links of macroalgal invertebrates, while helping shed light on the role of phytal copepods in the coastal food web.

Introduction to the Artsdatabanken Project: Mites of Unexplored and Cryptic Habitats (MUCH)

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We present a newly launched Artsdatabanken project on mites (Acari), outlining its scope, objectives, and initial progress. Despite their remarkable diversity and ecological importance, mites remain poorly studied in Norway. The project focuses on Innlandet, Norway's largest county, which remains largely a *terra incognita* with respect to mite biodiversity. Owing to its distinct climate and post-glacial colonization history, Innlandet is expected to host numerous species that differ from those recorded in the regions where mites have been studied most intensively to date, namely Western Norway, coastal areas, and Finnmark. The region's potential for novel discoveries is illustrated by the discovery of *Zercon hamaricus* Kaczmarek, Marquardt & Seniczak, 2021, a mesostigmatid mite species new to science, collected during opportunistic sampling near the popular tourist attraction Domkirkeodden in Hamar. Remarkably, all developmental stages of this species were collected and described. The project focuses on two important mite groups: the order Mesostigmata, including the poorly studied infraorder Uropodina (commonly known as tortoise mites), and the suborder Oribatida, the most species-rich group within the order Sarcoptiformes. Particular attention is given to ptyctimous mites (box mites), a taxonomically challenging and insufficiently explored group. To date, more than 150 samples have been collected from two peatlands (Stenfjellet and Lerbekkmyra) and a range of forest habitats, including old-growth pine and spruce forests, species-rich sandy pine forests, mesic calcareous spruce forests, floodplain forests, and species-rich mesic boreal deciduous forests. In addition to forest litter and mosses, the project investigates cryptic habitats such as insect galleries, ant nests, and bracket fungi. These habitats harbour diverse and specialized mite assemblages but remain largely unexplored from an acarological perspective in Norway. The project is expected to substantially improve our understanding of Norwegian mite diversity while providing a critical reassessment and validation of existing Oribatida and Mesostigmata checklists.

Promises and challenges of macrosynteny as a phylogenetic marker considering robusticity

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In the last decade, macrosynteny gains increasing consideration as a phylogenetic marker. Macrosynteny investigates genome architectures with respect to genic composition of chromosomes detecting conserved synteny groups called ancestral linkage groups (ALGs). While such groups generally lack collinearity, they are often stable over long evolutionary times. Large changes in ALGs can happen due to fissions or fusions, recognizing three fusion forms. In the first one, Robertsonian translocation, two or more ALGs merge without exchanging genes. In the second one, an ALG is inserted into another one without mixing their genes. Finally, in the third one, fusion-with-mixing, ALGs fuse and mix their genes. While the other two events are possibly reversable, the last one is supposedly irreversible, comparable to Shannon Entropy. Due to its irreversibility, this last event is therefore considered a very strong phylogenetic character. It is therefore increasingly exploited in answering challenging phylogenetic questions such as the first phylum to branch off within animals. In this presentation, it will show the potential of macrosynteny as a phylogenetic marker, but also show the challenges and problems associated with this approach. Using the phylogeny of Lophotrochozoa, I will show the remaining problems of the approach. First, a detailed analysis of possible macrosynteny events shows that convergent evolution of fusion-with-mixing events are rampant in the genomic evolution of Lophotrochozoa and convergent evolution is much more common than unique evolutionary events. Second, I will show that the detection of ALGs in the first place is affected by the large (N) problem in statistics. This means significant results are detected but are biologically meaningless. I will present a new jackknifing procedure allowing to as the robusticity of the detection of ALGs complementing the significance test. In combination, they allow for a more conservative but robust detection of ALGs.

Key insights from 20 years of DNA barcoding and integrative taxonomy on Chironomidae (Diptera).

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Two decades of DNA barcode research has revealed the power and pitfalls of DNA barcoding in non-biting midges (Insecta, Diptera, Chironomidae). The advantages of this taxon include the ease of obtaining sequences using universal primers, conflicting lineages due to *Wolbachia* infections are unknown, COI pseudogenes remain undetected, and there is in general good agreement between COI clusters and morphospecies. However, analyses of over 1900 BINs of 12 000 DNA barcodes, nuclear markers, genomes and morphology have shown that it is not always straight forward. Here we review some of our key findings over the last 20 years and argue for an integrative approach to taxonomy and a careful interpretation of barcode-generated species lists. We show that generation of partial barcodes from historical types is possible and useful to clarify taxonomy, but that the success rate is low, and that slide mounted types in general are inaccessible. We therefore argue that all descriptions of new species should include a DNA barcode. Moreover, our examination of the DNA barcodes for European Chironomidae has identified a need for a curated barcode reference library for non-biting midges to be efficiently utilized in biomonitoring of aquatic and terrestrial habitats.

