Package: dbscan (via r-universe)

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Title Density-Based Spatial Clustering of Applications with Noise (DBSCAN) and Related Algorithms

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Description A fast reimplementation of several density-based algorithms of the DBSCAN family. Includes the clustering algorithms DBSCAN (density-based spatial clustering of applications with noise) and HDBSCAN (hierarchical DBSCAN), the ordering algorithm OPTICS (ordering points to identify the clustering structure), shared nearest neighbor clustering, and the outlier detection algorithms LOF (local outlier factor) and GLOSH (global-local outlier score from hierarchies). The implementations use the kd-tree data structure (from library ANN) for faster k-nearest neighbor search. An R interface to fast kNN and fixed-radius NN search is also provided. Hahsler, Piekenbrock and Doran (2019) <doi:10.18637/jss.v091.i01>.

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BugReports https://github.com/mhahsler/dbscan/issues

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comps *Find Connected Components in a Nearest-neighbor Graph*

Description

Generic function and methods to find connected components in nearest neighbor graphs.

Usage

```
comps(x, ...)

## S3 method for class 'dist'
comps(x, eps, ...)

## S3 method for class 'kNN'
comps(x, mutual = FALSE, ...)

## S3 method for class 'sNN'
comps(x, ...)

## S3 method for class 'frNN'
comps(x, ...)
```

Arguments

x	the NN object representing the graph or a dist object
...	further arguments are currently unused.
eps	threshold on the distance
mutual	for a pair of points, do both have to be in each other's neighborhood?

Details

Note that for kNN graphs, one point may be in the kNN of the other but nor vice versa. `mutual = TRUE` requires that both points are in each other's kNN.

Value

an integer vector with component assignments.

Author(s)

Michael Hahsler

See Also

Other NN functions: NN, frNN(), kNN(), kNNdist(), sNN()

Examples

```
set.seed(665544)
n <- 100
x <- cbind(
  x=runif(10, 0, 5) + rnorm(n, sd = 0.4),
  y=runif(10, 0, 5) + rnorm(n, sd = 0.4)
  )
plot(x, pch = 16)

# Connected components on a graph where each pair of points
# with a distance less or equal to eps are connected
d <- dist(x)
components <- comps(d, eps = .8)
plot(x, col = components, pch = 16)

# Connected components in a fixed radius nearest neighbor graph
# Gives the same result as the threshold on the distances above
frnn <- frNN(x, eps = .8)
components <- comps(frnn)
plot(frnn, data = x, col = components)

# Connected components on a k nearest neighbors graph
knn <- kNN(x, 3)
components <- comps(knn, mutual = FALSE)
plot(knn, data = x, col = components)

components <- comps(knn, mutual = TRUE)
plot(knn, data = x, col = components)

# Connected components in a shared nearest neighbor graph
snn <- sNN(x, k = 10, kt = 5)
components <- comps(snn)
plot(snn, data = x, col = components)
```

---

dbcv *Density-Based Clustering Validation Index (DBCV)*

Description

Calculate the Density-Based Clustering Validation Index (DBCV) for a clustering.

Usage

```
dbcv(x, cl, d, metric = "euclidean", sample = NULL)
```

Arguments

x	a data matrix or a dist object.
cl	a clustering (e.g., a integer vector)

`d`	dimensionality of the original data if a dist object is provided.
`metric`	distance metric used. The available metrics are the methods implemented by `dist()` plus `"sqeuclidean"` for the squared Euclidean distance used in the original DBCV implementation.
`sample`	sample size used for large datasets.

Details

DBCV (Moulavi et al, 2014) computes a score based on the density sparseness of each cluster and the density separation of each pair of clusters.

The density sparseness of a cluster (DSC) is defined as the maximum edge weight of a minimal spanning tree for the internal points of the cluster using the mutual reachability distance based on the all-points-core-distance. Internal points are connected to more than one other point in the cluster. Since clusters of a size less than 3 cannot have internal points, they are ignored (considered noise) in this implementation.

The density separation of a pair of clusters (DSPC) is defined as the minimum reachability distance between the internal nodes of the spanning trees of the two clusters.

The validity index for a cluster is calculated using these measures and aggregated to a validity index for the whole clustering using a weighted average.

The index is in the range $[-1, 1]$. If the cluster density compactness is better than the density separation, a positive value is returned. The actual value depends on the separability of the data. In general, greater values of the measure indicating a better density-based clustering solution.

Noise points are included in the calculation only in the weighted average, therefore clustering with more noise points will get a lower index.

Performance note: This implementation calculates a distance matrix and thus can only be used for small or sampled datasets.

Value

A list with the DBCV `score` for the clustering, the density sparseness of cluster (`dsc`) values, the density separation of pairs of clusters (`dspc`) distances, and the validity indices of clusters (`v_c`).

Author(s)

Matt Piekenbrock and Michael Hahsler

References

Davoud Moulavi and Pablo A. Jaskowiak and Ricardo J. G. B. Campello and Arthur Zimek and Jörg Sander (2014). Density-Based Clustering Validation. In *Proceedings of the 2014 SIAM International Conference on Data Mining,* pages 839-847 doi:10.1137/1.9781611973440.96

Pablo A. Jaskowiak (2022). MATLAB implementation of DBCV. https://github.com/pajaskowiak/dbcv

Examples

```
# Load a test dataset
data(Dataset_1)
x <- Dataset_1[, c("x", "y")]
class <- Dataset_1$class

clplot(x, class)

# We use MinPts 3 and use the knee at eps = .1 for dbscan
kNNdistplot(x, minPts = 3)

cl <- dbscan(x, eps = .1, minPts = 3)
clplot(x, cl)

dbcv(x, cl)

# compare to the DBCV index on the original class labels and
# with a random partitioning
dbcv(x, class)
dbcv(x, sample(1:4, replace = TRUE, size = nrow(x)))

# find the best eps using dbcv
eps_grid <- seq(.05,.2, by = .01)
cls <- lapply(eps_grid, FUN = function(e) dbscan(x, eps = e, minPts = 3))
dbcvs <- sapply(cls, FUN = function(cl) dbcv(x, cl)$score)

plot(eps_grid, dbcvs, type = "l")

eps_opt <- eps_grid[which.max(dbcvs)]
eps_opt

cl <- dbscan(x, eps = eps_opt, minPts = 3)
clplot(x, cl)
```

DBCV_datasets *DBCV Paper Datasets*

Description

The four synthetic 2D datasets used in Moulavi et al (2014).

Format

Four data frames with the following 3 variables.

x a numeric vector

y a numeric vector

class an integer vector indicating the class label. 0 means noise.

Source

https://github.com/pajaskowiak/dbcv

References

Davoud Moulavi and Pablo A. Jaskowiak and Ricardo J. G. B. Campello and Arthur Zimek and Jörg Sander (2014). Density-Based Clustering Validation. In *Proceedings of the 2014 SIAM International Conference on Data Mining,* pages 839-847 doi:10.1137/1.9781611973440.96

Examples

```
data("Dataset_1")
clplot(Dataset_1[, c("x", "y")], cl = Dataset_1$class)

data("Dataset_2")
clplot(Dataset_2[, c("x", "y")], cl = Dataset_2$class)

data("Dataset_3")
clplot(Dataset_3[, c("x", "y")], cl = Dataset_3$class)

data("Dataset_4")
clplot(Dataset_4[, c("x", "y")], cl = Dataset_4$class)
```

---

dbscan *Density-based Spatial Clustering of Applications with Noise (DBSCAN)*

Description

Fast reimplementation of the DBSCAN (Density-based spatial clustering of applications with noise) clustering algorithm using a kd-tree.

Usage

```
dbscan(x, eps, minPts = 5, weights = NULL, borderPoints = TRUE, ...)

is.corepoint(x, eps, minPts = 5, ...)

## S3 method for class 'dbscan_fast'
predict(object, newdata, data, ...)
```

Arguments

x	a data matrix, a data.frame, a dist object or a frNN object with fixed-radius nearest neighbors.
eps	size (radius) of the epsilon neighborhood. Can be omitted if x is a frNN object.
minPts	number of minimum points required in the eps neighborhood for core points (including the point itself).

weights	numeric; weights for the data points. Only needed to perform weighted clustering.
borderPoints	logical; should border points be assigned to clusters. The default is TRUE for regular DBSCAN. If FALSE then border points are considered noise (see DBSCAN* in Campello et al, 2013).
...	additional arguments are passed on to the fixed-radius nearest neighbor search algorithm. See frNN() for details on how to control the search strategy.
object	clustering object.
newdata	new data points for which the cluster membership should be predicted.
data	the data set used to create the clustering object.

Details

The implementation is significantly faster and can work with larger data sets than fpc::dbscan() in **fpc**. Use dbscan::dbscan() (with specifying the package) to call this implementation when you also load package **fpc**.

The Algorithm:

This implementation of DBSCAN follows the original algorithm as described by Ester et al (1996). DBSCAN performs the following steps:

1. Estimate the density around each data point by counting the number of points in a user-specified eps-neighborhood and applies a used-specified minPts thresholds to identify
   - core points (points with more than minPts points in their neighborhood),
   - border points (non-core points with a core point in their neighborhood) and
   - noise points (all other points).
2. Core points form the backbone of clusters by joining them into a cluster if they are density-reachable from each other (i.e., there is a chain of core points where one falls inside the eps-neighborhood of the next).
3. Border points are assigned to clusters. The algorithm needs parameters eps (the radius of the epsilon neighborhood) and minPts (the density threshold).

Border points are arbitrarily assigned to clusters in the original algorithm. DBSCAN* (see Campello et al 2013) treats all border points as noise points. This is implemented with borderPoints = FALSE.

Specifying the Data:

If x is a matrix or a data.frame, then fast fixed-radius nearest neighbor computation using a kd-tree is performed using Euclidean distance. See frNN() for more information on the parameters related to nearest neighbor search. **Note** that only numerical values are allowed in x.

Any precomputed distance matrix (dist object) can be specified as x. You may run into memory issues since distance matrices are large.

A precomputed frNN object can be supplied as x. In this case eps does not need to be specified. This option is useful for large data sets, where a sparse distance matrix is available. See frNN() how to create frNN objects.

Setting Parameters for DBSCAN:

The parameters minPts and eps define the minimum density required in the area around core points which form the backbone of clusters. minPts is the number of points required in the neighborhood around the point defined by the parameter eps (i.e., the radius around the point). Both parameters depend on each other and changing one typically requires changing the other one as well. The parameters also depend on the size of the data set with larger datasets requiring a larger minPts or a smaller eps.

