Package ‘clst’

January 30, 2017

Type Package
Title Classification by local similarity threshold
Version 1.22.0
Depends R (>= 2.10)
Imports ROC, lattice
Suggests RUnit
LazyLoad yes
LazyData yes
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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
biocViews Classification
NeedsCompilation no

R topics documented:

clst-package ........................................... 2
actino ................................................. 3
bvseqs ................................................ 3
classify ............................................. 4
findThreshold ........................................ 7
plotDistances .......................................... 9
printClst ............................................ 10
scaleDistPlot ........................................ 10
strep ............................................... 12

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

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

Square matrices describing 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)

Description

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

Usage

data(bvseqs)
classify

Format

The format is:
List of 3

$ dmat: num [1:448, 1:448] 0.0494 0.0968 0.1002...
 ..- attr(*, "dimnames")=List of 2
 .. ..$: chr [1:448] "S001098970" "S000859776"...
 .. ..$: chr [1:448] "S001098970" "S000859776"...

$ 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"...
 ..- 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

descr

Description

Functions to perform classification by local similarity threshold.
classify

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)

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)

Arguments

dmat  Square matrix of pairwise distances.
gruops 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)
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 against 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 \( S \geq \text{minScore} \), 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 conveniently using the 'pull' function
findThreshold

```r
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)
```

**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**

```r
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 $SD$. 

`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 described 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 candidate 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**

```r
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 candidate 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 distances 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 describing 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

*Topic `textasciitildekwd1`
  printClst, 10
  scaleDistPlot, 10

*Topic `textasciitildekwd2`
  printClst, 10

*Topic `classify`
  classify, 4
  clst-package, 2
  findThreshold, 7
  plotDistances, 9

*Topic `datasets`
  actino, 3
  bvseqs, 3
  strep, 12

*Topic `package`
  clst-package, 2

actino, 3
bvseqs, 3
bwplot, 9

classifier (classify), 4
classify, 4, 8, 10
classifyIter, 10
classifyIter (classify), 4
clst (clst-package), 2
clst-package, 2
cmdscale, 2, 10, 11
findThreshold, 5, 6, 7, 9
partition, 7
partition (findThreshold), 7
plotDistances, 8, 9
plotMutinfo, 8
plotMutinfo (plotDistances), 9
printClst, 10
pull (classify), 4
pullTab (classify), 4
scaleDistPlot, 10
strep, 12
xyplot, 9, 11