

**Service Name:**

Meta-Barcoding of microbial communities

**Required activities - their description, range (eg number of samples, forest area), time perspective (requirements) etc.:**

- NGS Library preparation, NGS Library quantification and NGS Library sequencing of delivered pooled amplicons (from termites and termite related samples)
- The samples will be delivered as purified equimolarly pooled PCR products (amplicons) with specific NGS tagged-primers and known concentration (batch), so prepared for NGS library preparation (cca.475 amplicons in batch)
- Expected Number of library preparations: 15 libraries
- Expected Number of runs: 15 runs (i.e. Library sequencing)
- Platform required: Illumina MiSeq, paired-end, 250 bases on both sides, v2 chemistry, 10-15 million reads
- Quality check: NGS library quantification
- Data quantity for each sample of at least 100,000 tags with Q30> 75%.
- Sequential files, including raw reads, will be delivered in FASTA or FASTQ format either electronically via server or shared disk or on hard-drive/flash-drive
- Possibility to deliver low amount of single amplicons (purified PCR products with tagged primers) separately for sequencing, in rare cases (up to 100 for whole project)

**Methodological requirements**

- Sufficiently high-quality samples for aliquot mixture preparation are amplicons with the following minimum parameters: purified PCR amplicon concentration measured using fluorometer  $\geq 10$  ng/ $\mu$ l