Package ‘pRolocGUI’

October 14, 2021

Title Interactive visualisation of spatial proteomics data

Version 2.2.0

Description The package pRolocGUI comprises functions to
interactively visualise organelle (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, colourpicker, shinyhelper,
shinyWidgets, shinyjs, colorspace, shinydashboard, stats,
grDevices, grid, BiocGenerics

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

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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

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R topics documented:

pRolocVis *Interactive visualisation of spatial proteomics data*

Description

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",
  fig.height = "700px",
  nchar = 25,
  ...
)

pRolocVis_explore(
  object,
  fcol = "markers",
  fig.height = "700px",
  nchar = 25,
  ...
)
```

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.

`...` Additional parameters passed to `plot2D` for the `"explore"` (such as the dimensionality reduction technique, and methods), `"compare"` apps. For the `"aggregate"` app this is for additional parameters to be passed to `combineFeatures`.

`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. Default is `"700px"`.

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

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("hyperLOPITU2OS2018")
data("lopitdcU2OS2018")
xx <- MSnSetList(list(hyperLOPITU2OS2018, lopitdcU2OS2018))
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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