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gbm-package

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**gbm-package**

*Generalized Boosted Regression Models (GBMs)*

**Description**

This package implements extensions to Freund and Schapire’s AdaBoost algorithm and J. Friedman’s gradient boosting machine. Includes regression methods for least squares, absolute loss, logistic, Poisson, Cox proportional hazards partial likelihood, multinomial, t-distribution, AdaBoost exponential loss, Learning to Rank, and Huberized hinge loss.

**Details**

Further information is available in vignette: `browseVignettes(package = "gbm")`

**Author(s)**

Greg Ridgeway <gregridgeway@gmail.com> with contributions by Daniel Edwards, Brian Kriegler, Stefan Schroedl and Harry Southworth.
**References**


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**basehaz.gbm**

**Baseline hazard function**

**Description**

Computes the Breslow estimator of the baseline hazard function for a proportional hazard regression model.

**Usage**

`basehaz.gbm(t, delta, f.x, t.eval = NULL, smooth = FALSE, cumulative = TRUE)`

**Arguments**

- `t` The survival times.
- `delta` The censoring indicator.
- `f.x` The predicted values of the regression model on the log hazard scale.
- `t.eval` Values at which the baseline hazard will be evaluated.
- `smooth` If TRUE `basehaz.gbm` will smooth the estimated baseline hazard using Friedman’s super smoother `supsmu`.
- `cumulative` If TRUE the cumulative survival function will be computed.

**Details**

The proportional hazard model assumes h(t|x)=lambda(t)*exp(f(x)). `gbm` can estimate the f(x) component via partial likelihood. After estimating f(x), `basehaz.gbm` can compute the a nonparametric estimate of lambda(t).

**Value**

A vector of length equal to the length of t (or of length t.eval if t.eval is not NULL) containing the baseline hazard evaluated at t (or at t.eval if t.eval is not NULL). If cumulative is set to TRUE then the returned vector evaluates the cumulative hazard function at those values.
Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

References


See Also

survfit.gbm

calibrate.plot  Calibration plot

Description

An experimental diagnostic tool that plots the fitted values versus the actual average values. Currently only available when distribution = "bernoulli".

Usage

calibrate.plot(
  y,
  p,
  distribution = "bernoulli",
  replace = TRUE,
  line.par = list(col = "black"),
  shade.col = "lightyellow",
  shade.density = NULL,
  rug.par = list(side = 1),
  xlab = "Predicted value",
  ylab = "Observed average",
  xlim = NULL,
  ylim = NULL,
  knots = NULL,
  df = 6,
  ...
)

Arguments

y The outcome 0-1 variable.

p The predictions estimating E(y|x).
distribution The loss function used in creating p. bernoulli and poisson are currently the only special options. All others default to squared error assuming gaussian.
replace Determines whether this plot will replace or overlay the current plot. replace=FALSE is useful for comparing the calibration of several methods.
line.par Graphics parameters for the line.
shade.col Color for shading the 2 SE region. shade.col=NA implies no 2 SE region.
shade.density The density parameter for polygon.
rug.par Graphics parameters passed to rug.
xlab x-axis label corresponding to the predicted values.
ylab y-axis label corresponding to the observed average.
xlim, ylim x- and y-axis limits. If not specified function will select limits.
knots, df These parameters are passed directly to ns for constructing a natural spline smoother for the calibration curve.
... Additional optional arguments to be passed onto plot

Details
Uses natural splines to estimate E(y|p). Well-calibrated predictions imply that E(y|p) = p. The plot also includes a pointwise 95

Value
No return values.

Author(s)
Greg Ridgeway <gregridgeway@gmail.com>

References

Examples
# Don't want R CMD check to think there is a dependency on rpart
# so comment out the example
#library(rpart)
data(kyphosis)
y <- as.numeric(kyphosis$Kyphosis)-1
x <- kyphosis$Age
glm1 <- glm(y-poly(x,2),family=binomial)
p <- predict(glm1,type="response")
calibrate.plot(y, p, xlim=c(0,0.6), ylim=c(0,0.6))
Generalized Boosted Regression Modeling (GBM)

Description

Fits generalized boosted regression models. For technical details, see the vignette: utils::browseVignettes("gbm").

Usage

```r
gbm(
  formula = formula(data),
  distribution = "bernoulli",
  data = list(),
  weights,
  var.monotone = NULL,
  n.trees = 100,
  interaction.depth = 1,
  n.minobsinnode = 10,
  shrinkage = 0.1,
  bag.fraction = 0.5,
  train.fraction = 1,
  cv.folds = 0,
  keep.data = TRUE,
  verbose = FALSE,
  class.stratify.cv = NULL,
  n.cores = NULL
)
```

Arguments

- **formula**: A symbolic description of the model to be fit. The formula may include an offset term (e.g. `y~offset(n)+x`). If `keep.data = FALSE` in the initial call to `gbm` then it is the user’s responsibility to resupply the offset to `gbm.more`.
- **distribution**: Either a character string specifying the name of the distribution to use or a list with a component name specifying the distribution and any additional parameters needed. If not specified, `gbm` will try to guess: if the response has only 2 unique values, bernoulli is assumed; otherwise, if the response is a factor, multinomial is assumed; otherwise, if the response has class "Surv", coxph is assumed; otherwise, gaussian is assumed. Currently available options are "gaussian" (squared error), "laplace" (absolute loss), "tdist" (t-distribution loss), "bernoulli" (logistic regression for 0-1 outcomes), "huberized" (huberized hinge loss for 0-1 outcomes), classes), "adaboost" (the AdaBoost exponential loss for 0-1 outcomes), "poisson" (count outcomes), "coxph" (right censored observations), "quantile", or "pairwise" (ranking measure using the LambdaMart algorithm).
If quantile regression is specified, distribution must be a list of the form `list(name = "quantile", alpha = 0.25)` where alpha is the quantile to estimate. The current version’s quantile regression method does not handle non-constant weights and will stop.

If "tdist" is specified, the default degrees of freedom is 4 and this can be controlled by specifying `distribution = list(name = "tdist", df = DF)` where DF is your chosen degrees of freedom.

