Package ‘rfUtilities’

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Description Utilities for Random Forest model selection, class balance
correction, significance test, cross validation and partial dependency
plots.
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Description

Classification accuracy measures for pcc, kappa, users accuracy, producers accuracy

Usage

accuracy(x, y)

Arguments

x vector of predicted data or table/matrix contingency table
y vector of observed data, if x is not table/matrix contingency table
**accuracy**

**Value**

A list class object with the following components:

- PCC percent correctly classified (accuracy)
- auc Area Under the ROC Curve
- users.accuracy The users accuracy
- producers.accuracy The producers accuracy
- kappa Cohen’s Kappa (chance corrected accuracy)
- true.skill Hanssen-Kuiper skill score (aka true score statistic)
- sensitivity Sensitivity (aka, recall)
- specificity Specificity
- plr Positive Likelihood Ratio
- nlr Negative Likelihood Ratio
- typeI.error Type I error (omission)
- typeII.error Type II error (commission)
- gini Gini entropy index
- f.score F-score
- gain Information gain (aka precision)
- mcc Matthew’s correlation
- confusion A confusion matrix

**Note**

- sensitivity = true positives / ( true positives + false positives )
- specificity = true negatives / ( true negatives + false positives )
- Type I error = 1 - specificity
- Type II error = 1 - sensitivity
- Positive Likelihood Ratio = sensitivity / (1 - specificity)
- Negative Likelihood Ratio = (1 - sensitivity) / specificity
- gain = sensitivity / ( (true positives + true negatives) / n )
- auc = (tpr - fpr + 1) / 2
- F-Score = 2 * (precision * recall) / (precision + recall)
- Hanssen-Kuiper skill score (aka true score statistic) = [(tp * tn) - (fp * fn)] / [(tp + fn) + (fp + tn)], The true skill score has an expected -1 to +1, with 0 representing no discrimination.

Using the table function matrix positions for a 2x2 confusion matrix are TP(1), FN(3), FP(2), TN(4)

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References


Examples

# Two classes (vector)
observed <- sample(c(rep("Pres",50),rep("Abs",50)), 100, replace=TRUE )
accuracy(observed[sample(1:length(observed))], observed)

# Two classes (contingency table)
accuracy(cbind(c(15,11), c(2,123)))

# Multiple classes
accuracy(iris[sample(1:150),]$Species, iris$Species)

bivariate.partialDependence

Bivariate partial-dependency plot

Description

Bivariate partial dependence provides a graphical depiction of the marginal effect of two variables on the class probability (classification) or response (regression)

Usage

bivariate.partialDependence(x, pred.data, v1, v2, grid.size = 20, which.class = 2, plot = TRUE, col.ramp = c("#ffffff", "#2a2a2a"), ncols = 20, ...)

Arguments

x random forest object
pred.data data.frame of independent variables used in model
v1 Variable 1 used in partial dependency
v2 Variable 2 used in partial dependency
grid.size Number of grid cells (NxN) to integrate partial dependency for
which.class Index of class probability (only if classification)
plot (TRUE/FALSE) Plot 3D surface
col.ramp Colors used in building color ramp
ncols Number of colors in color ramp
... Arguments passed to persp
**Value**

A list object with vectors of \( v1 \) (p1) and \( v2 \) (p2) and a matrix (estimate), estimate of the averaged estimates.

**Note**

In deriving the partial-dependence, at each plotted point, the background variables are held at their median values.

**Author(s)**

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**References**


**See Also**

`persp` for persp ... plotting options

**Examples**

```r
library(randomForest)

data(iris)

iris$Species <- ifelse( iris$Species == "versicolor", 1, 0 )

# Add some noise
idx1 <- which(iris$Species %in% 1)
idx0 <- which( iris$Species %in% 0)
iris$Species[sample(idx1, 2)] <- 0
iris$Species[sample(idx0, 2)] <- 1

# Specify model
y = iris[,"Species"]
x = iris[,1:4]

set.seed(4364)
( rf.mdl1 <- randomForest(x=x, y=factor(y)) )

( bvpd <- bivariate.partialDependence(rf.mdl1, iris,
          v1 = "Petal.Length", v2 = "Petal.Width", shade = 0.6,
          shade = 0.6,
          v2 = "Petal.Width", shade = 0.6,
          v3 = "Petal.Length") )
```
logLoss

Description
Evaluation of estimate quality in binomial models using cross-entropy or log likelihood loss

Usage
logLoss(y, p, likelihood = FALSE, global = TRUE, eps = 0.000000000000001)

Arguments
y vector of observed binomial values 0,1
p vector of predicted probabilities 0-1
likelihood (FALSE/TRUE) return log likelihood loss, default is (FALSE) for log loss
global (TRUE/FALSE) return local or global log loss values, if FALSE local values are returned
eps epsilon scaling factor to avoid NaN values

Value
If likelihood TRUE the log likelihood loss will be returned. If global FALSE, a list with observed (y), probability (p) and log loss (log.loss) otherwise, a vector of global log loss value

Note
The log loss metric, based on cross-entropy, measures the quality of predictions rather than the accuracy. Effectively, the log loss is a measure that gages additional error coming the estimates as opposed to the true values.

As the estimated probability diverges from its observed value the log loss increases with an expected of [0-1] where 0 would be a perfect model. For a single sample with true value yt in 0,1 and estimated probability yp that yt = 1, the log loss is derived as: -log P(yt | yp) = -(yt log(yp) + (1 - yt) log(1 - yp)) eps is used where log loss is undefined for p=0 or p=1, so probabilities are clipped to: max(eps, min(1 - eps, p)) If likelihood is output, the eps and local arguments are ignored.

