

Package: zAMPEXplorer (via r-universe)

November 23, 2024

Type Package

Title zAMPEXplorer: A Versatile Shiny App for Microbiota Profiling in Clinical Microbiology

Version 0.1.0

Description A Shiny web application offering a user-friendly, accessible, and reproducible platform for downstream analysis of 16S rRNA-based metagenomics data. Key features include quality control visualizations (e.g., rarefaction curves), community composition plots, and statistical analyses for alpha- and beta-diversity. For deeper insights, the app incorporates community typing using Dirichlet multinomial modeling (DMM) and dynamically integrates metadata for sample stratification. This enables users to test microbial associations with clinical or experimental variables using redundancy analysis (RDA).

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

License GPL-3

Encoding UTF-8

LazyData true

biocViews Microbiology, Metabarcoding, Visualization, StatisticalMethod

Depends R (>= 3.5.0)

Imports shiny, shinydashboard, shinyWidgets, shinyFiles, fs, DT, ape, writexl, UpSetR, phyloseq, microViz, ggvenn, microbiome, ggplot2, cowplot, circlize, reshape2, dplyr, tidyr, vegan, gridExtra, Maaslin2, eulerr, MicEco, plotly, reticulate, webshot2, ggplotify, ComplexUpset, htmlwidgets, colourpicker, RColorBrewer, VennDiagram, ComplexHeatmap, MicrobiotaProcess, DirichletMultinomial, InteractiveComplexHeatmap, TreeSummarizedExperiment

Config/pak/sysreqs chromium cmake libfontconfig1-dev libfreetype6-dev
 libglpk-dev make libicu-dev libpng-dev libxml2-dev libssl-dev
 perl python3 zlib1g-dev

Repository <https://metagenlab.r-universe.dev>

RemoteUrl <https://github.com/metagenlab/zAMPExplorer>

RemoteRef HEAD

RemoteSha 8097e6084ca4c7bf66da0b2e9857dd9c4c8fe0ba

Contents

zAMPExplorer_app	2
Index	3

zAMPExplorer_app	<i>Launch the Shiny App</i>
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Description

This function launches the Shiny app.

Usage

zAMPExplorer_app()

Index

zAMPExplorer_app, [2](#)