If "pairwise" regression is specified, distribution must be a list of the form `list(name="pairwise",group=...,metric=...,max.rank=...)` (metric and max.rank are optional, see below). group is a character vector with the column names of data that jointly indicate the group an instance belongs to (typically a query in Information Retrieval applications). For training, only pairs of instances from the same group and with different target labels can be considered. metric is the IR measure to use, one of

- list("conc") Fraction of concordant pairs; for binary labels, this is equivalent to the Area under the ROC Curve
- list("mrr") Mean reciprocal rank of the highest-ranked positive instance
- list("map") Mean average precision, a generalization of mrr to multiple positive instances
- list("ndcg") Normalized discounted cumulative gain. The score is the weighted sum (DCG) of the user-supplied target values, weighted by log(rank+1), and normalized to the maximum achievable value. This is the default if the user did not specify a metric.

ndcg and conc allow arbitrary target values, while binary targets 0,1 are expected for map and mrr. For ndcg and mrr, a cut-off can be chosen using a positive integer parameter max.rank. If left unspecified, all ranks are taken into account.

Note that splitting of instances into training and validation sets follows group boundaries and therefore only approximates the specified train.fraction ratio (the same applies to cross-validation folds). Internally, queries are randomly shuffled before training, to avoid bias.

Weights can be used in conjunction with pairwise metrics, however it is assumed that they are constant for instances from the same group.

For details and background on the algorithm, see e.g. Burges (2010).

**data** an optional data frame containing the variables in the model. By default the variables are taken from `environment(formula)`, typically the environment from which gbm is called. If keep.data=TRUE in the initial call to gbm then gbm stores a copy with the object. If keep.data=FALSE then subsequent calls to gbm.more must resupply the same dataset. It becomes the user’s responsibility to resupply the same data at this point.

**weights** an optional vector of weights to be used in the fitting process. Must be positive but do not need to be normalized. If keep.data=FALSE in the initial call to gbm then it is the user’s responsibility to resupply the weights to gbm.more.
an optional vector, the same length as the number of predictors, indicating which variables have a monotone increasing (+1), decreasing (-1), or arbitrary (0) relationship with the outcome.

**n.trees** Integer specifying the total number of trees to fit. This is equivalent to the number of iterations and the number of basis functions in the additive expansion. Default is 100.

**interaction.depth** Integer specifying the maximum depth of each tree (i.e., the highest level of variable interactions allowed). A value of 1 implies an additive model, a value of 2 implies a model with up to 2-way interactions, etc. Default is 1.

**n.minobsinnode** Integer specifying the minimum number of observations in the terminal nodes of the trees. Note that this is the actual number of observations, not the total weight.

**shrinkage** a shrinkage parameter applied to each tree in the expansion. Also known as the learning rate or step-size reduction; 0.001 to 0.1 usually work, but a smaller learning rate typically requires more trees. Default is 0.1.

**bag.fraction** the fraction of the training set observations randomly selected to propose the next tree in the expansion. This introduces randomness into the model fit. If bag.fraction < 1 then running the same model twice will result in similar but different fits. gbm uses the R random number generator so set.seed can ensure that the model can be reconstructed. Preferably, the user can save the returned gbm.object using save. Default is 0.5.

**train.fraction** The first train.fraction * nrows(data) observations are used to fit the gbm and the remainder are used for computing out-of-sample estimates of the loss function.

**cv.folds** Number of cross-validation folds to perform. If cv.folds>1 then gbm, in addition to the usual fit, will perform a cross-validation, calculate an estimate of generalization error returned in cv.error.

**keep.data** a logical variable indicating whether to keep the data and an index of the data stored with the object. Keeping the data and index makes subsequent calls to gbm.more faster at the cost of storing an extra copy of the dataset.

**verbose** Logical indicating whether or not to print out progress and performance indicators (TRUE). If this option is left unspecified for gbm.more, then it uses verbose from object. Default is FALSE.

**class.stratify.cv** Logical indicating whether or not the cross-validation should be stratified by class. Defaults to TRUE for distribution = "multinomial" and is only implemented for "multinomial" and "bernoulli". The purpose of stratifying the cross-validation is to help avoiding situations in which training sets do not contain all classes.

**n.cores** The number of CPU cores to use. The cross-validation loop will attempt to send different CV folds off to different cores. If n.cores is not specified by the user, it is guessed using the detectCores function in the parallel package. Note that the documentation for detectCores makes clear that it is not failsafe and could return a spurious number of available cores.
gbm

Details

gbm.fit provides the link between R and the C++ gbm engine. gbm is a front-end to gbm.fit that uses the familiar R modeling formulas. However, model.frame is very slow if there are many predictor variables. For power-users with many variables use gbm.fit. For general practice gbm is preferable.

This package implements the generalized boosted modeling framework. Boosting is the process of iteratively adding basis functions in a greedy fashion so that each additional basis function further reduces the selected loss function. This implementation closely follows Friedman's Gradient Boosting Machine (Friedman, 2001).

In addition to many of the features documented in the Gradient Boosting Machine, gbm offers additional features including the out-of-bag estimator for the optimal number of iterations, the ability to store and manipulate the resulting gbm object, and a variety of other loss functions that had not previously had associated boosting algorithms, including the Cox partial likelihood for censored data, the poisson likelihood for count outcomes, and a gradient boosting implementation to minimize the AdaBoost exponential loss function.

Value

A gbm.object object.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>
Quantile regression code developed by Brian Kriegler <bk@stat.ucla.edu>
t-distribution, and multinomial code developed by Harry Southworth and Daniel Edwards
Pairwise code developed by Stefan Schroedl <schroedl@a9.com>

References

See Also

gbm.object, gbm.perf, plot.gbm, predict.gbm, summary.gbm, and pretty.gbm.tree.

