

Wednesday 9 November 2022

09:00 Registration

10:00 Welcome address **Hugo de Boer**

Chair Quentin Mauvisseau, Natural History Museum, Oslo

10:10 – 10:40 Keynote **Gentile Francesco Ficetola**, Dept of Environmental Science and Policy, University of Milan
What drives the changes of biotic communities after the global retreat of glaciers?

10:40 – 11:40 Talks (4x 15 min)

Micaela Hellström, MIX Research Sweden AB

Ecology, chemistry and eDNA analyses– effective monitoring tools for status in terrestrial and aquatic ecosystems. Case studies from Sweden.

Sonja Leidenberger, University of Skövde, School of Bioscience

Tracking of threatened aquatic invertebrates using eDNA – a Swedish showcase

Elianne Egge, Norwegian institute of water research - NIVA

Dispersion patterns of eDNA from four salmonid species, including the invasive pink salmon, in a river in Northern Norway.

Aloïs Revéret, The Arctic University Museum of Norway, UiT

Environmental DNA of aquatic macrophytes: potential for reconstructing past and present vegetation and environment

11:40 – 12:00 Coffee break

Chair Rakel Blaalid, University Museum of Bergen, Bergen

12:00 – 12:45 Talks (3x 15 min)

Veera Norros, Finnish Environment Institute SYKE

Roadmap for implementing environmental DNA (eDNA) and other molecular monitoring methods in Finland – Vision and action plan for 2022–2025

Marina Panova, University of Gothenburg, Department of Marine Sciences

eDNA in environmental monitoring and biodiversity assessment - remaining issues

Frode Fossøy, Norwegian institute for nature research - NINA

Examples of eDNA-based monitoring in Norwegian management

13:00 – 14:00 Lunch

Chair Torbjørn Ekrem, NTNU University Museum, Trondheim

14:00 – 14:30 Keynote **Tomas Roslin**, Swedish University of Agricultural Sciences (SLU), Dept of Ecology
DNA as a tool for dealing with arthropod diversity

14:30 – 15:35 Talks (1x 15 min) & Speed talks (10x 5 min)

Tommi Nyman, NIBIO, Dept of Ecosystems in the Barents Region, Svanhovd Research Station
Fungus–arthropod networks in Boreal forests: insights from metabarcoding

Marie Føreid Merkel, The Arctic University Museum of Norway, UiT
Any gaps to fill? The presence of the flora and fauna of Northern Norway in the database.

Peter Hollingsworth, Royal Botanic Garden Edinburgh
BIOSCAN Europe

Ann M. Evankow, Natural History Museum, UiO
Challenges & Unexpected Opportunities from constructing a Lichen DNA Barcode Database for Norway

Maria Kahlert, Swedish University of Agricultural Sciences - SLU, Dept of Aquatic Sciences and Assessment
Barcoding of freshwater taxa for improved assessment of biodiversity (FRESHBAR)

Monika Baranowska, Dept of Invertebrate Zoology and Hydrobiology, University of Lodz
Assessing biodiversity in 20 Norwegian ponds in the context of urbanization

Katarzyna Teresa Janik-Superson, Dept of Invertebrate Zoology and Hydrobiology, University of Lodz
Optimization of the ponds eDNA procedures for research prokaryote and eukaryote biodiversity

Quentin Mauvisseau, Natural History Museum, UiO
Environmental DNA-based tracking of species community in Norwegian freshwater systems

Lucas Elliott, The Arctic University Museum of Norway, UiT
Pipeline for metagenomic database construction from plant genome skims

Marie Louise Davey, Norwegian institute for nature research - NINA
Does it look like a duck? Quack like a duck? Capturing uncertainty in metabarcoding taxonomic assignments.

Dilli Prasad Rijal, The Arctic University Museum of Norway, UiT
Ancient DNA of bryophytes: current status and future potential

15:35 – 16:00 Coffee break

Chair Galina Gusarova, The Arctic University Museum of Norway, Tromsø

16:00 – 16:40 Talks & speed talks (2x 15 min & 2x 5 min)

Mika Helene Kirkhus, NTNU University Museum
Hidden diversity and host specificity of *Pertusaria*-residing *Tremella* fungi in Norway

Eivind Kverme Ronold, Dept of Biosciences, UiO
Unsuccessful mycorrhization of seedlings slow the advance of the tree- and forest line in alpine ecosystems

Monica Guilera Recoder, Dept of Biosciences, UiO
Who wins the battle? Interspecific combative interactions between wood-decay fungi

Rakel Blaalid, University Museum of Bergen, UiB
Fungi – facilitator or limitator for rhododendron invasion in western Norway

