Package: clst (via r-universe)

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Type Package

Title Classification by local similarity threshold

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Description Package for modified nearest-neighbor classification based on calculation of a similarity threshold distinguishing within-group from between-group comparisons.

License GPL-3

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Contents

clst-package 2
actino 3
bvseqs 4
classify 5
findThreshold 7
plotDistances 9
printClst 10
scaleDistPlot 11
strep 13

Index **14**

`clst-package` *Classification by local similarity threshold*

Description

Package for modified nearest-neighbor classification based on calculation of a similarity threshold distinguishing within-group from between-group comparisons.

Details

Package:	clst
Type:	Package
License:	GPL-3
Author:	Noah Hoffman <ngh2@uw.edu>

Index:

Further information is available in the following vignettes:

`clstDemo`	clst (source, pdf)

TODO: write package overview.

Author(s)

Noah Hoffman

Maintainer: <ngh2@uw.edu>

See Also

`cmdscale`

Examples

```
library(clst)
packageDescription("clst")
data(iris)
dmat <- as.matrix(dist(iris[,1:4], method="euclidean"))
groups <- iris$Species
i <- 1
cc <- classify(dmat, groups, dvect=dmat[i,])
cat('query at i =',i,'is species',paste('I.', groups[i]),'\n')
```

```
printClst(cc)
i <- 125
cc <- classify(dmat, groups, dvect=dmat[i,])
cat('query at i =',i,'is species',paste('I.', groups[i]),'\n')
printClst(cc)
```

---

actino *Actinomyces data set*

Description

Square matrices decsribing pairwise distances among 16s rRNA sequences.

Usage

```
data(actino)
```

Format

```
List of 5
 $ dmat1 : num [1:146, 1:146] 0 0.763 1.25 10.345 12.771 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:146] "200" "201" "202" "203" ...
  .. ..$ : chr [1:146] "200" "201" "202" "203" ...
 $ dmat2 : num [1:146, 1:146] 0 0.574 1.044 5.669 8.409 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:146] "200" "201" "202" "203" ...
  .. ..$ : chr [1:146] "200" "201" "202" "203" ...
 $ dmat3 : num [1:146, 1:146] 0 0.763 1.25 8.571 11.233 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:146] "200" "201" "202" "203" ...
  .. ..$ : chr [1:146] "200" "201" "202" "203" ...
 $ taxa  : Factor w/ 33 levels "Actinomyces bowdenii",..: 12 12 12 23 20 20 8 22 12 20 ...
 $ abbrev: Factor w/ 33 levels "A bowdenii","A canis",..: 12 12 12 23 20 20 8 22 12 20 ...
```

Details

The matrices `$dmat1`, `dmat2`, and `dmat3` contain percent nucleotide difference with indels penalized heavily, little, and somewhat, respectively.

`$taxa` is a factor of species names; abbreviations of the same names are found in `$abbrev`.

Examples

```
data(actino)
```

bvseqs *BV reference set.*

Description

Tree-derived pairwise distances and taxonomic assignments among 16S rRNA sequences representing bacteria represented in the vaginal mucosa.

Usage

```
data(bvseqs)
```

Format

```
  The format is:
List of 3
 $ dmat    : num [1:448, 1:448] 0 0.0494 0.0968 0.1002 0.1606 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:448] "S001098970" "S000859776" "S000539896" "S001352901" ...
  .. ..$ : chr [1:448] "S001098970" "S000859776" "S000539896" "S001352901" ...
 $ groupTab:'data.frame': 448 obs. of  12 variables:
  ..$ superkingdom    : chr [1:448] "2" "2" "2" "2" ...
  ..$ superphylum     : chr [1:448] NA NA NA NA ...
  ..$ phylum          : chr [1:448] "1224" "1224" "1224" "1224" ...
  ..$ class           : chr [1:448] "1236" "1236" "1236" "1236" ...
  ..$ subclass        : chr [1:448] NA NA NA NA ...
  ..$ order           : chr [1:448] "72274" "72274" "72274" "72274" ...
  ..$ suborder        : chr [1:448] NA NA NA NA ...
  ..$ family          : chr [1:448] "468" "468" "468" "468" ...
  ..$ genus           : chr [1:448] "469" "469" "469" "469" ...
  ..$ species_group   : chr [1:448] NA NA NA NA ...
  ..$ species_subgroup: chr [1:448] NA NA NA NA ...
  ..$ species         : chr [1:448] "470" "470" "471" "470" ...
 $ taxNames: Named chr [1:212] "Actinomyces urogenitalis" "Lactobacillus jensenii" "Proteobacteria" "Ga
  ..- attr(*, "names")= chr [1:212] "103621" "109790" "1224" "1236" ...
```

Details

(Describe creation of this data set)

Source

Sequences were assembled from both the RDP 16S rRNA database and from the laboratory of Dr. David Fredricks.

