Package ‘cccd’

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cccd

Class Cover Catch Digraph

Description

Constructs a class cover catch digraph from points or interpoint distance matrices.

Usage

cccd(x = NULL, y = NULL, dxx = NULL, dyx = NULL, method = NULL,
      k = NA, algorithm = 'cover_tree')
ccccd.rw(x=NULL,y=NULL,dxx=NULL,dyx=NULL,method=NULL,m=1,d=2)
ccccd.classifier(x,y,dom.method='greedy',proportion=1,...)
ccccd.classify(data, C,method=NULL)
ccccd.classifier.rw(x,y,m=1,d=2)
ccccd.multiclass.classifier(data, classes, dom.method='greedy',proportion=1,...)
ccccd.multiclass.classify(data,C,method=NULL)

## S3 method for class 'cccd'
plot(x, ..., plot.circles = FALSE, dominate.only = FALSE,
     D = NULL, vertex.size = 2, vertex.label = NA,
     vertex.color = "SkyBlue2", dom.color = "Blue",
     ypch = 20, ycex = 1.5, ycol = 2,
     use.circle.radii = FALSE, balls = FALSE,
     ball.color = gray(0.8), square = FALSE, xlim, ylim)

## S3 method for class 'cccdClassifier'
plot(x, ..., xcol=1,ycol=2,xpch=xpch,
     balls=FALSE,add=FALSE)

Arguments

x, y            the target class and non-target class points. Either x,y or dxx,dyx must be pro-
                vided. In the case of plot, x is an object of class cccd.
dxx,dyx         interpoint distances (x against x and y against x). If these are not provided they
                are computed using x and y.
method          the method used for the distance. See dist.
dom.method,proportion
k                the method used for the domination set computation, and the proportion of
                points required to dominate. See dominate.
algorithm       See get.knn.
m                slope of the null hypothesis curve
data             data to be classified
The class cover catch digraph is a graph with vertices defined by the points of \( x \) and edges defined according to the balls \( B(x, d(x, Y)) \). There is an edge between vertices \( x_1, x_2 \) if \( x_2 \in B(x_1, d(x_1, Y)) \). If \( \text{dyx} \) is not given and the method is 'euclidean', then \( \text{get.knnx} \) is used to find the nearest \( Y \) to each \( x \). If \( k \) is given, only the \( k \) nearest neighbors to each point are candidates for covering. Thus the \( \text{cccd} \) will be approximate, but the computation will (generally) be faster. Since \( \text{get.knn} \) uses Euclidean distance, these choices will only be valid for this distance metric. Since the graph will tend to be larger than otherwise, the dominating set computation will be slower, so one should trade-off speed of calculation, approximation, and the \( \text{prop} \) option to the dominating set (which can make that calculation faster at the cost of returning a subset of the dominating set).

**Details**

- **Value**
  - an object of class igraph. In addition, it contains the attributes:
    - \( \text{R} \): a vector of radii.
    - \( \text{Y} \): the \( Y \) vectors.
    - \( \text{layout} \): the \( x \) vectors.
  - In the case of the classifier, the attributes are:
    - \( \text{Rx, Ry} \): vectors of radii.
    - \( \text{Cx, Cy} \): the ball centers.
Note

The plotting assumes the cccd used Euclidean distance, and so the balls/circles will be Euclidean balls/circles. If the method used in the distance was some other metric, you’ll have to plot the balls/circles yourself if you want them to be correct on the plot.

Author(s)

David J. Marchette, david.marchette@navy.mil

References


See Also

ccd, rng, gg, dist, get.knn dominate

Examples

```r
set.seed(456330)
z <- matrix(runif(1000),ncol=2)
ind <- which(z[,1]<.5 & z[,2]<.5)
x <- z[ind,]
y <- z[-ind,]
g <- cccd(x,y)
C <- cccd.classifier(x,y)
z2 <- matrix(runif(1000),ncol=2)
ind <- which(z2[,1]<.5 & z2[,2]<.5)
cls <- rep(0,nrow(z2))
cls[ind] <- 1
out <- cccd.classify(z2,C)
sum(out != cls)/nrow(z2)
## Not run:
plot(g,plot.circles=TRUE,dominate.only=TRUE)
points(z2,col=2*(1-cls)+1,pch=20)
## End(Not run)
```
Description

construct the cluster catch digraph from a data matrix.

Usage

ccd(data, m = 1, alpha = 0.05, sequential = TRUE, method = NULL)

## S3 method for class 'ccd'
plot(x,...)

Arguments

data a matrix of observations.
m slope of the null hypothesis curve.
alpha alpha for the K-S test if sequential=T.
sequential use the sequential or non-sequential version.
method the method used for the distance. See dist.
x an object of class ccd.
... arguments passed to plot.cccd.

