Package ‘pRolocGUI’

May 29, 2024

Title  Interactive visualisation of spatial proteomics data

Version  2.14.0

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

Depends  methods, R (>= 3.1.0), pRoloc (>= 1.27.6), Biobase, MSnbase (>= 2.1.11)

Imports  shiny (>= 0.9.1), scales, dplyr, DT (>= 0.1.40), graphics, utils, ggplot2, shinydashboardPlus (>= 2.0.0), colourpicker, shinyhelper, shinyWidgets, shinyjs, colorspace, stats, grDevices, grid, BiocGenerics, shinydashboard

Suggests  pRolocdata, knitr, BiocStyle (>= 2.5.19), rmarkdown, testthat (>= 3.0.0)

License  GPL-2

URL  https://github.com/lgatto/pRolocGUI

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

VignetteBuilder  knitr

Video  https://www.youtube.com/playlist?list=PLvIXxpASLA2I0V5Sr52VBpJIYU1VJ4ow

biocViews  Proteomics, Visualization, GUI

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Interactive visualisation of spatial proteomics data

These functions allow one to explore spatial proteomics data interactively.

Usage

pRolocVis(object, app = "explore", fcol = "markers", ...)

pRolocVis_aggregate(
  object,
  fcol = "markers",
  groupBy,
  fig.height = "700px",
  nchar = 25,
  ...
)

pRolocVis_compare(
  object,
  fcol = "markers",
  classProfiles = FALSE,
  fig.height = "400px",
  nchar = 25,
  ...
)

pRolocVis_explore(
  object,
  fcol = "markers",
  classProfiles = FALSE,
  fig.height = "700px",
  nchar = 25,
  ...
)
**pRolocVis**

**Arguments**

- **object**
  An instance of class `MSnSet`, or an `MSnSetList` of length 2 if using "compare" application.

- **app**
  The type of application requested: "explore" (default), "compare" or "aggregate". See description below.

- **fcol**
  The feature meta-data label (`fData` column name) to be used for colouring. Default is "markers". If set to NULL, no annotation is expected. For the "compare" app, a character vector of length 2 is allowed to set different labels for each dataset. If only one label is specified, then this single label will be used to identify the annotation column in both datasets. Please see example herein.

- **groupBy**
  The feature meta-data label (`fData` column name) to be used for summarising the features to be combined.

- **fig.height**
  Height of the figure.

- **nchar**
  Maximum number of characters of the subcellular class names, before their names are truncated. Default is 25.

- **classProfiles**
  A logical indicating if a tab displaying individual class profile plots should be displayed. Default is `FALSE`.

**Details**

The function `pRolocVis` is a wrapper for `pRolocVis_pca`, `pRolocVis_compare`, and `pRolocVis_aggregate`. These Shiny apps allow to explore and analyse interactively spatial proteomics data.

The explore Shiny app allows exploration of quantitative data (1) visually through a projection of the dataset, (2) protein profiles, and (3) a searchable feature data table, allowing visualisation of sets of proteins of interest.

The compare Shiny app is meant for comparing protein localisation between two conditions, or two different experiments, replicates etc.

The aggregation Shiny app displays a scatter plot of the maximum or mean distances within each feature (e.g. protein group) according to its components (e.g. peptides) defined by the `groupBy` argument. A PCA plot of the components is also displayed. It can be used for visualising peptides, PSMs or any other features defined in the feature data of the `MSnSet` and their distributions.

**Author(s)**

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**See Also**

The package vignette: `vignette("pRolocGUI")`. 
Examples

library("pRoloc")
library("pRolocdata")

## Load the Explore app
data(hyperLOPIT2015)
if (interactive()) {
  pRolocVis(hyperLOPIT2015)
  pRolocVis(hyperLOPIT2015, method = "t-SNE")
  ## store the t-SNE coords and pass a matrix to pRolocVis
  xx <- plot2D(hyperLOPIT2015, method = "t-SNE")
  pRolocVis(xx, method = "none", methargs = list(hyperLOPIT2015))
}

## Load the Compare app
data("hyperLOPITU2018")
data("lopitdcU2018")
xx <- MSnSetList(list(hyperLOPITU2018, lopitdcU2018))
if (interactive()) {
  pRolocVis(xx, app = "compare", fcol = c("markers", "final.assignment"))
}

## Visualise the location and distribution of peptides per protein group
data("hyperLOPIT2015ms2psm")
if (interactive()) {
  ## Combine PSM data to peptides
  hl <- combineFeatures(hyperLOPIT2015ms2psm,
                        groupBy = fData(hyperLOPIT2015ms2psm)$Sequence,
                        method = median)
  ## Visualise peptides according to protein group
  pRolocVis(hl, app = "aggregate", fcol = "markers",
            groupBy = "Protein.Group.Accessions")
}
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