Package ‘pRolocGUI’

December 22, 2016

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=PLvIXxpatsLA2loV5Srs2VBpJIYULVJ4ow

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

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\%",
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.

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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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