Package 'adabag'

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Type Package

Title Applies Multiclass AdaBoost.M1, SAMME and Bagging

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Depends rpart, caret, foreach, doParallel

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Description It implements Freund and Schapire's Adaboost.M1 algorithm and Breiman's Bagging algorithm using classification trees as individual classifiers. Once these classifiers have been trained, they can be used to predict on new data. Also, cross validation estimation of the error can be done. Since version 2.0 the function margins() is available to calculate the margins for these classifiers. Also a higher flexibility is achieved giving access to the rpart.control() argument of 'rpart'. Four important new features were introduced on version 3.0, AdaBoost-SAMME (Zhu et al., 2009) is implemented and a new function errorevol() shows the error of the ensembles as a function of the number of iterations. In addition, the ensembles can be pruned using the option 'newmfinal' in the predict.bagging() and predict.boosting() functions and the posterior probability of

each class for observations can be obtained. Version 3.1 modifies the relative importance measure to take into account the gain of the Gini index given by a variable in each tree and the weights of these trees. Version 4.0 includes the margin-based ordered aggregation for Bagging pruning (Guo and Boukir, 2013) and a function to auto prune the 'rpart' tree. Moreover, three new plots are also available importanceplot(), plot.errorevol() and plot.margins(). Version 4.1 allows to predict on unlabeled data. Version 4.2 includes the parallel computation option for some of the functions.

License GPL (>= 2)

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Description

It implements Freund and Schapire's Adaboost.M1 algorithm and Breiman's Bagging algorithm using classification trees as individual classifiers. Once these classifiers have been trained, they can be used to predict on new data. Also, cross validation estimation of the error can be done. Since version 2.0 the function margins() is available to calculate the margins for these classifiers. Also a higher flexibility is achieved giving access to the rpart.control() argument of 'rpart'. Four important new features were introduced on version 3.0, AdaBoost-SAMME (Zhu et al., 2009) is implemented and a new function errorevol() shows the error of the ensembles as a function of the number of iterations. In addition, the ensembles can be pruned using the option 'newmfinal' in the predict.bagging() and predict.boosting() functions and the posterior probability of each class for observations can be obtained. Version 3.1 modifies the relative importance measure to take into account the gain of the Gini index given by a variable in each tree and the weights of these trees. Version 4.0 includes the margin-based ordered aggregation for Bagging pruning (Guo and Boukir, 2013) and a function to auto prune the 'rpart' tree. Moreover, three new plots are also available importanceplot(), plot.errorevol() and plot.margins(). Version 4.1 allows to predict on unlabeled data.

Details

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References

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Reverse cites: To the best of our knowledge this package has been cited by:

Andriyas, S. and McKee, M. (2013). Recursive partitioning techniques for modeling irrigation behavior. Environmental Modelling & Software, 47, 207–217.

Chan, J. C. W. and Paelinckx, D. (2008). Evaluation of Random Forest and Adaboost tree-based ensemble classification and spectral band selection for ecotope mapping using airborne hyperspectral imagery. Remote Sensing of Environment, 112(6), 2999–3011.

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Torgo, L. (2010). Data Mining with R: Learning with Case Studies. Series: Chapman & Hall/CRC Data Mining and Knowledge Discovery.

If you know any other work where this package is cited, please send us an email

See Also

autoprune, bagging, bagging.cv, boosting, boosting.cv, errorevol, importanceplot, margins, MarginOrderedPruning.Bagging, plot.errorevol, plot.margins, predict.bagging, predict.boosting

Examples

```
## rpart library should be loaded
data(iris)
iris.adaboost <- boosting(Species~., data=iris, boos=TRUE,
mfinal=3)
importanceplot(iris.adaboost)

sub <- c(sample(1:50, 35), sample(51:100, 35), sample(101:150, 35))
iris.bagging <- bagging(Species ~ ., data=iris[sub,], mfinal=3)
#Predicting with labeled data
iris.predbagging<-predict.bagging(iris.bagging, newdata=iris[-sub,])
iris.predbagging
#Predicting with unlabeled data
iris.predbagging<- predict.bagging(iris.bagging, newdata=iris[-sub,-5])
iris.predbagging</pre>
```

autoprune

Builds automatically a pruned tree of class rpart

Description

Builds automatically a pruned tree of class rpart looking in the cptable for the minimum cross validation error plus a standard deviation

Usage

```
autoprune(formula, data, subset=1:length(data[,1]), ...)
```

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Arguments

formula, as in the 1m function.

data a data frame in which to interpret the variables named in the formula.

subset optional expression saying that only a subset of the rows of the data should be

used in the fit, as in the rpart function.

... further arguments passed to or from other methods.

Details

The cross validation estimation of the error (xerror) has a random component. To avoid this randomness the 1-SE rule (or 1-SD rule) selects the simplest model with a xerror equal or less than the minimum xerror plus the standard deviation of the minimum xerror.

