# Package 'pRoloc'

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**Type** Package

**Title** A unifying bioinformatics framework for spatial proteomics

**Version** 1.42.0

**Author** Laurent Gatto, Oliver Crook and Lisa M. Breckels with contributions from Thomas Burger and Samuel Wieczorek

**Maintainer** Laurent Gatto <laurent.gatto@uclouvain.be>

**Description** The pRoloc package implements machine learning and visualisation methods for the analysis and interogation of quantitiative mass spectrometry data to reliably infer protein sub-cellular localisation.

**Depends** R (>= 3.5), MSnbase (>= 1.19.20), MLInterfaces (>= 1.67.10), methods, Rcpp (>= 0.10.3), BiocParallel

**Imports** stats4, Biobase, mclust (>= 4.3), caret, e1071, sampling, class, kernlab, lattice, nnet, randomForest, proxy, FNN, hexbin, BiocGenerics, stats, dendextend, RColorBrewer, scales, MASS, knitr, mvtnorm, LaplacesDemon, coda, mixtools, gtools, plyr, ggplot2, biomaRt, utils, grDevices, graphics

**Suggests** testthat, rmarkdown, pRolocdata (>= 1.9.4), roxygen2, xtable, rgl, BiocStyle (>= 2.5.19), hpar (>= 1.41.0), dplyr, akima, fields, vegan, GO.db, AnnotationDbi, Rtsne (>= 0.13), nipals, reshape, magick

**LinkingTo** Rcpp, RcppArmadillo

**License** GPL-2

**VignetteBuilder** knitr

**Video** https://www.youtube.com/playlist?list=PLvIXxpatSLA2loV5Srs2VBpJIYUlVJ4ow

**URL** https://github.com/lgatto/pRoloc

**BugReports** https://github.com/lgatto/pRoloc/issues

**biocViews** ImmunoOncology, Proteomics, MassSpectrometry, Classification, Clustering, QualityControl

**Collate** AllGenerics.R machinelearning-framework.R
machinelearning-framework-theta.R
machinelearning-framework-map.R
machinelearning-framework-mcmc.R machinelearning-utils.R
machinelearning-functions-knn.R
machinelearning-functions-ksvm.R machinelearning-functions-nb.R
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**RoxygenNote** 6.1.1

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# R **topics documented:**

addGoAnnotations             *Add GO annotations*

## Description

Adds GO annotations to the feature data

## Usage

```
addGoAnnotations(object, params, evidence, useID = FALSE,
  fcol = "GOAnnotations", ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| params | An instance of class AnnotationParams. If missing, [getAnnotationParams](#) will be used. |
| evidence | GO evidence filtering. |
| useID | Logical. Should GO term names or identifiers be used? If TRUE, identifiers will be used. If FALSE GO term names will be used. |
| fcol | Character. Name of the matrix of annotations to be added to the fData default is GOAnnotations |
| ... | Other arguments passed to makeGoSet |

## Value

An updated `MSnSet` with new feature data column called `GOAnnotations` containing a matrix of GO annotations

## Author(s)

Lisa M Breckels

## Examples

```
library(pRolocdata)
data(dunkley2006)
par <- setAnnotationParams(inputs =
                    c("Arabidopsis thaliana genes",
                    "Gene stable ID"))
## add protein sets/annotation information
xx <- addGoAnnotations(dunkley2006, par)
dim(fData(xx)$GOAnnotations)

## filter sets
xx <- filterMinMarkers(xx, n = 50)
dim(fData(xx)$GOAnnotations)
xx <- filterMaxMarkers(xx, p = .25)
dim(fData(xx)$GOAnnotations)

## Subset for specific protein sets
sub <- subsetMarkers(xx, keep = c("vacuole"))

## Order protein sets
res <- orderGoAnnotations(xx, k = 1:3, p = 1/3, verbose = FALSE)
if (interactive()) {
pRolocVis(res, fcol = "GOAnnotations")
}
```

---

addLegend                    *Adds a legend*

---

## Description

Adds a legend to a [plot2D](#) figure.

## Usage

```
addLegend(object, fcol = "markers", where = c("bottomleft", "bottom",
  "bottomright", "left", "topleft", "top", "topright", "right", "center",
  "other"), col, bty = "n", ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet |
| fcol | Feature meta-data label (fData column name) defining the groups to be differentiated using different colours. Default is markers. |
| where | One of "bottomleft" (default), "bottomright", "topleft", "topright" or "other" defining the location of the legend. "other" opens a new graphics device, while the other locations are passed to [legend](). |
| col | A character defining point colours. |
| bty | Box type, as in legend. Default is set to "n". |
| ... | Additional parameters passed to [legend](). |

## Details

The function has been updated in version 1.3.6 to recycle the default colours when more organelle classes are provided. See [plot2D]() for details.

## Value

Invisibly returns NULL

## Author(s)

Laurent Gatto

---

addMarkers                        *Adds markers to the data*

---

## Description

The function adds a 'markers' feature variable. These markers are read from a comma separated values (csv) spreadsheet file. This markers file is expected to have 2 columns (others are ignored) where the first is the name of the marker features and the second the group label. Alternatively, a markers named vector as provided by the [pRolocmarkers]() function can also be used.

## Usage

```
addMarkers(object, markers, mcol = "markers", fcol, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| markers | A character with the name the markers' csv file or a named character of markers as provided by [pRolocmarkers](). |
| mcol | A character of length 1 defining the feature variable label for the newly added markers. Default is "markers". |

| | |
|---|---|
| `fcol` | An optional feature variable to be used to match against the markers. If missing, the feature names are used. |
| `verbose` | A `logical` indicating if number of markers and marker table should be printed to the console. |

## Details

It is essential to assure that `featureNames(object)` (or `fcol`, see below) and marker names (first column) match, i.e. the same feature identifiers and case fold are used.

## Value

A new instance of class `MSnSet` with an additional `markers` feature variable.

## Author(s)

Laurent Gatto

## See Also

See [pRolocmarkers](#) for a list of spatial markers and [markers](#) for details about markers encoding.

## Examples

```
library("pRolocdata")
data(dunkley2006)
atha <- pRolocmarkers("atha")
try(addMarkers(dunkley2006, atha)) ## markers already exists
fData(dunkley2006)$markers.org <- fData(dunkley2006)$markers
fData(dunkley2006)$markers <- NULL
marked <- addMarkers(dunkley2006, atha)
fvarLabels(marked)
## if 'makers' already exists
marked <- addMarkers(marked, atha, mcol = "markers2")
fvarLabels(marked)
stopifnot(all.equal(fData(marked)$markers, fData(marked)$markers2))
plot2D(marked)
addLegend(marked, where = "topleft", cex = .7)
```

---

```
AnnotationParams-class
```
*Class* `"AnnotationParams"`

---

## Description

Class to store annotation parameters to automatically query a Biomart server, retrieve relevant annotation for a set of features of interest using, for example [getGOFromFeatures](#) and [makeGoSet](#).

## Objects from the Class

Objects can be created and set with the setAnnotationParams function. Object are created by calling without any arguments setAnnotationParams(), which will open an interactive interface. Depending on the value of "many.graphics" option, a graphical of a text-based menu will open (the text interface can be forced by setting the graphics argument to FALSE: setAnnotationParams(graphics = FALSE)). The menu will allow to select the species of interest first and the type of features (ENSEMBL gene identifier, Entrez id, ...) second.

The species that are available are those for which ENSEMBL data is available in Biomart and have a set of attributes of interest available. The compatible identifiers for downstream queries are then automatically filtered and displayed for user selection.

It is also possible to pass a parameter inputs, a character vector of length 2 containing a pattern uniquely matching the species of interest (in position 1) and a patterns uniquely matching the feature types (in position 2). If the matches are not unique, an error will be thrown.

A new instance of the AnnotationParams will be created to enable easy and automatic query of the Mart instance. The instance is invisibly returned and stored in a global variable in the **pRoloc** package's private environment for automatic retrieval. If a variable containing an AnnotationParams instance is already available, it can be set globally by passing it as argument to the setAnnotationParams function. Globally set AnnotationParams instances can be accessed with the getAnnotationParams function.

See the pRoloc-theta vignette for details.

## Slots

mart: Object of class "Mart" from the **biomaRt** package.

martname: Object of class "character" with the name of the mart instance.

dataset: Object of class "character" with the data set of the mart instance.

filter: Object of class "character" with the filter to be used when querying the mart instance.

date: Object of class "character" indicating when the current instance was created.

biomaRtVersion: Object of class "character" with the **biomaRt** version used to create the AnnotationParams instance.

.__classVersion__: Object of class "Versions" with the version of the AnnotationParams class of the current instance.

## Methods

**show** signature(object = "AnnotationParams"): to display objects.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## See Also

[getGOFromFeatures](), [makeGoSet]() and the pRoloc-theta vignette.

## Examples

```
data(andy2011params)
andy2011params
data(dunkley2006params)
dunkley2006params

try(setAnnotationParams(inputs = c("nomatch1", "nomatch2")))
setAnnotationParams(inputs = c("Human genes",
        "UniProtKB/Swiss-Prot ID"))
getAnnotationParams()
```

---

checkFeatureNamesOverlap
*Check feature names overlap*

---

## Description

Checks the marker and unknown feature overlap of two `MSnSet` instances.

## Usage

```
checkFeatureNamesOverlap(x, y, fcolx = "markers", fcoly,
  verbose = TRUE)
```

## Arguments

| | |
|---|---|
| x | An `MSnSet` instance. |
| y | An `MSnSet` instance. |
| fcolx | The feature variable to separate unknown (`fData(y)$coly == "unknown"`) from the marker features in the x object. |
| fcoly | As `fcolx`, for the y object. If missing, the value of `fcolx` is used. |
| verbose | If `TRUE` (default), the overlap is printed out on the console. |

## Value

Invisibly returns a named list of common markers, unique x markers, unique y markers in, common unknowns, unique x unknowns and unique y unknowns.

## Author(s)

Laurent Gatto

## Examples

```
library("pRolocdata")
data(andy2011)
data(andy2011goCC)
checkFeatureNamesOverlap(andy2011, andy2011goCC)
featureNames(andy2011goCC)[1] <- "ABC"
res <- checkFeatureNamesOverlap(andy2011, andy2011goCC)
res$markersX
res$markersY
```

---

checkFvarOverlap                *Compare a feature variable overlap*

---

## Description

Extracts qualitative feature variables from two `MSnSet` instances and compares with a contingency table.

## Usage

```
checkFvarOverlap(x, y, fcolx = "markers", fcoly, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| x | An `MSnSet` instance. |
| y | An `MSnSet` instance. |
| fcolx | The feature variable to separate unknown (`fData(y)$coly == "unknown"`) from the marker features in the x object. |
| fcoly | As `fcolx`, for the y object. If missing, the value of `fcolx` is used. |
| verbose | If `TRUE` (default), the contingency table of the the feature variables is printed out. |

## Value

Invisibly returns a named list with the values of the diagonal, upper and lower triangles of the contingency table.

## Author(s)

Laurent Gatto

## Examples

```
library("pRolocdata")
data(dunkley2006)
res <- checkFvarOverlap(dunkley2006, dunkley2006,
                        "markers", "markers.orig")
str(res)
```

---

chi2-methods | *The PCP 'chi square' method*

---

## Description

In the original protein correlation profiling (PCP), Andersen et al. use the peptide normalised profiles along gradient fractions and compared them with the reference profiles (or set of profiles) by computing $Chi^2$ values, $\frac{\sum(x_i-x_p)^2}{x_p}$, where $x_i$ is the normalised value of the peptide in fraction i and $x_p$ is the value of the marker (from Wiese et al., 2007). The protein $Chi^2$ is then computed as the median of the peptide $Chi^2$ values. Peptides and proteins with similar profiles to the markers will have small $Chi^2$ values.

The `chi2` methods implement this idea and compute such Chi^2 values for sets of proteins.

## Methods

signature(x = "matrix", y = "matrix", method = "character", fun = "NULL", na.rm = "logical")
    Compute nrow(x) times nrow(y) $Chi^2$ values, for each x, y feature pair. Method is one of
    "Andersen2003" or "Wiese2007"; the former (default) computed the $Chi^2$ as sum(y-x)^2/length(x),
    while the latter uses sum((y-x)^2/x). na.rm defines if missing values (NA and NaN) should be
    removed prior to summation. fun defines how to summarise the $Chi^2$ values; default, NULL,
    does not combine the $Chi^2$ values.

signature(x = "matrix", y = "numeric", method = "character", na.rm = "logical") Computes
    nrow(x) $Chi^2$ values, for all the $(x_i, y)$ pairs. See above for the other arguments.

signature(x = "numeric", y = "matrix", method = "character", na.rm = "logical") Computes
    nrow(y) $Chi^2$ values, for all the $(x, y_i)$ pairs. See above for the other arguments.

signature(x = "numeric", y = "numeric", method = "character", na.rm = "logical") Computes
    the $Chi^2$ value for the $(x, y)$ pairs. See above for the other arguments.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## References

Andersen, J. S., Wilkinson, C. J., Mayor, T., Mortensen, P. et al., Proteomic characterization of the human centrosome by protein correlation profiling. Nature 2003, 426, 570 - 574.

Wiese, S., Gronemeyer, T., Ofman, R., Kunze, M. et al., Proteomics characterization of mouse kidney peroxisomes by tandem mass spectrometry and protein correlation profiling. Mol. Cell. Proteomics 2007, 6, 2045 - 2057.

## See Also

empPvalues

## Examples

```
mrk <- rnorm(6)
prot <- matrix(rnorm(60), ncol = 6)
chi2(mrk, prot, method = "Andersen2003")
chi2(mrk, prot, method = "Wiese2007")

pepmark <- matrix(rnorm(18), ncol = 6)
pepprot <- matrix(rnorm(60), ncol = 6)
chi2(pepmark, pepprot)
chi2(pepmark, pepprot, fun = sum)
```

---

classWeights                    *Calculate class weights*

---

## Description

Calculates class weights to be used for parameter optimisation and classification such as `svmOptimisation` or `svmClassification` - see the *pRoloc tutorial* vignette for an example. The weights are calculated for all non-*unknown* classes the inverse of the number of observations.

## Usage

```
classWeights(object, fcol = "markers")
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet |
| fcol | The name of the features to be weighted |

## Value

A `table` of class weights

## Author(s)

Laurent Gatto

## Examples

```
library("pRolocdata")
data(hyperLOPIT2015)
classWeights(hyperLOPIT2015)
data(dunkley2006)
classWeights(dunkley2006)
```

---

| clustDist | *Pairwise Distance Computation for Protein Information Sets* |

---

## Description

This function computes the mean (normalised) pairwise distances for pre-defined sets of proteins.

## Usage

```
clustDist(object, k = 1:5, fcol = "GOAnnotations", n = 5,
  verbose = TRUE, seed)
```

## Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| k | The number of clusters to try fitting to the protein set. Default is k = 1:5. |
| fcol | The feature meta-data containing matrix of protein sets/ marker definitions. Default is GOAnnotations. |
| n | The minimum number of proteins per set. If protein sets contain less than n instances they will be ignored. Defualt is 5. |
| verbose | A logical defining whether a progress bar is displayed. |
| seed | An optional seed for the random number generator. |

## Details

The input to the function is a MSnSet dataset containing a matrix appended to the feature data slot identifying the membership of protein instances to a pre-defined set(s) e.g. a specific Gene Ontology term etc.

For each protein set, the clustDist function (i) extracts all instances belonging to the set, (ii) using the kmeans algorithm fits and tests k = c(1:5) (default) cluster components to each set, (iii) calculates the mean pairwise distance for each k tested.

Note: currently distances are calcualted in Euclidean space, but other distance metrics will be supported in the future).

The output is a list of ClustDist objects, one per information cluster. The ClustDist class summarises the algorithm information such as the number of k's tested for the kmeans, and mean and normalised pairwise Euclidean distances per numer of component clusters tested. See ?ClustDist for more details.

## Value

An instance of `"ClustDistList"` containing a `"ClustDist"` instance for every protein set, which summarises the algorithm information such as the number of k's tested for the kmeans, and mean and normalised pairwise Euclidean distances per numer of component clusters tested.

## Author(s)

Lisa Breckels

## See Also

For class definitions see "ClustDistList" and "ClustDist".

## Examples

