

# Package ‘miaDash’

December 6, 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 ( $\geq 4.4.0$ ), iSEE ( $\geq 2.19.4$ ), shiny

**Imports** ape, bluster, htmltools, iSEEtree ( $\geq 1.1.4$ ), mia, rintrojs, scater, scuttle, shinydashboard, shinyjs, shinyWidgets, S4Vectors, SingleCellExperiment, SummarizedExperiment, TreeSummarizedExperiment, utils, vegan

**Suggests** BiocStyle, knitr, philr, remotes, rmarkdown, testthat ( $\geq 3.0.0$ )

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

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

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constants

*Constants*

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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)**

Giulio Benedetti

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create\_observers      *Observers*

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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 = 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 <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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