Value

An object of class rpart

Author(s)

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References

Breiman, L., Friedman, J.H., Olshen, R. and Stone, C.J. (1984): "Classification and Regression Trees". Wadsworth International Group. Belmont

Therneau, T., Atkinson, B. and Ripley, B. (2014). rpart: Recursive Partitioning and Regression Trees. R package version 4.1-5

See Also

rpart

Examples

```
## rpart library should be loaded
library(rpart)
data(iris)
iris.prune<-autoprune(Species~., data=iris)
iris.prune

## Comparing the test error of rpart and autoprune
library(mlbench)
data(BreastCancer)
1 <- length(BreastCancer[,1])
sub <- sample(1:1,2*1/3)

BC.rpart <- rpart(Class~.,data=BreastCancer[sub,-1],cp=-1, maxdepth=5)
BC.rpart.pred <- predict(BC.rpart,newdata=BreastCancer[-sub,-1],type="class")</pre>
```

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```
tb <-table(BC.rpart.pred,BreastCancer$Class[-sub])
tb
1-(sum(diag(tb))/sum(tb))

BC.prune<-autoprune(Class~.,data=BreastCancer[,-1],subset=sub)
BC.rpart.pred <- predict(BC.prune,newdata=BreastCancer[-sub,-1],type="class")
tb <-table(BC.rpart.pred,BreastCancer$Class[-sub])
tb
1-(sum(diag(tb))/sum(tb))</pre>
```

bagging

Applies the Bagging algorithm to a data set

Description

Fits the Bagging algorithm proposed by Breiman in 1996 using classification trees as single classifiers.

Usage

```
bagging(formula, data, mfinal = 100, control, par=FALSE,...)
```

Arguments

formula	a formula, as in the 1m function.
data	a data frame in which to interpret the variables named in the formula
mfinal	an integer, the number of iterations for which boosting is run or the number of trees to use. Defaults to mfinal=100 iterations.
control	options that control details of the rpart algorithm. See rpart.control for more details.
par	if TRUE, the cross validation process is runned in parallel. If FALSE (by default), the function runs without parallelization.
	further arguments passed to or from other methods.

Details

Unlike boosting, individual classifiers are independent among them in bagging

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Value

An object of class bagging, which is a list with the following components:

formula the formula used.

trees the trees grown along the iterations.

votes a matrix describing, for each observation, the number of trees that assigned it to

each class.

prob a matrix describing, for each observation, the posterior probability or degree of

support of each class. These probabilities are calculated using the proportion of

votes in the final ensemble.

class the class predicted by the ensemble classifier.

samples the bootstrap samples used along the iterations.

importance returns the relative importance of each variable in the classification task. This

measure takes into account the gain of the Gini index given by a variable in each

tree.

Author(s)

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References

Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

Alfaro, E., Garcia, N., Gamez, M. and Elizondo, D. (2008): "Bankruptcy forecasting: An empirical comparison of AdaBoost and neural networks". Decision Support Systems, 45, pp. 110–122.

Breiman, L. (1996): "Bagging predictors". Machine Learning, Vol 24, 2, pp.123–140.

Breiman, L. (1998): "Arcing classifiers". The Annals of Statistics, Vol 26, 3, pp. 801–849.

See Also

```
predict.bagging, bagging.cv
```

Examples

```
## rpart library should be loaded
#This example has been hidden to fulfill execution time <5s
#library(rpart)
#data(iris)
#iris.bagging <- bagging(Species~., data=iris, mfinal=10)

# Data Vehicle (four classes)
library(rpart)
library(mlbench)
data(Vehicle)
1 <- length(Vehicle[,1])</pre>
```

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```
sub <- sample(1:1,2*1/3)
Vehicle.bagging <- bagging(Class ~.,data=Vehicle[sub, ],mfinal=5,
control=rpart.control(maxdepth=5, minsplit=15))
#Using the pruning option
Vehicle.bagging.pred <- predict.bagging(Vehicle.bagging,newdata=Vehicle[-sub, ], newmfinal=3)
Vehicle.bagging.pred$confusion
Vehicle.bagging.pred$error</pre>
```

bagging.cv

Runs v-fold cross validation with Bagging

Description

The data are divided into v non-overlapping subsets of roughly equal size. Then, bagging is applied on (v-1) of the subsets. Finally, predictions are made for the left out subsets, and the process is repeated for each of the v subsets.