```
library(pRolocdata)
data(dunkley2006)
par <- setAnnotationParams(inputs =
                    c("Arabidopsis thaliana genes",
                    "Gene stable ID"))
## add protein sets/annotation information
xx <- addGoAnnotations(dunkley2006, par)
## filter
xx <- filterMinMarkers(xx, n = 50)
xx <- filterMaxMarkers(xx, p = .25)
## get distances for protein sets
dd <- clustDist(xx)
## plot clusters for first 'ClustDist' object
## in the 'ClustDistList'
plot(dd[[1]], xx)
## plot distances for all protein sets
plot(dd)
## Extract normalised distances
## Normalise by n^1/3
minDist <- getNormDist(dd, p = 1/3)
## Get new order according to lowest distance
o <- order(minDist)
## Re-order GOAnnotations
fData(xx)$GOAnnotations <- fData(xx)$GOAnnotations[, o]
if (interactive()) {
pRolocVis(xx, fcol = "GOAnnotations")
}
```

---

ClustDist-class          *Class* "ClustDist"

---

## Description

The `ClustDist` summaries algorithm information, from running the `clustDist` function, such as
the number of k's tested for the kmeans, and mean and normalised pairwise (Euclidean) distances
per numer of component clusters tested.

## Objects from the Class

Object of this class are created with the `clustDist` function.

**Slots**

k: Object of class "numeric" storing the number of k clusters tested.

dist: Object of class "list" storing the list of distance matrices.

term: Object of class "character" describing GO term name.

id: Object of class "character" describing the GO term ID.

nrow: Object of class "numeric" showing the number of instances in the set

clustsz: Object of class "list" describing the number of instances for each cluster for each k tested

components: Object of class "vector" storing the class membership of each protein for each k tested.

fcol: Object of class "character" showing the feature column name in the corresponding MSnSet where the protein set information is stored.

**Methods**

**plot** Plots the kmeans clustering results.

**show** Shows the object.

**Author(s)**

Lisa M Breckels <lms79@cam.ac.uk>

**Examples**

```
showClass("ClustDist")

library('pRolocdata')
data(dunkley2006)
par <- setAnnotationParams(inputs =
                c("Arabidopsis thaliana genes",
                  "Gene stable ID"))

## add protein set/annotation information
xx <- addGoAnnotations(dunkley2006, par)

## filter
xx <- filterMinMarkers(xx, n = 50)
xx <- filterMaxMarkers(xx, p = .25)

## get distances for protein sets
dd <- clustDist(xx)

## plot clusters for first 'ClustDist' object
## in the 'ClustDistList'
plot(dd[[1]], xx)

## plot distances for all protein sets
plot(dd)
```

---

ClustDistList-class            *Storing multiple ClustDist instances*

---

**Description**

A class for storing lists of [ClustDist](#) instances.

**Objects from the Class**

Object of this class are created with the clustDist function.

**Slots**

x: Object of class list containing valid ClustDist instances.

log: Object of class list containing an object creation log, containing among other elements the call that generated the object.

.__classVersion__: The version of the instance. For development purposes only.

**Methods**

"[[" Extracts a single ClustDist at position.

"[" Extracts one of more ClustDists as ClustDistList.

length Returns the number of ClustDists.

names Returns the names of ClustDists, if available. The replacement method is also available.

show Display the object by printing a short summary.

lapply(x, FUN, ...) Apply function FUN to each element of the input x. If the application of FUN returns and ClustDist, then the return value is an ClustDistList, otherwise a list.

plot Plots a boxplot of the distance results per protein set.

**Author(s)**

Lisa M Breckels <lms79@cam.ac.uk>

**Examples**

```
library('pRolocdata')
data(dunkley2006)
par <- setAnnotationParams(inputs =
                  c("Arabidopsis thaliana genes",
                  "Gene stable ID"))

## add protein set/annotation information
xx <- addGoAnnotations(dunkley2006, par)

## filter
xx <- filterMinMarkers(xx, n = 50)
```

```
xx <- filterMaxMarkers(xx, p = .25)

## get distances for protein sets
dd <- clustDist(xx)

## plot distances for all protein sets
plot(dd)

names(dd)

## Extract first 4 ClustDist objects of the ClustDistList
dd[1:4]

## Extract 1st ClustDist object
dd[[1]]
```

---

Deprecated *pRoloc Deprecated and Defunct*

---

### Description

The function, class, or data object you have asked for has been deprecated or made defunct.

Deprecated: minClassScore; use the replacement [getPredictions](#)

Defunct:

Deprecated functions are provided for compatibility with older versions of the pRoloc package only, and will be defunct at the next release.

---

empPvalues *Estimate empirical p-values for $Chi\hat{\ }2$ protein correlations.*

---

### Description

Andersen et al. (2003) used a fixed $Chi^2$ threshold of 0.05 to identify organelle-specific candidates. This function computes empirical p-values by permutation the markers relative intensities and computed null $Chi^2$ values.

### Usage

```
empPvalues(marker, corMatrix, n = 100, ...)
```

### Arguments

| | |
|---|---|
| marker | A numerics with markers relative intensities. |
| corMatrix | A matrix of nrow(corMatrix) protein relative intensities to be compares against the marker. |
| n | The number of iterations. |
| ... | Additional parameters to be passed to chi2. |

## Value

A `numeric` of length `nrow(corMatrix)`.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## References

Andersen, J. S., Wilkinson, C. J., Mayor, T., Mortensen, P. et al., Proteomic characterization of the human centrosome by protein correlation profiling. Nature 2003, 426, 570 - 574.

## See Also

[chi2](#) for $Chi^2$ calculation.

## Examples

```
set.seed(1)
mrk <- rnorm(6, 5, 1)
prot <- rbind(matrix(rnorm(120, 5, 1), ncol = 6),
              mrk + rnorm(6))
mrk <- mrk/sum(mrk)
prot <- prot/rowSums(prot)
empPvalues(mrk, prot)
```

---

fDataToUnknown                  *Update a feature variable*

---

## Description

This function replaces a string or regular expression in a feature variable using the [sub](#) function.

## Usage

```
fDataToUnknown(object, fcol = "markers", from = "^$", to = "unknown",
  ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class `MSnSet`. |
| fcol | Feature variable to be modified. Default is `"markers"`. If NULL, all feature variables will updated. |
| from | A `character` defining the string or regular expression of the pattern to be replaced. Default is the empty string, i.e. the regular expression `"^$"`. See [sub](#) for details. If `NA`, then `NA` values are replaced by `to`. |
| to | A replacement for matched pattern. Default is `"unknown"`. See [sub](#) for details. |
| ... | Additional arguments passed to [sub](#). |

## Value

An updated MSnSet.

## Author(s)

Laurent Gatto

## Examples

```
library("pRolocdata")
data(dunkley2006)
getMarkers(dunkley2006, "markers")
dunkley2006 <- fDataToUnknown(dunkley2006,
                             from = "unknown", to = "unassigned")
getMarkers(dunkley2006, "markers")
```

---

filterBinMSnSet *Filter a binary MSnSet*

---

## Description

Removes columns or rows that have a certain proportion or absolute number of 0 values.

## Usage

```
filterBinMSnSet(object, MARGIN = 2, t, q, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| object | An MSnSet |
| MARGIN | 1 or 2. Default is 2. |
| t | Rows/columns that have t or less 1s, it will be filtered out. When t and q are missing, default is to use t = 1. |
| q | If a row has a higher quantile than defined by q, it will be filtered out. |
| verbose | A logical defining of a message is to be printed. Default is TRUE. |

## Value

A filtered MSnSet.

## Author(s)

Laurent Gatto

## See Also

zerosInBinMSnSet, filterZeroCols, filterZeroRows.

## Examples

```
set.seed(1)
m <- matrix(sample(0:1, 25, replace=TRUE), 5)
m[1, ] <- 0
m[, 1] <- 0
rownames(m) <- colnames(m) <- letters[1:5]
fd <- data.frame(row.names = letters[1:5])
x <- MSnSet(exprs = m, fData = fd, pData = fd)
exprs(x)
## Remove columns with no 1s
exprs(filterBinMSnSet(x, MARGIN = 2, t = 0))
## Remove columns with one 1 or less
exprs(filterBinMSnSet(x, MARGIN = 2, t = 1))
## Remove columns with two 1s or less
exprs(filterBinMSnSet(x, MARGIN = 2, t = 2))
## Remove columns with three 1s
exprs(filterBinMSnSet(x, MARGIN = 2, t = 3))
## Remove columns that have half or less of 1s
exprs(filterBinMSnSet(x, MARGIN = 2, q = 0.5))
```

---

filterMaxMarkers          *Removes class/annotation information from a matrix of candidate*
                          *markers that appear in the* fData.

---

## Description

Removes annotation information that contain more that a certain number/percentage of proteins

## Usage

```
filterMaxMarkers(object, n, p = 0.2, fcol = "GOAnnotations",
  verbose = TRUE)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| n | Maximum number of proteins allowed per class/information term. |
| p | Maximum percentage of proteins per column. Default is 0.2 i.e. remove columns that have information for greater than 20 of the total number of proteins in the dataset (note: this is useful for example, if information is GO terms, for removing very general and uninformative terms). |
| fcol | The name of the matrix of marker information. Default is GOAnnotations. |
| verbose | Number of marker candidates retained after filtering. |

## Value

An updated MSnSet

## See Also

addGoAnnotations and example therein.

---

| filterMinMarkers | *Removes class/annotation information from a matrix of candidate markers that appear in the* fData. |
| --- | --- |

---

## Description

Removes annotation information that contain less that a certain number/percentage of proteins

## Usage

```
filterMinMarkers(object, n = 10, p, fcol = "GOAnnotations",
  verbose = TRUE)
```

## Arguments

| | |
| --- | --- |
| object | An instance of class MSnSet. |
| n | Minimum number of proteins allowed per column. Default is 10. |
| p | Minimum percentage of proteins per column. |
| fcol | The name of the matrix of marker information. Default is GOAnnotations. |
| verbose | Number of marker candidates retained after filtering. |

## Value

An updated MSnSet.

## Author(s)

Lisa M Breckels

## See Also

addGoAnnotations and example therein.

---

filterZeroCols                    *Remove 0 columns/rows*

---

### Description

Removes all assay data columns/rows that are composed of only 0, i.e. have a `colSum`/`rowSum` of 0.

### Usage

```
filterZeroCols(object, verbose = TRUE)

filterZeroRows(object, verbose = TRUE)
```

### Arguments

| | |
|---|---|
| object | A MSnSet object. |
| verbose | Print a message with the number of filtered out columns/row (if any). |

### Value

An `MSnSet`.

### Author(s)

Laurent Gatto

### Examples

```
library("pRolocdata")
data(andy2011goCC)
any(colSums(exprs(andy2011goCC)) == 0)
exprs(andy2011goCC)[, 1:5] <- 0
ncol(andy2011goCC)
ncol(filterZeroCols(andy2011goCC))
```

---

GenRegRes-class                   *Class* "GenRegRes" *and* "ThetaRegRes"

---

### Description

Regularisation framework containers.

### Objects from the Class

Object of this class are created with the respective regularisation function: `knnOptimisation`, `svmOptimisation`, `plsdaOptimisation`, `knntlOptimisation`, ...

**Slots**

algorithm: Object of class "character" storing the machine learning algorithm name.

hyperparameters: Object of class "list" with the respective algorithm hyper-parameters tested.

design: Object of class "numeric" describing the cross-validation design, the test data size and the number of replications.

log: Object of class "list" with warnings thrown during the hyper-parameters regularisation.

seed: Object of class "integer" with the random number generation seed.

results: Object of class "matrix" of dimenstions times (see design) by number of hyperparameters + 1 storing the macro F1 values for the respective best hyper-parameters for each replication.

f1Matrices: Object of class "list" with respective times cross-validation F1 matrices.

cmMatrices: Object of class "list" with respective times contingency matrices.

testPartitions: Object of class "list" with respective times test partitions.

datasize: Object of class "list" with details about the respective inner and outter training and testing data sizes.

Only in ThetaRegRes:

predictions: A list of predictions for the optimisation iterations.

otherWeights: Alternative best theta weigts: a vector per iterations, NULL if no other best weights were found.

**Methods**

**getF1Scores** Returns a matrix of F1 scores for the optimisation parameters.

**f1Count** signature(object = "GenRegRes", t = "numeric") and signature(object = "ThetaRegRes", t = "numeric"): Constructs a table of all possible parameter combination and count how many have an F1 scores greater or equal than t. When t is missing (default), the best F1 score is used. This method is useful in conjunctin with plot.

**getParams** Returns the *best* parameters. It is however strongly recommended to inspect the optimisation results. For a ThetaRegRes optimisation result, the method to chose the best parameters can be "median" (default) or "mean" (the median or mean of the best weights is chosen), "max" (the first weights with the highest macro-F1 score, considering that multiple max scoring combinations are possible) or "count" (the observed weight that get the maximum number of observations, see f1Count). The favourP argument can be used to prioritise weights that favour the primary data (i.e. heigh weights). See favourPrimary below.

**getSeed** Returns the seed used for the optimisation run.

**getWarnings** signature(object = "GenRegRes"): Returns a vector of recorded warnings.

**levelPlot** signature(object = "GenRegRes"): Plots a heatmap of of the optimisation results. Only for "GenRegRes" instances.

**plot** Plots the optisisation results.

**show** Shows the object.

**Other functions**

Only for `ThetaRegRes`:

`combineThetaRegRes(object)` Takes a `list` of `ThetaRegRes` instances to be combined and returnes a new `ThetaRegRes` instance.

`favourPrimary(primary, auxiliary, object, verbose = TRUE)` Takes the `primary` and `auxiliary` data sources (two `MSnSet` instances) and a `ThetaRegRes` object and returns and updated `ThetaRegRes` instance containing best parameters/weigths (see the `getParams` function) favouring the primary data when multiple best theta weights are available.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**Examples**

```
showClass("GenRegRes")
showClass("ThetaRegRes")
```

---

getGOFromFeatures           *Retrieve GO terms for feature names*

---

**Description**

The function pulls the gene ontology (GO) terms for a set of feature names.

**Usage**

```
getGOFromFeatures(id, namespace = "cellular_component",
  evidence = NULL, params = NULL, verbose = FALSE, nmax = 500)
```

**Arguments**

| | |
|---|---|
| id | An character with feature names to be pulled from biomart. If and MSnSet is provided, then featureNames(id) is used. |
| namespace | The GO namespace. One of biological_process, cellular_component (default) or molecular_function. |
| evidence | The GO evidence code. See showGOEvidenceCodes for details. If NULL (default), no filtering based on the evidence code is performed. |
| params | An instance of class "AnnotationParams". |
| verbose | A logical defining verbosity of the function. Default is FALSE. |
| nmax | As described in https://support.bioconductor.org/p/86358/, the Biomart result can be unreliable for large queries. This argument splits the input in chunks of length nmax (default is 500). If set to NULL, the query is performed in full. |

## Value

A data.frame with relevant GO terms.

## Author(s)

Laurent Gatto

## Examples

```
library(pRolocdata)
data(dunkley2006)
data(dunkley2006params)
dunkley2006params
fn <- featureNames(dunkley2006)[1:5]
getGOFromFeatures(fn, params = dunkley2006params)
```

---

getMarkerClasses          *Returns the organelle classes in an 'MSnSet'*

---

## Description

Convenience accessor to the organelle classes in an 'MSnSet'. This function returns the organelle classes of an MSnSet instance. As a side effect, it prints out the classes.

