

# Package ‘pRolocGUI’

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**Title** Interactive visualisation of spatial proteomics data

**Version** 1.4.1

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**Description** The package pRolocGUI comprises functions to  
interactively visualise organelle (spatial) proteomics  
data on the basis of pRoloc, pRolocdata and shiny.

**Depends** R (>= 3.1.0), pRoloc (>= 1.5.12), MSnbase (>= 1.13.11),  
methods

**Imports** pRolocdata, shiny (>= 0.9.1), tools (>= 3.1.0), scales, DT

**Suggests** RUnit, BiocGenerics, knitr, knitrBootstrap, bibtex,  
knitcitations (>= 1.0-1)

**License** GPL-2

**URL** <http://ComputationalProteomicsUnit.github.io/pRolocGUI/>

**BugReports** <https://github.com/ComputationalProteomicsUnit/pRolocGUI/issues>

**VignetteBuilder** knitr

**Video** <https://www.youtube.com/playlist?list=PLvIXxpatSLA2loV5Srs2VBpJIYUIVJ4ow>

**biocViews** Proteomics, Visualization, GUI

**NeedsCompilation** no

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plotMat2D *Plot a matrix of markers*

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### Description

Shiny App for visualising a matrix of markers

### Usage

```
plotMat2D(object, fcol = "Markers", ncol., ...)
```

### Arguments

object	An instance of class MSnSet.
fcol	The name of the markers matrix. Default is "Markers".
ncol.	Number of columns to be used for the legend. The default value (4 or less) depends on the length of the labels. Reduce this if the labels are too long and the legend does not fit in the display panel.
...	Additional parameters that can be used to choose the dimensionality reduction method, as defined in <a href="#">plot2D</a> .

### Author(s)

Lisa M Breckels

### Examples

```
library("pRoloc")
library("pRolocdata")
data(dunkley2006)
## adds matrix markers
dunkley2006 <- mrkVecToMat(dunkley2006)
if (interactive())
  plotMat2D(dunkley2006)
```

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pRolocComp *pRolocVis/pRolocComp*

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### Description

pRolocVis and pRolocComp launch shiny sessions to interactively analyse and visualise proteomics data.

**Usage**

```
pRolocComp(object, method = "PCA")
```

```
pRolocVis(object, method = "PCA")
```

**Arguments**

**object** an object of class MSnSet or a list of MSnSets (pRolocVis), a list of length 2 of MSnSets (pRolocComp).

**method** The method to be used for dimensionality reduction. Default is "PCA". See plot2D for details.

**Details**

pRolocVis is a function to start a shiny session with one MSnSet data set or a list of MSnSets. pRolocComp launches with a list of two MSnSets.

The functions allow to explore and analyse interactively spatial proteomics data, especially LOPIT and PCP experiments. Both functions offer high interactivity for exploring Principle Component Analysis (PCA) plots, protein profile plots and quantitative and qualitative meta-data. Additionally, pRolocVis and pRolocComp support import/export abilities for past and new search results using the FeaturesOfInterest/FoICollection infrastructure defined in the MSnbase package.

pRolocVis enables to analyse one MSnSet at a time, while pRolocComp analyses and compares two MSnSets. pRolocComp is especially meant for analyses of data which looks at the change of proteins in protein localisation.

To load the vignette for the functions pRolocVis and pRolocGUI enter vignette("pRolocGUI") in the console. The vignette will give more information on how to use the shiny applications.

**Value**

An object pRolocGUI\_SearchResults of class FoICollection when the object existed already or when a new FoICollection was created during a session.

**Author(s)**

Thomas Naake <naake@stud.uni-heidelberg.de>

**Examples**

```
## load MSnSet data sets from the pRolocdata package
data(andy2011, package = "pRolocdata")
data(tan2009r1, package = "pRolocdata")
data(tan2009r2, package = "pRolocdata")
data(dunkley2006, package = "pRolocdata")

## create lists with unnamed and named objects
unnamedVis <- list(andy2011, tan2009r1, dunkley2006)
namedVis <- list(andy2011 = andy2011,
                tan2009r1 = tan2009r1,
                dunkley2006 = dunkley2006)
```

```

unnamedComp <- list(tan2009r1, tan2009r2)
namedComp <- list(tan2009r1 = tan2009r1,
                  tan2009r2 = tan2009r2)

## launch application by either assigning a MSnSet,
## an unnamed or a named list to the argument object
if (interactive()) {
  pRolocVis(object = andy2011)
  pRolocVis(object = unnamedVis)
  pRolocVis(object = namedVis)
  pRolocComp(object = unnamedComp)
  pRolocComp(object = namedComp)
}

```

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pRolocVis2

*Visualise your pRoloc data*


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## Description

pRoloc interactive visualisation

## Usage

```

pRolocVis2(object, fcol, foi, fig.height = "600px", fig.width = "100%",
           legend.width = "100%", legend.cex = 1, nchar = 15, all = FALSE, ...)

```

## Arguments

object	An instance of class MSnSet.
fcol	The name of the markers matrix (default is "Markers"). Can be missing if foi is available.
foi	A <a href="#">FeaturesOfInterest</a> or a <a href="#">FoICollection</a> , that will be available for display.
fig.height	Height of the figure. Default is "600px".
fig.width	Width of the figure. Default is "600px".
legend.width	Width of the legend. Default is "100%".
legend.cex	Character expansion for the vignette labels. Default is 1.
nchar	Maximum number of characters if the markers class names, before their names are truncated. Default is 10.
all	If there are more than 10 clusters, only the first three are displayed on start-up, unless all is set to TRUE. Default is FALSE.
...	Additional parameters that can be used to choose the dimensionality reduction method, as defined in <a href="#">plot2D</a> .

## Author(s)

Laurent Gatto

**Examples**

```
library("pRoloc")
library("pRolocdata")
data(dunkley2006)
## markers matrix ecoding
dunkley2006 <- mrkVecToMat(dunkley2006)
## order the fractions
dunkley2006 <- dunkley2006[, order(dunkley2006$fraction)]
if (interactive())
  pRolocGUI:::pRolocVis2(dunkley2006)
```

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