Usage

```
bagging.cv(formula, data, v = 10, mfinal = 100, control, par=FALSE)
```

Arguments

formula	a formula, as in the 1m function.
data	a data frame in which to interpret the variables named in formula
V	An integer, specifying the type of v-fold cross validation. Defaults to 10. If v is set as the number of observations, leave-one-out cross validation is carried out. Besides this, every value between two and the number of observations is valid and means that roughly every v-th observation is left out.
mfinal	an integer, the number of iterations for which boosting is run or the number of trees to use. Defaults to mfinal=100 iterations.
control	options that control details of the rpart algorithm. See rpart.control for more details.
par	if TRUE, the cross validation process is runned in parallel. If FALSE (by default), the function runs without parallelization.

Value

An object of class bagging.cv, which is a list with the following components:

class the class predicted by the ensemble classifier.

confusion the confusion matrix which compares the real class with the predicted one.

error returns the average error.

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Author(s)

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Breiman, L. (1996): "Bagging predictors". Machine Learning, Vol 24, 2, pp. 123-140.

Breiman, L. (1998). "Arcing classifiers". The Annals of Statistics, Vol 26, 3, pp. 801–849.

See Also

```
bagging, predict.bagging
```

Examples

```
## rpart library should be loaded
library(rpart)
data(iris)
iris.baggingcv <- bagging.cv(Species ~ ., v=2, data=iris, mfinal=3,
control=rpart.control(cp=0.01))
iris.baggingcv[-1]

## rpart and mlbench libraries should be loaded
## Data Vehicle (four classes)
#This example has been hidden to keep execution time <5s
#data(Vehicle)
#Vehicle.bagging.cv <- bagging.cv(Class ~.,data=Vehicle,v=5,mfinal=10,
#control=rpart.control(maxdepth=5))
#Vehicle.bagging.cv[-1]</pre>
```

boosting

Applies the AdaBoost.M1 and SAMME algorithms to a data set

Description

Fits the AdaBoost.M1 (Freund and Schapire, 1996) and SAMME (Zhu et al., 2009) algorithms using classification trees as single classifiers.

Usage

```
boosting(formula, data, boos = TRUE, mfinal = 100, coeflearn = 'Breiman',
control,...)
```

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Arguments

formula, as in the 1m function.

data a data frame in which to interpret the variables named in formula.

boos if TRUE (by default), a bootstrap sample of the training set is drawn using the

weights for each observation on that iteration. If FALSE, every observation is

used with its weights.

mfinal an integer, the number of iterations for which boosting is run or the number of

trees to use. Defaults to mfinal=100 iterations.

coeflearn if 'Breiman'(by default), alpha=1/2ln((1-err)/err) is used. If 'Freund'

alpha=ln((1-err)/err) is used. In both cases the AdaBoost.M1 algorithm is used and alpha is the weight updating coefficient. On the other hand, if co-

eflearn is 'Zhu' the SAMME algorithm is implemented with alpha=ln((1-err)/err)+

ln(nclasses-1).

control options that control details of the rpart algorithm. See rpart.control for more

details.

. . . further arguments passed to or from other methods.

Details

AdaBoost.M1 and SAMME are simple generalizations of AdaBoost for more than two classes. In AdaBoost-SAMME the individual trees are required to have an error lower than 1-1/nclasses instead of 1/2 of the AdaBoost.M1

Value

An object of class boosting, which is a list with the following components:

formula the formula used.

trees the trees grown along the iterations.

weights a vector with the weighting of the trees of all iterations.

votes a matrix describing, for each observation, the number of trees that assigned it to

each class, weighting each tree by its alpha coefficient.

prob a matrix describing, for each observation, the posterior probability or degree of

support of each class. These probabilities are calculated using the proportion of

votes in the final ensemble.

class the class predicted by the ensemble classifier.

importance returns the relative importance of each variable in the classification task. This

measure takes into account the gain of the Gini index given by a variable in a

tree and the weight of this tree.

Author(s)

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References

Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

Alfaro, E., Garcia, N., Gamez, M. and Elizondo, D. (2008): "Bankruptcy forecasting: An empirical comparison of AdaBoost and neural networks". Decision Support Systems, 45, pp. 110–122.

Breiman, L. (1998): "Arcing classifiers". The Annals of Statistics, Vol 26, 3, pp. 801–849.

Freund, Y. and Schapire, R.E. (1996): "Experiments with a new boosting algorithm". In Proceedings of the Thirteenth International Conference on Machine Learning, pp. 148–156, Morgan Kaufmann.

Zhu, J., Zou, H., Rosset, S. and Hastie, T. (2009): "Multi-class AdaBoost". Statistics and Its Interface, 2, pp. 349–360.

