Package ‘pRolocGUI’

March 23, 2017

Title Interactive visualisation of spatial proteomics data

Version 1.8.2

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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 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=PLvIXxpatSLA2loV5Sr2VBpJlYU1VJ4ow

biocViews Proteomics, Visualization, GUI

RoxygenNote 5.0.1

NeedsCompilation no

R topics documented:

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**pRolocVis**

*Interactive visualisation of spatial proteomics data*

**Description**

These functions allow one to explore spatial proteomics data interactively.

**Usage**

```r
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, ...)
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 the legend. Default is 1.

- **fcol1**
  If using the `compare` app this is the feature meta-data label (fData column name) for the first dataset in the `MSnSetList`. Default is markers.

- **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 "100%".

- **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.names(cols) <- myclasses Default is
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.

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)

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See Also

The package vignette: vignette("pRolocGUI").

Examples

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)
}
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