- minPts: The original DBSCAN paper (Ester et al, 1996) suggests to start by setting minPts $\geq d + 1$, the data dimensionality plus one or higher with a minimum of 3. Larger values are preferable since increasing the parameter suppresses more noise in the data by requiring more points to form clusters. Sander et al (1998) uses in the examples two times the data dimensionality. Note that setting minPts ≤ 2 is equivalent to hierarchical clustering with the single link metric and the dendrogram cut at height eps.
- eps: A suitable neighborhood size parameter eps given a fixed value for minPts can be found visually by inspecting the kNNdistplot() of the data using $k =$ minPts $- 1$ (minPts includes the point itself, while the k-nearest neighbors distance does not). The k-nearest neighbor distance plot sorts all data points by their k-nearest neighbor distance. A sudden increase of the kNN distance (a knee) indicates that the points to the right are most likely outliers. Choose eps for DBSCAN where the knee is.

Predict Cluster Memberships:

predict() can be used to predict cluster memberships for new data points. A point is considered a member of a cluster if it is within the eps neighborhood of a core point of the cluster. Points which cannot be assigned to a cluster will be reported as noise points (i.e., cluster ID 0). **Important note:** predict() currently can only use Euclidean distance to determine the neighborhood of core points. If dbscan() was called using distances other than Euclidean, then the neighborhood calculation will not be correct and only approximated by Euclidean distances. If the data contain factor columns (e.g., using Gower's distance), then the factors in data and query first need to be converted to numeric to use the Euclidean approximation.

Value

dbscan() returns an object of class dbscan_fast with the following components:

eps	value of the eps parameter.
minPts	value of the minPts parameter.
metric	used distance metric.
cluster	A integer vector with cluster assignments. Zero indicates noise points.

is.corepoint() returns a logical vector indicating for each data point if it is a core point.

Author(s)

Michael Hahsler

References

Hahsler M, Piekenbrock M, Doran D (2019). dbscan: Fast Density-Based Clustering with R. *Journal of Statistical Software,* 91(1), 1-30. doi:10.18637/jss.v091.i01

Martin Ester, Hans-Peter Kriegel, Joerg Sander, Xiaowei Xu (1996). A Density-Based Algorithm for Discovering Clusters in Large Spatial Databases with Noise. Institute for Computer Science, University of Munich. *Proceedings of 2nd International Conference on Knowledge Discovery and Data Mining (KDD-96),* 226-231. https://dl.acm.org/doi/10.5555/3001460.3001507

Campello, R. J. G. B.; Moulavi, D.; Sander, J. (2013). Density-Based Clustering Based on Hierarchical Density Estimates. Proceedings of the 17th Pacific-Asia Conference on Knowledge Discovery in Databases, PAKDD 2013, *Lecture Notes in Computer Science* 7819, p. 160. doi:10.1007/9783642374562_14

Sander, J., Ester, M., Kriegel, HP. et al. (1998). Density-Based Clustering in Spatial Databases: The Algorithm GDBSCAN and Its Applications. *Data Mining and Knowledge Discovery* 2, 169-194. doi:10.1023/A:1009745219419

See Also

Other clustering functions: `extractFOSC()`, `hdbscan()`, `jpclust()`, `ncluster()`, `optics()`, `sNNclust()`

Examples

```
## Example 1: use dbscan on the iris data set
data(iris)
iris <- as.matrix(iris[, 1:4])

## Find suitable DBSCAN parameters:
## 1. We use minPts = dim + 1 = 5 for iris. A larger value can also be used.
## 2. We inspect the k-NN distance plot for k = minPts - 1 = 4
kNNdistplot(iris, minPts = 5)

## Noise seems to start around a 4-NN distance of .7
abline(h=.7, col = "red", lty = 2)

## Cluster with the chosen parameters
res <- dbscan(iris, eps = .7, minPts = 5)
res

pairs(iris, col = res$cluster + 1L)
clplot(iris, res)

## Use a precomputed frNN object
fr <- frNN(iris, eps = .7)
dbscan(fr, minPts = 5)

## Example 2: use data from fpc
set.seed(665544)
n <- 100
x <- cbind(
  x = runif(10, 0, 10) + rnorm(n, sd = 0.2),
  y = runif(10, 0, 10) + rnorm(n, sd = 0.2)
  )

res <- dbscan(x, eps = .3, minPts = 3)
res
```

```
## plot clusters and add noise (cluster 0) as crosses.
plot(x, col = res$cluster)
points(x[res$cluster == 0, ], pch = 3, col = "grey")

clplot(x, res)
hullplot(x, res)

## Predict cluster membership for new data points
## (Note: 0 means it is predicted as noise)
newdata <- x[1:5,] + rnorm(10, 0, .3)
hullplot(x, res)
points(newdata, pch = 3 , col = "red", lwd = 3)
text(newdata, pos = 1)

pred_label <- predict(res, newdata, data = x)
pred_label
points(newdata, col = pred_label + 1L,  cex = 2, lwd = 2)

## Compare speed against fpc version (if microbenchmark is installed)
## Note: we use dbscan::dbscan to make sure that we do now run the
## implementation in fpc.
## Not run:
if (requireNamespace("fpc", quietly = TRUE) &&
    requireNamespace("microbenchmark", quietly = TRUE)) {
  t_dbscan <- microbenchmark::microbenchmark(
    dbscan::dbscan(x, .3, 3), times = 10, unit = "ms")
  t_dbscan_linear <- microbenchmark::microbenchmark(
    dbscan::dbscan(x, .3, 3, search = "linear"), times = 10, unit = "ms")
  t_dbscan_dist <- microbenchmark::microbenchmark(
    dbscan::dbscan(x, .3, 3, search = "dist"), times = 10, unit = "ms")
  t_fpc <- microbenchmark::microbenchmark(
    fpc::dbscan(x, .3, 3), times = 10, unit = "ms")

  r <- rbind(t_fpc, t_dbscan_dist, t_dbscan_linear, t_dbscan)
  r

  boxplot(r,
    names = c('fpc', 'dbscan (dist)', 'dbscan (linear)', 'dbscan (kdtree)'),
    main = "Runtime comparison in ms")

  ## speedup of the kd-tree-based version compared to the fpc implementation
  median(t_fpc$time) / median(t_dbscan$time)
}
## End(Not run)

## Example 3: manually create a frNN object for dbscan (dbscan only needs ids and eps)
nn <- structure(list(id = list(c(2,3), c(1,3), c(1,2,3), c(3,5), c(4,5)), eps = 1),
  class =  c("NN", "frNN"))
nn
dbscan(nn, minPts = 2)
```

dbscan_tidiers *Turn an dbscan clustering object into a tidy tibble*

Description

Provides tidy(), augment(), and glance() verbs for clusterings created with algorithms in package dbscan to work with tidymodels.

Usage

```
tidy(x, ...)

## S3 method for class 'dbscan'
tidy(x, ...)

## S3 method for class 'hdbscan'
tidy(x, ...)

## S3 method for class 'general_clustering'
tidy(x, ...)

augment(x, ...)

## S3 method for class 'dbscan'
augment(x, data = NULL, newdata = NULL, ...)

## S3 method for class 'hdbscan'
augment(x, data = NULL, newdata = NULL, ...)

## S3 method for class 'general_clustering'
augment(x, data = NULL, newdata = NULL, ...)

glance(x, ...)

## S3 method for class 'dbscan'
glance(x, ...)

## S3 method for class 'hdbscan'
glance(x, ...)

## S3 method for class 'general_clustering'
glance(x, ...)
```

Arguments

x	An dbscan object returned from dbscan().
...	further arguments are ignored without a warning.

data	The data used to create the clustering.
newdata	New data to predict cluster labels for.

See Also

generics::tidy(), generics::augment(), generics::glance(), dbscan()

Examples

```
data(iris)
x <- scale(iris[, 1:4])

## dbscan
db <- dbscan(x, eps = .9, minPts = 5)
db

# summarize model fit with tidiers
tidy(db)
glance(db)

# augment for this model needs the original data
augment(db, x)

# to augment new data, the original data is also needed
augment(db, x, newdata = x[1:5, ])

## hdbscan
hdb <- hdbscan(x, minPts = 5)

# summarize model fit with tidiers
tidy(hdb)
glance(hdb)

# augment for this model needs the original data
augment(hdb, x)

# to augment new data, the original data is also needed
augment(hdb, x, newdata = x[1:5, ])

## Jarvis-Patrick clustering
cl <- jpclust(x, k = 20, kt = 15)

# summarize model fit with tidiers
tidy(cl)
glance(cl)

# augment for this model needs the original data
augment(cl, x)

## Shared Nearest Neighbor clustering
cl <- sNNclust(x, k = 20, eps = 0.8, minPts = 15)
```

```
# summarize model fit with tidiers
tidy(cl)
glance(cl)

# augment for this model needs the original data
augment(cl, x)
```

---

dendrogram *Coercions to Dendrogram*

Description

Provides a new generic function to coerce objects to dendrograms with `stats::as.dendrogram()` as the default. Additional methods for hclust, hdbscan and reachability objects are provided.

Usage

```
as.dendrogram(object, ...)

## Default S3 method:
as.dendrogram(object, ...)

## S3 method for class 'hclust'
as.dendrogram(object, ...)

## S3 method for class 'hdbscan'
as.dendrogram(object, ...)

## S3 method for class 'reachability'
as.dendrogram(object, ...)
```

Arguments

`object`	the object
`...`	further arguments

Details

Coercion methods for hclust, hdbscan and reachability objects to dendrogram are provided.

The coercion from `hclust` is a faster C++ reimplementation of the coercion in package `stats`. The original implementation can be called using `stats::as.dendrogram()`.

The coercion from hdbscan builds the non-simplified HDBSCAN hierarchy as a dendrogram object.

DS3 *DS3: Spatial data with arbitrary shapes*

Description

Contains 8000 2-d points, with 6 "natural" looking shapes, all of which have an sinusoid-like shape that intersects with each cluster. The data set was originally used as a benchmark data set for the Chameleon clustering algorithm (Karypis, Han and Kumar, 1999) to illustrate the a data set containing arbitrarily shaped spatial data surrounded by both noise and artifacts.

Format

A data.frame with 8000 observations on the following 2 columns:

X a numeric vector

Y a numeric vector

Source

Obtained from the Clustering Datasets Repository, University of Joensuu, Finland.