Examples

# A least squares regression example

# Simulate data
set.seed(101)  # for reproducibility
N <- 1000
X1 <- runif(N)
X2 <- 2 * runif(N)
X3 <- ordered(sample(letters[1:4], N, replace = TRUE), levels = letters[4:1])
X4 <- factor(sample(letters[1:6], N, replace = TRUE))
X5 <- factor(sample(letters[1:3], N, replace = TRUE))
X6 <- 3 * runif(N)
mu <- c(-1, 0, 1, 2)[as.numeric(X3)]
SNR <- 10  # signal-to-noise ratio
Y <- X1 ^ 1.5 + 2 * (X2 ^ 0.5) + mu
sigma <- sqrt(var(Y) / SNR)
Y <- Y + rnorm(N, 0, sigma)
X1[sample(1:N, size = 500)] <- NA  # introduce some missing values
X4[sample(1:N, size = 300)] <- NA  # introduce some missing values
data <- data.frame(Y, X1, X2, X3, X4, X5, X6)

# Fit a GBM
set.seed(102)  # for reproducibility
gbm1 <- gbm(Y ~ ., data = data, var.monotone = c(0, 0, 0, 0, 0, 0),
            distribution = "gaussian", n.trees = 100, shrinkage = 0.1,
            interaction.depth = 3, bag.fraction = 0.5, train.fraction = 0.5,
            n.minobsinnode = 10, cv.folds = 5, keep.data = TRUE,
            verbose = FALSE, n.cores = 1)

# Check performance using the out-of-bag (OOB) error; the OOB error typically
# underestimates the optimal number of iterations
best.iter <- gbm.perf(gbm1, method = "OOB")
print(best.iter)

# Check performance using the 50% heldout test set
best.iter <- gbm.perf(gbm1, method = "test")
print(best.iter)

# Check performance using 5-fold cross-validation
best.iter <- gbm.perf(gbm1, method = "cv")
print(best.iter)

# Plot relative influence of each variable
par(mfrow = c(1, 2))
summary(gbm1, n.trees = 1)  # using first tree
summary(gbm1, n.trees = best.iter)  # using estimated best number of trees
# Compactly print the first and last trees for curiosity
print(pretty.gbm.tree(gbm1, i.tree = 1))
print(pretty.gbm.tree(gbm1, i.tree = gbm1$n.trees))

# Simulate new data
set.seed(103) # for reproducibility
N <- 1000
X1 <- runif(N)
X2 <- 2 * runif(N)
X3 <- ordered(sample(letters[1:4], N, replace = TRUE))
X4 <- factor(sample(letters[1:6], N, replace = TRUE))
X5 <- factor(sample(letters[1:3], N, replace = TRUE))
X6 <- 3 * runif(N)
mu <- c(-1, 0, 1, 2)[as.numeric(X3)]
Y <- X1 ^ 1.5 + 2 * (X2 ^ 0.5) + mu + rnorm(N, 0, sigma)
data2 <- data.frame(Y, X1, X2, X3, X4, X5, X6)

# Predict on the new data using the "best" number of trees; by default,
# predictions will be on the link scale
Yhat <- predict(gbm1, newdata = data2, n.trees = best.iter, type = "link")

# least squares error
print(sum((data2$Y - Yhat)^2))

# Construct univariate partial dependence plots
plot(gbm1, i.var = 1, n.trees = best.iter)
plot(gbm1, i.var = 2, n.trees = best.iter)
plot(gbm1, i.var = "X3", n.trees = best.iter) # can use index or name

# Construct bivariate partial dependence plots
plot(gbm1, i.var = 1:2, n.trees = best.iter)
plot(gbm1, i.var = c("X2", "X3"), n.trees = best.iter)
plot(gbm1, i.var = 3:4, n.trees = best.iter)

# Construct trivariate partial dependence plots
plot(gbm1, i.var = c(1, 2, 6), n.trees = best.iter, continuous.resolution = 20)
plot(gbm1, i.var = 1:3, n.trees = best.iter)
plot(gbm1, i.var = 2:4, n.trees = best.iter)
plot(gbm1, i.var = 3:5, n.trees = best.iter)

# Add more (i.e., 100) boosting iterations to the ensemble
gbm2 <- gbm.more(gbm1, n.new.trees = 100, verbose = FALSE)
Description

Workhorse function providing the link between R and the C++ gbm engine. gbm is a front-end to gbm.fit that uses the familiar R modeling formulas. However, model.frame is very slow if there are many predictor variables. For power-users with many variables use gbm.fit. For general practice gbm is preferable.

Usage

gbm.fit(
  x,
  y,
  offset = NULL,
  misc = NULL,
  distribution = "bernoulli",
  w = NULL,
  var.monotone = NULL,
  n.trees = 100,
  interaction.depth = 1,
  n.minobsinnode = 10,
  shrinkage = 0.001,
  bag.fraction = 0.5,
  nTrain = NULL,
  train.fraction = NULL,
  keep.data = TRUE,
  verbose = TRUE,
  var.names = NULL,
  response.name = "y",
  group = NULL
)

Arguments

x A data frame or matrix containing the predictor variables. The number of rows in x must be the same as the length of y.

y A vector of outcomes. The number of rows in x must be the same as the length of y.

offset A vector of offset values.

misc An R object that is simply passed on to the gbm engine. It can be used for additional data for the specific distribution. Currently it is only used for passing the censoring indicator for the Cox proportional hazards model.

distribution Either a character string specifying the name of the distribution to use or a list with a component name specifying the distribution and any additional parameters needed. If not specified, gbm will try to guess: if the response has only 2 unique values, bernoulli is assumed; otherwise, if the response is a factor, multinomial is assumed; otherwise, if the response has class "Surv", coxph is assumed; otherwise, gaussian is assumed.
Currently available options are "gaussian" (squared error), "laplace" (absolute loss), "tdist" (t-distribution loss), "bernoulli" (logistic regression for 0-1 outcomes), "huberized" (huberized hinge loss for 0-1 outcomes), classes), "adaboost" (the AdaBoost exponential loss for 0-1 outcomes), "poisson" (count outcomes), "coxph" (right censored observations), "quantile", or "pairwise" (ranking measure using the LambdaMart algorithm).

If quantile regression is specified, distribution must be a list of the form list(name = "quantile", alpha = 0.25) where alpha is the quantile to estimate. The current version's quantile regression method does not handle non-constant weights and will stop.

If "tdist" is specified, the default degrees of freedom is 4 and this can be controlled by specifying distribution = list(name = "tdist", df = DF) where DF is your chosen degrees of freedom.

