Package ‘MDSvis’

March 6, 2026

Title Plots of Multi Dimensional Scaling (MDS) results

Version 0.99.7

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 (>= 4.6)

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

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Contents

`MDSvis` *MDSvis package*

Description

`MDSvis` provides a shiny application for interactive visualisation of Multi Dimensional Scaling (MDS) results.

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See Also

CytoMDS

mdsvis_app

`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()
}
```

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