

# Package ‘streamMOA’

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**Title** Interface for MOA Stream Clustering Algorithms

**Description** Interface for data stream clustering algorithms implemented in the MOA (Massive Online Analysis) framework (Albert Bifet, Geoff Holmes, Richard Kirkby, Bernhard Pfahringer (2010). MOA: Massive Online Analysis, Journal of Machine Learning Research 11: 1601-1604).

**Depends** stream (>= 2.0-0), rJava (>= 1.0-1)

**Imports** graphics, stats, methods, proxy

**Suggests** RMOA (>= 1.1.0)

**SystemRequirements** Java (>= 8)

**BugReports** <https://github.com/mhahsler/streamMOA>

**License** GPL-3

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DSClassifier_MOA	<i>DSClassifier_MOA – MOA-based Stream Classifiers</i>
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### Description

Interface for MOA-based stream classification methods based on package **RMOA**.

### Usage

```
DSClassifier_MOA(formula, RMOA_classifier)

## S3 method for class 'DSClassifier_MOA'
update(object, dsd, n = 1, verbose = FALSE, block = 1000L, ...)

## S3 method for class 'DSClassifier_MOA'
predict(object, newdata, type = "response", ...)
```

### Arguments

formula	a formula for the classification problem.
RMOA_classifier	a RMOA_classifier object.
object	a DSC object.
dsd	a data stream object.
n	number of data points taken from the stream.
verbose	logical; show progress?
block	process blocks of data to improve speed.
...	further arguments.
newdata	dataframe with the new data.
type	prediction type (see <code>RMOA::predict.MOA_trainedmodel()</code> ).

## Details

DSClassifier\_MOA provides an interface to MOA-based stream classifiers using package **RMOA**. RMOA provides access to MOAs stream classifiers in the following groups:

- [RMOA::MOA\\_classification\\_trees](#)
- [RMOA::MOA\\_classification\\_bayes](#)
- [RMOA::MOA\\_classification\\_ensemblelearning](#)

Subsequent calls to `update()` update the current model.

## Value

An object of class DSClassifier\_MOA

## Author(s)

Michael Hahsler

## References

Wijffels, J. (2014) Connect R with MOA to perform streaming classifications. <https://github.com/jwijffels/RMOA>  
Bifet A, Holmes G, Pfahringer B, Kranen P, Kremer H, Jansen T, Seidl T (2010). MOA: Massive Online Analysis, a Framework for Stream Classification and Clustering. *Journal of Machine Learning Research (JMLR)*.

## Examples

```
## Not run:
library(streamMOA)
library(RMOA)

# create a data stream for the iris dataset
data <- iris[sample(nrow(iris)), ]
stream <- DSD_Memory(data)
stream

# define the stream classifier. MOAmodelOptions can be passed on as a control parameter
# to the call RMOA::HoeffdingTree(). See ? RMOA::MOAoptions
cl <- DSClassifier_MOA(
  Species ~ Sepal.Length + Sepal.Width + Petal.Length,
  RMOA::HoeffdingTree()
)

cl

# update the classifier with 100 points from the stream
update(cl, stream, 100)

# look at the classifier RMOA object
cl$RMOAobj
```

```

# predict the class for the next 50 points
newdata <- get_points(stream, n = 50)
pr <- predict(cl, newdata)
pr

table(pr, newdata$Species)

## End(Not run)

```

---

DSC\_BICO\_MOA

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


---

### Description

This is an interface to the MOA implementation of BICO. The original BICO implementation by Fichtenberger et al is also available as [stream::DSC\\_BICO](#).

### Usage

```

DSC_BICO_MOA(
  Cluster = 5,
  Dimensions,
  MaxClusterFeatures = 1000,
  Projections = 10,
  k = NULL,
  space = NULL,
  p = NULL
)

```

### Arguments

Cluster, k	Number of desired centers
Dimensions	The number of the dimensions of the input points (stream) need to be specified in advance
MaxClusterFeatures, space	Maximum size of the coreset
Projections, p	Number of random projections used for the nearest neighbor search

### Details

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.

