

Package ‘mcca’

April 13, 2026

Type Package

Title Multi-Category Classification Accuracy

Version 0.8.2

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Description It contains six common multi-category classification accuracy evaluation measures. All of these measures could be found in Li and Ming (2019) <[doi:10.1002/sim.8103](https://doi.org/10.1002/sim.8103)>. Specifically, Hypervolume Under Manifold (HUM), described in Li and Fine (2008) <[doi:10.1093/biostatistics/kxm050](https://doi.org/10.1093/biostatistics/kxm050)>. Correct Classification Percentage (CCP), Integrated Discrimination Improvement (IDI), Net Re-classification Improvement (NRI), R-Squared Value (RSQ), described in Li, Jiang and Fine (2013) <[doi:10.1093/biostatistics/kxs047](https://doi.org/10.1093/biostatistics/kxs047)>. Polytomous Discrimination Index (PDI), described in Van Calster et al. (2012) <[doi:10.1007/s10654-012-9733-3](https://doi.org/10.1007/s10654-012-9733-3)>. Li et al. (2018) <[doi:10.1177/0962280217692830](https://doi.org/10.1177/0962280217692830)>. PDI with variance estimation using Dover et al. (2021) <[doi:10.1002/sim.9187](https://doi.org/10.1002/sim.9187)>. We described all these above measures and our mcca package in Li, Gao and D'Agostino (2019) <[doi:10.1002/sim.8103](https://doi.org/10.1002/sim.8103)>.

License GPL

Encoding UTF-8

Imports nnet,rpart,e1071,MASS,stats,pROC,caret

Suggests rgl

URL <https://github.com/gaoming96/mcca>

BugReports <https://github.com/gaoming96/mcca/issues>

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-04-13 18:10:02 UTC

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 mcca-package

Diagnostic accuracy methods for classifiers

Description

Six common multi-category classification accuracy evaluation measures are included i.e., Correct Classification Percentage (CCP), Hypervolume Under Manifold (HUM), Integrated Discrimination Improvement (IDI), Net Reclassification Improvement (NRI), Polytomous Discrimination Index (PDI) and R-squared (RSQ). It allows users to fit many popular classification procedures, such as multinomial logistic regression, support vector machine, classification tree, and user computed risk values. Additionally, PDI with variance estimation using Dover et al. (2021) method is provided via the pdi function.

Details

Package: mcca
 Type: Package
 Version: 0.8.2
 Date: 2026-04-12
 License: GPL

Functions

<code>ccp</code>	Calculate CCP Value
<code>hum</code>	Calculate HUM Value
<code>plot.mcca.hum</code>	Plot 3D ROC curve
<code>idi</code>	Calculate IDI Value
<code>nri</code>	Calculate NRI Value
<code>pdi</code>	Calculate PDI Value with Optional Variance Estimation
<code>rsq</code>	Calculate RSQ Value
<code>pm</code>	Calculate Probability Matrix
<code>ests</code>	Estimated Information for Single Model Evaluation Value
<code>estp</code>	Estimated Information for Paired Model Evaluation Value

Installing and using

To install this package, make sure you are connected to the internet and issue the following command in the R prompt:

```
install.packages("mcca")
```

To load the package in R:

```
library(mcca)
```

Citation

Li J, Gao M, D'Agostino R. Evaluating classification accuracy for modern learning approaches. *Statistics in Medicine*. 2019;1-27. <https://doi.org/10.1002/sim.8103>

Author(s)

Ming Gao, Pan Liu, Jialiang Li

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References

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Li, Ming G., D'Agostino. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine*.

Li, J. and Fine, J. P. (2008): ROC analysis with multiple tests and multiple classes: methodology and applications in microarray studies. *Biostatistics*. 9 (3): 566-576.

Li, J., Chow, Y., Wong, W.K., and Wong, T.Y. (2014). Sorting Multiple Classes in Multi-dimensional ROC Analysis: Parametric and Nonparametric Approaches. *Biomarkers*. 19(1): 1-8.

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382-394.

Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

Feng, Q., Jia, T., Liu, P., Van Calster, B., Li J. (2026). Efficient variance estimation for the polytomous discrimination index. *Statistics in Medicine*.

Van Calster, B., Vergouwe, Y., Looman, C.W.N., Van Belle, V., Timmerman, D. and Steyerberg, E.W. Assessing the discriminative ability of risk models for more than two outcome categories. *European Journal of Epidemiology* 2012; 27: 761-770.

Li, J., Feng, Q., Fine, J.P., Pencina, M.J., Van Calster, B. (2018). Nonparametric estimation and inference for polytomous discrimination index. *Statistical Methods in Medical Research*. 27(10): 3092—3103.

See Also

CRAN packages **HUM** for HUM.

CRAN packages **nnet**, **rpart**, **e1071**, **MASS** employed in this package.

