Package 'pRolocGUI'

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Title Interactive visualisation of spatial proteomics data

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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=PLvIXxpatSLA2loV5Srs2VBpJIYUlVJ4ow

biocViews Proteomics, Visualization, GUI

RoxygenNote 5.0.1

NeedsCompilation no

R topics documented:

1

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pRolocVis   *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, ...)

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.
...	Additional parameters passed to the respective app.
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 "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.names(cols) <- myclasses Default is

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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