

# Package ‘MDSvis’

May 2, 2026

**Title** Plots of Multi Dimensional Scaling (MDS) results

**Version** 1.0.0

**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

**git\_url** <https://git.bioconductor.org/packages/MDSvis>

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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	<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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