

Package ‘miaDash’

November 20, 2025

Version 1.3.0

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>

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constants	<i>Constants</i>
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Description

Constant values used throughout the miaDash app.

Usage

- .miaDashDefaultPanels
- .miaDashOtherPanels
- .transformMethods
- .qualityMetrics
- .alphaMetrics
- .betaMetrics
- .betaMethods
- .clustMethods
- .DmmCriteria

Format

An object of class character of length 7.
 An object of class character of length 9.
 An object of class character of length 19.
 An object of class list of length 4.
 An object of class character of length 23.
 An object of class character of length 4.
 An object of class character of length 4.
 An object of class character of length 4.
 An object of class character of length 3.

Panel layout

.miaDashDefaultPanels List of panel names in the default layout of miaDash.
 .miaDashOtherPanels List of panel names not in the default layout of miaDash.
 .transformMethods List of transformations applicable to assays.
 .alphaMetrics List of alpha diversity metrics.
 .betaMetrics List of beta diversity metrics.
 .betaMethods List of beta diversity methods.
 .qualityMetrics List of metrics for quality control.

Author(s)

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create_observers	<i>Observers</i>
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Description

.create_observers and .create_launch_observers define the server to import and build TreeSE objects and track the state of the Build and Launch buttons.

Usage

```
.create_import_observers(input, rObjects)
.create_manipulate_observers(input, rObjects)
.create_estimate_observers(input, rObjects)
.update_observers(input, session, rObjects)
.create_launch_observers(FUN, input, session, rObjects)
```

Arguments

input	The Shiny input object from the server function.
rObjects	A reactive list of values generated in the landing page.

Value

Observers are created in the server function in which this is called. A NULL value is invisibly returned.

landing_page	<i>Landing page</i>
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Description

.landing_page creates the landing page of miaDash, where TreeSE objects can be built and iSEE can be launched.

Usage

```
.landing_page(FUN, input, output, session)
```

Value

The UI is defined by the function. A NULL value is invisibly returned.

miaDash	<i>miaDash</i>
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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)
}
```

render_output	<i>Outputs</i>
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Description

.render_overview and .render_download create the output of the UI, which consists of the overview of the TreeSE object and the download object, respectively.

Usage

```
.render_overview(output, rObjects)

.render_download(output, rObjects)
```

Arguments

output The Shiny output object from the server function.

Value

Adds a rendered item to output. A NULL value is invisibly returned.

utils	<i>miaDash utilities</i>
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Description

Helper functions to support the app functionality.

Usage

```
.import_datasets(selection)

.update_tse(tse, fun, fun.args = list())

.print_message(..., title = "Invalid input:")

.set_optarg(item, loader = NULL, alternative = NULL, ...)
```

```
.check_formula(form, tse)

.importBIOM(file, col.data = NULL, tree.file = NULL, ...)

.rownames2taxa(x)
```

Arguments

selection	Numeric vector. A list of indices for the mia datasets to return.
tse	a TreeSummarizedExperiment object.
fun	Function scalar. Function to apply to tse.
fun.args	Named list. A list of arguments to pass to fun.
...	Either a series of strings to form the message returned by .print_message or named arguments for loader.
title	Character scalar. The title of the error message to print. (Default: "Invalid input:")
item	Character scalar. The file path from which the object should be loaded.
loader	Function scalar. The function to load item. (Default: NULL)
alternative	an alternative output to return when at least one item and loader are not defined. (Default: NULL)
form	Character scalar The formula to be checked.

Value

- .import_datasets: returns the list of available mia datasets.
- .update_tse: returns a TreeSE object after applying fun with arguments fun.args. Eventual messages and errors are also printed.
- .print_message: returns a modalDialog with the error message specified with ... and titled title.
- .set_optarg: returns an optional element for a TreeSE constructor. The output is either an object located at the file path item and loaded with loader or alternative.
- .check_formula: returns TRUE or FALSE depending whether or not all variables included in form are present in se colData.

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