**Author(s)**

Matthias Carnein

**References**

Hendrik Fichtenberger, Marc Gille, Melanie Schmidt, Chris Schwiegelshohn, Christian Sohler: BICO: BIRCH Meets Coresets for k-Means Clustering. ESA 2013: 481-492

**See Also**

Other DSC\_MOA: [DSC\\_CluStream\(\)](#), [DSC\\_ClusTree\(\)](#), [DSC\\_DStream\\_MOA\(\)](#), [DSC\\_DenStream\(\)](#), [DSC\\_MCOD\(\)](#), [DSC\\_MOA\(\)](#), [DSC\\_StreamKM\(\)](#)

**Examples**

```
# data with 3 clusters and 2 dimensions
set.seed(1000)
stream <- DSD_Gaussians(k = 3, d = 2, noise = 0.05)

# cluster with BICO
bico <- DSC_BICO_MOA(Cluster = 3, Dimensions = 2)
update(bico, stream, 100)
bico

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

---

DSC\_CluStream

*CluStream Data Stream Clusterer*

---

**Description**

Class implements the CluStream cluster algorithm for data streams (Aggarwal et al, 2003).

**Usage**

```
DSC_CluStream(m = 100, horizon = 1000, t = 2, k = 5)
```

**Arguments**

m	Defines the maximum number of micro-clusters used in CluStream
horizon	Defines the time window to be used in CluStream
t	Maximal boundary factor (i.e., the kernel radius factor). When deciding to add a new data point to a micro-cluster, the maximum boundary is defined as a factor of t of the RMS deviation of the data points in the micro-cluster from the centroid.
k	Number of macro-clusters to produce using weighted k-means.

**Details**

This is an interface to the MOA implementation of CluStream.

If  $k$  is specified, then CluStream applies a weighted  $k$ -means algorithm for reclustering (see Examples section below).

**Value**

An object of class DSC\_CluStream (subclass of `stream::DSC_Micro`, `DSC_MOA` and `stream::DSC`).

**Author(s)**

Michael Hahsler and John Forrest

**References**

Aggarwal CC, Han J, Wang J, Yu PS (2003). "A Framework for Clustering Evolving Data Streams." In "Proceedings of the International Conference on Very Large Data Bases (VLDB '03)," pp. 81-92.

Bifet A, Holmes G, Pfahringer B, Kranen P, Kremer H, Jansen T, Seidl T (2010). MOA: Massive Online Analysis, a Framework for Stream Classification and Clustering. In Journal of Machine Learning Research (JMLR).

**See Also**

Other DSC\_MOA: `DSC_BICO_MOA()`, `DSC_ClusTree()`, `DSC_DStream_MOA()`, `DSC_DenStream()`, `DSC_MCOD()`, `DSC_MOA()`, `DSC_StreamKM()`

**Examples**

```
# data with 3 clusters and 5% noise
set.seed(1000)
stream <- DSD_Gaussians(k = 3, d = 2, noise = .05)

# cluster with CluStream
clustream <- DSC_CluStream(m = 50, horizon = 100, k = 3)
update(clustream, stream, 500)
clustream

plot(clustream, stream, type = "both")
```

---

DSC\_ClusTree

*ClusTree Data Stream Clusterer*

---

**Description**

Interface for the MOA implementation of the ClusTree data stream clustering algorithm (Kranen et al, 2009).

## Usage

```
DSC_ClusTree(horizon = 1000, maxHeight = 8, lambda = NULL, k = NULL)
```

## Arguments

horizon	Range of the (time) window.
maxHeight	The maximum height of the tree.
lambda	number used to override computed lambda (decay).
k	If specified, k-means with k clusters is used for reclustering.

## Details

ClusTree uses a compact and self-adaptive index structure for maintaining stream summaries. Kranen et al (2009) suggest EM or k-means for reclustering.

## Value

An object of class DSC\_ClusTree (subclass of `stream::DSC`, `DSC_MOA`, `stream::DSC_Micro`).

## Author(s)

Michael Hahsler and John Forrest

## References

Philipp Kranen, Ira Assent, Corinna Baldauf, and Thomas Seidl. 2009. Self-Adaptive Anytime Stream Clustering. In Proceedings of the 2009 Ninth IEEE International Conference on Data Mining (ICDM '09). IEEE Computer Society, Washington, DC, USA, 249-258. doi:10.1109/ICDM.2009.47

Bifet A, Holmes G, Pfahringer B, Kranen P, Kremer H, Jansen T, Seidl T (2010). MOA: Massive Online Analysis, a Framework for Stream Classification and Clustering. In Journal of Machine Learning Research (JMLR).

## See Also

Other DSC\_MOA: `DSC_BICO_MOA()`, `DSC_CluStream()`, `DSC_DStream_MOA()`, `DSC_DenStream()`, `DSC_MCOD()`, `DSC_MOA()`, `DSC_StreamKM()`

## Examples

