DNA metabarcoding diet analysis in reindeer is quantitative and integrates feeding over several weeks

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Abstract

Filtering of the SPER01 DNA metabarcoding raw data.

1. Github project

Every script and processed data are available from the RENIN-Project/Feeding-Experiment github project.

- https://github.com/RENIN-Project/Feeding-Experiment

2. Preprocessing of the raw data

The `OBITools` commands used to preprocess the data from the raw FASTQ files are described in the following bash script.

- Bash script for the preprocessing of the raw data

3. Filtering of the data

- For the *Eukaryota* `Euka03` marker
- For the *Chlorophyta* `Chlo01` marker
- For the *Chlorophyceae* `Chlo02` marker

4. Ecological analysis

Every code producing the presented results including the production of the figures is available here

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5. Processed data sets and results

Each processed dataset is composed of three coma separated values files (`.csv` files).

- For the *Eukaryota* `Euka03` marker
    - The MOTUs description file : Euka03.cleaned.motus.csv
    - The samples description file : Euka03.cleaned.samples.csv
    - The reads contengency table : Euka03.cleaned.reads.csv
- For the *Chlorophyta* `Chlo01` marker
    - The MOTUs description file : Chlo01.cleaned.motus.csv
    - The samples description file : Chlo01.cleaned.samples.csv
    - The reads contengency table : Chlo01.cleaned.reads.csv
- For the *Chlorophyceae* `Chlo02` marker
    - The MOTUs description file : Chlo02.cleaned.motus.csv
    - The samples description file : Chlo02.cleaned.samples.csv
    - The reads contengency table : Chlo02.cleaned.reads.csv

References