Package 'crossval'

June 9, 2023

Version 1.0.5

Date 2023-06-08

Title Generic Functions for Cross Validation

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Depends R (>= 3.0.2)

Imports stats

Suggests MASS, sda, care, binda

Description Contains generic functions for performing
    cross validation and for computing diagnostic errors.

License GPL (>= 3)

URL https://cran.r-project.org/package=crossval

NeedsCompilation no

Repository CRAN

Date/Publication 2023-06-08 22:40:02 UTC

R topics documented:

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crossval-package   *The crossval Package*

Description

The "crossval" package implements generic functions for performing cross validation and for computing diagnostic errors.

Author(s)

Korbinian Strimmer (<https://strimmerlab.github.io/>)

References

Website: <https://cran.r-project.org/package=crossval>

See Also

crossval, confusionMatrix, diagnosticErrors.

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confusionMatrix   *Compute Confusion Matrix*

Description

confusionMatrix computes the confusion matrix, i.e. it counts the number of false positives (FP), true positives (TP), true negatives (TN), and false negatives (FN).

Despite its name the functions returns a vector rather than an actual matrix for easier use with the crossval function.

Usage

```
confusionMatrix(actual, predicted, negative="control")
```

Arguments

actual	a vector containing the actual correct labels for each sample (e.g. "cancer" or "control").
predicted	a vector containing the predicted labels.
negative	the label of a negative "null" sample (default: "control").

Value

confusionMatrix returns a vector of length 4 containing the counts for FP, TP, TN, and FN.

Author(s)

Korbinian Strimmer (<https://strimmerlab.github.io>).

See Also

[diagnosticErrors](#).

Examples

```
# load crossval library
library("crossval")

# true labels
a = c("cancer", "cancer", "control", "control", "cancer", "control", "control")

# predicted labels
p = c("cancer", "control", "control", "control", "cancer", "control", "cancer")

# confusion matrix (a vector)
cm = confusionMatrix(a, p, negative="control")
cm
# FP TP TN FN
# 1  2  3  1
# attr(,"negative")
# [1] "control"

# corresponding accuracy, sensitivity etc.
diagnosticErrors(cm)
#       acc      sens      spec       ppv       npv       lor
# 0.7142857 0.6666667 0.7500000 0.6666667 0.7500000 1.7917595
# attr(,"negative")
# [1] "control"
```

---

crossval	*Generic Function for Cross Valdidation*

Description

crossval performs K-fold cross validation with B repetitions. If Y is a factor then balanced sampling is used (i.e. in each fold each category is represented in appropriate proportions).

Usage

```
crossval(predfun, X, Y, K=10, B=20, verbose=TRUE, ...)
```

Arguments

predfun	Prediction function (see details).
X	Matrix of predictors (columns correspond to variables).
Y	Univariate response variable.
K	Number of folds.
B	Number of repetitions.
verbose	If verbose=TRUE then status messages appear during cross validation.
...	optional arguments for predfun

Details

The argument predfun must be a function of the form predfun(Xtrain, Ytrain, Xtest, Ytest, ...).

Value

crossval returns a list with three entries:

stat.cv: the statistic returned by predfun for each cross validation run.

stat: the statistic returned by predfun averaged over all cross validation runs.

stat.se: the corresponding standard error.

Author(s)

Korbinian Strimmer (<https://strimmerlab.github.io>).

See Also

confusionMatrix.

Examples

```
# load "crossval" package
library("crossval")

# classification examples

# set up lda prediction function
predfun.lda = function(train.x, train.y, test.x, test.y, negative)
{
  require("MASS") # for lda function

  lda.fit = lda(train.x, grouping=train.y)
  ynew = predict(lda.fit, test.x)$class

  # count TP, FP etc.
  out = confusionMatrix(test.y, ynew, negative=negative)

  return( out )
```

```
  }


  # Student's Sleep Data
  data(sleep)
  X = as.matrix(sleep[,1, drop=FALSE]) # increase in hours of sleep
  Y = sleep[,2] # drug given
  plot(X ~ Y)
  levels(Y) # "1" "2"
  dim(X) # 20  1

  set.seed(12345)
  cv.out = crossval(predfun.lda, X, Y, K=5, B=20, negative="1")

  cv.out$stat
  diagnosticErrors(cv.out$stat)


  # linear regression example

  data("attitude")
  y = attitude[,1] # rating variable
  x = attitude[,-1] # date frame with the remaining variables
  is.factor(y) # FALSE

  summary( lm(y ~ . , data=x) )

  # set up lm prediction function
  predfun.lm = function(train.x, train.y, test.x, test.y)
  {
    lm.fit = lm(train.y ~ . , data=train.x)
    ynew = predict(lm.fit, test.x )

    # compute squared error risk (MSE)
    out = mean( (ynew - test.y)^2 )

    return( out )
  }


  # prediction MSE using all variables
  set.seed(12345)
  cv.out = crossval(predfun.lm, x, y, K=5, B=20)
  c(cv.out$stat, cv.out$stat.se)

  # and only two variables
  cv.out = crossval(predfun.lm, x[,c(1,3)], y, K=5, B=20)
  c(cv.out$stat, cv.out$stat.se)



  # for more examples (e.g. using cross validation in a regression or classification context)
  # see the R packages "sda", "care", or "binda".
```

diagnosticErrors	*Compute Diagnostic Errors: Accuracy, Sensitivity, Specificity, Positive Predictive Value, Negative Predictive Value, Log Odds Ratio*

Description

diagnosticErrors computes various diagnostic errors useful for evaluating the performance of a diagnostic test or a classifier: accuracy (acc), sensitivity (sens), specificity (spec), positive predictive value (ppv), negative predictive value (npv), and log-odds ratio (lor).

Usage

```
diagnosticErrors(cm)
```

Arguments

cm   a vector containing the true positives, false positives etc, as computed by [confusionMatrix](#).

Details

The diagnostic errors are computed as follows:

acc = (TP+TN)/(FP+TN+TP+FN)

sens = TP/(TP+FN)

spec = TN/(FP+TN)

ppv = TP/(FP+TP)

npv = TN/(TN+FN)

lor = log(TP*TN/(FN*FP))

Value

diagnostic errors returns a vector containing various diagnostic errors.

Author(s)

Korbinian Strimmer (<https://strimmerlab.github.io>).

See Also

[confusionMatrix](#).

Examples

```
# load crossval library
library("crossval")

# true labels
a = c("cancer", "cancer", "control", "control", "cancer", "control", "control")

# predicted labels
p = c("cancer", "control", "control", "control", "cancer", "control", "cancer")

# confusion matrix (a vector)
cm = confusionMatrix(a, p, negative="control")
cm
# FP TP TN FN
# 1  2  3  1
# attr(,"negative")
# [1] "control"


# corresponding accuracy, sensitivity etc.
diagnosticErrors(cm)
#       acc      sens      spec       ppv       npv       lor
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