```
# data with 3 clusters
set.seed(1000)
stream <- DSD_Gaussians(k = 3, d = 2, noise = 0.05)

clustree <- DSC_ClusTree(maxHeight = 3)
update(clustree, stream, 500)
clustree

plot(clustree, stream)
```

```
#' Use automatically the k-means reclusterer with k = 3 to create macro clusters
clustree <- DSC_ClusTree(maxHeight = 3, k = 3)
update(clustree, stream, 500)
clustree

plot(clustree, stream, type = "both")
```

---

DSC\_DenStream

*DenStream Data Stream Clusterer*


---

### Description

Interface for the DenStream cluster algorithm for data streams implemented in MOA.

### Usage

```
DSC_DenStream(
  epsilon,
  mu = 1,
  beta = 0.2,
  lambda = 0.001,
  initPoints = 100,
  offline = 2,
  processingSpeed = 1,
  recluster = TRUE,
  k = NULL
)
```

### Arguments

epsilon	defines the epsilon neighborhood which is the maximal radius of micro-clusters ( $r \leq \epsilon$ ). Range: 0 to 1.
mu	minpoints as the weight $w$ a core-micro-clusters needs to be created ( $w \geq \mu$ ). Range: 0 to $\max(\text{int})$ .
beta	multiplier for mu to detect outlier micro-clusters given their weight $w$ ( $w < \beta \times \mu$ ). Range: 0 to 1
lambda	decay constant.
initPoints	number of points to use for initialization via DBSCAN.
offline	offline multiplier for epsilon. Range: between 2 and 20). Used for reachability reclustering
processingSpeed	Number of incoming points per time unit (important for decay). Range: between 1 and 1000.
recluster	logical; should the offline DBSCAN-based (i.e., reachability at a distance of epsilon) be performed?
k	integer; tries to automatically chooses offline to find k macro-clusters.



## Details

DenStream applies reachability (from DBSCAN) between micro-clusters for reclustering using  $\epsilon \times \text{offline}$  (defaults to 2) as the reachability threshold.

If  $k$  is specified it automatically chooses the reachability threshold to find  $k$  clusters. This is achieved using single-link hierarchical clustering.

## Value

An object of class `DSC_DenStream` (subclass of `stream::DSC`, `DSC_MOA`, `stream::DSC_Micro`) or, for `recluster = TRUE`, an object of class `stream::DSC_TwoStage`.

## Author(s)

Michael Hahsler and John Forrest

## References

Cao F, Ester M, Qian W, Zhou A (2006). Density-Based Clustering over an Evolving Data Stream with Noise. In Proceedings of the 2006 SIAM International Conference on Data Mining, pp 326-337. SIAM.

Bifet A, Holmes G, Pfahringer B, Kranen P, Kremer H, Jansen T, Seidl T (2010). MOA: Massive Online Analysis, a Framework for Stream Classification and Clustering. In Journal of Machine Learning Research (JMLR).

## See Also

Other DSC\_MOA: `DSC_BICO_MOA()`, `DSC_CluStream()`, `DSC_ClusTree()`, `DSC_DStream_MOA()`, `DSC_MCOD()`, `DSC_MOA()`, `DSC_StreamKM()`

## Examples

```
# data with 3 clusters and 5% noise
set.seed(1000)
stream <- DSD_Gaussians(k = 3, d = 2, noise = 0.05)

# use Den-Stream with reachability reclustering
denstream <- DSC_DenStream(epsilon = .05)
update(denstream, stream, 500)
denstream

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

# plot micro-cluster
plot(denstream, stream, type = "micro")

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

# reclustering: Choose reclustering reachability threshold automatically to find 4 clusters
```

```
denstream2 <- DSC_DenStream(epsilon = .05, k = 4)
update(denstream2, stream, 500)
plot(denstream2, stream, type = "both")
```

---

DSC\_DStream\_MOA

*D-Stream Data Stream Clustering Algorithm*

---

## Description

This is an interface to the MOA implementation of D-Stream. A C++ implementation (including reclustering with attraction) is available as [stream::DSC\\_DStream](#).

## Usage

