

## Metabarcoding Data Delivery Specifications

### Output data info

- FASTQ.GZ files containing raw sequences.

Reads will be provided with adapter sequences masked. No quality clipping is provided with raw reads delivery.

### Metabarcoding bioinformatics analysis

- Absolute and relative taxonomical counts *i.e.* read counts for each single taxonomy label by each classification level (from phylum [L2] to species [L7]) in TXT format. For the relative taxonomical abundances, a bar-chart in HTML format is provided as well.
- Raw fragments count at OTU level for each sample and its relative taxonomic attribution in TXT format.
- FASTA-formatted file containing a representative sequence for each OTU present in the analysis.
- $\alpha$ - and  $\beta$ - diversity estimations provided as raw permutation tables, rarefaction curves, box plots distance matrix and principal coordinates analysis.
- A REPORT file describing the library preparation and analysis flow.