Examples

```
str(iris)
data <- iris[, 1:4]
label <- iris[, 5]
ccp(y = label, d = data, method = "multinom",maxit = 1000,MaxNWts = 2000,trace=FALSE)
ccp(y = label, d = data, method = "multinom")
ccp(y = label, d = data, method = "svm")
ccp(y = label, d = data, method = "svm",kernel="sigmoid",cost=4,scale=TRUE,coef0=0.5)
ccp(y = label, d = data, method = "tree")
p = as.numeric(label)
ccp(y = label, d = p, method = "label")
hum(y = label, d = data,method = "multinom")
hum(y = label, d = data,method = "svm")
hum(y = label, d = data,method = "svm",kernel="linear",cost=4,scale=TRUE)
hum(y = label, d = data, method = "tree")
ests(y = label, d = data,acc="hum",level=0.95,method = "multinom",trace=FALSE)

## $value
## [1] 0.9972

## $sd
## [1] 0.002051529

## $interval
## [1] 0.9935662 1.0000000
```

 ccp *Calculate CCP Value*

Description

compute the Correct Classification Percentage (CCP) value of two or three or four categories classifiers with an option to define the specific model or user-defined model.

Usage

```
ccp(y, d, method="multinom", ...)
```

Arguments

y	The multinomial response vector with two, three or four categories.
d	The set of candidate markers, including one or more columns. Can be a data frame or a matrix; if the method is "label", then d should be the label vector.
method	Specifies what method is used to construct the classifier based on the marker set in d. Available option includes the following methods:"multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet;"tree": Classification Tree method, requiring R package rpart;"svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071;"lda": Linear Discriminant Analysis, requiring R package lda;"label": d is a label vector resulted from any external classification algorithm obtained by the user, should be encoded from 1; "prob": d is a probability matrix resulted from any external classification algorithm obtained by the user.
...	Additional arguments in the chosen method's function.

Details

The function returns the CCP value for predictive markers based on a user-chosen machine learning method. Currently available methods include logistic regression (default), tree, lda, svm and user-computed risk values. This function is general since we can evaluate the accuracy for marker combinations resulted from complicated classification algorithms.

Value

Returns an object of class "mcca.ccp". The CCP value of the classification using a particular learning method on a set of marker(s).

An object of class "mcca.ccp" is a list containing at least the following components:

call	the matched call.
measure	the value of measure.
table	the category-specific value of measure.

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible evaluation is to consider "method=label" in which case the input d should be a label vector.

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References

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382-394.

Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

See Also

[pdi](#)

Examples

```
str(iris)
data <- iris[, 1:4]
label <- iris[, 5]
ccp(y = label, d = data, method = "multinom", maxit = 1000, MaxNWts = 2000, trace=FALSE)

## Call:
## ccp(y = label, d = data, method = "multinom", maxit = 1000,
##     MaxNWts = 2000, trace = FALSE)

## Overall Correct Classification Probability:
## 0.9866667

## Category-specific Correct Classification Probability:
## CATEGORIES VALUES PREVALENCE
## 1 setosa 1.00 0.3333333
## 2 versicolor 0.98 0.3333333
## 3 virginica 0.98 0.3333333

ccp(y = label, d = data, method = "multinom")
ccp(y = label, d = data, method = "svm")
ccp(y = label, d = data, method = "svm", kernel="sigmoid", cost=4, scale=TRUE, coef0=0.5)
ccp(y = label, d = data, method = "tree")
```

```

p = as.numeric(label)
ccp(y = label, d = p, method = "label")

table(mtcars$carb)
for (i in (1:length(mtcars$carb))) {
  if (mtcars$carb[i] == 3 | mtcars$carb[i] == 6 | mtcars$carb[i] == 8) {
    mtcars$carb_new[i] = 9
  }else{
    mtcars$carb_new[i] = mtcars$carb[i]
  }
}
}
data <- data.matrix(mtcars[, c(1)])
mtcars$carb_new <- factor(mtcars$carb_new)
label <- mtcars$carb_new
str(mtcars)
ccp(y = as.numeric(label), d = data, method = "svm",kernel="radial",cost=1,scale=TRUE)

## Call:
## ccp(y = as.numeric(label), d = data, method = "svm", kernel = "radial", cost = 1, scale = TRUE)

## Overall Correct Classification Probability:
## 0.4375

## Category-specific Correct Classification Probability:
##  CATEGORIES  VALUES PREVALENCE
## 1           1 0.5714286  0.21875
## 2           2 0.2000000  0.31250
## 3           3 0.8000000  0.31250
## 4           4 0.0000000  0.15625

```

estp

Inference for Accuracy Improvement Measures based on Bootstrap

Description

compute the bootstrap standard error and confidence interval for the classification accuracy improvement for a pair of nested models.

