**Workshop on “Metabarcoding analyses” in Oslo, 17-20 February 2020.**

Funded by the projects **Nansen Legacy and the University of Oslo.**

**Place:** Department of Biosciences (IBV), University of Oslo, Biologibygningen, Blindern.

**Time:** 17-20 February 2020. The workshop will start on Monday at 10:00 and end on Thursday evening.

**Organisers:** Anna Vader (UNIS), Bente Edvardsen, Karoline Saubrekka, Luka Supraha (UiO).

**Teachers:** Anders K. Krabberød, Laurent Fontaine, Alexander Eiler, Sandra Gran-Stadniczenko (UiO).

**Number of participants**: up to 15.

**Aim:**

The aim of the workshop is to train participants of AeN (PhDs, post docs, researchers and faculties) in analyses of high throughput metabarcoding data of marine protists and prokaryotes. The workshop will introduce the bioinformatic tools necessary for quality checking and filtering of high throughput sequencing data using Dada2 in the R environment, as well as taxonomic assignment of ASVs using databases for protist and prokaryote organisms. Additional relevant statistical methods for diversity and ecological studies (alpha and beta diversity analyses, multivariate analyses, and construction of association networks) will be performed using relevant packages in R (vegan, phyloseq, SpiecEasi). Another aim is to discuss and harmonise the choice of analyses and coordinate publications.

**Location and teachers:**

The place for the workshop will be at campus Blindern, Department of Biosciences of the University of Oslo. We will take advantage of the expertise in bioinformatics analyses of metabarcoding data available at IBV

**Prior knowledge**: Some knowledge and commands in R is required.

**Program:**

We plan to work with metabarcoding and environmental data from the AeN cruises in 2018 and 2019 which will be prepared before the workshop. Environmental data that will be used are CTD data, nutrients, chlorophyll *a* and if available, otherchemical parameters.

The first day will focus on quality filtering and denoising of high throughput sequencing data into amplicon sequence variants (ASVs) using the DADA2 pipeline, as well as taxonomic assignment of the ASVs and preparing the species matrix used for ecological and diversity analyses. During the following days we will analyse the alpha and beta diversity of microbes in the samples, construct association networks and perform multivariate statistical analyses. This will provide important insight into the distribution and ecology of protists and prokaryotes in the Arctic.

In addition to the training the workshop will contribute with a network among the AeN participants working with metabarcoding analyses and bioinformatics.

The planned accommodation is a hotel or pension near campus. Lunch will be prepared at section AQUA, IBV and dinner will be at a restaurant at campus or in town.

**Application** should be sent latest **10 January** by registration at <https://nettskjema.no/a/metabarcodingworkshop> . Travel and board expenses are covered for participants in the Nansen Legacy project. In the registration you will be asked about your name, e-mail address, affiliation, position and supervisor, background in R, motivation for participation and a brief description of your research project. If you have questions please contact Bente Edvardsen or Anna Vader.