Package ‘klaR’

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**Calculation of beta scaling parameters**

**Description**

Calculates the scaling parameter for `betascale`.

**Usage**

```r
b.scal(member, grouping, dis = FALSE, eps = 1e-04)
```

**Arguments**

- **member**: Membership values of an argmax classification method. Eg. posterior probabilities of `lda`. Row-wise values must sum up to 1 and must be in the interval [0,1].
- **grouping**: Class vector.
- **dis**: Logical, whether to optimize the dispersion parameter in `pbeta`.
- **eps**: Minimum variation of membership values. If variance is smaller than `eps`, the values are treated as one point.

**Details**

With `betascale` and `b.scal`, membership values of an argmax classifier are scaled in such a way, that the mean membership value of those values which are assigned to each class reflect the mean correctness rate of that values. This is done via `qbeta` and `pbeta` with the appropriate shape parameters. If `dis` is TRUE, it is tried that the variation of membership values is optimal for the accuracy relative to the correctness rate. If the variation of the membership values is less than `eps`, they are treated as one point and shifted towards the correctness rate.

**Value**

A list containing

- **model**: Estimated parameters for `betascale`.
- **eps**: Value of `eps` from the call.
- **member**: Scaled membership values.

**Author(s)**

Karsten Luebke (<karsten.luebke@fom.de>), Uwe Ligges

**References**

See Also

`betascale, e.scal`

Examples

```r
library(MASS)
data(B3)
pB3 <- predict(lda(PHASEN ~ ., data = B3))$posterior
pbB3 <- b.scal(pB3, B3$PHASEN, dis = TRUE)
ucpm(pB3, B3$PHASEN)
ucpm(pbB3$member, B3$PHASEN)
```

Description

West German Business Cycles 1955-1994

Usage

data(B3)

Format

A data frame with 157 observations on the following 14 variables.

- **PHASEN**: a factor with levels 1 (upswing), 2 (upper turning points), 3 (downswing), and 4 (lower turning points).
- **BSP91JW**: GNP (y)
- **CP91JW**: Private Consumption (y)
- **DEFRATE**: Government deficit (percent of GNP)
- **EWAJW**: Wage and salary earners (y)
- **EXIMRATE**: Net exports as (percent of GNP)
- **GM1JW**: Money supply M1 (y)
- **IAU91JW**: Investment in equipment (y)
- **IB91JW**: Investment in construction (y)
- **LSTKJW**: Unit labor cost (y)
- **PBSPJW**: GNP price deflator (y)
- **PCPJW**: Consumer price index (y)
- **ZINS**: Short term interest rate (nominal)
- **ZINSLR**: Long term interest rate (real)

where (y) stands for “yearly growth rates”.

Note that years and corresponding year quarters are given in the row names of the data frame, e.g. “1988,3” for the third quarter in 1988.
### Details

The West German Business Cycles data (1955-1994) is analyzed by the project B3 of the SFB475 (Collaborative Research Centre “Reduction of Complexity for Multivariate Data Structures”), supported by the Deutsche Forschungsgemeinschaft.

### Source

RWI (Rheinisch Westfälisches Institut für Wirtschaftsforschung), Essen, Germany.

### References


### See Also

For benchmarking on this data see also `benchB3`

### Examples

```r
data(B3)
summary(B3)
```

---

**Description**

Evaluates the performance of a classification method on the B3 data.

**Usage**

```r
benchB3(method, prior = rep(1/4, 4), sv = "4", scale = FALSE, ...)
```

**Arguments**

- `method`: classification method to use
- `prior`: prior probabilities of classes
- `sv`: class of the start of a business cycle
- `scale`: logical, whether to use `scale` first
- `...`: further arguments passed to `method`

**Details**

The performance of classification methods on cyclic data can be measured by a special form of cross-validation: Leave-One-Cycle-Out. That means that a complete cycle is used as test data and the others are used as training data. This is repeated for all complete cycles in the data.
betascale

Value
A list with elements

- MODEL: list with the model returned by method of the training data
- error: vector of test error rates in cycles
- l1co.error: leave-one-cycle-out error rate

Author(s)
Karsten Luebke, <karsten.luebke@fom.de>

See Also
bS

Examples

```r
perLDA <- benchB3("lda")
## Not run:
## due to parameter optimization rda takes a while
perRDA <- benchB3("rda")
library(rpart)
## rpart will not work with prior argument:
perRpart <- benchB3("rpart", prior = NULL)
## End(Not run)
```

---

**Description**

Performs the scaling for beta scaling learned by `b.scal`.

**Usage**

`betascale(betaobj, member)`

**Arguments**

- `betaobj`: A model learned by `b.scal`.
- `member`: Membership values to be scaled.

**Details**

See `b.scal`.
Value

A matrix with the scaled membership values.

See Also

b.scal, e.scal

Examples

library(MASS)
data(B3)
pB3 <- predict(lda(PHASEN ~ ., data = B3))$posterior
pbB3 <- b.scal(pB3, B3$PHASEN)
betascale(pbB3)

calc.trans

Calculation of transition probabilities

Description

Function to estimate the probabilities of a time series to stay or change the state.

Usage

calc.trans(x)

Arguments

x (factor) vector of states

Details

To estimate the transition probabilities the empirical frequencies are counted.

Value

The transition probabilities matrix. \( x[i,j] \) is the probability to change from state \( i \) to state \( j \).

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

Examples

data(B3)
calc.trans(B3$PHASEN)
centerlines  

*Lines from classborders to the center*

**Description**

Function which constructs the lines from the borders between two classes to the center. To be used in connection with *triplot* and *quadplot*.

**Usage**

```r
centerlines(n)
```

**Arguments**

- `n` number of classes. Meaningful are 3 or 4.

**Value**

A matrix with `n`-columns.

**Author(s)**

Karsten Luebke, <karsten.luebke@fom.de>

**See Also**

*triplot, quadplot*

**Examples**

```r
centerlines(3)
centerlines(4)
```

classscatter  

*Classification scatterplot matrix*

**Description**

Function to plot a scatterplot matrix with a classification result.

**Usage**

```r
classscatter(formula, data, method, col.correct = "black",
             col.wrong = "red", gs = NULL, ...)
```
cond.index

Arguments

formula formula of the form groups ~ x1 + x2 + ... . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data Data frame from which variables specified in formula are preferentially to be taken.
method character, name of classification function (e.g. "lda").
col.correct color to use for correct classified objects.
col.wrong color to use for missclassified objects.
gs group symbol (plot character), must have the same length as the data. If NULL, as.character(groups) is the default.

Value

The actual error rate.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

See Also

plot

Examples

data(B3)
library(MASS)
classscatter(PHASEN ~ BSP9JW + EWJW + LSTJW,
  data = B3, method = "lda")

cond.index Calculation of Condition Indices for Linear Regression

Description

Diagnosis of collinearity in X

Usage

cond.index(formula, data, ...)
Arguments

- **formula**: formula of the form `groups ~ x1 + x2 + ...`
- **data**: data frame (or matrix) containing the explanatory variables
- **...**: further arguments to be passed to `lm`

Details

Collinearities can inflate the variance of the estimated regression coefficients and numerical stability. The condition indices are calculated by the eigenvalues of the crossproduct matrix of the scaled but uncentered explanatory variables. Indices > 30 may indicate collinearity.

Value

A vector of the condition indices.

Author(s)

Andrea Preusser, Karsten Luebke (<karsten.luebke@fom.de>)

References


See Also

- `stepclass`, `manova`

Examples

```r
data(Boston)
condition_medv <- cond.index(medv ~ ., data = Boston)
condition_medv
```

`corclust` Function to identify groups of highly correlated variables for removing correlated features from the data for further analysis.

Description

A hierarchical clustering of variables using `hclust` is performed using 1 - the absolute correlation as a distance measure between two variables.

Usage

```r
corclust(x, cl = NULL, mincor = NULL, prnt = FALSE, method = "complete")
```
**Arguments**

- **x**: Either a data frame or a matrix consisting of numerical attributes.
- **cl**: Optional vector of ty factor indicating class levels, if class specific correlations should to be considered.
- **mincor**: Optional vector of degrees of correlation within a cluster of variables that will be indicated in the plot by a line.
- **prnt**: Logical indicating whether the matrix of distances should be printed.
- **method**: Linkage to be used for clustering. Default is `complete` linkage.

**Details**

The main output consists in the tree visualization of the clustered variables. Each cluster consists of a set of correlated variables according to the chosen clustering criterion. The default criterion is ‘complete’. This choice is meaningful as it represents the minimum absolute correlation between all variables of a cluster. Further proceeding would consist in choosing one variable of each cluster to obtain a subset of rather uncorrelated variables for further analysis. If an additional class vector `cl` is given to the function for any two variables their minimum correlation over all classes is used.

**Value**

- **min.abs.cor**: Matrix of distances used for clustering containing 1 - the absolute correlation between any two variables.
- **clustering**: Result object of the hierarchical clustering.

**Author(s)**

Gero Szepannek

**See Also**

See also `hclust`, for details on the clustering algorithm.

**Examples**

```r
data(iris)
classes <- iris$Species
variables <- iris[,1:4]
corclust(variables, classes, mincor = 0.6)
```
countries  

Socioeconomic data for the most populous countries.

Description

Socioeconomic data for the most populous countries.

Usage

data(countries)

Format

A data frame with 42 observations on the following 7 variables.

Country  name of the country.
Popul  population.
PopDens  population density.
GDPpp  GDP per inhabitant.
LifeEx  mean life expectation
InfMor  infant mortality
Illit  illiteracy rate

Source


Examples

data(countries)
summary(countries)

dkernel  

Estimate density of a given kernel

Description

Given an estimated kernel density this function estimates the density of a new vector.

Usage

dkernel(x, kernel = density(x), interpolate = FALSE, ...)

Arguments

- **x**: vector of which the density should be estimated
- **kernel**: object of class `density`
- **interpolate**: Interpolate or use `density` of nearest point? (currently not used.)

Value

Density of `x` in `kernel`.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

See Also

density, NaiveBayes

Examples

```r
kern <- density(rnorm(50))
x <- seq(-3, 3, len = 100)
y <- dkernel(x, kern)
plot(x, y, type = "l")
```

**Description**

Plot showing the classification of observations based on classification methods (e.g. `lda`, `qda`) for two variables. Moreover, the classification borders are displayed and the apparent error rates are given in each title.

**Usage**

```r
drawparti(grouping, x, y, method = "lda", prec = 100, xlab = NULL, ylab = NULL, col.correct = "black", col.wrong = "red", col.mean = "black", col.contour = "darkgrey", gs = as.character(grouping), pch.mean = 19, cex.mean = 1.3, print.err = 0.7, legend.err = FALSE, legend.bg = "white", imageplot = TRUE, image.colors = cm.colors(nc), plot.control = list(), ...)
```
Arguments

- **grouping**: factor specifying the class for each observation.
- **x**: first explanatory vector.
- **y**: second explanatory vector.
- **method**: the method the classification is based on, currently supported are: `lda`, `qda`, `rpart`, `naiveBayes`, `rda`, `sknn` and `svmlight`.
- **prec**: precision used to draw the classification borders (the higher the more precise; default: 100).
- **xlab**: a title for the x axis.
- **ylab**: a title for the y axis.
- **col.correct**: color for correct classified objects.
- **col.wrong**: color for wrong classified objects.
- **col.mean**: color for class means (only for methods `lda` and `qda`).
- **col.contour**: color of the contour lines (if `imageplot` = FALSE).
- **gs**: group symbol (plot character), must have the same length as **grouping**.
- **pch.mean**: plot character for class means (only for methods `lda` and `qda`).
- **cex.mean**: character expansion for class means (only for methods `lda` and `qda`).
- **print.err**: character expansion for text specifying the apparent error rate. If `print.err = 0`, nothing is printed.
- **legend.err**: logical; whether to plot the apparent error rate above the plot (if FALSE), or into a legend into the upper right corner of the plot (if TRUE). This argument is ignored, if `print.err = 0`, i.e. if no error rate is printed.
- **legend.bg**: background colour to use for the legend.
- **imageplot**: logical; whether to use an `image` plot or `contour` lines.
- **image.colors**: colors used for the `imageplot`, if TRUE.
- **plot.control**: A list containing further arguments passed to the underlying plot functions.
- **...**: Further arguments passed to the classification method.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>, Uwe Ligges, Irina Czogiel

See Also

- `partimat`
e.scal

**Function to calculate e- or softmax scaled membership values**

**Description**

Calculates the e- or softmax scaled membership values of an argmax based classification rule.