## Usage

```
getMarkerClasses(object, fcol = "markers", ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class ["MSnSet"](). |
| fcol | The name of the markers column in the featureData slot. Default is markers. |
| ... | Additional parameters passed to sort from the base package. |

## Value

A character vector of the organelle classes in the data.

## Author(s)

Lisa Breckels and Laurent Gatto

## See Also

[getMarkers]() to extract the marker proteins. See [markers]() for details about spatial markers storage and encoding.

## Examples

```
library("pRolocdata")
data(dunkley2006)
organelles <- getMarkerClasses(dunkley2006)
## same if markers encoded as a matrix
dunkley2006 <- mrkVecToMat(dunkley2006, mfcol = "Markers")
organelles2 <- getMarkerClasses(dunkley2006, fcol = "Markers")
stopifnot(all.equal(organelles, organelles2))
```

---

getMarkers *Get the organelle markers in an* MSnSet

---

## Description

Convenience accessor to the organelle markers in an MSnSet. This function returns the organelle markers of an MSnSet instance. As a side effect, it print out a marker table.

## Usage

```
getMarkers(object, fcol = "markers", names = TRUE, verbose = TRUE)
```

## Arguments

| object | An instance of class "MSnSet". |
|---|---|
| fcol | The name of the markers column in the featureData slot. Default is "markers". |
| names | A logical indicating if the markers vector should be named. Ignored if markers are encoded as a matrix. |
| verbose | If TRUE, a marker table is printed and the markers are returned invisibly. If FALSE, the markers are returned. |

## Value

A character (matrix) of length (ncol) ncol(object), depending on the vector or matrix encoding of the markers.

## Author(s)

Laurent Gatto

## See Also

See getMarkerClasses to get the classes only. See markers for details about spatial markers storage and encoding.

## Examples

```
library("pRolocdata")
data(dunkley2006)
## marker vectors
myVmarkers <- getMarkers(dunkley2006)
head(myVmarkers)
## marker matrix
dunkley2006 <- mrkVecToMat(dunkley2006, mfcol = "Markers")
myMmarkers <- getMarkers(dunkley2006, fcol = "Markers")
head(myMmarkers)
```

---

getNormDist                  *Extract Distances from a* "ClustDistList" *object*

---

## Description

This function computes and outputs normalised distances from a "[ClustDistList](#)" object.

## Usage

```
getNormDist(object, p = 1/3)
```

## Arguments

object          An instance of class "[ClustDistList](#)".

p               The normalisation factor. Default is 1/3.

## Value

An numeric of normalised distances, one per protein set in the ClustDistList.

## Author(s)

Lisa Breckels

## See Also

"[ClustDistList](#)", "[ClustDist](#)", and examples in clustDist.

---

getPredictions          *Returns the predictions in an 'MSnSet'*

---

## Description

Convenience accessor to the predicted feature localisation in an 'MSnSet'. This function returns the predictions of an MSnSet instance. As a side effect, it prints out a prediction table.

## Usage

```
getPredictions(object, fcol, scol, mcol = "markers", t = 0,
  verbose = TRUE)
```

## Arguments

| | |
|---|---|
| object | An instance of class "MSnSet". |
| fcol | The name of the prediction column in the featureData slot. |
| scol | The name of the prediction score column in the featureData slot. If missing, created by pasting '.scores' after fcol. |
| mcol | The feature meta data column containing the labelled training data. |
| t | The score threshold. Predictions with score < t are set to 'unknown'. Default is 0. It is also possible to define thresholds for each prediction class, in which case, t is a named numeric with names exactly matching the unique prediction class names. |
| verbose | If TRUE, a prediction table is printed and the predictions are returned invisibly. If FALSE, the predictions are returned. |

## Value

An instance of class "MSnSet" with fcol.pred feature variable storing the prediction results according to the chosen threshold.

## Author(s)

Laurent Gatto and Lisa Breckels

## See Also

orgQuants for calculating organelle-specific thresholds.

## Examples

```
library("pRolocdata")
data(dunkley2006)
res <- svmClassification(dunkley2006, fcol = "pd.markers",
                         sigma = 0.1, cost = 0.5)
fData(res)$svm[500:510]
fData(res)$svm.scores[500:510]
getPredictions(res, fcol = "svm", t = 0) ## all predictions
getPredictions(res, fcol = "svm", t = .9) ## single threshold
## 50% top predictions per class
ts <- orgQuants(res, fcol = "svm", t = .5)
getPredictions(res, fcol = "svm", t = ts)
```

---

goIdToTerm                    *Convert GO ids to/from terms*

---

## Description

Converts GO identifiers to/from GO terms, either explicitly or by checking if (any items in) the input contains "GO:".

## Usage

```
goIdToTerm(x, names = TRUE, keepNA = TRUE)

goTermToId(x, names = TRUE, keepNA = TRUE)

flipGoTermId(x, names = TRUE, keepNA = TRUE)

prettyGoTermId(x)
```

## Arguments

| | |
|---|---|
| x | A character of GO ids or terms. |
| names | Should a named character be returned? Default is TRUE. |
| keepNA | Should any GO term/id names that are missing or obsolete be replaced with a NA? Default is TRUE. If FALSE then the GO term/id names is kept. |

## Value

A character of GO terms (ids) if x were ids (terms).

## Author(s)

Laurent Gatto

## Examples

```
goIdToTerm("GO:0000001")
goIdToTerm("GO:0000001", names = FALSE)
goIdToTerm(c("GO:0000001", "novalid"))
goIdToTerm(c("GO:0000001", "GO:0000002", "notvalid"))
goTermToId("mitochondrion inheritance")
goTermToId("mitochondrion inheritance", name = FALSE)
goTermToId(c("mitochondrion inheritance", "notvalid"))
prettyGoTermId("mitochondrion inheritance")
prettyGoTermId("GO:0000001")
flipGoTermId("mitochondrion inheritance")
flipGoTermId("GO:0000001")
flipGoTermId("GO:0000001", names = FALSE)
```

---

highlightOnPlot                  *Highlight features of interest on a spatial proteomics plot*

---

### Description

Highlights a set of features of interest given as a FeaturesOfInterest instance on a PCA plot
produced by codeplot2D or plot3D. If none of the features of interest are found in the MSnset's
featureNames, an warning is thrown.

### Usage

```
highlightOnPlot(object, foi, labels, args = list(), ...)

highlightOnPlot3D(object, foi, labels, args = list(), radius = 0.1 * 3,
  ...)
```

### Arguments

| | |
|---|---|
| object | The main dataset described as an MSnSet or a matrix with the coordinates of the features on the PCA plot produced (and invisibly returned) by plot2D. |
| foi | An instance of [FeaturesOfInterest](), or, alternatively, a character of feautre names. |
| labels | A character of length 1 with a feature variable name to be used to label the features of interest. This is only valid if object is an MSnSet. Alternatively, if TRUE, then featureNames(object) (or coderownames(object), if object is a matrix) are used. Default is missing, which does not add any label.s |
| args | A named list of arguments to be passed to plot2D if the PCA coordinates are to be calculated. Ignored if the PCA coordinates are passed directly, i.e. object is a matrix. |
| ... | Additional parameters passed to points or text (when labels is TRUE) when adding to plot2D, or spheres3d or text3d when adding the plot3D |
| radius | Radius of the spheres to be added to the visualisation produced by plot3D. Default is 0.3 (i.e plot3D's radius1 * 3), to emphasise the features with regard to uknown (radius1 = 0.1) and marker (radius1 * 2) features. |

**Value**

NULL; used for its side effects.

**Author(s)**

Laurent Gatto

**Examples**

```
library("pRolocdata")
data("tan2009r1")
x <- FeaturesOfInterest(description = "A test set of features of interest",
                        fnames = featureNames(tan2009r1)[1:10],
                        object = tan2009r1)

## using FeaturesOfInterest or feature names
par(mfrow = c(2, 1))
plot2D(tan2009r1)
highlightOnPlot(tan2009r1, x)
plot2D(tan2009r1)
highlightOnPlot(tan2009r1, featureNames(tan2009r1)[1:10])

.pca <- plot2D(tan2009r1)
head(.pca)
highlightOnPlot(.pca, x, col = "red")
highlightOnPlot(tan2009r1, x, col = "red", cex = 1.5)
highlightOnPlot(tan2009r1, x, labels = TRUE)

.pca <- plot2D(tan2009r1, dims = c(1, 3))
highlightOnPlot(.pca, x, pch = "+", dims = c(1, 3))
highlightOnPlot(tan2009r1, x, args = list(dims = c(1, 3)))

.pca2 <- plot2D(tan2009r1, mirrorX = TRUE, dims = c(1, 3))
## previous pca matrix, need to mirror X axis
highlightOnPlot(.pca, x, pch = "+", args = list(mirrorX = TRUE))
## new pca matrix, with X mirrors (and 1st and 3rd PCs)
highlightOnPlot(.pca2, x, col = "red")

plot2D(tan2009r1)
highlightOnPlot(tan2009r1, x)
highlightOnPlot(tan2009r1, x, labels = TRUE, pos = 3)
highlightOnPlot(tan2009r1, x, labels = "Flybase.Symbol", pos = 1)

## in 3 dimensions
if (interactive()) {
  plot3D(tan2009r1, radius1 = 0.05)
  highlightOnPlot3D(tan2009r1, x, labels = TRUE)
  highlightOnPlot3D(tan2009r1, x)
}
```

---

knnClassification    *knn classification*

---

### Description

Classification using for the k-nearest neighbours algorithm.

### Usage

```
knnClassification(object, assessRes, scores = c("prediction", "all",
  "none"), k, fcol = "markers", ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class "MSnSet". |
| assessRes | An instance of class "GenRegRes", as generated by knnOptimisation. |
| scores | One of "prediction", "all" or "none" to report the score for the predicted class only, for all classes or none. |
| k | If assessRes is missing, a k must be provided. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| ... | Additional parameters passed to knn from package class. |

### Value

An instance of class "MSnSet" with knn and knn.scores feature variables storing the classification results and scores respectively.

### Author(s)

Laurent Gatto

### Examples

```
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space and iterations
params <- knnOptimisation(dunkley2006, k = c(3, 10), times = 3)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- knnClassification(dunkley2006, params)
getPredictions(res, fcol = "knn")
getPredictions(res, fcol = "knn", t = 0.75)
plot2D(res, fcol = "knn")
```

knnOptimisation              *knn parameter optimisation*

### Description

Classification parameter optimisation for the k-nearest neighbours algorithm.

### Usage

```
knnOptimisation(object, fcol = "markers", k = seq(3, 15, 2),
    times = 100, test.size = 0.2, xval = 5, fun = mean, seed,
    verbose = TRUE, ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| k | The hyper-parameter. Default values are seq(3, 15, 2). |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the xval macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A `logical` defining whether a progress bar is displayed. |
| ... | Additional parameters passed to [knn](#) from package class. |

### Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values are replaced by 0. This decision is motivated by the fact that any class that would have either a NA precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)). Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

### Value

An instance of class `"GenRegRes"`.

### Author(s)

Laurent Gatto

### See Also

[knnClassification](#) and example therein.

---

knntlClassification          *knn transfer learning classification*

---

### Description

Classification using a variation of the KNN implementation of Wu and Dietterich's transfer learning schema

### Usage

```
knntlClassification(primary, auxiliary, fcol = "markers", bestTheta, k,
  scores = c("prediction", "all", "none"), seed)
```

### Arguments

| | |
|---|---|
| primary | An instance of class ["MSnSet"](). |
| auxiliary | An instance of class ["MSnSet"](). |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| bestTheta | Best theta vector as output from knntlOptimisation, see knntlOptimisation for details |
| k | Numeric vector of length 2, containing the best k parameters to use for the primary and auxiliary datasets. If k k is not specified it will be calculated internally. |
| scores | One of "prediction", "all" or "none" to report the score for the predicted class only, for all classes or none. |
| seed | The optional random number generator seed. |

### Value

A character vector of the classifications for the unknowns

### Author(s)

Lisa Breckels

### See Also

[knntlOptimisation]()

### Examples

```
library(pRolocdata)
data(andy2011)
data(andy2011goCC)
## reducing calculation time of k by pre-running knnOptimisation
x <- c(andy2011, andy2011goCC)
k <- lapply(x, function(z)
```

```
            knnOptimisation(z, times=5,
                            fcol = "markers.orig",
                            verbose = FALSE))
k <- sapply(k, function(z) getParams(z))
k
## reducing parameter search with theta = 1,
## weights of only 1 or 0 will be considered
opt <- knntlOptimisation(andy2011, andy2011goCC,
                         fcol = "markers.orig",
                         times = 2,
                         by = 1, k = k)
opt
th <- getParams(opt)
plot(opt)
res <- knntlClassification(andy2011, andy2011goCC,
                           fcol = "markers.orig", th, k)
res
```

---

knntlOptimisation *theta parameter optimisation*

---

#### Description

Classification parameter optimisation for the KNN implementation of Wu and Dietterich's transfer learning schema

#### Usage

```
knntlOptimisation(primary, auxiliary, fcol = "markers", k, times = 50,
  test.size = 0.2, xval = 5, by = 0.5, length.out, th, xfolds,
  BPPARAM = BiocParallel::bpparam(), method = "Breckels",
  log = FALSE, seed)
```

#### Arguments

| | |
|---|---|
| primary | An instance of class "MSnSet". |
| auxiliary | An instance of class "MSnSet". |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| k | Numeric vector of length 2, containing the best k parameters to use for the primary (k[1]) and auxiliary (k[2]) datasets. See knnOptimisation for generating best k. |
| times | The number of times cross-validation is performed. Default is 50. |
| test.size | The size of test (validation) data. Default is 0.2 (20 percent). |
| xval | The number of rounds of cross-validation to perform. |
| by | The increment for theta, must be one of c(1, 0.5, 0.25, 0.2, 0.15, 0.1, 0.05) |

length.out        Alternative to using by parameter. Specifies the desired length of the sequence
                  of theta to test.

th                A matrix of theta values to test for each class as generated from the function
                  [thetas](), the number of columns should be equal to the number of classes con-
                  tained in fcol. Note: columns will be ordered according to getMarkerClasses(primary,
                  fcol). This argument is only valid if the default method 'Breckels' is used.

xfolds            Option to pass specific folds for the cross validation.

BPPARAM           Required for parallelisation. If not specified selects a default BiocParallelParam,
                  from global options or, if that fails, the most recently registered() back-end.

method            The k-NN transfer learning method to use. The default is 'Breckels' as described
                  in the Breckels et al (2016). If 'Wu' is specificed then the original method
                  implemented Wu and Dietterich (2004) is implemented.

log               A logical defining whether logging should be enabled. Default is FALSE. Note
                  that logging produes considerably bigger objects.

seed              The optional random number generator seed.

## Details

knntlOptimisation implements a variation of Wu and Dietterich's transfer learning schema: P.
Wu and T. G. Dietterich. Improving SVM accuracy by training on auxiliary data sources. In Pro-
ceedings of the Twenty-First International Conference on Machine Learning, pages 871 - 878. Mor-
gan Kaufmann, 2004. A grid search for the best theta is performed.

## Value

A list of containing the theta combinations tested, associated macro F1 score and accuracy for each
combination over each round (specified by times).

## Author(s)

Lisa Breckels

## References

Breckels LM, Holden S, Wonjar D, Mulvey CM, Christoforou A, Groen AJ, Kohlbacher O, Lil-
ley KS, Gatto L. Learning from heterogeneous data sources: an application in spatial proteomics.
bioRxiv. doi: http://dx.doi.org/10.1101/022152

Wu P, Dietterich TG. Improving SVM Accuracy by Training on Auxiliary Data Sources. Proceed-
ings of the 21st International Conference on Machine Learning (ICML); 2004.

## See Also

[knntlClassification]() and example therein.

---

ksvmClassification *ksvm classification*

---

### Description

Classification using the support vector machine algorithm.

### Usage

```
ksvmClassification(object, assessRes, scores = c("prediction", "all",
    "none"), cost, fcol = "markers", ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| assessRes | An instance of class `"GenRegRes"`, as generated by `ksvmOptimisation`. |
| scores | One of `"prediction"`, `"all"` or `"none"` to report the score for the predicted class only, for all classes or none. |
| cost | If `assessRes` is missing, a `cost` must be provided. |
| fcol | The feature meta-data containing marker definitions. Default is `markers`. |
| ... | Additional parameters passed to `ksvm` from package `kernlab`. |

### Value

An instance of class `"MSnSet"` with ksvm and ksvm.scores feature variables storing the classification results and scores respectively.

### Author(s)

Laurent Gatto

### Examples

```
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space and iterations
params <- ksvmOptimisation(dunkley2006, cost = 2^seq(-1,4,5), times = 3)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- ksvmClassification(dunkley2006, params)
getPredictions(res, fcol = "ksvm")
getPredictions(res, fcol = "ksvm", t = 0.75)
plot2D(res, fcol = "ksvm")
```

---

ksvmOptimisation | *ksvm parameter optimisation*

---

### Description

Classification parameter optimisation for the support vector machine algorithm.

