Package 'AbSolution'

May 6, 2026

Title Interactive Feature-Based Analysis of AIRR-Seq Data

Version 1.0.1

Description An interactive framework for the exploration and analysis of adaptive immune receptor repertoire sequencing (AIRR-seq) data. It enables large-scale computation and integrated analysis of sequence-derived features, including physicochemical properties, amino acid descriptor sets, sequence motifs, compositional patterns, and somatic hypermutation metrics. The application supports multiscale analysis across sequences, clones, and repertoires, with interactive visualizations and statistical feature selection. 'AbSolution' also facilitates reproducible research by enabling structured export of data, code, parameters, and computational environments. See <https://github.com/EDS-Bioinformatics-Laboratory/AbSolution> for more details.

License GPL (>= 3)

URL https://github.com/EDS-Bioinformatics-Laboratory/AbSolution,
https://eds-bioinformatics-laboratory.github.io/AbSolution/

BugReports https://github.com/EDS-Bioinformatics-Laboratory/AbSolution/issues

Depends R (>= 4.4.0)

Imports alakazam, attachment, benchmarkme, bigassertr, bigparallelr, bigstatsr, Biostrings, bs4Dash, callr, colourpicker, config (>= 0.3.2), dashboardthemes, data.table, dockerfiler, doParallel, dplyr, DT, foreach, fresh, fs, ggplot2, golem (>= 0.4.1), grDevices, htmlwidgets, IRanges, iterors, knitr, parallel, Peptides, plotly, pwalign, reactable, rlang, rmarkdown, seqinr, shiny (>= 1.7.4), shinycssloaders, shinyFiles, shinyjs, shinymanager, shinymeta, shinythemes, shinyWidgets, sortable, stats, stringdist, stringr, sunburstR, tools, umap, upsetjs, utils, viridis, xfun

Additional_repositories https://bioconductor.org/packages/release/bioc

Suggests testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

Language en-US

RoxygenNote 7.3.3

NeedsCompilation no

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`run_app` *Run the AbSolution Shiny Application Launches the interactive AbSolution Shiny application for exploring B-cell and T-cell receptor repertoire data. The application provides tools for loading AIRR-formatted datasets, inspecting sequence characteristics, visualizing clonotype distributions, and generating summary reports.*

Description

Internally, ‘run_app()‘ calls [‘shiny::shinyApp()‘] to start the application, using the UI defined in [`app_ui()`] and the server logic defined in [`app_server()`].

Usage

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

Arguments

`verbose`	Logical. If `FALSE` (default), suppresses all warnings and messages during app execution. Set to `TRUE` to see full console output for debugging.
`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.
`uiPattern`	A regular expression that will be applied to each `GET` request to determine whether the `ui` 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.
`...`	arguments to pass to golem_opts. See '?golem::get_golem_options' for more details.

Details

This function is the entry point that end-users should call after installing the package.

Examples

```
if (interactive()) {
  ### Launch the full application with default settings:
  run_app()
}
```

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