Package ‘stream’

December 2, 2020

Version 1.4-0
Date 2020-12-01
Encoding UTF-8
Title Infrastructure for Data Stream Mining
Description A framework for data stream modeling and associated data mining tasks such as clustering and classification. The development of this package was supported in part by NSF IIS-0948893 and NIH R21HG005912. Hahsler et al (2017) <doi:10.18637/jss.v076.i14>.
Depends R (>= 3.5.0), methods, proxy (>= 0.4-7)
Imports clue, cluster, clusterGeneration, dbscan (>= 1.0-0), fpc, graphics, grDevices, MASS, mlbench, Rcpp (>= 0.11.4), stats, utils
Suggests animation, DBI, rJava, RSQLite, testthat
URL https://github.com/mhahsler/stream
BugReports https://github.com/mhahsler/stream/issues
LinkingTo Rcpp, BH
License GPL-3
NeedsCompilation yes
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Repository CRAN
Date/Publication 2020-12-02 08:00:02 UTC
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animation

Animates the plotting of a DSD and the clustering process

Description

Generates an animation of a data stream or a data stream clustering. **Note:** You need to install package animation, and, if necessary, the libraries required for package magick.

Usage

```r
animate_data(dsd, horizon = 100, n = 1000, wait = .1, plot.args = NULL, ...)
animate_cluster(dsc, dsd, measure = NULL, horizon = 100, n = 1000,
   type=c("auto", "micro", "macro"), assign="micro",
   assignmentMethod=c("auto", "model", "nn"),
   noise = c("class", "exclude"),
   wait=.1, plot.args = NULL, ...)
```

Arguments

- `dsd` a DSD object
- `dsc` a DSC object
- `horizon` the number of points displayed at once/used for evaluation.
- `n` the number of points to be plotted
- `measure` the evaluation measure that should be graphed below the animation
- `type` evaluate "micro" or "macro"-clusters? "auto" chooses micro if dsc is of class DSC_micro and no macro is given. Otherwise macro is used.
- `assign` assign new points to the closest "micro" or "macro"-cluster to calculate the evaluation measure.
- `assignmentMethod` how to assign data points to micro-clusters. Options are "model" and "nn" (nearest neighbor). "auto" uses model if available and nn otherwise.
noise  how to handle noise for calculating the evaluation measure (as a separate class or excluded).
wait  the time interval between each frame
plot.args  a list with plotting parameters for the clusters.
...  extra arguments are added to plot.args.

Details
Animations are recorded using the library animation and can be replayed (which gives a smoother experience since there is no more computation done) and saved in various formats (see Examples section below).

Author(s)
Michael Hahsler

See Also
evaluate_cluster for stream evaluation without animation. See ani.replay for replaying and saving animations.

Examples
## Not run:
stream <- DSD_Benchmark(1)
animate_data(stream, horizon=100, n=5000, xlim=c(0,1), ylim=c(0,1))

### animations can be replayed with the animation package
library(animation)
apa::ani.options(interval=.1) ## change speed
ani.replay()

### animations can also be saved as HTML, animated gifs, etc.
saveHTML(ani.replay())

### animate the clustering process with evaluation
### Note: we choose to exclude noise points from the evaluation
### measure calculation, even if the algorithm would assign
### them to a cluster.
reset_stream(stream)
dbstream <- DSC_DBSTREAM(r=.04, lambda=.1, gaptime=100, Cm=3,
                         shared_density=TRUE, alpha=.2)
animate_cluster(dbstream, stream, horizon=100, n=5000,
               measure="crand", type="macro", assign="micro", noise="exclude",
               plot.args = list(xlim=c(0,1), ylim=c(0,1), shared = TRUE))

## End(Not run)
**clean_outliers**  
*Clean Outliers from the Outlier Detecting Clusterer*

**Description**
Removes all outliers from the outlier detecting clusterer.

**Usage**
```r
clean_outliers(x, ...)  
```

## S3 method for class 'DSC_Outlier'
```
clean_outliers(x, ...)
```

**Arguments**
- `x` : The DSC object.
- `...` : Additional parameters to pass to `clean_outliers` implementations.

**Details**
Removes all outliers from the outlier detecting clusterer.

**Author(s)**
- Dalibor Krleža

**See Also**
- `DSC_Outlier`

---

**DefaultEvalCallback-class**  
*Default Class for Evaluation Callbacks*

**Description**
The default callback class for the `stream` package. Implicitly instantiated for each `evaluate` call.

**Author(s)**
- Dalibor Krleža
Data Stream Clusterer Base Classes

Description

Abstract base classes for all DSC (Data Stream Clusterer) and DSC_R classes.

Details

The DSC and DSC_R classes cannot be instantiated (calling DSC() or DSC_R() produces errors), but they serve as a base class from which other DSC classes inherit. Class DSC provides several generic functions that can operate on all DSC subclasses: print(), plot(), nclusters() to get the current number of clusters, get_centers() to get the cluster centers, and get_weights() to get the cluster weights (if implemented). get_centers() and get_weights() are typically overwritten by subclasses of DSC. DSC_R provides these functions for R-based DSC implementations. Since DSC objects often contain external pointers, regular saving and reading operations will fail. Use saveDSC() and readDSC() which will serialize the objects first appropriately.

Author(s)

Michael Hahsler

See Also

animate_cluster, cluster, evaluate, get_assignment, get_centers, get_weights, get_copy, microToMacro, nclusters, plot, prune_clusters, recluster, readDSC, saveDSC

Abstract Class for Data Stream Classifiers

Description

Abstract class for data stream classifiers. Currently, stream does not implement classification algorithms.

Author(s)

Michael Hahsler

See Also

DST
**DSC_BICO**  

**BICO - Fast computation of k-means coresets in a data stream**

**Description**

BICO maintains a tree which is inspired by the clustering tree of BIRCH, a SIGMOD Test of Time award-winning clustering algorithm. Each node in the tree represents a subset of these points. Instead of storing all points as individual objects, only the number of points, the sum and the squared sum of the subset’s points are stored as key features of each subset. Points are inserted into exactly one node.

**Usage**

\[ \text{DSC_BICO}(k = 5, \text{space} = 10, p = 10, \text{iterations} = 10) \]

**Arguments**

- \( k \): number of centres
- \( \text{space} \): coreset size
- \( p \): number of random projections used for nearest neighbour search in first level
- \( \text{iterations} \): number of repetitions for the kmeans++ procedure in the offline component

**Details**

In this implementation, the nearest neighbour search on the first level of the tree is sped up by projecting all points to random 1-d subspaces. The first estimation of the optimal clustering cost is computed in a buffer phase at the beginning of the algorithm. This implementation interfaces the original C++ implementation available here: [http://ls2-www.cs.tu-dortmund.de/grav/de/bico](http://ls2-www.cs.tu-dortmund.de/grav/de/bico). For micro-clustering, the algorithm computes the coreset of the stream. Reclustering is performed by using the kmeans++ algorithm on the coreset.

**Author(s)**

R-Interface: Matthias Carnein (<Matthias.Carnein@uni-muenster.de>), Dennis Assenmacher.  
C-Implementation: Hendrik Fichtenberger, Marc Gille, Melanie Schmidt, Chris Schwiegelshohn, Christian Sohler.

**References**


**Examples**

```R
stream <- DSD_Gaussians(k = 3, d = 2)  
BICO <- DSC_BICO(k = 3, p = 10, space = 100, iterations = 10)  
update(BICO, stream, n = 500)  
plot(BICO, stream, type = "both")
```
**DSC_BIRCH**  
*Balanced Iterative Reducing Clustering using Hierarchies*

**Description**

BIRCH builds a balanced-tree of Clustering Features (CFs) to summarize the stream. A CF is a tuple \( (n, LS, SS) \) which represents a cluster by storing the number of elements \( n \), their linear sum \( LS \) and their squared sum \( SS \). Each new observation descends the tree by following its closest CF until a leaf node is reached. It is either merged into its closest leaf-CF or inserted as a new one. All leaf-CFs form the micro-clusters. Rebuilding the tree is realized by inserting all leaf-CF nodes into a new tree structure with an increased treshold.

**Usage**

```r
DSC_BIRCH(treshold, branching, maxLeaf, maxMem = 0, outlierThreshold = 0.25)
```

**Arguments**

- `treshold`: treshold used to check whether a new datapoint can be absorbed or not  
- `branching`: branching factor (maximum amount of child nodes for a nonleaf node) of the CF-Tree.  
- `maxLeaf`: maximum number of entries within a leaf node  
- `outlierThreshold`: threshold for identifying outliers when rebuilding the CF-Tree  
- `maxMem`: memory limitation for the whole CFTree in bytes. Default is 0, indicating no memory restriction.

**Author(s)**

Dennis Assenmacher (<Dennis.Assenmacher@uni-muenster.de>), Matthias Carnein (<Matthias.Carnein@uni-muenster.de>)

**References**


**Examples**

```r
stream <- DSD_Gaussians(k = 3, d = 2)

BIRCH <- DSC_BIRCH(treshold = .1, branching = 8, maxLeaf = 20)
update(BIRCH, stream, n = 500)
plot(BIRCH,stream)
```
## Description

Implements the DBSCAN algorithm for reclustering micro-clusterings.

## Usage

```r
DSC_DBSCAN(eps, MinPts = 5, weighted = TRUE, description=NULL)
```

## Arguments

- **eps**: radius of the eps-neighborhood.
- **MinPts**: minimum number of points required in the eps-neighborhood.
- **weighted**: logical indicating if a weighted version of DBSCAN should be used.
- **description**: optional character string to describe the clustering method.

## Details

DBSCAN is a weighted extended version of the implementation in fpc where each micro-cluster center considered a pseudo point. For weighting we use in the MinPts comparison the sum of weights of the micro-cluster instead of the number.

DBSCAN first finds core points based on the number of other points in its eps-neighborhood. Then core points are joined into clusters using reachability (overlapping eps-neighborhoods).

Note that this clustering cannot be updated iteratively and every time it is used for (re)clustering, the old clustering is deleted.

## Value

An object of class `DSC_DBSCAN` (a subclass of `DSC`, `DSC_R`, `DSC_Macro`).

## Author(s)

Michael Hahsler

## References


## See Also

`DSC`, `DSC_Macro`
Examples

# 3 clusters with 5% noise
stream <- DSD_Gaussians(k=3, d=2, noise=0.05)

# Use DBSCAN to recluster micro clusters (a sample)
sample <- DSC_Sample(k=100)
update(sample, stream, 500)

dbscan <- DSC_DBSCAN(eps = .05)
recluster(dbscan, sample)
plot(dbscan, stream, type="both")

# For comparison we can cluster some data with DBSCAN directly
# Note: DBSCAN is not suitable for data streams since it passes over the data
# several times.
dbscan <- DSC_DBSCAN(eps = .05)
update(dbscan, stream, 500)
plot(dbscan, stream)

DSC_DBSTREAM  DBSTREAM clustering algorithm

Description

Implements a simple density-based stream clustering algorithm that assigns data points to micro-clusters with a given radius and implements shared-density-based reclustering.

Usage

DSC_DBSTREAM(r, lambda = 0.001, gaptime = 1000L,
Cm = 3, metric = "Euclidean", shared_density = FALSE,
alpha=0.1, k=0, minweight = 0)
get_shared_density(x, use_alpha = TRUE)
change_alpha(x, alpha)
ge_cluster_assignments(x)

Arguments

r  The radius of micro-clusters.
lambda  The lambda used in the fading function.
gaptime  weak micro-clusters (and weak shared density entries) are removed every gaptime points.
Cm  minimum weight for a micro-cluster.
metric  metric used to calculate distances.
shared_density  Record shared density information. If set to TRUE then shared density is used for reclustering, otherwise reachability is used (overlapping clusters with less than $r \times (1 - alpha)$ distance are clustered together).
**DSC_DBSTREAM**

- **k** The number of macro clusters to be returned if macro is true.
- **alpha** For shared density: The minimum proportion of shared points between two clusters to warrant combining them (a suitable value for 2D data is .3). For reachability clustering it is a distance factor.
- **minweight** The proportion of the total weight a macro-cluster needs to have not to be noise (between 0 and 1).
- **x** A DSC_DBSTREAM object to get the shared density information from.
- **use_alpha** only return shared density if it exceeds alpha.