```
DSC_DStream_MOA(decayFactor = 0.998, Cm = 3, Cl = 0.8, Beta = 0.3)
```

## Arguments

decayFactor	The decay factor
Cm	Controls the threshold for dense grids
Cl	Controls the threshold for sparse grids
Beta	Adjusts the window of protection for renaming previously deleted grids as sporadic

## 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 decay factor.

### Notes:

- This implementation seems to use a 1 x 1 grid and therefore the range is increased in the example.
- The MOA implementation of D-Stream currently does not return micro clusters.

## Author(s)

Matthias Carnein

## References

Yixin Chen and Li Tu. 2007. Density-based clustering for real-time stream data. In Proceedings of the 13th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD '07). ACM, New York, NY, USA, 133-142.

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**

Other DSC\_MOA: [DSC\\_BICO\\_MOA\(\)](#), [DSC\\_CluStream\(\)](#), [DSC\\_ClusTree\(\)](#), [DSC\\_DenStream\(\)](#), [DSC\\_MCOD\(\)](#), [DSC\\_MOA\(\)](#), [DSC\\_StreamKM\(\)](#)

**Examples**

```
set.seed(1000)
stream <- DSD_Gaussians(k = 3, d = 2, noise = 0.05, space_limit = c(0, 10))

# cluster with D-Stream
dstream <- DSC_DStream_MOA(Cm = 3)
update(dstream, stream, 1000)
dstream

# plot macro-clusters
plot(dstream, stream, type= "macro")
```

DSC\_MCOD

*Micro-cluster Continuous Outlier Detector (MCOD)***Description**

Class interfaces the MOA implementation of the MCODE algorithm for distance-based data stream outlier detection.

**Usage**

```
DSC_MCOD(r = 0.1, t = 50, w = 1000, recheck_outliers = FALSE)
DSOutlier_MCOD(r = 0.1, t = 50, w = 1000, recheck_outliers = TRUE)
get_outlier_positions(x, ...)
recheck_outlier(x, outlier_correlated_id, ...)
clean_outliers(x, ...)
```

**Arguments**

r	Defines the micro-cluster radius.
t	Defines the number of neighbors (k in the article).
w	Defines the window width in data points.
recheck_outliers	Defines that the MCODE algorithm allows re-checking of detected outliers.
x	a DSC_MCOD object.
...	further arguments are currently ignored.
outlier_correlated_id	ids of outliers.

## Details

The algorithm detects density-based outliers. An object  $x$  is defined to be an outlier if there are less than  $t$  objects lying at distance at most  $r$  from  $x$ .

Outliers are stored and can be retrieved using `get_outlier_position()` and `recheck_outlier()`.

**Note:** The implementation updates the clustering when `predict()` is called.

## Value

An object of class DSC\_MCOD (subclass of `stream::DSC_Micro`, `DSC_MOA` and `stream::DSC`).

## Functions

- `get_outlier_positions()`: Returns spatial positions of all current outliers.
- `recheck_outlier()`: DSC\_MCOD Re-checks the outlier having `outlier_correlated_id`. If this object is still an outlier, the method returns TRUE.
- `clean_outliers()`: forget detected outliers from the outlier detector (currently not implemented).

## Author(s)

Dalibor Krleža

## References

Kontaki M, Gounaris A, Papadopoulos AN, Tsihlias K, and Manolopoulos Y (2016). Efficient and flexible algorithms for monitoring distance-based outliers over data streams. *Information Systems*, Vol. 55, pp. 37-53. doi:10.1109/ICDE.2011.5767923

## See Also

Other DSC\_MOA: `DSC_BICO_MOA()`, `DSC_CluStream()`, `DSC_ClusTree()`, `DSC_DStream_MOA()`, `DSC_DenStream()`, `DSC_MOA()`, `DSC_StreamKM()`

## Examples

```
# Example 1: Clustering with MCOD
stream <- DSD_Gaussians(k = 3, d = 2, noise = 0.05)
mcod <- DSC_MCOD(r = .1, t = 3, w = 100)
update(mcod, stream, 100)
mcod

plot(mcod, stream, n = 100)

# Example 2: Predict outliers (have a class label of NA)
stream <- DSD_Gaussians(k = 3, d = 2, noise = 0.05)
mcod <- DSOutlier_MCOD(r = .1, t = 3, w = 100)
update(mcod, stream, 100)

plot(mcod, stream, n = 100)
```

```
# MCOB can retried the outliers
get_outlier_positions(mcod)

# Example 3: evaluate on a stream
evaluate_static(mcod, stream, n = 100, type = "micro",
  measure = c("crand", "noisePrecision", "outlierjaccard"))
```

---

DSC\_MOA

*DSC\_MOA Class*

---

## Description

An abstract class that inherits from the base class [stream::DSC](#) and provides the common functions needed to interface MOA clusterers.

## Usage

