

Package ‘miaDash’

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Version 1.2.0

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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Author Giulio Benedetti [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-8732-7692>>),
Akwak Jeba [ctb] (ORCID: <<https://orcid.org/0009-0007-1347-7552>>),
Leo Lahti [aut] (ORCID: <<https://orcid.org/0000-0001-5537-637X>>)

Maintainer Giulio Benedetti <giulio.benedetti@utu.fi>

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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)

Giulio Benedetti

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

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