### Usage

```
ksvmOptimisation(object, fcol = "markers", cost = 2^(-4:4),
  times = 100, test.size = 0.2, xval = 5, fun = mean, seed,
  verbose = TRUE, ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| cost | The hyper-parameter. Default values are 2^-4:4. |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the xval macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A `logical` defining whether a progress bar is displayed. |
| ... | Additional parameters passed to `ksvm` from package kernlab. |

### Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values are replaced by 0. This decision is motivated by the fact that any class that would have either a NA precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)). Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

### Value

An instance of class `"GenRegRes"`.

### Author(s)

Laurent Gatto

### See Also

`ksvmClassification` and example therein.

---

makeGoSet                    *Creates a GO feature* MSnSet

---

### Description

Creates a new "MSnSet" instance populated with a GO term binary matrix based on an original object.

### Usage

```
makeGoSet(object, params, namespace = "cellular_component",
  evidence = NULL)
```

### Arguments

| | |
|---|---|
| object | An instance of class "MSnSet" or a character of feature names. |
| params | An instance of class "AnnotationParams", compatible with featureNames(object)'s format. |
| namespace | The ontology name space. One or several of "biological_process", "cellular_component" or "molecular_function". |
| evidence | GO evidence filtering. |

### Value

A new "MSnSet" with the GO terms for the respective features in the original object.

### Author(s)

Laurent Gatto

### Examples

```
library("pRolocdata")
data(dunkley2006)
data(dunkley2006params)
goset <- makeGoSet(dunkley2006[1:10, ],
                   dunkley2006params)
goset
exprs(goset)[1:10, 1:5]
image(goset)
```

---

MAPParams-class                    *The 'logPosteriors' function can be used to extract the log-posteriors*
                                   *at each iteration of the EM algorithm to check for convergence.*

---

### Description

These functions implement the T augmented Gaussian mixture (TAGM) model for mass spectrometry-based spatial proteomics datasets using the maximum a posteriori (MAP) optimisation routine.

### Usage

```
## S4 method for signature 'MAPParams'
show(object)

logPosteriors(x)

tagmMapTrain(object, fcol = "markers", method = "MAP", numIter = 100,
  mu0 = NULL, lambda0 = 0.01, nu0 = NULL, S0 = NULL,
  beta0 = NULL, u = 2, v = 10, seed = NULL)

tagmMapPredict(object, params, fcol = "markers", probJoint = FALSE,
  probOutlier = TRUE)
```

### Arguments

| | |
|---|---|
| object | An [MSnbase::MSnSet](#) containing the spatial proteomics data to be passed to tagmMapTrain and tagmPredict. |
| x | An object of class 'MAPParams'. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| method | A charachter() describing the inference method for the TAGM algorithm. Default is "MAP". |
| numIter | The number of iterations of the expectation-maximisation algorithm. Default is 100. |
| mu0 | The prior mean. Default is colMeans of the expression data. |
| lambda0 | The prior shrinkage. Default is 0.01. |
| nu0 | The prior degreed of freedom. Default is ncol(exprs(object)) + 2 |
| S0 | The prior inverse-wishary scale matrix. Empirical prior used by default. |
| beta0 | The prior Dirichlet distribution concentration. Default is 1 for each class. |
| u | The prior shape parameter for Beta(u, v). Default is 2 |
| v | The prior shape parameter for Beta(u, v). Default is 10. |
| seed | The optional random number generator seed. |
| params | An instance of class [MAPParams](#), as generated by [tagmMapTrain()](#). |

probJoint        A `logical(1)` indicating whether to return the joint probability matrix, i.e. the probability for all classes as a new `tagm.map.joint` feature variable.

probOutlier      A `logical(1)` indicating whether to return the probability of being an outlier as a new `tagm.map.outlier` feature variable. A high value indicates that the protein is unlikely to belong to any annotated class (and is hence considered an outlier).

### Details

The `tagmMapTrain` function generates the MAP parameters (object or class `MAPParams`) based on an annotated quantitative spatial proteomics dataset (object of class `MSnbase::MSnSet`). Both are then passed to the `tagmPredict` function to predict the sub-cellular localisation of protein of unknown localisation. See the *pRoloc-bayesian* vignette for details and examples. In this implementation, if numerical instability is detected in the covariance matrix of the data a small multiple of the identity is added. A message is printed if this conditioning step is performed.

### Value

`tagmMapTrain` returns an instance of class `MAPParams()`.

`tagmPredict` returns an instance of class `MSnbase::MSnSet` containing the localisation predictions as a new `tagm.map.allocation` feature variable.

### Slots

method A `character()` storing the TAGM method name.

priors A `list()` with the priors for the parameters

seed An `integer()` with the random number generation seed.

posteriors A `list()` with the updated posterior parameters and log-posterior of the model.

datasize A `list()` with details about size of data

### Author(s)

Laurent Gatto

Oliver M. Crook

### References

*A Bayesian Mixture Modelling Approach For Spatial Proteomics* Oliver M Crook, Claire M Mulvey, Paul D. W. Kirk, Kathryn S Lilley, Laurent Gatto bioRxiv 282269; doi: https://doi.org/10.1101/282269

### See Also

The `plotEllipse()` function can be used to visualise TAGM models on PCA plots with ellipses. The `tagmMapTrain()` function to use the TAGM MAP method.

---

**markerMSnSet**                              *Extract marker/unknown subsets*

---

### Description

These function extract the marker or unknown proteins into a new `MSnSet`.

### Usage

```
markerMSnSet(object, fcol = "markers")

unknownMSnSet(object, fcol = "markers")
```

### Arguments

| | |
|---|---|
| `object` | An instance of class `MSnSet` |
| `fcol` | The name of the feature data column, that will be used to separate the markers from the proteins of unknown localisation. When the markers are encoded as vectors, features of unknown localisation are defined as `fData(object)[, fcol] == "unknown"`. For matrix-encoded markers, unlabelled proteins are defined as `rowSums(fData(object)[, fcol]) == 0`. Default is `"markers"`. |

### Value

An new `MSnSet` with marker/unknown proteins only.

### Author(s)

Laurent Gatto

### See Also

[sampleMSnSet](#) [testMSnSet](#) and [markers](#) for markers encoding.

### Examples

```
library("pRolocdata")
data(dunkley2006)
mrk <- markerMSnSet(dunkley2006)
unk <- unknownMSnSet(dunkley2006)
dim(dunkley2006)
dim(mrk)
dim(unk)
table(fData(dunkley2006)$markers)
table(fData(mrk)$markers)
table(fData(unk)$markers)
## matrix-encoded markers
dunkley2006 <- mrkVecToMat(dunkley2006)
dim(markerMSnSet(dunkley2006, "Markers"))
```

```
stopifnot(all.equal(featureNames(markerMSnSet(dunkley2006, "Markers")),
                     featureNames(markerMSnSet(dunkley2006, "markers"))))
dim(unknownMSnSet(dunkley2006, "Markers"))
stopifnot(all.equal(featureNames(unknownMSnSet(dunkley2006, "Markers")),
                     featureNames(unknownMSnSet(dunkley2006, "markers"))))
```

---

MartInstance-class      *Class* "MartInstance"

---

### Description

Internal infrastructure to query/handle several individual mart instance. See `MartInterface.R` for details.

### Author(s)

Laurent Gatto <lg390@cam.ac.uk>

---

MCMCChains-class      *Instrastructure to store and process MCMC results*

---

### Description

The `MCMCParams` infrastructure is used to store and process Marchov chain Monte Carlo results for the T-Augmented Gaussian Mixture model (TAGM) from Crook et al. (2018).

### Usage

```
chains(object)

## S4 method for signature 'MCMCParams'
show(object)

## S4 method for signature 'ComponentParam'
show(object)

## S4 method for signature 'MCMCChain'
show(object)

## S4 method for signature 'MCMCChains'
length(x)

## S4 method for signature 'MCMCParams'
length(x)

## S4 method for signature 'MCMCChains,ANY,ANY'
```

```
x[[i, j = "missing",
  drop = "missing"]]

## S4 method for signature 'MCMCParams,ANY,ANY'
x[[i, j = "missing",
  drop = "missing"]]

## S4 method for signature 'MCMCChains,ANY,ANY,ANY'
x[i, j = "missing",
  drop = "missing"]

## S4 method for signature 'MCMCParams,ANY,ANY,ANY'
x[i, j = "missing",
  drop = "missing"]

## S4 method for signature 'MCMCChains'
show(object)
```

## Arguments

| | |
|---|---|
| object | An instance of appropriate class. |
| x | Object to be subset. |
| i | An integer(). Should be of length 1 for [[. |
| j | Missing. |
| drop | Missing. |

## Details

Objects of the MCMCParams class are created with the tagmMcmcTrain() function. These objects store the *priors* of the generative TAGM model and the results of the MCMC chains, which themselves are stored as an instance of class MCMCChains and can be accessed with the chains() function. A summary of the MCMC chains (or class MCMCSummary) can be further computed with the tagmMcmcProcess() function.

See the *pRoloc-bayesian* vignette for examples.

## Slots

chains list() containing the individual full MCMC chain results in an MCMCChains instance. Each element must be a valid MCMCChain instance.

posteriorEstimates A data.frame documenting the prosterior priors in an MCMCSummary instance. It contains N rows and columns tagm.allocation, tagm.probability, tagm.outlier, tagm.probability.lowerquantile, tagm.probability.upperquantile and tagm.mean.shannon.

diagnostics A matrix of dimensions 1 by 2 containing the MCMCSummary diagnostics.

tagm.joint A matrix of dimensions N by K storing the joint probability in an MCMCSummary instance.

method character(1) describing the method in the MCMCParams object.

chains Object of class `MCMCChains` containing the full MCMC chain results stored in the `MCMCParams` object.

priors `list()`

summary Object of class `MCMCSummary` the summarised MCMC results available in the `MCMCParams` instance.

n `integer(1)` indicating the number of MCMC interactions. Stored in an `MCMCChain` instance.

K `integer(1)` indicating the number of components. Stored in an `MCMCChain` instance.

N `integer(1)` indicating the number of proteins. Stored in an `MCMCChain` instance.

Component `matrix(N, n)` component allocation results of an `MCMCChain` instance.

ComponentProb `matrix(N, n, K)` component allocation probabilities of an `MCMCChain` instance.

Outlier `matrix(N, n)` outlier allocation results.

OutlierProb `matrix(N, n, 2)` outlier allocation probabilities of an `MCMCChain` instance.

## See Also

The function `tagmMcmcTrain()` to construct object of this class.

---

mcmc_get_outliers *Number of outlier at each iteration of MCMC*

---

## Description

Helper function to get the number of outlier at each MCMC iteration.

Helper function to get mean component allocation at each MCMC iteration.

Helper function to get mean probability of belonging to outlier at each iteration.

Wrapper for the geweke diagnostics from coda package also return p-values.

Helper function to pool chains together after processing

Helper function to burn n iterations from the front of the chains

Helper function to subsample the chains, known informally as thinning.

Produces a violin plot with the protein posterior probabilities distributions for all organelles.

## Usage

```
mcmc_get_outliers(x)

mcmc_get_meanComponent(x)

mcmc_get_meanoutliersProb(x)

geweke_test(k)

mcmc_pool_chains(param)
```

```
mcmc_burn_chains(x, n = 50)

mcmc_thin_chains(x, freq = 5)

## S4 method for signature 'MCMCParams,character'
plot(x, y, ...)
```

## Arguments

| | |
|---|---|
| x | Object of class `MCMCParams` |
| k | A `list` of [coda::mcmc](#) objects, as returned by `mcmc_get_outliers`, `mcmc_get_meanComponent` and `mcmc_get_meanoutliersProb`. |
| param | An object of class `MCMCParams`. |
| n | `integer(1)` defining number of iterations to burn. The default is 50 |
| freq | Thinning frequency. The function retains every 'freq'th iteration and is an 'integer(1)'. The default thinning frequency is '5'. |
| y | A 'character(1)' with a protein name. |
| ... | Currently ignored. |

## Value

A `list` of length `length(x)`.

A `list` of length `length(x)`.

A `list` of length `length(x)`.

A `matrix` with the test z- and p-values for each chain.

A pooled `MCMCParams` object.

An updated `MCMCParams` object.

A thinned 'MCMCParams' object.

A ggplot2 object.

## Author(s)

Laurent Gatto

---

minMarkers                    *Creates a reduced marker variable*

---

## Description

This function updates an `MSnSet` instances and sets markers class to unknown if there are less than n instances.

## Usage

```
minMarkers(object, n = 10, fcol = "markers")
```

## Arguments

| | |
|---|---|
| object | An instance of class ["MSnSet"](). |
| n | Minumum of marker instances per class. |
| fcol | The name of the markers column in the featureData slot. Default is markers. |

## Value

An instance of class ["MSnSet"]() with a new feature variables, named after the original fcol variable and the n value.

## Author(s)

Laurent Gatto

## See Also

[getPredictions]() to filter based on classification scores.

## Examples

```
library(pRolocdata)
data(dunkley2006)
d2 <- minMarkers(dunkley2006, 20)
getMarkers(dunkley2006)
getMarkers(d2, fcol = "markers20")
```

---

mixing_posterior_check

*Model calibration plots*

---

## Description

Model calibration model with posterior z-scores and posterior shrinkage

## Usage

```
mixing_posterior_check(object, params, priors, fcol = "markers")
```

## Arguments

| | |
|---|---|
| object | A valid object of class MSnset |
| params | A valid object of class MCMCParams that has been processed and checked for convergence |
| priors | The prior that were used in the model |
| fcol | The columns of the feature data which contain the marker data. |

## Value

Used for side effect of producing plot. Invisibily returns an ggplot object that can be further manipulated

## Author(s)

Oliver M. Crook <omc25@cam.ac.uk>

## Examples

```
## Not run:
library("pRoloc")
data("tan2009r1")

tanres <- tagmMcmcTrain(object = tan2009r1)
tanres <- tagmMcmcProcess(tanres)
tan2009r1 <- tagmMcmcPredict(object = tan2009r1, params = tanres, probJoint = TRUE)
myparams <- chains(e14Tagm_converged_pooled)[[1]]
myparams2 <- chains(mcmc_pool_chains(tanres))[[1]]
priors <- tanres@priors
pRoloc:::mixing_posterior_check(object = tan2009r1, params = myparams2, priors = priors)

## End(Not run)
```

---

MLearn-methods          *The* MLearn *interface for machine learning*

---

## Description

This method implements MLInterfaces' MLean method for instances of the class *"MSnSet"*.

## Methods

signature(formula = "formula", data = "MSnSet", .method = "learnerSchema", trainInd = "numeric")
   The learning problem is stated with the formula and applies the .method schema on the MSnSet data input using the trainInd numeric indices as train data.

signature(formula = "formula", data = "MSnSet", .method = "learnerSchema", trainInd = "xvalSpec")
   In this case, an instance of xvalSpec is used for cross-validation.

signature(formula = "formula", data = "MSnSet", .method = "clusteringSchema", trainInd = "missing")
   Hierarchical (hclustI), k-means (kmeansI) and partitioning around medoids (pamI) clustering algorithms using MLInterface's MLearn interface.

## See Also

The MLInterfaces package documentation, in particular MLearn.

## move2Ds
*Displays a spatial proteomics animation*

### Description

Given two MSnSet instances of one MSnSetList with at least two items, this function produces an animation that shows the transition from the first data to the second.

### Usage

```
move2Ds(object, pcol, fcol = "markers", n = 25, hl)
```

### Arguments

| | |
|---|---|
| object | An linkS4class{MSnSet} or a MSnSetList. In the latter case, only the two first elements of the list will be used for plotting and the others will be silently ignored. |
| pcol | If object is an MSnSet, a factor or the name of a phenotype variable (phenoData slot) defining how to split the single MSnSet into two or more data sets. Ignored if object is a MSnSetList. |
| fcol | Feature meta-data label (fData column name) defining the groups to be differentiated using different colours. Default is markers. Use NULL to suppress any colouring. |
| n | Number of frames, Default is 25. |
| hl | An optional instance of class linkS4class{FeaturesOfInterest} to track features of interest. |

### Value

Used for its side effect of producing a short animation.

### Author(s)

Laurent Gatto

### See Also

[plot2Ds](#) to a single figure with the two datasets.

### Examples

```
library("pRolocdata")
data(dunkley2006)

## Create a relevant MSnSetList using the dunkley2006 data
xx <- split(dunkley2006, "replicate")
xx1 <- xx[[1]]
```

```
xx2 <- xx[[2]]
fData(xx1)$markers[374] <- "Golgi"
fData(xx2)$markers[412] <- "unknown"
xx@x[[1]] <- xx1
xx@x[[2]] <- xx2

## The features we want to track
foi <- FeaturesOfInterest(description = "test",
                          fnames = featureNames(xx[[1]])[c(374, 412)])

## (1) visualise each experiment separately
par(mfrow = c(2, 1))
plot2D(xx[[1]], main = "condition A")
highlightOnPlot(xx[[1]], foi)
plot2D(xx[[2]], mirrorY = TRUE, main = "condition B")
highlightOnPlot(xx[[2]], foi, args = list(mirrorY = TRUE))

## (2) plot both data on the same plot
par(mfrow = c(1, 1))
tmp <- plot2Ds(xx)
highlightOnPlot(data1(tmp), foi, lwd = 2)
highlightOnPlot(data2(tmp), foi, pch = 5, lwd = 2)

## (3) create an animation
move2Ds(xx, pcol = "replicate")
move2Ds(xx, pcol = "replicate", hl = foi)
```

---

mrkConsProfiles            *Marker consensus profiles*

---

### Description

A function to calculate average marker profiles.

### Usage

```
mrkConsProfiles(object, fcol = "markers", method = mean)
```

### Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| fcol | Feature meta-data label (fData column name) defining the groups to be differentiated using different colours. Default is markers. |
| method | A function to average marker profiles. Default is mean. |

### Value

A matrix of dimensions *number of clusters* (exluding unknowns) by *number of fractions*.

## Author(s)

Laurent Gatto and Lisa M. Breckels

## See Also

The [mrkHClust](mrkHClust) function to produce a hierarchical cluster.

## Examples

```
library("pRolocdata")
data(dunkley2006)
mrkConsProfiles(dunkley2006)
mrkConsProfiles(dunkley2006, method = median)
mm <- mrkConsProfiles(dunkley2006)
## Reorder fractions
o <- order(dunkley2006$fraction)
## Plot mean organelle profiles using the
## default pRoloc colour palette.
matplot(t(mm[, o]), type = "l",
        xlab = "Fractions", ylab = "Relative intensity",
        main = "Mean organelle profiles",
        col = getStockcol(), lwd = 2, lty = 1)
## Add a legend
addLegend(markerMSnSet(dunkley2006), where = "topleft")
```

---

mrkHClust                     *Draw a dendrogram of subcellular clusters*

---

## Description

This functions calculates an average protein profile for each marker class (proteins of unknown localisation are ignored) and then generates a dendrogram representing the relation between marker classes. The colours used for the dendrogram labels are taken from the default colours (see [getStockcol](getStockcol)) so as to match the colours with other spatial proteomics visualisations such as [plot2D](plot2D).

## Usage

```
mrkHClust(object, fcol = "markers", distargs, hclustargs,
  method = mean, plot = TRUE, ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| fcol | Feature meta-data label (fData column name) defining the groups to be differentiated using different colours. Default is markers. |
| distargs | A list of arguments to be passed to the [dist](dist) function. |
| hclustargs | A list of arguments to be passed to the [hclust](hclust) function. |

| method | A `function` to average marker profiles. Default is `mean`. |
| plot | A `logical` defining whether the dendrogram should be plotted. Default is `TRUE`. |
| ... | Additional parameters passed when plotting the [dendrogram](). |

## Value

Invisibly returns a dendrogram object, containing the hierarchical cluster as computed by `hclust`.