Author(s)
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References
Examples

```r
require(randomForest)
data(iris)
iris$Species <- ifelse( iris$Species == "versicolor", 1, 0 )
# Add some noise
idx1 <- which(iris$Species %in% 1)
idx0 <- which( iris$Species %in% 0)
iris$Species[sample(idx1, 2)] <- 0
iris$Species[sample(idx0, 2)] <- 1

( mdl <- randomForest(x=iris[,1:4], y=as.factor(iris[,"Species"])) )

# Global log loss
logLoss(y = iris$Species, p = predict(mdl, iris[,1:4], type="prob")[,2])

# Local log loss
( ll <- logLoss(y = iris$Species, p = predict(mdl, iris[,1:4],
                type="prob")[,2], global = FALSE) )

# Log likelihood loss
logLoss(y = iris$Species, p = predict(mdl, iris[,1:4],
        type="prob")[,2], likelihood = TRUE)
```

---

**multi.collinear**

*Multi-collinearity test*

**Description**

Test for multi-collinearity in data using qr-matrix decomposition

**Usage**

```r
multi.collinear(x, perm = FALSE, leave.out = FALSE, n = 99,
                p = 0.0000001, na.rm = FALSE)
```

**Arguments**

- `x`: data.frame or matrix object
- `perm`: (FALSE/TRUE) Should a permutation be applied
- `leave.out`: (FALSE/TRUE) Should a variable be left out at each permutation
- `n`: Number of permutations
- `p`: multi-collinearity threshold
- `na.rm`: (FALSE/TRUE) Remove NA values
Value

If perm == TRUE a data.frame of indicating the frequency that a variable was collinear and, if leave.out = TRUE the number of times it was omitted. Otherwise, a vector of collinear variables is returned. If no collinear variables are identified a NULL is returned.

Note

A permutation approach is not available where, at each iteration, the columns are randomly rearranged and a parameter dropped. The frequency that a variable is identified as collinear is accumulated. The multi-collinearity threshold needs to be adjusted based on number of parameters. For small number(s) of variables (<20) use ~1e-07 and for larger ~0.05

Author(s)

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References


Examples

```r
# Single test
( cl <- multi.collinear(test) )

# Permutated test with leave out
( cl.test <- multi.collinear(test, perm = TRUE, leave.out = TRUE, n = 999) )
  cl.test[cl.test$frequency > 0,]$variables

# Remove identified variable(s)
head( test[-which(names(test) %in% cl.test[cl.test$frequency > 0,]$variables)] )
```

Description

A statistical sensitivity test for occurrence probability thresholds
Usage

occurrence.threshold(x, xdata, class, p = seq(0.1, 0.7, 0.02),
   type = "delta.ss")

Arguments

x A classification randomForest model object
xdata Independent data used to build model
class What class to test
p Vector of probability thresholds
type What statistic to use in evaluation ("delta.ss", "sum.ss", "kappa")

Details

Available threshold evaluation statistics:

- kappa - The Kappa statistic is maximized
- sum.ss - The sum of sensitivity and specificity is maximized
- delta.ss - The absolute value of the difference between sensitivity and specificity is minimized

Value

An "occurrence.threshold" class object containing a "thresholds" vector object with evaluation statistic and probability thresholds as names.

Author(s)

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References


Examples

library(randomForest)
data(imports85)
imp85 <- imports85[, -2]
imp85 <- imp85[complete.cases(imp85), ]
imp85[] <- lapply(imp85, function(x) if (is.factor(x)) x[, drop=TRUE] else x)
y <- ifelse( imp85$numOfDoors != "four", "0", "1")
( rf.mdl <- randomForest(y = as.factor(y), x = imp85[, -5]) )
( delta.ss.t <- occurrence.threshold(rf.mdl, imp85[, -5], class = "1") )
( sum.ss.t <- occurrence.threshold(rf.mdl, imp85[, -5], class = "1",
   type = "sum.ss") )
( kappa.ss.t <- occurrence.threshold(rf.mdl, imp85[, -5], class = "1", type = "kappa") )

par(mfrow = c(2, 2))
plot(sum.ss.t)
plot(delta.ss.t)
plot(kappa.ss.t)

plot.occurrence.threshold

Plot occurrence thresholds

Description
Plot function for occurrence.threshold object

Usage
## S3 method for class 'occurrence.threshold'
plot(x, ...)

Arguments
x A occurrence.threshold object
...
Additional arguments passed to plot

Author(s)
Jeffrey S. Evans <jeffrey_evans@tnc.org>

plot.rf.cv

Plot random forests cross-validation

Description
Plot function for rf.cv object

Usage
## S3 method for class 'rf.cv'
plot(x, type = "cv", stat = "kappa", ...)
plot.rf.modelSel

Arguments

x
A rf.cv object

type
Which result to evaluate c("cv","model")

stat
Which statistic to plot: classification: "users.accuracy", "producers.accuracy", "kappa", "oob", regression: "rmse", "mse", "var.exp", "mae", "mbb"

... Additional arguments passed to plot

Author(s)

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Description

Dot plot function for rf.modelSel importance values

Usage

## S3 method for class 'rf.modelSel'
plot(x, imp = "sel", ...)

Arguments

x
A rf.modelSel object

imp
Plot selected ("sel") or all ("all") importance used in model selection

... Additional arguments passed to plot

Author(s)