Usage

```
estp(y, m1, m2, acc="idi", level=0.95, method="multinom", B=250, balance=FALSE, ...)
```

Arguments

y The multinomial response vector with two, three or four categories. It can be factor or integer-valued.

m1	The set of marker(s) included in the baseline model, can be a data frame or a matrix; if the method is "prob", then m1 should be the prediction probability matrix of the baseline model.
m2	The set of additional marker(s) included in the improved model, can be a data frame or a matrix; if the method is "prob", then m2 should be the prediction probability matrix of the improved model.
acc	Accuracy measure to be evaluated. Allow two choices: "idi", "nri".
level	The confidence level. Default value is 0.95.
method	Specifies what method is used to construct the classifier based on the marker set in m1 & m2. Available option includes the following methods:"multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet;"tree": Classification Tree method, requiring R package rpart;"svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071;"lda": Linear Discriminant Analysis, requiring R package lda;"prob": m1 & m2 are risk matrices resulted from any external classification algorithm obtained by the user.
B	Number of bootstrap resamples.
balance	Logical, if TRUE, the class prevalence of the bootstrap sample is forced to be identical to the class prevalence of the original sample. Otherwise the prevalence of the bootstrap sample may be random.
...	Additional arguments in the chosen method's function.

Details

The function returns the standard error and confidence interval for a paired model evaluation method. All the other arguments are the same as the function [hum](#).

Value

value	The specific value of the classification using a particular learning method on a set of marker(s).
se	The standard error of the value.
interval	The confidence interval of the value.

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible evaluation is to consider "method=prob" in which case the input m1 & m2 should be a matrix of membership probabilities with k columns and each row of m1 & m2 should sum to one.

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See Also[ests](#)**Examples**

```

table(mtcars$carb)
for (i in (1:length(mtcars$carb))) {
  if (mtcars$carb[i] == 3 | mtcars$carb[i] == 6 | mtcars$carb[i] == 8) {
    mtcars$carb_new[i] = 9
  }else{
    mtcars$carb_new[i] = mtcars$carb[i]
  }
}
data <- data.matrix(mtcars[, c(1,2)])
mtcars$carb_new <- factor(mtcars$carb_new)
label <- mtcars$carb_new
str(mtcars)
estp(y = label, m1 = data[, 1], m2 = data[, 2], acc="idi",method="lda", B=10)

## $value
## [1] 0.1235644

## $se
## [1] 0.07053541

## $interval
## [1] 0.05298885 0.21915088

estp(y = label, m1 = data[, 1], m2 = data[, 2], acc="nri",method="tree",B=5)

## $value
## [1] 0.05

## $se
## [1] 0.09249111

## $interval
## [1] 0.0000000 0.1458333

```

Description

compute the bootstrap standard error and confidence interval for the classification accuracy for a single classification model.

Usage

```
ests(y, d, acc="hum", level=0.95, method="multinom", B=250, balance=FALSE, ...)
```

Arguments

y	The multinomial response vector with two, three or four categories. It can be factor or integer-valued.
d	The set of candidate markers, including one or more columns. Can be a data frame or a matrix; if the method is "prob", then d should be the probability matrix.
acc	Accuracy measure to be evaluated. Allow four choices: "hum", "pdi", "ccp" and "rsq".
level	The confidence level. Default value is 0.95.
method	Specifies what method is used to construct the classifier based on the marker set in d. Available option includes the following methods: "multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet; "tree": Classification Tree method, requiring R package rpart; "svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071; "lda": Linear Discriminant Analysis, requiring R package lda; "label": d is a label vector resulted from any external classification algorithm obtained by the user, should be encoded from 1; "prob": d is a probability matrix resulted from any external classification algorithm obtained by the user.
B	Number of bootstrap resamples.
balance	Logical, if TRUE, the class prevalence of the bootstrap sample is forced to be identical to the class prevalence of the original sample. Otherwise the prevalence of the bootstrap sample may be random.
...	Additional arguments in the chosen method's function.

Details

The function returns the standard error and confidence interval for a single model evaluation method. All the other arguments are the same as the function [hum](#).

Value

value	The specific value of the classification using a particular learning method on a set of marker(s).
se	The standard error of the value.
interval	The confidence interval of the value.

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible

evaluation is to consider "method=prob" in which case the input d should be a matrix of membership probabilities with k columns and each row of d should sum to one.

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See Also

[estp](#)

Examples

```
str(iris)
data <- iris[, 1:4]
label <- iris[, 5]
ests(y = label, d = data, acc="hum", level=0.95, method = "multinom", B=10, trace=FALSE)

## $value
## [1] 0.9972

## $se
## [1] 0.002051529

## $interval
## [1] 0.9935662 1.0000000

ests(y = label, d = data, acc="pdi", level=0.85, method = "tree", B=10)

## $value
## [1] 0.9213333

## $se
## [1] 0.02148812

## $interval
## [1] 0.9019608 0.9629630

table(mtcars$carb)
for (i in (1:length(mtcars$carb))) {
  if (mtcars$carb[i] == 3 | mtcars$carb[i] == 6 | mtcars$carb[i] == 8) {
    mtcars$carb_new[i] = 9
  }else{
    mtcars$carb_new[i] = mtcars$carb[i]
  }
}
data <- data.matrix(mtcars[, c(1:2)])
mtcars$carb_new <- factor(mtcars$carb_new)
label <- mtcars$carb_new
str(mtcars)
```

```
ests(y = label, d = data, acc="hum", level=0.95, method = "multinom", trace=FALSE, B=5)

## $value
## [1] 0.2822857

## $se
## [1] 0.170327

## $interval
## [1] 0.2662500 0.4494643
```

hum

Calculate HUM Value

Description

compute the Hypervolume Under Manifold (HUM) value of two or three or four categories classifiers with an option to define the specific model or user-defined model.