If "pairwise" regression is specified, distribution must be a list of the form list(name="pairwise", group=..., metric=..., max.rank=...) (metric and max.rank are optional, see below). group is a character vector with the column names of data that jointly indicate the group an instance belongs to (typically a query in Information Retrieval applications). For training, only pairs of instances from the same group and with different target labels can be considered. metric is the IR measure to use, one of

list("conc") Fraction of concordant pairs; for binary labels, this is equivalent to the Area under the ROC Curve

list("mrr") Mean reciprocal rank of the highest-ranked positive instance

list("map") Mean average precision, a generalization of mrr to multiple positive instances

list("ndcg") Normalized discounted cumulative gain. The score is the weighted sum (DCG) of the user-supplied target values, weighted by log(rank+1), and normalized to the maximum achievable value. This is the default if the user did not specify a metric.

ndcg and conc allow arbitrary target values, while binary targets 0,1 are expected for map and mrr. For ndcg and mrr, a cut-off can be chosen using a positive integer parameter max.rank. If left unspecified, all ranks are taken into account.

Note that splitting of instances into training and validation sets follows group boundaries and therefore only approximates the specified train.fraction ratio (the same applies to cross-validation folds). Internally, queries are randomly shuffled before training, to avoid bias.

Weights can be used in conjunction with pairwise metrics, however it is assumed that they are constant for instances from the same group.

For details and background on the algorithm, see e.g. Burges (2010).

w A vector of weights of the same length as the y.
var.monotone  an optional vector, the same length as the number of predictors, indicating which variables have a monotone increasing (+1), decreasing (-1), or arbitrary (0) relationship with the outcome.

n.trees   the total number of trees to fit. This is equivalent to the number of iterations and the number of basis functions in the additive expansion.

interaction.depth   The maximum depth of variable interactions. A value of 1 implies an additive model, a value of 2 implies a model with up to 2-way interactions, etc. Default is 1.

n.minobsinnode   Integer specifying the minimum number of observations in the trees terminal nodes. Note that this is the actual number of observations not the total weight.

shrinkage   The shrinkage parameter applied to each tree in the expansion. Also known as the learning rate or step-size reduction; 0.001 to 0.1 usually work, but a smaller learning rate typically requires more trees. Default is 0.1.

bag.fraction   The fraction of the training set observations randomly selected to propose the next tree in the expansion. This introduces randomness into the model fit. If bag.fraction < 1 then running the same model twice will result in similar but different fits. gbm uses the R random number generator so set.seed can ensure that the model can be reconstructed. Preferably, the user can save the returned gbm.object using save. Default is 0.5.

nTrain   An integer representing the number of cases on which to train. This is the preferred way of specification for gbm.fit; The option train.fraction in gbm.fit is deprecated and only maintained for backward compatibility. These two parameters are mutually exclusive. If both are unspecified, all data is used for training.

train.fraction   The first train.fraction * nrows(data) observations are used to fit the gbm and the remainder are used for computing out-of-sample estimates of the loss function.

keep.data   Logical indicating whether or not to keep the data and an index of the data stored with the object. Keeping the data and index makes subsequent calls to gbm.more faster at the cost of storing an extra copy of the dataset.

verbose   Logical indicating whether or not to print out progress and performance indicators (TRUE). If this option is left unspecified for gbm.more, then it uses verbose from object. Default is FALSE.

var.names   Vector of strings of length equal to the number of columns of x containing the names of the predictor variables.

response.name   Character string label for the response variable.

group   The group to use when distribution = "pairwise".

Details
This package implements the generalized boosted modeling framework. Boosting is the process of iteratively adding basis functions in a greedy fashion so that each additional basis function further reduces the selected loss function. This implementation closely follows Friedman’s Gradient Boosting Machine (Friedman, 2001).
In addition to many of the features documented in the Gradient Boosting Machine, \texttt{gbm} offers additional features including the out-of-bag estimator for the optimal number of iterations, the ability to store and manipulate the resulting \texttt{gbm} object, and a variety of other loss functions that had not previously had associated boosting algorithms, including the Cox partial likelihood for censored data, the poisson likelihood for count outcomes, and a gradient boosting implementation to minimize the AdaBoost exponential loss function.

**Value**

A \texttt{gbm.object} object.

**Author(s)**

Greg Ridgeway <gregridgeway@gmail.com>  
Quantile regression code developed by Brian Kriegler <bk@stat.ucla.edu>  
t-distribution, and multinomial code developed by Harry Southworth and Daniel Edwards  
Pairwise code developed by Stefan Schroedl <schroedl@a9.com>

**References**


**See Also**

\texttt{gbm.object}, \texttt{gbm.perf}, \texttt{plot.gbm}, \texttt{predict.gbm}, \texttt{summary.gbm}, and \texttt{pretty.gbm.tree}.
\textbf{Description}

Adds additional trees to a \texttt{gbm.object} object.

\textbf{Usage}

\begin{verbatim}
gbm.more(
  object,
  n.new.trees = 100,
  data = NULL,
  weights = NULL,
  offset = NULL,
  verbose = NULL
)
\end{verbatim}

\textbf{Arguments}

- \texttt{object} \hspace{1cm} A \texttt{gbm.object} object created from an initial call to \texttt{gbm}.
- \texttt{n.new.trees} \hspace{1cm} Integer specifying the number of additional trees to add to \texttt{object}. Default is 100.
- \texttt{data} \hspace{1cm} An optional data frame containing the variables in the model. By default the variables are taken from \texttt{environment(formula)}, typically the environment from which \texttt{gbm} is called. If \texttt{keep.data=TRUE} in the initial call to \texttt{gbm} then \texttt{gbm} stores a copy with the object. If \texttt{keep.data=FALSE} then subsequent calls to \texttt{gbm.more} must resupply the same dataset. It becomes the user’s responsibility to resupply the same data at this point.
- \texttt{weights} \hspace{1cm} An optional vector of weights to be used in the fitting process. Must be positive but do not need to be normalized. If \texttt{keep.data=FALSE} in the initial call to \texttt{gbm} then it is the user’s responsibility to resupply the weights to \texttt{gbm.more}.
- \texttt{offset} \hspace{1cm} A vector of offset values.
- \texttt{verbose} \hspace{1cm} Logical indicating whether or not to print out progress and performance indicators (TRUE). If this option is left unspecified for \texttt{gbm.more}, then it uses \texttt{verbose} from \texttt{object}. Default is FALSE.

\textbf{Value}

A \texttt{gbm.object} object.

