

Package ‘DBCVindex’

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Title Calculates the Density-Based Clustering Validation Index (DBCV) Index

Version 1.1

Description A metric called 'Density-Based Clustering Validation index' (DBCV) index to evaluate clustering results, following the <<https://github.com/FelSiq/DBCV>> 'Python' implementation by Felipe Alves Siqueira. Original 'DBCV' index article: Moulavi, D., Jaskowiak, P. A., Campello, R. J., Zimek, A., & Sander, J. (2014, April). ``Density-based clustering validation", Proceedings of SDM 2014 -- the 2014 SIAM International Conference on Data Mining (pp. 839-847), <[doi:10.1137/1.9781611973440.96](https://doi.org/10.1137/1.9781611973440.96)>.

Depends R (>= 4.0.0)

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URL <https://github.com/davidechicco/DBCVindex>

Imports pacman, Matrix, stats

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.2

NeedsCompilation no

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`compute_pair_to_pair_dists`*Function to compute pairwise distances and ensure matrix format*

Description

Function to compute pairwise distances and ensure matrix format

Usage

```
compute_pair_to_pair_dists(data, metric = "euclidean")
```

Arguments

<code>data</code>	input clustering results
<code>metric</code>	metric of the distance, Euclidean by default

Value

a pairwise distances' matrix

Examples

```
n = 300; noise = 0.05; seed = 1782;
theta <- seq(0, pi, length.out = n / 2)
x1 <- cos(theta) + rnorm(n / 2, sd = noise)
y1 <- sin(theta) + rnorm(n / 2, sd = noise)
x2 <- cos(theta + pi) + rnorm(n / 2, sd = noise)
y2 <- sin(theta + pi) + rnorm(n / 2, sd = noise)
X <- rbind(cbind(x1, y1), cbind(x2, y2))

dist_matrix <- compute_pair_to_pair_dists(X)
```

`dbcv`*Function that calculates the Density-Based Clustering Validation index (DBCv) of clustering results*

Description

Function that calculates the Density-Based Clustering Validation index (DBCv) of clustering results

Usage

```
dbcv(data, labels, metric = "euclidean", noise_id = -1)
```

Arguments

data	input clustering results
labels	labels of the clustering
metric	metric of the distance, Euclidean by default
noise_id	the code of the noise cluster points, -1 by default

Value

a real value containing the Saturn coefficient

Examples

```
n = 300; noise = 0.05; seed = 1782;
theta <- seq(0, pi, length.out = n / 2)
x1 <- cos(theta) + rnorm(n / 2, sd = noise)
y1 <- sin(theta) + rnorm(n / 2, sd = noise)
x2 <- cos(theta + pi) + rnorm(n / 2, sd = noise)
y2 <- sin(theta + pi) + rnorm(n / 2, sd = noise)
X <- rbind(cbind(x1, y1), cbind(x2, y2))
y <- c(rep(0, n / 2), rep(1, n / 2))

cat("dbcv(X, y) = ", dbcv(X, y), "\n", sep="")
```

remove_duplicates	<i>Function to remove duplicate samples from the input data</i>
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Description

Function to remove duplicate samples from the input data

Usage

```
remove_duplicates(data, labels)
```

Arguments

data	input clustering results
labels	labels of the clustering

Value

a list of data and labels without duplicates

Examples

```
n = 300; noise = 0.05; seed = 1782;
theta <- seq(0, pi, length.out = n / 2)
x1 <- cos(theta) + rnorm(n / 2, sd = noise)
y1 <- sin(theta) + rnorm(n / 2, sd = noise)
x2 <- cos(theta + pi) + rnorm(n / 2, sd = noise)
y2 <- sin(theta + pi) + rnorm(n / 2, sd = noise)
X <- rbind(cbind(x1, y1), cbind(x2, y2))
y <- c(rep(0, n / 2), rep(1, n / 2))

cat("remove_duplicates(X, y) = ")
print(remove_duplicates(X, y))
```

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