Usage

```
hum(y, d, method="multinom", ...)
```

Arguments

y	The multinomial response vector with two, three or four categories. It can be factor or integer-valued.
d	The set of candidate markers, including one or more columns. Can be a data frame or a matrix; if the method is "prob", then d should be the probability matrix.
method	Specifies what method is used to construct the classifier based on the marker set in d. Available option includes the following methods: "multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet; "tree": Classification Tree method, requiring R package rpart; "svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071; "lda": Linear Discriminant Analysis, requiring R package lda; "prob": d is a risk matrix resulted from any external classification algorithm obtained by the user.
...	Additional arguments in the chosen method's function.

Details

The function returns the HUM value for predictive markers based on a user-chosen machine learning method. Currently available methods include logistic regression (default), tree, lda, svm and user-computed risk values. For binary outcome, one can use AUC value (HUM reduces to AUC in such case). This function is more general than the package HUM, since we can evaluate the accuracy for marker combinations resulted from complicated classification algorithms.

Value

The HUM value of the classification using a particular learning method on a set of marker(s).

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible evaluation is to consider "method=prob" in which case the input d should be a matrix of membership probabilities with k columns and each row of d should sum to one.

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References

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Li, J. and Fine, J. P. (2008): ROC analysis with multiple tests and multiple classes: methodology and applications in microarray studies. *Biostatistics*. 9 (3): 566-576.

Li, J., Chow, Y., Wong, W.K., and Wong, T.Y. (2014). Sorting Multiple Classes in Multi-dimensional ROC Analysis: Parametric and Nonparametric Approaches. *Biomarkers*. 19(1): 1-8.

See Also

[pdi](#)

Examples

```
str(iris)
data <- iris[, 1:4]
label <- iris[, 5]
hum(y = label, d = data, method = "multinom")
## [1] 0.9972
hum(y = label, d = data, method = "svm")
## [1] 0.9964
hum(y = label, d = data, method = "svm", type="C", kernel="linear", cost=4, scale=TRUE)
## [1] 0.9972
hum(y = label, d = data, method = "tree")
## [1] 0.998

data <- data.matrix(iris[, 1:4])
label <- as.numeric(iris[, 5])
# multinomial
require(nnet)
```

```

# model
fit <- multinom(label ~ data, maxit = 1000, MaxNWts = 2000)
predict.probs <- predict(fit, type = "probs")
pp<- data.frame(predict.probs)
# extract the probability assessment vector
head(pp)
hum(y = label, d = pp, method = "prob")
## [1] 0.9972

table(mtcars$carb)
for (i in (1:length(mtcars$carb))) {
  if (mtcars$carb[i] == 3 | mtcars$carb[i] == 6 | mtcars$carb[i] == 8) {
    mtcars$carb_new[i] = 9
  }else{
    mtcars$carb_new[i] = mtcars$carb[i]
  }
}
data <- data.matrix(mtcars[, c(1:10)])
mtcars$carb_new <- factor(mtcars$carb_new)
label <- mtcars$carb_new
str(mtcars)

hum(y = label, d = data, method = "tree", control = rpart::rpart.control(minsplit = 5))
## [1] 1
hum(y = label, d = data, method = "svm", kernel="linear", cost=0.7, scale=TRUE)
## [1] 1
hum(y = label, d = data, method = "svm", kernel = "radial", cost=0.7, scale=TRUE)
## [1] 0.53

```

idi

Calculate IDI Value

Description

compute the integrated discrimination improvement (IDI) value of two or three or four categories classifiers with an option to define the specific model or user-defined model.

Usage

```
idi(y, m1, m2, method="multinom", ...)
```

Arguments

y	The multinomial response vector with two, three or four categories. It can be factor or integer-valued.
m1	The set of marker(s) included in the baseline model, can be a data frame or a matrix; if the method is "prob", then m1 should be the prediction probability matrix of the baseline model.

m2	The set of additional marker(s) included in the improved model, can be a data frame or a matrix; if the method is "prob", then m2 should be the prediction probability matrix of the improved model.
method	Specifies what method is used to construct the classifier based on the marker set in m1 & m2. Available option includes the following methods:"multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet;"tree": Classification Tree method, requiring R package rpart;"svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071;"lda": Linear Discriminant Analysis, requiring R package lda;"prob": m1 & m2 are risk matrices resulted from any external classification algorithm obtained by the user.
...	Additional arguments in the chosen method's function.

Details

The function returns the IDI value for predictive markers based on a user-chosen machine learning method. Currently available methods include logistic regression (default), tree, lda, svm and user-computed risk values. This function is general since we can evaluate the accuracy for marker combinations resulted from complicated classification algorithms.

