Easy16S

Easy16S, a user-friendly web application for statistical exploration of amplicon sequencing metagenomics data

Summary

Easy16S is a user-friendly web application enabling to easily explore, visualize and analyze amplicon sequencing metagenomics data. Easy16S takes as input data in BIOM, tabulated or RData format. The data must have been processed beforehand by amplicon sequencing metagenomics pipelines such as FROGS or DADA2.

Within the application, it is possible to select samples of interest, and to numerically transform data (e.g. data normalization). Among others, barplots can be generated; multivariate analysis can be performed, with a dynamical mapping of co-variates of interest. R scripts and plots can be exported for further use. The Easy16S application is developed in R Shiny and it is based mainly on the phyloseq package.

It is hosted by the INRAE MIGALE bioinformatics facility and freely accessible:
shiny.migale.inrae.fr/app/easy16S

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Easy16S server

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