References

Karypis, George, Eui-Hong Han, and Vipin Kumar (1999). Chameleon: Hierarchical clustering using dynamic modeling. *Computer* 32(8): 68-75.

Examples

```
data(DS3)
plot(DS3, pch = 20, cex = 0.25)
```

extractFOSC *Framework for the Optimal Extraction of Clusters from Hierarchies*

Description

Generic reimplementation of the *Framework for Optimal Selection of Clusters* (FOSC; Campello et al, 2013) to extract clusterings from hierarchical clustering (i.e., hclust objects). Can be parameterized to perform unsupervised cluster extraction through a stability-based measure, or semisupervised cluster extraction through either a constraint-based extraction (with a stability-based tiebreaker) or a mixed (weighted) constraint and stability-based objective extraction.

Usage

```
extractFOSC(
  x,
  constraints,
  alpha = 0,
  minPts = 2L,
  prune_unstable = FALSE,
  validate_constraints = FALSE
)
```

Arguments

x	a valid hclust object created via `hclust()` or `hdbscan()`.
constraints	Either a list or matrix of pairwise constraints. If missing, an unsupervised measure of stability is used to make local cuts and extract the optimal clusters. See details.
alpha	numeric; weight between $[0, 1]$ for mixed-objective semi-supervised extraction. Defaults to 0.
minPts	numeric; Defaults to 2. Only needed if class-less noise is a valid label in the model.
prune_unstable	logical; should significantly unstable subtrees be pruned? The default is `FALSE` for the original optimal extraction framework (see Campello et al, 2013). See details for what `TRUE` implies.
validate_constraints	logical; should constraints be checked for validity? See details for what are considered valid constraints.

Details

Campello et al (2013) suggested a *Framework for Optimal Selection of Clusters* (FOSC) as a framework to make local (non-horizontal) cuts to any cluster tree hierarchy. This function implements the original extraction algorithms as described by the framework for hclust objects. Traditional cluster extraction methods from hierarchical representations (such as hclust objects) generally rely on global parameters or cutting values which are used to partition a cluster hierarchy into a set of disjoint, flat clusters. This is implemented in R in function `stats::cutree()`. Although such methods are widespread, using global parameter settings are inherently limited in that they cannot capture patterns within the cluster hierarchy at varying *local* levels of granularity.

Rather than partitioning a hierarchy based on the number of the cluster one expects to find (k) or based on some linkage distance threshold (H), the FOSC proposes that the optimal clusters may exist at varying distance thresholds in the hierarchy. To enable this idea, FOSC requires one parameter (minPts) that represents *the minimum number of points that constitute a valid cluster.* The first step of the FOSC algorithm is to traverse the given cluster hierarchy divisively, recording new clusters at each split if both branches represent more than or equal to minPts. Branches that contain less than minPts points at one or both branches inherit the parent clusters identity. Note that using FOSC, due to the constraint that minPts must be greater than or equal to 2, it is possible that the optimal cluster solution chosen makes local cuts that render parent branches of sizes less than minPts as noise, which are denoted as 0 in the final solution.

Traversing the original cluster tree using minPts creates a new, simplified cluster tree that is then post-processed recursively to extract clusters that maximize for each cluster C_i the cost function

$$\max_{\delta_2,\ldots,\delta_k} J = \sum_{i=2}^{k} \delta_i S(C_i)$$

where $S(C_i)$ is the stability-based measure as

$$S(C_i) = \sum_{x_j \in C_i} (\frac{1}{h_{min}(x_j, C_i)} - \frac{1}{h_{max}(C_i)})$$

δ_i represents an indicator function, which constrains the solution space such that clusters must be disjoint (cannot assign more than 1 label to each cluster). The measure $S(C_i)$ used by FOSC is an unsupervised validation measure based on the assumption that, if you vary the linkage/distance threshold across all possible values, more prominent clusters that survive over many threshold variations should be considered as stronger candidates of the optimal solution. For this reason, using this measure to detect clusters is referred to as an unsupervised, *stability-based* extraction approach. In some cases it may be useful to enact *instance-level* constraints that ensure the solution space conforms to linkage expectations known *a priori*. This general idea of using preliminary expectations to augment the clustering solution will be referred to as *semisupervised clustering*. If constraints are given in the call to `extractFOSC()`, the following alternative objective function is maximized:

$$J = \frac{1}{2n_c} \sum_{j=1}^{n} \gamma(x_j)$$

n_c is the total number of constraints given and $\gamma(x_j)$ represents the number of constraints involving object x_j that are satisfied. In the case of ties (such as solutions where no constraints were given), the unsupervised solution is used as a tiebreaker. See Campello et al (2013) for more details.

As a third option, if one wishes to prioritize the degree at which the unsupervised and semisupervised solutions contribute to the overall optimal solution, the parameter α can be set to enable the extraction of clusters that maximize the `mixed` objective function

$$J = \alpha S(C_i) + (1 - \alpha)\gamma(C_i))$$

FOSC expects the pairwise constraints to be passed as either 1) an $n(n-1)/2$ vector of integers representing the constraints, where 1 represents should-link, -1 represents should-not-link, and 0 represents no preference using the unsupervised solution (see below for examples). Alternatively, if only a few constraints are needed, a named list representing the (symmetric) adjacency list can be used, where the names correspond to indices of the points in the original data, and the values correspond to integer vectors of constraints (positive indices for should-link, negative indices for should-not-link). Again, see the examples section for a demonstration of this.

The parameters to the input function correspond to the concepts discussed above. The `minPts` parameter to represent the minimum cluster size to extract. The optional `constraints` parameter contains the pairwise, instance-level constraints of the data. The optional `alpha` parameters controls whether the mixed objective function is used (if `alpha` is greater than 0). If the `validate_constraints` parameter is set to true, the constraints are checked (and fixed) for symmetry (if point A has a should-link constraint with point B, point B should also have the same constraint). Asymmetric constraints are not supported.

Unstable branch pruning was not discussed by Campello et al (2013), however in some data sets it may be the case that specific subbranches scores are significantly greater than sibling and parent branches, and thus sibling branches should be considered as noise if their scores are cumulatively lower than the parents. This can happen in extremely nonhomogeneous data sets, where there exists locally very stable branches surrounded by unstable branches that contain more than `minPts` points. `prune_unstable = TRUE` will remove the unstable branches.

Value

A list with the elements:

`cluster`	A integer vector with cluster assignments. Zero indicates noise points (if any).
hc	The original hclust object with additional list elements `"stability"`, `"constraint"`, and `"total"` for the $n - 1$ cluster-wide objective scores from the extraction.

Author(s)

Matt Piekenbrock

References

Campello, Ricardo JGB, Davoud Moulavi, Arthur Zimek, and Joerg Sander (2013). A framework for semi-supervised and unsupervised optimal extraction of clusters from hierarchies. *Data Mining and Knowledge Discovery* 27(3): 344-371. doi:10.1007/s1061801303114

See Also

`hclust()`, `hdbscan()`, `stats::cutree()`

Other clustering functions: `dbscan()`, `hdbscan()`, `jpclust()`, `ncluster()`, `optics()`, `sNNclust()`

Examples

```
data("moons")

## Regular HDBSCAN using stability-based extraction (unsupervised)
cl <- hdbscan(moons, minPts = 5)
cl$cluster

## Constraint-based extraction from the HDBSCAN hierarchy
## (w/ stability-based tiebreaker (semisupervised))
cl_con <- extractFOSC(cl$hc, minPts = 5,
  constraints = list("12" = c(49, -47)))
cl_con$cluster

## Alternative formulation: Constraint-based extraction from the HDBSCAN hierarchy
## (w/ stability-based tiebreaker (semisupervised)) using distance thresholds
dist_moons <- dist(moons)
cl_con2 <- extractFOSC(cl$hc, minPts = 5,
  constraints = ifelse(dist_moons < 0.1, 1L,
                ifelse(dist_moons > 1, -1L, 0L)))
```

```
cl_con2$cluster # same as the second example
```

---

frNN *Find the Fixed Radius Nearest Neighbors*

Description

This function uses a kd-tree to find the fixed radius nearest neighbors (including distances) fast.

Usage

```
frNN(
  x,
  eps,
  query = NULL,
  sort = TRUE,
  search = "kdtree",
  bucketSize = 10,
  splitRule = "suggest",
  approx = 0
)

## S3 method for class 'frNN'
sort(x, decreasing = FALSE, ...)

## S3 method for class 'frNN'
adjacencylist(x, ...)

## S3 method for class 'frNN'
print(x, ...)
```

Arguments

x	a data matrix, a dist object or a frNN object.
eps	neighbors radius.
query	a data matrix with the points to query. If query is not specified, the NN for all the points in x is returned. If query is specified then x needs to be a data matrix.
sort	sort the neighbors by distance? This is expensive and can be done later using sort().
search	nearest neighbor search strategy (one of "kdtree", "linear" or "dist").
bucketSize	max size of the kd-tree leafs.
splitRule	rule to split the kd-tree. One of "STD", "MIDPT", "FAIR", "SL_MIDPT", "SL_FAIR" or "SUGGEST" (SL stands for sliding). "SUGGEST" uses ANNs best guess.

approx	a positive number useed for approximate nearest neighbors. All NN up to a distance of a factor of 1 + approx eps may be used. Some actual NN may be omitted leading to spurious clusters and noise points. However, the algorithm will enjoy a significant speedup.
decreasing	sort in decreasing order?
...	further arguments

Details

If x is specified as a data matrix, then Euclidean distances and fast nearest neighbor lookup using a kd-tree are used.

To create a frNN object from scratch, you need to supply at least the elements id with a list of integer vectors with the nearest neighbor ids for each point and eps (see below).

Self-matches: Self-matches are not returned!

Value

frNN() returns an object of class frNN (subclass of NN) containing a list with the following components:

id	a list of integer vectors. Each vector contains the ids (row numbers) of the fixed radius nearest neighbors.
dist	a list with distances (same structure as id).
eps	neighborhood radius eps that was used.
metric	used distance metric.

adjacencylist() returns a list with one entry per data point in x. Each entry contains the id of the nearest neighbors.

Author(s)

Michael Hahsler

References

David M. Mount and Sunil Arya (2010). ANN: A Library for Approximate Nearest Neighbor Searching, http://www.cs.umd.edu/~mount/ANN/.