References

RDP url here.

Examples

```
data(bvseqs)
## maybe str(bvseqs) ; plot(bvseqs) ...
```

`classify` *classify*

Description

Functions to perform classification by local similarity threshold.

Usage

```
classify(dmat, groups, dvect, method = "mutinfo", minScore = 0.45,
         doffset = 0.5, dStart = NA, maxDepth = 10, minGroupSize = 2,
         objNames = names(dvect), keep.data = TRUE, ..., verbose =
         FALSE)

classifyIter(dmat, groupTab, dvect, dStart = NA, multiple = FALSE,
             keep.data = TRUE, ..., verbose = FALSE)

classifier(dmat, groups, dvect, method = 'mutinfo', minScore = 0.45,
           doffset = 0.5, dStart = NA, minGroupSize = 2,
           objNames = names(dvect), keep.data = TRUE, ..., verbose = FALSE,
           depth = 1)

pull(dmat, groups, index)

pullTab(dmat, groupTab, index)
```

Arguments

`dmat`	Square matrix of pairwise distances.
`groups`	Object coercible to a factor identifying group membership of objects corresponding to either edge of `dmat`.
`groupTab`	a data.frame representing a taxonomy, with columns in increasing order of specificity from left to right (ie, Kingdom –> Species). Column names are used to name taxonomic ranks. Rows correspond to margins of dmat.
`dvect`	numeric vector of distance from query sequence to each reference corresponding to margins of dmat.
`method`	The method for calculating the threshold; only 'mutinfo' is currently implemented.
`minScore`	Threshold value for the match score to define a match.

doffset	Offset used in the denominator of the expression to calculate match score to penalize very small groups of reference objects.
dStart	start with this value of D.
multiple	if TRUE, stops at the rank that yields at least one match; if FALSE, continues to perform classification until exactly one match is identified.
maxDepth	Maximum number of iterations that will be attempted to perform classification.
minGroupSize	The minimal number of members comprising at least one group required to attempt classification.
objNames	Optional character identifiers for objects corresponding to margin of dmat.
keep.data	Populates thresh$distances (see findThreshold) if TRUE.
verbose	Terminal output is produced if TRUE.
index	an integer specifying an element in dmat
...	see Details
depth	specifies iteration number (not meant to be user-defined)

Details

classify performs iterative classification. See the vignette vignette for package **clst** for a description of the classification algorithm.

classifier performs non-iterative classification, and is typically not called directly by the user.

The functions pull and pullTab are used to remove a single element of dmat for the purpose of performing classification agains the remaining elements. The value of these two functions (a list) can be passed directly to classify or classifyIter directly (see examples).

Value

classify and classifyIter return x, a list of lists, one for each iteration of the classifier. Each sub-list contains the following named elements:

depth	An integer indicating the number of the iteration (where x[[i]]$depth == i)
tally	a data.frame with one row for each group or reference objects. Columns below and above contain counts of reference objects with distance values greater than or less than *D*, respectively; score, containing match score S; match is 1 if $S \geq minScore$, 0 otherwise; and the minimum, median, and maximum values of distances to all members of the indicated group.
details	a list of two matrices, named "below" and "above", itemizing each object with index *i* in the reference set with distances below or above the distance threshold *D*, respectively. Columns include index, the index *i*; dist, the distance between the object and the query; and group, indicating the classification of the object.
matches	Character vector naming groups to which query object belongs.
thresh	object returned by findThreshold
params	a list of input arguments and their values
input	list containing copies of dvect and groups

Author(s)

Noah Hoffman

See Also

findThreshold

Examples

```
## illustrate classification using the Iris data set
data(iris)
dmat <- as.matrix(dist(iris[,1:4], method="euclidean"))
groups <- iris$Species

## remove one element from the data set and perform classification using
## the remaining elements as the reference set
ind <- 1
cat(paste('class of "unknown" sample is Iris',groups[ind]),fill=TRUE)
cc <- classify(dmat[-ind,-ind], groups[-ind], dvect=dmat[ind, -ind])
printClst(cc)

## this operation can be performed conveinetly using the `pull` function
ind <- 51
cat(paste('class of "unknown" sample is Iris',groups[ind]),fill=TRUE)
cc <- do.call(classify, pull(dmat, groups, ind))
printClst(cc)
str(cc)
```

---

findThreshold *findThreshold*

Description

Identify a distance threshold predicting whether a pairwise distance represents a comparison between objects in the same class (within-group comparison) or different classes (between-group comparison) given a matrix providing distances between objects and the group membership of each object.

