Package 'pRolocGUI'

Title Interactive visualisation of spatial proteomics data

Version 1.2.0

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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)

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

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URL http://ComputationalProteomicsUnit.github.io/pRolocGUI/

BugReports https://github.com/ComputationalProteomicsUnit/pRolocGUI/issues

VignetteBuilder knitr

Video https://www.youtube.com/playlist?list=PLvIXxpatSLA2loV5Srs2VBpJIYUlVJ4ow

biocViews Proteomics, Visualization, GUI

NeedsCompilation no

R topics documented:

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pRolocVis/pRolocComp   *pRolocVis/pRolocComp*

Description

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

Usage

```
pRolocVis(object)
```

Arguments

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

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 quantatative 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.

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Examples

```
## Not run:

## 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
pRolocVis(object = andy2011)
pRolocVis(object = unnamedVis)
pRolocVis(object = namedVis)

pRolocComp(object = unnamedComp)
pRolocComp(object = namedComp)

## End(Not run)
```

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