Package ‘miaDash’

May 2, 2026

Version 1.5.0

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

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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, 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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Contents

`constants` *Constants*

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)

Giulio Benedetti

`create_observers` *Observers*

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` *Landing page*

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` *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)
}
```

`render_output` *Outputs*

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` *miaDash utilities*

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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