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**plot.significance**

*Plot random forests significance*

**Description**

Plot function for significance object

**Usage**

```r
## S3 method for class 'significance'
plot(x, ...)
```

**Arguments**

- `x` A significance object
- `...` Additional arguments passed to `plot`

**Author(s)**

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---

**print.accuracy**

*Print accuracy*

**Description**

print method for class "accuracy"

**Usage**

```r
## S3 method for class 'accuracy'
print(x, ...)
```

**Arguments**

- `x` Object of class accuracy
- `...` Ignored
**print.occurrence.threshold**

*Print occurrence.threshold*

### Description

Print method for occurrence.threshold objects

### Usage

```r
## S3 method for class 'occurrence.threshold'
print(x, ...)
```

### Arguments

- `x` Object of class occurrence.threshold
- `...` Ignored

---

**print.rf.cv**

*Print random forests cross-validation*

### Description

Print method for rf.cv objects

### Usage

```r
## S3 method for class 'rf.cv'
print(x, ...)
```

### Arguments

- `x` Object of class rf.cv
- `...` Ignored
### print.rf.ensembles
*Print for combined random forests ensembles*

**Description**

print method for combined random forests ensembles

**Usage**

```r
## S3 method for class 'rf.ensembles'
print(x, ...)  
```

**Arguments**

- `x` Object of class rf.ensembles
- `...` Ignored

### print.rf.modelSel
*Print random forests model selection*

**Description**

Print method for rf.modelSel objects

**Usage**

```r
## S3 method for class 'rf.modelSel'
print(x, ...)  
```

**Arguments**

- `x` Object of class rf.modelSel
- `...` Ignored
print.significance

print.significance

Description

print method for class "significance"

Usage

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

Arguments

x
Object of class significance

... Ignored

probability.calibration

Isotonic probability calibration

Description

Performs an isotonic regression calibration of posterior probability to minimize log loss.

Usage

probability.calibration(y, p, regularization = FALSE)

Arguments

y
Binomial response variable used to fit model

p
Estimated probabilities from fit model

regularization (FALSE/TRUE) should regularization be performed on the probabilities? (see notes)

Value

a vector of calibrated probabilities

Note

Isotonic calibration can correct for monotonic distortions.

regularization defines new minimum and maximum bound for the probabilities using:

\[ p_{\text{max}} = \frac{(n1 + 1)}{(n1 + 2)}, \quad p_{\text{min}} = \frac{1}{(n0 + 2)}; \] where \( n1 \) = number of prevalence values and \( n0 \) = number of null values
Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

References


Examples

library(randomForest)
data(iris)
iris$Species <- ifelse( iris$Species == "versicolor", 1, 0 )

# Add some noise
idx1 <- which(iris$Species %in% 1)
idx0 <- which( iris$Species %in% 0)
iris$Species[sample(idx1, 2)] <- 0
iris$Species[sample(idx0, 2)] <- 1

# Specify model
y = iris[,"Species"]
x = iris[,1:4]
set.seed(4364)
( rf.mdl <- randomForest(x=x, y=factor(y)) )
y.hat <- predict(rf.mdl, iris[,1:4], type="prob")[,2]

# Calibrate probabilities
calibrated.y.hat <- probability.calibration(y, y.hat, regularization = TRUE)

# Plot calibrated against original probability estimate
plot(density(y.hat), col="red", xlim=c(0,1), ylab="Density", xlab="probabilities",
main="Calibrated probabilities")
lines(density(calibrated.y.hat), col="blue")
legend("topleft", legend=c("original","calibrated"), lty = c(1,1), col=c("red","blue"))

rf.class.sensitivity  Random Forests class-level sensitivity analysis

Description

Performs a sensitivity analysis on a specified class in a random forests model
rf.class.sensitivity

Usage

rf.class.sensitivity(x, xdata, d = "1", p = 0.05, nperm = 999,
plot = TRUE, seed = NULL, ...)

Arguments

  x  randomForest class object
  xdata  Independent variables used in model
  d  Which class to perturb
  p  Proportion of class to be randomized
  nperm  Number of permutations
  plot  Plot results (TRUE/FALSE)
  seed  Random seed value
  ...  Additional arguments passed to randomForest

Value

List object with following components: @return mean.error Mean of RMSE @return sd.error Standard deviation of RMSE @return rmse Root mean squared error (RMSE) for each perturbed probability @return probs data.frame with "true" estimate in first column and perturbed probabilities in subsequent columns.

Note

Wildlife survey data likely decreases the proportion of imperfect detection (false absences or presences) but can still be a source of error. Because of this it is often necessary to test the model sensitivity of a given class (e.g., used versus available habitat).

Model sensitivity of false absences is evaluated by randomly assigning a proportion of the specified positive class to the other, refitting the model and estimating the probabilities. Each perturbed estimate is compared against the "true" estimate. Currently only supports binomial models.