**Details**

The DBSTREAM algorithm checks for each new data point in the incoming stream, if it is below the threshold value of dissimilarity value of any existing micro-clusters, and if so, merges the point with the micro-cluster. Otherwise, a new micro-cluster is created to accommodate the new data point.

Although DSC_DBSTREAM is a micro clustering algorithm, macro clusters and weights are available.

get_cluster_assignments() can be used to extract the MC assignment for each data point clustered during the last update operation (note: update needs to be called with assignments = TRUE and the block size needs to be large enough). The function returns the MC index (in the current set of MCs obtained with, e.g., get_centers()) and as an attribute the permanent MC ids.

plot() for DSC_DBSTREAM has two extra logical parameters called assignment and shared_density which show the assignment area and the shared density graph, respectively.

**Value**

An object of class DSC_DBSTREAM (subclass of DSC, DSC_R, DSC_Micro).

**Author(s)**

Michael Hahsler and Matthew Bolanos

**References**


**See Also**

DSC, DSC_Micro

**Examples**

```r
set.seed(0)
stream <- DSD_Gaussians(k = 3, noise = 0.05)
# create clusterer with r = 0.05
```
dbstream <- DSC_DBSTREAM(r = .05)
update(dbstream, stream, 1000)
dbstream

# check micro-clusters
nclusters(dbstream)
head(get_centers(dbstream))
plot(dbstream, stream)

# plot macro-clusters
plot(dbstream, stream, type = "both")

# plot micro-clusters with assignment area
plot(dbstream, stream, type = "both", assignment = TRUE)

# DBSTREAM with shared density
dbstream <- DSC_DBSTREAM(r = .05, shared_density = TRUE, Cm = 5)
update(dbstream, stream, 1000)
dbstream
plot(dbstream, stream, type = "both")
# plot the shared density graph (several options)
plot(dbstream, stream, type = "both", shared_density = TRUE)
plot(dbstream, stream, type = "micro", shared_density = TRUE)
plot(dbstream, stream, type = "micro", shared_density = TRUE, assignment = TRUE)
plot(dbstream, stream, type = "none", shared_density = TRUE, assignment = TRUE)

# see how micro and macro-clusters relate
# each microcluster has an entry with the macro-cluster id
# Note: unassigned micro-clusters (noise) have an NA
microToMacro(dbstream)

# do some evaluation
evaluate(dbstream, stream, measure = "purity")
evaluate(dbstream, stream, measure = "cRand", type = "macro")

# use DBSTREAM for conventional clustering (with assignments = TRUE so we can
# later retrieve the cluster assignments for each point)
data("iris")

dbstream <- DSC_DBSTREAM(r = 1)
update(dbstream, iris[, -5], assignments = TRUE)
dbstream

cl <- get_cluster_assignments(dbstream)
cl

# micro-clusters
plot(iris[, -5], col = cl, pch = cl)

# macro-clusters
plot(iris[, -5], col = microToMacro(dbstream, cl))
DSC_DStream

Description

Implements the D-Stream data stream clustering algorithm.

Usage

DSC_DStream(gridsize, lambda = 1e-3, gaptime=1000L,
            Cm=3, Cl=.8, attraction=FALSE, epsilon=.3, Cm2=Cm, k=NULL, N = 0)

get_attraction(x, relative=FALSE, grid_type = "dense", dist=FALSE)

Arguments

gridsize
    Size of grid cells.

lambda
    Fading constant used function to calculate the decay factor \(2^{-\lambda}\). (Note: in the paper the authors use \(\lambda\) to denote the decay factor and not the fading constant!)

gaptime
    Sporadic grids are removed every gaptime number of points.

Cm
    Density threshold used to detect dense grids as a proportion of the average expected density (\(Cm > 1\)). The average density is given by the total weight of the clustering over \(N\), the number of grid cells.

Cl
    Density threshold to detect sporadic grids (\(0 > Cl > Cm\)). Transitional grids have a density between \(Cl\) and \(Cm\).

attraction
    Compute and store information about the attraction between adjacent grids. If TRUE then attraction is used to create macro-clusters, otherwise macro-clusters are created by merging adjacent dense grids.

epsilon
    Overlap parameter for attraction as a proportion of gridsize.

Cm2
    Threshold on attraction to join two dense grid cells (as a proportion on the average expected attraction). In the original algorithm \(Cm2\) is equal to \(Cm\).

k
    Alternative to \(Cm2\) (not in the original algorithm). Create \(k\) clusters based on attraction. In case of more than \(k\) unconnected components, closer groups of MCs are joined.

N
    Fix the number of grid cells used for the calculation of the density thresholds with \(Cl\) and \(Cm\). If \(N\) is not given (0) then the algorithm tries to determine \(N\) from the data. Note that this means that \(N\) potentially increases over time and outliers might produce an extremely large value which will lead to a sudden creation of too many dense micro-clusters. The original paper assumed that \(N\) is known a priori.

x
    DSC_DStream object to get attraction values from.

relative
    Calculates relative attraction (normalized by the cluster weight).

grid_type
    The attraction between what grid types should be returned?

dist
    Make attraction symmetric and transform into a distance.
Details

D-Stream creates an equally spaced grid and estimates the density in each grid cell using the count of points falling in the cells. Grid cells are classified based on density into dense, transitional and sporadic cells. The density is faded after every new point by a factor of $2^{-\lambda}$. Every gaptime number of points sporadic grid cells are removed.

For reclustering D-Stream (2007 version) merges adjacent dense grids to form macro-clusters and then assigns adjacent transitional grids to macro-clusters. This behavior is implemented as attraction=FALSE.

The 2009 version of the algorithm adds the concept of attraction between grid cells. If attraction=TRUE is used then the algorithm produces macro-clusters based on attraction between dense adjacent grids (uses $C_m^2$ which in the original algorithm is equal to $C_m$).

For many functions (e.g., get_centers(), plot()), D-Stream adds a parameter grid_type with possible values of "dense", "transitional", "sparse", "all" and "used". This only returns the selected type of grid cells. "used" includes dense and adjacent transitional cells which are used in D-Stream for reclustering.

For plot D-Stream also provides extra parameters "grid" and "grid_type" to show micro-clusters as grid cells (density represented by gray values).

Note that DSC_DStream can at this point not be saved to disk using save() or saveRDS(). This functionality will be added later!

Value

An object of class DSC_DStream (subclass of DSC, DSC_R, DSC_Micro).

Author(s)

Michael Hahsler

References


Li Tu and Yixin Chen. 2009. Stream data clustering based on grid density and attraction. ACM Transactions on Knowledge Discovery from Data, 3(3), Article 12 (July 2009), 27 pages.

See Also

DSC, DSC_Micro

Examples

```r
stream <- DSD_BarsAndGaussians(noise=.05)
plot(stream)

# we set Cm=.8 to pick up the lower density clusters
dstream1 <- DSC_DStream(gridsize=1, Cm=1.5)
update(dstream1, stream, 1000)
dstream1
```
# micro-clusters (these are "used" grid cells)
nclusters(dstream1)
head(get_centers(dstream1))

# plot (DStream provides additional grid visualization)
plot(dstream1, stream)
plot(dstream1, stream, grid=TRUE)

# look only at dense grids
nclusters(dstream1, grid_type="dense")
plot(dstream1, stream, grid=TRUE, grid_type="dense")

# look at transitional and sparse cells
plot(dstream1, stream, grid=TRUE, grid_type="transitional")
plot(dstream1, stream, grid=TRUE, grid_type="sparse")

### Macro-clusters

# standard D-Stream uses reachability
nclusters(dstream1, type="macro")
get_centers(dstream1, type="macro")
plot(dstream1, stream, type="both", grid=TRUE)
evaluate(dstream1, stream, measure="crand", type="macro")

# use attraction for reclustering
dstream2 <- DSC_DStream(gridsize=1, attraction=TRUE, Cm=1.5)
update(dstream2, stream, 1000)
dstream2

plot(dstream2, stream, type="both", grid=TRUE)
evaluate(dstream2, stream, measure="crand", type="macro")

---

### DSC_EA

#### Evolutionary Algorithm

**Description**

Reclustering using an evolutionary algorithm. This approach was designed for evoStream but can also be used for other micro-clustering algorithms. The evolutionary algorithm uses existing clustering solutions and creates small variations of them by combining and randomly modifying them. The modified solutions can yield better partitions and thus can improve the clustering over time. The evolutionary algorithm is incremental, which allows to improve existing macro-clusters instead of recomputing them every time.

**Usage**

DSC_EA(k, generations = 2000, crossoverRate = 0.8, mutationRate = 0.001, populationSize = 100)
Arguments

- **k**: number of macro-clusters
- **generations**: number of EA generations performed during reclustering
- **crossoverRate**: cross-over rate for the evolutionary algorithm
- **mutationRate**: mutation rate for the evolutionary algorithm
- **populationSize**: number of solutions that the evolutionary algorithm maintains

Author(s)

Matthias Carnein <Matthias.Carnein@uni-muenster.de>

References


Examples

```r
stream <- DSD_Memory(DSD_Gaussians(k = 3, d = 2), 1000)

## online algorithm
dbstream <- DSC_DBSTREAM(r=0.1)

## offline algorithm
EA <- DSC_EA(k=3, generations=1000)

two <- DSC_TwoStage(dbstream, EA)
update(two, stream, n=1000)

## plot resut
reset_stream(stream)
plot(two, stream, type="both")

## if we have time, evaluate additional generations. This can be
## called at any time, also between observations.
two$macro_dsc$RObj$recluster(2000)

## plot improved result
reset_stream(stream)
plot(two, stream, type="both")

## alternatively: do not create twostage but apply directly
reset_stream(stream)
update(dbstream, stream, n = 1000)
recluster(EA, dbstream)
reset_stream(stream)
plot(EA, stream)
```
**DSC_evoStream**

**Description**

Stream clustering algorithm based on evolutionary optimization. The online component uses a simplified version of DBSTREAM to generate micro-clusters. The micro-clusters are then incrementally reclastered using an evolutionary algorithm. Evolutionary algorithms create slight variations by combining and randomly modifying existing solutions. By iteratively selecting better solutions, an evolutionary pressure is created which improves the clustering over time. Since the evolutionary algorithm is incremental, it is possible to apply it between observations, e.g. in the idle time of the stream. Whenever there is idle time, we can call the recluster function of the reference class to improve the macro-clusters (see example). The evolutionary algorithm can also be applied as a traditional reclustering step, or a combination of both. In addition, this implementation also allows to evaluate a fixed number of generations after each observation.

**Usage**

```r
DSC_evoStream(r, lambda = 0.001, tgap = 100, k = 2,
  crossoverRate = 0.8, mutationRate = 0.001, populationSize = 100,
  initializeAfter = 2 * k, incrementalGenerations = 1,
  reclusterGenerations = 1000)
```

**Arguments**

- `r` radius threshold for micro-cluster assignment
- `lambda` decay rate
- `tgap` time-interval between outlier detection and clean-up
- `k` number of macro-clusters
- `crossoverRate` cross-over rate for the evolutionary algorithm
- `mutationRate` mutation rate for the evolutionary algorithm
- `populationSize` number of solutions that the evolutionary algorithm maintains
- `initializeAfter` number of micro-cluster required for the initialization of the evolutionary algorithm.
- `incrementalGenerations` number of EA generations performed after each observation
- `reclusterGenerations` number of EA generations performed during reclustering

**Author(s)**

Matthias Carnein <Matthias.Carnein@uni-muenster.de>
References

Examples
stream <- DSD_Memory(DSD_Gaussians(k = 3, d = 2), 500)

## init evoStream
evoStream <- DSC_evoStream(r = 0.05, k = 3,
                           incrementalGenerations = 1, reclusterGenerations = 500)

## insert observations
update(evoStream, stream, n = 500)

## micro clusters
gc(c = evoStream, type = "micro")

## micro weights
gw(c = evoStream, type = "micro")

## macro clusters
gc(c = evoStream, type = "macro")

## macro weights
gw(c = evoStream, type = "macro")

## plot result
reset_stream(stream)
plot(evoStream, stream, type = "both")

## if we have time, evaluate additional generations.
## This can be called at any time, also between observations.
## by default, 1 generation is evaluated after each observation and
## 1000 generations during reclustering but we set it here to 500
evoStream$RObj$recluster(500)

## plot improved result
reset_stream(stream)
plot(evoStream, stream, type = "both")

## get assignment of micro to macro clusters
microToMacro(evoStream)

---

DSC_Hierarchical  
*Hierarchical Micro-Cluster Reclusterer*

Description
Implementation of hierarchical clustering to recluster a set of micro-clusters.
DSC_Hierarchical

Usage

DSC_Hierarchical(k=NULL, h=NULL, method = "complete", min_weight=NULL, description=NULL)

Arguments

k
The number of desired clusters.

h
Height where to cut the dendrogram.

method
the agglomeration method to be used. This should be (an unambiguous abbreviation of) one of "ward", "single", "complete", "average", "mcquitty", "median" or "centroid".

min_weight
micro-clusters with a weight less than this will be ignored for reclustering.

description
optional character string to describe the clustering method.