\textbf{Examples}

\begin{verbatim}
# # A least squares regression example
#
\end{verbatim}
# Simulate data
set.seed(101)  # for reproducibility
N <- 1000
X1 <- runif(N)
X2 <- 2 * runif(N)
X3 <- ordered(sample(letters[1:4], N, replace = TRUE), levels = letters[4:1])
X4 <- factor(sample(letters[1:6], N, replace = TRUE))
X5 <- factor(sample(letters[1:3], N, replace = TRUE))
X6 <- 3 * runif(N)
mu <- c(-1, 0, 1, 2)[as.numeric(X3)]
SNR <- 10  # signal-to-noise ratio
Y <- X1 ^ 1.5 + 2 * (X2 ^ 0.5) + mu
sigma <- sqrt(var(Y) / SNR)
Y <- Y + rnorm(N, 0, sigma)
X1[sample(1:N, size=500)] <- NA  # introduce some missing values
X4[sample(1:N, size=300)] <- NA  # introduce some missing values
data <- data.frame(Y, X1, X2, X3, X4, X5, X6)

# Fit a GBM
set.seed(102)  # for reproducibility
gbm1 <- gbm(Y ~ ., data = data, var.monotone = c(0, 0, 0, 0, 0, 0),
            distribution = "gaussian", n.trees = 100, shrinkage = 0.1,
            interaction.depth = 3, bag.fraction = 0.5, train.fraction = 0.5,
            n.minobsinnode = 10, cv.folds = 5, keep.data = TRUE,
            verbose = FALSE, n.cores = 1)

# Check performance using the out-of-bag (OOB) error; the OOB error typically
# underestimates the optimal number of iterations
best.iter <- gbm.perf(gbm1, method = "OOB")
print(best.iter)

# Check performance using the 50% heldout test set
best.iter <- gbm.perf(gbm1, method = "test")
print(best.iter)

# Check performance using 5-fold cross-validation
best.iter <- gbm.perf(gbm1, method = "cv")
print(best.iter)

# Plot relative influence of each variable
par(mfrow = c(1, 2))
summary(gbm1, n.trees = 1)  # using first tree
summary(gbm1, n.trees = best.iter)  # using estimated best number of trees

# Compactly print the first and last trees for curiosity
print(pretty.gbm.tree(gbm1, i.tree = 1))
print(pretty.gbm.tree(gbm1, i.tree = gbm1$n.trees))

# Simulate new data
set.seed(103)  # for reproducibility
N <- 1000
X1 <- runif(N)
X2 <- 2 * runif(N)
X3 <- ordered(sample(letters[1:4], N, replace = TRUE))
X4 <- factor(sample(letters[1:6], N, replace = TRUE))
X5 <- factor(sample(letters[1:3], N, replace = TRUE))
X6 <- 3 * runif(N)
mu <- c(-1, 0, 1, 2)[as.numeric(X3)]
Y <- X1 ^ 1.5 + 2 * (X2 ^ 0.5) + mu + rnorm(N, 0, sigma)
data2 <- data.frame(Y, X1, X2, X3, X4, X5, X6)

# Predict on the new data using the "best" number of trees; by default,
# predictions will be on the link scale
Yhat <- predict(gbm1, newdata = data2, n.trees = best.iter, type = "link")

# least squares error
print(sum((data2$Y - Yhat)^2))

# Construct univariate partial dependence plots
plot(gbm1, i.var = 1, n.trees = best.iter)
plot(gbm1, i.var = 2, n.trees = best.iter)
plot(gbm1, i.var = "X3", n.trees = best.iter)  # can use index or name

# Construct bivariate partial dependence plots
plot(gbm1, i.var = 1:2, n.trees = best.iter)
plot(gbm1, i.var = c("X2", "X3"), n.trees = best.iter)
plot(gbm1, i.var = 3:4, n.trees = best.iter)

# Construct trivariate partial dependence plots
plot(gbm1, i.var = c(1, 2, 6), n.trees = best.iter, continuous.resolution = 20)
plot(gbm1, i.var = 1:3, n.trees = best.iter)
plot(gbm1, i.var = 2:4, n.trees = best.iter)
plot(gbm1, i.var = 3:5, n.trees = best.iter)

# Add more (i.e., 100) boosting iterations to the ensemble
gbm2 <- gbm.more(gbm1, n.new.trees = 100, verbose = FALSE)

---

### gbm.object

**Generalized Boosted Regression Model Object**

**Description**

These are objects representing fitted gbms.

**Value**

- **initF**: The "intercept" term, the initial predicted value to which trees make adjustments.
- **fit**: A vector containing the fitted values on the scale of regression function (e.g. log-odds scale for bernoulli, log scale for poisson).
- **train.error**: A vector of length equal to the number of fitted trees containing the value of the loss function for each boosting iteration evaluated on the training data.
valid.error A vector of length equal to the number of fitted trees containing the value of the loss function for each boosting iteration evaluated on the validation data.

cv.error If cv.folds < 2 this component is NULL. Otherwise, this component is a vector of length equal to the number of fitted trees containing a cross-validated estimate of the loss function for each boosting iteration.

oobag.improve A vector of length equal to the number of fitted trees containing an out-of-bag estimate of the marginal reduction in the expected value of the loss function. The out-of-bag estimate uses only the training data and is useful for estimating the optimal number of boosting iterations. See gbm.perf.

trees A list containing the tree structures. The components are best viewed using pretty.gbm.tree.

c.splits A list of all the categorical splits in the collection of trees. If the trees[[i]] component of a gbm object describes a categorical split then the splitting value will refer to a component of c.splits. That component of c.splits will be a vector of length equal to the number of levels in the categorical split variable. -1 indicates left, +1 indicates right, and 0 indicates that the level was not present in the training data.

cv.fitted If cross-validation was performed, the cross-validation predicted values on the scale of the linear predictor. That is, the fitted values from the i-th CV-fold, for the model having been trained on the data in all other folds.

Structure

The following components must be included in a legitimate gbm object.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

See Also

gbm

Description

Estimates the optimal number of boosting iterations for a gbm object and optionally plots various performance measures

Usage

gbm.perf(object, plot.it = TRUE, oobag.curve = FALSE, overlay = TRUE, method)
gbm.roc.area

Arguments

object  A gbm.object created from an initial call to gbm.
plot.it  An indicator of whether or not to plot the performance measures. Setting plot.it = TRUE creates two plots. The first plot plots object$train.error (in black) and object$valid.error (in red) versus the iteration number. The scale of the error measurement, shown on the left vertical axis, depends on the distribution argument used in the initial call to gbm.
oobag.curve  Indicates whether to plot the out-of-bag performance measures in a second plot.
overlay  If TRUE and oobag.curve=TRUE then a right y-axis is added to the training and test error plot and the estimated cumulative improvement in the loss function is plotted versus the iteration number.
method  Indicate the method used to estimate the optimal number of boosting iterations. method = "OOB" computes the out-of-bag estimate and method = "test" uses the test (or validation) dataset to compute an out-of-sample estimate. method = "cv" extracts the optimal number of iterations using cross-validation if gbm was called with cv.folds > 1.