Author(s)

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References


Examples

```r
library(randomForest)
data(iris)
y <- as.factor(ifelse(iris$Species == "setosa" | iris$Species == "virginica", 1, 0))
xdata <- iris[,1:4]
rf.mdl <- randomForest(xdata, y, ntree=501)
ua <- rf.class.sensitivity(rf.mdl, xdata=xdata, nperm=20, ntree=501, plot=TRUE)
```

rf.classBalance

### Random Forest Class Balance (Zero Inflation Correction) Model

**Description**


**Usage**

`rf.classBalance(ydata, xdata, p = 0.005, cbf = 3, sf = 2, seed = NULL, ...)`

**Arguments**

- `ydata`: Response variable using index (i.e., `[,2]` or `[,"SPP"]`)
- `xdata`: Independent variables using index (i.e., `[3:14]` or `[3:ncol(data)]`)
- `p`: p-value of covariance convergence (do not recommend changing)
- `cbf`: Scaling factor to test if problem is imbalanced, default is size of majority class * 3
- `sf`: Majority subsampling factor. If sf=1 then random sample would be perfectly balanced with smallest class \[s | 0 = n | 1\] whereas; sf=2 provides \[s | 0 = (n | 1 * 2)\]
- `seed`: Sets random seed in R global environment
- `...`: Additional arguments passed to randomForest

**Value**

A `rf.balanced` object with the following components: @return model Final Combined Random Forests ensemble (randomForest object) @return OOB.error Out-of-bag error for each model (vector) @return confusion Confusion matrix for each model (list)

**Note**

This approach runs independent Random Forest models using random subsets of the majority class until covariance convergences on full data. The final model is obtained by combining independent ensembles.
rf.combine

Description

Combine two or more random forests models into a single ensemble.

Usage

rf.combine(...)
Arguments

... two or more randomForest class objects as individual objects or a list containing models

Value

An object of class randomForest

Note

The confusion, err.rate, mse and rsq components (as well as the corresponding components in the test component, if exist) are averaged across ensembles. This is a modification of the randomForest combine function that returns averaged validation statistics

Author(s)

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See Also

randomForest for randomForest details
combine for original combine function details

Examples

library(randomForest)
data(iris)
c1 <- randomForest(Species ~ ., iris, ntree=50, norm.votes=FALSE)
c2 <- randomForest(Species ~ ., iris, ntree=50, norm.votes=FALSE)
c3 <- randomForest(Species ~ ., iris, ntree=50, norm.votes=FALSE)
(class.combine <- rf.combine(c1,c2,c3) )
data(airquality)
set.seed(131)
r1 <- randomForest(Ozone ~ ., data=airquality, mtry=3,
                   importance=TRUE, na.action=na.omit)
r2 <- randomForest(Ozone ~ ., data=airquality, mtry=3,
                   importance=TRUE, na.action=na.omit)
r3 <- randomForest(Ozone ~ ., data=airquality, mtry=3,
                   importance=TRUE, na.action=na.omit)
(regress.combine <- rf.combine(r1,r2,r3) )
**rf.crossValidation**  
*Random Forest Classification or Regression Model Cross-validation*

**Description**

Implements a permutation test cross-validation for Random Forests models.

**Usage**

```r
rf.crossValidation(x, xdata, ydata = NULL, p = 0.1, n = 99,  
seed = NULL, normalize = FALSE, bootstrap = FALSE, trace = FALSE,  
...)
```

**Arguments**

- `x` random forest object
- `xdata` x data used in model
- `ydata` optional y data used in model, default is to use x$y from model object
- `p` Proportion data withheld (default p=0.10)
- `n` Number of cross validations (default n=99)
- `seed` Sets random seed in R global environment
- `normalize` (FALSE/TRUE) For regression, should rmse, mbe and mae be normalized using (max(y) - min(y))
- `bootstrap` (FALSE/TRUE) Should a bootstrap sampling be applied. If FALSE, an n-th percent withhold will be conducted
- `trace` Print iterations
- `...` Additional arguments passed to Random Forests

**Details**

For classification problems, the cross-validation statistics are based on the prediction error on the withheld data: Total observed accuracy represents the percent correctly classified (aka, PCC) and is considered as a naive measure of agreement. The diagonal of the confusion matrix represents correctly classified observations where off-diagonals represent cross-classification error. The primary issue with this evaluation is that does not reveal if error was evenly distributed between classes. To represent the balance of error one can use omission and commission statistics such as estimates of users and producers accuracy. User’s accuracy corresponds to error of commission (inclusion), observations being erroneously included in a given class. The commission errors are represented by row sums of the matrix. Producer’s accuracy corresponds to error of omission (exclusion), observations being erroneously excluded from a given class. The omission errors are represented by column sums of the matrix. None of the previous statistics account for random agreement influencing the accuracy measure. The kappa statistic is a chance corrected metric that reflects the difference between observed agreement and agreement expected by random chance. A kappa of k=0.85 would indicate that there is 85
• pcc = [Number of correct observations / total number of observations]

• producers accuracy = [Number of correct / total number of correct and omission errors]

• k = (observed accuracy - chance agreement) / (1 - chance agreement) where; change agreement = sum[product of row and column totals for each class]

For regression problems, a Bootstrap is constructed and the subset models MSE and percent variance explained is reported. Additional, the RMSE between the withheld response variable (y) and the predicted subset model

Value

For classification a "rf.cv"", "classification" class object with the following components:

• cross.validation$cv.users.accuracy Class-level users accuracy for the subset cross validation data

• cross.validation$cv.producers.accuracy Class-level producers accuracy for the subset cross validation data

• cross.validation$cv.oob Global and class-level OOB error for the subset cross validation data

• model$model.users.accuracy Class-level users accuracy for the model

• model$model.producers.accuracy Class-level producers accuracy for the model

• model$model.oob Global and class-level OOB error for the model

For regression a "rf.cv", "regression" class object with the following components:

• fit.var.exp Percent variance explained from specified fit model

• fit.mse Mean Squared Error from specified fit model

• y.rmse Root Mean Squared Error (observed vs. predicted) from each Bootstrap iteration (cross-validation)

• y.mbe Mean Bias Error from each Bootstrapped model

• y.mae Mean Absolute Error from each Bootstrapped model

• D Test statistic from Kolmogorov-Smirnov distribution Test (y and estimate)

• p.val p-value for Kolmogorov-Smirnov distribution Test (y and estimate)

• model.mse Mean Squared Error from each Bootstrapped model

• model.varExp Percent variance explained from each Bootstrapped model

Author(s)

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References


See Also

randomForest for randomForest ... options

Examples

## Not run:
library(randomForest)

# For classification
data(iris)
  iris$Species <- as.factor(iris$Species)
  set.seed(1234)
  ( rf.mdl <- randomForest(iris[,1:4], iris[,"Species"], ntree=501) )
  ( rf.cv <- rf.crossValidation(rf.mdl, iris[,1:4], p=0.10, n=99, ntree=501) )

  # Plot cross validation versus model producers accuracy
  par(mfrow=c(1,2))
  plot(rf.cv, type = "cv", main = "CV producers accuracy")
  plot(rf.cv, type = "model", main = "Model producers accuracy")

  # Plot cross validation versus model oob
  par(mfrow=c(1,2))
  plot(rf.cv, type = "cv", stat = "oob", main = "CV oob error")
  plot(rf.cv, type = "model", stat = "oob", main = "Model oob error")

# For regression
data(airquality)
  airquality <- na.omit(airquality)
  rf.mdl <- randomForest(y=airquality[,"Ozone"], x=airquality[,2:4])
  ( rf.cv <- rf.crossValidation(rf.mdl, airquality[,2:4],
                               p=0.10, n=99, ntree=501) )
  par(mfrow=c(2,2))
  plot(rf.cv)
  plot(rf.cv, stat = "mse")
  plot(rf.cv, stat = "var.exp")
  plot(rf.cv, stat = "mae")

## End(Not run)
rf.effectSize

Random Forest effect size

Description
Parameter effect size based on partial dependency (Cafri & Bailey, 2016)

Usage
rf.effectSize(x, y, ...)

Arguments
x  A randomForest model object
y  A vector represent the independent variable of interest
... Arguments passed to the partial dependency function, requires x.var, pred.data,

Value
A vector (single value) of the parameter effect size

Note
Effect size based on partial dependency and parameter-weighted OLS (does not support factorial or dichotomous variables) The algorithm follows: 1) Grow a forest 2) Estimate partial dependence (for a single variable). a. Create datasets for all observation in the dataset only let them take on one value for the variable of interest while keeping values of all other variables unchanged. b. Pass the dataset through each tree and average the predictions over the trees in the forest. 3) Construct a point estimate of the proposed effect size by fitting a weighted least squares model with response based on the tree-averaged predicted values obtained in Step 2, the explanatory variable corresponding to the value used to generate each tree-averaged prediction, and weight based on the frequency each value the explanatory variable takes on in the original data. 4) For confidence intervals, repeat Steps 1-3 for as many bootstrap samples as desired Modified partialPlot function uses distinct X values to construct partial dependence for non-factor variables