Mortierellaceae in Norway: a highly abundant but neglected fungal family

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Globally, only about 5% of fungal species' diversity is thought to have been discovered and described. A large proportion of the undescribed and unmapped fungal diversity likely belongs to non-Dikarya fungi that mostly do not produce macroscopic aboveground structures, making them easy to overlook. Mortierellaceae is one such group. Even though eDNA analyses indicate that they might be the most abundant soil fungal group in Norway, we lack basic knowledge about their diversity and distribution. In this project, we therefore aim to describe the diversity and map the distribution of Mortierellaceae in Norway. Our main focuses are to obtain cultures of Mortierellaceae specimens from Norwegian soils, perform morphological descriptions and DNA-barcoding, as well as eDNA based long-read metabarcoding analyses of soil samples collected throughout Norway. In this talk, our project objectives, progress to date, and preliminary results will be presented.

Retreating glaciers, emerging ecosystems: Invertebrate diversity and the refuge potential of glacier forefield ponds and lakes in Arctic and Alpine environments

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Glacier retreat is reshaping cryospheric landscapes in arctic and alpine regions, resulting in the formation of new ponds and lakes across glacier forefields. These newly emerging aquatic ecosystems provide novel habitat opportunities and therefore reshape biodiversity patterns, however our understanding of the invertebrate diversity, both for zooplankton and benthic organisms within these ponds and lakes remains limited. In this study we investigated the freshwater invertebrate fauna inhabiting forefield ponds and lakes across eight glaciers located in Svalbard, Northern Norway and the Austrian Alps. Additionally, we assessed the invertebrate diversity in cryoconite holes and ponds situated at lower elevation within the same valley as the glacier to better understand colonization patterns. Organisms were identified to the lowest achievable taxonomic level using morphological and molecular approaches. This study found that ponds and lakes formed as a result of deglaciation can harbour a complex freshwater invertebrate composition, having a higher diversity compared to cryoconite holes but being less diverse than ponds at lower elevations. A total of eight higher taxonomic groups has been identified and Tardigrada, followed by Rotifera, Nematoda and Chironomidae were the most dominant. In total two species exhibited an overlap between lower elevated ponds and ponds in the glacier forefield. In contrast, seven species, previously identified as true glacier species, were found to be present in forefield ponds and lakes, suggesting that these habitats may serve as a potential refugia for glacier-adapted taxa in the future. As glaciers are expected to further decline and landscapes are transforming from ice dominated systems to paraglacial systems, these ponds and lakes are becoming increasingly important for freshwater biodiversity. However, the future dynamics of these ecosystems remain uncertain, particularly in the context of continued glacier retreat, global warming and potential competition between typical glacier species and taxa from lower elevations. Future studies and monitoring programs are needed to fully understand the ecological dynamics in these recently formed ecosystems.

Rapid loss of arctic plant and animal diversity in the Baltic at the onset of Holocene revealed by sedimentary ancient DNA

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The Pleistocene-Holocene transition allows reconstruction and assessment of past ecological responses to rapid climatic warming. We reconstruct dynamics of 220 plants and 19 animals detected in the southeastern Baltic between the Late Glacial to early Holocene (14.4–9.6 ka) using metabarcoding of sedimentary ancient DNA (sedaDNA) from three lake sediment records (Prossa, Nakri, and Lielais Svētiņu). The Late Glacial communities were dominated by cold-adapted, open-habitat plant and animal communities, but a major and abrupt shift occurred near the onset of the Holocene that caused a disproportionate disappearance of cold-adapted taxa at all sites, most of which remain absent from the region today. At the same time, boreal diversity increased, but with delayed tree establishment and slight variation in timing and persistence among sites. Community weighted plant indicator traits imply broad environmental change near the Late Glacial-Holocene transition, with increased heat requirement, declined cold requirement, increased association with nitrogen rich and wetter soils, and decreased light demand. European beaver (*Castor fiber*) detections during Allerød and Younger Dryas at the southern lake Svētiņu and Allerød at central lake Nakri aligned with presence of trees (mainly *Pinus* and *Populus tremula*). The sedaDNA records demonstrate the large-scale consequences of climatic warming during the Holocene onset in the eastern Baltic. The loss of cold-adapted flora co-occurred with expansion of shrub diversity, argued to have caused competitive exclusion, in combination with other effects of climatic warming.

Aquatic hyphomycete communities from headwaters to the sea in the Målselv catchment

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Submerged leaf litter is a major constituent of carbon available in streams. The decomposition of submerged leaf litter is largely affected by abiotic factors, and the community composition of microorganisms on these leaves. However, knowledge about which species are present in the different parts of the subarctic river continuum, from headwaters to the sea is lacking. This study aims to investigate the species richness and community structure of aquatic hyphomycetes on two types of submerged leaves, alder and birch, in different parts of the Målselv river system in Northern Norway. Through experimental transfer of leaves placed in the river in litter bags, I also investigate how the communities change when leaves flow downstream towards the sea. I found that the headwater station had a higher species richness than the stations in the river's lower reach, estuary and fjord, confirming the hypothesis that turbulent headwaters have higher species richness of aquatic hyphomycetes. I also found that the species richness decreased when leaves were transferred from the headwater to the lower reach. Similarity of the communities was investigated, and the estuarine community was found to consist of species from other parts of the river, while some species were unique to the headwaters or the lower reach communities. The more nutrient-rich leaves of gray alder contained a higher species richness than the leaves of birch. This study shows how aquatic hyphomycete communities change during leaf transport events from headwater towards the fjord, and the discovery of fungi new to Norway highlights the need for more focused studies on aquatic fungi in northern latitudes.

