Package: MDSvis (via r-universe)

November 25, 2026

Title Plots of Multi Dimensional Scaling (MDS) results

Version 1.2.0

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

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

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/roxygen2/version 8.1.0

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 Bioconductor 3.24

Date/Publication 2026-11-23 22:55:09 UTC

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

RemoteRef RELEASE_3_24

RemoteSha 0adb2365ee32d228bf780441984d52961bf3e9c2

Contents

mdsvis_app 2

Index **3**

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

Description

Launch shiny app for MDS projection visualization

Usage

```
mdsvis_app(preLoadDemoDataset = FALSE, maxUploadSize = 50 * 1024^2)
```

Arguments

`preLoadDemoDataset`	if TRUE, pre-load the *Krieg_Anti_PD_1* dataset
`maxUploadSize`	maximum size for file upload (50MB by default)

Value

no return value

Examples

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

Index

mdsvis_app, 2