See Also

```
predict.boosting.cv
```

Examples

```
## rpart library should be loaded
data(iris)
iris.adaboost <- boosting(Species~., data=iris, boos=TRUE, mfinal=3)</pre>
iris.adaboost
## Data Vehicle (four classes)
library(mlbench)
data(Vehicle)
1 <- length(Vehicle[,1])</pre>
sub <- sample(1:1,2*1/3)
mfinal <- 3
maxdepth <- 5
Vehicle.rpart <- rpart(Class~.,data=Vehicle[sub,],maxdepth=maxdepth)</pre>
Vehicle.rpart.pred <- predict(Vehicle.rpart,newdata=Vehicle[-sub, ],type="class")</pre>
tb <- table(Vehicle.rpart.pred, Vehicle$Class[-sub])</pre>
error.rpart <- 1-(sum(diag(tb))/sum(tb))</pre>
tb
error.rpart
Vehicle.adaboost <- boosting(Class ~.,data=Vehicle[sub, ],mfinal=mfinal, coeflearn="Zhu",</pre>
control=rpart.control(maxdepth=maxdepth))
Vehicle.adaboost.pred <- predict.boosting(Vehicle.adaboost,newdata=Vehicle[-sub, ])</pre>
Vehicle.adaboost.pred$confusion
Vehicle.adaboost.pred$error
#comparing error evolution in training and test set
errorevol(Vehicle.adaboost,newdata=Vehicle[sub, ])->evol.train
errorevol(Vehicle.adaboost,newdata=Vehicle[-sub, ])->evol.test
```

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plot.errorevol(evol.test,evol.train)

boosting.cv

Runs v-fold cross validation with AdaBoost.M1 or SAMME

Description

The data are divided into v non-overlapping subsets of roughly equal size. Then, boosting is applied on (v-1) of the subsets. Finally, predictions are made for the left out subsets, and the process is repeated for each of the v subsets.

Usage

```
boosting.cv(formula, data, v = 10, boos = TRUE, mfinal = 100,
coeflearn = "Breiman", control, par=FALSE)
```

Arguments

formula a formula, as in the lm function.

data a data frame in which to interpret the variables named in formula

boos if TRUE (by default), a bootstrap sample of the training set is drawn using the

weights for each observation on that iteration. If FALSE, every observation is

used with its weights.

v An integer, specifying the type of v-fold cross validation. Defaults to 10. If v is

set as the number of observations, leave-one-out cross validation is carried out. Besides this, every value between two and the number of observations is valid

and means that roughly every v-th observation is left out.

mfinal an integer, the number of iterations for which boosting is run or the number of

trees to use. Defaults to mfinal=100 iterations.

coeflearn if 'Breiman' (by default), alpha=1/2ln((1-err)/err) is used. If 'Freund'

alpha=ln((1-err)/err) is used. In both cases the AdaBoost.M1 algorithm is used and alpha is the weight updating coefficient. On the other hand, if co-

eflearn is 'Zhu' the SAMME algorithm is implemented with alpha=ln((1-err)/err)+

ln(nclasses-1).

control options that control details of the rpart algorithm. See rpart.control for more

details.

par if TRUE, the cross validation process is runned in parallel. If FALSE (by default),

the function runs without parallelization.

Value

An object of class boosting.cv, which is a list with the following components:

class the class predicted by the ensemble classifier.

confusion the confusion matrix which compares the real class with the predicted one.

error returns the average error.

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Author(s)

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Alfaro, E., Garcia, N., Gamez, M. and Elizondo, D. (2008): "Bankruptcy forecasting: An empirical comparison of AdaBoost and neural networks". Decision Support Systems, 45, pp. 110–122.

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Freund, Y. and Schapire, R.E. (1996): "Experiments with a new boosting algorithm". In Proceedings of the Thirteenth International Conference on Machine Learning, pp. 148–156, Morgan Kaufmann.

Zhu, J., Zou, H., Rosset, S. and Hastie, T. (2009): "Multi-class AdaBoost". Statistics and Its Interface, 2, pp. 349–360.

See Also

```
boosting, predict.boosting
```

Examples

```
## rpart library should be loaded
data(iris)
iris.boostcv <- boosting.cv(Species ~ ., v=2, data=iris, mfinal=5,
control=rpart.control(cp=0.01))
iris.boostcv[-1]

## rpart and mlbench libraries should be loaded
## Data Vehicle (four classes)
#This example has been hidden to fulfill execution time <5s
#data(Vehicle)
#Vehicle.boost.cv <- boosting.cv(Class ~.,data=Vehicle,v=5, mfinal=10, coeflearn="Zhu",
#control=rpart.control(maxdepth=5))
#Vehicle.boost.cv[-1]</pre>
```

errorevol

Shows the error evolution of the ensemble

Description

Calculates the error evolution of an AdaBoost.M1, AdaBoost-SAMME or Bagging classifier for a data frame as the ensemble size grows

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Usage

errorevol(object, newdata)

Arguments

object This object must be the output of one of the functions bagging or boosting.

This is assumed to be the result of some function that produces an object with two components named formula and trees, as those returned for instance by

the bagging function.

newdata Could be the same data frame used in object or a new one

Details

This can be useful to see how fast Bagging, boosting reduce the error of the ensemble. in addition, it can detect the presence of overfitting and, therefore, the convenience of pruning the ensemble using predict.bagging or predict.boosting.