**Usage**

```r
e.scal(x, k = 1, tc = NULL)
```

**Arguments**

- `x`: matrix of membership values
- `k`: parameter for e-scaling (1 for softmax)
- `tc`: vector of true classes (required if `k` has to be optimized)

**Details**

For any membership vector \( y \), \( \exp(y \cdot k) / \sum \exp(y \cdot k) \) is calculated. If \( k=1 \), the classical softmax scaling is used. If the true classes are given, \( k \) is optimized so that the apparent error rate is minimized.

**Value**

A list containing elements

- `sv`: Scaled values
- `k`: Optimal \( k \)

**Author(s)**

Karsten Luebke, <karsten.luebke@fom.de>

**References**


**Examples**

```r
library(MASS)
data(iris)
ldaobj <- lda(Species ~ ., data = iris)
ldapred <- predict(ldaobj)$posterior
e.scal(ldapred)
e.scal(ldapred, tc = iris$Species)
```
Description

Produces an object of class EDAM which is a two dimensional representation of data in a rectangular, equally spaced grid as known from Self-Organizing Maps.

Usage

EDAM(EV0, nzx = 0, iter.max = 10, random = TRUE, standardize = FALSE,
    wghts = 0, classes = 0, sa = TRUE, temp.in = 0.5, temp.fin = 1e-07,
    temp.gamma = 0)

Arguments

EV0 either a symmetric dissimilarity matrix or a matrix of arbitrary dimensions whose n rows correspond to cases and whose k columns correspond to variables.

nzx an integer specifying the number of vertical bars in the grid. By default, nzx is chosen automatically, so that the grid gets closest do a square. If n is no multiple of nzx, all surplus objects are skipped.

iter.max an integer giving the maximum number of iterations to perform for the same neighborhood size.

random logical. If TRUE, the initial order is drawn from a uniform distribution.

standardize logical. If TRUE, the measurements in EV0 are standardized before calculating Euclidean distances. Measurements are standardized for each variable by dividing by the variable's standard deviation. Meaningless if EV0 is a dissimilarity matrix.

wghts an optional vector of length k giving relative weights of the variables in computing Euclidean distances. Meaningless if EV0 is a dissimilarity matrix.

classes an optional vector of length n specifying the membership to classes for all objects.

sa logical. If TRUE, the optimization is obtained by Simulated Annealing.

temp.in numeric giving the initial temperature, if sa is set to TRUE.

temp.fin numeric giving the final temperature, if sa is set to TRUE. Meaningless if temp.gamma is greater than 0.

temp.gamma numeric giving the relative change of the temperature from one iteration to the other, if sa is set to TRUE.
Details

The data given by \text{evP} is visualized by the EDAM-algorithm. This method approximates the best visualization where goodness is measured by \text{S}, a transformation of the criterion \text{stress} as i.e. known from \text{sammon}. The target space of the visualization is restricted to a grid so the problem has a discrete solution space. Originally this restriction was made to make the results comparable to those of Kohonen Self-Organizing Maps. But it turns out that also for reasons of a clear arrangement the representation in a grid can be more favorable than in the hole plane.

During the computation of EDAM 3 values indicating its progress are given online. The first is the number of the actual iteration, the second the maximum number of overall performed iterations. The latter may reduce during computation, since the neighborhood reduces in case of convergence before the last iteration. The last number gives the actual criterion \text{S}. The default plot method \text{plot.edam} for objects of class EDAM is \text{shardsplot}.

Value

EDAM returns an object of class \text{EDAM}, which is a list containing the following components:

\begin{itemize}
  \item \text{preimages} the re-ordered data; the position of the i-th object is where \text{Z} equals i.
  \item \text{Z} a matrix representing the positions of the \text{preimages} in the grid by their numbers.
  \item \text{Z.old.terms} a matrix representing the positions of the data in original order in the grid by their numbers.
  \item \text{cl.ord} a vector giving the re-ordered classes. All elements equal 1 if argument \text{classes} is undefined.
  \item \text{S} the criterion of the map
\end{itemize}

Author(s)

Nils Raabe

References

\url{http://www.statistik.tu-dortmund.de/de/content/einrichtungen/lehrstuehle/personen/raabe/Diplomarbeit.pdf}.

See Also

\text{shardsplot, TopoS}

Examples

\begin{verbatim}
# Compute an Eight Directions Arranged Map for a random sample
# of the iris data.
data(iris)
set.seed(1234)
iris.sample <- sample(150, 42)
\end{verbatim}
errormatrix

Tabulation of prediction errors by classes

Description

Cross-tabulates true and predicted classes with the option to show relative frequencies.

Usage

errormatrix(true, predicted, relative = FALSE)

Arguments

describe the code:

true Vector of true classes.
predicted Vector of predicted classes.
relative Logical. If TRUE rows are normalized to show relative frequencies (see below).
Details

Given vectors of true and predicted classes, a (symmetric) table of misclassifications is constructed. Element \([i,j]\) shows the number of objects of class \(i\) that were classified as class \(j\); so the main diagonal shows the correct classifications. The last row and column show the corresponding sums of misclassifications, the lower right element is the total sum of misclassifications.

If ‘relative’ is TRUE, the rows are normalized so they show relative frequencies instead. The lower right element now shows the total error rate, and the remaining last row sums up to one, so it shows “where the misclassifications went”.

Value

A (named) matrix.

Note

Concerning the case that ‘relative’ is TRUE:

If a prior distribution over the classes is given, the misclassification rate that is returned as the lower right element (which is only the fraction of misclassified data) is not an estimator for the expected misclassification rate.

In that case you have to multiply the individual error rates for each class (returned in the last column) with the corresponding prior probabilities and sum these up (see example below).

Both error rate estimates are equal, if the fractions of classes in the data are equal to the prior probabilities.

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

See Also

table

Examples

data(iris)
library(MASS)
x <- lda(Species ~ Sepal.Length + Sepal.Width, data=iris)
y <- predict(x, iris)

# absolute numbers:
errormatrix(iris$Species, y$class)

# relative frequencies:
errormatrix(iris$Species, y$class, relative = TRUE)

# percentages:
round(100 * errormatrix(iris$Species, y$class, relative = TRUE), 0)

# expected error rate in case of class prior:
friedman.data

```r
indiv.rates <- errormatrix(iris$Species, y$class, relative = TRUE)[1:3, 4]
prior <- c("setosa" = 0.2, "versicolor" = 0.3, "virginica" = 0.5)
total.rate <- t(indiv.rates) %% prior
total.rate
```

friedman.data Friedman’s classification benchmark data

Description

Function to generate 3-class classification benchmarking data as introduced by J.H. Friedman (1989).

Usage

```
friedman.data(setting = 1, p = 6, samplesize = 40, asmatrix = FALSE)
```

Arguments

- `setting` the problem setting (integer 1,2,...,6).
- `p` number of variables (6, 10, 20 or 40).
- `samplesize` sample size (number of observations, >=6).
- `asmatrix` if TRUE, results are returned as a matrix, otherwise as a data frame (default).

Details

When J.H. Friedman introduced the Regularized Discriminant Analysis (`rda`) in 1989, he used artificially generated data to test the procedure and to examine its performance in comparison to Linear and Quadratic Discriminant Analysis (see also `lda` and `qda`).

6 different settings were considered to demonstrate potential strengths and weaknesses of the new method:

1. equal spherical covariance matrices,
2. unequal spherical covariance matrices,
3. equal, highly ellipsoidal covariance matrices with mean differences in low-variance subspace,
4. equal, highly ellipsoidal covariance matrices with mean differences in high-variance subspace,
5. unequal, highly ellipsoidal covariance matrices with zero mean differences and
6. unequal, highly ellipsoidal covariance matrices with nonzero mean differences.

For each of the 6 settings data was generated with 6, 10, 20 and 40 variables.

Classification performance was then measured by repeatedly creating training-datasets of 40 observations and estimating the misclassification rates by test sets of 100 observations.

The number of classes is always 3, class labels are assigned randomly (with equal probabilities) to observations, so the contributions of classes to the data differs from dataset to dataset. To make sure covariances can be estimated at all, there are always at least two observations from each class in a dataset.
Value

Depending on asmatrix either a data frame or a matrix with samplesize rows and \( p + 1 \) columns, the first column containing the class labels, the remaining columns being the variables.

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

References


See Also

rda

Examples

```r
# Reproduce the 1st setting with 6 variables.
# Error rate should be somewhat near 9 percent.
training <- friedman.data(1, 6, 40)
x <- rda(class ~ ., data = training, gamma = 0.74, lambda = 0.77)
test <- friedman.data(1, 6, 100)
y <- predict(x, test[, -1])
errormatrix(test[,1], y$class)
```

GermanCredit  Statlog German Credit

Description

The dataset contains data of past credit applicants. The applicants are rated as good or bad. Models of this data can be used to determine if new applicants present a good or bad credit risk.

Usage

```r
data("GermanCredit")
```

Format

A data frame containing 1,000 observations on 21 variables.

- **status**: factor variable indicating the status of the existing checking account, with levels \( \ldots < 100 \text{ DM}, 0 \leq \ldots < 200 \text{ DM}, \ldots \geq 200 \text{ DM/salary for at least 1 year and no checking account.} \)
- **duration**: duration in months.
**credit_history** factor variable indicating credit history, with levels no credits taken/all credits paid back duly, all credits at this bank paid back duly, existing credits paid back duly till now, delay in paying off in the past and critical account/other credits existing.

**purpose** factor variable indicating the credit's purpose, with levels car (new), car (used), furniture/equipment, radio/television, domestic appliances, repairs, education, retraining, business and others.

**amount** credit amount.

**savings** factor. savings account/bonds, with levels ... < 100 DM, 100 <= ... < 500 DM, 500 <= ... < 1000 DM, ... >= 1000 DM and unknown/no savings account.

**employment_duration** ordered factor indicating the duration of the current employment, with levels unemployed, ... < 1 year, 1 <= ... < 4 years, 4 <= ... < 7 years and ... >= 7 years.

**installment_rate** installment rate in percentage of disposable income.

**personal_status_sex** factor variable indicating personal status and sex, with levels male: divorced/separated, female: divorced/separated/married, male: single, male: married/widowed and female: single.

**other_debtors** factor. Other debtors, with levels none, co-applicant and guarantor.

**present_residence** present residence since?

**property** factor variable indicating the client's highest valued property, with levels real estate, building society savings agreement/life insurance, car or other and unknown/no property.

**age** client's age.

**other_installment_plans** factor variable indicating other installment plans, with levels bank, stores and none.

**housing** factor variable indicating housing, with levels rent, own and for free.

**number_credits** number of existing credits at this bank.

**job** factor indicating employment status, with levels unemployed/unskilled - non-resident, unskilled - resident, skilled employee/official and management/self-employed/highly qualified employee.

**people LIABLE** Number of people being liable to provide maintenance.

**telephone** binary variable indicating if the customer has a registered telephone number.

**foreign_worker** binary variable indicating if the customer is a foreign worker.

**credit_risk** binary variable indicating credit risk, with levels good and bad.

**Source**

The original data was provided by:

Professor Dr. Hans Hofmann, Institut fuer Statistik und Oekonometrie, Universitaet Hamburg, FB Wirtschaftswissenschaften, Von-Melle-Park 5, 2000 Hamburg 13


It was published this way in CRAN package evtree (maintainer: Thomas Grubinger) that has been archived from CRAN on May 31, 2014. Afterwards the exactly same data object has been copied from the evtree package to klaR.
Stepwise forward variable selection for classification

Description

Performs a stepwise forward variable/model selection using the Wilk’s Lambda criterion.

