

Package: miaDash (via r-universe)

October 8, 2026

Version 1.5.1

Title Dashboard for the interactive analysis and exploration of microbiome data

Description miaDash provides a Graphical User Interface for the exploration of microbiome data. This way, no knowledge of programming is required to perform analyses. Datasets can be imported, manipulated, analysed and visualised with a user-friendly interface.

biocViews Microbiome, Software, Visualization, GUI, ShinyApps, DataImport

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Encoding UTF-8

Depends R (>= 4.4.0), iSEE (>= 2.19.4), shiny

Imports ape, bluster, htmltools, iSEEtree (>= 1.1.4), mia, rbiom, rintrojs, scater, scuttle, shinyAce, shinydashboard, shinyjs, shinyWidgets, S4Vectors, SingleCellExperiment, SummarizedExperiment, TreeSummarizedExperiment, utils, vegan

Suggests BiocStyle, dada2, knitr, philr, remotes, rmarkdown, testthat (>= 3.0.0)

URL <https://github.com/microbiome/miaDash>

BugReports <https://github.com/microbiome/miaDash/issues>

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs

libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libgsl0-dev libcud-
dev libjpeg-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl libx11-dev zlib1g-dev

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

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Description

miaDash is a web app that provides an interface to build and explore [TreeSummarizedExperiment](#) (TreeSE) objects by means of [iSEE](#).

Usage

`miaDash()`

Value

An [iSEE](#) app with a custom landing page to build TreeSE objects and explore [mia datasets](#).

See Also

[iSEE mia miaViz](#)

Examples

```
app <- miaDash()

if (interactive()) {
  shiny::runApp(app)
}
```

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