Value

The IDI value of the classification using a particular learning method on a set of marker(s).

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible evaluation is to consider "method=prob" in which case the input m1 & m2 should be a matrix of membership probabilities with k columns and each row of m1 & m2 should sum to one.

Author(s)

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References

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382—394.

Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

See Also[nri](#)**Examples**

```

table(mtcars$carb)
for (i in (1:length(mtcars$carb))) {
  if (mtcars$carb[i] == 3 | mtcars$carb[i] == 6 | mtcars$carb[i] == 8) {
    mtcars$carb_new[i] = 9
  }else{
    mtcars$carb_new[i] = mtcars$carb[i]
  }
}
data <- data.matrix(mtcars[, c(1,5)])
mtcars$carb_new <- factor(mtcars$carb_new)
label <- mtcars$carb_new
str(mtcars)

idi(y = label, m1 = data[, 1], m2 = data[, 2], "tree")
## [1] 0.09979413
idi(y = label, m1 = data[, 1], m2 = data[, 2], "tree", control=rpart::rpart.control(minsplit=4))
## [1] 0.2216707

```

nri

*Calculate NRI Value***Description**

compute the net reclassification improvement (NRI) value of two or three or four categories classifiers with an option to define the specific model or user-defined model.

Usage

```
nri(y, m1, m2, method="multinom", ...)
```

Arguments

- | | |
|----|--|
| y | The multinomial response vector with two, three or four categories. It can be factor or integer-valued. |
| m1 | The set of marker(s) included in the baseline model, can be a data frame or a matrix; if the method is "prob", then m1 should be the prediction probability matrix of the baseline model. |
| m2 | The set of additional marker(s) included in the improved model, can be a data frame or a matrix; if the method is "prob", then m2 should be the prediction probability matrix of the improved model. |

method Specifies what method is used to construct the classifier based on the marker set in m1 & m2. Available option includes the following methods:"multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet;"tree": Classification Tree method, requiring R package rpart;"svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071;"lda": Linear Discriminant Analysis, requiring R package lda;"label": m1 & m2 are label vectors resulted from any external classification algorithm obtained by the user;"prob": m1 & m2 are probability matrices resulted from any external classification algorithm obtained by the user.

... Additional arguments in the chosen method's function.

Details

The function returns the NRI value for predictive markers based on a user-chosen machine learning method. Currently available methods include logistic regression (default), tree, lda, svm and user-computed risk values. This function is general since we can evaluate the accuracy for marker combinations resulted from complicated classification algorithms.

Value

The NRI value of the classification using a particular learning method on a set of marker(s).

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible evaluation is to consider "method=prob" in which case the input m1 & m2 should be a matrix of membership probabilities with k columns and each row of m1 & m2 should sum to one.

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References

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382—394.

Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

See Also

[idi](#)

Examples

```

table(mtcars$carb)
for (i in (1:length(mtcars$carb))) {
  if (mtcars$carb[i] == 3 | mtcars$carb[i] == 6 | mtcars$carb[i] == 8) {
    mtcars$carb_new[i] = 9
  }else{
    mtcars$carb_new[i] = mtcars$carb[i]
  }
}
data <- data.matrix(mtcars[, c(1,5)])
mtcars$carb_new <- factor(mtcars$carb_new)
label <- mtcars$carb_new
str(mtcars)

nri(y = label, m1 = data[, 1], m2 = data[, 2], "lda")
## [1] 0.09375
nri(y = label, m1 = data[, 1], m2 = data[, 2], "tree")
## [1] 0.0625
nri(y = label, m1 = data[, 1], m2 = data[, 2], "tree", control=rpart::rpart.control(minsplit=4))
## [1] 0.1875

```

pdi

Calculate PDI Value

Description

compute the Polytomous Discrimination Index (PDI) value for a classifier, with optional variance estimation, using either a specified built-in classification method or user-supplied class probabilities.

Usage

```
pdi(y, d, method="multinom", withTies = TRUE, Var = FALSE, level = 0.95, ...)
```

Arguments

- | | |
|--------|---|
| y | A multinomial response vector with two or more categories. It can be a factor or an integer-valued vector. |
| d | A set of candidate markers with one or more columns. It can be a data frame or a matrix. If method = "prob", then d should be a matrix of predicted class probabilities. |
| method | The method used to construct the classifier based on the marker set in d. Available options are "multinom" (multinomial logistic regression; default; requires package nnet), "tree" (classification tree; requires package rpart), "svm" (support vector machine classification; requires package e1071), "lda" (linear discriminant analysis; requires package MASS), and "prob" (user-supplied predicted class probabilities). |

withTies	A logical value indicating whether tied predicted probabilities may occur in the PDI calculation. This argument is only used when Var = TRUE. The default is TRUE.
Var	A logical value indicating whether to compute the variance and confidence interval of the PDI. The default is FALSE.
level	The confidence level for confidence interval construction. The default is 0.95.
...	Additional arguments passed to the function corresponding to the chosen classification method.

