**Planning the workshop in metabarcoding analyses**

**Meeting 17.12 kl 11-12**

1. the content, which methods/analyses to demonstrate and practice

2. what material should we send out beforehand and use

3. which data do we have that we can use. how large dataset is feasible?

4. what do they need to download on their computers

5. how many students can we handle assuming we will be 2-3 teachers at all practical’s.

There are some material on the internet:

Daniel Vaulot has a tutorial for R dada2 metabarcoding analyses

<https://vaulot.github.io/tutorials/R_dada2_tutorial.html>

<https://github.com/vaulot/metabarcodes_tutorials/tree/master/R_dada2>

and he has a tutorial for phyloseq:

<https://vaulot.github.io/tutorials/Phyloseq_tutorial.html>

and Daniel maintains the database PR2 for taxonomic assignations of eukaryotes in the 18S rRNA gene (4.12 as the last version)

<https://github.com/pr2database/pr2database>

2. Data Camp has tutorials for R.

**Minutes from meeting:**

Present: Anders, Karoline, Bente

1. We looked at the tutorials by Vaulot and Anders thought they looked very nice and clean and easy to read and covers all what we will need for the workshop. We suggest that this can be the material to use, if Alex also agrees.

Additional method could be the EPA to place OTUs/AVEs to a phylogenetic tree by phylogenetic placement. Anders has the scripts and a eukaryotic tree we can use.

2. If we agree on using Vaulot’s material we can send the links to those resources and ask everyone to down load R, R studio and the libraries listed before they come.

If they need some training in R they can e.g. use the Data Camp tutorial for R.

3. Which data can we use. We can use Karolines data from her Masters thesis. She will run these Illumina V4 18S metabarcodes through the dada2 pipeline beforehand. It includes ca 33 samples and if it takes too long time with the complete dataset she will take out a subset.

4. If we get the AeN metabarcoding data from Canada, well in time before the workshop, we can also use a subsample from there. These are 115 eukaryotic and 115 prokaryotic metabarcoding samples, and have to be subsampled if we will use them. We should have had time to run the pipeline of a subsample, if we use them.

5. How many students. With two teachers present at all times Anders suggest up to 25. This means that we can take several local students in addition to those at AeN. We will use room 4436 (Bente book).

The students will use their own computers and will have to down load all software beforehand. Dead line for submitting application is 10 January.