Value

gbm.perf  Returns the estimated optimal number of iterations. The method of computation depends on the method argument.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

See Also

gbm, gbm.object

Description

Functions to compute Information Retrieval measures for pairwise loss for a single group. The function returns the respective metric, or a negative value if it is undefined for the given group.

Usage

gbm.roc.area(obs, pred)

gbm.conc(x)

ir.measure.conc(y.f, max.rank = 0)
```r
ir.measure.auc(y.f, max.rank = 0)
ir.measure.mrr(y.f, max.rank)
ir.measure.map(y.f, max.rank = 0)
ir.measure.ndcg(y.f, max.rank)
perf.pairwise(y, f, group, metric = "ndcg", w = NULL, max.rank = 0)
```

### Arguments
- `obs` Observed value.
- `pred` Predicted value.
- `x` Numeric vector.
- `y, y.f, f, w, group, max.rank` Used internally.
- `metric` What type of performance measure to compute.

### Details
For simplicity, we have no special handling for ties; instead, we break ties randomly. This is slightly inaccurate for individual groups, but should have only a small effect on the overall measure.

`gbm.conc` computes the concordance index: Fraction of all pairs (i,j) with i<j, x[i]!=x[j], such that x[j]<x[i].

If `obs` is binary, then `gbm.roc.area(obs, pred) = gbm.conc(obs[order(-pred)])`.

`gbm.conc` is more general as it allows non-binary targets, but is significantly slower.

### Value
The requested performance measure.

### Author(s)
Stefan Schroedl

### References

### See Also
`gbm`
gbmCrossVal  

Cross-validate a gbm

Description

Functions for cross-validating gbm. These functions are used internally and are not intended for end-user direct usage.

Usage

```r
gbmCrossVal(
  cv.folds,
  nTrain,
  n.cores,
  class.stratify.cv,
  data,
  x,
  y,
  offset,
  distribution,
  w,
  var.monotone,
  n.trees,
  interaction.depth,
  n.minobsinnode,
  shrinkage,
  bag.fraction,
  var.names,
  response.name,
  group
)

gbmCrossValErr(cv.models, cv.folds, cv.group, nTrain, n.trees)

gbmCrossValPredictions(
  cv.models,
  cv.folds,
  cv.group,
  best.iter.cv,
  distribution,
  data,
  y
)

gbmCrossValModelBuild(
  cv.folds,
  cv.group,
```
gbmCrossVal

n.cores,  
i.train,  
x,  
y,  
offset,  
distribution,  
w,  
var.monotone,  
n.trees,  
interaction.depth,  
n.minobsinnode,  
shrinkage,  
bag.fraction,  
var.names,  
response.name,  
group  
)

gbmDoFold(  
  x,  
  i.train,  
  x,  
  y,  
  offset,  
  distribution,  
  w,  
  var.monotone,  
  n.trees,  
  interaction.depth,  
  n.minobsinnode,  
  shrinkage,  
  bag.fraction,  
  var.names,  
  response.name,  
  group,  
s  
)

Arguments

cv.folds     The number of cross-validation folds.
nTrain       The number of training samples.
n.cores      The number of cores to use.
class.stratify.cv  Whether or not stratified cross-validation samples are used.
data         The data.
x            The model matrix.
gbmCrossVal

y
offset
distribution
w
var.monotone
n.trees
interaction.depth
n.minobsinnode
shrinkage
bag.fraction
var.names
response.name
group
cv.models
cv.group
best.iter.cv
i.train
X
s

The response variable.
The offset.
The type of loss function. See gbm.
Observation weights.
See gbm.
The number of trees to fit.
The degree of allowed interactions. See gbm.
See gbm.
See gbm.
See gbm.
See gbm.
See gbm.
Used when distribution = "pairwise". See gbm.
A list containing the models for each fold.
A vector indicating the cross-validation fold for each member of the training set.
The iteration with lowest cross-validation error.
Items in the training set.
Index (cross-validation fold) on which to subset.
Random seed.

Details

These functions are not intended for end-user direct usage, but are used internally by gbm.

Value

A list containing the cross-validation error and predictions.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

References


See Also

gbm
guessDist

gbm internal functions

Description
Helper functions for preprocessing data prior to building a "gbm" object.

Usage
guessDist(y)

getCVgroup(distribution, class.stratify.cv, y, i.train, cv.folds, group)

getStratify(strat, d)

checkMissing(x, y)

checkWeights(w, n)

checkID(id)

checkOffset(o, y)

getVarNames(x)

gbmCluster(n)

Arguments

y The response variable.
class.stratify.cv Whether or not to stratify, if provided by the user.
i.train Computed internally by gbm.
cv.folds The number of cross-validation folds.
group The group, if using distribution = "pairwise".
strat Whether or not to stratify.
d, distribution The distribution, either specified by the user or implied.
x The design matrix.
w The weights.
n The number of cores to use in the cluster.
id The interaction depth.
o The offset.
Details

These are functions used internally by gbm and not intended for direct use by the user.

---

interact.gbm  Estimate the strength of interaction effects

Description

Computes Friedman’s H-statistic to assess the strength of variable interactions.

Usage

```r
interact.gbm(x, data, i.var = 1, n.trees = x$n.trees)
```

Arguments

- `x`: A `gbm.object` fitted using a call to `gbm`.
- `data`: The dataset used to construct `x`. If the original dataset is large, a random sub-sample may be used to accelerate the computation in `interact.gbm`.
- `i.var`: A vector of indices or the names of the variables for compute the interaction effect. If using indices, the variables are indexed in the same order that they appear in the initial `gbm` formula.
- `n.trees`: The number of trees used to generate the plot. Only the first `n.trees` trees will be used.

