

# Package ‘miaDash’

April 4, 2025

**Version** 0.99.11

**Title** Shiny app 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, shiny

**Imports** ape, biomformat, htmltools, iSEEtree (>= 1.1.4), mia, rintrojs, scater, shinydashboard, shinyjs, 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** 7.3.2

**VignetteBuilder** knitr

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constants	<i>Constants</i>
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## Description

Constant values used throughout the miaDash app.

## Usage

.miaDashDefaultPanels

.miaDashOtherPanels

.transformMethods

.alphaMetrics

.betaMetrics

.betaMethods

## 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 character of length 23.

An object of class character of length 4.

An object of class character of length 4.

**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.

**Author(s)**

Giulio Benedetti

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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.

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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.

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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)
}
```

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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.

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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)
```

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

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

```
.check_formula(form, tse)
```

### Arguments

selection	Numeric vector. A list of indices for the mia datasets to return.
tse	a <a href="#">TreeSummarizedExperiment</a> 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 <code>.print_message</code> 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 <code>item</code> and <code>loader</code> 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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