Author(s)
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References

See Also
partialPlot for ... options
randomForest for randomForest details
Examples

```r
cat("Example 1:\n")
library(randomForest)
data(airquality)
airquality <- na.omit(airquality)
fit.reg <- randomForest(Ozone ~ ., data=airquality)

# Parameter effect sizes
rf.effectSize(fit.reg, y = airquality$Wind, pred.data = airquality, x.var = Wind)
rf.effectSize(fit.reg, y = airquality$Temp, pred.data = airquality, x.var = Temp)
rf.effectSize(fit.reg, y = airquality$Month, pred.data = airquality, x.var = Month)
rf.effectSize(fit.reg, y = airquality$Day, pred.data = airquality, x.var = Day)

## Not run:
# Bootstrap of effect size for Wind and Temp
B = 999
n = nrow(airquality)
es.boot.wind <- vector()
es.boot.temp <- vector()
for(i in 1:B) {
  boot.samples <- airquality[sample(1:nrow(airquality), n, replace = TRUE),]
  fmla <- stats::as.formula(paste(paste("Ozone","~","", sep=""), paste(".", collapse=""))
  fit <- randomForest(fmla, data = boot.samples)
  es.boot.wind <- append(es.boot.wind, rf.effectSize(fit, y = boot.samples$Wind,
                                          pred.data = boot.samples, x.var = Wind))
  es.boot.temp <- append(es.boot.temp, rf.effectSize(fit, y = boot.samples$Temp,
                                          pred.data = boot.samples, x.var = Temp))
}
se <- function(x) sqrt(var(x, na.rm = TRUE) / length(na.omit(x)))
cat("Bootstrap variance for Wind:, var(es.boot.wind), \"n\")
cat("Bootstrap standard error for Wind:, se(es.boot.wind), \"n","n")
cat("Bootstrap variance for Temp:, var(es.boot.temp), \"n\")
cat("Bootstrap standard error for Temp:, se(es.boot.temp), \"n")

# Confidence intervals of Bootstrap of effect size for Wind
p=0.95
y <- sort(es.boot.wind)
x <- 1:length(y)
plx <- stats::predict(stats::loess(y ~ x), se=TRUE)
cli = plx$fit - stats::qt(p, plx$df) * plx$se.fit
uci = plx$fit + stats::qt(p, plx$df) * plx$se.fit
graphics::plot(x, y, type="n", main="Effect size Bootstrap CI for Wind",
sub=paste("confidence intervals at", p))
graphics::polygon(c(x,rev(x)), c(cli, rev(uci)), col="grey86")
graphics::points(x, y, pch=3, cex=0.7)
graphics::lines(x, plx[["fit"]], lty=3)

# Confidence intervals of Bootstrap of effect size for Temp
p=0.95
y <- sort(es.boot.temp)
x <- 1:length(y)
plx <- stats::predict(stats::loess(y ~ x), se=TRUE)
```
```r
lci = plx$fit - stats::qt(p, plx$df) * plx$se.fit
uci = plx$fit + stats::qt(p, plx$df) * plx$se.fit

graphics::plot(x, y, type="n", main="Effect size Bootstrap CI for Temp",
sub=paste("confidence intervals at", p))
graphics::polygon(c(x,rev(x)), c(lci, rev(uci)), col="grey86")
graphics::points(x, y, pch=20, cex=0.70)
graphics::lines(x, plx["fit"], lty=3)

# Plot bootstrap of wind effect size
pdf <- density(es.boot.wind)
plot(pdf, type="n", main="Bootstrap of effect size wind (n=99)",
     ylab="p", xlab="effect size")
polygon(pdf, col="grey")
abline(v=mean(es.boot.wind))
abline(v=mean(es.boot.wind)-sd(es.boot.wind), col="blue", lty=3)
abline(v=mean(es.boot.wind)+sd(es.boot.wind), col="blue", lty=3)

# Plot bootstrap of temp effect size
pdf <- density(es.boot.temp)
plot(pdf, type="n", main="Bootstrap of effect size temp (n=99)",
     ylab="p", xlab="effect size")
polygon(pdf, col="grey")
abline(v=mean(es.boot.temp))
abline(v=mean(es.boot.temp)-sd(es.boot.temp), col="blue", lty=3)
abline(v=mean(es.boot.temp)+sd(es.boot.temp), col="blue", lty=3)

## End(Not run)
```

---

**rf.imp.freq**

**Random Forest variable selection frequency**

**Description**

Evaluates the frequency that an independent variables are selected greater-than/equal-to defined importance threshold

**Usage**

```
rf.imp.freq(x, p = 0.6, plot = TRUE)
```

**Arguments**

- **x**: random forest object
- **p**: Threshold of row standardized importance values
- **plot**: Plot frequencies (TRUE/FALSE)
rf.modelSel

Value

A list class object with the following components: frequency: var - names of independent variables used in model global - if a variable greater-than/equal-to importance threshold, else NA column for each class where greater-than/equal-to importance threshold, else NA var.freq - frequency a variable is selected for global and local importance >= importance threshold

importance: Standardized importance matrix from randomForest model

Note

Evaluates the number of times a variable is selected greater-than/equal-to defined threshold (p) for the global and local (class level) importances. This allow one to evaluate if a given variable is important to the overall model or specific classes.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```r
require(randomForest)
data(iris)
iris.rf <- randomForest(Species ~ ., data=iris, importance=TRUE)
rf.imp.freq(iris.rf, p = 0.30)
```

rf.modelSel

Random Forest Model Selection

Description


Usage