## Author(s)

Laurent Gatto

## Examples

```
library("pRolocdata")
data(dunkley2006)
mrkHClust(dunkley2006)
```

---

mrkVecToMat                    *Create a marker vector or matrix.*

---

## Description

Functions producing a new vector (matrix) marker vector set from an existing matrix (vector) marker set.

## Usage

```
mrkVecToMat(object, vfcol = "markers", mfcol = "Markers")

mrkMatToVec(object, mfcol = "Markers", vfcol = "markers")

mrkMatAndVec(object, vfcol = "markers", mfcol = "Markers")

showMrkMat(object, mfcol = "Markers")

isMrkMat(object, fcol = "Markers")

isMrkVec(object, fcol = "markers")

mrkEncoding(object, fcol = "markers")
```

## Arguments

| object | An `MSnSet` object |
| vfcol | The name of the *vector* marker feature variable. Default is `"markers"`. |
| mfcol | The name of the *matrix* marker feature variable. Default is `"Markers"`. |
| fcol | A marker feature variable name. |

### Details

Sub-cellular markers can be encoded in two different ways. Sets of spatial markers can be represented as character *vectors* (character or factor, to be accurate), stored as feature metadata, and proteins of unknown or uncertain localisation (unlabelled, to be classified) are marked with the "unknown" character. While very handy, this encoding suffers from some drawbacks, in particular the difficulty to label proteins that reside in multiple (possible or actual) localisations. The markers vector feature data is typically named markers. A new *matrix* encoding is also supported. Each spatial compartment is defined in a column in a binary markers matrix and the resident proteins are encoded with 1s. The markers matrix feature data is typically named Markers. If proteins are assigned unique localisations only (i.e. no multi-localisation) or their localisation is unknown (unlabelled), then both encodings are equivalent. When the markers are encoded as vectors, features of unknown localisation are defined as fData(object)[, fcol] == "unknown". For matrix-encoded markers, unlabelled proteins are defined as rowSums(fData(object)[, fcol]) == 0.

The mrkMatToVec and mrkVecToMat functions enable the conversion from matrix (vector) to vector (matrix). The mrkMatAndVec function generates the missing encoding from the existing one. If the destination encoding already exists, or, more accurately, if the feature variable of the destination encoding exists, an error is thrown. During the conversion from matrix to vector, if multiple possible label exists, they are dropped, i.e. they are converted to "unknown". Function isMrkVec and isMrkMat can be used to test if a marker set is encoded as a vector or a matrix. mrkEncoding returns either "vector" or "matrix" depending on the nature of the markers.

### Value

An updated MSnSet with a new vector (matrix) marker set.

### Author(s)

Laurent Gatto and Lisa Breckels

### See Also

Other functions that operate on markers are getMarkers, getMarkerClasses and markerMSnSet. To add markers to an existing MSnSet, see the addMarkers function and pRolocmarkers, for a list of suggested markers.

### Examples

```
library("pRolocdata")
data(dunkley2006)
dunk <- mrkVecToMat(dunkley2006)
head(fData(dunk)$Markers)
fData(dunk)$markers <- NULL
dunk <- mrkMatToVec(dunk)
stopifnot(all.equal(fData(dunkley2006)$markers,
                    fData(dunk)$markers))
```

---

nbClassification *nb classification*

---

### Description

Classification using the naive Bayes algorithm.

### Usage

```
nbClassification(object, assessRes, scores = c("prediction", "all",
  "none"), laplace, fcol = "markers", ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| assessRes | An instance of class `"GenRegRes"`, as generated by `nbOptimisation`. |
| scores | One of `"prediction"`, `"all"` or `"none"` to report the score for the predicted class only, for all classes or none. |
| laplace | If `assessRes` is missing, a `laplace` must be provided. |
| fcol | The feature meta-data containing marker definitions. Default is `markers`. |
| ... | Additional parameters passed to `naiveBayes` from package e1071. |

### Value

An instance of class `"MSnSet"` with nb and nb.scores feature variables storing the classification results and scores respectively.

### Author(s)

Laurent Gatto

### Examples

```
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space and iterations
params <- nbOptimisation(dunkley2006, laplace = c(0, 5),  times = 3)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- nbClassification(dunkley2006, params)
getPredictions(res, fcol = "naiveBayes")
getPredictions(res, fcol = "naiveBayes", t = 1)
plot2D(res, fcol = "naiveBayes")
```

---

nbOptimisation *nb paramter optimisation*

---

### Description

Classification algorithm parameter for the naive Bayes algorithm.

### Usage

```
nbOptimisation(object, fcol = "markers", laplace = seq(0, 5, 0.5),
  times = 100, test.size = 0.2, xval = 5, fun = mean, seed,
  verbose = TRUE, ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| laplace | The hyper-parameter. Default values are seq(0, 5, 0.5). |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the xval macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A `logical` defining whether a progress bar is displayed. |
| ... | Additional parameters passed to [naiveBayes](naiveBayes) from package e1071. |

### Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values are replaced by 0. This decision is motivated by the fact that any class that would have either a NA precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)). Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

### Value

An instance of class `"GenRegRes"`.

### Author(s)

Laurent Gatto

### See Also

[nbClassification](nbClassification) and example therein.

---

nicheMeans2D                    *Uncertainty plot organelle means*

---

### Description

Produces a pca plot with uncertainty in organelle means projected onto the PCA plot with contours.

### Usage

```
nicheMeans2D(object, params, priors, dims = c(1, 2), fcol = "markers",
  aspect = 0.5)
```

### Arguments

| | |
|---|---|
| object | A valid object of class `MSnset` |
| params | A valid object of class `MCMCParams` that has been processed and checked for convergence |
| priors | The prior that were used in the model |
| dims | The PCA dimension in which to project he data, default is `c(1,2)` |
| fcol | The columns of the feature data which contain the marker data. |
| aspect | A argument to change the plotting aspect of the PCA |

### Value

Used for side effect of producing plot. Invisibily returns an ggplot object that can be further manipulated

### Author(s)

Oliver M. Crook <omc25@cam.ac.uk>

### Examples

```
## Not run:
library("pRolocdata")
data("tan2009r1")

tanres <- tagmMcmcTrain(object = tan2009r1)
tanres <- tagmMcmcProcess(tanres)
tan2009r1 <- tagmMcmcPredict(object = tan2009r1, params = tanres, probJoint = TRUE)
myparams <- chains(e14Tagm_converged_pooled)[[1]]
myparams2 <- chains(mcmc_pool_chains(tanres))[[1]]
priors <- tanres@priors
pRloc:::nicheMeans2D(object = tan2009r1, params = myparams2, priors = priors)

## End(Not run)
```

---

nndist-methods *Nearest neighbour distances*

---

### Description

Methods computing the nearest neighbour indices and distances for `matrix` and `MSnSet` instances.

### Methods

`signature(object = "matrix", k = "numeric", dist = "character", ...)` Calculates indices and distances to the k (default is 3) nearest neighbours of each feature (row) in the input matrix `object`. The distance `dist` can be either of `"euclidean"` or `"mahalanobis"`. Additional parameters can be passed to the internal function `FNN::get.knn`. Output is a matrix with 2 * k columns and `nrow(object)` rows.

`signature(object = "MSnSet", k = "numeric", dist = "character", ...)` As above, but for an MSnSet input. The indices and distances to the k nearest neighbours are added to the object's feature metadata.

`signature(object = "matrix", query = "matrix", k = "numeric", ...)` If two matrix instances are provided as input, the k (default is 3) indices and distances of the nearest neighbours of `query` in `object` are returned as a matrix of dimensions 2 * k by `nrow(query)`. Additional parameters are passed to `FNN::get.knnx`. Only euclidean distance is available.

### Examples

```
library("pRolocdata")
data(dunkley2006)

## Using a matrix as input
m <- exprs(dunkley2006)
m[1:4, 1:3]
head(nndist(m, k = 5))
tail(nndist(m[1:100, ], k = 2, dist = "mahalanobis"))

## Same as above for MSnSet
d <- nndist(dunkley2006, k = 5)
head(fData(d))

d <- nndist(dunkley2006[1:100, ], k = 2, dist = "mahalanobis")
tail(fData(d))

## Using a query
nndist(m[1:100, ], m[101:110, ], k = 2)
```

---

nnetClassification          *nnet classification*

---

### Description

Classification using the artificial neural network algorithm.

### Usage

```
nnetClassification(object, assessRes, scores = c("prediction", "all",
  "none"), decay, size, fcol = "markers", ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class "MSnSet". |
| assessRes | An instance of class "GenRegRes", as generated by nnetOptimisation. |
| scores | One of "prediction", "all" or "none" to report the score for the predicted class only, for all classes or none. |
| decay | If assessRes is missing, a decay must be provided. |
| size | If assessRes is missing, a size must be provided. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| ... | Additional parameters passed to nnet from package nnet. |

### Value

An instance of class "MSnSet" with nnet and nnet.scores feature variables storing the classification results and scores respectively.

### Author(s)

Laurent Gatto

### Examples

```
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space and iterations
params <- nnetOptimisation(dunkley2006, decay = 10^(c(-1, -5)), size = c(5, 10), times = 3)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- nnetClassification(dunkley2006, params)
getPredictions(res, fcol = "nnet")
getPredictions(res, fcol = "nnet", t = 0.75)
plot2D(res, fcol = "nnet")
```

---

nnetOptimisation *nnet parameter optimisation*

---

#### Description

Classification parameter optimisation for artificial neural network algorithm.

#### Usage

```
nnetOptimisation(object, fcol = "markers", decay = c(0, 10^(-1:-5)),
  size = seq(1, 10, 2), times = 100, test.size = 0.2, xval = 5,
  fun = mean, seed, verbose = TRUE, ...)
```

#### Arguments

| | |
|---|---|
| object | An instance of class ["MSnSet"](MSnSet). |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| decay | The hyper-parameter. Default values are c(0, 10^(-1:-5)). |
| size | The hyper-parameter. Default values are seq(1, 10, 2). |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the xval macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A logical defining whether a progress bar is displayed. |
| ... | Additional parameters passed to [nnet](nnet) from package nnet. |

#### Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values
are replaced by 0. This decision is motivated by the fact that any class that would have either a NA
precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)).
Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

#### Value

An instance of class ["GenRegRes"](GenRegRes).

#### Author(s)

Laurent Gatto

#### See Also

[nnetClassification](nnetClassification) and example therein.

orderGoAnnotations          *Orders annotation information*

**Description**

For a given matrix of annotation information, this function returns the information ordered according to the best fit with the data.

**Usage**

```
orderGoAnnotations(object, fcol = "GOAnnotations", k = 1:5, n = 5,
  p = 1/3, verbose = TRUE, seed)
```

**Arguments**

| | |
|---|---|
| object | An instance of class MSnSet. |
| fcol | The name of the annotations matrix. Default is GOAnnotations. |
| k | The number of clusters to test. Default is k = 1:5 |
| n | The minimum number of proteins per component cluster. |
| p | The normalisation factor, per k tested |
| verbose | A logical indicating if a progress bar should be displayed. Default is TRUE. |
| seed | An optional random number generation seed. |

**Details**

As there are typically many protein/annotation sets that may fit the data we order protein sets by best fit i.e. cluster tightness, by computing the mean normalised Euclidean distance for all instances per protein set.

For each protein set i.e. proteins that have been labelled with a specified term/information criteria, we find the best k cluster components for the set (the default is to testk = 1:5) according to the minimum mean normalised pairwise Euclidean distance over all component clusters. (Note: when testing k if any components are found to have less than n proteins these components are not included and k is reduced by 1).

Each component cluster is normalised by N^p (where N is the total number of proteins per component, and p is the power). Hueristally, p = 1/3 and normalising by N^1/3 has been found the optimum normalisation factor.

Candidates in the matrix are ordered according to lowest mean normalised pairwise Euclidean distance as we expect high density, tight clusters to have the smallest mean normalised distance.

This function is a wrapper for running clustDist, getNormDist, see the "Annotating spatial proteomics data" vignette for more details.

**Value**

An updated MSnSet containing the newly ordered fcol matrix.

## Author(s)

Lisa M Breckels

## See Also

addGoAnnotations and example therein.

---

orgQuants                    *Returns organelle-specific quantile scores*

---

## Description

This function produces organelle-specific quantiles corresponding to the given classification scores.

## Usage

```
orgQuants(object, fcol, scol, mcol = "markers", t, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| object | An instance of class ["MSnSet"](). |
| fcol | The name of the prediction column in the featureData slot. |
| scol | The name of the prediction score column in the featureData slot. If missing, created by pasting '.scores' after fcol. |
| mcol | The name of the column containing the training data in the featureData slot. Default is markers. |
| t | The quantile threshold. |
| verbose | If TRUE, the calculated threholds are printed. |

## Value

A named vector of organelle thresholds.

## Author(s)

Lisa Breckels

## See Also

[getPredictions]() to get organelle predictions based on calculated thresholds.

## Examples

```
library("pRolocdata")
data(dunkley2006)
res <- svmClassification(dunkley2006, fcol = "pd.markers",
                         sigma = 0.1, cost = 0.5)
## 50% top predictions per class
ts <- orgQuants(res, fcol = "svm", t = .5)
getPredictions(res, fcol = "svm", t = ts)
```

---

perTurboClassification

*perTurbo classification*

---

## Description

Classification using the PerTurbo algorithm.

## Usage

```
perTurboClassification(object, assessRes, scores = c("prediction", "all",
  "none"), pRegul, sigma, inv, reg, fcol = "markers")
```

## Arguments

| | |
|---|---|
| object | An instance of class "MSnSet". |
| assessRes | An instance of class "GenRegRes", as generated by svmRegularisation. |
| scores | One of "prediction", "all" or "none" to report the score for the predicted class only, for all classes or none. |
| pRegul | If assessRes is missing, a pRegul must be provided. See perTurboOptimisation for details. |
| sigma | If assessRes is missing, a sigma must be provided. See perTurboOptimisation for details. |
| inv | The type of algorithm used to invert the matrix. Values are : "Inversion Cholesky" (chol2inv), "Moore Penrose" (ginv), "solve" (solve), "svd" (svd). Default value is "Inversion Cholesky". |
| reg | The type of regularisation of matrix. Values are "none", "trunc" or "tikhonov". Default value is "tikhonov". |
| fcol | The feature meta-data containing marker definitions. Default is markers. |

## Value

An instance of class "MSnSet" with perTurbo and perTurbo.scores feature variables storing the classification results and scores respectively.

## Author(s)

Thomas Burger and Samuel Wieczorek

## References

N. Courty, T. Burger, J. Laurent. "PerTurbo: a new classification algorithm based on the spectrum perturbations of the Laplace-Beltrami operator", The European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML-PKDD 2011), D. Gunopulos et al. (Eds.): ECML PKDD 2011, Part I, LNAI 6911, pp. 359 - 374, Athens, Greece, September 2011.