See Also

Other NN functions: NN, comps(), kNN(), kNNdist(), sNN()

Examples

```
data(iris)
x <- iris[, -5]

# Example 1: Find fixed radius nearest neighbors for each point
nn <- frNN(x, eps = .5)
```

```
nn

# Number of neighbors
hist(lengths(adjacencylist(nn)),
  xlab = "k", main="Number of Neighbors",
  sub = paste("Neighborhood size eps =", nn$eps))

# Explore neighbors of point i = 10
i <- 10
nn$id[[i]]
nn$dist[[i]]
plot(x, col = ifelse(seq_len(nrow(iris)) %in% nn$id[[i]], "red", "black"))

# get an adjacency list
head(adjacencylist(nn))

# plot the fixed radius neighbors (and then reduced to a radius of .3)
plot(nn, x)
plot(frNN(nn, eps = .3), x)

## Example 2: find fixed-radius NN for query points
q <- x[c(1,100),]
nn <- frNN(x, eps = .5, query = q)

plot(nn, x, col = "grey")
points(q, pch = 3, lwd = 2)
```

`glosh` *Global-Local Outlier Score from Hierarchies*

Description

Calculate the Global-Local Outlier Score from Hierarchies (GLOSH) score for each data point using a kd-tree to speed up kNN search.

Usage

```
glosh(x, k = 4, ...)
```

Arguments

`x`	an hclust object, data matrix, or dist object.
`k`	size of the neighborhood.
`...`	further arguments are passed on to `kNN()`.

Details

GLOSH compares the density of a point to densities of any points associated within current and child clusters (if any). Points that have a substantially lower density than the density mode (cluster) they most associate with are considered outliers. GLOSH is computed from a hierarchy a clusters.

Specifically, consider a point *x* and a density or distance threshold *lambda*. GLOSH is calculated by taking 1 minus the ratio of how long any of the child clusters of the cluster *x* belongs to "survives" changes in *lambda* to the highest *lambda* threshold of x, above which x becomes a noise point.

Scores close to 1 indicate outliers. For more details on the motivation for this calculation, see Campello et al (2015).

Value

A numeric vector of length equal to the size of the original data set containing GLOSH values for all data points.

Author(s)

Matt Piekenbrock

References

Campello, Ricardo JGB, Davoud Moulavi, Arthur Zimek, and Joerg Sander. Hierarchical density estimates for data clustering, visualization, and outlier detection. *ACM Transactions on Knowledge Discovery from Data (TKDD)* 10, no. 1 (2015). doi:10.1145/2733381

See Also

Other Outlier Detection Functions: `kNNdist()`, `lof()`, `pointdensity()`

Examples

```
set.seed(665544)
n <- 100
x <- cbind(
  x=runif(10, 0, 5) + rnorm(n, sd = 0.4),
  y=runif(10, 0, 5) + rnorm(n, sd = 0.4)
  )

### calculate GLOSH score
glosh <- glosh(x, k = 3)

### distribution of outlier scores
summary(glosh)
hist(glosh, breaks = 10)

### simple function to plot point size is proportional to GLOSH score
plot_glosh <- function(x, glosh){
  plot(x, pch = ".", main = "GLOSH (k = 3)")
  points(x, cex = glosh*3, pch = 1, col = "red")
  text(x[glosh > 0.80, ], labels = round(glosh, 3)[glosh > 0.80], pos = 3)
```

```
}
plot_glosh(x, glosh)

### GLOSH with any hierarchy
x_dist <- dist(x)
x_sl <- hclust(x_dist, method = "single")
x_upgma <- hclust(x_dist, method = "average")
x_ward <- hclust(x_dist, method = "ward.D2")

## Compare what different linkage criterion consider as outliers
glosh_sl <- glosh(x_sl, k = 3)
plot_glosh(x, glosh_sl)

glosh_upgma <- glosh(x_upgma, k = 3)
plot_glosh(x, glosh_upgma)

glosh_ward <- glosh(x_ward, k = 3)
plot_glosh(x, glosh_ward)

## GLOSH is automatically computed with HDBSCAN
all(hdbscan(x, minPts = 3)$outlier_scores == glosh(x, k = 3))
```

---

hdbscan *Hierarchical DBSCAN (HDBSCAN)*

Description

Fast C++ implementation of the HDBSCAN (Hierarchical DBSCAN) and its related algorithms.

Usage

```
hdbscan(
  x,
  minPts,
  cluster_selection_epsilon = 0,
  gen_hdbscan_tree = FALSE,
  gen_simplified_tree = FALSE,
  verbose = FALSE
)

## S3 method for class 'hdbscan'
print(x, ...)

## S3 method for class 'hdbscan'
plot(
  x,
  scale = "suggest",
  gradient = c("yellow", "red"),
  show_flat = FALSE,
```

```
  main = "HDBSCAN*",
  ylab = "eps value",
  leaflab = "none",
  ...
)

coredist(x, minPts)

mrdist(x, minPts, coredist = NULL)

## S3 method for class 'hdbscan'
predict(object, newdata, data, ...)
```

Arguments

x	a data matrix (Euclidean distances are used) or a dist object calculated with an arbitrary distance metric.
minPts	integer; Minimum size of clusters. See details.
cluster_selection_epsilon	double; a distance threshold below which
gen_hdbscan_tree	logical; should the robust single linkage tree be explicitly computed (see cluster tree in Chaudhuri et al, 2010).
gen_simplified_tree	logical; should the simplified hierarchy be explicitly computed (see Campello et al, 2013).
verbose	report progress.
...	additional arguments are passed on.
scale	integer; used to scale condensed tree based on the graphics device. Lower scale results in wider colored trees lines. The default 'suggest' sets scale to the number of clusters.
gradient	character vector; the colors to build the condensed tree coloring with.
show_flat	logical; whether to draw boxes indicating the most stable clusters.
main	Title of the plot.
ylab	the label for the y axis.
leaflab	a string specifying how leaves are labeled (see stats::plot.dendrogram()).
coredist	numeric vector with precomputed core distances (optional).
object	clustering object.
newdata	new data points for which the cluster membership should be predicted.
data	the data set used to create the clustering object.

Details

This fast implementation of HDBSCAN (Campello et al., 2013) computes the hierarchical cluster tree representing density estimates along with the stability-based flat cluster extraction. HDBSCAN essentially computes the hierarchy of all DBSCAN* clusterings, and then uses a stability-based extraction method to find optimal cuts in the hierarchy, thus producing a flat solution.

HDBSCAN performs the following steps:

1. Compute mutual reachability distance mrd between points (based on distances and core distances).
2. Use mdr as a distance measure to construct a minimum spanning tree.
3. Prune the tree using stability.
4. Extract the clusters.

Additional, related algorithms including the "Global-Local Outlier Score from Hierarchies" (GLOSH; see section 6 of Campello et al., 2015) is available in function `glosh()` and the ability to cluster based on instance-level constraints (see section 5.3 of Campello et al. 2015) are supported. The algorithms only need the parameter `minPts`.

Note that `minPts` not only acts as a minimum cluster size to detect, but also as a "smoothing" factor of the density estimates implicitly computed from HDBSCAN.

When using the optional parameter `cluster_selection_epsilon`, a combination between DBSCAN* and HDBSCAN* can be achieved (see Malzer & Baum 2020). This means that part of the tree is affected by `cluster_selection_epsilon` as if running DBSCAN* with `eps = cluster_selection_epsilon`. The remaining part (on levels above the threshold) is still processed by HDBSCAN*'s stability-based selection algorithm and can therefore return clusters of variable densities. Note that there is not always a remaining part, especially if the parameter value is chosen too large, or if there aren't enough clusters of variable densities. In this case, the result will be equal to DBSCAN*. where HDBSCAN* produces too many small clusters that need to be merged, while still being able to extract clusters of variable densities at higher levels.

`coredist()`: The core distance is defined for each point as the distance to the `MinPts - 1`'s neighbor. It is a density estimate equivalent to `kNNdist()` with `k = MinPts -1`.

`mrdist()`: The mutual reachability distance is defined between two points as `mrd(a, b) = max(coredist(a), coredist(b), dist(a, b))`. This distance metric is used by HDBSCAN. It has the effect of increasing distances in low density areas.

`predict()` assigns each new data point to the same cluster as the nearest point if it is not more than that points core distance away. Otherwise the new point is classified as a noise point (i.e., cluster ID 0).

Value

`hdbscan()` returns object of class `hdbscan` with the following components:

`cluster`	A integer vector with cluster assignments. Zero indicates noise points.
`minPts`	value of the `minPts` parameter.
`cluster_scores`	The sum of the stability scores for each salient (flat) cluster. Corresponds to cluster IDs given the in `"cluster"` element.

`membership_prob` The probability or individual stability of a point within its clusters. Between 0 and 1.

`outlier_scores` The GLOSH outlier score of each point.

`hc` An hclust object of the HDBSCAN hierarchy.

`coredist()` returns a vector with the core distance for each data point.

`mrdist()` returns a dist object containing pairwise mutual reachability distances.

Author(s)

Matt Piekenbrock

Claudia Malzer (added cluster_selection_epsilon)

References

Campello RJGB, Moulavi D, Sander J (2013). Density-Based Clustering Based on Hierarchical Density Estimates. Proceedings of the 17th Pacific-Asia Conference on Knowledge Discovery in Databases, PAKDD 2013, *Lecture Notes in Computer Science* 7819, p. 160. doi:10.1007/9783642-374562_14

Campello RJGB, Moulavi D, Zimek A, Sander J (2015). Hierarchical density estimates for data clustering, visualization, and outlier detection. *ACM Transactions on Knowledge Discovery from Data (TKDD),* 10(5):1-51. doi:10.1145/2733381

Malzer, C., & Baum, M. (2020). A Hybrid Approach To Hierarchical Density-based Cluster Selection. In 2020 IEEE International Conference on Multisensor Fusion and Integration for Intelligent Systems (MFI), pp. 223-228. doi:10.1109/MFI49285.2020.9235263

See Also

Other clustering functions: `dbscan()`, `extractFOSC()`, `jpclust()`, `ncluster()`, `optics()`, `sNNclust()`