Value

An object of class errorevol, which is a list with only one component:

error a vector with the error evolution.

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References

Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

Alfaro, E., Garcia, N., Gamez, M. and Elizondo, D. (2008): "Bankruptcy forecasting: An empirical comparison of AdaBoost and neural networks". Decision Support Systems, 45, pp. 110–122.

Breiman, L. (1996): "Bagging predictors". Machine Learning, Vol 24, 2, pp.123-140.

Freund, Y. and Schapire, R.E. (1996): "Experiments with a new boosting algorithm". In Proceedings of the Thirteenth International Conference on Machine Learning, pp. 148–156, Morgan Kaufmann.

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See Also

boosting, predict.boosting, bagging, predict.bagging

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Examples

```
library(mlbench)
data(BreastCancer)
1 <- length(BreastCancer[,1])
sub <- sample(1:1,2*1/3)
cntrl <- rpart.control(maxdepth = 3, minsplit = 0, cp = -1)

BC.adaboost <- boosting(Class ~.,data=BreastCancer[sub,-1],mfinal=5, control=cntrl)
BC.adaboost.pred <- predict.boosting(BC.adaboost,newdata=BreastCancer[-sub,-1])
errorevol(BC.adaboost,newdata=BreastCancer[-sub,-1])->evol.test
errorevol(BC.adaboost,newdata=BreastCancer[sub,-1])->evol.train

plot.errorevol(evol.test,evol.train)
abline(h=min(evol.test[[1]]), col="red",lty=2,lwd=2)
abline(h=min(evol.train[[1]]), col="blue",lty=2,lwd=2)
```

importanceplot

Plots the variables relative importance

Description

Plots the relative importance of each variable in the classification task. This measure takes into account the gain of the Gini index given by a variable in a tree and, in the boosting case, the weight of this tree.

Usage

```
importanceplot(object, ...)
```

Arguments

object

fitted model object of class boosting or bagging. This is assumed to be the result of some function that produces an object with a component named importance

as that returned by the boosting and bagging functions.

... further arguments passed to or from other methods.

Details

For this goal, the varImp function of the caret package is used to get the gain of the Gini index of the variables in each tree.

Value

A labeled plot is produced on the current graphics device (one being opened if needed).

Author(s)

Esteban Alfaro-Cortes <Esteban.Alfaro@uclm.es>, Matias Gamez-Martinez <Matias.Gamez@uclm.es> and Noelia Garcia-Rubio <Noelia.Garcia@uclm.es>

References

Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

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Freund, Y. and Schapire, R.E. (1996): "Experiments with a new boosting algorithm". In Proceedings of the Thirteenth International Conference on Machine Learning, pp. 148–156, Morgan Kaufmann.

Zhu, J., Zou, H., Rosset, S. and Hastie, T. (2009): "Multi-class AdaBoost". Statistics and Its Interface, 2, pp. 349–360.

See Also

boosting, bagging,

Examples

```
#Examples
#Iris example
library(rpart)
data(iris)
sub <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
iris.adaboost <- boosting(Species ~ ., data=iris[sub,], mfinal=3)
importanceplot(iris.adaboost)

#Examples with bagging
#iris.bagging <- bagging(Species ~ ., data=iris[sub,], mfinal=5)
#importanceplot(iris.bagging, horiz=TRUE, cex.names=.6)</pre>
```

MarginOrderedPruning.Bagging

MarginOrderedPruning.Bagging

Description

Margin-based ordered aggregation for bagging pruning

Usage

```
MarginOrderedPruning.Bagging(baggingObject, trainingset, pruningset,
marginType = "unsupervised", doTrace = TRUE)
```

Arguments

baggingObject fitted model object of class bagging
trainingset the training set of the bagging object
pruningset a set aside dataset for bagging pruning

marginType if "unsupervised" (by default) the margin is the difference between the propor-

tions of votes of the first and second most popular classes. Else the margin is calculated as the difference between the proportion of votes of the correct class

and the most popular among the other classes

doTrace If set to TRUE, give a more verbose output as MarginOrderedPruning. Bagging

is running

Value

Returns a list with the following components:

```
prunedBagging a pruned bagging object
AccuracyOrderedEnsemblePruningSet
```

Accuracy of each ordered ensemble on pruning set

Note

Questions about this function should be sent to Li Guo

Author(s)

```
Li Guo <guoli84@hotmail.com>
```

References

Guo, L. and Boukir, S. (2013): "Margin-based ordered aggregation for ensemble pruning". Pattern Recognition Letters, 34(6), 603-609.