```r
rf.modelSel(xdata, ydata, imp.scale = "mir", r = c(0.25, 0.5, 0.75), final.model = FALSE, seed = NULL, parsimony = NULL, ...)
```

Arguments

- `xdata`: X Data for model
- `ydata`: Y Data for model
- `imp.scale`: Type of scaling for importance values (mir or se), default is mir
- `r`: Vector of importance percentiles to test i.e., c(0.1, 0.2, 0.5, 0.7, 0.9)
- `final.model`: Run final model with selected variables (TRUE/FALSE)
- `seed`: Sets random seed in the R global environment. This is highly suggested.
parsimony  Threshold for competing model (0-1)

Additional arguments to pass to randomForest (e.g., ntree=1000, replace=TRUE, proximity=TRUE)

Details

If you want to run classification, make sure that y is a factor, otherwise the randomForest model runs in regression mode. For classification problems the model selection criteria is: smallest OOB error, smallest maximum within class error, and fewest parameters. For regression problems, the model selection criteria is; largest

The "mir" scale option performs a row standardization and the "se" option performs normalization using the "standard errors" of the permutation-based importance measure. Both options result in a 0-1 range but, "se" sums to 1. The scaled importance measures are calculated as: \( \text{mir} = i / \max(i) \) and \( \text{se} = (i / \text{se}) / (\sum(i) / \text{se}) \). The parsimony argument is the percent of allowable error surrounding competing models. For example, if there are two competing models, a selected model with 5 parameters and a competing model with 3 parameters, and parsimony = 0.05, if there is +/- 5 the fewer parameter model it will be selected at the final model.

Value

A list class object with the following components:

- "rf.final" Final selected model, if final = TRUE(randomForest model object)
- "sel.vars" Final selected variables (vector)
- "test" Validation parameters used on model selection (data.frame)
- "sel.importance" Importance values for selected model (data.frame)
- "importance" Importance values for all models (data.frame)
- "parameters" Variables used in each tested model (list)
- "s" Type of scaling used for importance

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References


See Also

randomForest for randomForest ... model options
Examples

# Classification on iris data
require(randomForest)
data(iris)
iris$Species <- as.factor(iris$Species)
(rf.class <- rf.modelSel(iris[,1:4], iris[,"Species"], seed=1234, imp.scale="mir") )
(rf.class <- rf.modelSel(iris[,1:4], iris[,"Species"], seed=1234, imp.scale="mir", parsimony=0.03) )
plot(rf.class) # plot importance for selected variables
plot(rf.class, imp = "all") # plot importance for all variables

vars <- rf.class$selvars
(rf.fit <- randomForest(x=iris[,vars], y=iris[,"Species"]))

# Regression on airquality data
data(airquality)
airquality <- na.omit(airquality)
(rf.regress <- rf.modelSel(airquality[,2:6], airquality[,1], imp.scale="se") )
(rf.regress <- rf.modelSel(airquality[,2:6], airquality[,1], imp.scale="se", parsimony=0.03) )
plot(rf.regress) # plot importance for selected variables
plot(rf.regress, imp = "all") # plot importance for all variables

# To use parameters from competing model
vars <- rf.regress$parameters[[3]]

# To use parameters from selected model
vars <- rf.regress$selvars
(rf.fit <- randomForest(x=airquality[,vars], y=airquality[,1]))

rf.partial.ci
Random Forests regression partial dependency plot with confidence intervals

Description

Plots the partial dependency, and associated confidence intervals, of a random forests regression model

Usage

rf.partial.ci(m, x, yname, xname, lci = 0.25, uci = 0.75, delta = FALSE)
rf.partial.prob

Random Forest probability scaled partial dependency plots

Description

Produces partial dependency plots with probability distribution based on scaled margin distances.

Usage

rf.partial.prob(x, pred.data, xname, which.class, w, prob = TRUE, plot = TRUE, smooth, conf = TRUE, smooth.parm = NULL, pts = FALSE, raw.line = FALSE, rug = FALSE, n.pt, xlab, ylab, main, ...)
Arguments

- **x**: Object of class randomForest
- **pred.data**: Training data.frame used for constructing the plot,
- **xname**: Name of the variable for calculating partial dependence
- **which.class**: The class to focus on
- **w**: Weights to be used in averaging (if not supplied, mean is not weighted)
- **prob**: Scale distances to probabilities
- **plot**: (TRUE/FALSE) Plot results
- **smooth**: c(spline, loess) Apply spline.smooth or loess to
- **conf**: (TRUE/FALSE) Should confidence intervals be calculated for smoothing
- **smooth.parm**: An appropriate smoothing parameter passed to loess or smooth.spline
- **pts**: (FALSE/TRUE) Add raw points
- **raw.line**: (FALSE/TRUE) Plot raw line (non-smoothed)
- **rug**: Draw hash marks on plot representing deciles of x
- **n.pt**: Number of points on the grid for evaluating partial dependence.
- **xlab**: x-axis plot label
- **ylab**: y-axis plot label
- **main**: Plot label for main
- **...**: Additional graphical parameters passed to plot

Value

A list class object with fit x,y. If smooth=c("spline","loess") y represents smoothed scaled margin distance values

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References


See Also

smooth.spline for smooth.spline details on spar smoothing argument
loess for loess details of span smoothing argument
Examples

```r
require(randomForest)
data(iris)
iris.rf <- randomForest(iris[,1:4], iris[,5])

# plot all parameters
par(mfrow=c(2,2))
for(i in names(iris)[1:4]) {
  rf.partial.prob(iris.rf, iris, i, "setosa", smooth="spline",
                n.pt=70, smooth.parm = 0.5)
}

# Plot spline and loess smoothing for one parameter, with raw points and line
par(mfrow=c(1,2))
rf.partial.prob(x = iris.rf, pred.data = iris, xname = "Sepal.Length",
                which.class = "setosa", smooth = "spline", smooth.parm = 0.5,
                n.pt = 70, pts = TRUE, raw.line = TRUE, rug = TRUE)
rf.partial.prob(x = iris.rf, pred.data = iris, xname = "Sepal.Length",
                which.class = "setosa", smooth = "loess", smooth.parm = 0.20,
                n.pt = 70, pts = TRUE, raw.line = TRUE, rug = TRUE)
```

**rf.regression.fit**

*Random Forest fit statistics*

**Description**

Evaluates fit and overfit of random forests regression

**Usage**

```r
rf.regression.fit(x)
```

**Arguments**

- `x` randomForest regression object

**Value**

A list and rf.fit class object with "fit" matrix of fit statistics and "message" indicating overfit risk.

**Author(s)**

Jeffrey S. Evans &lt;jeffrey_evans@tnc.org&gt;
**Examples**

```r
library(randomForest)
set.seed(131)
data(airquality)
airquality <- na.omit(airquality)
( rf.aq <- randomForest(airquality[,1:3], airquality[,"Ozone"] )
rf.regression.fit(rf.aq)
```

---

**rf.significance**

Random Forest model significance test

**Description**

Performs significance test for classification and regression Random Forests models.

**Usage**