Details

The function returns the PDI value for predictive markers based on a user-chosen machine learning method. Currently available methods include logistic regression (default), tree, lda, svm and user-computed risk values. This function is general since we can evaluate the accuracy for marker combinations resulted from complicated classification algorithms.

Value

Returns an object of class "mcca.pdi". The PDI value of the classifier obtained using a particular learning method on a set of marker(s).

An object of class "mcca.pdi" is a list containing at least the following components:

call	the matched call.
measure	the value of the PDI.
table	the category-specific values of the PDI.

If Var = TRUE, the list also contains the following:

se	the calculated standard error of the overall PDI.
ci	the confidence interval for the overall PDI.
level	the confidence level used.

and component table also contains the standard errors and confidence intervals of the category-specific PDI values.

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible evaluation is to consider "method=prob" in which case the input d should be a matrix of membership probabilities with k columns and each row of d should sum to one.

Author(s)

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Jialiang Li: stalj@nus.edu.sg

References

- Feng, Q., Jia, T., Liu, P., Van Calster, B., Li J. (2026). Efficient variance estimation for the polytomous discrimination index. *Statistics in Medicine*.
- Dover, D.C., Savu, A., Engel, B. (2021). Polytomous discrimination index: Estimation and inference. *Statistics in Medicine*.
- Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.
- Van Calster, B., Vergouwe, Y., Looman, C.W.N., Van Belle, V., Timmerman, D. and Steyerberg, E.W. Assessing the discriminative ability of risk models for more than two outcome categories. *European Journal of Epidemiology* 2012; 27: 761-770.
- Li, J., Feng, Q., Fine, J.P., Pencina, M.J., Van Calster, B. (2018). Nonparametric estimation and inference for polytomous discrimination index. *Statistical Methods in Medical Research*. 27(10): 3092—3103.

See Also

[hum](#)

Examples

```
str(iris)
data <- iris[, 3]
label <- iris[, 5]
pdi(y = label, d = data, method = "multinom")

## Call:
## pdi(y = label, d = data, method = "multinom")

## Overall Polytomous Discrimination Index:
## 0.9881333

## Category-specific Polytomous Discrimination Index:
## CATEGORIES VALUES
## 1 setosa 1.0000
## 2 versicolor 0.9822
## 3 virginica 0.9822

# PDI with variance estimation
pdi(y = label, d = data, method = "multinom", Var = TRUE)

## Call:
## pdi(y = label, d = data, method = "multinom", Var = TRUE)

## Overall Polytomous Discrimination Index:
## 0.9881333

## Standard Error:
## 0.006440373

## 95% Confidence Interval:
```

```
## [0.9755104, 1.0000000]

## Category-specific Polytomous Discrimination Index:
## CATEGORIES VALUES SE LOWER_CI UPPER_CI
## setosa 1.0000 0.0000 1.0000 1.0000
## versicolor 0.9822 0.0097 0.9633 1.0000
## virginica 0.9822 0.0097 0.9633 1.0000

pdi(y = label, d = data, method = "tree")
pdi(y = label, d = data, method = "tree", control = rpart::rpart.control(minsplit = 200))

data <- data.matrix(iris[, 3])
label <- as.numeric(iris[, 5])
# multinomial
require(nnet)
# model
fit <- multinom(label ~ data, maxit = 1000, MaxNWts = 2000)
predict.probs <- predict(fit, type = "probs")
pp <- data.frame(predict.probs)
# extract the probability assessment vector
head(pp)
pdi(y = label, d = pp, method = "prob")
```

plot.mcca.hum

Plot 3D ROC surface

Description

plot the 3D ROC surface for a three-category classifier using the 3-dimensional point coordinates, computed by obj which is a mcca.hum class.

Usage

```
## S3 method for class 'mcca.hum'
plot(x, labs=levels(x$y), coords=1:3, nticks=5, filename='fig.png', cex=0.7, ...)
```

Arguments

x	An mcca.hum class object, containing probability matrix and labels.
labs	The label names of three coordinates. Default is 'levels(x\$y)'.
coords	The coordinates markers. Default is 'c(1,2,3)', which means labs[1] is the x-axis (class 1), labs[2] is the z-axis (class 3) and labs[3] is the y-axis (class 2).
nticks	Suggested number of ticks.
filename	Filename to save snapshot.
cex	Size for text.
...	further arguments to 'plot.default'.

Details

This function is to plot the 3D ROC surface according to the correct classification probabilities for the three categories, resulted from any statistical or machine learning methods. This function complements the HUM package which can only plot 3D ROC surface for a single diagnostic test or biomarker for three classes.

Value

The function doesn't return any value.

Author(s)

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References

Li, J., and Zhou, X. H. (2009). Nonparametric and semiparametric estimation of the three way receiver operating characteristic surface. *Journal of Statistical Planning and Inference*. 139: 4133—4142.

