

# Package ‘clst’

May 20, 2024

**Type** Package

**Title** Classification by local similarity threshold

**Version** 1.53.0

**Depends** R (>= 2.10)

**Imports** ROC, lattice

**Suggests** RUnit

**LazyLoad** yes

**LazyData** yes

**Author** Noah Hoffman

**Maintainer** Noah Hoffman <ngh2@uw.edu>

**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

**git\_url** <https://git.bioconductor.org/packages/clst>

**git\_branch** devel

**git\_last\_commit** d898425

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-05-20

## Contents

clst-package . . . . .	2
actino . . . . .	3
bvseqs . . . . .	4
classify . . . . .	5
findThreshold . . . . .	7
plotDistances . . . . .	9

printClst . . . . .	10
scaleDistPlot . . . . .	11
strep . . . . .	13

<b>Index</b>	<b>14</b>
--------------	-----------

---

clst-package	<i>Classification by local similarity threshold</i>
--------------	---

---

## 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 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)
```

---

```
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 <a href="#">findThreshold</a> ) 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 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 $S \geq minScore$ , 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 <a href="#">findThreshold</a>
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
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**

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

<code>D</code>	The distance threshold (distance cutoff corresponding to the PMMI).
<code>pmmi</code>	Value of the point of maximal mutual information (PMMI)
<code>interval</code>	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**

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

---

plotDistances	<i>Visualize results of</i> <code>link{findThreshold}</code>
---------------	--

---

**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 <code>findThreshold</code>
breaks	The \$breaks element of the output value of <code>findThreshold</code>
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 <a href="#">xyplot</a>

**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, 0=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

## \* **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](#)