



(Meta)barcoding for research and environmental monitoring

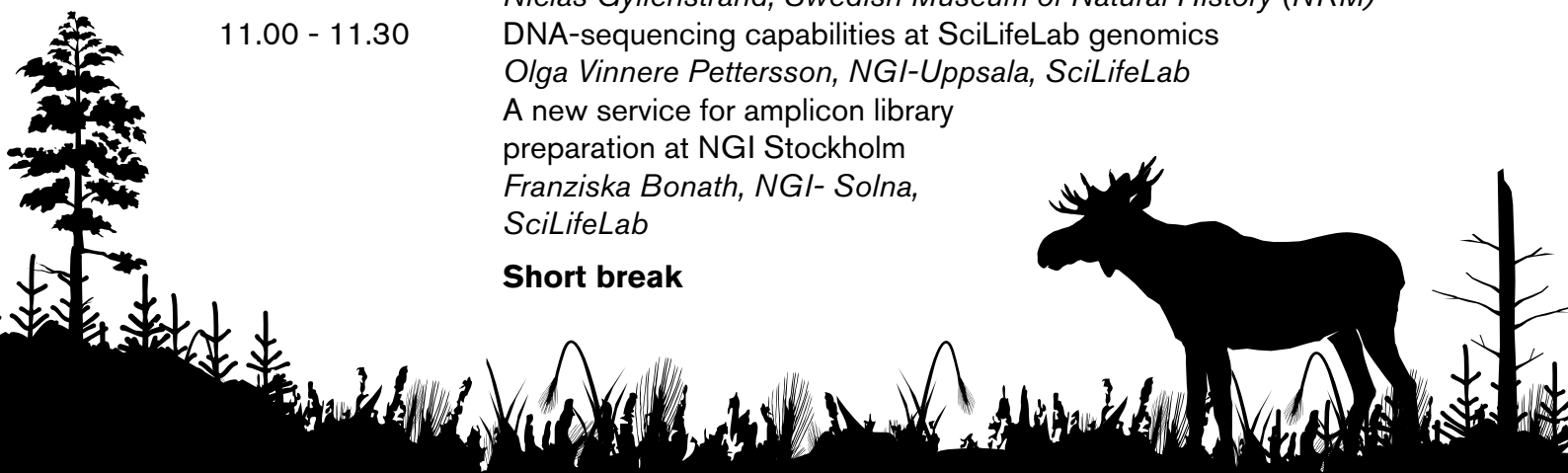
7 November 2019, 8.00-17.00

Venue: Lennart Kennes sal, BioC, Ultuna

Morning session

(Meta)-barcoding activities with focus on Environmental Assessment in Sweden

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| 8.00 – 8.30 | Coffee, registration |
| 8.30 – 8.40 | Welcome
<i>Åke Olson & Maria Kahlert, SLU</i> |
| 8.40 - 10.00 | Projects Environmental Assessment with focus on the “Miljöforskningsanslaget” (Environmental Research Grants) projects, call DNA-methods-in-environmental-monitoring (2019-2021), funded by The Swedish Environmental Protection Agency (SEPA) and The Swedish Agency for Marine and Water Management (SwAM) |
| 8.40 – 9.05 | Keynote: Identification of macroinvertebrates
<i>Professor Tomas Roslin, SLU</i> |
| 9.05 – 9.30 | Keynote: Monitoring of biodiversity in Swedish forest soils
<i>Professor Björn Lindahl, SLU</i> |
| 9.30 - 9.45 | ePIKE - Testing the applicability of eDNA for monitoring pike (<i>Esox lucius</i> L) abundance
<i>Erik Karlsson and Patrik Bohman, SLU</i> |
| 9.45 - 10.00 | DNA-barcoding of marine phytoplankton
<i>Agneta Andersson, Umeå University</i> |
| 10.00 - 10.15 | Coffee |
| 10.15 - 11.30 | Infrastructure |
| 10.15 - 10.30 | Integrating metabarcoding data into the Swedish Biodiversity Data Infrastructure (SBDI)
<i>Anders Andersson, KTH / SciLifeLab</i> |
| 10.30 - 10.45 | The SLU Metabarcoding Laboratory - UMBLA
<i>Åke Olson, SLU</i> |
| 10.45 - 11.00 | eDNA service at the Swedish Museum of Natural History
<i>Niclas Gyllenstrand, Swedish Museum of Natural History (NRM)</i> |
| 11.00 - 11.30 | DNA-sequencing capabilities at SciLifeLab genomics
<i>Olga Vinnere Pettersson, NGI-Uppsala, SciLifeLab</i>
A new service for amplicon library preparation at NGI Stockholm
<i>Franziska Bonath, NGI- Solna, SciLifeLab</i> |
| | Short break |



11.35 - 12.45

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Projects Environmental Assessment

Barcoding of freshwater taxa for improved assessment of biodiversity (FRESHBAR)

Maria Kahlert, SLU

11.45 - 12.00

Establishing DNA-barcode libraries of Swedish clitellate worms (Annelida)

Christer Erséus, Gothenburg University

12.00 - 12.15

NEMOte BARCODing: Advancing monitoring of Baltic benthic ecosystems

Francisco Nascimento, Stockholm University

12.15 - 12.30

Life-DNAquatic

Micaela Hellström, AquaBiota Water Research (ABWR AB)

12.30 - 12.45

eDNA – promises and challenges

Helena Wiklund, Gothenburg University

12.45 - 13.45

Lunch (provided for all participants)

Afternoon session

Molecular identification of species and communities in research projects

13.45 – 14.15

Keynote: Microbial communities as indicators of environmental change

Professor Sara Hallin, SLU

14.15 – 14.30

Untargeted barcoding: Exploring shotgun metagenomics for microbial systems assessment

Stefan Bertilsson, SLU

14.30 – 14.45

Target capture probe design for green plants; a novel tool for environmental DNA sequencing

Kevin Nota, Uppsala University

14.45 - 15.00

Vegetation shapes fungal spore arrival within a forest–agricultural mosaic landscape

Miguel-Angel Redondo, SLU

15.00 - 15.30

Coffee

15.30 – 15.45

Tracking marine and freshwater threatened invertebrates

Sonja Leidenberger, University of Skövde

15.45 – 16.00

DOs and DON'Ts of switching from bulk samples to eDNA for environmental monitoring: a case-study with terrestrial insects

Daniel Marquina, Swedish Museum of Natural History (NRM)

16.00 – 16.15

Exploring microbial eukaryotic diversity with long-read metabarcoding

Mahwash Jamy, Uppsala University

16.15 – 16.30

Optimized metabarcoding protocol using Pacific Biosciences sequencing of the ITS2 region allows semiquantitative analysis of fungal communities

Carles Castaño Soler, SLU

16.30 – 16.45

Detecting bioimmigrants – metabarcoding of plant pathogenic oomycetes in soil from the rhizosphere of imported woody plants

Simeon Rossmann

16.45 – 17.00

Concluding remarks