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Examples

```
data <- iris[, 1]
label <- iris[, 5]
a=hum(y = label, d = data,method = "multinom")
#plot(a,filename='fig.png')
```

pm

Calculate Probability Matrix

Description

compute the probability matrix of two or three or four categories classifiers with an option to define the specific model or user-defined model.

Usage

```
pm(y, d, method="multinom", ...)
```

Arguments

y	The multinomial response vector with two, three or four categories. It can be factor or integer-valued.
d	The set of candidate markers, including one or more columns. Can be a data frame or a matrix.
method	Specifies what method is used to construct the classifier based on the marker set in d. Available option includes the following methods:"multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet;"tree": Classification Tree method, requiring R package rpart;"svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071;"lda": Linear Discriminant Analysis, requiring R package lda.
...	Additional arguments in the chosen method's function.

Details

The function returns the probability matrix for predictive markers based on a user-chosen machine learning method. Currently available methods include logistic regression (default), tree, lda, svm and user-computed risk values.

Value

The probability matrix of the classification using a particular learning method on a set of marker(s).

Author(s)

Ming Gao: gaoming@umich.edu

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References

Li, J. and Fine, J. P. (2008): ROC analysis with multiple tests and multiple classes: methodology and applications in microarray studies. *Biostatistics*. 9 (3): 566-576.

Li, J., Chow, Y., Wong, W.K., and Wong, T.Y. (2014). Sorting Multiple Classes in Multi-dimensional ROC Analysis: Parametric and Nonparametric Approaches. *Biomarkers*. 19(1): 1-8.

See Also

[pdi](#)

Examples

```
str(iris)
data <- iris[, 1:4]
label <- iris[, 5]
pm(y = label, d = data, method = "multinom")
```

print.mcca.ccp	<i>Print Method for mcca ccp class</i>
----------------	--

Description

An S3 method for the print generic. It is designed for a quick look at CCP values.

Usage

```
## S3 method for class 'mcca.ccp'  
print(x, ...)
```

Arguments

x	object of class 'mcca.ccp'.
...	further arguments to 'print.default'.

Value

An object of class "mcca.ccp" is a list containing at least the following components:

call	the matched call.
measure	the value of measure.
table	the category-specific value of measure.

Author(s)

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References

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382-394.

Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

Examples

```
data = iris[, 1:4]  
label = iris[, 5]  
ccp_object=ccp(y = label, d = data, method = "multinom",maxit = 1000,MaxNWts = 2000,trace=FALSE)  
print(ccp_object)
```

print.mcca.hum	<i>Print Method for mcca hum class</i>
----------------	--

Description

An S3 method for the print generic. It is designed for a quick look at hum values.

Usage

```
## S3 method for class 'mcca.hum'  
print(x, ...)
```

Arguments

x	object of class 'mcca.hum'.
...	further arguments to 'print.default'.

Value

An object of class "mcca.hum" is a list containing at least the following components:

call	the matched call.
measure	the value of measure.
table	the category-specific value of measure.

Author(s)

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References

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382-394.

Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

Examples

```
data = iris[, 1:4]  
label = iris[, 5]  
hum_object=hum(y = label, d = data, method = "multinom",maxit = 1000,MaxNWts = 2000,trace=FALSE)  
print(hum_object)
```

print.mcca.pdi *Print Method for mcca pdi class*

Description

An S3 method for the print generic. It is designed for a quick look at pdi values.

Usage

```
## S3 method for class 'mcca.pdi'  
print(x, ...)
```

Arguments

x object of class 'mcca.pdi'.
... further arguments to 'print.default'.

Value

An object of class "mcca.pdi" is a list containing at least the following components:

call the matched call.
measure the value of measure.
table the category-specific value of measure.

Author(s)

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Jialiang Li: stalj@nus.edu.sg

References

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382-394.
Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

Examples

```
data = iris[, 1:4]  
label = iris[, 5]  
pdi_object=pdi(y = label, d = data, method = "multinom",maxit = 1000,MaxNWts = 2000,trace=FALSE)  
print(pdi_object)
```

print.mcca.pdi.var *Print Method for mcca.pdi.var class*

Description

An S3 method for the print generic. It is designed for a quick look at PDI values with variance estimation.

Usage

```
## S3 method for class 'mcca.pdi.var'  
print(x, ...)
```

Arguments

x object of class 'mcca.pdi.var'.
... further arguments to 'print.default'.

Value

An object of class "mcca.pdi.var" is a list containing at least the following components:

call	the matched call.
measure	the overall PDI value.
se	the calculated standard error of the overall PDI.
ci	the confidence interval for the overall PDI.
level	the confidence level used.
table	a data frame with category-specific PDI values, standard errors, and confidence intervals.

Author(s)

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References

Feng, Q., Jia, T., Liu, P., Van Calster, B., Li J. (2026). Efficient variance estimation for the polytomous discrimination index. *Statistics in Medicine*.

Dover, D.C., Savu, A., Engel, B. (2021). Polytomous discrimination index: Estimation and inference. *Statistics in Medicine*.