Usage

```r
greedy.wilks(X, ...)  # Default S3 method:
greedy.wilks(X, grouping, niveau = 0.2, ...)  # S3 method for class 'formula'
greedy.wilks(formula, data = NULL, ...)
```

Arguments

- `X`: matrix or data frame (rows=cases, columns=variables)
- `grouping`: class indicator vector
- `formula`: formula of the form `groups ~ x1 + x2 + ...`
- `data`: data frame (or matrix) containing the explanatory variables
- `niveau`: level for the approximate F-test decision
- `...`: further arguments to be passed to the default method, e.g. `niveau`

Details

A stepwise forward variable selection is performed. The initial model is defined by starting with the variable which separates the groups most. The model is then extended by including further variables depending on the Wilk’s lambda criterion: Select the one which minimizes the Wilk’s lambda of the model including the variable if its p-value still shows statistical significance.

Value

A list of two components, a formula of the form `response ~ list of selected variables`, and a data.frame `results` containing the following variables:

- `vars`: the names of the variables in the final model in the order of selection.
- `Wilks.lambda`: the appropriate Wilks' lambda for the selected variables.
- `F.statistics.overall`: the approximated F-statistic for the so far selected model.
- `p.value.overall`: the appropriate p-value of the F-statistic.
- `F.statistics.diff`: the approximated F-statistic of the partial Wilk’s lambda (for comparing the model including the new variable with the model not including it).
- `p.value.diff`: the appropriate p-value of the F-statistic of the partial Wilk’s lambda.
Author(s)

Andrea Preusser, Karsten Luebke (<karsten.luebke@fom.de>)

References


See Also

`stepclass`, `manova`

Examples

data(B3)
gw_obj <- greedy.wilks(PHASEN ~ ., data = B3, niveau = 0.1)
gw_obj
## now you can say stuff like
## lda(gw_obj$formula, data = B3)

---

**hmm.sop**

*Calculation of HMM Sum of Path*

Description

A Hidden Markov Model for the classification of states in a time series. Based on the transition probabilities and the so called emission probabilities \( p(\text{class}|x) \) the ‘prior probabilities’ of states (classes) in time period \( t \) given all past information in time period \( t \) are calculated.

Usage

```r
hmm.sop(sv, trans.matrix, prob.matrix)
```

Arguments

- `sv`: state at time 0
- `trans.matrix`: matrix of transition probabilities
- `prob.matrix`: matrix of \( p(\text{class}|x) \)

Value

Returns the ‘prior probabilities’ of states.

Author(s)

Daniel Fischer, Reinald Oetsch
kmodes

K-Modes Clustering

Description

Perform k-modes clustering on categorical data.

Usage

kmodes(data, modes, iter.max = 10, weighted = FALSE)

Arguments

data A matrix or data frame of categorical data. Objects have to be in rows, variables in columns.

modes Either the number of modes or a set of initial (distinct) cluster modes. If a number, a random set of (distinct) rows in data is chosen as the initial modes.

iter.max The maximum number of iterations allowed.

weighted Whether usual simple-matching distance between objects is used, or a weighted version of this distance.

References


See Also

calc.trans

Examples

library(MASS)
data(B3)
trans.matrix <- calc.trans(B3$PHASEN)

# Calculate posterior prob. for the classes via lda
prob.matrix <- predict(lda(PHASEN ~ ., data = B3))$post
errormatrix(B3$PHASEN, apply(prob.matrix, 1, which.max))
prior.prob <- hmm sop("2", trans.matrix, prob.matrix)
errormatrix(B3$PHASEN, apply(prior.prob, 1, which.max))
Details

The $k$-modes algorithm (Huang, 1997) an extension of the $k$-means algorithm by MacQueen (1967). The data given by data is clustered by the $k$-modes method (Huang, 1997) which aims to partition the objects into $k$ groups such that the distance from objects to the assigned cluster modes is minimized.

By default simple-matching distance is used to determine the dissimilarity of two objects. It is computed by counting the number of mismatches in all variables. Alternative this distance is weighted by the frequencies of the categories in data (see Huang, 1997, for details).

If an initial matrix of modes is supplied, it is possible that no object will be closest to one or more modes. In this case less cluster than supplied modes will be returned and a warning is given.

Value

An object of class "kmodes" which is a list with components:

- **cluster**: A vector of integers indicating the cluster to which each object is allocated.
- **size**: The number of objects in each cluster.
- **modes**: A matrix of cluster modes.
- **withindiff**: The within-cluster simple-matching distance for each cluster.
- **iterations**: The number of iterations the algorithm has run.
- **weighted**: Whether weighted distances were used or not.

Author(s)

Christian Neumann, <christian2.neumann@tu-dortmund.de>

References


Examples

```R
## a 5-dimensional toy-example:

## generate data set with two groups of data:
set.seed(1)
x <- rbind(matrix(rbinom(250, 2, 0.25), ncol = 5),
           matrix(rbinom(250, 2, 0.75), ncol = 5))
colnames(x) <- c("a", "b", "c", "d", "e")

## run algorithm on x:
(cl <- kmodes(x, 2))
```
## Description
A localized version of Linear Discriminant Analysis.

## Usage
```r
loclda(x, ...)  
## S3 method for class 'formula'
loclda(formula, data, ..., subset, na.action)
## Default S3 method:
loclda(x, grouping, weight.func = function(x) 1/exp(x),
    k = nrow(x), weighted.apriori = TRUE, ...)
## S3 method for class 'data.frame'
loclda(x, ...)
## S3 method for class 'matrix'
loclda(x, grouping, ..., subset, na.action)
```

## Arguments
- **formula**: Formula of the form `groups ~ x1 + x2 + ...`.
- **data**: Data frame from which variables specified in `formula` are to be taken.
- **x**: Matrix or data frame containing the explanatory variables (required, if `formula` is not given).
- **grouping**: (required if no `formula` principal argument is given.) A factor specifying the class for each observation.
- **weight.func**: Function used to compute local weights. Must be finite over the interval [0,1]. See Details below.
- **k**: Number of nearest neighbours used to construct localized classification rules. See Details below.
- **weighted.apriori**: Logical: if `TRUE`, class prior probabilities are computed using local weights (see Details below). If `FALSE`, equal priors for all classes actually occurring in the train data are used.
- **subset**: An index vector specifying the cases to be used in the training sample.
na.action A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit which leads to rejection of cases with missing values on any required variable.

... Further arguments to be passed to loclda.default.

Details

This is an approach to apply the concept of localization described by Tutz and Binder (2005) to Linear Discriminant Analysis. The function loclda generates an object of class loclda (see Value below). As localization makes it necessary to build an individual decision rule for each test observation, this rule construction has to be handled by predict.loclda. For convenience, the rule building procedure is still described here.

To classify a test observation \( x_s \), only the \( k \) nearest neighbours of \( x_s \) within the train data are used. Each of these \( k \) train observations \( x_i, i = 1, \ldots, k \), is assigned a weight \( w_i \) according to

\[
w_i = K \left( \frac{||x_i - x_s||}{d_k} \right), \quad i = 1, \ldots, k
\]

where \( K \) is the weighting function given by weight.func, \( ||x_i - x_s|| \) is the euclidian distance of \( x_i \) and \( x_s \) and \( d_k \) is the euclidian distance of \( x_s \) to its \( k \)-th nearest neighbour. With these weights for each class \( A_g, g = 1, \ldots, G \), its weighted empirical mean \( \hat{\mu}_g \) and weighted empirical covariance matrix are computed. The estimated pooled (weighted) covariance matrix \( \hat{\Sigma} \) is then calculated from the individual weighted empirical class covariance matrices. If weighted.apriori is TRUE (the default), prior class probabilities are estimated according to:

\[
prior_g := \frac{\sum_{i=1}^{k} (w_i \cdot I(x_i \in A_g))}{\sum_{i=1}^{k} (w_i)}
\]

where \( I \) is the indicator function. If FALSE, equal priors for all classes are used. In analogy to Linear Discriminant Analysis, the decision rule for \( x_s \) is

\[
\hat{A} := \text{argmax}_{g \in 1, \ldots, G}(\text{posterior}_g)
\]

where

\[
\text{posterior}_g := \text{prior}_g \cdot \exp \left( -\frac{1}{2} t(x_s - \hat{\mu}_g) \hat{\Sigma}^{-1} (x_s - \hat{\mu}_g) \right)
\]

If \( \text{posterior}_g < 10^{-150} \forall g \in \{1, \ldots, G\} \), \( \text{posterior}_g \) is set to \( \frac{1}{G} \) for all \( g \in 1, \ldots, G \) and the test observation \( x_s \) is simply assigned to the class whose weighted mean has the lowest euclidian distance to \( x_s \).

Value

A list of class loclda containing the following components:

call The (matched) function call.
learn Matrix containing the values of the explanatory variables for all train observations.

grouping Factor specifying the class for each train observation.
**locpvs**

```
weight.func Value of the argument weight.func.
k Value of the argument k.
weighted.apriori Value of the argument weighted.apriori.
```

**Author(s)**

Marc Zentgraf (<marc-zentgraf@gmx.de>) and Karsten Luebke (<karsten.luebke@fom.de>)

**References**


**See Also**

`predict.loclda, lda`

**Examples**

```r
benchB3("lda")$llco.error
benchB3("loclda")$llco.error
```

---

**locpvs**

*Pairwise variable selection for classification in local models*

**Description**

Performs pairwise variable selection on subclasses.

**Usage**

```r
locpvs(x, subclasses, subclass.labels, prior=NULL, method="lda",
      vs.method = c("ks.test", "stepclass", "greedy.wilks"),
      niveau=0.05, fold=10, impr=0.1, direct="backward", out=FALSE, ...)
```

**Arguments**

- `x`: matrix or data frame containing the explanatory variables. `x` must consist of numerical data only.
- `subclasses`: vector indicating the subclasses (a factor)
- `subclass.labels`: must be a matrix with 2 columns, where the first column specifies the subclass and the second column the according upper class
- `prior`: prior probabilities for the classes. If not specified the prior probabilities will be set according to proportion in “subclasses”. If specified the order of prior probabilities must be the same as in “subclasses”.
- `method`: character, name of classification function (e.g. “lda” (default)).
vs.method  character, name of variable selection method. Must be one of "ks.test" (default), "stepclass" or "greedy.wilks".

niveau    used niveau for "ks.test"

fold      parameter for cross-validation, if "stepclass" is chosen 'vs.method'

impr      least improvement of performance measure desired to include or exclude any variable (<=1), if "stepclass" is chosen 'vs.method'

direct    direction of variable selection, if "stepclass" is chosen 'vs.method'. Must be one if "forward", "backward" (default) or "both".

out       indicator (logical) for textoutput during computation (slows down computation!), if "stepclass" is chosen 'vs.method'

...      further parameters passed to classification function ('method') or variable selection method ("vs.method")

Details

A call on pvs is performed using "subclasses" as grouping variable. See pvs for further details.

Value

An object of class 'locpvs' containing the following components:
pvs.result the complete output of the call to pvs (see pvs for further details
subclass.labels the subclass.labels as specified in function call

Author(s)

Gero Szepannek, <szepannek@statistik.tu-dortmund.de>, Christian Neumann

References


See Also

predict.locpvs for predicting 'locpvs' models and pvs

Examples

## this example might be a bit artificial, but it sufficiently shows how locpvs has to be used
## learn a locpvs-model on the Vehicle dataset
library("mlbench")
data("Vehicle")
subclass <- Vehicle$Class # use four car-types in dataset as subclasses
## meclight.default

### Minimal Error Classification

**Description**

Computer intensive method for linear dimension reduction that minimizes the classification error directly.

**Usage**

```r
meclight(x, ...)  
```

**Arguments**

- `x` (required if no formula is given as the principal argument.) A matrix or data frame containing the explanatory variables.
- `grouping` (required if no formula principal argument is given.) A factor specifying the class for each observation.
- `r` Dimension of projected subspace.
- `fold` Number of Bootstrap samples.
formula A formula of the form groups ~ x1 + x2 + .... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data Data frame from which variables specified in formula are preferentially to be taken.
subset An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
na.action A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)

... Further arguments passed to \texttt{lda}.