Details

Please refer to hclust for more details on the behavior of the algorithm.

Note that this clustering cannot be updated iteratively and every time it is used for (re)clustering, the old clustering is deleted.

Value

A list of class DSC, DSC_R, DSC_Macro, and DSC_Hierarchical. The list contains the following items:

description
The name of the algorithm in the DSC object.

RObj
The underlying R object.

Author(s)

Michael Hahsler

See Also

DSC, DSC_Macro

Examples

# Cassini dataset
stream <- DSD_mlbenchGenerator("cassini")

# Use hierarchical clustering to recluster micro-clusters
dbstream <- DSC_DBSTREAM(r = .05)
update(dbstream, stream, 500)

# reclustering using single-link and specifying k
hc <- DSC_Hierarchical(k = 3, method = "single")
recluster(hc, dbstream)
DSC_Kmeans

Kmeans Macro-clusterer

Description

Class implements the k-means algorithm for reclustering a set of micro-clusters.

Usage

DSC_Kmeans(k, weighted = TRUE, iter.max = 10, nstart = 1,
algorithm = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"),
min_weight = NULL, description=NULL)

Arguments

k either the number of clusters, say k, or a set of initial (distinct) cluster centers.
If a number, a random set of (distinct) rows in x is chosen as the initial centers.
weighted use a weighted k-means (algorithm is ignored).
iter.max the maximum number of iterations allowed.
nstart if centers is a number, how many random sets should be chosen?
algorithm character: may be abbreviated.
min_weight micro-clusters with a weight less than this will be ignored for reclustering.
description optional character string to describe the clustering method.

Details

Please refer to function kmeans in stats for more details on the algorithm.
Note that this clustering cannot be updated iteratively and every time it is used for (re)clustering, the old clustering is deleted.
Value

An object of class DSC_Kmeans (subclass of DSC, DSC_R, DSC_Macro)

Author(s)

Michael Hahsler

See Also

DSC, DSC_Macro

Examples

stream <- DSD_Gaussians(k=3, noise=0)

# create micro-clusters via sampling
sample <- DSC_Sample(k=20)
update(sample, stream, 500)
sample

# reclustering micro-clusters
kmeans <- DSC_Kmeans(k=3)
recluster(kmeans, sample)
plot(kmeans, stream, type="both")

# For comparison we use k-means directly to cluster data
# Note: k-means is not a data stream clustering algorithm
kmeans <- DSC_Kmeans(k=3)
update(kmeans, stream, 500)
plot(kmeans, stream)

Abstract Class for Macro Clusterers

Description

Abstract class for all DSC Macro Clusterers.

Details

DSC_Macro cannot be instantiated. Calling DSC_Macro() results in an error.

Author(s)

Michael Hahsler

See Also

DSC
DSC_Micro

Abstract Class for Micro Clusterers

Description

Abstract class for all DSC Micro Clusterers.

Details

DSC_Micro cannot be instantiated. Calling DSC_Micro() results in an error.

Author(s)

Michael Hahsler

See Also

DSC

DSC_Outlier-class

Abstract Class for Outlier Detection Clusterers

Description

The abstract class for all outlier detection clusterers. Cannot be instantiated. Must be inherited. An implementation is available in package streamMOA.

Methods

clean_outliers(x, ...) A method that requires removal of all outliers from the addressed outlier detection clusterer.

get_outlier_positions(x, ...) Returns spatial positions of all current outliers.

recheck_outlier(x, outlier_correlated_id, ...) Re-checks the outlier having outlier_correlated_id. If this object is still an outlier, the method returns TRUE.

noutliers(x, ...) Returns the current number of outliers.

print(x, ...) Prints out the general info and statistics about the outlier detection clusterer.

get_assignment(x, points, type=c("auto", "micro", "macro"), method=c("auto", "nn", "model"), outlier_threshold, ...) Calculates assignments and outlier marks for the points data frame. Points are assigned to an outlier only if they are inside outlier_threshold distance from its position. This implementation is heavily dependant on the Euclidean distance measure and should be overwritten by concrete outlier detection clusterer implementations.

Author(s)

Dalibor Krleža
Reachability Micro-Cluster Reclusterer

Description

Implementation of reachability clustering (based on DBSCAN’s concept of reachability) to recluster a set of micro-clusters. Two micro-clusters are directly reachable if they are within each other’s epsilon-neighborhood (i.e., the distance between the centers is less than epsilon). Two micro-clusters are reachable if they are connected by a chain of pairwise directly reachable micro-clusters. All mutually reachable micro-clusters are put in the same cluster.

Usage

DSC_Reachability(epsilon, min_weight=NULL, description=NULL)

Arguments

- epsilon: radius of the epsilon-neighborhood.
- min_weight: micro-clusters with a weight less than this will be ignored for reclustering.
- description: optional character string to describe the clustering method.

Details

Reachability uses internally DSC_Hierarchical with single link.

Note that this clustering cannot be updated iteratively and every time it is used for (re)clustering, the old clustering is deleted.

Value

An object of class DSC_Reachability. The object contains the following items:

- description: The name of the algorithm in the DSC object.
- RObj: The underlying R object.

Author(s)

Michael Hahsler

References


See Also

DSC, DSC_Macro
Examples

```r
stream <- DSD_mlbenchGenerator("cassini")

# Recluster micro-clusters from DSC_Sample with reachability
sample <- DSC_Sample(k = 200)
update(sample, stream, 1000)
reach <- DSC_Reachability(epsilon=0.3)
recluster(reach, sample)
plot(reach, stream, type="both")

# For comparison we using reachability clustering directly on data points
# Note: reachability is not a data stream clustering algorithm taking O(n^2)
# time and space.
reach <- DSC_Reachability(epsilon=0.2)
update(reach, stream, 500)
reach
plot(reach, stream)
```

---

**DSC_Sample**

Extract a Fixed-size Sample from a Data Stream

Description

Extracts a sample form a data stream using Reservoir Sampling. The sample is stored as a set of micro-clusters to be compatible with other data DSC stream clustering algorithms.

Usage

```r
DSC_Sample(k = 100, biased = FALSE)
```

Arguments

- **k**
  the number of points to be sampled from the stream.

- **biased**
  if FALSE then a regular (unbiased) reservoir sampling is used. If true then the sample is biased towards keeping more recent data points (see Details section).

Details

If biased=FALSE then the reservoir sampling algorithm by McLeod and Bellhouse (1983) is used. This sampling makes sure that each data point has the same chance to be sampled. All sampled points will have a weight of 1. Note that this might not be ideal for an evolving stream since very old data points have the same chance to be in the sample as newer points.

If bias=TRUE then sampling prefers newer points using the modified reservoir sampling algorithm 2.1 by Aggarwal (2006). New points are always added. They replace a random point in the reservoir with a probability of reservoir size over k. This an exponential bias function of \(2^{-\lambda} = \frac{1}{k}\).
Value

An object of class DSC_Sample (subclass of DSC, DSC_R, DSC_Micro).

Author(s)

Michael Hahsler

References


See Also

DSC, DSC_Micro

Examples

```r
stream <- DSD_Gaussians(k=3, noise=0.05)

sample <- DSC_Sample(k=20)
update(sample, stream, 500)
sample

# plot micro-clusters
plot(sample, stream)

# reclustering
kmeans <- DSC_Kmeans(3)
recluster(kmeans, sample)
plot(kmeans, stream, type="both")

# sample from an evolving stream
stream <- DSD_Benchmark(1)
sample <- DSC_Sample(k=20)
update(sample, stream, 1000)
plot(sample, stream)
# Note: the clusters move from left to right and the sample keeps many outdated points

# use a biased sample to keep more recent data points
stream <- DSD_Benchmark(1)
sample <- DSC_Sample(k=20, biased=TRUE)
update(sample, stream, 1000)
plot(sample, stream)
```
DSC_Static  
Create as Static Copy of a Clustering

Description

This representation cannot perform clustering anymore, but it also does not need the supporting data structures. It only stores the cluster centers and weights.

Usage

DSC_Static(x, type=c("auto", "micro", "macro"), k_largest=NULL, min_weight=NULL)

Arguments

x The clustering (a DSD object) to copy.
type which clustering to copy.
k_largest only copy the k largest (highest weight) clusters.
min_weight only copy clusters with a weight larger or equal to min_weight.

Value

An object of class DSC_Static (sub class of DSC, DSC_R). The list also contains either DSC_Micro or DSC_Macro depending on what type of clustering was copied.
DSC_TwoStage

Author(s)
Michael Hahsler

See Also
DSC, DSC_Micro, DSC_Macro

Examples

```r
stream <- DSD_Gaussians(k=3, noise=0.05)

dstream <- DSC_DStream(gridsize=0.05)
update(dstream, stream, 500)
dstream
plot(dstream, stream)

# create a static copy of the clustering
static <- DSC_Static(dstream)
static
plot(static, stream)

# copy only the 5 largest clusters
static2 <- DSC_Static(dstream, k_largest=5)
static2
plot(static2, stream)

# copy all clusters with a weight of at least .3
static3 <- DSC_Static(dstream, min_weight=.3)
static3
plot(static3, stream)
```

DSC_TwoStage

TwoStage Clustering Process

Description
Combines a micro and a macro clustering algorithm into a single process.

Usage

DSC_TwoStage(micro, macro)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>micro</td>
<td>Clustering algorithm used in the online stage (DSC_micro)</td>
</tr>
<tr>
<td>macro</td>
<td>Clustering algorithm used for reclustering in the offline stage (DSC_macro)</td>
</tr>
</tbody>
</table>
Details
update() runs the micro-clustering stage and only when macro cluster centers/weights are requested, then the offline stage reclustering is automatically performed.

Value
An object of class DSC_TwoStage (subclass of DSC, DSC_Macro).

Author(s)
Michael Hahsler

See Also
DSC, DSC_Macro

Examples
stream <- DSD_Gaussians(k=3)

# Create a clustering process that uses a window for the online stage and
# k-means for the offline stage (reclustering)
win_km <- DSC_TwoStage(
  micro=DSC_Window(horizon=100),
  macro=DSC_Kmeans(k=3)
)
win_km

update(win_km, stream, 200)
win_km
plot(win_km, stream, type="both")
evaluate(win_km, stream, assign="macro")

---

DSC_Window

A sliding window from a Data Stream

Description
Implements a sliding window which keeps a fixed amount (window length) of the most recent data points of the stream.

Usage
DSC_Window(horizon = 100, lambda=0)

Arguments

horizon the window length.
lambda decay factor damped window model. lambda=0 means no dampening.
Details

If \( \lambda \) is greater than 0 then the weight uses a damped window model (Zhu and Shasha, 2002). The weight for points in the window follows \( 2^{-\lambda t} \) where \( t \) is the age of the point.

Value

An object of class `DSC_Window` (subclass of `DSC`, `DSC_R`, `DSC_Micro`).