Examples

```
## cluster the moons data set with HDBSCAN
data(moons)

res <- hdbscan(moons, minPts = 5)
res

plot(res)
clplot(moons, res)

## cluster the moons data set with HDBSCAN using Manhattan distances
res <- hdbscan(dist(moons, method = "manhattan"), minPts = 5)
plot(res)
clplot(moons, res)

## Example for HDBSCAN(e) using cluster_selection_epsilon
# data with clusters of various densities.
```

```
X <- data.frame(
 x = c(
  0.08, 0.46, 0.46, 2.95, 3.50, 1.49, 6.89, 6.87, 0.21, 0.15,
  0.15, 0.39, 0.80, 0.80, 0.37, 3.63, 0.35, 0.30, 0.64, 0.59, 1.20, 1.22,
  1.42, 0.95, 2.70, 6.36, 6.36, 6.36, 6.60, 0.04, 0.71, 0.57, 0.24, 0.24,
  0.04, 0.04, 1.35, 0.82, 1.04, 0.62, 0.26, 5.98, 1.67, 1.67, 0.48, 0.15,
  6.67, 6.67, 1.20, 0.21, 3.99, 0.12, 0.19, 0.15, 6.96, 0.26, 0.08, 0.30,
  1.04, 1.04, 1.04, 0.62, 0.04, 0.04, 0.04, 0.82, 0.82, 1.29, 1.35, 0.46,
  0.46, 0.04, 0.04, 5.98, 5.98, 6.87, 0.37, 6.47, 6.47, 6.47, 6.67, 0.30,
  1.49, 3.21, 3.21, 0.75, 0.75, 0.46, 0.46, 0.46, 0.46, 3.63, 0.39, 3.65,
  4.09, 4.01, 3.36, 1.43, 3.28, 5.94, 6.35, 6.87, 5.60, 5.99, 0.12, 0.00,
  0.32, 0.39, 0.00, 1.63, 1.36, 5.67, 5.60, 5.79, 1.10, 2.99, 0.39, 0.18
  ),
 y = c(
  7.41, 8.01, 8.01, 5.44, 7.11, 7.13, 1.83, 1.83, 8.22, 8.08,
  8.08, 7.20, 7.83, 7.83, 8.29, 5.99, 8.32, 8.22, 7.38, 7.69, 8.22, 7.31,
  8.25, 8.39, 6.34, 0.16, 0.16, 0.16, 1.66, 7.55, 7.90, 8.18, 8.32, 8.32,
  7.97, 7.97, 8.15, 8.43, 7.83, 8.32, 8.29, 1.03, 7.27, 7.27, 8.08, 7.27,
  0.79, 0.79, 8.22, 7.73, 6.62, 7.62, 8.39, 8.36, 1.73, 8.29, 8.04, 8.22,
  7.83, 7.83, 7.83, 8.32, 8.11, 7.69, 7.55, 7.20, 7.20, 8.01, 8.15, 7.55,
  7.55, 7.97, 7.97, 1.03, 1.03, 1.24, 7.20, 0.47, 0.47, 0.47, 0.79, 8.22,
  7.13, 6.48, 6.48, 7.10, 7.10, 8.01, 8.01, 8.01, 8.01, 5.99, 8.04, 5.22,
  5.82, 5.14, 4.81, 7.62, 5.73, 0.55, 1.31, 0.05, 0.95, 1.59, 7.99, 7.48,
  8.38, 7.12, 2.01, 1.40, 0.00, 9.69, 9.47, 9.25, 2.63, 6.89, 0.56, 3.11
 )
)

## HDBSCAN splits one cluster
hdb <- hdbscan(X, minPts = 3)
plot(hdb, show_flat = TRUE)
hullplot(X, hdb, main = "HDBSCAN")

## DBSCAN* marks the least dense cluster as outliers
db <- dbscan(X, eps = 1, minPts = 3, borderPoints = FALSE)
hullplot(X, db, main = "DBSCAN*")

## HDBSCAN(e) mixes HDBSCAN AND DBSCAN* to find all clusters
hdbe <- hdbscan(X, minPts = 3, cluster_selection_epsilon = 1)
plot(hdbe, show_flat = TRUE)
hullplot(X, hdbe, main = "HDBSCAN(e)")
```

`hullplot` *Plot Clusters*

Description

This function produces a two-dimensional scatter plot of data points and colors the data points according to a supplied clustering. Noise points are marked as `x`. `hullplot()` also adds convex hulls to clusters.

Usage

```
hullplot(
  x,
  cl,
  col = NULL,
  pch = NULL,
  cex = 0.5,
  hull_lwd = 1,
  hull_lty = 1,
  solid = TRUE,
  alpha = 0.2,
  main = "Convex Cluster Hulls",
  ...
)

clplot(x, cl, col = NULL, pch = NULL, cex = 0.5, main = "Cluster Plot", ...)
```

Arguments

x	a data matrix. If more than 2 columns are provided, then the data is plotted using the first two principal components.
cl	a clustering. Either a numeric cluster assignment vector or a clustering object (a list with an element named `cluster`).
col	colors used for clusters. Defaults to the standard palette. The first color (default is black) is used for noise/unassigned points (cluster id 0).
pch	a vector of plotting characters. By default `o` is used for points and `x` for noise points.
cex	expansion factor for symbols.
hull_lwd, hull_lty	line width and line type used for the convex hull.
solid, alpha	draw filled polygons instead of just lines for the convex hulls? alpha controls the level of alpha shading.
main	main title.
...	additional arguments passed on to plot.

Author(s)

Michael Hahsler

Examples

```
set.seed(2)
n <- 400

x <- cbind(
  x = runif(4, 0, 1) + rnorm(n, sd = 0.1),
  y = runif(4, 0, 1) + rnorm(n, sd = 0.1)
```

```
  )
cl <- rep(1:4, times = 100)


### original data with true clustering
clplot(x, cl, main = "True clusters")
hullplot(x, cl, main = "True clusters")
### use different symbols
hullplot(x, cl, main = "True clusters", pch = cl)
### just the hulls
hullplot(x, cl, main = "True clusters", pch = NA)
### a version suitable for b/w printing)
hullplot(x, cl, main = "True clusters", solid = FALSE,
  col = c("grey", "black"), pch = cl)


### run some clustering algorithms and plot the results
db <- dbscan(x, eps = .07, minPts = 10)
clplot(x, db, main = "DBSCAN")
hullplot(x, db, main = "DBSCAN")

op <- optics(x, eps = 10, minPts = 10)
opDBSCAN <- extractDBSCAN(op, eps_cl = .07)
hullplot(x, opDBSCAN, main = "OPTICS")

opXi <- extractXi(op, xi = 0.05)
hullplot(x, opXi, main = "OPTICSXi")

# Extract minimal 'flat' clusters only
opXi <- extractXi(op, xi = 0.05, minimum = TRUE)
hullplot(x, opXi, main = "OPTICSXi")

km <- kmeans(x, centers = 4)
hullplot(x, km, main = "k-means")

hc <- cutree(hclust(dist(x)), k = 4)
hullplot(x, hc, main = "Hierarchical Clustering")
```

`jpclust` *Jarvis-Patrick Clustering*

Description

Fast C++ implementation of the Jarvis-Patrick clustering which first builds a shared nearest neighbor graph (k nearest neighbor sparsification) and then places two points in the same cluster if they are in each others nearest neighbor list and they share at least kt nearest neighbors.

Usage

```
jpclust(x, k, kt, ...)
```

Arguments

x	a data matrix/data.frame (Euclidean distance is used), a precomputed dist object or a kNN object created with kNN().
k	Neighborhood size for nearest neighbor sparsification. If x is a kNN object then k may be missing.
kt	threshold on the number of shared nearest neighbors (including the points themselves) to form clusters. Range: $[1, k]$
...	additional arguments are passed on to the k nearest neighbor search algorithm. See kNN() for details on how to control the search strategy.

Details

Following the original paper, the shared nearest neighbor list is constructed as the k neighbors plus the point itself (as neighbor zero). Therefore, the threshold kt needs to be in the range $[1, k]$.

Fast nearest neighbors search with kNN() is only used if x is a matrix. In this case Euclidean distance is used.

Value

A object of class general_clustering with the following components:

cluster	A integer vector with cluster assignments. Zero indicates noise points.
type	name of used clustering algorithm.
metric	the distance metric used for clustering.
param	list of used clustering parameters.

Author(s)

Michael Hahsler

References

R. A. Jarvis and E. A. Patrick. 1973. Clustering Using a Similarity Measure Based on Shared Near Neighbors. *IEEE Trans. Comput. 22,* 11 (November 1973), 1025-1034. doi:10.1109/T-C.1973.223640

See Also

Other clustering functions: dbscan(), extractFOSC(), hdbscan(), ncluster(), optics(), sNNclust()

Examples

```
data("DS3")

# use a shared neighborhood of 20 points and require 12 shared neighbors
cl <- jpclust(DS3, k = 20, kt = 12)
cl
```

```
clplot(DS3, cl)
# Note: JP clustering does not consider noise and thus,
# the sine wave points chain clusters together.

# use a precomputed kNN object instead of the original data.
nn <- kNN(DS3, k = 30)
nn

cl <- jpclust(nn, k = 20, kt = 12)
cl

# cluster with noise removed (use low pointdensity to identify noise)
d <- pointdensity(DS3, eps = 25)
hist(d, breaks = 20)
DS3_noiseless <- DS3[d > 110,]

cl <- jpclust(DS3_noiseless, k = 20, kt = 10)
cl

clplot(DS3_noiseless, cl)
```

---

kNN *Find the k Nearest Neighbors*

Description

This function uses a kd-tree to find all k nearest neighbors in a data matrix (including distances) fast.

Usage

```
kNN(
  x,
  k,
  query = NULL,
  sort = TRUE,
  search = "kdtree",
  bucketSize = 10,
  splitRule = "suggest",
  approx = 0
)

## S3 method for class 'kNN'
sort(x, decreasing = FALSE, ...)

## S3 method for class 'kNN'
adjacencylist(x, ...)

## S3 method for class 'kNN'
print(x, ...)
```

Arguments

x	a data matrix, a dist object or a kNN object.
k	number of neighbors to find.
query	a data matrix with the points to query. If query is not specified, the NN for all the points in x is returned. If query is specified then x needs to be a data matrix.
sort	sort the neighbors by distance? Note that some search methods already sort the results. Sorting is expensive and sort = FALSE may be much faster for some search methods. kNN objects can be sorted using sort().
search	nearest neighbor search strategy (one of "kdtree", "linear" or "dist").
bucketSize	max size of the kd-tree leafs.
splitRule	rule to split the kd-tree. One of "STD", "MIDPT", "FAIR", "SL_MIDPT", "SL_FAIR" or "SUGGEST" (SL stands for sliding). "SUGGEST" uses ANNs best guess.
approx	use approximate nearest neighbors. All NN up to a distance of a factor of 1 + approx eps may be used. Some actual NN may be omitted leading to spurious clusters and noise points. However, the algorithm will enjoy a significant speedup.
decreasing	sort in decreasing order?
...	further arguments

Details

Handling of ties and self-matches

- **Ties:** If the kth and the (k+1)th nearest neighbor are tied, then the neighbor found first is returned and the other one is ignored.
- **Self-matches:** If no query is specified, then self-matches are removed.