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Examples

```
data = iris[, 1:4]
label = iris[, 5]
pdi_var_object = pdi(y = label, d = data, method = "multinom", Var = TRUE)
print(pdi_var_object)
```

```
print.mcca.rsq      Print Method for mcca rsq class
```

Description

An S3 method for the print generic. It is designed for a quick look at rsq values.

Usage

```
## S3 method for class 'mcca.rsq'
print(x, ...)
```

Arguments

x	object of class 'mcca.rsq'.
...	further arguments to 'print.default'.

Value

An object of class "mcca.rsq" is a list containing at least the following components:

call	the matched call.
measure	the value of measure.
table	the category-specific value of measure.

Author(s)

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 Jialiang Li: stalj@nus.edu.sg

References

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382-394.
 Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

Examples

```
data = iris[, 1:4]
label = iris[, 5]
rsq_object=rsq(y = label, d = data, method = "multinom",maxit = 1000,MaxNWts = 2000,trace=FALSE)
print(rsq_object)
```

rsq

*Calculate RSQ Value***Description**

compute the R-squared (RSQ) value of two or three or four categories classifiers with an option to define the specific model or user-defined model.

Usage

```
rsq(y, d, method="multinom", ...)
```

Arguments

y	The multinomial response vector with two, three or four categories. It can be factor or integer-valued.
d	The set of candidate markers, including one or more columns. Can be a data frame or a matrix; if the method is "prob", then d should be the probability matrix.
method	Specifies what method is used to construct the classifier based on the marker set in d. Available option includes the following methods:"multinom": Multinomial Logistic Regression which is the default method, requiring R package nnet;"tree": Classification Tree method, requiring R package rpart;"svm": Support Vector Machine (C-classification and radial basis as default), requiring R package e1071;"lda": Linear Discriminant Analysis, requiring R package lda;"prob": d is a risk matrix resulted from any external classification algorithm obtained by the user.
...	Additional arguments in the chosen method's function.

Details

The function returns the RSQ value for predictive markers based on a user-chosen machine learning method. Currently available methods include logistic regression (default), tree, lda, svm and user-computed risk values. This function is general since we can evaluate the accuracy for marker combinations resulted from complicated classification algorithms.

Value

Returns an object of class "mcca.rsq". The RSQ value of the classification using a particular learning method on a set of marker(s).

An object of class "mcca.rsq" is a list containing at least the following components:

call	the matched call.
measure	the value of measure.
table	the category-specific value of measure.

Note

Users are advised to change the operating settings of various classifiers since it is well known that machine learning methods require extensive tuning. Currently only some common and intuitive options are set as default and they are by no means the optimal parameterization for a particular data analysis. Users can put machine learning methods' parameters after tuning. A more flexible evaluation is to consider "method=prob" in which case the input d should be a matrix of membership probabilities with k columns and each row of d should sum to one.

Author(s)

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Jialiang Li: stalj@nus.edu.sg

References

Li, J., Gao, M., D'Agostino, R. (2019). Evaluating Classification Accuracy for Modern Learning Approaches. *Statistics in Medicine (Tutorials in Biostatistics)*. 38(13): 2477-2503.

Li, J., Jiang, B. and Fine, J. P. (2013). Multicategory reclassification statistics for assessing Improvements in diagnostic accuracy. *Biostatistics*. 14(2): 382-394.

Li, J., Jiang, B., and Fine, J. P. (2013). Letter to Editor: Response. *Biostatistics*. 14(4): 809-810.

See Also

[ccp](#)

Examples

```
str(iris)
data <- iris[, 1:4]
label <- iris[, 5]
rsq(y = label, d = data, method="multinom")

## Call:
## rsq(y = label, d = data, method = "multinom")

## Overall R-squared value:
## 0.9637932
```

```

## Category-specific R-squared value:
## CATEGORIES VALUES
## 1 setosa 0.9999824
## 2 versicolor 0.9456770
## 3 virginica 0.9457203

rsq(y = label, d = data, method = "tree")

data <- data.matrix(iris[, 1:4])
label <- as.numeric(iris[, 5])
# multinomial
require(nnet)
# model
fit <- multinom(label ~ data, maxit = 1000, MaxNWts = 2000)
predict.probs <- predict(fit, type = "probs")
pp <- data.frame(predict.probs)
# extract the probability assessment vector
head(pp)
rsq(y = label, d = pp, method = "prob")

table(mtcars$carb)
for (i in (1:length(mtcars$carb))) {
  if (mtcars$carb[i] == 3 | mtcars$carb[i] == 6 | mtcars$carb[i] == 8) {
    mtcars$carb_new[i] = 9
  }else{
    mtcars$carb_new[i] = mtcars$carb[i]
  }
}
data <- data.matrix(mtcars[, c(1)])
mtcars$carb_new <- factor(mtcars$carb_new)
label <- mtcars$carb_new
str(mtcars)

rsq(y = label, d = data, method="tree")
rsq(y = label, d = data, method="lda")
rsq(y = label, d = data, method="lda",prior = c(100,1,1,1)/103)

```

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