Author(s)

Michael Hahsler

References


See Also

`DSC`, `DSC_Micro`

Examples

```r
stream <- DSD_Gaussians(k=3, d=2, noise=0.05)

window <- DSC_Window(horizon=100)

update(window, stream, 200)

# plot micro-clusters
plot(window, stream)

# animation for a window using a damped window model. The weight decays with a half-life of 25
## Not run:
window <- DSC_Window(horizon=25, lambda=1/25)
animate_cluster(window, stream, horizon=1, n=100, xlim=c(0,1), ylim=c(0,1))
## End(Not run)
```

---

**DSD**

*Data Stream Data Generator Base Classes*

**Description**

Abstract base classes for DSD (Data Stream Data Generator).
Details

The DSD class cannot be instantiated, but it serves as a abstract base class from which all DSD objects inherit.

DSD_R inherits from DSD and is the abstract parent class for DSD implemented in R. To create a new R-based implementation there are only two function that needs to be implemented for a new DSD subclass: A creator function (the name should start with DSD_) and a method get_points() for that class.

DSD provides common functionality like print(), plot(), etc.
Note that calling DSD() or DSD_R() results in an error since both are abstract classes.

Author(s)

Michael Hahsler

See Also

animate_data, animate_cluster, cluster, evaluate, get_points, plot, recluster, write_stream.DSD

Examples

# create data stream with three clusters in 3-dimensional space
stream <- DSD_Gaussians(k=3, d=3)

# get points from stream
get_points(stream, n=5)

# get points with true cluster assignment
p <- get_points(stream, n=5, cluster=TRUE)
attr(p, "cluster")

# plotting the data (scatter plot matrix, first and third dimension, and first
# two principal components)
plot(stream)
plot(stream, dim=c(1,3))
plot(stream, method="pc")

DSD_BarsAndGaussians  Data Stream Generator for Bars and Gaussians

Description

A data stream generator which creates the shape of two bars and two Gaussians clusters with different density.

Usage

DSD_BarsAndGaussians(angle= NULL, noise = 0)
Description
A data stream generator that generates several dynamic streams intended to be benchmarks to compare data stream clustering algorithms.

Usage
DSD_Benchmark(i=1)

Arguments
i number of the benchmark.

Details
Currently available benchmarks are 1 and 2.

Value
Returns a DSD object.
**Author(s)**

Michael Hahsler

**See Also**

DSD

**Examples**

```r
stream <- DSD_Benchmark(i=1)
## Not run:
animate_data(stream, n=10000, horizon=100, xlim=c(0,1), ylim=c(0,1))
## End(Not run)
```

---

**DSD_Cubes**

*Static Cubes Data Stream Generator*

**Description**

A data stream generator that produces a data stream with static (hyper) cubes filled uniformly with data points.

**Usage**

```r
DSD_Cubes(k=2, d=2, center, size, p, noise = 0, noise_range)
```

**Arguments**

- **k**: Determines the number of clusters.
- **d**: Determines the number of dimensions.
- **center**: A matrix of means for each dimension of each cluster.
- **size**: A k times d matrix with the cube dimensions.
- **p**: A vector of probabilities that determines the likelihood of generated a data point from a particular cluster.
- **noise**: Noise probability between 0 and 1. Noise is uniformly distributed within noise range (see below).
- **noise_range**: A matrix with d rows and 2 columns. The first column contains the minimum values and the second column contains the maximum values for noise.

**Value**

Returns a DSD_Cubes object (subclass of DSD_R, DSD).

**Author(s)**

Michael Hahsler
A data stream generator that produces a data stream with a mixture of static Gaussians.

Usage

DSD_Gaussians(k=2, d=2, mu, sigma, p, noise = 0, noise_range,
  separation_type=c("auto","Euclidean","Mahalanobis"), separation=0.2,
  space_limit = c(0.2, 0.8), variance_limit = 0.01,
  outliers = 0, outlier_options = NULL, verbose=FALSE)

Arguments

  k  Determines the number of clusters.
  d  Determines the number of dimensions.
  mu A matrix of means for each dimension of each cluster.
  sigma A list of length k of covariance matrices.
  p   A vector of probabilities that determines the likelihood of generated a data point
       from a particular cluster.
  noise Noise probability between 0 and 1. Noise is uniformly distributed within noise
       range (see below).
  noise_range A matrix with d rows and 2 columns. The first column contains the minimum
              values and the second column contains the maximum values for noise.
  separation_type The type of the separation distance calculation. It can be either Euclidean norm
              or Mahalanobis distance.
  separation Depends on the separation_type parameter. It means minimum separation
              distance between all generated constructs. When k>0, generated constructs in-
              clude clusters. When outliers>0, generated constructs include outliers.
  space_limit Defines the space bounds. All constructs are generated inside these bounds. For
              clusters this means that their centroids must be within these space bounds.
DSD_Gaussians

DSD_Gaussians creates a mixture of \( k \) static clusters and \( \text{outliers} \) outliers in a \( d \)-dimensional space. The cluster centers \( \mu \) and the covariance matrices \( \sigma \) can be supplied or will be randomly generated. The probability vector \( p \) defines for each cluster the probability that the next data point will be chosen from it (defaults to equal probability). The outlier spatial positions \( \text{predefined_outlier_space_positions} \) and the outlier stream positions \( \text{predefined_outlier_stream_positions} \) can be supplied or will be randomly generated.

Separation between generated clusters and outliers can be imposed by using Euclidean or Mahalanobis distance, which is controlled by the \( \text{separation_type} \) parameter. Separation value then is supplied in the \( \text{separation} \) parameter.

The generation method is similar to the one suggested by Jain and Dubes (1988).

Value

Returns a DSD_Gaussians object (subclass of DSD_R, DSD) which is a list of the defined params. The params are either passed in from the function or created internally. They include:

- **description**:
  A brief description of the DSD object.

- **k**:
  The number of clusters.

- **d**:
  The number of dimensions.
DSD_Gaussians

mu The matrix of means of the dimensions in each cluster.
sigma The covariance matrix.
p The probability vector for the clusters.
noise A flag that determines if or if not noise is generated.
outs Outlier spatial positions.
outs_pos Outlier stream positions.
outs_vv Outlier virtual variance.

Author(s)
Michael Hahsler, Dalibor Krleža

References

See Also
DSD

Examples

# create data stream with three clusters in 3-dimensional data space
stream1 <- DSD_Gaussians(k=3, d=3)
plot(stream1)

# create data stream with specified cluster positions, # 20% noise in a given bounding box and # with different densities (1 to 9 between the two clusters)
stream2 <- DSD_Gaussians(k=2, d=2,
  mu=rbind(c(-.5,-.5), c(.5,.5)),
  noise=0.2, noise_range=rbind(c(-1,1),c(-1,1)),
  p=c(.1,.9))
plot(stream2)

# create 2 clusters and 2 outliers. Clusters and outliers # are separated by Euclidean distance of 0.5 or more.
stream3 <- DSD_Gaussians(k=2, d=2,
  separation_type="Euclidean", separation=0.5,
  space_limit=c(0,1),
  outliers=2)
plot(stream3)

# create 2 clusters and 2 outliers separated by a Mahalanobis # distance of 6 or more.
stream4 <- DSD_Gaussians(k=2, d=2,
  separation_type="Mahalanobis", separation=6,
  space_limit=c(0,25), variance_limit=2,
outliers=2)
plot(stream4)

# spread outliers over 20000 data instances
stream5 <- DSD_Gaussians(k=2, d=2,
    separation_type="Mahalanobis", separation=6,
    space_limit=c(0,45), variance_limit=2,
    outliers=20, outlier_options=list(
        outlier_horizon=20000,
        outlier_virtual_variance = 0.3))
plot(stream5, n=20000)

---

DSD_Memory  A Data Stream Interface for Data Stored in Memory

Description

This class provides a data stream interface for data stored in memory as matrix-like objects (including data frames). All or a portion of the stored data can be replayed several times.

Usage

DSD_Memory(x, n, k=NA, loop=FALSE, class = NULL, outlier = NULL,
    description=NULL)

Arguments

x  A matrix-like object containing the data. If x is a DSD object then a data frame for n data points from this DSD is created.

n  Number of points used if x is a DSD object. If x is a matrix-like object then n is ignored.

k  Optional: The known number of clusters in the data

loop  Should the stream start over when it reaches the end?

class  Vector with the class/cluster label (only used if x is not a DSD object).

outlier  A logical vector with outlier marks (only used if x is not a DSD object). FALSE = the corresponding data instance in the x data frame is not an outlier, TRUE = the corresponding data instance in the x data frame is an outlier.

description  character string with a description.

Details

In addition to regular data.frames other matrix-like objects that provide subsetting with the bracket operator can be used. This includes ffddf (large data.frames stored on disk) from package ff and big.matrix from bigmemory.
DSD_Memory

Value

Returns a DSD_Memory object (subclass of DSD_R, DSD).

Author(s)

Michael Hahsler, Dalibor Krleža

See Also

DSD, reset_stream

Examples

# store 1000 points from a stream
stream <- DSD_Gaussians(k=3, d=2)
replayer <- DSD_Memory(stream, k=3, n=1000)
replayer
plot(replayer)

# creating 2 clusterers of different algorithms
dsc1 <- DSC_DBSTREAM(r=0.1)
dsc2 <- DSC_DStream(gridsize=0.1, Cm=1.5)

# clustering the same data in 2 DSC objects
reset_stream(replayer) # resetting the replayer to the first position
update(dsc1, replayer, 500)
reset_stream(replayer)
update(dsc2, replayer, 500)

# plot the resulting clusterings
reset_stream(replayer)
plot(dsc1, replayer, main="DBSTREAM")
reset_stream(replayer)
plot(dsc2, replayer, main="D-Stream")

### use a data.frame to create a stream (3rd col. contains the assignment)

df <- data.frame(x=runif(100), y=runif(100),
class=sample(1:3, 100, replace=TRUE))
head(df)
### add some outliers
out <- runif(100) > .95
### re-assign classes for outliers
df[which(out), "class"] <- sample(4:(4+sum(out)-1), sum(out), replace=FALSE)

stream <- DSD_Memory(df[,c("x", "y")], class=df[,"class"], outlier=out)
stream
reset_stream(stream)
plot(stream, n=100)
**DSD_MG**

**DSD Moving Generator**

**Description**

Creates an evolving DSD that consists of several MGCs.

**Usage**

```r
DSD_MG(dimension = 2, ..., labels=NULL, description=NULL)
```

```r
add_cluster(x, c, label=NULL)
get_clusters(x)
remove_cluster(x, i)
```

**Arguments**

- `dimension`: the dimension of the DSD object
- `...`: initial set of MGCs
- `x`: A DSD_MG object.
- `c`: The cluster that should be added to the DSD_MG object.
- `i`: The index of the cluster that should be removed from the DSD_MG object.
- `label, labels`: integer representing the cluster label. NA represents noise. If labels are not specified, then each new cluster gets a new label.
- `description`: An optional string used by print to describe the data generator.

**Details**

This DSD is able to generate complex datasets that are able to evolve over a period of time. Its behavior is determined by the MGCs it is composed of.

**Author(s)**

Matthew Bolanos

**See Also**

*MGC_Function, MGC_Linear, MGC_Noise, MGC_Random* for details on the different MGC objects.

**Examples**

```r
### create an empty DSD_MG
stream <- DSD_MG(dim = 2)
stream

### add two clusters
```
c1 <- MGC_Random(density=50, center=c(50,50), parameter=1, randomness = )
add_cluster(stream, c1)
stream

c2 <- MGC_Noise(density=1, range=rbind(c(-20,120), c(-20,120)))
add_cluster(stream, c2)
stream

get_clusters(stream)
plot(stream, xlim=c(-20,120), ylim=c(-20,120))

## Not run:
animate_data(stream, n=5000, xlim=c(-20,120), ylim=c(-20,120))
## End(Not run)

### remove cluster 1
remove_cluster(stream,1)

get_clusters(stream)
plot(stream, xlim=c(-20,120), ylim=c(-20,120))

### create a more complicated cluster structure (using 2 clusters with the same
### label to form an L shape)
stream <- DSD_MG(dim=2,
  MGC_Static(density=10, center=c(.5,.2), par=c(.4,.2), shape=MGC_Shape_Block),
  MGC_Static(density=10, center=c(.6,.5), par=c(.2,.4), shape=MGC_Shape_Block),
  MGC_Static(density=5, center=c(.39,.53), par=c(.16,.35), shape=MGC_Shape_Block),
  MGC_Noise(density=1, range=rbind(c(0,1), c(0,1))),
  labels= c(1, 1, 2, NA)
)
plot(stream, xlim=c(0,1), ylim=c(0,1))

### simulate the clustering of a splitting cluster
C1 <- MGC_Linear(dim = 2, keyframelist = list(
  keyframe(time = 1, dens = 20, center = c(0,0), param = 10),
  keyframe(time = 50, dens = 10, center = c(50,50), param = 10),
  keyframe(time = 100,dens = 10, center = c(50,100),param = 10)
))

### Note: Second cluster appearch at time=50
C2 <- MGC_Linear(dim = 2, keyframelist = list(
  keyframe(time = 50, dens = 10, center = c(50,50), param = 10),
  keyframe(time = 100,dens = 10, center = c(100,50),param = 10)
))

stream <- DSD_MG(dim = 2, c1, c2)
stream
dbstream <- DSC_DBSTREAM(r=10, lambda=0.1)
## Not run:

```r
purity <- animate_cluster(dbstream, stream, n=2500, type="both",
    xlim=c(-10,120), ylim=c(-10,120), evaluationMeasure="purity", horizon=100)
```

## End(Not run)

---

### DSD_mlbenchData

**Stream Interface for Data Sets From mlbench**

#### Description

Provides a convenient stream interface for data sets from the mlbench package.