Details on the search parameters:

- search controls if a kd-tree or linear search (both implemented in the ANN library; see Mount and Arya, 2010). Note, that these implementations cannot handle NAs. search = "dist" precomputes Euclidean distances first using R. NAs are handled, but the resulting distance matrix cannot contain NAs. To use other distance measures, a precomputed distance matrix can be provided as x (search is ignored).
- bucketSize and splitRule influence how the kd-tree is built. approx uses the approximate nearest neighbor search implemented in ANN. All nearest neighbors up to a distance of eps / (1 + approx) will be considered and all with a distance greater than eps will not be considered. The other points might be considered. Note that this results in some actual nearest neighbors being omitted leading to spurious clusters and noise points. However, the algorithm will enjoy a significant speedup. For more details see Mount and Arya (2010).

Value

An object of class kNN (subclass of NN) containing a list with the following components:

dist	a matrix with distances.

id	a matrix with ids.
k	number k used.
metric	used distance metric.

Author(s)

Michael Hahsler

References

David M. Mount and Sunil Arya (2010). ANN: A Library for Approximate Nearest Neighbor Searching, http://www.cs.umd.edu/~mount/ANN/.

See Also

Other NN functions: NN, comps(), frNN(), kNNdist(), sNN()

Examples

```
data(iris)
x <- iris[, -5]

# Example 1: finding kNN for all points in a data matrix (using a kd-tree)
nn <- kNN(x, k = 5)
nn

# explore neighborhood of point 10
i <- 10
nn$id[i,]
plot(x, col = ifelse(seq_len(nrow(iris)) %in% nn$id[i,], "red", "black"))

# visualize the 5 nearest neighbors
plot(nn, x)

# visualize a reduced 2-NN graph
plot(kNN(nn, k = 2), x)

# Example 2: find kNN for query points
q <- x[c(1,100),]
nn <- kNN(x, k = 10, query = q)

plot(nn, x, col = "grey")
points(q, pch = 3, lwd = 2)

# Example 3: find kNN using distances
d <- dist(x, method = "manhattan")
nn <- kNN(d, k = 1)
plot(nn, x)
```

kNNdist *Calculate and Plot k-Nearest Neighbor Distances*

Description

Fast calculation of the k-nearest neighbor distances for a dataset represented as a matrix of points. The kNN distance is defined as the distance from a point to its k nearest neighbor. The kNN distance plot displays the kNN distance of all points sorted from smallest to largest. The plot can be used to help find suitable parameter values for `dbscan()`.

Usage

```
kNNdist(x, k, all = FALSE, ...)

kNNdistplot(x, k, minPts, ...)
```

Arguments

`x`	the data set as a matrix of points (Euclidean distance is used) or a precalculated dist object.
`k`	number of nearest neighbors used for the distance calculation. For `kNNdistplot()` also a range of values for `k` or `minPts` can be specified.
`all`	should a matrix with the distances to all k nearest neighbors be returned?
`...`	further arguments (e.g., kd-tree related parameters) are passed on to `kNN()`.
`minPts`	to use a k-NN plot to determine a suitable `eps` value for `dbscan()`, `minPts` used in dbscan can be specified and will set `k = minPts - 1`.

Value

`kNNdist()` returns a numeric vector with the distance to its k nearest neighbor. If `all = TRUE` then a matrix with k columns containing the distances to all 1st, 2nd, ..., kth nearest neighbors is returned instead.

Author(s)

Michael Hahsler

See Also

Other Outlier Detection Functions: `glosh()`, `lof()`, `pointdensity()`

Other NN functions: `NN`, `comps()`, `frNN()`, `kNN()`, `sNN()`

Examples

```
data(iris)
iris <- as.matrix(iris[, 1:4])

## Find the 4-NN distance for each observation (see ?kNN
## for different search strategies)
kNNdist(iris, k = 4)

## Get a matrix with distances to the 1st, 2nd, ..., 4th NN.
kNNdist(iris, k = 4, all = TRUE)

## Produce a k-NN distance plot to determine a suitable eps for
## DBSCAN with MinPts = 5. Use k = 4 (= MinPts -1).
## The knee is visible around a distance of .7
kNNdistplot(iris, k = 4)

## Look at all k-NN distance plots for a k of 1 to 10
## Note that k-NN distances are increasing in k
kNNdistplot(iris, k = 1:20)

cl <- dbscan(iris, eps = .7, minPts = 5)
pairs(iris, col = cl$cluster + 1L)
## Note: black points are noise points
```

---

lof *Local Outlier Factor Score*

Description

Calculate the Local Outlier Factor (LOF) score for each data point using a kd-tree to speed up kNN search.

Usage

```
lof(x, minPts = 5, ...)
```

Arguments

x	a data matrix or a dist object.
minPts	number of nearest neighbors used in defining the local neighborhood of a point (includes the point itself).
...	further arguments are passed on to kNN(). Note: sort cannot be specified here since lof() uses always sort = TRUE.

Details

LOF compares the local reachability density (lrd) of a point to the lrd of its neighbors. A LOF score of approximately 1 indicates that the lrd around the point is comparable to the lrd of its neighbors and that the point is not an outlier. Points that have a substantially lower lrd than their neighbors are considered outliers and produce scores significantly larger than 1.

If a data matrix is specified, then Euclidean distances and fast nearest neighbor search using a kd-tree is used.

Note on duplicate points: If there are more than `minPts` duplicates of a point in the data, then LOF the local readability distance will be 0 resulting in an undefined LOF score of 0/0. We set LOF in this case to 1 since there is already enough density from the points in the same location to make them not outliers. The original paper by Breunig et al (2000) assumes that the points are real duplicates and suggests to remove the duplicates before computing LOF. If duplicate points are removed first, then this LOF implementation in **dbscan** behaves like the one described by Breunig et al.

Value

A numeric vector of length `nrow(x)` containing LOF values for all data points.

Author(s)

Michael Hahsler

References

Breunig, M., Kriegel, H., Ng, R., and Sander, J. (2000). LOF: identifying density-based local outliers. In *ACM Int. Conf. on Management of Data,* pages 93-104. doi:10.1145/335191.335388

See Also

Other Outlier Detection Functions: `glosh()`, `kNNdist()`, `pointdensity()`

Examples

```
set.seed(665544)
n <- 100
x <- cbind(
  x=runif(10, 0, 5) + rnorm(n, sd = 0.4),
  y=runif(10, 0, 5) + rnorm(n, sd = 0.4)
  )

### calculate LOF score with a neighborhood of 3 points
lof <- lof(x, minPts = 3)

### distribution of outlier factors
summary(lof)
hist(lof, breaks = 10, main = "LOF (minPts = 3)")

### plot sorted lof. Looks like outliers start around a LOF of 2.
plot(sort(lof), type = "l",  main = "LOF (minPts = 3)",
```

```
  xlab = "Points sorted by LOF", ylab = "LOF")

### point size is proportional to LOF and mark points with a LOF > 2
plot(x, pch = ".", main = "LOF (minPts = 3)", asp = 1)
points(x, cex = (lof - 1) * 2, pch = 1, col = "red")
text(x[lof > 2,], labels = round(lof, 1)[lof > 2], pos = 3)
```

`moons` *Moons Data*

Description

Contains 100 2-d points, half of which are contained in two moons or "blobs"" (25 points each blob), and the other half in asymmetric facing crescent shapes. The three shapes are all linearly separable.

Format

A data frame with 100 observations on the following 2 variables.

X a numeric vector

Y a numeric vector

Details

This data was generated with the following Python commands using the SciKit-Learn library:

```
import sklearn.datasets as data

moons = data.make_moons(n_samples=50, noise=0.05)
blobs = data.make_blobs(n_samples=50,
                        centers=[(-0.75,2.25), (1.0, 2.0)],
                        cluster_std=0.25)
test_data = np.vstack([moons, blobs])
```

Source

See the HDBSCAN notebook from github documentation: https://hdbscan.readthedocs.io/en/latest/how_hdbscan_works.html

References

Pedregosa, Fabian, Gael Varoquaux, Alexandre Gramfort, Vincent Michel, Bertrand Thirion, Olivier Grisel, Mathieu Blondel et al. Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research* 12, no. Oct (2011): 2825-2830.

Examples

```
data(moons)
plot(moons, pch=20)
```

ncluster *Number of Clusters, Noise Points, and Observations*

Description

Extract the number of clusters or the number of noise points for a clustering. This function works with any clustering result that contains a list element named `cluster` with a clustering vector. In addition, `nobs` (see `stats::nobs()`) is also available to retrieve the number of clustered points.

Usage

```
ncluster(object, ...)

nnoise(object, ...)
```

Arguments

`object`	a clustering result object containing a `cluster` element.
`...`	additional arguments are unused.

Value

returns the number if clusters or noise points.

See Also

Other clustering functions: `dbscan()`, `extractFOSC()`, `hdbscan()`, `jpclust()`, `optics()`, `sNNclust()`

Examples

```
data(iris)
iris <- as.matrix(iris[, 1:4])

res <- dbscan(iris, eps = .7, minPts = 5)
res

ncluster(res)
nnoise(res)
nobs(res)

# the functions also work with kmeans and other clustering algorithms.
cl <- kmeans(iris, centers = 3)
ncluster(cl)
nnoise(cl)
nobs(res)
```

NN *NN — Nearest Neighbors Superclass*

Description

NN is an abstract S3 superclass for the classes of the objects returned by `kNN()`, `frNN()` and `sNN()`. Methods for sorting, plotting and getting an adjacency list are defined.

Usage

```
adjacencylist(x, ...)

## S3 method for class 'NN'
adjacencylist(x, ...)

## S3 method for class 'NN'
sort(x, decreasing = FALSE, ...)

## S3 method for class 'NN'
plot(x, data, main = NULL, pch = 16, col = NULL, linecol = "gray", ...)
```

Arguments

`x`	a `NN` object
`...`	further parameters past on to `plot()`.
`decreasing`	sort in decreasing order?
`data`	that was used to create `x`
`main`	title
`pch`	plotting character.
`col`	color used for the data points (nodes).
`linecol`	color used for edges.