19:00 Dinner, Scandic Nidelven Hotel

Thursday 10 November 2022

Chair Glenn Dunshea, NTNU University Museum, Trondheim

09:00 – 09:30 Keynote **Sophie Arnaud-Haond**, Ifremer

eDNAbyss: Setting up a standardized chain of protocols to achieve a FAIR pipeline for the DNA-based exploration of the largest biome on Earth

09:30 – 10:00 Talks (2x 15 min)

Sune Agersnap

A national scale “BioBlitz” using citizen science and eDNA metabarcoding for monitoring coastal marine fish

Mikołaj Mazurkiewicz, Institute of Oceanology, Polish Academy of Sciences

Biodiversity assessment of benthic fauna in an Arctic glacier-influenced fjord based on morphological and eDNA metabarcoding survey

10:00 – 10:15 Coffee break

Chair Stefaniya Kamenova, University of Oslo & Norwegian University of Life Sciences, Ås

10:15 – 11:30 Talks (5x 15 min)

Jon T. Hestetun, NORCE Climate and Environment

Assessing the performance of benthic metabarcoding for environmental monitoring and baseline biodiversity of the Norwegian Shelf

Elizaveta A. Ershova, Institute of Marine Research (IMR)

Developing methods for routine monitoring of marine zooplankton communities using metabarcoding

Nathan Mertz, NTNU Dept of Biology & Norwegian institute for nature research - NINA

Refining enumeration of planktonic sea lice larvae detected by ddPCR; calibration by serial spiking

Youri Lammers, The Arctic University Museum of Norway, UiT

Multiplexing markers: Increasing the amount of data that can be obtained from a single amplification reaction

Inger Greve Alsos, The Arctic University Museum of Norway, UiT

Reconstructing past communities and environments using sedaDNA: where are we now?

11:30 – 12:30 Lunch

Chair Hugo de Boer, Natural History Museum, Oslo

12:30 – 13:00 Keynote **Kristine Bohmann**, Globe Institute, University of Copenhagen

Monitoring terrestrial biodiversity using airborne eDNA



13:00 – 14:00 Talks (4x 15 min)

Marcel Polling, Wageningen Environmental Research, Wageningen University and Research
Quantification using DNA metabarcoding: the case of airborne pollen

Vid Švara, UNESCO Chair (MCA), Carinthia University of Applied Sciences
The applicability of eDNA-based assessment of biodiversity in Austrian protected areas

Terje Klemetsen, UiT - The Arctic University of Norway & ELIXIR UiT Node
Integrating Molecular Biodiversity – ELIXIR3 Norway

Stefaniya Kamenova, University of Oslo - NMBU
Long-term management history affects seasonal diet composition of semi-domesticated reindeer

14:00 – 14:30 Coffee break

Chair Inger Greve Alsos, The Arctic University Museum of Norway, Tromsø

14:30 – 15:35 Talks (1x15 min) & speed talks (10x 5 min)

Christopher Hempel, University of Guelph, Dept of Integrative Biology
Metagenomics vs. total RNA sequencing: most accurate data-processing tools, microbial identification accuracy, and implications for freshwater assessments

Caroline Karlsson, NMBU, Faculty of Environmental Sciences and Natural Resource Management
The effect of *Silene acaulis* on soil bacterial communities across elevational and latitudinal gradients in Scandinavia

Embla Elen Stokke, University of Oslo, Department of Biosciences
Applying long-read sequencing to environmental DNA to map Eukaryote diversity in soil

Chenyu Jin, SMNH & Centre for Palaeogenetics & Department of Zoology, Stockholm University
Genome-wide analysis of eDNA

Helle Tessand Baalsrud, NMBU, Centre of Integrative Genetics (CIGENE)
Earth BioGenome Project (EBP) - Sequencing Life for the Future of Life

Anna J. Székely, SLU, Dept of Aquatic Sciences and Assessment
eDNA capacities for aquatic biodiversity assessment at the Swedish University of Agricultural Sciences (SLU)

Kristiina Marita Vuorio, Finnish Environment Institute SYKE
Utilization of eDNA methods in water status and biodiversity assessment (eDNA-monitor)

Tulug Gulce Ataman, The Arctic University Museum of Norway, UiT
Spatial distribution of sedDNA in small catchments and lakes: Is single core enough?

Stefania Piarulli, Dept of Climate and Environment, SINTEF Ocean AS
Environmental DNA as part of an observational toolkit for marine biodiversity monitoring in a global change context: The ABOVE-DNA project

Alexander Eiler, Dept of Biosciences and Center of Biogeochemistry in the Anthropocene, UiO
UiO Research and Training program: Coastal Biodiversity Dynamics under anthropogenic pressures

Ngoc-Loi Nguyen, Institute of Oceanology Polish Academy of Science
Nordic Seas metabarcoding and eDNA taphonomy

15:35 –16:00'ish Closing