#### Usage

```r
DSD_mlbenchData(data=NULL, loop = FALSE, random = FALSE, scale = FALSE)
```

#### Arguments

- `data`: The name of the dataset from mlbench. If missing then a list of all available data sets is shown and returned.
- `loop`: A flag that tells the stream to loop or not to loop over the data frame.
- `random`: A flag that determines if the data should be in a random order.
- `scale`: A flag that determines if the data should be scaled.

#### Details

The `DSD_mlbenchData` class is designed to be a wrapper class for data that is held in memory in either a data frame or matrix form. It is a subclass of `DSD_Memory`. Call `DSD_mlbenchData` with a missing value for data to get a list of all available data sets.

#### Value

Returns a `DSD_mlbenchData` object which is also of class `DSD_Memory`.

#### Author(s)

Michael Hahsler and Matthew Bolanos

#### See Also

`DSD`, `DSD_Memory`, `reset_stream`

#### Examples

```r
stream <- DSD_mlbenchData("Shuttle")
stream
plot(stream, n=100)
```
DSD_mlbenchGenerator  mlbench Data Stream Generator

Description
A data stream generator class that interfaces data generators found in mlbench.

Usage
DSD_mlbenchGenerator(method, ...)

Arguments
method  The name of the mlbench data generator.
...  Parameters for the mlbench data generator.

Details
The DSD_mlbenchGenerator class is designed to be a wrapper class for data created by data generators in the mlbench library.
Call DSD_mlbenchGenerator with missing method to get a list of available methods.

Value
Returns a DSD_mlbenchGenerator object (subclass of DSD_R, DSD) which is a list of the defined parameters. The parameters are either passed in from the function or created internally. They include:

description  The name of the class of the DSD object.
method  The name of the mlbench data generator.
variables  The variables for the mlbench data generator.

Author(s)
John Forrest

See Also
DSD

Examples
stream <- DSD_mlbenchGenerator(method="cassini")
plot(stream, n=500)
**DSD_ReadCSV**

**Read a Data Stream from File**

**Description**

A DSD class that reads a data stream from a file or any R connection.

**Usage**

DSD_ReadCSV(file, k=NA, o=NA, take=NULL, class=NULL, outlier=NULL, loop=FALSE, sep="," , header=FALSE, skip=0, colClasses = NA, ...)

close_stream(dsd)

**Arguments**

- **file**: A file/URL or an open connection.
- **k**: Number of true clusters, if known.
- **o**: Number of outliers, if known.
- **take**: indices of columns to extract from the file.
- **class**: column index for the class attribute/cluster label. If take is specified then it needs to also include the class/label column.
- **outlier**: column index for the outlier mark. If take is specified then it needs to also include the outlier column.
- **loop**: If enabled, the object will loop through the stream when the end has been reached. If disabled, the object will warn the user upon reaching the end.
- **sep**: The character string that separates dimensions in data points in the stream.
- **header**: Does the first line contain variable names?
- **skip**: the number of lines of the data file to skip before beginning to read data.
- **colClasses**: A vector of classes to be assumed for the columns passed on to read.table.
- **...**: Further arguments are passed on to read.table. This can for example be used for encoding, quotes, etc.
- **dsd**: A object of class DSD_ReadCSV.

**Details**

DSD_ReadCSV uses read.table() to read in data from an R connection. The connection is responsible for maintaining where the stream is currently being read from. In general, the connections will consist of files stored on disk but have many other possibilities (see connection).

The implementation tries to gracefully deal with slightly corrupted data by dropping points with inconsistent reading and producing a warning. However, this might not always be possible resulting in an error instead.

The position in the file can be reset to the beginning using reset_stream(). The connection can be closed using close_stream().
**DSD_ReadCSV**

**Value**

An object of class `DSD_ReadCSV` (subclass of `DSD_R, DSD`).

**Author(s)**

Michael Hahsler, Dalibor Krleža

**See Also**

`DSD, reset_stream, read.table`.

**Examples**

```r
# creating data and writing it to disk
stream <- DSD_Gaussians(k=3, d=5, outliers=1, space_limit=c(0,2),
outlier_options = list(outlier_horizon=10))
write_stream(stream, "data.txt", n=10, header = TRUE, sep=" ", class=TRUE, write_outliers=TRUE)

# reading the same data back (as a loop)
stream2 <- DSD_ReadCSV(k=3, o=1, "data.txt", sep=" ", header = TRUE, loop=TRUE, class="class",
outlier="outlier")
stream2

# get points (first a single point and then 20 using loop)
get_points(stream2)
p <- get_points(stream2, n=20, outlier=TRUE)
message(paste("Outliers",sum(attr(p,"outlier"))))

# clean up
close_stream(stream2)
file.remove("data.txt")

# example with a part of the kddcup1999 data (take only cont. variables)
file <- system.file("examples", "kddcup10000.data.gz", package="stream")
stream <- DSD_ReadCSV(gzfile(file),
 take=c(1, 5, 6, 8:11, 13:20, 23:42), class=42, k=7)
stream

get_points(stream, 5, class = TRUE)

# plot 100 points (projected on the first two principal components)
plot(stream, n=100, method="pc")

close_stream(stream)
```
DSD_ReadDB

Read a Data Stream from an open DB Query

Description

A DSD class that reads a data stream from an open DB result set from a relational database with using R's data base interface (DBI).

Usage

DSD_ReadDB(result, k=NA, o=NA, class=NULL, outlier=NULL, description=NULL)

Arguments

result  An open DBI result set.
k       Number of true clusters, if known.
o       Number of outliers, if known.
class   column index for the class/cluster assignment.
outlier column index for the outlier mark.
description a character string describing the data.

Details

This class provides a streaming interface for result sets from a data base with via DBI. You need to connect to the data base and submit a SQL query using dbGetQuery() to obtain a result set. Make sure that your query only includes the columns that should be included in the stream (including class and outlier marking columns). Do not forget to close the result set and the data base connection.

Value

An object of class DSD_ReadDB (subclass of DSD_R, DSD).

Author(s)

Michael Hahsler, Dalibor Krleža

See Also

DSD, dbGetQuery
Examples

```r
### create a data base with a table with 3 Gaussians
library("RSQlite")
con <- dbConnect(RSQLite::SQLite(), ":memory:\")

points <- get_points(DSD_Gaussians(k=3, d=2, outliers=1,
    outlier_options=list(outlier_horizon=600)), 600,
    class = TRUE, outlier = TRUE)
points <- cbind(points, outlier=attr(points,"outlier"))
head(points)

dbWriteTable(con, "gaussians", points)

### prepare a query result set
res <- dbSendQuery(con, "SELECT X1, X2, class, outlier FROM gaussians")
res

### create a stream interface to the result set
stream <- DSD_ReadDB(res, k=3, o=1, class = 3, outlier = 4)

### get points
get_points(stream, 5, class = TRUE, outlier=TRUE)
plot(stream)

### clean up
dbClearResult(res)
dbDisconnect(con)
```

DSD_ScaleStream

Scale a Stream from a DSD

Description

Make an unscaled data stream into a scaled data stream.

Usage

```
DSD_ScaleStream(dsd, center=TRUE, scale=TRUE, n=1000, reset=FALSE)
```

Arguments

- `dsd`: A object of class DSD that will be scaled.
- `center, scale`: logical or a numeric vector of length equal to the number of columns used for centering/scaling (see function scale).
- `n`: The number of points used to creating the centering/scaling
- `reset`: Try to reset the stream to its beginning after taking n points for scaling.
Details

scale_stream() estimates the values for centering and scaling (see scale in base) using n points from the stream.

Value

An object of class DSD_ScaleStream (subclass of DSD_R, DSD).

Author(s)

Michael Hahsler

See Also

DSD, reset_stream, scale in base.

Examples

stream <- DSD_Gaussians(k=3, d=3)
plot(stream)

# scale stream using 100 points
stream_scaled <- DSD_ScaleStream(stream, n=100)
plot(stream_scaled)

---

DSD_Target

Target Data Stream Generator

Description

A data stream generator that generates a data stream in the shape of a target. It has a single Gaussian cluster in the center and a ring that surrounds it.

Usage

DSD_Target(center_sd = 0.05, center_weight = 0.5, ring_r = 0.2,
            ring_sd = 0.02, noise = 0)

Arguments

center_sd | standard deviation of center
center_weight | proportion of points in center
ring_r | average ring radius
ring_sd | standard deviation of ring radius
noise | proportion of noise
**Details**

DSD_Target is a DSD generator for stream data. It has been implemented entirely in R, so there is no computational overhead with communicating to the Java Runtime Interface (JRI) or native C code. This DSD will produce a singular Gaussian cluster in the center with a ring around it.

**Value**

Returns a DSD_Target object which is a list of the defined params. The params are either passed in from the function or created internally. They include:

- **description**: A brief description of the DSD object.
- **k**: The number of clusters.
- **d**: The number of dimensions.

**Author(s)**

Michael Hahsler

**See Also**

DSD

**Examples**

```r
# create data stream with three clusters in 2D
stream <- DSD_Target()
# plotting the data
plot(stream)
```

---

**DSD_UniformNoise**

*Uniform Noise Data Stream Generator*

**Description**

This generator produces uniform noise in a d-dimensional unit (hyper) cube.

**Usage**

```r
DSD_UniformNoise(d=2, range=NULL)
```

**Arguments**

- **d**: Determines the number of dimensions.
- **range**: A matrix with two columns and d rows giving the minimum and maximum for each dimension. Defaults to the range of [0, 1].
Value

Returns a DSD_UniformNoise object (subclass of DSD_R, DSD).

Author(s)

Michael Hahsler

See Also

DSD

Examples

# create data stream with three clusters in 2D
stream <- DSD_UniformNoise(d=2)
plot(stream, n=100)

# specify a different range for each dimension
stream <- DSD_UniformNoise(d=3, range=rbind(c(0,1), c(0,10), c(0,5)))
plot(stream, n=100)
Data Stream Operator Base Classes

Description
Abstract base classes for all DSO (Data Stream Operator) classes.

Details
The DSO class cannot be instantiated (calling DSO() produces errors), but it serve as a base class from which other DSO classes inherit.

Data stream operators use update() to process new data from the stream. The result of the operator can be obtained via get_points() and get_weights().

Author(s)
Michael Hahsler

See Also
update, get_points, get_weights, DSO_Window, DSO_Sample

Sampling from a Data Stream (Data Stream Operator)

Description
Extracts a sample from a data stream using Reservoir Sampling.

Usage
DSO_Sample(k = 100, biased = FALSE)

Arguments
k
the number of points to be sampled from the stream.

biased
if FALSE then a regular (unbiased) reservoir sampling is used. If true then the sample is biased towards keeping more recent data points (see Details section).
Details

If `biased=False` then the reservoir sampling algorithm by McLeod and Bellhouse (1983) is used. This sampling makes sure that each data point has the same chance to be sampled. All sampled points will have a weight of 1. Note that this might not be ideal for an evolving stream since very old data points have the same chance to be in the sample as newer points.

