Package ‘pRolocGUI’

March 23, 2017

Title Interactive visualisation of spatial proteomics data

Version 1.9.4

Author Lisa M Breckels, Thomas Naake and Laurent Gatto

Maintainer Laurent Gatto <lg390@cam.ac.uk>,
Lisa M Breckels <lms79@cam.ac.uk>

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 (>= 1.11.1), Biobase, MSnbase
(>= 1.13.11)

Imports shiny (>= 0.9.1), scales, dplyr, DT (>= 0.1.40), graphics,
utils

Suggests pRolocdata, knitr, BiocStyle, rmarkdown

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=PLv1IXxpISLAl/oV5Srs2VBpJlYUIVJ4ow

biocViews Proteomics, Visualization, GUI

RoxygenNote 5.0.1

NeedsCompilation no

R topics documented:

  pRolocVis ................................................................. 2

Index 5
Interactive visualisation of spatial proteomics data

Description

These functions allow one to explore spatial proteomics data interactively.

Usage

pRolocVis(object, app = "main", fcol, ...)

pRolocVis_classify(object, fcol, scol, mcol = "markers", legend.cex = 1, ...)

pRolocVis_compare(object, fcol1, fcol2, foi, fig.height = "600px", fig.width = "100%", legend.width = "200%", legend.cex = 1, remap = TRUE, nchar = 40, all = TRUE, mirrorX = FALSE, mirrorY = FALSE, ...)

pRolocVis_pca(object, fcol = "markers", foi, fig.height = "600px", fig.width = "100%", legend.width = "200%", legend.cex = 1, nchar = 40, all = TRUE, ...)

Arguments

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

app The type of application requested: "main" (default), "classify", "compare". See description below.

fcol The feature meta-data label (fData column name) to be used for colouring. Default is "markers". This will correspond to the prediction column if using "classify", or the markers (labelled data) to be plotted otherwise. If set to NULL, no annotation is expected.

scol The feature meta data column containing the classification scores.

mcol The feature meta data column containing the labelled training data, for use with "classify".

legend.cex Point character expansion for the legend. Default is 1.

fcol2 If using the compare app this is the feature meta-data label (fData column name) for the second dataset in the MSnSetList. Default is markers.

foi A FeaturesOfInterest or FoICollection object.

fig.height Height of the figure. Default is "600px".

fig.width Width of the figure. Default is "100px".

legend.width Width of the legend. Default is "200%".

remap A logical indicating whether the second dataset in the MSnSetList should be remapped to the first dataset. The default is TRUE.
pRolocVis

nchar

Maximum number of characters of the markers class names, before their names are truncated. Default is 10.

all

If TRUE all clusters are displayed on startup, if the total number of clusters is less than including 15. If FALSE or otherwise, only the first cluster in the list is displayed.

mirrorX

Should the first PC of the second MSnSet in object be mirrored (default is FALSE). Only relevant when remap is FALSE.

mirrorY

Should the second PC of the second MSnSet in object be mirrored (default is FALSE). Only relevant when remap is FALSE.

... Additional parameters passed to plot2D. Note that mirrorX and mirrorY are currently silently ignored other than for the compare app.

Details

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

The main Shiny app allows exploration of quantitative data (1) visually through Principle Component Analysis (PCA), (2) protein profiles, and (3) a searchable feature data table, allowing visualisation of particular proteins of interest.

The classify Shiny app is used to visualise classification results and set user-specified thresholds for sub-cellular location predictions.

The compare Shiny app is meant for comparing protein localisation between two conditions, or two different experiments, replicates etc. Please note that passing the argument method to ... will not work as it is already specified internally.

Value

For classify a numeric vector of thresholds, one per class, to use with getPredictions

For compare and main a character vector of the featureNames of the proteins selected is invisibly returned.

For pca a character of protein names, of the proteins selected upon application closure.

Author(s)

Laurent Gatto, Lisa Breckels and Thomas Naake

See Also

The package vignette: vignette("pRolocGUI").

Examples

```r
library("pRoloc")
library("pRolocdata")
data(hyperLOPIT2015)
if (interactive()) {
pRolocVis(hyperLOPIT2015)
}
## Load classification results from hyperLOPIT stored in fData
if (interactive()) {
  myThreshold <- pRolocVis(hyperLOPIT2015, app = "classify",
                           fcol = "svm.classification",
```
scol = "svm.score"
newPredictions <- getPredictions(hyperLOPIT2015, fcol = "svm.classification",
                                 scol = "svm.score", t = myThreshold)
Index

FeaturesOfInterest, 2
FoICollection, 2

getPredictions, 3

pRolocVis, 2
pRolocVis_classify (pRolocVis), 2
pRolocVis_compare (pRolocVis), 2
pRolocVis_pca (pRolocVis), 2