## Examples

```
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space
params <- perTurboOptimisation(dunkley2006,
                               pRegul = 2^seq(-2,2,2),
                               sigma = 10^seq(-1, 1, 1),
                               inv = "Inversion Cholesky",
                               reg ="tikhonov",
                               times = 3)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- perTurboClassification(dunkley2006, params)
getPredictions(res, fcol = "perTurbo")
getPredictions(res, fcol = "perTurbo", t = 0.75)
plot2D(res, fcol = "perTurbo")
```

---

perTurboOptimisation      *PerTurbo parameter optimisation*

---

## Description

Classification parameter optimisation for the PerTurbo algorithm

## Usage

```
perTurboOptimisation(object, fcol = "markers", pRegul = 10^(seq(from =
  -1, to = 0, by = 0.2)), sigma = 10^(seq(from = -1, to = 1, by = 0.5)),
  inv = c("Inversion Cholesky", "Moore Penrose", "solve", "svd"),
  reg = c("tikhonov", "none", "trunc"), times = 1, test.size = 0.2,
  xval = 5, fun = mean, seed, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| pRegul | The hyper-parameter for the regularisation (values are in ]0,1] ). If reg =="trunc", pRegul is for the percentage of eigen values in matrix. If reg =="tikhonov", then 'pRegul' is the parameter for the tikhonov regularisation. Available configurations are : "Inversion Cholesky" - ("tikhonov" / "none"), "Moore Penrose" - ("tikhonov" / "none"), "solve" - ("tikhonov" / "none"), "svd" - ("tikhonov" / "none" / "trunc"). |
| sigma | The hyper-parameter. |
| inv | The type of algorithm used to invert the matrix. Values are : "Inversion Cholesky" ([chol2inv](#)), "Moore Penrose" ([ginv](#)), "solve" ([solve](#)), "svd" ([svd](#)). Default value is `"Inversion Cholesky"`. |
| reg | The type of regularisation of matrix. Values are "none", "trunc" or "tikhonov". Default value is `"tikhonov"`. |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the times macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A `logical` defining whether a progress bar is displayed. |

## Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values are replaced by 0. This decision is motivated by the fact that any class that would have either a NA precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)). Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

## Value

An instance of class `"GenRegRes"`.

## Author(s)

Thomas Burger and Samuel Wieczorek

## See Also

[perTurboClassification](#) and example therein.

---

| phenoDisco | *Runs the* phenoDisco *algorithm.* |

---

## Description

phenoDisco is a semi-supervised iterative approach to detect new protein clusters.

## Usage

```
phenoDisco(object, fcol = "markers", times = 100, GS = 10,
  allIter = FALSE, p = 0.05, ndims = 2,
  modelNames = mclust.options("emModelNames"), G = 1:9, BPPARAM,
  tmpfile, seed, verbose = TRUE, dimred = c("PCA", "t-SNE"), ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| fcol | A character indicating the organellar markers column name in feature metadata. Default is markers. |
| times | Number of runs of tracking. Default is 100. |
| GS | Group size, i.e how many proteins make a group. Default is 10 (the minimum group size is 4). |
| allIter | logical, defining if predictions for all iterations should be saved. Default is FALSE. |
| p | Significance level for outlier detection. Default is 0.05. |
| ndims | Number of principal components to use as input for the disocvery analysis. Default is 2. Added in version 1.3.9. |
| modelNames | A vector of characters indicating the models to be fitted in the EM phase of clustering using Mclust. The help file for mclust::mclustModelNames describes the available models. Default model names are c("EII", "VII", "EEI", "VEI", "EVI", "VVI", "EEE","EEV", "VEV", "VVV"), as returned by mclust.options("emModelNames"). Note that using all these possible models substantially increases the running time. Legacy models are c("EEE","EEV","VEV","VVV"), i.e. only ellipsoidal models. |
| G | An integer vector specifying the numbers of mixture components (clusters) for which the BIC is to be calculated. The default is G=1:9 (as in Mclust). |
| BPPARAM | Support for parallel processing using the BiocParallel infrastructure. When missing (default), the default registered BiocParallelParam parameters are used. Alternatively, one can pass a valid BiocParallelParam parameter instance: SnowParam, MulticoreParam, DoparParam, . . . see the BiocParallel package for details. To revert to the origianl serial implementation, use NULL. |
| tmpfile | An optional character to save a temporary MSnSet after each iteration. Ignored if missing. This is useful for long runs to track phenotypes and possibly kill the run when convergence is observed. If the run completes, the temporary file is deleted before returning the final result. |

seed      An optional `numeric` of length 1 specifing the random number generator seed to be used. Only relevant when executed in serialised mode with `BPPARAM = NULL`. See `BPPARAM` for details.

verbose      Logical, indicating if messages are to be printed out during execution of the algorithm.

dimred      A `characater` defining which of Principal Component Analysis (`"PCA"`) or t-Distributed Stochastic Neighbour Embedding (`"t-SNE"`) should be use to reduce dimensions prior to running phenoDisco novelty detection.

...      Additional arguments passed to the dimensionality reduction method. For both PCA and t-SNE, the data is scaled and centred by default, and these parameters (`scale` and `centre` for PCA, and `pca_scale` and `pca_center` for t-SNE can't be set). When using t-SNE however, it is important to tune the perplexity and max iterations parameters. See the *Dimensionality reduction* section in the pRoloc vignette for details.

## Details

The algorithm performs a phenotype discovery analysis as described in Breckels et al. Using this approach one can identify putative subcellular groupings in organelle proteomics experiments for more comprehensive validation in an unbiased fashion. The method is based on the work of Yin et al. and used iterated rounds of Gaussian Mixture Modelling using the Expectation Maximisation algorithm combined with a non-parametric outlier detection test to identify new phenotype clusters.

One requires 2 or more classes to be labelled in the data and at a very minimum of 6 markers per class to run the algorithm. The function will check and remove features with missing values using the [filterNA](#) method.

A parallel implementation, relying on the `BiocParallel` package, has been added in version 1.3.9. See the `BPPARAM` arguent for details.

Important: Prior to version 1.1.2 the row order in the output was different from the row order in the input. This has now been fixed and row ordering is now the same in both input and output objects.

## Value

An instance of class `MSnSet` containing the `phenoDisco` predictions.

## Author(s)

Lisa M. Breckels <lms79@cam.ac.uk>

## References

Yin Z, Zhou X, Bakal C, Li F, Sun Y, Perrimon N, Wong ST. Using iterative cluster merging with improved gap statistics to perform online phenotype discovery in the context of high-throughput RNAi screens. BMC Bioinformatics. 2008 Jun 5;9:264. PubMed PMID: 18534020.

Breckels LM, Gatto L, Christoforou A, Groen AJ, Lilley KS and Trotter MWB. The Effect of Organelle Discovery upon Sub-Cellular Protein Localisation. J Proteomics. 2013 Aug 2;88:129-40. doi: 10.1016/j.jprot.2013.02.019. Epub 2013 Mar 21. PubMed PMID: 23523639.

## Examples

```
## Not run:
library(pRolocdata)
data(tan2009r1)
pdres <- phenoDisco(tan2009r1, fcol = "PLSDA")
getPredictions(pdres, fcol = "pd", scol = NULL)
plot2D(pdres, fcol = "pd")

## to pre-process the data with t-SNE instead of PCA
pdres <- phenoDisco(tan2009r1, fcol = "PLSDA", dimred = "t-SNE")

## End(Not run)
```

---

plot2D                          *Plot organelle assignment data and results.*

---

## Description

Generate 2 or 3 dimensional feature distribution plots to illustrate localistation clusters. Rows/features containing NA values are removed prior to dimension reduction except for the "nipals" method. For this method, it is advised to set the method argument 'ncomp' to a low number of dimensions to avoid computing all components when analysing large datasets.

## Usage

```
plot2D(object, fcol = "markers", fpch, unknown = "unknown",
  dims = 1:2, score = 1, method = "PCA", methargs,
  axsSwitch = FALSE, mirrorX = FALSE, mirrorY = FALSE, col, pch, cex,
  index = FALSE, idx.cex = 0.75, addLegend, identify = FALSE,
  plot = TRUE, grid = TRUE, ...)

## S4 method for signature 'MSnSet'
plot3D(object, fcol = "markers", dims = c(1, 2, 3),
  radius1 = 0.1, radius2 = radius1 * 2, plot = TRUE, ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| fcol | Feature meta-data label (fData column name) defining the groups to be differentiated using different colours. Default is markers. Use NULL to suppress any colouring. |
| fpch | Featre meta-data label (fData column name) desining the groups to be differentiated using different point symbols. |
| unknown | A character (default is "unknown") defining how proteins of unknown/un-labelled localisation are labelled. |
| dims | A numeric of length 2 (or 3 for plot3D) defining the dimensions to be plotted. Defaults are c(1,2) and c(1, 2, 3). Always 1:2 for MDS. |

| score | A numeric specifying the minimum organelle assignment score to consider features to be assigned an organelle. (not yet implemented). |
|---|---|
| method | A character describe how to transform the data or what to plot. One of "PCA" (default), "MDS", "kpca", "nipals", "t-SNE" or "lda", defining what dimensionality reduction is applied: principal component analysis (see prcomp), classical multidimensional scaling (see cmdscale), kernel PCA (see kpca), nipals (principal component analysis by NIPALS, non-linear iterative partial least squares which support missing values; see nipals) t-SNE (see Rtsne) or linear discriminant analysis (see lda). The last method uses fcol to defined the subcellular clusters so that the ration between within ad between cluster variance is maximised. All the other methods are unsupervised and make use fcol only to annotate the plot. Prior to t-SNE, duplicated features are removed and a message informs the user if such filtering is needed. |
| | "scree" can also be used to produce a scree plot. "hexbin" applies PCA to the data and uses bivariate binning into hexagonal cells from hexbin to emphasise cluster density. |
| | If none is used, the data is plotted as is, i.e. without any transformation. In this case, object can either be an MSnSet or a matrix (as invisibly returned by plot2D). This enables to re-generate the figure without computing the dimensionality reduction over and over again, which can be time consuming for certain methods. If object is a matrix, an MSnSet containing the feature metadata must be provided in methargs (see below for details). |
| | Available methods are listed in plot2Dmethods. |
| methargs | A list of arguments to be passed when method is called. If missing, the data will be scaled and centred prior to PCA and t-SNE (i.e. Rtsne's arguments pca_center and pca_scale are set to TRUE). If method = "none" and object is a matrix, then the first and only argument of methargs must be an MSnSet with matching features with object. |
| axsSwitch | A logical indicating whether the axes should be switched. |
| mirrorX | A logical indicating whether the x axis should be mirrored? |
| mirrorY | A logical indicating whether the y axis should be mirrored? |
| col | A character of appropriate length defining colours. |
| pch | A character of appropriate length defining point character. |
| cex | Character expansion. |
| index | A logical (default is FALSE, indicating of the feature indices should be plotted on top of the symbols. |
| idx.cex | A numeric specifying the character expansion (default is 0.75) for the feature indices. Only relevant when index is TRUE. |
| addLegend | A character indicating where to add the legend. See addLegendfor details. If missing (default), no legend is added. |
| identify | A logical (default is TRUE) defining if user interaction will be expected to identify individual data points on the plot. See also identify. |
| plot | A logical defining if the figure should be plotted. Useful when retrieving data only. Default is TRUE. |

| grid | A logical indicating whether a grid should be plotted. Default is TRUE. |
| --- | --- |
| ... | Additional parameters passed to plot and points. |
| radius1 | A numeric specifying the radius of feature of unknown localisation. Default is 0.1, which is specidied on the data scale. See plot3d for details. |
| radius2 | A numeric specifying the radius of marker feature. Default is radius * 2. |

## Details

plot3D relies on the ##' rgl package, that will be loaded automatically.

- Note that plot2D has been update in version 1.3.6 to support more organelle classes than colours defined in getStockcol. In such cases, the default colours are recycled using the default plotting characters defined in getStockpch. See the example for an illustration. The alpha argument is also depreciated in version 1.3.6. Use setStockcol to set colours with transparency instead. See example below.
- Version 1.11.3: to plot data as is, i.e. without any transformation, method can be set to "none" (as opposed to passing pre-computed values to method as a matrix, in previous versions). If object is an MSnSet, the untransformed values in the assay data will be plotted. If object is a matrix with coordinates, then a matching MSnSet must be passed to methargs.

## Value

Used for its side effects of generating a plot. Invisibly returns the 2 or 3 dimensions that are plotted.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## See Also

addLegend to add a legend to plot2D figures (the legend is added by default on plot3D) and plotDist for alternative graphical representation of quantitative organelle proteomics data. plot2Ds to overlay 2 data sets on the same PCA plot. The plotEllipse function can be used to visualise TAGM models on PCA plots with ellipses.

## Examples

```
library("pRolocdata")
data(dunkley2006)
plot2D(dunkley2006, fcol = NULL)
plot2D(dunkley2006, fcol = NULL, col = "black")
plot2D(dunkley2006, fcol = "markers")
addLegend(dunkley2006,
          fcol = "markers",
          where = "topright",
          cex = 0.5, bty = "n", ncol = 3)
title(main = "plot2D example")
## available methods
plot2Dmethods
plot2D(dunkley2006, fcol = NULL, method = "kpca", col = "black")
```

```
plot2D(dunkley2006, fcol = NULL, method = "kpca", col = "black",
       methargs = list(kpar = list(sigma = 1)))
plot2D(dunkley2006, method = "lda")
plot2D(dunkley2006, method = "hexbin")
## Using transparent colours
setStockcol(paste0(getStockcol(), "80"))
plot2D(dunkley2006, fcol = "markers")
## New behaviour in 1.3.6 when not enough colours
setStockcol(c("blue", "red", "green"))
getStockcol() ## only 3 colours to be recycled
getMarkers(dunkley2006)
plot2D(dunkley2006)
## reset colours
setStockcol(NULL)
plot2D(dunkley2006, method = "none") ## plotting along 2 first fractions
plot2D(dunkley2006, dims = c(3, 5), method = "none") ## plotting along fractions 3 and 5
## pre-calculate PC1 and PC2 coordinates
pca <- plot2D(dunkley2006, plot=FALSE)
head(pca)
plot2D(pca, method = "none", methargs  = list(dunkley2006))

## plotting in 3 dimenstions
plot3D(dunkley2006)
plot3D(dunkley2006, radius2 = 0.3)
plot3D(dunkley2006, dims = c(2, 4, 6))
```

---

plot2Ds                         *Draw 2 data sets on one PCA plot*

---

### Description

Takes 2 linkS4class{MSnSet} instances as input to plot the two data sets on the same PCA plot.
The second data points are projected on the PC1 and PC2 dimensions calculated for the first data
set.

### Usage

```
plot2Ds(object, pcol, fcol = "markers", cex.x = 1, cex.y = 1,
  pch.x = 21, pch.y = 23, col, mirrorX = FALSE, mirrorY = FALSE,
  plot = TRUE, ...)
```

### Arguments

| | |
|---|---|
| object | An MSnSet or a MSnSetList. In the latter case, only the two first elements of the list will be used for plotting and the others will be silently ignored. |
| pcol | If object is an MSnSet, a factor or the name of a phenotype variable (phenoData slot) defining how to split the single MSnSet into two or more data sets. Ignored if object is a MSnSetList. |

| fcol | Feature meta-data label (fData column name) defining the groups to be differentiated using different colours. Default is markers. Use NULL to suppress any colouring. |
|------|-------------------------------------------------------------------------------------------------|
| cex.x | Character expansion for the first data set. Default is 1. |
| cex.y | Character expansion for the second data set. Default is 1. |
| pch.x | Plotting character for the first data set. Default is 21. |
| pch.y | Plotting character for the second data set. Default is 23. |
| col | A vector of colours to highlight the different classes defined by fcol. If missing (default), default colours are used (see [getStockcol](#)). |
| mirrorX | A logical indicating whether the x axis should be mirrored? |
| mirrorY | A logical indicating whether the y axis should be mirrored? |
| plot | If TRUE (default), a plot is produced. |
| ... | Additinal parameters passed to plot and points. |

### Value

Used for its side effects of producing a plot. Invisibly returns an object of class plot2Ds, which is a list with the PCA analyses results (see [prcomp](#)) of the first data set and the new coordinates of the second data sets, as used to produce the plot and the respective point colours. Each of these elements can be accessed with data1, data2, col1 and code2 respectively.

### Author(s)

Laurent Gatto

### See Also

See [plot2D](#) to plot a single data set and [move2Ds](#) for a animation.

### Examples

```
library("pRolocdata")
data(tan2009r1)
data(tan2009r2)
msnl <- MSnSetList(list(tan2009r1, tan2009r2))
plot2Ds(msnl)
## tweaking the parameters
plot2Ds(list(tan2009r1, tan2009r2),
        fcol = NULL, cex.x = 1.5)
## input is 1 MSnSet containing 2 data sets
data(dunkley2006)
plot2Ds(dunkley2006, pcol = "replicate")
## no plot, just the data
res <- plot2Ds(dunkley2006, pcol = "replicate",
               plot = FALSE)
res
head(data1(res))
head(col1(res))
```

---

plotConsProfiles          *Plot marker consenses profiles.*

---

### Description

The function plots marker consensus profiles obtained from mrkConsProfile

### Usage

```
plotConsProfiles(object, order = NULL, plot = TRUE)
```

### Arguments

| | |
|---|---|
| object | A matrix containing marker consensus profiles as output from [mrkConsProfiles()](#). |
| order | Order for markers (optional). |
| plot | A logical(1) defining whether the heatmap should be plotted. Default is TRUE. |

### Value

Invisibly returns ggplot2 object.

### Author(s)

Tom Smith

### Examples

```
library("pRolocdata")
data(E14TG2aS1)
hc <- mrkHClust(E14TG2aS1, plot = FALSE)
mm <- getMarkerClasses(E14TG2aS1)
ord <- levels(factor(mm))[order.dendrogram(hc)]
fmat <- mrkConsProfiles(E14TG2aS1)
plotConsProfiles(fmat, order = ord)
```

---

plotDist                  *Plots the distribution of features across fractions*

---

### Description

Produces a line plot showing the feature abundances across the fractions.

### Usage

```
plotDist(object, markers, fcol = NULL, mcol = "steelblue",
  pcol = getUnknowncol(), alpha = 0.3, type = "b", lty = 1,
  fractions = sampleNames(object), ylab = "Intensity",
  xlab = "Fractions", ylim, ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| markers | A character, numeric or logical of appropriate length and or content used to subset object and define the organelle markers. |
| fcol | Feature meta-data label (fData column name) defining the groups to be differentiated using different colours. If NULL (default) ignored and mcol and pcol are used. |
| mcol | A character define the colour of the marker features. Default is "steelblue". |
| pcol | A character define the colour of the non-markers features. Default is the colour used for features of unknown localisation, as returned by [getUnknowncol](). |
| alpha | A numeric defining the alpha channel (transparency) of the points, where 0 <= alpha <= 1, 0 and 1 being completely transparent and opaque. |
| type | Character string defining the type of lines. For example "p" for points, "l" for lines, "b" for both. See plot for all possible types. |
| lty | Vector of line types for the marker profiles. Default is 1 (solid). See [par]() for details. |
| fractions | A character defining the phenoData variable to be used to label the fraction along the x axis. Default is to use sampleNames(object). |
| ylab | y-axis label. Default is "Intensity". |
| xlab | x-axis label. Default is "Fractions". |
| ylim | A numeric vector of length 2, giving the y coordinates range. |
| ... | Additional parameters passed to [plot](). |

## Value

Used for its side effect of producing a feature distribution plot. Invisibly returns the data matrix.

