Package: scSimEvalStudio (via r-universe)

November 19, 2026

Type Package

Title Interactive Shiny Studio for scSimEval Single-Cell Multiomics Benchmarking

Version 0.99.1

Description Companion graphical Shiny web interface for the 'scSimEval' Bioconductor package. Enables interactive uploading of single-cell RNA-seq, scATAC-seq, and paired or unpaired multiomics SingleCellExperiment datasets, execution of the 56-measure evaluation suite, interactive bubble-matrix and ordination exploration, and export of publication-quality figures and tabular reports.

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URL https://kabilanbio.github.io/scSimEvalStudio/, https://github.com/kabilanbio/scSimEvalStudio

BugReports https://github.com/kabilanbio/scSimEvalStudio/issues

biocViews GUI, Software, SingleCell, Transcriptomics, ATACSeq, QualityControl, Visualization

Encoding UTF-8

VignetteBuilder knitr

Depends R (>= 4.3.0)

Imports scSimEval, shiny, bslib, bsicons, DT, ggplot2, plotly, Matrix, SingleCellExperiment, SummarizedExperiment, openxlsx, writexl, zip

Suggests testthat (>= 3.0.0), knitr, rmarkdown

Config/roxygen2/version 8.1.1

Config/pak/sysreqs cmake libglpk-dev make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev zlib1g-dev

Repository https://biocstaging.r-universe.dev

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RemoteUrl https://github.com/BiocStaging/scSimEvalStudio

RemoteRef HEAD

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`launch_scSimEval_app` *Launch Interactive scSimEval Benchmarking Studio*

Description

Launches the companion Shiny web application bundled in **scSimEvalStudio**. Provides a graphical interface to upload `SingleCellExperiment` biological reference and simulated datasets (scRNA-seq, scATAC-seq, paired or unpaired multiomics), inspect 56 evaluation metrics, explore diagnostic figures interactively, and export high-resolution plots and Excel/PDF reports.

Usage

```
launch_scSimEval_app(
  port = NULL,
  host = "127.0.0.1",
  launch.browser = interactive(),
  maxRequestSize = 10 * 1024^3
)
```

Arguments

`port`	Optional port number for the local web server. Default is `NULL` (random open port).
`host`	Character string specifying the IP address to listen on. Defaults to `"127.0.0.1"`.
`launch.browser`	Logical, whether to automatically open the default web browser. Defaults to `interactive()`.
`maxRequestSize`	Numeric maximum upload file size in bytes. Defaults to `10 * 1024^3` (10 GiB).

Value

A `shiny.appobj` returned invisibly when `shiny::runApp()` exits cleanly.

Examples

```
app_dir <- system.file("shiny", "scSimEvalApp", package = "scSimEvalStudio")
nzchar(app_dir)
if (interactive()) {
  launch_scSimEval_app()
}
```

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