```r
rf.significance(x, xdata, q = 0.99, p = 0.05, nperm = 999, ...)
```

**Arguments**

- `x`: randomForest class object
- `xdata`: Independent variables (x) used in model
- `q`: Quantile threshold to test classification models
- `p`: p-value to test for significance in regression models
- `nperm`: Number of permutations
- `...`: Additional Random Forests arguments

**Value**

A list class object with the following components:

For Regression problems:
- `RandRsquare`: Vector of random R-square values
- `Rsquare`: The R-square of the "true" model
- `Accept`: Is the model significant at specified p-value (TRUE/FALSE)
- `TestQuantile`: Quantile threshold used in significance plot
- `pValueThreshold`: Specified p-value
- `pValue`: p-values of randomizations
- `nPerm`: Number of permutations

For Classification problems:
- `RandOOB`: Vector of random out-of-bag (OOB) values
RandMaxError Maximum error of randomizations

test.OOB Error if the "true" model

Accept Is the model significant at specified p-value (TRUE/FALSE)

TestQuantile Quantile threshold used in significance plot

pValueThreshold Specified p-value

pValue p-values of randomizations

nPerm Number of permutations

Author(s)

Jeffrey S. Evans <jeffrey.evans@tnc.org>

References


Examples

```r
## Not run:
# Regression
require(randomForest)
set.seed(1234)
data(airquality)
airquality <- na.omit(airquality)
( rf.mdl <- randomForest(x=airquality[,2:6], y=airquality[,1]) )
( rf.perm <- rf.significance(rf.mdl, airquality[,2:6], nperm=99, ntree=501) )

# Classification
require(randomForest)
set.seed(1234)
data(iris)
iris$Species <- as.factor(iris$Species)
( rf.mdl <- randomForest(iris[,1:4], iris[,"Species"], ntree=501) )
( rf.perm <- rf.significance(rf.mdl, iris[,1:4], nperm=99, ntree=501) )

## End(Not run)
```
rf.unsupervised

Unsupervised Random Forests

Description
Performs an unsupervised Random Forests for returning clustering, based on dissimilarity, and optional neighbor distance.

Usage
rf.unsupervised(x, n = 2, proximity = FALSE, silhouettes = FALSE, clara = FALSE, ...)

Arguments
- x: A matrix/data/frame object to cluster
- n: Number of clusters
- proximity: (FALSE/TRUE) Return matrix of neighbor distances based on proximity
- silhouettes: (FALSE/TRUE) Return adjusted silhouette values
- clara: (FALSE/TRUE) Use clara partitioning, for large data
- ...: Additional Random Forests arguments

Value
A vector of clusters or list class object of class "unsupervised", containing the following components:
- distances: Scaled proximity matrix representing dissimilarity neighbor distances
- k: Vector of cluster labels using adjusted silhouettes
- silhouette.values: Adjusted silhouette cluster labels and silhouette values

Note
Clusters (k) are derived using the random forests proximity matrix, treating it as dissimilarity neighbor distances.
The clusters are identified using a Partitioning Around Medoids where negative silhouette values are assigned to the nearest neighbor.

Author(s)
Jeffrey S. Evans <jeffrey_evans@tnc.org>
References


See Also

randomForest for ... options
pam for details on Partitioning Around Medoids (PAM)
clara for details on Clustering Large Applications (clara)

Examples

library(randomForest)
data(iris)
n = 4
clust.iris <- rf.unsupervised(iris[,1:4], n=n, proximity = TRUE,
   silhouettes = TRUE)
clust.iris$k

mds <- stats:::cmdscale(clust.iris$distances, eig=TRUE, k=n)
colnames(mds$points) <- paste("Dim", 1:n)
mds.col <- ifelse(clust.iris$k == 1, rainbow(4)[1],
   ifelse(clust.iris$k == 2, rainbow(4)[2],
   ifelse(clust.iris$k == 3, rainbow(4)[3],
   ifelse(clust.iris$k == 4, rainbow(4)[4], NA)))
plot(mds$points[,1:2],col=mds.col, pch=20)
pairs(mds$points, col=mds.col, pch=20)

rfu.news

rfUtilities news

Description

Displays release notes

Usage

rfu.news(...)
**summary.accuracy**

### Summarizing accuracy

**Description**

Summary method for class "accuracy".

**Usage**

```r
## S3 method for class 'accuracy'
summary(object, ...)
```

**Arguments**

- `object` Object of class accuracy
- `...` Ignored

---

**summary.occurrence.threshold**

### Summarizing occurrence.threshold

**Description**

Summarize occurrence.threshold

**Usage**

```r
## S3 method for class 'occurrence.threshold'
summary(object, ...)
```

**Arguments**

- `object` Object of occurrence.threshold
- `...` Ignored
### summary.rf.cv

**Summarizing cross-validation**

**Description**

Summarizing of the rf.crossValidation function

**Usage**

```r
## S3 method for class 'rf.cv'
summary(object, ...)
```

**Arguments**

- **object**: Object of class rf.cv
- **...**: Ignored

### summary.rf.ensembles

**Summary for combined random forests ensembles**

**Description**

summary method for combined random forests ensembles

**Usage**

```r
## S3 method for class 'rf.ensembles'
summary(object, ...)
```

**Arguments**

- **object**: Object of class rf.ensembles
- **...**: Ignored
summarize.rf.modelSel  

**Summary of random forests model selection**

**Description**
Summarizing of the rf.modelSel function

**Usage**
```r
define S3 method for class 'rf.modelSel'
summary(object, ...)
```

**Arguments**
- `object` Object of class rf.modelSel
- `...` Ignored

**summary.significance**  

**Summary of significance**

**Description**
Summarizing of a rf.significance object

**Usage**
```r
define S3 method for class 'significance'
summary(object, ...)
```

**Arguments**
- `object` Object of class significance
- `...` Ignored
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