Exploring the concept of rarity in Dark Taxa

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The overarching objective of this study is to investigate how rarity is structured within hyperdiverse insect communities and how patterns of rarity emerge with increasing sampling completeness. The project focuses on scuttle flies (Diptera: Phoridae) which are extremely abundant yet remain poorly described taxonomically and ecologically. As such, they exemplify the long tail of rare species that dominate species abundance distributions in insect communities. The samples are collected from a large-scale insect inventory project in Sweden compiled from 2018 and 2019. We selected three ecologically distinct sites representing a latitudinal gradient, with representatives in the south (Öland), middle (Runmarö), and north (Abisko) of Sweden. Most species in ecological communities are rare, though the definition of rarity is still being discussed and is not agreed upon. Rather than treating rarity as a discrete category, this project approaches it as a continuum along species abundance distributions. Several statistical distributions like log-series, log-normal and negative binomial have been proposed to describe the general form species abundance distributions take across different communities of taxa. This project aims to exhaust species accumulation curves and analyze the distribution of species and investigate if the structure of rarity reflects a biological universality or artefacts of uneven sampling and taxonomic completeness. In this project I will aim to answer the following research questions: What level and structure of sampling effort is required for species accumulation curves to approach an asymptote in hyperdiverse dark taxa? How does the proportion of rare species, and patterns of rarity change through successive sampling rounds, space and time? Are species abundance distributions consistent across sites, or do communities differ in the prevalence and structure of rare species?

Generation time under clonal reproduction: module founding in the peat moss *Sphagnum*

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Generation time sets the timescale for population dynamics, scales rates in molecular evolution, and underlies coalescent and effective-population-size theory. In sexually reproducing organisms a single event, meiosis followed by fertilization, delimits one generation from the next and discharges four functions at once: demographic replacement, genealogical linkage, genetic sampling, and the transmission of accumulated mutation. In clonal, modular organisms these functions come apart. Growth, physiological independence, and reproduction are spread across the life cycle, and it is no longer obvious which event should count as a generation, or whether the concept applies at all. This study set out to establish that, in modular clonal plants, the founding of a new module is the event that defines a generation in population-genetic terms. When a module is founded through a single apical cell bottleneck, it acts as the point of genealogical linkage and genetic sampling. On this view generation time is the mean interval between successive foundings along a lineage. This quantity distinct from the lifespan of a module, the age at physical separation, or the turnover time of the whole clone. We estimate this in the hummock-forming peat moss *Sphagnum austinii* and *S. papillosum* because module founding is preserved in the accumulating peat cores. From surface peat cores we build stage-structured population matrices and calculate an asexual generation time T from the transition rates among stages. In addition, to test whether this asexual generation time behaves as a coalescent unit, we simulate module founding and turnover in an individual-based model. Mean pairwise coalescence time scales as the product of effective population size and T ($E[T_2] = N_e \cdot T$) across wide ranges of population size and turnover rate.

Rapid, unbiased and precise phenotyping using the ALPHA3D pipeline

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Phenotypic variation is produced through the interactions between genotype and environment. Despite its importance, our ability to characterize phenomes still remains behind our ability to characterize genomes. There is therefore an urgency to develop techniques that enable the rapid and efficient acquisition of high-dimensional phenotypic data. Traditionally landmarks have been collected manually and in two dimensions, but these two phenotyping bottlenecks have recently been addressed by the availability of 3D technologies and the advent of automated landmark-placement methods. In this study, we introduce the phenomic pipeline *Automated Landmarking and Photogrammetry Acquisition in 3D* (ALPHA3D) that combines photogrammetry (a fast, portable and cheap way to create 3D models) with automated landmark placement. This highly automated pipeline is designed to rapidly acquire traits. Its speed enables a faster measurement of morphological structures such as the mammalian cranium, including those of polar bears (*Ursus maritimus*) used in this study. With ALPHA3D, it takes approximately 20 minutes to progress from photographing a skull to obtain a fully automatically annotated 3D model. We assessed the measurement error (imprecision and bias) of ALPHA3D in extracting size (measured as centroid size), and linear measurements. The results showed that photographing and making of the 3D model did not contribute significantly to measurement error. Automated landmarking accounted for most of the error introduced by the pipeline but was for the most part negligible relative to the biological (true) variance among the specimens. We quantified imprecision as the pairwise variance between two measurements (σ^2), which approximates the relative measurement error. The mean σ^2 across all linear distances was found low, at 0.13%. We detect negligible bias for most traits. Lastly we found a strong correlation between P-matrices obtained manually (P_{ML}) and automatically (P_{AL}), confirming the close agreement between results from ALPHA3D and from manual landmarking. Overall, our results show how ALPHA3D can be used as a rapid, unbiased and precise phenotyping tool to extract morphological traits from mammalian skulls.

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