Subclasses

kNN, frNN and sNN

Author(s)

Michael Hahsler

See Also

Other NN functions: `comps()`, `frNN()`, `kNN()`, `kNNdist()`, `sNN()`

Examples

```
data(iris)
x <- iris[, -5]

# finding kNN directly in data (using a kd-tree)
nn <- kNN(x, k=5)
nn

# plot the kNN where NN are shown as line conecting points.
plot(nn, x)

# show the first few elements of the adjacency list
head(adjacencylist(nn))

## Not run:
# create a graph and find connected components (if igraph is installed)
library("igraph")
g <- graph_from_adj_list(adjacencylist(nn))
comp <- components(g)
plot(x, col = comp$membership)

# detect clusters (communities) with the label propagation algorithm
cl <- membership(cluster_label_prop(g))
plot(x, col = cl)

## End(Not run)
```

---

optics *Ordering Points to Identify the Clustering Structure (OPTICS)*

Description

Implementation of the OPTICS (Ordering points to identify the clustering structure) point ordering algorithm using a kd-tree.

Usage

```
optics(x, eps = Inf, minPts = 5, ...)

## S3 method for class 'optics'
print(x, ...)

## S3 method for class 'optics'
plot(x, cluster = TRUE, predecessor = FALSE, ...)

## S3 method for class 'optics'
as.reachability(object, ...)
```

```
## S3 method for class 'optics'
as.dendrogram(object, ...)

extractDBSCAN(object, eps_cl)

extractXi(object, xi, minimum = FALSE, correctPredecessors = TRUE)

## S3 method for class 'optics'
predict(object, newdata, data, ...)
```

Arguments

x	a data matrix or a dist object.
eps	maximum epsilon neighborhood size only used for performance. When set to Inf, then the actual maximal needed radius is estimated from minPts and the data. The upper limit can be further reduced to improve performance. If set too low then many reachability values will erroneously become Inf shown as dashed lines in the reachability plot. eps should be increased.
minPts	the parameter is used to identify dense neighborhoods and the reachability distance is calculated as the distance to the minPts nearest neighbor. Controls the smoothness of the reachability distribution. Default is 5 points.
...	additional arguments are passed on to fixed-radius nearest neighbor search algorithm. See frNN() for details on how to control the search strategy.
cluster, predecessor	plot clusters and predecessors.
object	clustering object.
eps_cl	Threshold to identify clusters (eps_cl <= eps).
xi	Steepness threshold to identify clusters hierarchically using the Xi method.
minimum	logical, representing whether or not to extract the minimal (non-overlapping) clusters in the Xi clustering algorithm.
correctPredecessors	logical, correct a common artifact by pruning the steep up area for points that have predecessors not in the cluster–found by the ELKI framework, see details below.
newdata	new data points for which the cluster membership should be predicted.
data	the data set used to create the clustering object.

Details

The Algorithm:

This implementation of OPTICS implements the original algorithm as described by Ankerst et al (1999). OPTICS is an ordering algorithm with methods to extract a clustering from the ordering. While using similar concepts as DBSCAN, minPts in OPTICS has a different effect than in DBSCAN. Since it is also used to calculate the reachability distance, larger values will make the reachability distance plot smoother. The parameter eps is optional and defaults to Inf. It

represents an upper limit for the neighborhood size used to reduce computational complexity which is helpful for large data sets.

OPTICS linearly orders the data points such that points which are spatially closest become neighbors in the ordering. The closest analog to this ordering is dendrogram in single-link hierarchical clustering. The algorithm also calculates the reachability distance for each point. `plot()` (see reachability_plot) produces a reachability plot which shows each points reachability distance between two consecutive points where the points are sorted by OPTICS. Valleys represent clusters (the deeper the valley, the more dense the cluster) and high points indicate points between clusters.

Specifying the Data:

If `x` is specified as a data matrix, then Euclidean distances and fast nearest neighbor lookup using a kd-tree are used. See `kNN()` for details on the parameters for the kd-tree.

Extracting a Clustering:

Several methods to extract a clustering from the order returned by OPTICS are implemented:

- `extractDBSCAN()` extracts a clustering from an OPTICS ordering that is similar to what DBSCAN would produce with an eps set to `eps_cl` (see Ankerst et al, 1999). The only difference to a DBSCAN clustering is that OPTICS is not able to assign some border points and reports them instead as noise.
- `extractXi()` extract clusters hierarchically specified in Ankerst et al (1999) based on the steepness of the reachability plot. One interpretation of the `xi` parameter is that it classifies clusters by change in relative cluster density. The used algorithm was originally contributed by the ELKI framework and is explained in Schubert et al (2018), but contains a set of fixes.

Predict Cluster Memberships:

`predict()` requires an extracted DBSCAN clustering with `extractDBSCAN()` and then uses predict for `dbscan()`.

Value

An object of class `optics` with components:

`eps`	value of `eps` parameter.
`minPts`	value of `minPts` parameter.
`order`	optics order for the data points in `x`.
`reachdist`	reachability distance for each data point in `x`.
`coredist`	core distance for each data point in `x`.

For `extractDBSCAN()`, in addition the following components are available:

`eps_cl`	the value of the `eps_cl` parameter.
`cluster`	assigned cluster labels in the order of the data points in `x`.

For `extractXi()`, in addition the following components are available:

`xi`	Steepness threshold `xi`.
`cluster`	assigned cluster labels in the order of the data points in `x`.
`clusters_xi`	data.frame containing the start and end of each cluster found in the OPTICS ordering.

Author(s)

Michael Hahsler and Matthew Piekenbrock

References

Mihael Ankerst, Markus M. Breunig, Hans-Peter Kriegel, Joerg Sander (1999). OPTICS: Ordering Points To Identify the Clustering Structure. *ACM SIGMOD international conference on Management of data.* ACM Press. pp. doi:10.1145/304181.304187

Hahsler M, Piekenbrock M, Doran D (2019). dbscan: Fast Density-Based Clustering with R. *Journal of Statistical Software*, 91(1), 1-30. doi:10.18637/jss.v091.i01

Erich Schubert, Michael Gertz (2018). Improving the Cluster Structure Extracted from OPTICS Plots. In *Lernen, Wissen, Daten, Analysen (LWDA 2018),* pp. 318-329.

See Also

Density reachability.

Other clustering functions: `dbscan()`, `extractFOSC()`, `hdbscan()`, `jpclust()`, `ncluster()`, `sNNclust()`

Examples

```
set.seed(2)
n <- 400

x <- cbind(
  x = runif(4, 0, 1) + rnorm(n, sd = 0.1),
  y = runif(4, 0, 1) + rnorm(n, sd = 0.1)
  )

plot(x, col=rep(1:4, times = 100))

### run OPTICS (Note: we use the default eps calculation)
res <- optics(x, minPts = 10)
res

### get order
res$order

### plot produces a reachability plot
plot(res)

### plot the order of points in the reachability plot
plot(x, col = "grey")
polygon(x[res$order, ])

### extract a DBSCAN clustering by cutting the reachability plot at eps_cl
res <- extractDBSCAN(res, eps_cl = .065)
res

plot(res)  ## black is noise
hullplot(x, res)
```

```
### re-cut at a higher eps threshold
res <- extractDBSCAN(res, eps_cl = .07)
res
plot(res)
hullplot(x, res)

### extract hierarchical clustering of varying density using the Xi method
res <- extractXi(res, xi = 0.01)
res

plot(res)
hullplot(x, res)

# Xi cluster structure
res$clusters_xi

### use OPTICS on a precomputed distance matrix
d <- dist(x)
res <- optics(d, minPts = 10)
plot(res)
```

`pointdensity` *Calculate Local Density at Each Data Point*

Description

Calculate the local density at each data point as either the number of points in the eps-neighborhood (as used in `dbscan()`) or perform kernel density estimation (KDE) using a uniform kernel. The function uses a kd-tree for fast fixed-radius nearest neighbor search.

Usage

```
pointdensity(
  x,
  eps,
  type = "frequency",
  search = "kdtree",
  bucketSize = 10,
  splitRule = "suggest",
  approx = 0
)
```

Arguments

`x`	a data matrix or a dist object.
`eps`	radius of the eps-neighborhood, i.e., bandwidth of the uniform kernel). For the Gaussian kde, this parameter specifies the standard deviation of the kernel.

type "frequency", "density", or "gaussian". should the raw count of points inside the eps-neighborhood, the eps-neighborhood density estimate, or a Gaussian density estimate be returned?

search, bucketSize, splitRule, approx
algorithmic parameters for frNN().

Details

dbscan() estimates the density around a point as the number of points in the eps-neighborhood of the point (including the query point itself). Kernel density estimation (KDE) using a uniform kernel, which is just this point count in the eps-neighborhood divided by $(2\, eps\, n)$, where n is the number of points in x.

Alternatively, type = "gaussian" calculates a Gaussian kernel estimate where eps is used as the standard deviation. To speed up computation, a kd-tree is used to find all points within 3 times the standard deviation and these points are used for the estimate.

Points with low local density often indicate noise (see e.g., Wishart (1969) and Hartigan (1975)).

Value

A vector of the same length as data points (rows) in x with the count or density values for each data point.

Author(s)

Michael Hahsler

References

Wishart, D. (1969), Mode Analysis: A Generalization of Nearest Neighbor which Reduces Chaining Effects, in *Numerical Taxonomy,* Ed., A.J. Cole, Academic Press, 282-311.

John A. Hartigan (1975), *Clustering Algorithms,* John Wiley & Sons, Inc., New York, NY, USA.

See Also

frNN(), stats::density().

Other Outlier Detection Functions: glosh(), kNNdist(), lof()

Examples

```
set.seed(665544)
n <- 100
x <- cbind(
  x=runif(10, 0, 5) + rnorm(n, sd = 0.4),
  y=runif(10, 0, 5) + rnorm(n, sd = 0.4)
  )
plot(x)

### calculate density around points
d <- pointdensity(x, eps = .5, type = "density")
```

```
### density distribution
summary(d)
hist(d, breaks = 10)

### plot with point size is proportional to Density
plot(x, pch = 19, main = "Density (eps = .5)", cex = d*5)

### Wishart (1969) single link clustering after removing low-density noise
# 1. remove noise with low density
f <- pointdensity(x, eps = .5, type = "frequency")
x_nonoise <- x[f >= 5,]

# 2. use single-linkage on the non-noise points
hc <- hclust(dist(x_nonoise), method = "single")
plot(x, pch = 19, cex = .5)
points(x_nonoise, pch = 19, col= cutree(hc, k = 4) + 1L)
```

`reachability` *Reachability Distances*

Description

Reachability distances can be plotted to show the hierarchical relationships between data points. The idea was originally introduced by Ankerst et al (1999) to visualize the order generated by OPTICS. Later, Sanders et al (2003) showed that the visualization is useful for other hierarchical structures and introduced an algorithm to convert dendrogram representation to reachability plots. We implement dendrogram conversion and reachability plots.