Details

Computer intensive method for linear dimension reduction that minimizes the classification error in the projected subspace directly. Classification is done by \texttt{lda}. In contrast to the reference function minimization is done by Nelder-Mead in \texttt{optim}.

Value

\begin{itemize}
  \item \texttt{method.model} An object of class ‘\texttt{lda}’.
  \item \texttt{Proj.matrix} Projection matrix.
  \item \texttt{B.error} Estimated bootstrap error rate.
  \item \texttt{B.impro} Improvement in \texttt{lda} error rate.
\end{itemize}

Author(s)

Maria Eveslage, Karsten Luebke, \texttt{<karsten.luebke@fom.de>}

References


See Also

\texttt{predict.meclight}

Examples

\begin{verbatim}
data(iris)
meclight.obj <- meclight(Species ~ ., data = iris)
meclight.obj
\end{verbatim}
Naive Bayes Classifier

Description

Computes the conditional a-posterior probabilities of a categorical class variable given independent predictor variables using the Bayes rule.

Usage

```r
## S3 method for class 'formula'
NaiveBayes(formula, data, ..., subset, na.action = na.pass)
## Default S3 method:
NaiveBayes(x, grouping, prior, usekernel = FALSE, fl = 0, ...)
```

Arguments

- `x`: a numeric matrix, or a data frame of categorical and/or numeric variables.
- `grouping`: class vector (a factor).
- `formula`: a formula of the form `class ~ x1 + x2 + ...`. Interactions are not allowed.
- `data`: a data frame of predictors (categorical and/or numeric).
- `prior`: the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If present, the probabilities should be specified in the order of the factor levels.
- `usekernel`: if TRUE a kernel density estimate (density) is used for density estimation. If FALSE a normal density is estimated.
- `fl`: Factor for Laplace correction, default factor is 0, i.e. no correction.
- `...`: arguments passed to `density`.
- `subset`: for data given in a data frame, an index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
- `na.action`: a function to specify the action to be taken if NAs are found. The default action is not to count them for the computation of the probability factors. An alternative is `na.omit`, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)

Details

This implementation of Naive Bayes as well as this help is based on the code by David Meyer in the package e1071 but extended for kernel estimated densities and user specified prior probabilities.

The standard naive Bayes classifier (at least this implementation) assumes independence of the predictor variables.
Value

An object of class "NaiveBayes" including components:

- **apriori**: Class distribution for the dependent variable.
- **tables**: A list of tables, one for each predictor variable. For each categorical variable a table giving, for each attribute level, the conditional probabilities given the target class. For each numeric variable, a table giving, for each target class, mean and standard deviation of the (sub-)variable or a object of class `density`.

Author(s)

Karsten Luebke,<karsten.luebke@fom.de>

See Also

- `predict.NaiveBayes`, `plot.NaiveBayes`, `naiveBayes`, `qda`

Examples

```r
data(iris)
m <- NaiveBayes(Species ~ ., data = iris)
```

---

**Nearest Mean Classification**

Description

Function for nearest mean classification.

Usage

```r
nm(x, ...)
```

## Default S3 method:
```r
nm(x, grouping, gamma = 0, ...)
```

## S3 method for class 'data.frame'
```r
nm(x, ...)
```

## S3 method for class 'matrix'
```r
nm(x, grouping, ..., subset, na.action = na.fail)
```

## S3 method for class 'formula'
```r
nm(formula, data = NULL, ..., subset, na.action = na.fail)
```
Arguments

- **x**: matrix or data frame containing the explanatory variables (required, if `formula` is not given)
- **grouping**: factor specifying the class for each observation (required, if `formula` is not given)
- **formula**: formula of the form `groups ~ x1 + x2 + ...`. That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators
- **data**: Data frame from which variables specified in `formula` are preferentially to be taken
- **gamma**: gamma parameter for rbf weight of the distance to mean. If `gamma=0` the posterior is 1 for the nearest class (mean) and 0 else.
- **subset**: An index vector specifying the cases to be used in the training sample. (Note: If given, this argument must be named!)
- **na.action**: specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is `na.omit`, which leads to rejection of cases with missing values on any required variable. (Note: If given, this argument must be named.)
- **...**: further arguments passed to the underlying `sknn` function

Details

`nm` is calling `sknn` with the class means as observations. If `gamma>0` a gaussian like density is used to weight the distance to the class means `weight=exp(-gamma*distance)`. This is similar to an rbf kernel. If the distances are large it may be useful to `scale` the data first.

Value

A list containing the function call and the class means (`learn`).

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

See Also

- `sknn`, `rda`, `knn`

Examples

```r
data(B3)
x <- nm(PHASEN ~ ., data = B3)
x$learn
x <- nm(PHASEN ~ ., data = B3, gamma = 0.1)
predict(x)$post
```
Description

Provides a multiple figure array which shows the classification of observations based on classification methods (e.g. lda, qda) for every combination of two variables. Moreover, the classification borders are displayed and the apparent error rates are given in each title.

Usage

```
partimat(x,...)
```

## Default S3 method:
```
partimat(x, grouping, method = "lda", prec = 100,
  nplots.vert, nplots.hor, main = "Partition Plot", name, mar,
  plot.matrix = FALSE, plot.control = list(), ...)
```

## S3 method for class 'data.frame'
```
partimat(x, ...)
```

## S3 method for class 'matrix'
```
partimat(x, grouping, ..., subset, na.action = na.fail)
```

## S3 method for class 'formula'
```
partimat(formula, data = NULL, ..., subset, na.action = na.fail)
```

Arguments

- **x**: matrix or data frame containing the explanatory variables (required, if `formula` is not given).
- **grouping**: factor specifying the class for each observation (required, if `formula` is not given).
- **formula**: formula of the form `groups ~ x1 + x2 + ....` That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
- **method**: the method the classification is based on, currently supported are: lda, qda, rpart, naiveBayes, rda, sknn and svmlight.
- **prec**: precision used to draw the classification borders (the higher the more precise; default: 100).
- **data**: Data frame from which variables specified in formula are preferentially to be taken.
- **nplots.vert**: number of rows in the multiple figure array
- **nplots.hor**: number of columns in the multiple figure array
- **subset**: index vector specifying the cases to be used in the training sample. (Note: If given, this argument must be named.)
**na.action**  
specify the action to be taken if NAs are found. The default action is for the  
procedure to fail. An alternative is **na.omit**, which leads to rejection of cases  
with missing values on any required variable. (Note: If given, this argument  
must be named.)

**main**  
title

**name**  
Variable names to be printed at the axis / into the diagonal.

**mar**  
umerical vector of the form c(bottom, left, top, right) which gives  
the lines of margin to be specified on the four sides of the plot. Defaults are  
rep(0, 4) if plot.matrix = TRUE, c(5, 4, 2, 1) + 0.1 otherwise.

**plot.matrix**  
logical; if TRUE, like a scatterplot matrix; if FALSE (default) uses less space and  
aranges the plots “optimal” (using a fuzzy algorithm) in an array by plotting  
each pair of variables once.

**plot.control**  
A list containing further arguments passed to the underlying plot functions (and  
to **drawparti**).

...  
Further arguments passed to the classification method (through **drawparti**).

**Note**

Warnings such as ‘parameter “xyz” couldn’t be set in high-level plot function’ are expected, if  
making use of ....

**Author(s)**

Karsten Luebke, <karsten.luebke@fom.de>, Uwe Ligges, Irina Czogiel

**See Also**

for much more fine tuning see **drawparti**

**Examples**

```
library(MASS)
data(iris)
partimat(Species ~ ., data = iris, method = "lda")
## Not run:
partimat(Species ~ ., data = iris, method = "lda",
         plot.matrix = TRUE, imageplot = FALSE) # takes some time ...

## End(Not run)
```
plineplot  

Plotting marginal posterior class probabilities

Description

For a given variable the posteriori probabilities of the classes given by a classification method are plotted. The variable need not be used for the actual classification.

Usage

plineplot(formula, data, method, x, col.wrong = "red", ylim = c(0, 1), loo = FALSE, mfrow, ...)

Arguments

formula   formula of the form groups ~ x1 + x2 + .... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data      Data frame from which variables specified in formula are preferentially to be taken.
method    character, name of classification function (e.g. "lda").
x         variable that should be plotted. See examples.
col.wrong color to use for misclassified objects.
ylim      ylim for the plot.
loo       logical, whether leave-one-out estimate is used for prediction
mfrow     number of rows and columns in the graphics device, see par. If missing, number of rows equals number of classes, and 1 column.
...       further arguments passed to the underlying classification method or plot functions.

Value

The actual error rate.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

See Also

partimat
plot.NaiveBayes

Examples

library(MASS)

# The name of the variable can be used for x
data(B3)
plineplot(PHASEN ~ ., data = B3, method = "lda",
          x = "EWAJW", xlab = "EWAJW")

# The plotted variable need not be in the data
data(iris)
iris2 <- iris[, c(1,3,5)]
plineplot(Species ~ ., data = iris2, method = "lda",
          x = iris[, 4], xlab = "Petal.Width")

Description

Visualizes the marginal probabilities of predictor variables given the class.

Usage

### S3 method for class 'NaiveBayes'
plot(x, vars, n = 1000, legendplot = TRUE, lty, col,
     ylab = "Density", main = "Naive Bayes Plot", ...)

Arguments

- **x**: an object of class `NaiveBayes`
- **vars**: variables to be plotted. If missing, all predictor variables are plotted.
- **n**: number of points used to plot the density line.
- **legendplot**: logical, whether to print a `legend`
- **lty**: line type for different classes, defaults to the first `length(x$apriori)` colors of the current palette in use.
- **col**: color for different classes, defaults to `rainbow(length(x$apriori))`.
- **ylab**: label for y-axis.
- **main**: title of the plots.
- **...**: further arguments passed to the underlying plot functions.

Details

For metric variables the estimated density is plotted. For categorial variables `mosaicplot` is called.
Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

See Also

NaiveBayes

Examples

data(iris)

mN <- NaiveBayes(Species ~ ., data = iris)
plot(mN)

mK <- NaiveBayes(Species ~ ., data = iris, usekernel = TRUE)
plot(mK)

Description

Barplot of information values to compare discriminator of the transformed variables.

Usage

## S3 method for class 'woe'
plot(x, type = c("IV", "woes"), ...)

Arguments

x

An object of class woe.

type

Character to specify the plot type, see below. Either "IV" (default) or "woes".

... Further arguments to be passed to the barplot function.

Details

For type="IV" a barplot of information values for all transformed variables. A thumb rule of interpretation is that Values above 0.3 are considered as strongly discriminative where values below 0.02 are considered to characterize unpredictable variables. For type="woes" for each variable the relative frequencies of all transformed levels are plotted.

Value

No value is returned.

Author(s)

Gero Szepannek
References


See Also

`woe`, `predict.woe`

Examples

```r
# see examples in ?woe
```

---

`predict.loclda`  
*Localized Linear Discriminant Analysis (LocLDA)*

Description

Classifies new observations using parameters determined by the `loclda`-function.

Usage

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

Arguments

- `object`: Object of class `loclda`.
- `newdata`: Data frame of cases to be classified.
- `...`: Further arguments are ignored.

Value

A list with components:

- `class`: Vector (of class `factor`) of classifications.
- `posterior`: Posterior probabilities for the classes. For details of computation see `loclda` (+ normalization so posterior-values add up to 1 for each observation).
- `all.zero`: Vector (of class `integer`) indicating for which rows of `newdata` all corresponding posterior-values are $< 10^{-150}$ before normalization. Those observations are assigned to the class to whose (locally weighted) centroid they have the lowest euclidian distance.

Author(s)

Marc Zentgraf (<marc-zentgraf@gmx.de>) and Karsten Luebke (<karsten.luebke@fom.de>)
predict.locpvs

See Also
   loclda

Examples

data(B3)
x <- loclda(PHASEN ~ ., data = B3, subset = 1:80)
predict(x, B3[-(1:80),])

Description

Prediction of class membership and posterior probabilities in local models using pairwise variable selection.

