Package: MDSvis (via r-universe)

May 30, 2026

Title Plots of Multi Dimensional Scaling (MDS) results

Version 1.1.0

Description This package implements visulization of Multi Dimensional Scaling (MDS) results.

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

BugReports `https://github.com/UCLouvain-CBIO/MDSvis/issues`

URL `https://uclouvain-cbio.github.io/MDSvis`

biocViews FlowCytometry, QualityControl, DimensionReduction, MultidimensionalScaling, Software, Visualization

Depends R (>= 4.5)

Imports CytoMDS (>= 1.3.5), rlang, ggplot2, plotly, shiny, shinyjs, methods

Suggests knitr, rmarkdown, BiocStyle, HDCytoData, flowCore, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs cmake libfontconfig1-dev libfreetype6-dev make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl libx11-dev zlib1g-dev

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

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RemoteUrl https://github.com/bioc/MDSvis

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Contents

`mdsvis_app` *Launch shiny app for MDS projection visualization*

Description

Launch shiny app for MDS projection visualization

Usage

```
mdsvis_app(preLoadDemoDataset = FALSE)
```

Arguments

`preLoadDemoDataset`	if TRUE, pre-load the *Krieg_Anti_PD_1* dataset

Value

no return value

Examples

```
if (interactive()) {
  mdsvis_app()
}
```

Index