```
DSC_MOA(...)
```

## Arguments

... further arguments.

## Details

DSC\_MOA is a subclass of [stream::DSC](#) for MOA-based clusterers. DSC\_MOA classes operate in a different way in that the centers of the micro-clusters have to be extracted from the underlying Java object. This is done by using **rJava** to perform method calls directly in the JRI and converting the multi-dimensional Java array into a local R data type.

**Note:** The formula interface is currently not implemented for MOA-based clusterers. Use [stream::DSF](#) to select features instead.

## Author(s)

Michael Hahsler and John Forrest

## References

Albert Bifet, Geoff Holmes, Richard Kirkby, Bernhard Pfahringer (2010). MOA: Massive Online Analysis, Journal of Machine Learning Research 11: 1601-1604

## See Also

Other DSC\_MOA: [DSC\\_BICO\\_MOA\(\)](#), [DSC\\_CluStream\(\)](#), [DSC\\_ClusTree\(\)](#), [DSC\\_DStream\\_MOA\(\)](#), [DSC\\_DenStream\(\)](#), [DSC\\_MCOD\(\)](#), [DSC\\_StreamKM\(\)](#)

---

DSC_StreamKM	<i>streamKM++</i>
--------------	-------------------

---

### Description

This is an interface to the MOA implementation of streamKM++.

### Usage

```
DSC_StreamKM(sizeCoreset = 10000, numClusters = 5, length = 100000L, ...)
```

### Arguments

sizeCoreset	Size of the coreset
numClusters	Number of clusters to compute
length	Length of the data stream
...	Further arguments ignored.

### Details

streamKM++ uses a tree-based sampling strategy to obtain a small weighted sample of the stream called coreset. The MOA implementation applies the k-means++ algorithm to find a given number of centers in the coreset.

#### Notes:

- The cluster can only cluster the number of points specified in length and then produces an `ArrayIndexOutOfBoundsException` error.
- The coreset (micro-clusters are not accessible), only the macro-clusters can be requested.

### Author(s)

Matthias Carnein

### References

Marcel R. Ackermann, Christiane Lammersen, Marcus Maertens, Christoph Raupach, Christian Sohler, Kamil Swierkot. StreamKM++: A Clustering Algorithm for Data Streams. In: *Proceedings of the 12th Workshop on Algorithm Engineering and Experiments (ALENEX '10)*, 2010.

### See Also

Other DSC\_MOA: [DSC\\_BICO\\_MOA\(\)](#), [DSC\\_CluStream\(\)](#), [DSC\\_ClusTree\(\)](#), [DSC\\_DStream\\_MOA\(\)](#), [DSC\\_DenStream\(\)](#), [DSC\\_MCOD\(\)](#), [DSC\\_MOA\(\)](#)

**Examples**

```
set.seed(1000)
stream <- DSD_Gaussians(k = 3, d = 2, noise = 0.05)

# cluster with streamKM++
streamkm <- DSC_StreamKM(sizeCoreset = 100, numClusters = 3, length = 1000)
update(streamkm, stream, 100)
streamkm

# plot macro-clusters (no access to micro-clusters)
plot(streamkm, stream)
```

---

DSD\_MOA

*Base class for MOA-based Data Stream Generators*

---

**Description**

Abstract base class for MOA-based data stream generators directly inherits from [stream::DSD](#).

**Usage**

```
DSD_MOA(...)
```

**Arguments**

```
...          further arguments.
```

**Value**

The abstract class cannot be instantiated and produces an error.

**Author(s)**

Michael Hahsler

**References**

MOA: Massive Online Analysis, a Framework for Stream Classification and Clustering Albert Bifet, Geoff Holmes, Bernhard Pfahringer, Philipp Kranen, Hardy Kremer, Timm Jansen, Thomas Seidl. Journal of Machine Learning Research (JMLR).

**See Also**

Other DSD\_MOA: [DSD\\_RandomRBFGeneratorEvents\(\)](#)

**Examples**

```
DSD()
```

---

DSD\_RandomRBFGeneratorEvents

*Random RBF Generator Events Data Stream Generator*


---

## Description

A class that generates random data based on RandomRBFGeneratorEvents implemented in MOA.

## Usage