Usage
   ## S3 method for class 'locpvs'
   predict(object, newdata, quick = FALSE, return.subclass.prediction = TRUE, ...)

Arguments

object                  an object of class `locpvs`, as that created by the function `locpvs`
newdata                a data frame or matrix containing new data. If not given the same datas as used for training the `pvs`-model are used.
quick                 indicator (logical), whether a quick, but less accurate computation of posterior probabilities should be used or not.
return.subclass.prediction
                       indicator (logical), whether the returned object includes posterior probabilities for each date in each subclass
...               Further arguments are passed to underlying predict calls.

Details

Posterior probabilities are predicted as if object is a standard `pvs`-model with the subclasses as classes. Then the posterior probabilities are summed over all subclasses for each class. The class with the highest value becomes the prediction.

If `quick=FALSE` the posterior probabilities for each case are computed using the pairwise coupling algorithm presented by Hastie, Tibshirani (1998). If `quick=FALSE` a much quicker solution is used, which leads to less accurate posterior probabilities. In almost all cases it doesn’t have a negative effect on the classification result.
Value

a list with components:

- **class**: the predicted (upper) classes
- **posterior**: posterior probabilities for the (upper) classes
- **subclass.posterior**
  (only if "return.subclass.prediction=TRUE". A matrix containing posterior probabilities for the subclasses.

Author(s)

Gero Szepannek, <szepannek@statistik.tu-dortmund.de>, Christian Neumann

References


See Also

- locpvs for learning `locpvs`-models and examples for applying this predict method, pvs for pairwise variable selection without modeling subclasses, predict.pvs for predicting `pvs`-models

---

**Description**

Classify multivariate observations in conjunction with meclight and lda.

**Usage**

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

**Arguments**

- **object**: Object of class meclight.
- **newdata**: Data frame of cases to be classified or, if object has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector.
- **...**
  currently ignored

**Details**

Classify multivariate observations in conjunction with meclight and lda.
predict.NaiveBayes

Value

class The estimated class (factor).
posterior Posterior probabilities for the classes.

Author(s)
Karsten Luebke, <karsten.luebke@fom.de>

References

See Also
meclight

Examples

data(iris)
meclight.obj <- meclight(Species ~ ., data = iris)
predict(meclight.obj, iris)

predict.NaiveBayes  Naive Bayes Classifier

Description
Computes the conditional a-posterior probabilities of a categorical class variable given independent predictor variables using the Bayes rule.

Usage

## S3 method for class 'NaiveBayes'
predict(object, newdata, threshold = 0.001, ...)

Arguments

object An object of class "naiveBayes".
newdata A dataframe with new predictors.
threshold Value replacing cells with 0 probabilities.
... passed to dkernel function if neccessary.
This implementation of Naive Bayes as well as this help is based on the code by David Meyer in the package e1071 but extended for kernel estimated densities. The standard naive Bayes classifier (at least this implementation) assumes independence of the predictor variables. For attributes with missing values, the corresponding table entries are omitted for prediction.

A list with the conditional a-posterior probabilities for each class and the estimated class are returned.

Karsten Luebke, <karsten.luebke@fom.de>

NaiveBayes, dkernelnaiveBayes, qda

data(iris)
m <- NaiveBayes(Species ~ ., data = iris)
predict(m)

predict.pvs       predict method for pvs objects

Prediction of class membership and posterior probabilities using pairwise variable selection.

## S3 method for class 'pvs'
predict(object, newdata, quick = FALSE, detail = FALSE, ...)

object an object of class `pvs`, as that created by the function “pvs”
newdata a data frame or matrix containing new data. If not given the same datas as used for training the ‘pvs’-model are used.
quick indicator (logical), whether a quick, but less accurate computation of posterior probabilities should be used or not.
detail indicator (logical), whether the returned object includes additional information about the posterior probabilities for each date in each submodel.
... Further arguments are passed to underlying predict calls.
Details

If “quick=FALSE” the posterior probabilities for each case are computed using the pairwise coupling algorithm presented by Hastie, Tibshirani (1998). If “quick=FALSE” a much quicker solution is used, which leads to less accurate posterior probabilities. In almost all cases it doesn’t have a negative effect on the classification result.

Value

a list with components:

- **class**: the predicted classes
- **posterior**: posterior probabilities for the classes
- **details** (only if “details=TRUE”. A list containing matrices of posterior probabilities computed by the classification method for each case and class pair.

Author(s)

Gero Szepannek, <szepannek@statistik.tu-dortmund.de>, Christian Neumann

References


See Also

For more details and examples how to use this predict method, see *pvs*.

---

**predict.rda**

*Regularized Discriminant Analysis (RDA)*

Description

Classifies new observations using parameters determined by the *rda*-function.

Usage

```r
## S3 method for class 'rda'
predict(object, newdata, posterior = TRUE,
        aslist = TRUE, ...)
```
predict.sknn

Arguments

object Object of class rda.
newdata Data frame (or matrix) of cases to be classified.
posterior Logical; indicates whether a matrix of posterior probabilities over all classes for each observation shall be returned in addition to classifications.
aslist Logical; if TRUE, a list containing classifications and posterior probabilities is returned, otherwise a vector with an attribute 'posterior'.
... currently unused

Value

Depends on the value of argument 'aslist':

Either a vector (of class factor) of classifications that (optionally) has an attribute 'posterior' containing the posterior probability matrix, or

A list with elements 'class' and 'posterior'.

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

See Also

rda

Examples

data(iris)
x <- rda(Species ~ ., data = iris, gamma = 0.05, lambda = 0.2)
predict(x, iris[, 1:4])

predict.sknn Simple k Nearest Neighbours Classification

Description

Classifies new observations using the sknn learned by the sknn-function.

Usage

## S3 method for class 'sknn'
predict(object, newdata,...)

Arguments

object Object of class sknn.
newdata Data frame (or matrix) of cases to be classified.
... ...
Value

A list with elements ‘class’ and ‘posterior’.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

See Also

sknn, knn

Examples

data(iris)
x <- sknn(Species ~ ., data = iris)
predict(x, iris)
x <- sknn(Species ~ ., gamma = 10, kn = 10, data = iris)
predict(x, iris)

Description

Predicts new observations using the SVM learned by the svmlight-function.

Usage

## S3 method for class 'svmlight'
predict(object, newdata, scal = TRUE, ...)

Arguments

object Object of class svmlight.
newdata Data frame (or matrix) of cases to be predicted.
scal Logical, whether to scale membership values via e.scal.
...

Value

If a classification is learned (type="C") in svmlight a list with elements ‘class’ and ‘posterior’ (scaled, if scal = TRUE).

If a Regression is learned (type="R") in svmlight the predicted values.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>
predict.woe

See Also

svmlight, svm

Examples

## Not run:
data(iris)
x <- svmlight(Species ~ ., data = iris)
predict(x, iris)

## End(Not run)

<table>
<thead>
<tr>
<th>predict.woe</th>
<th>Weights of evidence</th>
</tr>
</thead>
</table>

Description

Applies weight of evidence transform of factor variables for binary classification based on a model of class woe.

Usage

## S3 method for class 'woe'
predict(object, newdata, replace = TRUE, ...)

Arguments

- **object**: Object resulting from a call of woe.
- **newdata**: A matrix or data frame where WOE transform should be applied of the same dimension as the data used for training the woe object.
- **replace**: Logical flag specifying whether the original factor variables should be kept in the output.
- **...**: Currently not used.

Value

Data frame including the transformed numeric woe variables.

Author(s)

Gero Szepannek

References

Pairwise variable selection for classification

Description

Pairwise variable selection for numerical data, allowing the use of different classifiers and different variable selection methods.

Usage

```r
pvs(x, ...) # Default S3 method:
pvs(x, grouping, prior=NULL, method="lda",
   vs.method=c("ks.test","stepclass","greedy.wilks"), niveau=0.05,
   fold=10, impr=0.1, direct="backward", out=FALSE, ...)

# S3 method for class 'formula'
pvs(formula, data = NULL, ...)
```

Arguments

- `x` matrix or data frame containing the explanatory variables (required, if `formula` is not given). `x` must consist of numerical data only.
- `formula` A formula of the form `groups ~ x1 + x2 + ...`. That is, the response is the grouping factor (the classes) and the right hand side specifies the (numerical) discriminators. Interaction terms are not supported.
- `data` data matrix (rows=cases, columns=variables)
- `grouping` class indicator vector (a factor)
- `prior` prior probabilities for the classes. If not specified the prior probabilities will be set according to proportion in “grouping”. If specified the order of prior probabilities must be the same as in “grouping”.
- `method` character, name of classification function (e.g. “lda” (default)).
- `vs.method` character, name of variable selection method. Must be one of “ks.test” (default), “stepclass” or “greedy.wilks”.
- `niveau` used niveau for “ks.test”
- `fold` parameter for cross-validation, if “stepclass” is chosen ‘vs.method’
impr least improvement of performance measure desired to include or exclude any variable (<=1), if “stepclass” is chosen ‘vs.method’
direct direction of variable selection, if “stepclass” is chosen ‘vs.method’. Must be one if “forward”, “backward” (default) or “both”.
out indicator (logical) for textoutput during computation (slows down computation!), if “stepclass” is chosen ‘vs.method’

... further parameters passed to classification function (‘method’) or variable selection method (‘vs.method’)

Details

The classification “method” (e.g. ‘lda’) must have its own ‘predict’ method (like ‘predict.lda’ for ‘lda’) returns a list with an element ‘posterior’ containing the posterior probabilities. It must be able to deal with matrices as in method(x, grouping, ...). Examples of such classification methods are ‘lda’, ‘qda’, ‘rda’, ‘NaiveBayes’ or ‘sknn’.

For the classification methods “svm” and “randomForest” there are special routines implemented, to make them work with ‘pvs’ method even though their ‘predict’ methods don’t provide the demanded posteriors. However those two classifiers can not be used together with variable selection method “stepclass”.

‘pvs’ performs a variable selection using the selection method chosen in ‘vs.method’ for each pair of classes in ‘x’. Then for each pair of classes a submodel using ‘method’ is trained (using only the earlier selected variables for this class-pair).

If ‘method’ is “ks.test”, then for each variable the empirical distribution functions of the cases of both classes are compared via “ks.test”. Only variables with a p-values below ‘niveau’ are used for training the submodel for this pair of classes.

If ‘method’ is “stepclass” the variable selection is performed using the “stepclass” method.

If ‘method’ is “greedy.wilks” the variable selection is performed using Wilk’s lambda criterion.

Value

An object of class ‘pvs’ containing the following components:

- classes: the classes in grouping
- prior: used prior probabilities
- method: name of used classification function
- vs.method: name of used function for variable selection
- submodels: containing a list of submodels. For each pair of classes there is a list element being another list of 3 containing the class-pair of this submodel, the selected variables for the subspace of classes and the result of the trained classification function.
- call: the (matched) function call

Author(s)

Gero Szepannek, <szepannek@statistik.tu-dortmund.de>, Christian Neumann
References


See Also

predict.pvs for predicting ‘pvs’ models and locpvs for pairwise variable selection in local models of several subclasses

Examples

```r
## Example 1: learn an "lda" model on the waveform data using pairwise variable
## selection (pvs) using "ks.test" and compare it to using lda without pvs

library("mlbench")
trainset <- mlbench.waveform(300)
pvsmodel <- pvs(trainset$x, trainset$classes, niveau=0.05) # default: using method="lda"
## short summary, showing the class-pairs of the submodels and the selected variables
pvsmodel

testset <- mlbench.waveform(500)
## prediction of the test data set:
prediction <- predict(pvsmodel, testset$x)

## calculating the test error rate
1-sum(testset$classes==prediction$class)/length(testset$classes)
## Bayes error is 0.149

## comparison to performance of simple lda
ldamodel <- lda(trainset$x, trainset$classes)
LDAprediction <- predict(ldamodel, testset$x)

## test error rate
1-sum(testset$classes==LDAprediction$class)/length(testset$classes)

## Example 2: learn a "qda" model with pvs on half of the Satellite dataset,
## using "ks.test"

library("mlbench")
data("Satellite")

model <- pvs(classes ~ ., Satellite[1:3218,], method="qda", vs.method="ks.test")
## short summary, showing the class-pairs of the submodels and the selected variables
model
```
quadplot

## now predict on the rest of the data set:
## pred <- predict(model, Satellite[3219:6435,]) # takes some time
pred <- predict(model, Satellite[3219:6435,], quick=TRUE) # that's much quicker

## now you can look at the predicted classes:
pred$class
## or the posterior probabilities:
pred$posterior

---

### Description

For a 4 class discrimination problem the membership values of each class are visualized in a 3 dimensional barycentric coordinate system.