If `bias=True` then sampling prefers newer points using the modified reservoir sampling algorithm 2.1 by Aggarwal (2006). New points are always added. They replace a random point in the reservoir with a probability of reservoir size over `k`. This an exponential bias function of $2^{-\lambda/k}$ with $\lambda = 1/k$.

Value

An object of class DSO_Sample (subclass of DSO).

Author(s)

Michael Hahsler

References


See Also

DSO

Examples

```r
stream <- DSD_Gaussians(k=3, noise=0.05)
sample <- DSO_Sample(k=20)
update(sample, stream, 500)
sample
# plot points in sample
plot(get_points(sample))
```
**DSO_Window**

*Sliding Window (Data Stream Operator)*

**Description**

Implements a sliding window data stream operator which keeps a fixed amount (window length) of the most recent data points of the stream.

**Usage**

```
DSO_Window(horizon = 100, lambda=0)
```

**Arguments**

- **horizon**: the window length.
- **lambda**: decay factor damped window model. \( \lambda=0 \) means no dampening.

**Details**

If \( \lambda \) is greater than 0 then the weight uses a damped window model (Zhu and Shasha, 2002). The weight for points in the window follows \( 2^{-\lambda \cdot t} \) where \( t \) is the age of the point.

**Value**

An object of class `DSO_Window` (subclass of `DSO`).

**Author(s)**

Michael Hahsler

**References**


**See Also**

*DSO*

**Examples**

```r
stream <- DSD_Gaussians(k=3, d=2, noise=0.05)

window <- DSO_Window(horizon=100)
window

update(window, stream, 200)
window
```
# plot points in window
plot(get_points(window))

---

**DST**  
*Abstract Base Class for All Data Stream Mining Tasks*

**Description**

Abstract base class for all data stream mining tasks. Current tasks are data stream clustering DSC, classification on data streams DSClassify and frequent pattern mining on data streams DSFP.

**Author(s)**

Michael Hahsler

**See Also**

DSC, DSClassify, DSFP

---

**EvalCallback-class**  
*Abstract Class for Evaluation Callbacks*

**Description**

The abstract class for all evaluation callbacks. Cannot be instantiated. Must be inherited. Evaluation is the process of the clustering quality assessment. This assessment can include clustering results, as well as the clustering process, e.g., duration, spatial query performance, and similar. The stream package has some measurements (see evaluate for details) already implemented. All other measurements can be externally implemented without need to extend the stream package, by using callbacks.

**Fields**

- `all_measures` A list of all measures this object contributes to the evaluation. Union of all callback measures defines measures the end-user can use.
- `internal_measures` A list of internal measures. A subset of all_measures.
- `external_measures` A list of external measures. A subset of all_measures.
- `outlier_measures` A list of outlier measures. A subset of all_measures.
**EvalCallback-class**

**Methods**

```r
evaluate_callback(cb_obj, dsc, measure, points, actual, predict, outliers, predict_outliers, predict_outliers_corrid, centers, noise, ...)
```

A method that allows callback for external clustering results evaluation.

- `cb_obj` - The callback object (`EvalCallback`).
- `dsc` - The clusterer object (`DSC`).
- `measure` - The requested measures.
- `points` - A data frame containing all data items.
- `actual` - Actual assignments for the related data instance in `points`, given by the used data stream generator.
- `predict` - Assignments for the related data instance in `points`, given by the clusterer.
- `outliers` - Outlier marks for the related data instance in `points`, marked by the used data stream generator.
- `predict_outliers` - Outlier marks for the related data instance in `points`, marked by the clusterer.
- `predict_outliers_corrid` - Outlier identifiers assigned by the clusterer.
- `centers` - Cluster centers given by the clusterer.
- `noise` - Noise assignments (NA) for the related data instance in `points`, for all data instances that cannot be classified neither into clusters or outliers.

**Author(s)**

Dalibor Krleža

**Examples**

```r
CustomCallback <- function() {
  env <- environment()
  all_measures <- c("LowestWeightPercentage")
  internal_measures <- c()
  external_measures <- all_measures
  outlier_measures <- c()
  this <- list(description = "Custom evaluation callback",
                env = environment())
  class(this) <- c("CustomCallback", "EvalCallback")
  this
}
evaluate_callback.CustomCallback <- function(cb_obj, dsc, measure, points,
                                             actual, predict, outliers,
                                             predict_outliers,
                                             predict_outliers_corrid,
                                             centers, noise) {
  r <- list()
  if("LowestWeightPercentage" %in% measure)
    r$LowestWeightPercentage = min(get_weights(dsc))/sum(get_weights(dsc))
  r
}
stream <- DSD_Gaussians(k = 3, d = 2, p = c(0.2, 0.4, 0.4))
km <- DSC_Kmeans(3)
update(km, stream, n=500)
```
evaluate_with_callbacks(km, stream, type="macro", n=500,
measure = c("crand","LowestWeightPercentage"),
callbacks = list(cc=CustomCallback()))

Description

Evaluate Clusterings

Gets evaluation measures for micro or macro-clusters from a DSC object given the original DSD object.

Usage

evaluate(dsc, dsd, measure, n = 100, type=c("auto", "micro", "macro"),
assign="micro", assignmentMethod=c("auto", "model", "nn"),
noise = c("class", "exclude"), ...)
evaluate_with_callbacks(dsc, dsd, measure, callbacks=NULL, n = 100,
type=c("auto", "micro", "macro"), assign="micro",
assignmentMethod=c("auto", "model", "nn"), noise = c("class", "exclude"), ...)
evaluate_cluster(dsc, dsd, measure, n = 1000,
type=c("auto", "micro", "macro"),
assign="micro", assignmentMethod=c("auto", "model", "nn"),
horizon=100, verbose=FALSE, noise = c("class", "exclude"), ...)
evaluate_cluster_with_callbacks(dsc, dsd, measure, callbacks=NULL,
n = 1000, type=c("auto", "micro", "macro"),
assign="micro", assignmentMethod=c("auto", "model", "nn"),
horizon=100, verbose=FALSE, noise = c("class", "exclude"), ...)

Arguments

dsc The DSC object that the evaluation measure is being requested from.
dsd The DSD object that holds the initial training data for the DSC.
measure Evaluation measure(s) to use. If missing then all available measures are returned.
n The number of data points being requested.
type Use micro- or macro-clusters for evaluation. Auto used the class of dsc to decide.
assign Assign points to micro or macro-clusters?
assignmentMethod How are points assigned to clusters for evaluation (see get_assignment)?
horizon Evaluation is done using horizon many previous points (see detail section).
verbose Report progress?
o10ne How to handle noise points in the data. Options are to treat as a separate class (default) or to exclude them from evaluation.
callbacks A list of EvalCallback objects, invoked when measurement is calculated.
... Unused arguments are ignored.
Details

For evaluation each data points are assigned to its nearest cluster using Euclidean distance to the cluster centers. Then for each cluster the majority class is determined. Based on the majority class several evaluation measures can be computed.

For `evaluate_cluster` the most commonly used method of prequential error estimation (see Gama, Sebastiao and Rodrigues; 2013). The data points in the horizon are first used to calculate the evaluation measure and then they are used for updating the cluster model. Many evaluation measures are calculated with code from the packages `cluster`, `clue` and `fpc`. Detailed documentation can be found in these packages (see Section See Also.)

The following information items are available:

- "numMicroClusters" number of micro-clusters
- "numMacroClusters" number of macro-clusters
- "numClasses" number of classes

The following noise-related items are available:

- "noisePredicted" Number data points predicted as noise
- "noiseActual" Number of data points which are actually noise
- "noisePrecision" Precision of the predicting noise (i.e., number of correctly predicted noise points over the total number of points predicted as noise)

The following internal evaluation measures are available:

- "SSQ" within cluster sum of squares. Assigns each non-noise point to its nearest center from the clustering and calculates the sum of squares
- "silhouette" average silhouette width (actual noise points which stay unassigned by the clustering algorithm are removed; regular points that are unassigned by the clustering algorithm will form their own noise cluster) (`cluster`)
- "average.between" average distance between clusters (`fpc`)
- "average.within" average distance within clusters (`fpc`)
- "max.diameter" maximum cluster diameter (`fpc`)
- "min.separation" minimum cluster separation (`fpc`)
- "ave.within.cluster.ss" a generalization of the within clusters sum of squares (half the sum of the within cluster squared dissimilarities divided by the cluster size) (`fpc`)
- "g2" Goodman and Kruskal’s Gamma coefficient (`fpc`)
- "pearsongamma" correlation between distances and a 0-1-vector where 0 means same cluster, 1 means different clusters (`fpc`)
- "dunn" Dunn index (minimum separation / maximum diameter) (`fpc`)
- "dunn2" minimum average dissimilarity between two cluster / maximum average within cluster dissimilarity (`fpc`)
- "entropy" entropy of the distribution of cluster memberships (`fpc`)
- "wb.ratio" average.within/average.between (`fpc`)

The following external evaluation measures are available:
• "precision", "recall", "F1" F1. A true positive (TP) decision assigns two points in the same true cluster also to the same cluster, a true negative (TN) decision assigns two points from two different true clusters to two different clusters. A false positive (FP) decision assigns two points from the same true cluster to two different clusters. A false negative (FN) decision assigns two points from the same true cluster to different clusters.

\[ \text{precision} = \frac{TP}{TP+FP} \]
\[ \text{recall} = \frac{TP}{TP+FN} \]

The F1 measure is the harmonic mean of precision and recall.

• "purity" Average purity of clusters. The purity of each cluster is the proportion of the points of the majority true group assigned to it (see Cao et al. (2006))

• "Euclidean" Euclidean dissimilarity of the memberships (see Dimitriadou, Weingessel and Hornik (2002)) (clue)

• "Manhattan" Manhattan dissimilarity of the memberships (clue)

• "Rand" Rand index (see Rand (1971)) (clue)

• "cRand" Adjusted Rand index (see Hubert and Arabie (1985)) (clue)

• "NMI" Normalized Mutual Information (see Strehl and Ghosh (2002)) (clue)

• "KP" Katz-Powell index (see Katz and Powell (1953)) (clue)

• "angle" maximal cosine of the angle between the agreements (clue)

• "diag" maximal co-classification rate (clue)

• "FM" Fowlkes and Mallows’s index (see Fowlkes and Mallows (1983)) (clue)

• "Jaccard" Jaccard index (clue)

• "PS" Prediction Strength (see Tibshirani and Walter (2005)) (clue)

• "vi" variation of information (VI) index (fpc)

Many measures are the average over all clusters. For example, purity is the average purity over all clusters.

For DSC_Micro objects, data points are assigned to micro-clusters and then each micro-cluster is evaluated. For DSC_Macro objects, data points by default (assign="micro") also assigned to micro-clusters, but these assignments are translated to macro-clusters. The evaluation is here done for macro-clusters. This is important when macro-clustering is done with algorithms which do not create spherical clusters (e.g, hierarchical clustering with single-linkage or DBSCAN) and this assignment to the macro-clusters directly (i.e., their center) does not make sense.

Using type and assign, the user can select how to assign data points and ad what level (micro or macro) to evaluate.

Many of the above measures are implemented package clue in function cl_agreement().

The following outlier measures are available:

• "OutlierJaccard" - A variant of the Jaccard index used to assess outlier detection accuracy (see Krleza et al (2020)). Outlier Jaccard index is calculated as \( TP/(TP+FP+\text{UNDETECTED}) \).

Outlier measures are taken as external measures, and can be applied only for DSD that can mark outliers (see DSD_Gaussians) and outlier detection clusterers that inherits DSC_Outlier class.

evaluate_cluster() is used to evaluate an evolving data stream using the method described by Wan et al. (2009). Of the \( n \) data points horizon many points are clustered and then the evaluation
measure is calculated on the same data points. The idea is to find out if the clustering algorithm was able to adapt to the changing stream.

evaluate_with_callbacks() and evaluate_cluster_with_callbacks() can be used to add external measure calculations, without need to update stream package. At the end of each evaluation, a set of callbacks is done. Measurements described hereby are placed in the DefaultEvalCallback class. All other callbacks are done through objects inheriting the EvalCallback class.

