# Package ‘MDSvis’

May 12, 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 (>= 4.6)

**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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## `MDSvis` *MDSvis package*

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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

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

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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_1* dataset |

### Value

no return value

### Examples

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

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