Usage

```
findThreshold(dmat, groups, distances, method = "mutinfo", prob = 0.5,
              na.rm = FALSE, keep.dists = TRUE, roundCuts = 2, minCuts =
              20, maxCuts = 300, targetCuts = 100, verbose = FALSE,
              depth = 1, ...)

partition(dmat, groups, include, verbose = FALSE)
```

Arguments

dmat	Square matrix of pairwise distances.
groups	Object coercible to a factor identifying group membership of objects corresponding to either edge of dmat.
include	vector (numeric or boolean) indicating which elements to retain in the output; comparisons including an excluded element will have a value of NA
distances	Optional output of partition provided in the place of dmat and groups
method	The method for calculating the threshold; only 'mutinfo' is currently implemented.
prob	Sets the upper and lower bounds of D as some quantile of the within class distances and between-class differences, respectively.
na.rm	If TRUE, excludes NA elements in groups and corresponding rows and columns in dmat. Ignored if distances is provided.
keep.dists	If TRUE, the output will contain the distances element (output of partition).
roundCuts	Number of digits to round cutoff values (see Details)
minCuts	Minimal length of vector of cutoffs (see Details).
maxCuts	Maximal length of vector of cutoffs (see Details)
targetCuts	Length of vector of cutoffs if conditions met by minCuts and maxCuts are not met (see Details).
verbose	Terminal output is produced if TRUE.
depth	Private argument used to track level of recursion.
...	Extra arguments are ignored.

Details

findThreshold is used internally in classify, but may also be used to calculate a starting value of D.

partition is used to transform a square (or lower triangular) distance matrix into a data.frame containing a column of distances ($vals) along with a factor ($comparison) defining each distance as a within- or between-group comparison. Columns $row and $col provide indices of corresponding rows and columns of dmat.

Value

In the case of findThreshold, output is a list with elements decsribed below. In the case of partition, output is the data.frame returned as the element named $distances in the output of findThreshold.

D	The distance threshold (distance cutoff corresponding to the PMMI).
pmmi	Value of the point of maximal mutual information (PMMI)
interval	A vector of length 2 indicating the upper and lower bounds over which values for the threshold are evaluated.

breaks	A data.frame with columns x and y providing candidiate breakpoints and corresponding mutual information values, respectively.
distances	If keep.distances is TRUE, a data.frame containing pairwise distances identified as within- or between classes.
method	Character corresponding to input argument method.
params	Additional input parameters.

Author(s)

Noah Hoffman

See Also

plotDistances, plotMutinfo

Examples

```
data(iris)
dmat <- as.matrix(dist(iris[,1:4], method="euclidean"))
groups <- iris$Species
thresh <- findThreshold(dmat, groups, type="mutinfo")
str(thresh)
```

---

plotDistances *Visualize results of* link{findThreshold}

Description

The functions plotDistances and plotMutinfo are used to visualize the distance threshold calculated by findThreshold in the context of pairwise distances among objects in the reference set.

Usage

```
plotDistances(distances, D = NA, interval = NA,
              ylab = "distances", ...)

plotMutinfo(breaks, D = NA, interval = NA,
            xlab = "distance", ylab = "mutual information", ...)
```

Arguments

distances	The $distances element of the output value of findThreshold
breaks	The $breaks element of the output value of findThreshold
D	The distance threshold
interval	The range of values over which candidiate values of PMMI are evaluated.
xlab	Label the x axis of the plot.

ylab	Label the y axis of the plot.
...	Additional arguments are passed to bwplot (plotDistances) or xyplot (plotMutinfo)

Details

plotDistances produces a box-and-whisker plot contrasting within- and between-group distances. plotMutinfo produces a plot of cutpoints vs mutual information scores.

Value

Returns a lattice grid object.

Author(s)

Noah Hoffman

See Also

findThreshold

Examples

```
data(iris)
dmat <- as.matrix(dist(iris[,1:4], method="euclidean"))
groups <- iris$Species
thresh <- findThreshold(dmat, groups)
do.call(plotDistances, thresh)
do.call(plotMutinfo, thresh)
```

---

printClst *Print a summary of the classifier output.*

Description

Prints a description of the output of classify.

Usage

```
printClst(cc, rows = 8, nameWidth = 30, groupNames)
```

Arguments

cc	Output of classify
rows	Number of rows corresponding to groups of reference objects to show.
nameWidth	Character width of group names.
groupNames	a named vector containing replacement names for groups keyed by categories in groups (classify) or groupTab (classifyIter).

Value

Output value is NULL; output is to stdout.