Value

evaluate returns an object of class stream_eval which is a numeric vector of the values of the requested measures and two attributes, "type" and "assign", to see at what level the evaluation was done.

Author(s)

Michael Hahsler, Matthew Bolanos, John Forrest, and Dalibor Krleža

References


L. Katz and J. H. Powell (1953). A proposed index of the conformity of one sociometric measurement to another. Psychometrika, 18, 249-256.


L Wan, W.K. Ng, X.H. Dang, P.S. Yu and K. Zhang (2009). Density-Based Clustering of Data Streams at Multiple Resolutions, ACM Transactions on Knowledge Discovery from Data, 3(3).


See Also

animate_cluster, cl_agreement in clue, cluster.stats in fpc, silhouette in cluster.
Examples


code

stream <- DSD_Gaussians(k=3, d=2)
dstream <- DSC_DStream(gridsize=0.05, Cm=1.5)
update(dstream, stream, 500)
plot(dstream, stream)
# Evaluate micro-clusters
# Note: we use here only n=500 points for evaluation to speed up execution
evaluate(dstream, stream, measure=c("numMicro","numMacro","purity","crand", "SSQ"), n=100)

# DStream also provides macro clusters. Evaluate macro clusters with type="macro"
plot(dstream, stream, type="macro")
evaluate(dstream, stream, type="macro",
measure=c("numMicro","numMacro","purity","crand", "SSQ"), n=100)

# Points are by default assigned to the closest micro clusters for evaluation.
# However, points can also be assigned to the closest macro-cluster using
# assign="macro".
evaluate(dstream, stream, type="macro", assign="macro",
measure=c("numMicro","numMacro","purity","crand", "SSQ"), n=100)

# Evaluate an evolving data stream
stream <- DSD_Benchmark(1)
dstream <- DSC_DStream(gridsize=0.05, lambda=0.1)
evaluate_cluster(dstream, stream, type="macro", assign="micro",
measure=c("numMicro","numMacro","purity","crand"),
n=600, horizon=100)

# Not run:
# animate the clustering process
reset_stream(stream)
dstream <- DSC_DStream(gridsize=0.05, lambda=0.1)
animate_cluster(dstream, stream, horizon=100, n=5000,
measure=c("crand"), type="macro", assign="micro",
plot.args = list(type="both", xlim=c(0,1), ylim=c(0,1)))

# End(Not run)

# a simple callback example
# this example requires DSC_MCOD in the streamMOA package
CustomCallback <- function() {
  env <- environment()
  all_measures <- c("LowestWeightPercentage")
  internal_measures <- c()
  external_measures <- all_measures
  outlier_measures <- c()
  this <- list(description = "Custom evaluation callback",
                env = environment())
  class(this) <- c("CustomCallback", "EvalCallback")
  this
}
evaluate_callback.CustomCallback <- function(cb_obj, dsc, measure, points, actual, predict, outliers, predict_outliers, predict_outliers_corrid, centers, noise) {
  r <- list()
  if("LowestWeightPercentage" %in% measure)
    r$LowestWeightPercentage=min(get_weights(dsc))/sum(get_weights(dsc))
  r
}
stream <- DSD_Gaussians(k = 3, d = 2, p = c(0.2, 0.4, 0.4))
km <- DSC_Kmeans(3)
update(km, stream, n=500)
evaluate_with_callbacks(km, stream, type="macro", n=500, measure = c("crand","LowestWeightPercentage"), callbacks = list(cc=CustomCallback()))

get_assignment

Assignment Data Points to Clusters

Description

Get the assignment of data points to clusters in a DSC using the model’s assignment rules or nearest neighbor assignemnt. The clustering is not modified.

Usage

get_assignment(dsc, points, type = c("auto", "micro", "macro"), method = "auto", ...)

Arguments

dsc
points

type
method

The DSC object with the clusters for assignment.
The points to be assigned as a data.frame.
Use micro- or macro-clusters in DSC for assignment. Auto used the class of dsc to decide.
assignment method

- "model" uses the assignment method of the underlying algorithm (unassigned points return NA). Not all algorithms implement this option.
- "nn" performs nearest neighbor assignment using Euclidean distance.
- "auto" uses the model assignment method. If this method is not implemented/available then nn assignment is used instead.

... Additional arguments are passed on.
get_centers

**Details**

Each data point is assigned either using the original model’s assignment rule or Euclidean nearest neighbor assignment. If the user specifies the model’s assignment strategy, but is not available, then nearest neighbor assignment is used and a warning is produced.

**Value**

A vector containing the assignment of each point. NA means that a data point was not assigned to a cluster.

**Author(s)**

Michael Hahsler

**See Also**

DSC

**Examples**

```r
stream <- DSD_Gaussians(k = 3, d = 2, noise = .05)

dbstream <- DSC_DBSTREAM(r = .1)
update(dbstream, stream, n = 100)

# find the assignment for the next 100 points to # micro-clusters in dsc. This uses the model’s assignemnt function
points <- get_points(stream, n = 100)
a <- get_assignment(dbstream, points)
a

# show the MC assignment areas. Assigned points as blue circles and
# the unassigned points as red dots
plot(dbstream, stream, assignment = TRUE, type = "none")
points(points[!is.na(a),], col = "blue")
points(points[is.na(a),], col = "red", pch = 20)

# use nearest neighbor assignment instead
get_assignment(dbstream, points, method = "nn")
```

---

**Description**

Gets the cluster centers (micro- or macro-clusters) from a DSC object.

**Usage**

```r
get_centers(x, type=c("auto", "micro", "macro"), ...)
```
get_copy

Arguments

x The DSC object the centers are being requested from.
type get centers for micro- or macro-clusters. Auto used the class of dsc to decide.
... Additional parameters.

Value
A data.frame with the micro- or macro-cluster centers as rows.

Author(s)
Michael Hahsler

See Also
DSC

Examples
stream <- DSD_Gaussians(k=3, d=2)
dstream <- DSC_DStream(gridsize=.1)
update(dstream, stream, 500)
dstream

# getting the micro-cluster centers
get_centers(dstream)

# D-Stream also has macro-clusters
get_centers(dstream, type="macro")

---

get_copy Create a Deep Copy of a DSC Object

Description
DSC objects contain reference classes or Java data structures (for MOA). Therefore, we provide a mechanism to create deep copies.

Usage
get_copy(x)

Arguments

x The DSC object being copied.

Value
A deep copy of the original DSC.
get_points

Description

Gets points from a DSD object.

Usage

get_points(x, n=1, outofpoints=c("stop", "warn", "ignore"), ...)

Arguments

x 
The DSD object.
n 
Request up to n points from the stream.
outofpoints 
Action taken if less than n data points are available. The default is to stop with an error. For warn and ignore all available (possibly zero) points are returned.
... 
Additional parameters to pass to get_points() implementations.

Details

Each DSD object has a unique way for returning data points, but they all are called through the generic function, get_points(). This is done by using the S3 class system. See the man page for the specific DSD class on the semantics for each implementation of get_points().

Value

Returns a matrix of x$d columns and n rows.

Author(s)

Michael Hahsler

See Also

DSD

Examples

stream <- DSD_Gaussians()
get_points(stream, 100)
get_weights  
*Get Cluster Weights*

**Description**
Get the weights of the clusters in the DSC

**Usage**
```r
get_weights(x, type=c("auto", "micro", "macro"), scale=NULL, ...)
```

**Arguments**
- `x`: The DSC object the weights are being requested from.
- `type`: Return weights of micro- or macro-clusters in `x`. Auto uses the class of `x` to decide.
- `scale`: a range (from, to) to scale the weights. Returns by default the raw weights.
- `...`: Additional arguments are passed on.

**Details**
The cluster weights are typically a function of how many points were assigned to each cluster.

**Value**
A vector containing the weight of each micro-cluster or macro-cluster. Internally the call is delegated to the appropriate `get_microweights()` or `get_macroweights()` method.

**Author(s)**
Michael Hahsler

**See Also**
- DSC

**Examples**
```r
stream <- DSD_Gaussians(k=3, d=2)
dstream <- DSC_DStream(gridsize=.1)
update(dstream, stream, 500)
dstream

# getting the micro-cluster weights
get_weights(dstream)

# D-Stream also has macro-clusters
get_weights(dstream, type="macro")
```
Moving Generator Cluster

Description

Creates an evolving cluster for a DSD_MG.

Usage

MGC_Static(density, center, parameter, shape = NULL)
MGC_Function(density, center, parameter, shape = NULL)
MGC_Random(density, center, parameter, randomness = 1, shape = NULL)
MGC_Noise(density, range)
MGC_Linear(dimension = 2, keyframelist = NULL, shape = NULL)
keyframe(time, density, center, parameter, reset = FALSE)
add_keyframe(x, time, density, center, parameter, reset = FALSE)
get_keyframes(x)
remove_keyframe(x, time)

Arguments

center A list that defines the center of the cluster. The list should have a length equal to the dimensionality. For MGC_Function, this list consists of functions that define the movement of the cluster. For MGC_Random, this attribute defines the beginning location for the MGC before it begins moving.
density The density of the cluster. For MGC_Function, this attribute is a function and defines the density of a cluster at a given timestamp.
dimension Dimensionality of the data stream.
keyframelist a list of keyframes to initialize the MGC_Linear object with.
parameter Parameters for the shape. For the default shape MGC_Shape_Gaussian the parameter is the standard deviation, one per dimension. If a single value is specified then it is recycled for all dimensions.
randomness The maximum amount the cluster will move during one time step.
range The area in which the noise should appear.
reset Should the cluster reset to the first keyframe (time 0) after this keyframe is finished?
shape A function creating the shape of the cluster. It gets passed on the parameters argument from above. Available functions are MGC_Shape_Gaussian (the parameters are a vector containing standard deviations) and MGC_Shape_Block (parameters are the dimensions of the uniform block).
time The time stamp the keyframe should be located or which keyframe should be removed.
x An object of class MGC_Linear.
Details

An MGC describes a single cluster for use within an DSD_MG. There are currently four different MGCs that allow a user to express many different behaviors within a single data stream.

An MGC_Linear creates an evolving Gaussian cluster for a DSD_MG who’s behavior is determined by several keyframes. Keyframes can be added and removed.
An MGC_Function allows for a creation of a DSD_MG that is defined by functions of time.
An MGC_Random allows for a creation of a DSD_MG that moves randomly.
An MGC_Noise allows for a creation of noise within a DSD_MG.

Author(s)

Matthew Bolanos

See Also

DSD_MG for details on how to use an MGC within a DSD

Examples

### Two static clusters
```
stream <- DSD_MG(dim=2,
    MGC_Static(den = 1, center=c(1, 0), par=.1),
    MGC_Static(den = 1, center=c(2, 0), par=.4, shape=MGC_Shape_Block),
)

plot(stream)
```

### Example of several MGC_Randoms
```
stream <- DSD_MG(dimension=2,
    MGC_Random(den = 100, center=c(1, 0), par=.1, rand=.1),
    MGC_Random(den = 100, center=c(2, 0), par=.4, shape=MGC_Shape_Block, rand=.1),
)
```

## Not run:
```
animate_data(stream, 2500, xlim=c(0,3), ylim=c(-2,2), horizon=100)
```

## End(Not run)

### Example of several MGC_Functions
```
stream <- DSD_MG(dim = 2)

### block-shaped cluster moving from bottom-left to top-right increasing size
cl <- MGC_Function(
    density = function(t){100},
    parameter = function(t){t*t},
    center = function(t) c(t,t),
    shape = MGC_Shape_Block
)
add_cluster(stream,cl)
```
### cluster moving in a circle (default shape is Gaussian)

c2 <- MGC_Function(
  density = function(t){25},
  parameter = function(t){5},
  center= function(t) c(sin(t/10)*50+50, cos(t/10)*50+50)
)
add_cluster(stream,c2)

## Not run:
animate_data(stream,10000,xlim=c(-20,120),ylim=c(-20,120), horizon=100)

## End(Not run)

### Example of several MGC_Linears: A single cluster splits at time 50 into two.
### Note that c2 starts at time=50!
stream <- DSD_MG(dim = 2)
c1 <- MGC_Linear(dim = 2)
add_keyframe(c1, time=1, dens=50, par=5, center=c(0,0))
add_keyframe(c1, time=50, dens=50, par=5, center=c(50,50))
add_keyframe(c1, time=100,dens=50, par=5, center=c(50,100))
add_cluster(stream,c1)

c2 <- MGC_Linear(dim = 2, shape=MGC_Shape_Block)
add_keyframe(c2, time=50, dens=25, par=c(10,10), center=c(50,50))
add_keyframe(c2, time=100,dens=25, par=c(30,30), center=c(100,50))
add_cluster(stream,c2)

## Not run:
animate_data(stream,5000,xlim=c(0,100),ylim=c(0,100), horiz=100)

## End(Not run)

### two fixed and a moving cluster
stream <- DSD_MG(dim = 2,
  MGC_Static(dens=1, par=.1, center=c(0,0)),
  MGC_Static(dens=1, par=.1, center=c(1,1)),
  MGC_Linear(dim=2,list(
    keyframe(time = 0, dens=1, par=.1, center=c(0,0)),
    keyframe(time = 1000, dens=1, par=.1, center=c(1,1)),
    keyframe(time = 2000, dens=1, par=.1, center=c(0,0), reset=TRUE)
  )))

noise <- MGC_Noise(dens=.1, range=rbind(c(-.2,1.2),c(-.2,1.2)))
add_cluster(stream, noise)

## Not run:
animate_data(stream, n=2000*3.1, xlim=c(-.2,1.2), ylim=c(-.2,1.2), horiz=200)

## End(Not run)
Translate Micro-cluster IDs to Macro-cluster IDs

Description
Translates micro-cluster ids into macro-cluster ids for a DSC_Macro object.