```
DSD_RandomRBFGeneratorEvents(
    k = 3,
    d = 2,
    numClusterRange = 3L,
    kernelRadius = 0.07,
    kernelRadiusRange = 0,
    densityRange = 0,
    speed = 100L,
    speedRange = 0L,
    noiseLevel = 0.1,
    noiseInCluster = FALSE,
    eventFrequency = 30000L,
    eventMergeSplitOptions = FALSE,
    eventDeleteCreate = FALSE,
    modelSeed = NULL,
    instanceSeed = NULL
)
```

## Arguments

k	The average number of centroids in the model.
d	The dimensionality of the data.
numClusterRange	Range for number of clusters.
kernelRadius	The average radius of the micro-clusters.
kernelRadiusRange	Deviation of the number of centroids in the model.
densityRange	Density range.
speed	Kernels move a predefined distance of 0.01 every X points.
speedRange	Speed/Velocity point offset.
noiseLevel	Noise level.
noiseInCluster	Allow noise to be placed within a cluster.
eventFrequency	Frequency of events.



eventMergeSplitOptions	Merge and split?
eventDeleteCreate	Delete and create?
modelSeed	Random seed for the model.
instanceSeed	Random seed for the instances.

### Details

There are an assortment of parameters available for the underlying MOA data structure, however, we have currently limited the available parameters to the arguments above. Currently the `modelSeed` and `instanceSeed` are set to default values every time a [DSD\\_MOA](#) is created, therefore the generated data will be the same. Because of this, it is important to set the seed manually when different data is needed.

The default behavior is to create a data stream with 3 clusters and concept drift. The locations of the clusters will change slightly, and they will merge with one another as time progresses.

### Value

An object of class `DSD_RandomRBFGeneratorEvent` (subclass of [DSD\\_MOA](#), `stream::DSD`).

### Author(s)

Michael Hahsler and John Forrest

### References

Albert Bifet, Geoff Holmes, Bernhard Pfahringer, Philipp Kranen, Hardy Kremer, Timm Jansen, Thomas Seidl. MOA: Massive Online Analysis, a Framework for Stream Classification and Clustering *Journal of Machine Learning Research (JMLR)*, 2010.

### See Also

Other `DSD_MOA`: [DSD\\_MOA\(\)](#)

### Examples

```
stream <- DSD_RandomRBFGeneratorEvents()
get_points(stream, 10)

if (interactive()) {
  animate_data(stream, n = 5000, horizon = 100, xlim = c(0, 1), ylim = c(0, 1))
}
```

---

DSRegressor\_MOA      *DSRegressor\_MOA – MOA-based Stream Regressors*


---

### Description

Interface for MOA-based stream regression methods based on package **RMOA**.

### Usage

```
DSRegressor_MOA(formula, RMOA_regressor)

## S3 method for class 'DSRegressor_MOA'
update(object, dsd, n = 1, verbose = FALSE, block = 1000L, ...)

## S3 method for class 'DSRegressor_MOA'
predict(object, newdata, type = "response", ...)
```

### Arguments

formula	a formula for the regression problem.
RMOA_regressor	a RMOA_regressors object.
object	a DSC object.
dsd	a data stream object.
n	number of data points taken from the stream.
verbose	logical; show progress?
block	process blocks of data to improve speed.
...	further arguments.
newdata	dataframe with the new data.
type	prediction type (see <a href="#">RMOA::predict.MOA_trainedmodel()</a> ).

### Details

DSRegressor\_MOA provides an interface to MOA-based stream regressors using package **RMOA**. Available regressors can be found at [RMOA::MOA\\_regressors](#).

Subsequent calls to `update()` update the current model.

### Value

An object of class `DSRegressor_MOA`

### Author(s)

Michael Hahsler

## References

- Wijffels, J. (2014) Connect R with MOA to perform streaming classifications. <https://github.com/jwijffels/RMOA>
- Bifet A, Holmes G, Pfahringer B, Kranen P, Kremer H, Jansen T, Seidl T (2010). MOA: Massive Online Analysis, a Framework for Stream Classification and Clustering. *Journal of Machine Learning Research (JMLR)*.

## Examples

```
## Not run:
library(streamMOA)
library(RMOA)

# create a data stream for the iris dataset
data <- iris[sample(nrow(iris)), ]
stream <- DSD_Memory(data)
stream

# define a stream regression model.
cl <- DSRegressor_MOA(
  Sepal.Length ~ Species + Sepal.Width + Petal.Length,
  RMOA::Perceptron()
)

cl

# update the model with 100 points from the stream
update(cl, stream, 100)

# look at the RMOA model object
cl$RMOAObj

# make predictions for the next 50 points
newdata <- get_points(stream, n = 50)
pr <- predict(cl, newdata)
pr

plot(pr, newdata$Sepal.Length, xlim = c(0,10), ylim = c(0,10))
abline(a = 0, b = 1, col = "red")

## End(Not run)
```

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