Package: miaDash (via r-universe)

May 29, 2026

Version 1.4.0

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

License Artistic-2.0

Encoding UTF-8

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

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

Suggests BiocStyle, 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 libfribidi-dev libglpk-dev make libgsl0-dev libharfbuzz-dev libicu-dev libjpeg-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev perl zlib1g-dev

Repository https://bioc-release.r-universe.dev

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Contents

`miaDash` *miaDash*

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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