### Usage

```r
quadplot(e = NULL, f = NULL, g = NULL, h = NULL, angle = 75,
          scale.y = 0.6, label = 1:4, labelcol = rainbow(4),
          labelpch = 19, labelcex = 1.5, main = "", s3d.control = list(),
          simplex.control = list(), legend.control = list(), ...) #
```

### Arguments

- `e`: either a matrix with 4 columns representing the membership values or a vector with the membership values of the first class
- `f`: vector with the membership values of the second class
- `g`: vector with the membership values of the third class
- `h`: vector with the membership values of the fourth class
- `angle`: angle between x and y axis
- `scale.y`: scale of y axis related to x- and z axis
- `label`: label for the classes
- `labelcol`: colors to use for the labels
- `labelpch`: pch for the labels
- `labelcex`: cex for the labels
- `main`: main title of the plot
- `s3d.control`: a list with further arguments passed to the underlying `scatterplot3d` function call that sets up the plot
- `simplex.control`: a list with further arguments passed to the underlying function call that draws the barycentric coordinate system
- `legend.control`: a list with further arguments passed to the underlying function call that adds the legend
- `...`: further arguments passed to the underlying plot function that draws the data points
Details

The membership values are calculated with `quadtrafo` and plotted with `scatterplot3d`.

Value

A `scatterplot3d` object.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>, and Uwe Ligges

References


See Also

`triplot`, `scatterplot3d`

Examples

```r
library("MASS")
data(B3)
opar <- par(mfrow = c(1, 2), pty = "s")
posterior <- predict(lda(PHASEN ~ ., data = B3))$post
s3d <- quadplot(posterior, col = rainbow(4)[B3$PHASEN],
  labelpch = 22:25, labelcex = 0.8,
  pch = (22:25)[apply(posterior, 1, which.max)],
  main = "LDA posterior assignments")
quadlines(centerlines(4), sp = s3d, lty = "dashed")
posterior <- predict(qda(PHASEN ~ ., data = B3))$post
s3d <- quadplot(posterior, col = rainbow(4)[B3$PHASEN],
  labelpch = 22:25, labelcex = 0.8,
  pch = (22:25)[apply(posterior, 1, which.max)],
  main = "QDA posterior assignments")
quadlines(centerlines(4), sp = s3d, lty = "dashed")
par(opar)
```

---

**rda**

*Regularized Discriminant Analysis (RDA)*

**Description**

Builds a classification rule using regularized group covariance matrices that are supposed to be more robust against multicollinearity in the data.
Usage

rda(x, ...)

## Default S3 method:
rda(x, grouping = NULL, prior = NULL, gamma = NA,
    lambda = NA, regularization = c(gamma = gamma, lambda = lambda),
    crossval = TRUE, fold = 10, train.fraction = 0.5,
    estimate.error = TRUE, output = FALSE, startsimplex = NULL,
    max.iter = 100, trafo = TRUE, simAnn = FALSE, schedule = 2,
    T.start = 0.1, halflife = 50, zero.temp = 0.01, alpha = 2,
    K = 100, ...)

## S3 method for class 'formula'
rda(formula, data, ...)

Arguments

x Matrix or data frame containing the explanatory variables (required, if formula is not given).

formula Formula of the form `groups ~ x1 + x2 + ...`.

data A data frame (or matrix) containing the explanatory variables.

grouping (Optional) a vector specifying the class for each observation; if not specified, the first column of `data` is taken.

prior (Optional) prior probabilities for the classes. Default: proportional to training sample sizes. "prior=1" indicates equally likely classes.

gamma, lambda, regularization One or both of the rda-parameters may be fixed manually. Unspecified parameters are determined by minimizing the estimated error rate (see below).

crossval Logical. If TRUE, in the optimization step the error rate is estimated by Cross-Validation, otherwise by drawing several training- and test-samples.

fold The number of Cross-Validation- or Bootstrap-samples to be drawn.

train.fraction In case of Bootstrapping: the fraction of the data to be used for training in each Bootstrap-sample; the remainder is used to estimate the misclassification rate.

estimate.error Logical. If TRUE, the apparent error rate for the final parameter set is estimated.

output Logical flag to indicate whether text output during computation is desired.

startsimplex (Optional) a starting simplex for the Nelder-Mead-minimization.

max.iter Maximum number of iterations for Nelder-Mead.

trafo Logical; indicates whether minimization is carried out using transformed parameters.

simAnn Logical; indicates whether Simulated Annealing shall be used.

schedule Annealing schedule 1 or 2 (exponential or polynomial).

T.start Starting temperature for Simulated Annealing.

halflife Number of iterations until temperature is reduced to a half (schedule 1).

zero.temp Temperature at which it is set to zero (schedule 1).
alpha     Power of temperature reduction (linear, quadratic, cubic,...) (schedule 2).
K         Number of iterations until temperature = 0 (schedule 2).
...       currently unused

Details

J.H. Friedman (see references below) suggested a method to fix almost singular covariance matrices in discriminant analysis. Basically, individual covariances as in QDA are used, but depending on two parameters ($\gamma$ and $\lambda$), these can be shifted towards a diagonal matrix and/or the pooled covariance matrix. For ($\gamma = 0$, $\lambda = 0$) it equals QDA, for ($\gamma = 0$, $\lambda = 1$) it equals LDA.

You may fix these parameters at certain values or leave it to the function to try to find “optimal” values. If one parameter is given, the other one is determined using the R-function 'optimize'. If no parameter is given, both are determined numerically by a Nelder-Mead-(Simplex-)algorithm with the option of using Simulated Annealing. The goal function to be minimized is the (estimated) misclassification rate; the misclassification rate is estimated either by Cross-Validation or by repeatedly dividing the data into training- and test-sets (Boostrapping).

Warning: If these sets are small, optimization is expected to produce almost random results. We recommend to adjust the parameters manually in such a case. In all other cases it is recommended to run the optimization several times in order to see whether stable results are gained.

Since the Nelder-Mead-algorithm is actually intended for continuous functions while the observed error rate by its nature is discrete, a greater number of Bootstrap-samples might improve the optimization by increasing the smoothness of the response surface (and, of course, by reducing variance and bias). If a set of parameters leads to singular covariance matrices, a penalty term is added to the misclassification rate which will hopefully help to maneuver back out of singularity (so do not worry about error rates greater than one during optimization).

Value

A list of class rda containing the following components:

call     The (matched) function call.
regularization vector containing the two regularization parameters (gamma, lambda)
classes the names of the classes
prior the prior probabilities for the classes
error.rate apparent error rate (if computation was not suppressed), and, if any optimization took place, the final (cross-validated or bootstrapped) error rate estimate as well.
means Group means.
covariances Array of group covariances.
covpooled Pooled covariance.
converged (Logical) indicator of convergence (only for Nelder-Mead).
iter Number of iterations actually performed (only for Nelder-Mead).
More details

The explicit definition of $\gamma$, $\lambda$ and the resulting covariance estimates is as follows:

The pooled covariance estimate $\hat{\Sigma}$ is given as well as the individual covariance estimates $\hat{\Sigma}_k$ for each group.

First, using $\lambda$, a convex combination of these two is computed:

$$\hat{\Sigma}_k(\lambda) := (1 - \lambda)\hat{\Sigma}_k + \lambda\hat{\Sigma}.$$ 

Then, another convex combination is constructed using the above estimate and a (scaled) identity matrix:

$$\hat{\Sigma}_k(\lambda, \gamma) = (1 - \gamma)\hat{\Sigma}_k(\lambda) + \gamma\frac{1}{d}\text{tr}[\hat{\Sigma}_k(\lambda)]I.$$

The factor $\frac{1}{d}\text{tr}[\hat{\Sigma}_k(\lambda)]$ in front of the identity matrix $I$ is the mean of the diagonal elements of $\hat{\Sigma}_k(\lambda)$, so it is the mean variance of all $d$ variables assuming the group covariance $\hat{\Sigma}_k(\lambda)$.

For the four extremes of $(\gamma, \lambda)$ the covariance structure reduces to special cases:

- $(\gamma = 0, \lambda = 0)$: QDA - individual covariance for each group.
- $(\gamma = 0, \lambda = 1)$: LDA - a common covariance matrix.
- $(\gamma = 1, \lambda = 0)$: Conditional independent variables - similar to Naive Bayes, but variable variances within group (main diagonal elements) are equal.
- $(\gamma = 1, \lambda = 1)$: Classification using euclidean distance - as in previous case, but variances are the same for all groups. Objects are assigned to group with nearest mean.

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

References


See Also

predict.rda, lda, qda

Examples

data(iris)
x <- rda(Species ~ ., data = iris, gamma = 0.05, lambda = 0.2)
predict(x, iris)
shardsplot

Plotting Eight Direction Arranged Maps or Self-Organizing Maps

Description

Plotting method for objects of class EDAM or som.

Usage

```r
shardsplot(object, plot.type = c("eight", "four", "points", "n"),
            expand = 1, stk = TRUE, grd = FALSE, standardize = FALSE,
            data.or = NA, label = FALSE, plot = TRUE, classes = 0,
            vertices = TRUE, classcolors = "rainbow", wghts = 0,
            xlab = "Dimension 1", ylab = "Dimension 2", xaxs = "i",
            yaxs = "i", plot.data.column = NA,
            log.classes = FALSE, revert.colors = FALSE, ...)

level_shardsplot(object, par.names, rows = 1:NCOL(object$data),
                  centers = rep(NA, length(par.names)), class.labels = NA,
                  revert.colors = rep(FALSE, length(par.names)),
                  log.classes = rep(FALSE, length(par.names)),
                  centeredcolors = colorRamp(c("red", "white", "blue")),
                  mfrow = c(2, 2), plot.type = c("eight", "four", "points", "n"),
                  expand = 1, stk = TRUE, grd = FALSE, standardize = FALSE,
                  label = FALSE, plot = TRUE, vertices = TRUE, classcolors = "topo",
                  wghts = 0, xlab = "Dimension 1", ylab = "Dimension 2",
                  xaxs = "i", yaxs = "i", ...)
```

## S3 method for class 'EDAM'

plot(...)

Arguments

- **object**: an object of class EDAM or som.
- **par.names**: names used to label the data columns
- **rows**: vector with indices of columns to be plotted
- **centers**: vector of type numeric defining the class centers for the data. NA if data does not have a center.
- **class.labels**: matrix of type text and dimension(3, NROW(object$data)) defining the labels to be used for maximum, minimum and central value.
- **centeredcolors**: colors to represent the classes with a central value
- **mfrow**: parameter defining number of plots on a page. see `par`
- **plot.type**: a character giving the shape of the shards. Available are "eight" and "four" for octagons resp. rectangles, and "points" for points. If plot.type is "n", no shards are plotted at all.
expand a numeric giving the relative expansion of the axes. A value greater than one implies smaller shards. Varying expand can be sensible for visual reasons.

stck logical. If TRUE the cells are varied continuously corresponding to the differences of direct neighbors in the origin space. Within this variation the relative order of the cells is always preserved.

grd logical. If TRUE (which automatically sets stck to TRUE), the variation of cells is restricted to their original discrete values.

standardize logical. If TRUE, then the measurements in object$preimages are standardized before calculating Euclidean distances. Measurements are standardized for each variable by dividing by the variable’s standard deviation. Meaningless if object$preimages is a dissimilarity matrix.

data.or original data and classes where the first k columns are variables and the (k+1)-th column are the classes. If defined and class of object is som, data.or is used to assign a class to each codebook. There a codebook receives the class, from which the majority of its assigned objects origins.

label logical. If TRUE, the shards are labeled by the rownames of the preimages.

plot logical. If FALSE, all graphical output is suppressed.

classes a vector giving alternative classes for objects of class EDAM; classes have to be given in the original order of the data to which EDAM was applied.

vertices logical. If TRUE the grid is drawn.

classcolors colors to represent the classes, or a character giving the colorscale for the classes. Since now available scales are rainbow, topo and gray.

wghts an optional vector of length k giving relative weights of the variables in computing Euclidean distances. Meaningless if object$preimages is a dissimilarity matrix.

xaxs see par

yaxs see par

xlab see par

ylab see par

... further plotting parameters.

plot.data.column column index defining from data.or providing the data used to calculate the coloring of the cells.

log.classes boolean indicating that the data should be transformed with the logarithmic function before calculating the cell coloring

revert.colors boolean indicating that the colorscale should be reverted.

