

Package ‘Holomics’

November 15, 2025

Type Package

Title A User-Friendly R 'shiny' Application for Multi-Omics Data
Integration and Analysis

Version 1.2.1

Description A 'shiny' application, which allows you to perform single- and multi-omics analyses using your own omics datasets. After the upload of the omics datasets and a metadata file, single-omics is performed for feature selection and dataset reduction. These datasets are used for pairwise- and multi-omics analyses, where automatic tuning is done to identify correlations between the datasets - the end goal of the recommended 'Holomics' workflow. Methods used in the package were implemented in the package 'mixomics' by Florian Rohart, Benoît Gautier, Amrit Singh, Kim-Anh Lê Cao (2017) <[doi:10.1371/journal.pcbi.1005752](https://doi.org/10.1371/journal.pcbi.1005752)> and are described there in further detail.

License GPL (>= 3)

URL <https://github.com/MolinLab/Holomics>

BugReports <https://github.com/MolinLab/Holomics/issues>

Depends R (>= 4.0)

Imports bs4Dash (>= 2.0.2), config, dplyr, DT, ggplot2, golem, igraph, openxlsx, readxl, shiny (>= 1.6.0), shinyalert, shinybusy, shinyjs, shinyvalidate, shinyWidgets, stringr, tippy, visNetwork, mixOmics, BiocParallel

Suggests bookdown, knitr, rmarkdown, badger

VignetteBuilder knitr

Encoding UTF-8

Language en-US

RoxygenNote 7.3.2

NeedsCompilation no

Author Katharina Munk [aut, cre],
Eva M. Molin [aut, ctb],
Günter Brader [ctb],
Lisa Ziemba [ctb],
AIT Austrian Institute of Technology GmbH [cph]
Maintainer Katharina Munk <katharinamunk@yahoo.de>
Repository CRAN
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Description

Run the Shiny Application

Usage

```
run_app(  
  onStart = NULL,  
  options = list(),  
  enableBookmarking = NULL,  
  uiPattern = "/",  
  ...  
)
```

Arguments

- | | |
|-------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| onStart | A function that will be called before the app is actually run. This is only needed for shinyAppObj, since in the shinyAppDir case, a global.R file can be used for this purpose. |
| options | Named options that should be passed to the runApp call (these can be any of the following: "port", "launch.browser", "host", "quiet", "display.mode" and "test.mode"). You can also specify width and height parameters which provide a hint to the embedding environment about the ideal height/width for the app. |
| enableBookmarking | Can be one of "url", "server", or "disable". The default value, NULL, will respect the setting from any previous calls to enableBookmarking() . See enableBookmarking() for more information on bookmarking your app. |

<code>uiPattern</code>	A regular expression that will be applied to each GET request to determine whether the <code>ui</code> should be used to handle the request. Note that the entire request path must match the regular expression in order for the match to be considered successful.
<code>...</code>	arguments to pass to <code>golem_opts</code> . See <code>'?golem::get_golem_options'</code> for more details.

Value

No return value, called to start the Shiny application

Examples

```
## Not run:  
# Start app in the current working directory  
run_app()  
  
## End(Not run)
```

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