See Also

```
bagging, predict.bagging
```

Examples

```
## mlbench package should be loaded
library(mlbench)
data(Satellite)
## Separate data into 3 parts: training set, pruning set and test set
ind <- sample(3, nrow(Satellite), replace = TRUE, prob=c(0.3, 0.2,0.5))
## create bagging with training set
#increase mfinal in your own execution of this example to see
#the real usefulness of this function
Satellite.bagging<-bagging(classes~.,data=Satellite[ind==1,],mfinal=3)
#Satellite.bagging.pred<-predict(Satellite.bagging,Satellite[ind==3,])</pre>
```

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```
##pruning bagging
Satellite.bagging.pruning<-MarginOrderedPruning.Bagging(Satellite.bagging,
Satellite[ind==1,],Satellite[ind==2,])
#Satellite.bagging.pruning.pred<-predict(Satellite.bagging.pruning$prunedBagging,
#Satellite[ind==3,])

## create bagging with training and pruning set
#This example has been hidden to fulfill execution time <5s
#Satellite.bagging2<-bagging(classes~.,data=Satellite[ind!=3,],25)
#Satellite.bagging2.pred<-predict(Satellite.bagging2,Satellite[ind==3,])</pre>
```

margins

Calculates the margins

Description

Calculates the margins of an AdaBoost.M1, AdaBoost-SAMME or Bagging classifier for a data frame

Usage

```
margins(object, newdata)
```

Arguments

object This object must be the output of one of the functions bagging, boosting,

predict.bagging or predict.boosting. This is assumed to be the result of some function that produces an object with two components named formula

and class, as those returned for instance by the bagging function.

newdata The same data frame used for building the object

Details

Intuitively, the margin for an observation is related to the certainty of its classification. It is calculated as the difference between the support of the correct class and the maximum support of an incorrect class

Value

An object of class margins, which is a list with only one component:

margins a vector with the margins.

Author(s)

Esteban Alfaro-Cortes <Esteban.Alfaro@uclm.es>, Matias Gamez-Martinez <Matias.Gamez@uclm.es> and Noelia Garcia-Rubio <Noelia.Garcia@uclm.es>

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Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

Alfaro, E., Garcia, N., Gamez, M. and Elizondo, D. (2008): "Bankruptcy forecasting: An empirical comparison of AdaBoost and neural networks". Decision Support Systems, 45, pp. 110–122.

Schapire, R.E., Freund, Y., Bartlett, P. and Lee, W.S. (1998): "Boosting the margin: A new explanation for the effectiveness of voting methods". The Annals of Statistics, vol 26, 5, pp. 1651–1686.

See Also

```
bagging, boosting, plot.margins, predict.boosting, predict.bagging
```

Examples

```
#Iris example
library(rpart)
data(iris)
sub <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
iris.adaboost <- boosting(Species ~ ., data=iris[sub,], mfinal=3)</pre>
margins(iris.adaboost,iris[sub,])->iris.margins # training set
plot.margins(iris.margins)
# test set
iris.predboosting<- predict.boosting(iris.adaboost, newdata=iris[-sub,])</pre>
margins(iris.predboosting,iris[-sub,])->iris.predmargins
plot.margins(iris.predmargins,iris.margins)
#Examples with bagging
iris.bagging <- bagging(Species ~ ., data=iris[sub,], mfinal=3)</pre>
margins(iris.bagging,iris[sub,])->iris.bagging.margins # training set
iris.predbagging<- predict.bagging(iris.bagging, newdata=iris[-sub,])</pre>
margins(iris.predbagging,iris[-sub,])->iris.bagging.predmargins # test set
par(bg="lightyellow")
plot.margins(iris.bagging.predmargins,iris.bagging.margins)
```

plot.errorevol

Plots the error evolution of the ensemble

Description

Plots the previously calculated error evolution of an AdaBoost.M1, AdaBoost-SAMME or Bagging classifier for a data frame as the ensemble size grows

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Usage

```
## S3 method for class 'errorevol'
plot(x, y = NULL, ...)
```

Arguments

X	An object of class errorevol. This is assumed to be the result of some function
	that produces an object with a component named error as that returned by the
	errorevol function.

y This argument can be used to represent in the same plot the evolution of the test and train errors, x and y, respectively. Should be NULL (by default) or an object of class errorevol.

. . . further arguments passed to or from other methods.

Details

This can be useful to see how fast bagging or boosting reduce the error of the ensemble. in addition, it can detect the presence of overfitting and, therefore, the convenience of pruning the ensemble using predict.bagging or predict.boosting.

Value

A labeled plot is produced on the current graphics device (one being opened if needed).

Author(s)

Esteban Alfaro-Cortes <Esteban.Alfaro@uclm.es>, Matias Gamez-Martinez <Matias.Gamez@uclm.es> and Noelia Garcia-Rubio <Noelia.Garcia@uclm.es>

References

Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

Alfaro, E., Garcia, N., Gamez, M. and Elizondo, D. (2008): "Bankruptcy forecasting: An empirical comparison of AdaBoost and neural networks". Decision Support Systems, 45, pp. 110–122.

Breiman, L. (1996): "Bagging predictors". Machine Learning, Vol 24, 2, pp.123–140.

Freund, Y. and Schapire, R.E. (1996): "Experiments with a new boosting algorithm". In Proceedings of the Thirteenth International Conference on Machine Learning, pp. 148–156, Morgan Kaufmann.

Zhu, J., Zou, H., Rosset, S. and Hastie, T. (2009): "Multi-class AdaBoost". Statistics and Its Interface, 2, pp. 349–360.

See Also

boosting, predict.boosting, bagging, predict.bagging, errorevol

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Examples