Details

level_shardsplot uses multiple shardsplot representations of a SOM in order to depict how the data used to calculate the SOM is distribution across the map. Two representations are possible for the data, first with a single color ramp from the minimum value to the maximum value. The second representation is useful for data for which a basic value exists somewhere between minimum and maximum for which a special color representation should be used (e.g. 0 is indicated with white).
If `plotNtype` is "four" or "eight", the shape of each shard depends on the relative distances of the actual object or codebook to its up to eight neighbours. If `plotNtype` is "eight", shardsplot corresponds to the representation method suggested by Cottrell and de Bodt (1996) for Kohonen Self-Organizing Maps. If `plotNtype` is "points", shardsplot reduces to a usual scatter plot.

Value

The following list is (invisibly) returned:

- `Cells.ex` - the images of the visualized data
- `S` - the criterion of the visualization

Author(s)

Nils Raabe, `level_shardsplot` function from Dominik Reusser

References


See Also

- CRAN package `EDAM`, `TopoS`, `som`

Examples

```r
# Compute clusters and an Eight Directions Arranged Map for the country data. Plotting the result.
data(countries)
logcount <- log(countries[, 2:7])
sdlogcount <- apply(logcount, 2, sd)
logstand <- t((t(logcount) / sdlogcount) * c(1, 2, 6, 5, 3))
cclasses <- cutree(hclust(dist(logstand)), k = 6)
countryEDAM <- EDAM(logstand, classes = cclasses, sa = FALSE, iter.max = 10, random = FALSE)
plot(countryEDAM, vertices = FALSE, label = TRUE, stck = FALSE)

# Compute and plot a Self-Organizing Map for the iris data
data(iris)
library(som)
irissom <- som(iris[, 1:4], xdim = 6, ydim = 14)
shardsplot(irissom, data.or = iris, vertices = FALSE)

opar <- par(xpd = NA)
legend(7.5, 6.1, col = rainbow(3), xjust = 0.5, yjust = 0,
      legend = levels(iris[, 5]), pch = 16, horiz = TRUE)
par(opar)

level_shardsplot(irissom, par.names = names(iris),
                 class.labels = NA, mfrow = c(2,2))
```
Description

Function for simple knn classification.

Usage

sknn(x, ...)

## Default S3 method:
sknn(x, grouping, kn = 3, gamma=0, ...)
## S3 method for class 'data.frame'
sknn(x, ...)
## S3 method for class 'matrix'
sknn(x, grouping, ..., subset, na.action = na.fail)
## S3 method for class 'formula'
sknn(formula, data = NULL, ..., subset, na.action = na.fail)

Arguments

x             matrix or data frame containing the explanatory variables (required, if formula is not given).
grouping      factor specifying the class for each observation (required, if formula is not given).
formula       formula of the form groups ~ x1 + x2 + .... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data          Data frame from which variables specified in formula are preferentially to be taken.
kn            Number of nearest neighbours to use.
gamma         gamma parameter for rbf in knn. If gamma=0 ordinary knn classification is used.
subset        An index vector specifying the cases to be used in the training sample. (Note: If given, this argument must be named.)
na.action     specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit, which leads to rejection of cases with missing values on any required variable. (Note: If given, this argument must be named.)
...           currently unused

Details

If gamma>0 an gaussian like density is used to weight the classes of the kn nearest neighbors. weight=exp(-gamma*distance). This is similar to an rbf kernel. If the distances are large it may be useful to scale the data first.
Value

A list containing the function call.

Author(s)

Karsten Luebke, <karsten.luebke@fom.de>

See Also

predict.sknn.knn

Examples

data(iris)
x <- sknn(Species ~ ., data = iris)
x <- sknn(Species ~ ., gamma = 4, data = iris)

stepclass

Stepwise variable selection for classification

Description

Forward/backward variable selection for classification using any specified classification function
and selecting by estimated classification performance measure from ucppm.

Usage

stepclass(x, ...)

## Default S3 method:
stepclass(x, grouping, method, improvement = 0.05, maxvar = Inf,
start.vars = NULL, direction = c("both", "forward", "backward"),
criterion = "CR", fold = 10, cv.groups = NULL, output = TRUE,
min1var = TRUE, ...)
## S3 method for class 'formula'
stepclass(formula, data, method, ...)

Arguments

x
matrix or data frame containing the explanatory variables (required, if formula is not given).

formula
A formula of the form groups ~ x1 + x2 + .... That is, the response is the
 Grouping factor and the right hand side specifies the (non-factor) discriminators.
Interaction terms are not supported.

data
data matrix (rows=cases, columns=variables)

grouping
class indicator vector (a factor)
**method**
character, name of classification function (e.g. "lda").

**improvement**
least improvement of performance measure desired to include or exclude any variable (<=1)

**maxvar**
maximum number of variables in model

**start.vars**
set variables to start with (indices or names). Default is no variables if ‘direction’ is “forward” or “both”, and all variables if ‘direction’ is “backward”.

**direction**
“forward”, “backward” or “both” (default)

**criterion**
performance measure taken from `ucpm`.

**fold**
parameter for cross-validation; omitted if ‘cvNgroups’ is specified.

**cvNgroups**
vector of group indicators for cross-validation. By default assigned automatically.

**output**
indicator (logical) for textoutput during computation (slows down computation!)

**minQvar**
logical, whether to include at least one variable in the model, even if the prior itself already is a reasonable model.

... further parameters passed to classification function (’method’), e.g. priors etc.

### Details

The classification “method” (e.g. ‘lda’) must have its own ‘predict’ method (like ‘predict.lda’ for ‘lda’) that either returns a matrix of posterior probabilities or a list with an element ‘posterior’ containing that matrix instead. It must be able to deal with matrices as in `methodHxL groupingL NNNI`.

Then a stepwise variable selection is performed. The initial model is defined by the provided starting variables; in every step new models are generated by including every single variable that is not in the model, and by excluding every single variable that is in the model. The resulting performance measure for these models are estimated (by cross-validation), and if the maximum value of the chosen criterion is better than ‘improvement’ plus the value so far, the corresponding variable is in- or excluded. The procedure stops, if the new best value is not good enough, or if the specified maximum number of variables is reached.

If ‘direction’ is “forward”, the model is only extended (by including further variables), if ‘direction’ is “backward”, the model is only reduced (by excluding variables from the model).

### Value

An object of class ‘stepclass’ containing the following components:

**call**
the (matched) function call.

**method**
name of classification function used (e.g. “lda”).

**start.variables**
vector of starting variables.

**process**
data frame showing selection process (included/excluded variables and performance measure).

**model**
the final model: data frame with 2 columns; indices and names of variables.

**performance.measure**
value of the criterion used by `ucpm`

**formula**
formula of the form ‘response ~ list + of + selected + variables’
svmlight

Description

Function to call SVMlight from R for classification. Multiple group classification is done with the one-against-rest partition of data.

Usage

svmlight(x, ...)

## Default S3 method:
svmlight(x, grouping, temp.dir = NULL, pathsvm = NULL,
       del = TRUE, type = "C", class.type = "oaa", svm.options = NULL,
       prior = NULL, out = FALSE, ...)

## S3 method for class 'data.frame'
svmlight(x, ...)

## S3 method for class 'matrix'
svmlight(x, grouping, ..., subset, na.action = na.fail)

## S3 method for class 'formula'
svmlight(formula, data = NULL, ..., subset,
          na.action = na.fail)

Examples

data(iris)
library(MASS)
iris.d <- iris[,1:4]  # the data
iris.c <- iris[,5]   # the classes
sc_obj <- stepclass(iris.d, iris.c, "lda", start.vars = "Sepal.Width")
sc_obj
plot(sc_obj)

## or using formulas:
sc_obj <- stepclass(Species ~ ., data = iris, method = "qda",
                    start.vars = "Sepal.Width", criterion = "AS")  # same as above
sc_obj
## now you can say stuff like
## qda(sc_obj$formula, data = B3)
Arguments

- **x**: matrix or data frame containing the explanatory variables (required, if `formula` is not given).
- **grouping**: factor specifying the class for each observation (required, if `formula` is not given).
- **formula**: formula of the form `groups ~ x1 + x2 + ...`. That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
- **data**: Data frame from which variables specified in `formula` are preferentially to be taken.
- **temp.dir**: directory for temporary files.
- **pathsvm**: Path to SVMlight binaries (required, if path is unknown by the OS).
- **del**: Logical: whether to delete temporary files.
- **type**: Perform "C"=Classification or "R"=Regression.
- **class.type**: Multiclass scheme to use. See details.
- **svm.options**: Optional parameters to SVMlight.
- **prior**: A Priori probabilities of classes.
- **out**: Logical: whether SVMlight output should be printed on console (only for Windows OS.)
- **subset**: An index vector specifying the cases to be used in the training sample. (Note: If given, this argument must be named.)
- **na.action**: specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is `na.omit`, which leads to rejection of cases with missing values on any required variable. (Note: If given, this argument must be named.)

... currently unused

Details

Function to call SVMlight from R for classification (`type="C"`). SVMlight is an implementation of Vapnik’s Support Vector Machine. It is written in C by Thorsten Joachims. On the homepage (see below) the source-code and several binaries for SVMlight are available. If more then two classes are given the SVM is learned by the one-against-all scheme (`class.type="oaa"`). That means that each class is trained against the other K-1 classes. The class with the highest decision function in the SVM wins. So K SVMs have to be learned. If `class.type="oao"` each class is tested against every other and the final class is elected by a majority vote.

If `type="R"` a SVM Regression is performed.

Value

A list containing the function call and the result of SVMlight.

Requirements

SVMlight (http://svmlight.joachims.org/) must be installed before using this interface.
Author(s)
Karsten Luebke, <karsten.luebke@fom.de>, Andrea Preusser

References
http://svmlight.joachims.org/

See Also
predict.svmlight.svm,

Examples
```
## Not run:
## Only works if the svmlight binaries are in the path.
data(iris)
x <- svmlight(Species ~ ., data = iris)
## Using RBF-Kernel with gamma=0.1:
data(B3)
x <- svmlight(PHASEN ~ ., data = B3, svm.options = "-t 2 -g 0.1")
## End(Not run)
```

Description
Barycentric plots

Function to add a frame to an existing (barycentric) plot.

Usage
```
triframe(label = 1:3, label.col = 1, cex = 1, ...)
```

Arguments
```
label
  labels for the three corners of the plot.
label.col
  text color for labels.
cex
  Magnification factor for label text relative to the default.
...
  Further graphical parameters passed to trilines.
```

Author(s)
Christian Röver, <roever@statistik.tu-dortmund.de>

See Also
triplot, trilines, trigrid, centerlines
Examples

```r
triplot(grid = TRUE, frame = FALSE)  # plot without frame
some.triangle <- rbind(c(0, 0.65, 0.35), c(0.53, 0.47, 0),
                       c(0.72, 0, 0.28))[c(1:3, 1), ]
trilines(some.triangle, col = "red", pch = 16, type = "b")
triframe(label = c("left", "top", "right"), col = "blue",
         label.col = "green3")  # frame on top of points
```

Description

Function to add a grid to an existing (barycentric) plot.