## Author(s)

Laurent Gatto

## Examples

```
library("pRolocdata")
data(tan2009r1)
j <- which(fData(tan2009r1)$markers == "mitochondrion")
i <- which(fData(tan2009r1)$PLSDA == "mitochondrion")
plotDist(tan2009r1[i, ], markers = featureNames(tan2009r1)[j])
plotDist(tan2009r1[i, ], markers = featureNames(tan2009r1)[j],
         fractions = "Fractions")
## plot and colour all marker profiles
tanmrk <- markerMSnSet(tan2009r1)
plotDist(tanmrk, fcol = "markers")
```

---

plotEllipse                *A function to plot probabiltiy ellipses on marker PCA plots to visualise and assess TAGM models.*

---

## Description

Note that when running PCA, this function does not scale the data (centring is performed), as opposed to [plot2D()]. Only marker proteins are displayed; the protein of unknown location, that are not used to estimate the MAP parameters, are filtered out.

## Usage

```
plotEllipse(object, params, dims = c(1, 2), method = "MAP", ...)
```

## Arguments

| | |
|---|---|
| object | An ['MSnbase::MSnset'] containing quantitative spatial proteomics data. |
| params | An ['MAPParams'] with the TAGM-MAP parameters, as generated by 'tagmMapTrain'. |
| dims | A 'numeric(2)' with the principal components along which to project the data. Default is 'c(1, 2)'. |
| method | The method used. Currently '"MAP"' only. |
| ... | Additional parameters passed to [plot2D()]. |

## Value

A PCA plot of the marker data with probability ellipises. The outer ellipse contains 99 probability whilst the middle and inner ellipses contain 95 and 90 clusters are represented by black circumpunct (circled dot).

## See Also

[plot2D()] to visualise spatial proteomics data using various dimensionality reduction methods. For details about TAGM models, see [tagmPredict()] and the *pRoloc-bayesian* vignette.

---

plsdaClassification        *plsda classification*

---

## Description

Classification using the partial least square distcriminant analysis algorithm.

## Usage

```
plsdaClassification(object, assessRes, scores = c("prediction", "all",
  "none"), ncomp, fcol = "markers", ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| assessRes | An instance of class `"GenRegRes"`, as generated by `plsdaOptimisation`. |
| scores | One of `"prediction"`, `"all"` or `"none"` to report the score for the predicted class only, for all classes or none. |
| ncomp | If `assessRes` is missing, a `ncomp` must be provided. |
| fcol | The feature meta-data containing marker definitions. Default is `markers`. |
| ... | Additional parameters passed to `plsda` from package `caret`. |

## Value

An instance of class `"MSnSet"` with `plsda` and `plsda.scores` feature variables storing the classification results and scores respectively.

## Author(s)

Laurent Gatto

## Examples

```
## not running this one for time considerations
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space and iterations
params <- plsdaOptimisation(dunkley2006, ncomp = c(3, 10),  times = 2)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- plsdaClassification(dunkley2006, params)
getPredictions(res, fcol = "plsda")
getPredictions(res, fcol = "plsda", t = 0.9)
plot2D(res, fcol = "plsda")
```

---

plsdaOptimisation        *plsda parameter optimisation*

---

## Description

Classification parameter optimisation for the partial least square distcriminant analysis algorithm.

## Usage

```
plsdaOptimisation(object, fcol = "markers", ncomp = 2:6, times = 100,
  test.size = 0.2, xval = 5, fun = mean, seed, verbose = TRUE, ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class ["MSnSet"](). |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| ncomp | The hyper-parameter. Default values are 2:6. |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the xval macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A logical defining whether a progress bar is displayed. |
| ... | Additional parameters passed to [plsda]() from package caret. |

## Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values are replaced by 0. This decision is motivated by the fact that any class that would have either a NA precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)). Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

## Value

An instance of class ["GenRegRes"]().

## Author(s)

Laurent Gatto

## See Also

[plsdaClassification]() and example therein.

---

pRolocmarkers                    *Organelle markers*

---

## Description

This function retrieves a list of organelle markers or, if no species is provided, prints a description of available marker sets. The markers can be added to and MSnSet using the [addMarkers]() function.

## Usage

```
pRolocmarkers(species)
```

## Arguments

species          The species of interest.

## Details

The markers have been contributed by various members of the Cambridge Centre for Proteomics, in particular Dr Dan Nightingale for yeast, Dr Andy Christoforou and Dr Claire Mulvey for human, Dr Arnoud Groen for Arabodopsis and Dr Claire Mulvey for mouse. In addition, original (curated) markers from the pRolocdata datasets have been extracted (see pRolocdata for details and references). Curation involved verification of publicly available subcellular localisation annotation based on the curators knowledge of the organelles/proteins considered and tracing the original statement in the literature.

These markers are provided as a starting point to generate reliable sets of organelle markers but still need to be verified against any new data in the light of the quantitative data and the study conditions.

## Value

Prints a description of the available marker lists if species is missing or a named character with organelle markers.

## Author(s)

Laurent Gatto

## See Also

[addMarkers](#) to add markers to an MSnSet and [markers](#) for more information about marker encoding.

## Examples

```
pRolocmarkers()
table(pRolocmarkers("atha"))
table(pRolocmarkers("hsap"))
```

---

QSep-class                    *Quantify resolution of a spatial proteomics experiment*

---

## Description

The QSep infrastructure provide a way to quantify the resolution of a spatial proteomics experiment, i.e. to quantify how well annotated sub-cellular clusters are separated from each other.

The QSep function calculates all between and within cluster average distances. These distances are then divided column-wise by the respective within cluster average distance. For example, for a dataset with only 2 spatial clusters, we would obtain

$$
\begin{array}{ccc}
 & c_1 & c_2 \\
c_1 & d_1 1 & d_1 2 \\
c_2 & d_2 1 & d_2 2
\end{array}
$$

Normalised distance represent the ratio of between to within average distances, i.e. how much bigger the average distance between cluster $c_i$ and $c_j$ is compared to the average distance within cluster $c_i$.

$$
\begin{array}{ccc}
 & c_1 & c_2 \\
c_1 & 1 & \frac{d_1 2}{d_2 2} \\
c_2 & \frac{d_2 1}{d_1 1} & 1
\end{array}
$$

Note that the normalised distance matrix is not symmetric anymore and the normalised distance ratios are proportional to the tightness of the reference cluster (along the columns).

Missing values only affect the fractions containing the NA when the distance is computed (see the example below) and further used when calculating mean distances. Few missing values are expected to have negligible effect, but data with a high proportion of missing data will will produce skewed distances. In QSep, we take a conservative approach, using the data as provided by the user, and expect that the data missingness is handled before proceeding with this or any other analysis.

### Objects from the Class

Objects can be created by calls using the constructor QSep (see below).

### Slots

x: Object of class "matrix" containing the pairwise distance matrix, accessible with qseq(., norm = FALSE).

xnorm: Object of class "matrix" containing the normalised pairwise distance matrix, accessible with qsep(.,norm = TRUE) or qsep(.).

object: Object of class "character" with the variable name of [MSnSet](#) object that was used to generate the QSep object.

.__classVersion__: Object of class "Versions" storing the class version of the object.

### Extends

Class ["Versioned"](#), directly.

### Methods and functions

**QSeq** signature(object = "MSnSet", fcol = "character"): constructor for QSep objects. The fcol argument defines the name of the feature variable that annotates the sub-cellular clusters. Non-marker proteins, that are marked as "unknown" are automatically removed prior to distance calculation.

**qsep** signature{object = "QSep", norm = "logical"}: accessor for the normalised (when norm is TRUE, which is default) and raw (when norm is FALSE) pairwise distance matrices.

**names** signature{object = ″QSep″}: method to retrieve the names of the sub-celluar clusters originally defined in QSep's fcol argument. A replacement method names(.) <- is also available.

**summary** signature(object = ″QSep″, ..., verbose = ″logical″): Invisible return all between cluster average distances and prints (when verbose is TRUE, default) a summary of those.

**levelPlot** signature(object = ″QSep″, norm = ″logical″,...): plots an annotated heatmap of all normalised pairwise distances. norm (default is TRUE) defines whether normalised distances should be plotted. Additional arguments ... are passed to the levelplot.

**plot** signature(object = ″QSep″, norm = ″logical″...): produces a boxplot of all normalised pairwise distances. The red points represent the within average distance and black points between average distances. norm (default is TRUE) defines whether normalised distances should be plotted.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## References

Assessing sub-cellular resolution in spatial proteomics experiments Laurent Gatto, Lisa M Breckels, Kathryn S Lilley bioRxiv 377630; doi: https://doi.org/10.1101/377630

## Examples

```
## Test data from Christoforou et al. 2016
library("pRolocdata")
data(hyperLOPIT2015)

## Create the object and get a summary
hlq <- QSep(hyperLOPIT2015)
hlq
summary(hlq)

## mean distance matrix
qsep(hlq, norm = FALSE)

## normalised average distance matrix
qsep(hlq)

## Update the organelle cluster names for better
## rendering on the plots
names(hlq) <- sub("/", "\n", names(hlq))
names(hlq) <- sub(" - ", "\n", names(hlq))
names(hlq)

## Heatmap of the normalised intensities
levelPlot(hlq)

## Boxplot of the normalised intensities
par(mar = c(3, 10, 2, 1))
```

```
plot(hlq)

## Boxplot of all between cluster average distances
x <- summary(hlq, verbose = FALSE)
boxplot(x)

## Missing data example, for 4 proteins and 3 fractions
x <- rbind(c(1.1, 1.2, 1.3), rep(1, 3), c(NA, 1, 1), c(1, 1, NA))
rownames(x) <- paste0("P", 1:4)
colnames(x) <- paste0("F", 1:3)

## P1 is the reference, against which we will calculate distances. P2
## has a complete profile, producing the *real* distance. P3 and P4 have
## missing values in the first and last fraction respectively.
x

## If we drop F1 in P3, which represents a small difference of 0.1, the
## distance only considers F2 and F3, and increases. If we drop F3 in
## P4, which represents a large distance of 0.3, the distance only
## considers F1 and F2, and decreases.  dist(x)
```

---

rfClassification            *rf classification*

---

### Description

Classification using the random forest algorithm.

### Usage

```
rfClassification(object, assessRes, scores = c("prediction", "all",
  "none"), mtry, fcol = "markers", ...)
```

### Arguments

| | |
|---|---|
| object | An instance of class ["MSnSet"](). |
| assessRes | An instance of class ["GenRegRes"](), as generated by [rfOptimisation](). |
| scores | One of "prediction", "all" or "none" to report the score for the predicted class only, for all classes or none. |
| mtry | If assessRes is missing, a mtry must be provided. |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| ... | Additional parameters passed to [randomForest]() from package randomForest. |

### Value

An instance of class ["MSnSet"]() with rf and rf.scores feature variables storing the classification results and scores respectively.

## Author(s)

Laurent Gatto

## Examples

```
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space and iterations
params <- rfOptimisation(dunkley2006, mtry = c(2, 5, 10),  times = 3)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- rfClassification(dunkley2006, params)
getPredictions(res, fcol = "rf")
getPredictions(res, fcol = "rf", t = 0.75)
plot2D(res, fcol = "rf")
```

---

rfOptimisation            *svm parameter optimisation*

---

## Description

Classification parameter optimisation for the random forest algorithm.

## Usage

```
rfOptimisation(object, fcol = "markers", mtry = NULL, times = 100,
  test.size = 0.2, xval = 5, fun = mean, seed, verbose = TRUE, ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class "MSnSet". |
| fcol | The feature meta-data containing marker definitions. Default is markers. |
| mtry | The hyper-parameter. Default value is NULL. |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the xval macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A logical defining whether a progress bar is displayed. |
| ... | Additional parameters passed to randomForest from package randomForest. |

## Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values
are replaced by 0. This decision is motivated by the fact that any class that would have either a NA
precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)).
Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

## Value

An instance of class *"GenRegRes"*.

## Author(s)

Laurent Gatto

## See Also

[rfClassification](#) and example therein.

---

sampleMSnSet                    *Extract a stratified sample of an* MSnSet

---

## Description

This function extracts a stratified sample of an MSnSet.

## Usage

```
sampleMSnSet(object, fcol = "markers", size = 0.2, seed)
```

## Arguments

| | |
|---|---|
| object | An instance of class [MSnSet](#) |
| fcol | The feature meta-data column name containing the marker (vector or matrix) definitions on which the MSnSet will be stratified. Default is markers. |
| size | The size of the stratified sample to be extracted. Default is 0.2 (20 percent). |
| seed | The optional random number generator seed. |

## Value

A stratified sample (according to the defined fcol) which is an instance of class *"MSnSet"*.

## Author(s)

Lisa Breckels

## See Also

[testMSnSet](#) [unknownMSnSet](#) [markerMSnSet](#). See [markers](#) for details about markers encoding.

## Examples

```
library(pRolocdata)
data(tan2009r1)
dim(tan2009r1)
smp <- sampleMSnSet(tan2009r1, fcol = "markers")
dim(smp)
getMarkers(tan2009r1)
getMarkers(smp)
```

---

setLisacol                    *Manage default colours and point characters*

---

## Description

These functions allow to get/set the colours and point character that are used when plotting organelle clusters and unknown features. These values are parametrised at the session level. Two palettes are available: the default palette (previously *Lisa's colours*) containing 30 colours and the old (original) palette, containing 13 colours.

## Usage

```
setLisacol()

getLisacol()

getOldcol()

setOldcol()

getStockcol()

setStockcol(cols)

getStockpch()

setStockpch(pchs)

getUnknowncol()

setUnknowncol(col)

getUnknownpch()

setUnknownpch(pch)
```

## Arguments

| | |
|---|---|
| cols | A vector of colour characters or NULL, which sets the colours to the default values. |
| pchs | A vector of numeric or NULL, which sets the point characters to the default values. |
| col | A colour character or NULL, which sets the colour to #E7E7E7 (grey91), the default colour for unknown features. |
| pch | A numeric vector of length 1 or NULL, which sets the point character to 21, the default. |

## Value

The set functions set (and invisibly returns) colours. The get functions returns a character vector of colours. For the pch functions, numerics rather than characters.

## Author(s)

Laurent Gatto

## Examples

```
## defaults for clusters
getStockcol()
getStockpch()
## unknown features
getUnknownpch()
getUnknowncol()
## an example
library(pRolocdata)
data(dunkley2006)
par(mfrow = c(2, 1))
plot2D(dunkley2006, fcol = "markers", main = 'Default colours')
setUnknowncol("black")
plot2D(dunkley2006, fcol = "markers", main = 'setUnknowncol("black")')
getUnknowncol()
setUnknowncol(NULL)
getUnknowncol()
getStockcol()
getOldcol()
```

---

showGOEvidenceCodes    *GO Evidence Codes*

---

## Description

This function prints a textual description of the Gene Ontology evidence codes.

## Usage

```
showGOEvidenceCodes()

getGOEvidenceCodes()
```

## Value

These functions are used for their side effects of printing evidence codes and their description.

## Author(s)

Laurent Gatto

## Examples

```
showGOEvidenceCodes()
getGOEvidenceCodes()
```

---

spatial2D                    *Uncertainty plot in localisation probabilities*

---

## Description

Produces a pca plot with spatial variation in localisation probabilities

## Usage