Details

`interact.gbm` computes Friedman’s H-statistic to assess the relative strength of interaction effects in non-linear models. H is on the scale of [0-1] with higher values indicating larger interaction effects. To connect to a more familiar measure, if \( x_1 \) and \( x_2 \) are uncorrelated covariates with mean 0 and variance 1 and the model is of the form

\[
y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3
\]

then

\[
H = \frac{\beta_3}{\sqrt{\beta_1^2 + \beta_2^2 + \beta_3^2}}
\]

Note that if the main effects are weak, the estimated H will be unstable. For example, if (in the case of a two-way interaction) neither main effect is in the selected model (relative influence is zero), the result will be 0/0. Also, with weak main effects, rounding errors can result in values of \( H > 1 \) which are not possible.

Value

Returns the value of \( H \).
plot.gbm

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

References


See Also

gbm, gbm.object

plot.gbm  
Marginal plots of fitted gbm objects

Description

Plots the marginal effect of the selected variables by "integrating" out the other variables.

Usage

## S3 method for class 'gbm'
plot(
  x,
  i.var = 1,
  n.trees = x$n.trees,
  continuous.resolution = 100,
  return.grid = FALSE,
  type = c("link", "response"),
  level.plot = TRUE,
  contour = FALSE,
  number = 4,
  overlap = 0.1,
  col.regions = viridis::viridis,
  ...
)

Arguments

x  
A gbm.object that was fit using a call to gbm.

i.var  
Vector of indices or the names of the variables to plot. If using indices, the variables are indexed in the same order that they appear in the initial gbm formula. If length(i.var) is between 1 and 3 then plot.gbm produces the plots. Otherwise, plot.gbm returns only the grid of evaluation points and their average predictions.

n.trees  
Integer specifying the number of trees to use to generate the plot. Default is to use x$n.trees (i.e., the entire ensemble).
continuous.resolution

Integer specifying the number of equally space points at which to evaluate continuous predictors.

return.grid

Logical indicating whether or not to produce graphics FALSE or only return the grid of evaluation points and their average predictions TRUE. This is useful for customizing the graphics for special variable types, or for higher dimensional graphs.

type

Character string specifying the type of prediction to plot on the vertical axis. See predict.gbm for details.

level.plot

Logical indicating whether or not to use a false color level plot (TRUE) or a 3-D surface (FALSE). Default is TRUE.

contour

Logical indicating whether or not to add contour lines to the level plot. Only used when level.plot = TRUE. Default is FALSE.

number

Integer specifying the number of conditional intervals to use for the continuous panel variables. See co.intervals and equal.count for further details.

overlap

The fraction of overlap of the conditioning variables. See co.intervals and equal.count for further details.

col.regions

Color vector to be used if level.plot is TRUE. Defaults to the wonderful Matplotlib 'viridis' color map provided by the viridis package. See viridis for details.

...

Additional optional arguments to be passed onto plot.

Details

plot.gbm produces low dimensional projections of the gbm.object by integrating out the variables not included in the i.var argument. The function selects a grid of points and uses the weighted tree traversal method described in Friedman (2001) to do the integration. Based on the variable types included in the projection, plot.gbm selects an appropriate display choosing amongst line plots, contour plots, and lattice plots. If the default graphics are not sufficient the user may set return.grid = TRUE, store the result of the function, and develop another graphic display more appropriate to the particular example.

Value

If return.grid = TRUE, a grid of evaluation points and their average predictions. Otherwise, a plot is returned.

Note

More flexible plotting is available using the partial and plotPartial functions.

References


predict.gbm

Description

Predicted values based on a generalized boosted model object

Usage

## S3 method for class 'gbm'
predict(object, newdata, n.trees, type = "link", single.tree = FALSE, ...)

Arguments

object
Object of class inheriting from (gbm.object)

newdata
Data frame of observations for which to make predictions

n.trees
Number of trees used in the prediction. n.trees may be a vector in which case predictions are returned for each iteration specified

type
The scale on which gbm makes the predictions

single.tree
If single.tree=TRUE then predict.gbm returns only the predictions from tree(s)

n.trees

... further arguments passed to or from other methods

Details

predict.gbm produces predicted values for each observation in newdata using the first n.trees iterations of the boosting sequence. If n.trees is a vector than the result is a matrix with each column representing the predictions from gbm models with n.trees[1] iterations, n.trees[2] iterations, and so on.

The predictions from gbm do not include the offset term. The user may add the value of the offset to the predicted value if desired.

If object was fit using gbm.fit there will be no Terms component. Therefore, the user has greater responsibility to make sure that newdata is of the same format (order and number of variables) as the one originally used to fit the model.

Value

Returns a vector of predictions. By default the predictions are on the scale of f(x). For example, for the Bernoulli loss the returned value is on the log odds scale, poisson loss on the log scale, and coxph is on the log hazard scale.

If type="response" then gbm converts back to the same scale as the outcome. Currently the only effect this will have is returning probabilities for bernoulli and expected counts for poisson. For the other distributions "response" and "link" return the same.
pretty.gbm.tree

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

See Also

gbm, gbm.object

Description

gbm stores the collection of trees used to construct the model in a compact matrix structure. This function extracts the information from a single tree and displays it in a slightly more readable form. This function is mostly for debugging purposes and to satisfy some users’ curiosity.

Usage

## S3 method for class 'gbm.tree'
pretty(object, i.tree = 1)

Arguments

object a gbm.object initially fit using gbm
i.tree the index of the tree component to extract from object and display

Value

pretty.gbm.tree returns a data frame. Each row corresponds to a node in the tree. Columns indicate

SplitVar index of which variable is used to split. -1 indicates a terminal node.
SplitCodePred if the split variable is continuous then this component is the split point. If the split variable is categorical then this component contains the index of object$c.split that describes the categorical split. If the node is a terminal node then this is the prediction.
LeftNode the index of the row corresponding to the left node.
RightNode the index of the row corresponding to the right node.
ErrorReduction the reduction in the loss function as a result of splitting this node.
Weight the total weight of observations in the node. If weights are all equal to 1 then this is the number of observations in the node.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>
Description

Display basic information about a gbm object.

Usage

## S3 method for class 'gbm'
print(x, ...)

show.gbm(x, ...)

Arguments

x an object of class gbm.

... arguments passed to print.default.