Author(s)

Noah Hoffman

See Also

classify, classifyIter

Examples

```
data(iris)
dmat <- as.matrix(dist(iris[,1:4], method="euclidean"))
groups <- iris$Species
```

---

scaleDistPlot *Annotated multidimensional scaling plots.*

Description

Produces annotated representations of two-dimensional multidimensional scaling plots using cmdscale.

Usage

```
scaleDistPlot(dmat, groups, fill, X, O, indices = "no",
              include, display, labels,
              shuffleGlyphs = NA, key = "top",
              keyCols = 4, glyphs,
              xflip = FALSE, yflip = FALSE, ...)
```

Arguments

dmat	Square matrix of pairwise distances.
groups	Object coercible to a factor identifying group membership of objects corresponding to either edge of dmat.
fill	vector (logical or indices) of points to fill
X	vector of points to mark with an X
O	vector of points to mark with a circle
indices	label points with indices (all points if 'yes', or a subset indicated by a vector)
include	boolean or numeric vector of elements to include in call to cmdscale
display	boolean or numeric vector of elements to include in call to display

labels	list or data frame with parameters $i indicating indices and $text containing labels.
shuffleGlyphs	modify permutation of shapes and colors given an integer to serve as a random seed.
key	'right' (single column), 'top' (variable number of columns), or NULL for no key
keyCols	number of columns in key
glyphs	a data.frame with columns named col and pch corresponding to elements of unique(groups)
xflip	if TRUE, flip orientation of x-axis
yflip	if TRUE, flip orientation of y-axis
...	additional arguments are passed to xyplot

Value

Returns a lattice grid object.

Author(s)

Noah Hoffman

See Also

cmdscale, xyplot

Examples

```
data(iris)
dmat <- as.matrix(dist(iris[,1:4], method="euclidean"))
groups <- iris$Species

## visualize pairwise euclidean dstances among items in the Iris data set
fig <- scaleDistPlot(dmat, groups)
plot(fig)

## leave-one-out analysis of the classifier
loo <- lapply(seq_along(groups), function(i){
  do.call(classify, pull(dmat, groups, i))
})
matches <- lapply(loo, function(x) rev(x)[[1]]$matches)
result <- sapply(matches, paste, collapse='-')
confusion <- sapply(matches, length) > 1
no_match <- sapply(matches, length) < 1
plot(scaleDistPlot(dmat, groups, fill=confusion, O=confusion, X=no_match))
```

strep *Streptococcus data set.*

Description

Square matrices decsribing pairwise distances among 16s rRNA sequences.

Usage

```
data(strep)
```

Format

```
List of 5
 $ dmat1 : num [1:150, 1:150] 0 5.81 8.38 10.28 10.64 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:150] "197" "199" "207" "208" ...
  .. ..$ : chr [1:150] "197" "199" "207" "208" ...
 $ dmat2 : num [1:150, 1:150] 0 5.09 3.82 7.21 7.59 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:150] "197" "199" "207" "208" ...
  .. ..$ : chr [1:150] "197" "199" "207" "208" ...
 $ dmat3 : num [1:150, 1:150] 0 5.63 5.81 8.77 9.14 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:150] "197" "199" "207" "208" ...
  .. ..$ : chr [1:150] "197" "199" "207" "208" ...
 $ taxa  : Factor w/ 50 levels "Streptococcus acidominimus",..: 31 44 26 4 4 31 32 39 42 31 ...
 $ abbrev: Factor w/ 50 levels "S acidominimus",..: 31 44 26 4 4 31 32 39 42 31 ...
```

Details

The matrices `$dmat1`, `dmat2`, and `dmat3` contain percent nucleotide difference with indels penalized heavily, little, and somewhat, respectively.

`$taxa` is a factor of species names; abbreviations of the same names are found in `$abbrev`.

Examples

```
data(strep)
```

Index

∗ **classif**
  classify, 5
  clst-package, 2
  findThreshold, 7
  plotDistances, 9
∗ **datasets**
  actino, 3
  bvseqs, 4
  strep, 13
∗ **package**
  clst-package, 2

actino, 3

bvseqs, 4
bwplot, *10*

classifier *(*classify*)*, 5
classify, 5, *8*, *10, 11*
classifyIter, *10, 11*
classifyIter *(*classify*)*, 5
clst *(*clst-package*)*, 2
clst-package, 2
cmdscale, *2*, *11, 12*

findThreshold, *6*, 7, *7*, *9, 10*

partition, *8*
partition *(*findThreshold*)*, 7
plotDistances, 9, *9*
plotMutinfo, *9*
plotMutinfo *(*plotDistances*)*, 9
printClst, 10
pull *(*classify*)*, 5
pullTab *(*classify*)*, 5

scaleDistPlot, 11
strep, 13

xyplot, *10*, *12*