

Package ‘MDSvis’

March 2, 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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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	<i>Launch shiny app for MDS projection visualization</i>
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Description

Launch shiny app for MDS projection visualization

Usage

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

Arguments

preLoadDemoDataset
if TRUE, pre-load the *Krieg_Anti_PD_I* dataset

Value

no return value

Examples

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

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