Usage

```r
trigrid(x = seq(0.1, 0.9, by = 0.1), y = NULL, z = NULL,
        lty = "dashed", col = "grey", ...)```

Arguments

- `x`: Values along which to draw grid lines for first dimension (or all dimensions if `y` and `z` omitted). For NO grid lines in some dimensions just supply an NA.
- `y`: Grid lines for second dimension.
- `z`: Grid lines for third dimension.
- `lty`: Line type (see `par`).
- `col`: Line colour (see `par`).
- `...`: Further graphical parameters passed to `trilines`.

Details

Grid lines illustrate the set of points for which one of the dimensions is held constant; e.g. horizontal lines contain all points with a certain value `y` for the second dimension, connecting the two extreme points (0,y,1-y) and (1-y,y,0).

Grids may be designed more flexible than with `triplot`'s grid option.

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

See Also

`triplot`, `trilines`, `triframe`, `centerlines`
Examples

```r
triplot(grid = FALSE)
trigrid(c(1/3, 0.5))  # same grid for all 3 dimensions

triplot(grid = c(1/3, 0.5))  # (same effect)

triplot(grid = FALSE)
# different grids for all dimensions:
trigrid(x = 1/3, y = 0.5, z = seq(0.2, 0.8, by=0.2))

triplot(grid = FALSE)
# grid for third dimension only:
trigrid(x = NA, y = NA, z = c(0.1, 0.2, 0.4, 0.8))
```

---

**triperplines**  
*Barycentric plots*

Description

Function to add a point and the corresponding perpendicular lines to all three sides to an existing (barycentric) plot.

Usage

```r
triperplines(x, y = NULL, z = NULL, lcol = "red", pch = 17, ...)
```

Arguments

- `x`  
  fraction of first component OR 3-element vector (for all three components, omitting `y` and `z`).
- `y`  
  (optional) fraction of second component.
- `z`  
  (optional) fraction of third component.
- `lcol`  
  line color
- `pch`  
  plotting character. `pch = 0` for no point
- `...`  
  Further graphical parameters (see `points`, `lines` and `par`).

Details

Adds a (single!) point and lines to an existing plot (generated by `triplot`). The lines originate from the point and run (perpendicular) towards all three sides. The lengths (and proportions) of these lines are identical to those of `x`, `y` and `z`.

Value

a 2-column-matrix containing plot coordinates.
**Author(s)**
Christian Röver, <roever@statistik.tu-dortmund.de>

**See Also**
triplot, tripoints, trilines, tritrafo

**Examples**
```r
triplot()  # empty plot
triplines(1/2, 1/3, 1/6)
```

---

**triplot**  
*Barycentric plots*

**Description**
Function to produce triangular (barycentric) plots illustrating proportions of 3 components, e.g. discrete 3D-distributions or mixture fractions that sum up to 1.

**Usage**
```r
triplot(x = NULL, y = NULL, z = NULL, main = "", frame = TRUE,
       label = 1:3, grid = seq(0.1, 0.9, by = 0.1), center = FALSE,
       set.par = TRUE, ...)
```

**Arguments**
- **x**  
  Vector of fractions of first component OR 3-column matrix containing all three components (omitting y and z) OR 3-element vector (for all three components, omitting y and z).
- **y**  
  (Optional) vector of fractions of second component.
- **z**  
  (Optional) vector of fractions of third component.
- **main**  
  Main title
- **frame**  
  Controls whether a frame (triangle) and labels are drawn.
- **label**  
  (Character) vector of labels for the three corners.
- **grid**  
  Values along which grid lines are to be drawn (or FALSE for no grid at all). Default is steps of 10 percent.
- **center**  
  Controls whether or not to draw centerlines at which there is a ‘tie’ between any two dimensions (see also centerlines).
- **set.par**  
  Controls whether graphical parameter mar is set so the plot fills the window (see par).
- **...**  
  Further graphical parameters passed to trilines.
Details

The barycentric plot illustrates the set of points \((x,y,z)\) with \(x,y,z\) between 0 and 1 and \(x+y+z=1\); that is, the triangle spanned by \((1,0,0)\), \((0,1,0)\) and \((0,0,1)\) in 3-dimensional space. The three dimensions \(x\), \(y\) and \(z\) correspond to lower left, upper and lower right corner of the plot. The greater the share of \(x\) in the proportion, the closer the point is to the lower left corner; Points on the opposite (upper right) side have a zero \(x\)-fraction. The grid lines show the points at which one dimension is held constant, horizontal lines for example contain points with a constant second dimension.

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

See Also

`tripoints`, `trilines`, `triperplines`, `trigrid`, `triframe` for points, lines and layout, `tritrafo` for placing labels, and `quadplot` for the same in 4 dimensions.

Examples

```r
# illustrating probabilities:
triplet(label = c("1", "2 or 3", "4 or 5", "6"),
       main = "die rolls: probabilities", pch = 17)
tiperplines(1/2, 1/3, 1/6)

# expected...
triplet(1/2, 1/3, 1/6, label = c("1", "2 or 3", "4 or 5", "6"),
       main = "die rolls: expected and observed frequencies", pch = 17)
# ... and observed frequencies.
dierolls <- matrix(sample(1:3, size = 50*20, prob = c(1/2, 1/3, 1/6),
                      replace = TRUE), ncol = 50)
frequencies <- t(apply(dierolls, 1,
                      function(x)(summary(factor(x, levels = 1:3)))) / 50)
tipoints(frequencies)

# LDA classification posterior:
data(iris)
require(MASS)
pred <- predict(lda(Species ~ ., data = iris),iris)
plotchar <- rep(1,150)
plotchar[pred$class != iris$Species] <- 19
triplet(pred$posterior, label = colnames(pred$posterior),
        main = "LDA posterior assignments", center = TRUE,
        pch = plotchar, col = rep(c("blue", "green3", "red"), rep(50, 3)),
        grid = TRUE)
legend(x = -0.6, y = 0.7, col = c("blue", "green3", "red"),
       pch = 15, legend = colnames(pred$posterior))
```
tripoints

Barycentric plots

Description

Function to add points or lines to an existing (barycentric) plot.

Usage

tripoints(x, y = NULL, z = NULL, ...)  
trilines(x, y = NULL, z = NULL, ...)

Arguments

x       Vector of fractions of first component OR 3-column matrix containing all three components (omitting y and z) OR 3-element vector (for all three components, omitting y and z).

y       (optional) vector of fractions of second component.

z       (optional) vector of fractions of third component.

...     Further graphical parameters (see points and par).

Details

 Adds points or lines to an existing plot (generated by triplot).

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

See Also

points, lines, triplot, tritrafo, centerlines

Examples

tripoints()  # empty plot
tripoints(0.1, 0.2, 0.7)  # a point
tripoints(c(0.2, 0.6), c(0.3, 0.3), c(0.5, 0.1),
          pch = c(2, 6))  # two points
trilines(c(0.1, 0.6), c(0.2, 0.3), c(0.7, 0.1),
         col = "blue", lty = "dotted")  # a line
trilines(centerlines(3))
tritrafo  

Barycentric plots

Description

Function to carry out the transformation into 2D space for triplot, trilines etc.

Usage

tritrafo(x, y = NULL, z = NULL, check = TRUE, tolerance = 0.0001)

Arguments

x  Vector of fractions of first component OR 3-column matrix containing all three components (omitting y and z) OR 3-element vector (for all three components, omitting y and z).

y  (optional) vector of fractions of second component.

z  (optional) vector of fractions of third component.

check  if TRUE, it is checked whether x+y+z=1 and x, y, z>=0 for all cases.

tolerance  tolerance for above sum check.

Details

Projects the mixture given by x, y, and z with x, y, z between one and zero and x+y+z=1 into a two-dimensional space.

For further details see triplot.

Value

A matrix with two columns corresponding to the two dimensions.

Author(s)

Christian Röver, <roever@statistik.tu-dortmund.de>

See Also

triplot, tripoints, trilines, trigrid

Examples

tritrafo(0.1, 0.2, 0.7)
tritrafo(0.1, 0.2, 0.6) # warning

triplot()
points(tritrafo(0.1, 0.2, 0.7), col="red")
tripoints(0.1, 0.2, 0.7, col="green")  # the same
ucpm

tritrafo(c(0.1,0.2), c(0.3,0.4), c(0.6,0.4))
tritrafo(diag(3))

point <- c(0.25,0.6,0.15)
triplot(point, pch=16)
text(tritrafo(point), "(0.25, 0.60, 0.15)", adj=c(0.5,2)) # add a label

ucpm                  Uschi's classification performance measures

Description
Function to calculate the Correctness Rate, the Accuracy, the Ability to Separate and the Confidence of a classification rule.

Usage
ucpm(m, tc, ec = NULL)

Arguments
m             matrix of (scaled) membership values
 tc            vector of true classes
 ec            vector of estimated classes (only required if scaled membership values are used)

Details
- The correctness rate is the estimator for the correctness of a classification rule (1-error rate).
- The accuracy is based on the euclidean distances between (scaled) membership vectors and the vectors representing the true class corner. These distances are standardized so that a measure of 1 is achieved if all vectors lie in the correct corners and 0 if they all lie in the center.
- Analogously, the ability to separate is based on the distances between (scaled) membership vectors and the vector representing the corresponding assigned class corner.
- The confidence is the mean of the membership values of the assigned classes.

Value
A list with elements:

CR  Correctness Rate
AC  Accuracy
AS  Ability to Separate
CF  Confidence
CFvec  Confidence for each (true) class
Weights of evidence

Computes weight of evidence transform of factor variables for binary classification.

Usage

```r
library(MASS)
data(iris)
ucpm(predict(lda(Species ~ ., data = iris))$posterior, iris$Species)
```

Arguments

- `x` A matrix or data frame containing the explanatory variables.
- `grouping` A factor specifying the binary class for each observation.
- `formula` A formula of the form `grouping ~ x1 + x2 + ...` That is, the response is the grouping factor and the right hand side specifies the discriminators.
- `data` Data frame from which variables specified in formula are to be taken.
- `zeroadj` Additive constant to be added for a level with 0 observations in a class.
- `ids` Vector of either indices or variable names that specifies the variables to be transformed.
- `appont` Application on training data: logical indicating whether the transformed values for the training data should be returned by recursive calling of `predict.woe`.
- `...` For `woe.formula`: Further arguments passed to function `woe.default` such as `ids`. For `woe.default`: `replace = FALSE` can be passed to recursive call of `predict.woe` if `appont`.
Details

To each factor level \( x \) a numeric value \( WOE(x) = \ln(f(x|1)/f(x|2)) \) is assigned where 1 and 2 denote the class labels. The WOE transform is motivated for subsequent modelling by logistic regression. Note that the frequencies of the classes should be investigated before. Information values heuristically quantify the discriminatory power of a variable by \( IV = (f(x|1) - f(x|2))\ln(f(x|1)/f(x|2)) \).

Value

Returns an object of class \( woe \) that can be applied to new data.

- \( \text{woe} \): WOE coefficients for factor2numeric transformation of each (specified) variable.
- \( \text{IV} \): Vector of information values of all transformed variables.
- \( \text{newx} \): Data frame of transformed data if \( \text{appont} \).

Author(s)

Gero Szepannek

References


See Also

- \( \text{predict.woe} \), \( \text{plot.woe} \)

Examples

```r
## load German credit data
data("GermanCredit")

## training/validation split
train <- sample(nrow(GermanCredit), round(0.6*nrow(GermanCredit)))

woemodel <- woe(credit_risk~., data = GermanCredit[train,], zeroadj=0.5, applyontrain = TRUE)

## plot variable information values and woes
plot(woemodel)
plot(woemodel, type = "woes")

## apply woes
traindata <- predict(woemodel, GermanCredit[train,], replace = TRUE)
str(traindata)

## fit logistic regression model
glmmodel  <- glm(credit_risk~., traindata, family=binomial)
```
summary(glmodel)
pred.trn <- predict(glmodel, traindata, type = "response")

## predict validation data
validata <- predict(woemodel, GermanCredit[-train,], replace = TRUE)
pred.val <- predict(glmodel, validata, type = "response")
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