Usage
microToMacro(x, micro=NULL)

Arguments
x
a DSC_Macro object that also contains information about micro-clusters.
micro
A vector with micro-cluster ids. If NULL then the assignments for all micro-clusters in x are returned.

Value
A vector of the same length as micro with the macro-cluster ids.

Author(s)
Michael Hahsler

See Also
DSC_Macro

Examples
stream <- DSD_Gaussians(k=3, d=2, noise=0.05, p=c(.2,.4,.6))

# recluster a micro-clusters
micro <- DSC_DStream(gridsize=0.05)
update(micro, stream, 500)

macro <- DSC_Kmeans(k=3)
recluster(macro, micro)

# translate all micro-cluster ids
microToMacro(macro)

# plot some data points in gray
plot(stream, col="gray", cex=.5, xlim=c(0,1), ylim=c(0,1))
# add micro-clusters and use the macro-cluster ids as color and weights as size
points(get_centers(macro, type="micro"),
       col=microToMacro(macro),
       cex=get_weights(macro, type="micro", scale=c(.5,3)))
# add macro-cluster centers (size is weight)
points(get_centers(macro, type="macro"),
  cex = get_weights(macro, type="macro", scale=c(2,5)),
  pch=3,lwd=3, col=1:3)

**nclusters**

**Description**

Returns the number of micro-clusters from the DSC object.

**Usage**

```r
nclusters(x, type=c("auto", "micro", "macro"), ...)
```

**Arguments**

- `x` A DSC object.
- `type` Return the number of micro- or macro-clusters in DSC. Auto used the class of dsc to decide.
- `...` Additional arguments are passed on.

**Value**

An integer; the number of micro- or macro-clusters in the clustering.

**Author(s)**

Michael Hahsler

**See Also**

*DSC*

**Examples**

```r
# setting up the objects
stream <- DSD_Gaussians(k=3)
dstream <- DSC_DStream(gridsize=0.1)
update(dstream, stream, 500)

# retrieving the results
get_centers(dstream)
nclusters(dstream)
```
plot  

Plotting Data Stream Data and Clusterings

Description

Methods to plot data stream data and clusterings.

Usage

```r
## S3 method for class 'DSD'
plot(x, n = 500, col = NULL, pch = NULL, ..., method = "pairs", dim = NULL, alpha = 0.6)

## S3 method for class 'DSC'
plot(x, dsd = NULL, n = 500, col_points = NULL, col_clusters = c("red", "blue", "green"), weights = TRUE, scale = c(1, 5), cex = 1, pch = NULL, method = "pairs", dim = NULL, type = c("auto", "micro", "macro", "both", "all", "outliers"), assignment = FALSE, ...)
```

Arguments

- **x**: the DSD or DSC object to be plotted.
- **dsd**: a DSD object to plot the data in the background.
- **n**: number of plots taken from the dsd to plot.
- **col, col_points, col_clusters**: colors used for plotting.
- **weights**: the size of the symbols for micro- and macro-clusters represents its weight.
- **scale**: range for the symbol sizes used.
- **cex**: size factor for symbols.
- **pch**: symbol type.
- **method**: method used for plotting: "pairs" (pairs plot), "scatter" (scatter plot) or "pc" (plot first 2 principal components).
- **dim**: an integer vector with the dimensions to plot. If NULL then for methods "pairs" and "pc" all dimensions are used and for "scatter" the first two dimensions are plotted.
- **alpha**: alpha shading used to plot the points.
- **type**: Plot micro clusters (type="micro"), macro clusters (type="macro"), both micro and macro clusters (type="both"), outliers(type="outliers"), or everything together (type="all"). type="auto" leaves to the class of dsc to decide.
- **assignment**: logical; show assignment area of micro-clusters.
- **...**: further arguments are passed on to plot or pairs in `graphics`.

Author(s)

Michael Hahsler
See Also

DSC, DSD

Examples

stream <- DSD_Gaussians(k=3, d=3)

## plot data
plot(stream, n=500)
plot(stream, method="pc", n=500)
plot(stream, method="scatter", dim=c(1,3), n=500)

## create and plot micro-clusters
dstream <- DSC_DStream(gridsize=0.1)
update(dstream, stream, 500)
plot(dstream)

## plot with data, projected on the first two principal components
## and dimensions 2 and 3
plot(dstream, stream)
plot(dstream, stream, method="pc")
plot(dstream, stream, dim=c(2,3))

## plot micro and macro-clusters
plot(dstream, stream, type="both")

---

prune_clusters

Prune Clusters from a Clustering

Description

Creates a (static) copy of a clustering where a fraction of the weight or the number of clusters with the lowest weights were pruned.

Usage

prune_clusters(dsc, threshold= 0.05, weight = TRUE)

Arguments

dsc                The DSC object to be pruned.
threshold          The numeric vector of probabilities for the quantile.
weight             should a fraction of the total weight in the clustering be pruned? Otherwise a fraction of clusters is pruned.

Value

Returns an object of class DSC_Static.
recluster

Author(s)

Michael Hahsler

See Also

DSC_Static

Examples

# 3 clusters with 10% noise
stream <- DSD_Gaussians(k=3, noise=0.1)

dbstream <- DSC_DBSTREAM(r=0.1)
update(dbstream, stream, 500)
dbstream
plot(dbstream, stream)

# prune lightest micro-clusters for 20% of the weight of the clustering
static <- prune_clusters(dbstream, threshold=0.2)
static
plot(static, stream)

recluster  Re-clustering micro-clusters

Description

Use a macro clustering algorithm to recluster micro-clusters into a final clustering.

Usage

recluster(macro, micro, type="auto", ...)

Arguments

macro a macro clustering algorithm (class "DSC_Macro")
micro a DSC object containing micro-clusters.
type controls which clustering is used from dsc (typically micro-clusters).
... additional arguments passed on.

Details

Takes centers and weights of the micro-clusters and applies the macro clustering algorithm.

Value

The object macro is altered and contains the clustering.
**reset_stream**

### Description

Resets the counter in a DSD object to the beginning or any other position in the stream.

### Usage

```r
reset_stream(dsd, pos = 1)
```

### Arguments

- `dsd` 
  An object of class a subclass of DSD which implements a reset function.
- `pos` 
  Position in the stream (the beginning of the stream is position 1).

### Details

Resets the counter of the stream object. For example, for DSD_Memory, the counter stored in the environment variable is moved back to 1. For DSD_ReadCSV objects, this is done by calling `seek()` on the underlying connection.

### Author(s)

Michael Hahsler

### See Also

[DSD_ReadCSV, DSD_MG, DSD_ScaleStream, DSD_Memory]
Examples

# initializing the objects
stream <- DSD_Gaussians(k=3, d=2)
replayer <- DSD_Memory(stream, 100)
replayer

p <- get_points(replayer, 50)
replayer

# reset replayer to the beginning of the stream
reset_stream(replayer)
replayer

# set replayer to position 21
reset_stream(replayer, pos=21)
replayer

---

Save and Read DSC Objects

Description

Save and Read DSC objects safely (serializes the underlying data structure). This also works for streamMOA DSC objects.

Usage

saveDSC(object, file, ...)  
readDSC(file)

Arguments

object a DSC object.
file filename.
... further arguments.

Author(s)

Michael Hahsler

See Also

saveRDS and readRDS.
Examples

```r
stream <- DSD_Gaussians(k = 3, noise = 0.05)

# create clusterer with r = 0.05
dbstream1 <- DSC_DBSTREAM(r = .05)
update(dbstream1, stream, 1000)
dbstream1

saveDSC(dbstream1, file="dbstream.Rds")

dbstream2 <- readDSC("dbstream.Rds")
dbstream2

## cleanup
unlink("dbstream.Rds")
```

---

**update**

*Update a Data Stream Clustering Model*

**Description**

Update a clustering model by clustering a number of input points from a data stream into a clustering object.

**Usage**

```r
## S3 method for class 'DSC_R'
update(object, dsd, n = 1, verbose = FALSE, block=10000L, ...)
## S3 method for class 'DSC_TwoStage'
update(object, dsd, n = 1, verbose = FALSE, block=10000L, ...)
## S3 method for class 'DSO_Sample'
update(object, dsd, n = 1, verbose = FALSE, ...)
## S3 method for class 'DSO_Window'
update(object, dsd, n = 1, verbose = FALSE, ...)
```

**Arguments**

- **object**: an object of a subclass of DST (data stream mining task).
- **dsd**: a DSD object (data stream).
- **n**: number of points to cluster.
- **verbose**: report progress.
- **block**: maximal number of data points passed on at once to the algorithm. This only is used since R loops are very slow.
- **...**: extra arguments for clusterer.
write_stream

Details

update takes n times a single data points out of the DSD updates the model in object. Note that update directly modifies the object (which is a reference class) and thus the result does not need to be reassigned to the object name.

Value

The updated model is returned invisibly for reassignment (however, this is not necessary).

To obtain the updated model for a DSC (data stream clustering model), call get_centers() on the DSC object.

Author(s)

Michael Hahsler

See Also

DSC, DSD, and animation for producing an animation of the clustering process.

Examples

stream <- DSD_Gaussians(k=3)
dstream <- DSC_DStream(gridsize=.05)

update(dstream, stream, 500)
plot(dstream, stream)

write_stream

Write a Data Stream to a File

Description

Writes points from a data stream DSD object to a file or a connection.

Usage

write_stream(dsd, file, n=100, block=100000L,
class=FALSE, append = FALSE, sep="","", header=FALSE, row.names=FALSE, ...)
## S3 method for class 'DSD'
write_stream(dsd, file, n=100, block=100000L,
class=FALSE, append = FALSE, sep="","", header=FALSE, row.names=FALSE,
write_outliers=FALSE, ...)
Arguments

dsd The DSD object that will generate the data points for output.
file A file name or a R connection to be written to.
n The number of data points to be written.
block Write stream in blocks to improve file I/O speed.
class Save the class/cluster labels of the points as the last column.
sep The character that will separate attributes in a data point.
append Append the data to an existing file.
header A flag that determines if column names will be output (equivalent to col.names in write.table()).
row.names A flag that determines if row names will be output.
write_outliers A flag that determines if outliers will be output.
... Additional parameters that are passed to write.table().

Value

There is no value returned from this operation.

Author(s)

Michael Hahsler, Dalibor Krleža

See Also

write.table, DSD

Examples

# creating data and writing it to disk
stream <- DSD_Gaussians(k=3, d=5, outliers=1,
    outlier_options=list(outlier_horizon=10))
write_stream(stream, file="data.txt", n=10, class=TRUE, write_outliers=TRUE)

#file.show("data.txt")

# clean up
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