Details

Prints some information about the model object. In particular, this method prints the call to gbm(), the type of loss function that was used, and the total number of iterations.

If cross-validation was performed, the 'best' number of trees as estimated by cross-validation error is displayed. If a test set was used, the 'best' number of trees as estimated by the test set error is displayed.

The number of available predictors, and the number of those having non-zero influence on predictions is given (which might be interesting in data mining applications).

If multinomial, bernoulli or adaboost was used, the confusion matrix and prediction accuracy are printed (objects being allocated to the class with highest probability for multinomial and bernoulli). These classifications are performed on the entire training data using the model with the 'best' number of trees as described above, or the maximum number of trees if the 'best' cannot be computed.

If the 'distribution' was specified as gaussian, laplace, quantile or t-distribution, a summary of the residuals is displayed. The residuals are for the training data with the model at the 'best' number of trees, as described above, or the maximum number of trees if the 'best' cannot be computed.

Author(s)

Harry Southworth, Daniel Edwards

See Also

gbm
Examples

data(iris)
iris.mod <- gbm(Species ~ ., distribution="multinomial", data=iris,
    n.trees=2000, shrinkage=0.01, cv.folds=5,
    verbose=FALSE, n.cores=1)
iris.mod
#data(lung)
#lung.mod <- gbm(Surv(time, status) ~ ., distribution="coxph", data=lung,
#    n.trees=2000, shrinkage=0.01, cv.folds=5, verbose =FALSE)
#lung.mod

quantile.rug          Quantile rug plot

Description

Marks the quantiles on the axes of the current plot.

Usage

## S3 method for class 'rug'
quantile(x, prob = 0:10/10, ...)

Arguments

x          A numeric vector.
prob       The quantiles of x to mark on the x-axis.
...         Additional optional arguments to be passed onto rug

Value

No return values.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>.

See Also

plot, quantile, jitter, rug.

Examples

x <- rnorm(100)
y <- rnorm(100)
plot(x, y)
quantile.rug(x)
reconstructGBMdata  Reconstruct a GBM’s Source Data

Description

Helper function to reconstitute the data for plots and summaries. This function is not intended for
the user to call directly.

Usage

reconstructGBMdata(x)

Arguments

x a gbm.object initially fit using gbm

Value

Returns a data used to fit the gbm in a format that can subsequently be used for plots and summaries

Author(s)

Harry Southworth

See Also

gbm, gbm.object

relative.influence  Methods for estimating relative influence

Description

Helper functions for computing the relative influence of each variable in the gbm object.

Usage

relative.influence(object, n.trees, scale. = FALSE, sort. = FALSE)

permutation.test.gbm(object, n.trees)

gbm.loss(y, f, w, offset, dist, baseline, group = NULL, max.rank = NULL)
Arguments

object

a gbm object created from an initial call to gbm.

n.trees

the number of trees to use for computations. If not provided, the function will guess: if a test set was used in fitting, the number of trees resulting in lowest test set error will be used; otherwise, if cross-validation was performed, the number of trees resulting in lowest cross-validation error will be used; otherwise, all trees will be used.

scale.

whether or not the result should be scaled. Defaults to FALSE.

sort.

whether or not the results should be (reverse) sorted. Defaults to FALSE.

y, f, w, offset, dist, baseline

For gbm.loss: These components are the outcome, predicted value, observation weight, offset, distribution, and comparison loss function, respectively.

group, max.rank

Used internally when distribution = 'pairwise'.

Details

This is not intended for end-user use. These functions offer the different methods for computing the relative influence in summary.gbm. gbm.loss is a helper function for permutation.test.gbm.

Value

By default, returns an unprocessed vector of estimated relative influences. If the scale. and sort. arguments are used, returns a processed version of the same.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

References


See Also

summary.gbm
**Summary of a gbm object**

**Description**
Computes the relative influence of each variable in the gbm object.

**Usage**

```r
## S3 method for class 'gbm'
summary(
  object,
  cBars = length(object$var.names),
  n.trees = object$n.trees,
  plotit = TRUE,
  order = TRUE,
  method = relative.influence,
  normalize = TRUE,
  ...
)
```

**Arguments**

- `object` a gbm object created from an initial call to `gbm`.
- `cBars` the number of bars to plot. If `order=TRUE` the only the variables with the `cBars` largest relative influence will appear in the barplot. If `order=FALSE` then the first `cBars` variables will appear in the plot. In either case, the function will return the relative influence of all of the variables.
- `n.trees` the number of trees used to generate the plot. Only the first `n.trees` trees will be used.
- `plotit` an indicator as to whether the plot is generated.
- `order` an indicator as to whether the plotted and/or returned relative influences are sorted.
- `method` The function used to compute the relative influence. `relative.influence` is the default and is the same as that described in Friedman (2001). The other current (and experimental) choice is `permutation.test.gbm`. This method randomly permutes each predictor variable at a time and computes the associated reduction in predictive performance. This is similar to the variable importance measures Breiman uses for random forests, but gbm currently computes using the entire training dataset (not the out-of-bag observations).
- `normalize` if FALSE then `summary.gbm` returns the unnormalized influence.
- `...` other arguments passed to the plot function.
Details

For distribution="gaussian" this returns exactly the reduction of squared error attributable to each variable. For other loss functions this returns the reduction attributable to each variable in sum of squared error in predicting the gradient on each iteration. It describes the relative influence of each variable in reducing the loss function. See the references below for exact details on the computation.

Value

Returns a data frame where the first component is the variable name and the second is the computed relative influence, normalized to sum to 100.

Author(s)

Greg Ridgeway <gregridgeway@gmail.com>

References


See Also

gbm

test.gbm  Test the gbm package.

Description

Run tests on gbm functions to perform logical checks and reproducibility.

Usage

test.gbm()

Details

The function uses functionality in the RUnit package. A fairly small validation suite is executed that checks to see that relative influence identifies sensible variables from simulated data, and that predictions from GBMs with Gaussian, Cox or binomial distributions are sensible.

Value

An object of class RUnitTestData. See the help for RUnit for details.
Note

The test suite is not comprehensive.

Author(s)

Harry Southworth

See Also

gbm

Examples

# Uncomment the following lines to run - commented out to make CRAN happy
#library(RUnit)
#val <- validate.texmex()
#printHTMLProtocol(val, "texmexReport.html")
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