Usage

```
## S3 method for class 'reachability'
print(x, ...)

## S3 method for class 'reachability'
plot(
  x,
  order_labels = FALSE,
  xlab = "Order",
  ylab = "Reachability dist.",
  main = "Reachability Plot",
  ...
)

as.reachability(object, ...)

## S3 method for class 'dendrogram'
as.reachability(object, ...)
```

Arguments

x	object of class reachability.
...	graphical parameters are passed on to plot(), or arguments for other methods.
order_labels	whether to plot text labels for each points reachability distance.
xlab	x-axis label.
ylab	y-axis label.
main	Title of the plot.
object	any object that can be coerced to class reachability, such as an object of class optics or stats::dendrogram.

Details

Reachability Plots:

A reachability plot displays the points as vertical bars, were the height is the reachability distance between two consecutive points. Reachability distances can be undefined when a point does not have enough neighbors in the epsilon neighborhood. We represent these undefined cases as Inf and represent them in the plot as a dashed line. If many dashed lines show up for OPTICS then you need to increase eps there. The reachability distance for the first point is by definition not defined (it has no preceding point).

The central idea behind reachability plots is that the ordering in which points are plotted identifies underlying hierarchical density representation as mountains and valleys of high and low reachability distance.

Different hierarchical representations, such as dendrograms or reachability plots, may be preferable depending on the context. In smaller datasets, cluster memberships may be more easily identifiable through a dendrogram representation, particularly is the user is already familiar with tree-like representations. For larger datasets however, a reachability plot may be preferred for visualizing macro-level density relationships.

Reachability Plots for OPTICS:

The original ordering algorithm OPTICS as described by Ankerst et al (1999) introduced the notion of reachability plots. OPTICS linearly orders the data points such that points which are spatially closest become neighbors in the ordering. Valleys represent clusters, which can be represented hierarchically. Although the ordering is crucial to the structure of the reachability plot, it's important to note that OPTICS, like DBSCAN, is not entirely deterministic and, just like the dendrogram, isomorphisms may exist. Reachability plots were shown to essentially convey the same information as the more traditional dendrogram structure by Sanders et al (2003).

A variety of cluster extraction methods have been proposed using reachability plots. Because both cluster extraction depend directly on the ordering OPTICS produces, they are part of the optics() interface. Nonetheless, reachability plots can be created directly from other types of linkage trees, and vice versa.

Value

An object of class reachability with components:

order	order to use for the data points in x.
reachdist	reachability distance for each data point in x.

Author(s)

Matthew Piekenbrock

References

Ankerst, M., M. M. Breunig, H.-P. Kriegel, J. Sander (1999). OPTICS: Ordering Points To Identify the Clustering Structure. *ACM SIGMOD international conference on Management of data.* ACM Press. pp. 49–60.

Sander, J., X. Qin, Z. Lu, N. Niu, and A. Kovarsky (2003). Automatic extraction of clusters from hierarchical clustering representations. *Pacific-Asia Conference on Knowledge Discovery and Data Mining.* Springer Berlin Heidelberg.

See Also

`optics()`, `as.dendrogram()`, and `stats::hclust()`.

Examples

```
set.seed(2)
n <- 20

x <- cbind(
  x = runif(4, 0, 1) + rnorm(n, sd = 0.1),
  y = runif(4, 0, 1) + rnorm(n, sd = 0.1)
)

plot(x, xlim = range(x), ylim = c(min(x) - sd(x), max(x) + sd(x)), pch = 20)
text(x = x, labels = seq_len(nrow(x)), pos = 3)

### run OPTICS
res <- optics(x, eps = 10,  minPts = 2)
res

### plot produces a reachability plot.
plot(res)

### Manually extract reachability components from OPTICS
reach <- as.reachability(res)
reach

### plot still produces a reachability plot; points ids
### (rows in the original data) can be displayed with order_labels = TRUE
plot(reach, order_labels = TRUE)

### Reachability objects can be directly converted to dendrograms
dend <- as.dendrogram(reach)
dend
plot(dend)

### A dendrogram can be converted back into a reachability object
plot(as.reachability(dend))
```

sNN *Find Shared Nearest Neighbors*

Description

Calculates the number of shared nearest neighbors and creates a shared nearest neighbors graph.

Usage

```
sNN(
  x,
  k,
  kt = NULL,
  jp = FALSE,
  sort = TRUE,
  search = "kdtree",
  bucketSize = 10,
  splitRule = "suggest",
  approx = 0
)

## S3 method for class 'sNN'
sort(x, decreasing = TRUE, ...)

## S3 method for class 'sNN'
print(x, ...)
```

Arguments

x	a data matrix, a dist object or a kNN object.
k	number of neighbors to consider to calculate the shared nearest neighbors.
kt	minimum threshold on the number of shared nearest neighbors to build the shared nearest neighbor graph. Edges are only preserved if kt or more neighbors are shared.
jp	In regular sNN graphs, two points that are not neighbors can have shared neighbors. Javis and Patrick (1973) requires the two points to be neighbors, otherwise the count is zeroed out. TRUE uses this behavior.
sort	sort by the number of shared nearest neighbors? Note that this is expensive and sort = FALSE is much faster. sNN objects can be sorted using sort().
search	nearest neighbor search strategy (one of "kdtree", "linear" or "dist").
bucketSize	max size of the kd-tree leafs.
splitRule	rule to split the kd-tree. One of "STD", "MIDPT", "FAIR", "SL_MIDPT", "SL_FAIR" or "SUGGEST" (SL stands for sliding). "SUGGEST" uses ANNs best guess.

approx	use approximate nearest neighbors. All NN up to a distance of a factor of (1 + approx) eps may be used. Some actual NN may be omitted leading to spurious clusters and noise points. However, the algorithm will enjoy a significant speedup.
decreasing	logical; sort in decreasing order?
...	additional parameters are passed on.

Details

The number of shared nearest neighbors of two points p and q is the intersection of the kNN neighborhood of two points. Note: that each point is considered to be part of its own kNN neighborhood. The range for the shared nearest neighbors is $[0, k]$. The result is a n-by-k matrix called shared. Each row is a point and the columns are the point's k nearest neighbors. The value is the count of the shared neighbors.

The shared nearest neighbor graph connects a point with all its nearest neighbors if they have at least one shared neighbor. The number of shared neighbors can be used as an edge weight. Javis and Patrick (1973) use a slightly modified (see parameter jp) shared nearest neighbor graph for clustering.

Value

An object of class sNN (subclass of kNN and NN) containing a list with the following components:

id	a matrix with ids.
dist	a matrix with the distances.
shared	a matrix with the number of shared nearest neighbors.
k	number of k used.
metric	the used distance metric.

Author(s)

Michael Hahsler

References

R. A. Jarvis and E. A. Patrick. 1973. Clustering Using a Similarity Measure Based on Shared Near Neighbors. *IEEE Trans. Comput.* 22, 11 (November 1973), 1025-1034. doi:10.1109/T-C.1973.223640

See Also

Other NN functions: NN, comps(), frNN(), kNN(), kNNdist()

Examples

```
data(iris)
x <- iris[, -5]

# finding kNN and add the number of shared nearest neighbors.
k <- 5
nn <- sNN(x, k = k)
nn

# shared nearest neighbor distribution
table(as.vector(nn$shared))

# explore number of shared points for the k-neighborhood of point 10
i <- 10
nn$shared[i,]

plot(nn, x)

# apply a threshold to create a sNN graph with edges
# if more than 3 neighbors are shared.
nn_3 <- sNN(nn, kt = 3)
plot(nn_3, x)

# get an adjacency list for the shared nearest neighbor graph
adjacencylist(nn_3)
```

---

sNNclust *Shared Nearest Neighbor Clustering*

Description

Implements the shared nearest neighbor clustering algorithm by Ertoz, Steinbach and Kumar (2003).

Usage

```
sNNclust(x, k, eps, minPts, borderPoints = TRUE, ...)
```

Arguments

x	a data matrix/data.frame (Euclidean distance is used), a precomputed dist object or a kNN object created with kNN().
k	Neighborhood size for nearest neighbor sparsification to create the shared NN graph.
eps	Two objects are only reachable from each other if they share at least eps nearest neighbors. Note: this is different from the eps in DBSCAN!
minPts	minimum number of points that share at least eps nearest neighbors for a point to be considered a core points.

borderPoints	should border points be assigned to clusters like in DBSCAN?
...	additional arguments are passed on to the k nearest neighbor search algorithm. See kNN() for details on how to control the search strategy.

Details

Algorithm:

1. Constructs a shared nearest neighbor graph for a given k. The edge weights are the number of shared k nearest neighbors (in the range of $[0, k]$).
2. Find each points SNN density, i.e., the number of points which have a similarity of eps or greater.
3. Find the core points, i.e., all points that have an SNN density greater than MinPts.
4. Form clusters from the core points and assign border points (i.e., non-core points which share at least eps neighbors with a core point).

Note that steps 2-4 are equivalent to the DBSCAN algorithm (see dbscan()) and that eps has a different meaning than for DBSCAN. Here it is a threshold on the number of shared neighbors (see sNN()) which defines a similarity.

Value

A object of class general_clustering with the following components:

cluster	A integer vector with cluster assignments. Zero indicates noise points.
type	name of used clustering algorithm.
param	list of used clustering parameters.

Author(s)

Michael Hahsler

References

Levent Ertoz, Michael Steinbach, Vipin Kumar, Finding Clusters of Different Sizes, Shapes, and Densities in Noisy, High Dimensional Data, *SIAM International Conference on Data Mining,* 2003, 47-59. doi:10.1137/1.9781611972733.5

See Also

Other clustering functions: dbscan(), extractFOSC(), hdbscan(), jpclust(), ncluster(), optics()

Examples

```
data("DS3")

# Out of k = 20 NN 7 (eps) have to be shared to create a link in the sNN graph.
# A point needs a least 16 (minPts) links in the sNN graph to be a core point.
# Noise points have cluster id 0 and are shown in black.
```

```
cl <- sNNclust(DS3, k = 20, eps = 7, minPts = 16)
cl

clplot(DS3, cl)
```

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