```
spatial2D(object, dims = c(1, 2), cov.function = fields::wendland.cov,
  theta = 1, derivative = 2, k = 1, breaks = c(0.99, 0.95, 0.9,
  0.85, 0.8, 0.75, 0.7), aspect = 0.5)
```

## Arguments

| | |
|---|---|
| object | A valid object of class MSnset with mcmc prediction results from tagmMCMCpredict |
| dims | The PCA dimension in which to project he data, default is c(1,2) |
| cov.function | The covariance function used default is wendland.cov. See fields package. |
| theta | A hyperparameter to the covariance function. See fields package. Default is 1. |
| derivative | The number of derivative of the wendland kernel. See fields package. Default is 2. |
| k | A hyperparamter to the covariance function. See fields package. Default is 1. |
| breaks | Probability values at which to draw the contour bands. Default is c(0.99, 0.95, 0.9, 0.85, 0.8, 0.75, 0.7) |
| aspect | A argument to change the plotting aspect of the PCA |

## Value

Used for side effect of producing plot. Invisibily returns an ggplot object that can be further manipulated

## Author(s)

Oliver M. Crook <omc25@cam.ac.uk>

## Examples

```
## Not run:
library("pRolocdata")
data("tan2009r1")

tanres <- tagmMcmcTrain(object = tan2009r1)
tanres <- tagmMcmcProcess(tanres)
tan2009r1 <- tagmMcmcPredict(object = tan2009r1, params = tanres, probJoint = TRUE)
spatial2D(object = tan2009r1)

## End(Not run)
```

---

SpatProtVis-class　　　　　　*Class* SpatProtVis

---

## Description

A class for spatial proteomics visualisation, that upon instantiation, pre-computes all defined visualisations. Objects can be created with the SpatProtVis constructor and visualised with the plot method.

The class is essentially a wrapper around several calls to [plot2D](#) that stores the dimensionality reduction outputs, and is likely to be updated in the future.

## Usage

```
SpatProtVis(x, methods, dims, methargs, ...)
```

## Arguments

| | |
|---|---|
| x | An instance of class [MSnSet](#) to visualise. |
| methods | Dimensionality reduction methods to be used to visualise the data. Must be contained in [plot2Dmethods](#) (except "scree"). See [plot2D](#) for details. |
| dims | A list of numerics defining dimensions used for plotting. Default are 1 and 2. If provided, the length of this list must be identical to the length of methods. |
| methargs | A list of additional arguments to be passed for each visualisation method. If provided, the length of this list must be identical to the length of methods. |
| ... | Additional arguments. Currently ignored. |

**Slots**

vismats: A "list" of matrices containing the feature projections in 2 dimensions.

data: The original spatial proteomics data stored as an "MSnSet".

methargs: A "list" of additional plotting arguments.

objname: A "character" defining how to name the dataset. By default, this is set using the variable name used at object creation.

**Methods**

plot: Generates the figures for the respective methods and additional arguments defined in the constructor. If used in an interactive session, the user is prompted to press 'Return' before new figures are displayed.

show: A simple textual summary of the object.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

The data for the individual visualisations is created by plot2D.

**Examples**

```
library("pRolocdata")
data(dunkley2006)
## Default parameters for a set of methods
## (in the interest of time, don't use t-SNE)
m <- c("PCA", "MDS", "kpca")
vis <- SpatProtVis(dunkley2006, methods = m)
vis
plot(vis)
plot(vis, legend = "topleft")

## Setting method arguments
margs <- c(list(kpar = list(sigma = 0.1)),
           list(kpar = list(sigma = 1.0)),
           list(kpar = list(sigma = 10)),
           list(kpar = list(sigma = 100)))
vis <- SpatProtVis(dunkley2006,
                   methods = rep("kpca", 4),
                   methargs = margs)
par(mfrow = c(2, 2))
plot(vis)

## Multiple PCA plots but different PCs
dims <- list(c(1, 2), c(3, 4))
vis <- SpatProtVis(dunkley2006, methods = c("PCA", "PCA"), dims = dims)
plot(vis)
```

---

subsetMarkers                    *Subsets markers*

---

### Description

Subsets a matrix of markers by specific terms

### Usage

```
subsetMarkers(object, fcol = "GOAnnotations", keep)
```

### Arguments

| | |
|---|---|
| object | An instance of class MSnSet. |
| fcol | The name of the markers matrix. Default is GOAnnotations. |
| keep | Integer or character vector specifying the columns to keep in the markers matrix, as defined by fcol. |

### Value

An updated MSnSet

### Author(s)

Lisa M Breckels

### See Also

addGoAnnotations and example therein.

---

svmClassification                *svm classification*

---

### Description

Classification using the support vector machine algorithm.

### Usage

```
svmClassification(object, assessRes, scores = c("prediction", "all",
  "none"), cost, sigma, fcol = "markers", ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| assessRes | An instance of class `"GenRegRes"`, as generated by `svmOptimisation`. |
| scores | One of `"prediction"`, `"all"` or `"none"` to report the score for the predicted class only, for all classes or none. |
| cost | If `assessRes` is missing, a `cost` must be provided. |
| sigma | If `assessRes` is missing, a `sigma` must be provided. |
| fcol | The feature meta-data containing marker definitions. Default is `markers`. |
| ... | Additional parameters passed to `svm` from package e1071. |

## Value

An instance of class `"MSnSet"` with `svm` and `svm.scores` feature variables storing the classification results and scores respectively.

## Author(s)

Laurent Gatto

## Examples

```
library(pRolocdata)
data(dunkley2006)
## reducing parameter search space and iterations
params <- svmOptimisation(dunkley2006, cost = 2^seq(-2,2,2), sigma = 10^seq(-1, 1, 1), times = 3)
params
plot(params)
f1Count(params)
levelPlot(params)
getParams(params)
res <- svmClassification(dunkley2006, params)
getPredictions(res, fcol = "svm")
getPredictions(res, fcol = "svm", t = 0.75)
plot2D(res, fcol = "svm")
```

---

svmOptimisation             *svm parameter optimisation*

---

## Description

Classification parameter optimisation for the support vector machine algorithm.

## Usage

```
svmOptimisation(object, fcol = "markers", cost = 2^(-4:4),
  sigma = 10^(-3:2), times = 100, test.size = 0.2, xval = 5,
  fun = mean, seed, verbose = TRUE, ...)
```

## Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| fcol | The feature meta-data containing marker definitions. Default is `markers`. |
| cost | The hyper-parameter. Default values are `2^-4:4`. |
| sigma | The hyper-parameter. Default values are `10^(-2:3)`. |
| times | The number of times internal cross-validation is performed. Default is 100. |
| test.size | The size of test data. Default is 0.2 (20 percent). |
| xval | The n-cross validation. Default is 5. |
| fun | The function used to summarise the xval macro F1 matrices. |
| seed | The optional random number generator seed. |
| verbose | A `logical` defining whether a progress bar is displayed. |
| ... | Additional parameters passed to `svm` from package `e1071`. |

## Details

Note that when performance scores precision, recall and (macro) F1 are calculated, any NA values are replaced by 0. This decision is motivated by the fact that any class that would have either a NA precision or recall would result in an NA F1 score and, eventually, a NA macro F1 (i.e. mean(F1)). Replacing NAs by 0s leads to F1 values of 0 and a reduced yet defined final macro F1 score.

## Value

An instance of class `"GenRegRes"`.

## Author(s)

Laurent Gatto

## See Also

`svmClassification` and example therein.

---

tagmMcmcTrain          *Localisation of proteins using the TAGM MCMC method*

---

## Description

These functions implement the T augmented Gaussian mixture (TAGM) model for mass spectrometry-based spatial proteomics datasets using Markov-chain Monte-Carlo (MCMC) for inference.

## Usage

```
tagmMcmcTrain(object, fcol = "markers", method = "MCMC",
  numIter = 1000L, burnin = 100L, thin = 5L, mu0 = NULL,
  lambda0 = 0.01, nu0 = NULL, S0 = NULL, beta0 = NULL, u = 2,
  v = 10, numChains = 4L, BPPARAM = BiocParallel::bpparam())

tagmMcmcPredict(object, params, fcol = "markers", probJoint = FALSE,
  probOutlier = TRUE)

tagmPredict(object, params, fcol = "markers", probJoint = FALSE,
  probOutlier = TRUE)

tagmMcmcProcess(params)
```

## Arguments

| | |
|---|---|
| object | An [MSnbase::MSnSet](MSnbase::MSnSet) containing the spatial proteomics data to be passed to `tagmMcmcTrain` and `tagmPredict`. |
| fcol | The feature meta-data containing marker definitions. Default is `markers`. |
| method | A `charachter()` describing the inference method for the TAGM algorithm. Default is `"MCMC"`. |
| numIter | The number of iterations of the MCMC algorithm. Default is 1000. |
| burnin | The number of samples to be discarded from the begining of the chain. Default is 100. |
| thin | The thinning frequency to be applied to the MCMC chain. Default is 5. |
| mu0 | The prior mean. Default is `colMeans` of the expression data. |
| lambda0 | The prior shrinkage. Default is 0.01. |
| nu0 | The prior degreed of freedom. Default is `ncol(exprs(object)) + 2` |
| S0 | The prior inverse-wishart scale matrix. Empirical prior used by default. |
| beta0 | The prior Dirichlet distribution concentration. Default is 1 for each class. |
| u | The prior shape parameter for Beta(u, v). Default is 2 |
| v | The prior shape parameter for Beta(u, v). Default is 10. |
| numChains | The number of parrallel chains to be run. Default it 4. |
| BPPARAM | Support for parallel processing using the `BiocParallel` infrastructure. When missing (default), the default registered `BiocParallelParam` parameters are used. Alternatively, one can pass a valid `BiocParallelParam` parameter instance: `SnowParam`, `MulticoreParam`, `DoparParam`, ... see the `BiocParallel` package for details. |
| params | An instance of class `MCMCParams`, as generated by [tagmMcmcTrain()](tagmMcmcTrain()). |
| probJoint | A `logical(1)` indicating whether to return the joint probability matrix, i.e. the probability for all classes as a new `tagm.mcmc.joint` feature variable. |
| probOutlier | A `logical(1)` indicating whether to return the probability of being an outlier as a new `tagm.mcmc.outlier` feature variable. A high value indicates that the protein is unlikely to belong to any annotated class (and is hence considered an outlier). |

**Details**

The `tagmMcmcTrain` function generates the samples from the posterior distributions (object or class MCMCParams) based on an annotated quantitative spatial proteomics dataset (object of class `MSnbase::MSnSet`). Both are then passed to the `tagmPredict` function to predict the sub-cellular localisation of protein of unknown localisation. See the *pRoloc-bayesian* vignette for details and examples. In this implementation, if numerical instability is detected in the covariance matrix of the data a small multiple of the identity is added. A message is printed if this conditioning step is performed.

**Value**

`tagmMcmcTrain` returns an instance of class `MCMCParams`.

`tagmMcmcPredict` returns an instance of class `MSnbase::MSnSet` containing the localisation predictions as a new `tagm.mcmc.allocation` feature variable. The allocation probability is encoded as `tagm.mcmc.probability` (corresponding to the mean of the distribution probability). In additionm the upper and lower quantiles of the allocation probability distribution are available as `tagm.mcmc.probability.lowerquantile` and `tagm.mcmc.probability.upperquantile` feature variables. The Shannon entropy is available in the `tagm.mcmc.mean.shannon` feature variable, measuring the uncertainty in the allocations (a high value representing high uncertainty; the highest value is the natural logarithm of the number of classes).

`tagmMcmcProcess` returns an instance of class `MCMCParams` with its summary slot populated.

**References**

*A Bayesian Mixture Modelling Approach For Spatial Proteomics* Oliver M Crook, Claire M Mulvey, Paul D. W. Kirk, Kathryn S Lilley, Laurent Gatto bioRxiv 282269; doi: https://doi.org/10.1101/282269

**See Also**

The `plotEllipse()` function can be used to visualise TAGM models on PCA plots with ellipses.

---

testMarkers                     *Tests marker class sizes*

---

**Description**

Tests if the marker class sizes are large enough for the parameter optimisation scheme, i.e. the size is greater that xval + n, where the default xval is 5 and n is 2. If the test is unsuccessful, a warning is thrown.

**Usage**

```
testMarkers(object, xval = 5, n = 2, fcol = "markers",
  error = FALSE)
```

## Arguments

| | |
|---|---|
| object | An instance of class `"MSnSet"`. |
| xval | The number cross-validation partitions. See the `xval` argument in the parameter optimisation function(s). Default is 5. |
| n | Number of additional examples. |
| fcol | The name of the prediction column in the `featureData` slot. Default is `"markers"`. |
| error | A `logical` specifying if an error should be thown, instead of a warning. |

## Details

In case the test indicates that a class contains too few examples, it is advised to either add some or, if not possible, to remove the class altogether (see `minMarkers`) as the parameter optimisation is likely to fail or, at least, produce unreliable results for that class.

## Value

If successfull, the test invisibly returns NULL. Else, it invisibly returns the names of the classes that have too few examples.

## Author(s)

Laurent Gatto

## See Also

`getMarkers` and `minMarkers`

## Examples

```
library("pRolocdata")
data(dunkley2006)
getMarkers(dunkley2006)
testMarkers(dunkley2006)
toosmall <- testMarkers(dunkley2006, xval = 15)
toosmall
try(testMarkers(dunkley2006, xval = 15, error = TRUE))
```

---

testMSnSet             *Create a stratified 'test'* MSnSet

---

## Description

This function creates a stratified 'test' MSnSet which can be used for algorihtmic development. A `"MSnSet"` containing only the marker proteins, as defined in fcol, is returned with a new feature data column appended called test in which a stratified subset of these markers has been relabelled as 'unknowns'.

## Usage

```
testMSnSet(object, fcol = "markers", size = 0.2, seed)
```

## Arguments

| | |
|---|---|
| object | An instance of class ["MSnSet"](#) |
| fcol | The feature meta-data column name containing the marker definitions on which the data will be stratified. Default is markers. |
| size | The size of the data set to be extracted. Default is 0.2 (20 percent). |
| seed | The optional random number generator seed. |

## Value

An instance of class *"MSnSet"* which contains only the proteins that have a labelled localisation i.e. the marker proteins, as defined in fcol and a new column in the feature data slot called test which has part of the labels relabelled as "unknown" class (the number of proteins renamed as "unknown" is according to the parameter size).

## Author(s)

Lisa Breckels

## See Also

[sampleMSnSet](#) [unknownMSnSet](#) [markerMSnSet](#)

## Examples

```
library(pRolocdata)
data(tan2009r1)
sample <- testMSnSet(tan2009r1)
getMarkers(sample, "test")
all(dim(sample) == dim(markerMSnSet(tan2009r1)))
```

---

thetas                          *Draw matrix of thetas to test*

---

## Description

The possible weights to be considered is a sequence from 0 (favour auxiliary data) to 1 (favour primary data). Each possible combination of weights for nclass classes must be tested. The thetas function produces a weight matrix for nclass columns (one for each class) with all possible weight combinations (number of rows).

## Usage

```
thetas(nclass, by = 0.5, length.out, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| `nclass` | Number of marker classes |
| `by` | The increment of the weights. One of `1`, `0.5`, `0.25`, `2`, `0.1` or `0.05`. |
| `length.out` | The desired length of the weight sequence. |
| `verbose` | A `logical` indicating if the weight sequences should be printed out. Default is `TRUE`. |

## Value

A matrix with all possible theta weight combinations.

## Author(s)

Lisa Breckels

## Examples

```
dim(thetas(4, by = 0.5))
dim(thetas(4, by = 0.2))
dim(thetas(5, by = 0.2))
dim(thetas(5, length.out = 5))
dim(thetas(6, by = 0.2))
```

---

| undocumented | *Undocumented/unexported entries* |
|---|---|

---

## Description

This is just a dummy entry for methods from unexported classes that generate warnings during package checking.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

---

zerosInBinMSnSet            *Compute the number of non-zero values in each marker classes*

---

### Description

The function assumes that its input is a binary MSnSet and computes, for each marker class, the number of non-zero expression profiles. The function is meant to be used to produce heatmaps (see the example) and visualise binary (such as GO) MSnSet objects and assess their utility: all zero features/classes will not be informative at all (and can be filtered out with [filterBinMSnSet](#)) while features/classes with many annotations (GO terms) are likely not be be informative either.

### Usage

```
zerosInBinMSnSet(object, fcol = "markers", as.matrix = TRUE,
  percent = TRUE)
```

### Arguments

| | |
|---|---|
| object | An instance of class MSnSet with binary data. |
| fcol | A character defining the feature data variable to be used as markers. Default is "markers". |
| as.matrix | If TRUE (default) the data is formatted and returned as a matrix. Otherwise, a list is returned. |
| percent | If TRUE, percentages are returned. Otherwise, absolute values. |

### Value

A matrix or a list indicating the number of non-zero value per marker class.

### Author(s)

Laurent Gatto

### See Also

[filterBinMSnSet](#)

### Examples

```
library(pRolocdata)
data(hyperLOPIT2015goCC)
zerosInBinMSnSet(hyperLOPIT2015goCC)
zerosInBinMSnSet(hyperLOPIT2015goCC, percent = FALSE)
pal <- colorRampPalette(c("white", "blue"))
library(lattice)
levelplot(zerosInBinMSnSet(hyperLOPIT2015goCC),
          xlab = "Number of non-0s",
          ylab = "Marker class",
          col.regions = pal(140))
```

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