```
data(iris)
train <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))

cntrl<-rpart.control(maxdepth=1)
#increase mfinal in your own execution of this example to see
#the real usefulness of this function
iris.adaboost <- boosting(Species ~ ., data=iris[train,], mfinal=10, control=cntrl)

#Error evolution along the iterations in training set
errorevol(iris.adaboost,iris[train,])->evol.train
plot.errorevol(evol.train)

#comparing error evolution in training and test set
errorevol(iris.adaboost,iris[-train,])->evol.test
plot.errorevol(evol.test, evol.train)

# See the help of the functions error evolution and boosting
# for more examples of the use of the error evolution
```

plot.margins

Plots the margins of the ensemble

Description

Plots the previously calculated margins of an AdaBoost.M1, AdaBoost-SAMME or Bagging classifier for a data frame

Usage

```
## S3 method for class 'margins'
plot(x, y = NULL, ...)
```

Arguments

У

X	An object of class margins. This is assumed to be the result of some function
	that produces an object with a component named margins as that returned by
	the margins function.

This argument can be used to represent in the same plot the margins in the test and train sets, x and y, respectively. Should be NULL (by default) or an object of class margins.

... further arguments passed to or from other methods.

Details

Intuitively, the margin for an observation is related to the certainty of its classification. It is calculated as the difference between the support of the correct class and the maximum support of an incorrect class

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Value

A labeled plot is produced on the current graphics device (one being opened if needed).

Author(s)

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Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

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Schapire, R.E., Freund, Y., Bartlett, P. and Lee, W.S. (1998): "Boosting the margin: A new explanation for the effectiveness of voting methods". The Annals of Statistics, vol 26, 5, pp. 1651–1686.

See Also

```
margins, boosting, predict.boosting, bagging, predict.bagging
```

Examples

```
library(mlbench)
data(BreastCancer)
1 <- length(BreastCancer[,1])
sub <- sample(1:1,2*1/3)
cntrl <- rpart.control(maxdepth = 3, minsplit = 0, cp = -1)

BC.adaboost <- boosting(Class ~.,data=BreastCancer[sub,-1],mfinal=5, control=cntrl)
BC.adaboost.pred <- predict.boosting(BC.adaboost,newdata=BreastCancer[-sub,-1])

BC.margins<-margins(BC.adaboost,BreastCancer[sub,-1]) # training set
BC.predmargins<-margins(BC.adaboost.pred,BreastCancer[-sub,-1]) # test set
plot.margins(BC.predmargins,BC.margins)</pre>
```

predict.bagging

Predicts from a fitted bagging object

Description

Classifies a dataframe using a fitted bagging object.

Usage

```
## S3 method for class 'bagging'
predict(object, newdata, newmfinal=length(object$trees), ...)
```

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Arguments

object fitted model object of class bagging. This is assumed to be the result of some

function that produces an object with the same named components as that re-

turned by the bagging function.

newdata data frame containing the values at which predictions are required. The predic-

tors referred to in the right side of formula(object) must be present by name

in newdata.

newmfinal The number of trees of the bagging object to be used in the prediction. This

argument allows the user to prune the ensemble. By default all the trees in the

bagging object are used

further arguments passed to or from other methods.

Value

An object of class predict.bagging, which is a list with the following components:

formula the formula used.

votes a matrix describing, for each observation, the number of trees that assigned it to

each class.

prob a matrix describing, for each observation, the posterior probability or degree of

support of each class. These probabilities are calculated using the proportion of

votes in the final ensemble.

class the class predicted by the ensemble classifier.

confusion the confusion matrix which compares the real class with the predicted one.

error returns the average error.

Author(s)

Esteban Alfaro-Cortes <Esteban. Alfaro@uclm.es>, Matias Gamez-Martinez <Matias. Gamez@uclm.es> and Noelia Garcia-Rubio <Noelia. Garcia@uclm.es>

References

Alfaro, E., Gamez, M. and Garcia, N. (2013): "adabag: An R Package for Classification with Boosting and Bagging". Journal of Statistical Software, Vol 54, 2, pp. 1–35.

Alfaro, E., Garcia, N., Gamez, M. and Elizondo, D. (2008): "Bankruptcy forecasting: An empirical comparison of AdaBoost and neural networks". Decision Support Systems, 45, pp. 110–122.

Breiman, L. (1996): "Bagging predictors". Machine Learning, Vol 24, 2, pp. 123-140.

Breiman, L. (1998). "Arcing classifiers". The Annals of Statistics, Vol 26, 3, pp. 801–849.

See Also

bagging, bagging.cv

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Examples

