

Package ‘popsom’

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Title Functions for Constructing and Evaluating Self-Organizing Maps

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Imports som,class,fields, graphics, ggplot2

Description State of the art functions for constructing and evaluating self-organizing maps.

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URL <http://homepage.cs.uri.edu/faculty/hamel/>

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`map.build`*Build Map*

Description

Constructs a SOM, returns an object of class 'map'.

Usage

```
map.build(data, labels=NULL, xdim=10, ydim=5, alpha=0.3, train=1000, algorithm="vsom")
```

Arguments

<code>data</code>	a dataframe where each row contains an unlabeled training instance.
<code>labels</code>	a vector or dataframe with one label for each observation in data.
<code>xdim</code>	the x-dimension of the map. (default=10)
<code>ydim</code>	the y-dimension of the map. (default=5)
<code>alpha</code>	the learning rate, should be a positive non-zero real number. (default=0.3)
<code>train</code>	the number of training iterations. (default=1000)
<code>algorithm</code>	training algorithm selection switch. (default="vsom")

Value

object of type 'map'.

Note

You have a choice of training algorithms:

- "vsom" - vectorized stochastic learning, this is a highly optimized version of stochastic training written in FORTRAN 9X.
- "som" - the traditional stochastic learning algorithm written in C++/TNT.
- "batchsom" - batch version of the SOM training algorithm, written in C.
- "experimental" - experimental implementation of vectorized stochastic learning implemented directly in R.

Note

If your training data does not have any labels you can construct a simple label vector as follows: `labels <- 1:nrow(training.data)`. If you let the labels default to the NULL value then no labels will be shown in the map visualization.

Author(s)

Lutz Hamel, Benjamin Ott, Gregory Breard

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)
```

map.convergence *SOM Quality Assessment*

Description

Evaluate the quality of a SOM using embedding accuracy and estimated topographical accuracy.

Usage

```
map.convergence(map, conf.int=.95, k=50, verb=FALSE, ks=FALSE)
```

Arguments

map	an object of type 'map'.
conf.int	is the confidence interval of the quality assessment (default 95%)
k	number of samples to use in the computation of the estimated topographical accuracy (default=50)
verb	if true reports the two convergence components separately, otherwise it will report a linear combination of the two indices (default=FALSE)
ks	if true uses the Kolmogorov-Smirnov convergence test otherwise a convergence test based on variance and means is performed (default=FALSE)

Value

A single value or a pair of values: 1) embedding accuracy 2) estimated topographic accuracy.

Author(s)

Lutz Hamel

References

"SOM Quality Measures: A Statistical Approach," Lutz Hamel, WSOM16, 2016.

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## map quality
map.convergence(m)
```

map.embed

Map Embedding Accuracy

Description

Evaluates how well a map models the underlying training data distribution.

Usage

```
map.embed(map, conf.int = 0.95, verb=FALSE, ks=FALSE)
```

Arguments

map	an object of type 'map'.
conf.int	the confidence interval of the embedding test (default 95 percent).
verb	a switch controlling the structure of the output value (default=FALSE)
ks	if true uses the Kolmogorov-Smirnov convergence test otherwise a convergence test based on variance and means is performed (default=FALSE)

Value

The embedding accuracy of the map. If the switch verb=TRUE then a vector of the individual feature embedding accuracies are returned.

Author(s)

Lutz Hamel, Benjamin Ott, Gregory Breard, Robert Tatroian

References

"A Population Based Convergence Criterion for Self-Organizing Maps," Lutz Hamel and Benjamin Ott. Proceeding of the 2012 International Conference on Data Mining (DMIN'12), pp98-104, July 16-19, 2012, Las Vegas Nevada, USA.

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## display the embedding accuracy of the map
map.embed(m)

## display the embedding accuracies of the individual features
data.frame(names(df),map.embed(m,verb=TRUE))
```

map.marginal

Plot Marginal Distribution

Description

Generate a plot that shows the marginal probability distribution of the neurons and data.

Usage

```
map.marginal(map,marginal)
```

Arguments

map an object of type 'map'.
marginal is the name of a training data frame dimension or index.

Author(s)

Lutz Hamel, Robert Tatioian

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## display marginal distribution of dimension 1
map.marginal(m,1)
```

map.neuron	<i>Return a Map Neuron</i>
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Description

Returns the contents of a neuron at (x,y) on the map as a vector.