Details

cluster cover digraph. plot.ccd is just a call to plot.cccd.

Value

an object of class igraph. In addition, this contains the attributes:

R the radii.
stats the K-S statistics.
layout the data vectors.
waks the y-values of the random walks.
fs the null hypothesis curve.
A the adjacency matrix.
m,alpha arguments passed to ccd.

Author(s)

David J. Marchette david.marchette@navy.mil
References


See Also

cccd

Examples

```r
x <- matrix(rnorm(100),ncol=2)
G <- ccd(x)
## Not run:
plot(G)
## End(Not run)
```

---

**dominate**

### Dominating Sets

#### Description

find maximum dominating sets in (di)graphs.

#### Usage

```r
dominate(g, method = "greedy",proportion=1.0)
```

#### Arguments

- `g` an adjacency matrix.
- `method` one of "greedy", "random", "byRadius", "greedyProportion".
- `proportion` proportion of points to cover.

#### Details

dominate is the main program which calls the others, as indicated by method. Greedy is the greedy dominating algorithm. In the greedy method ties are broken by first index (a la `which.max`). The byRadius method uses the radii to break ties while the random routine breaks ties randomly. If proportion is given, the algorithm stops after proportion points are covered.

#### Value

a vector of vertices corresponding to the dominating set.

#### Author(s)

David J. Marchette david.marchette@navy.mil
References

Examples

```r
x <- matrix(runif(100), ncol=2)
y <- matrix(runif(100, -2, 2), ncol=2)
G <- cccd(x, y)
D <- dominate(G)
## Not run:
plot(G, balls=TRUE, D=D)
## End(Not run)
```

---

**gg**  
*Gabriel Graph*

Description
A Gabriel graph is one where the vertices are points and there is an edge between two points if the maximal ball between the points contains no other points.

Usage

```r
gg(x, r = 1, method = NULL, usedeldir = TRUE, open = TRUE,  
k = NA, algorithm = 'cover_tree')
```

Arguments

- **x**: a matrix of observations.
- **r**: a multiplier on the ball radius.
- **method**: the method used for the distance. See `dist`.
- **usedeldir**: logical. Whether to use the deldir package or not.
- **open**: logical. If TRUE, open balls are used in the definition.
- **k**: If given, get.knn is used from FNN to approximate the Gabriel graph. Only the k nearest neighbors to the points are used to determine whether an edge should be made or not. This will be much faster and use less memory for large data sets, but is an approximation unless k is sufficiently large.
- **algorithm**: See `get.knn`.

Details
places an edge between two points \(i, j\) if the ball centered between the points with radius \(rd(i, j)/2\) contains no other points.
juggling

Value

an object of class igraph. In addition it contains the attributes:

layout the data.
r,p arguments passed to gg

Author(s)

David J. Marchette

References


See Also

rng, dist, get.knn

Examples

x <- matrix(runif(100),ncol=2)
g <- gg(x)
## Not run:
plot(g)
## End(Not run)

Description

a resampled version of the CCCD classifier.

Usage

juggle(data, classes, sampled = TRUE, sample.dim = FALSE,
num = 100, sample.proportion = 0.1, k = 2, method = NULL)
juggle.classify(data,J,tdata,indices)
Arguments

data, tdata training data from which to build the classifier. In the case of juggler.classify, tdata is the training data and data is the test data.

classes class labels.
sampled whether the data are subsampled.
sample.dim if TRUE, the dimensions (variates) are also sampled.
num number of juggles (resamples).
sample.proportion proportion of the data to sample. If 1 or greater, the data are sampled with replacement.
k number of variates to sample when sample.dim is TRUE.
J the juggled classifier.
indices the indices of the juggles to use.
method the method used for the distance. See dist

Details

The idea of juggling is to sample the data, compute a CCCD classifier, then repeat. The resampling is controlled by the two sampling variables, which basically determine whether the data are sampled with replacement, or whether a subsample is used. If sample.dim is TRUE, the variates are also sampled, with k indicating how many are sampled.

Value

juggler.classify returns a matrix holding the classification probabilities for each observation in data. a list consisting of:

S the dominating sets.
R the radii.
dimension the dimension of the data.
vars in the case of sample.dim=TRUE, the variables sampled each time.

Only the indices into the training data are stored in J, which is why the classifier requires the original training data in tdata.

Author(s)

David J. Marchette, david.marchette@navy.mil

See Also

cccd, dist
**Nearest Neighbor Graphs**

**Description**

nearest neighbor, k-nearest neighbor, and mutual k-nearest neighbor (di)graphs.