```
#library(rpart)
#data(iris)
#sub <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
#iris.bagging <- bagging(Species ~ ., data=iris[sub,], mfinal=5)</pre>
#iris.predbagging<- predict.bagging(iris.bagging, newdata=iris[-sub,])</pre>
#iris.predbagging
## rpart and mlbench libraries should be loaded
library(rpart)
library(mlbench)
data(BreastCancer)
1 <- length(BreastCancer[,1])</pre>
sub <- sample(1:1,2*1/3)
BC.bagging <- bagging(Class ~., data=BreastCancer[,-1], mfinal=5,
control=rpart.control(maxdepth=3))
BC.bagging.pred <- predict.bagging(BC.bagging,newdata=BreastCancer[-sub,-1])
BC.bagging.pred$prob
BC.bagging.pred$confusion
BC.bagging.pred$error
```

predict.boosting

Predicts from a fitted boosting object

Description

Classifies a dataframe using a fitted boosting object.

Usage

```
## S3 method for class 'boosting'
predict(object, newdata, newmfinal=length(object$trees), ...)
```

Arguments

object fitted model object of class boosting. This is assumed to be the result of some

function that produces an object with the same named components as that re-

turned by the boosting function.

newdata data frame containing the values at which predictions are required. The predic-

tors referred to in the right side of formula(object) must be present by name

in newdata.

newmfinal The number of trees of the boosting object to be used in the prediction. This

argument allows the user to prune the ensemble. By default all the trees in

object are used

. . . further arguments passed to or from other methods.

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Value

An object of class predict.boosting, which is a list with the following components:

formula the formula used.

votes a matrix describing, for each observation, the number of trees that assigned it to

each class, weighting each tree by its alpha coefficient.

prob a matrix describing, for each observation, the posterior probability or degree of

support of each class. These probabilities are calculated using the proportion of

votes in the final ensemble.

class the class predicted by the ensemble classifier.

confusion the confusion matrix which compares the real class with the predicted one.

error returns the average error.

Author(s)

Esteban Alfaro-Cortes < Esteban . Alfaro@uclm.es >, Matias Gamez-Martinez < Matias . Gamez@uclm.es > and Noelia Garcia-Rubio < Noelia . Garcia@uclm.es >

References

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Breiman, L. (1998): "Arcing classifiers". The Annals of Statistics, Vol 26, 3, pp. 801–849.

Freund, Y. and Schapire, R.E. (1996): "Experiments with a new boosting algorithm". En Proceedings of the Thirteenth International Conference on Machine Learning, pp. 148–156, Morgan Kaufmann.

Zhu, J., Zou, H., Rosset, S. and Hastie, T. (2009): "Multi-class AdaBoost". Statistics and Its Interface, 2, pp. 349–360.

See Also

boosting, boosting.cv

Examples

```
## rpart library should be loaded
#This example has been hidden to fulfill execution time <5s
#library(rpart)
#data(iris)
#sub <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
#iris.adaboost <- boosting(Species ~ ., data=iris[sub,], mfinal=10)
#iris.predboosting<- predict.boosting(iris.adaboost, newdata=iris[-sub,])
#iris.predboosting$prob</pre>
## rpart and mlbench libraries should be loaded
```

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```
## Comparing the test error of rpart and adaboost.M1
library(rpart)
library(mlbench)
data(BreastCancer)
1 <- length(BreastCancer[,1])</pre>
sub <- sample(1:1,2*1/3)</pre>
BC.rpart <- rpart(Class~.,data=BreastCancer[sub,-1], maxdepth=3)</pre>
BC.rpart.pred <- predict(BC.rpart,newdata=BreastCancer[-sub,-1],type="class")
tb <-table(BC.rpart.pred,BreastCancer$Class[-sub])</pre>
error.rpart <- 1-(sum(diag(tb))/sum(tb))</pre>
tb
error.rpart
BC.adaboost <- boosting(Class ~.,data=BreastCancer[,-1],mfinal=10, coeflearn="Freund",
boos=FALSE , control=rpart.control(maxdepth=3))
#Using the pruning option
BC.adaboost.pred <- predict.boosting (BC.adaboost, newdata=BreastCancer[-sub,-1], newmfinal=10)\\
BC.adaboost.pred$confusion
BC.adaboost.pred$error
```

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