Usage

```
map.neuron(map, x, y)
```

Arguments

map	an object of type 'map'.
x	map x-coordinate of neuron.
y	map y-coordinate of neuron.

Value

A vector representing the neuron.

Author(s)

Lutz Hamel

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## display the neuron at position (1,1)
map.neuron(m,1,1)
```

map.projection	<i>Map Projection</i>
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Description

Prints the association of labels with map elements.

Usage

```
map.projection(map)
```

Arguments

map an object of type 'map'.

Value

a dataframe containing the projection onto the map for each training observation.

Author(s)

Lutz Hamel, Benjamin Ott, Gregory Breard

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## display the label association for the map
map.projection(m)
```

map.significance	<i>Compute Significance Of Features</i>
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Description

Computes the relative significance of each feature and plots it.

Usage

```
map.significance(map, graphics = TRUE, feature.labels = TRUE)
```

Arguments

map an object of type 'map'.
graphics a switch that controls whether a plot is generated or not.
feature.labels a switch to allow the plotting of feature names vs feature indices.

Value

if graphics=FALSE a vector containing the significance for each feature is returned.

Note

We use a Bayesian approach to compute the relative significance of features based on variance.

Author(s)

Lutz Hamel, Benjamin Ott, Gregory Breard

References

"Bayesian Probability Approach to Feature Significance for Infrared Spectra of Bacteria," Lutz Hamel, Chris W. Brown, Applied Spectroscopy, Volume 66, Number 1, 2012.

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## show the relative feature significance for each feature
data.frame(names(df),map.significance(m,graphics=FALSE))

## display the relative feature significance graphically
map.significance(m)
```

map.starburst

Generate Starburst For Map

Description

Computes and displays the starburst representation of clusters on a map.

Usage

```
map.starburst(map, explicit = FALSE, smoothing = 2, merge.clusters=TRUE, merge.range=.25)
```


Arguments

map	an object of type 'map'.
explicit	controls the shape of the connected components.
smoothing	controls the smoothing level of the map display (NULL, 0, >0).
merge.clusters	is a switch that controls if the starburst clusters are merged together
merge.range	is a range that is used as a percentage of a certain distance in the code to determine whether components are closer to their centroids or centroids closer to each other.

Author(s)

Lutz Hamel, Benjamin Ott, Gregory Breard, Robert Tatioian, Vishakh Gopu

References

"Improved Interpretability of the Unified Distance Matrix with Connected Components," Lutz Hamel and Chris W. Brown. Proceeding of the 7th International Conference on Data Mining (DMIN'11), July 18-21, 2011, Las Vegas Nevada, USA, ISBN: 1-60132-168-6, pp338-343, CSREA Press, 2011.

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## display the starburst for the map
map.starburst(m)
```

map.topo

Estimated Topographical Accuracy

Description

Evaluate the topological quality of a SOM using the estimated topographical accuracy.

Usage

```
map.topo(map,k=50,conf.int = 0.95,verb=FALSE,interval=TRUE)
```

Arguments

map	an object of type 'map'.
k	number of samples to use in the computation of the estimated topographical accuracy (default=50)
conf.int	the confidence interval of the estimated topographical accuracy (default 95 percent).
verb	a switch controlling the structure of the output value (default=FALSE)
interval	a switch that controls whether the confidence interval is computed (default=TRUE)

Value

1) The value of the estimated topographical accuracy. 2) The low value of the confidence interval and the high value of the confidence interval 'conf.int' if interval=TRUE. 3) If verb=TRUE then map.accuracy will return a vector with the accuracies of the individual k samples.

Author(s)

Lutz Hamel

References

"SOM Quality Measures: A Statistical Approach," Lutz Hamel, WSOM16, 2016'.

Examples

```
data(iris)

## set data frame and labels
df <- subset(iris,select=-Species)
labels <- subset(iris,select=Species)

## build a map
m <- map.build(df, labels, xdim=15, ydim=10, train=1000)

## display estimated topographical accuracy of the map
map.topo(m)
```

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