

Anacapa in R Testing

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Documentation Link

Setup

- `BiocManager::install("multtest")`
- `BiocManager::install("phyloseq")`
- Install devtools
- `devtools::install_github("gauravsk/ranacapa")`
- There is also a terminal option if desired

```
library(devtools)
```

```
## Loading required package: usethis
```

```
## Warning: package 'usethis' was built under R version 4.3.1
```

```
library(ranacapa)
```

What is Anacapa?

- Input file: Anacapa output file, aka biom file
 - One column of full taxonomic path, one column for each sample, sometimes one column for unique sequence identifiers (this identifier is useful only if you need to go back to a FASTA file and find the sequence)
- Other input file: Mapping file with the sample metadata. The first column values must match the sample names (Anacapa output column names)

The main purpose of `ranacapa` is to convert between Anacapa output and `phyloseq` objects

Anacapa Functions

- `group_anacapa_by_taxonomy()` If two rows have the same taxonomic path, group those rows and add up the sample column values. This cleans duplicates for `phyloseq`.

- `convert_anacapa_to_phyloseq()` does what it says on the tin, requiring two input files (Anacapa output and mapping file) and spitting out one **phyloseq** object
 - Note: Phyloseq is a package and an object class