**Usage**

```r
nng(x = NULL, dx = NULL, k = 1, mutual = FALSE, method = NULL,
    use.fnn = FALSE, algorithm = 'cover_tree')
```

**Arguments**

- `x`: a data matrix. Either `x` or `dx` is required
- `dx`: interpoint distance matrix
- `k`: number of neighbors
- `mutual`: logical. if true the neighbors must be mutual. See details.
- `method`: the method used for the distance. See `dist`
- `use.fnn`: logical. If TRUE, `get.knn` from the FNN package is used to obtain the neighbors.
- `algorithm`: see `get.knn`.

**Details**

A k-nearest neighbor graph is a digraph where each vertex is associated with an observation and there is a directed edge between the vertex and it’s k nearest neighbors. A mutual k-nearest neighbor graph is a graph where there is an edge between x and y if x is one of the k nearest neighbors of y AND y is one of the k nearest neighbors of x.

**Value**

an object of class igraph with the extra attributes

- `layout`: the x vectors.
- `k, mutual, p`: arguments given to `nn`.

**Author(s)**

David J. Marchette david.marchette@navy.mil

**References**

prune

See Also
dist get.knn

Examples

x <- matrix(runif(100),ncol=2)
G1 <- nng(x,k=1)
## Not run:
par(mfrow=c(2,2))
plot(G1)
## End(Not run)
G2 <- nng(x,k=2)
## Not run:
plot(G2)
## End(Not run)
G5 <- nng(x,k=5)
## Not run:
plot(G5)
## End(Not run)
G5m <- nng(x,k=5,mutual=TRUE)
## Not run:
plot(G5m)
par(mfrow=c(1,1))
## End(Not run)

---

<table>
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</table>

Description

a nearest neighbor pruning using neighborhood graphs.

Usage

prune(x, classes, prox = "Gabriel", ignore.ties = TRUE, ...)

nng
Arguments

- **x**: a data matrix.
- **classes**: a vector of class labels.
- **prox**: type of proximity graph.
- **ignore.ties**: do not prune if there is a tie vote.
- **...**: arguments passed to the proximity graph.

Details

First a proximity graph is computed on the data. Then points are marked if their neighbors have a different class than they do: if the most common class among the neighbors is different than the point. Then all marked points are removed.

Value

A list with attributes:

- **x**: the pruned data.
- **v**: the indices of the retained data.
- **g**: the proximity graph.

Author(s)

David J. Marchette, david.marchette@navy.mil

References


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**rng**

*Relative Neighborhood Graph.*

Description

the relative neighborhood graph defined by a set of points.

Usage

```r
rng(x=NULL, dx=NULL, r = 1, method = NULL, usedeldir = TRUE, open = TRUE, k = NA, algorithm = 'cover_tree')
```
Arguments

- **x**: a data matrix. Either x or dx must be provided.
- **dx**: an interpoint distance matrix.
- **r**: a multiplier to grow the balls.
- **method**: the method used for the distance. See `dist`.
- **usedeldir**: a logical. If true and the data are two dimensional and the deldir package is installed, the Delaunay triangularization is first computed, and this is used to compute the relative neighborhood graph.
- **open**: logical. If TRUE, open balls are used in the definition.
- **k**: If given, get.knn is used from FNN to approximate the relative neighborhood graph. Only the k nearest neighbors to the points are used to determine whether an edge should be made or not. This will be much faster and use less memory for large data sets, but is an approximation unless k is sufficiently large.
- **algorithm**: See `get.knn`.

Details

The relative neighborhood graph is defined in terms of balls centered at observations. For two observations, the balls are set to have radius equal to the distance between the observations (or r times this distance if r is not 1). There is an edge between the vertices associated with the observations if and only if there are no vertices in the lune defined by the intersection of the balls.

The flag open should make no difference for most applications, but there are very specific cases (see the example section below) where setting it to be TRUE will give the wrong answer (thanks to Luke Mathieson for pointing this out to me).

Value

- an object of class igraph, with the additional attributes
- **layout**: the x matrix.
- **r,p**: arguments given to rng.

Author(s)

David J. Marchette david.marchette@navy.mil

References


See Also

- `gg, cccd, ccd, dist, get.knn`
Examples

```r
x <- matrix(runif(100), ncol=2)

g <- rng(x)
## Not run:
plot(g)
## End(Not run)

## Example using 'open':
g <- graph.full(5, directed=FALSE)

g1 <- rng(x=get.adjacency(g, sparse=FALSE), open=TRUE)
ecount(g1)
g2 <- rng(x=get.adjacency(g, sparse=FALSE), open=FALSE)
graph.isomorphic(g2, g)
```
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