

Package ‘ROCRegression’

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Description The ROCRegression package allows the user to estimate the effect of covariates on the Receiver Operating Characteristic (ROC) curve. Various approaches to regression analysis of ROC curves have been implemented, allowing the user to choose between the “Normal Method”, the “Semiparametric Method”, the “Parametric ROC-GLM Method” and the “Semiparametric ROC-GLM Method”. The package can be used to fit ROC regression models including a set of continuous and/or categorical covariates, and their possible interactions. As a result, the user easily obtain numerical and graphical output for all models.

License GPL

LazyLoad yes

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ROCRegression-package *Receiver Operating Characteristic (ROC) regression analysis*

Description

This package allows the user to estimate the effect of covariates on the ROC curve. Various approaches to regression analysis of ROC curves have been implemented, including the "normal" method of Faraggi (2003), the "semiparametric" method of Pepe (1998), the "parametric ROC-GLM" method of Alonzo and Pepe (2002) and the "semiparametric ROC-GLM" method of Cai (2004). The package functions can be used to fit ROC regression models with a vector of continuous and/or categorical covariates, and their possible interactions. Numerical and graphical output for all models is easily obtained.

Details

Package:	ROCRegression
Type:	Package
Version:	1.0
Date:	2011-01-14
License: GPL LazyLoad:	yes

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

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References

- Alonzo, T.A. and Pepe M.S. (2002). Distribution-free ROC analysis using binary regression techniques. *Biostatistics* **3**, 421–432.
- Faraggi, D. (2003). Adjusting receiver operating characteristic curves and related indices for covariates. *The Statistician* **52**, 179–192.
- Cai, T. (2004). Semi-parametric ROC regression analysis with placement values. *Biostatistics* **5**, 45–60.
- Pepe, M.S. (1998). Three approaches to regression analysis of receiver operating characteristic curves for continuous test results. *Biometrics* **54**, 124–135.

controlROCreg

Setting ROC regression fitting defaults

Description

Used to set various parameters controlling the ROC regression fitting process

Usage

```
controlROCreg(step.h = 0.02, card.T = 10,
ROC.model = c("binormal", "logistic"), nboot = 500,
resample.m = c("coutcome", "ncoutcome"), FPFint = NULL,
est.surv = c("normal", "empirical"))
```

Arguments

step.h	a numeric value meaningful only in the "SROCGLM" method. ROC curve values are estimated for false positive fractions in the sequence 0, step.h, 2*step.h, ..., 1. The default is 0.02.
card.T	a numeric value meaningful only in the "PROCGLM" method. It specifies the cardinality of the set of false positive fractions. The default is 10.
ROC.model	a character string meaningful only in the "PROCGLM" method. It specifies the ROC model to be fitted: "binormal" for a binormal model, and "logistic" for a bilogistic model. The default is "binormal".
nboot	the number of bootstrap resamples. The default is 500.
resample.m	a character string specifying whether the resampling should be done with or without regard to the disease status. The option "coutcome" indicates that the data is resampled with regard to the disease status (e.g., in a case-control study), and "ncoutcome" indicates that the data is resampled without regard to the disease status. The default is "coutcome".
FPFint	a right-hand formula meaningful only in the "PROCGLM" method. It specifies the interaction model between the covariates and the false positive fraction. The default is NULL.
est.surv	a character string meaningful only in the "PROCGLM" and "SROCGLM" methods. It indicates how the conditional survival function of the healthy population, $S_{X\bar{D}}$, is estimated. Options are "normal" and "empirical" (see details). The default is "normal".

Details

The value returned by this function is used as the control argument of the ROCreg() function.

The estimation procedure of both the "PROCGLM" and the "SROCGLM" methods requires the estimation of the conditional survival function in the healthy population, $S_{X\bar{D}}(y) = P[Y \geq y | \bar{D}X]$. In this package, two estimators have been implemented. In both cases, a parametric location model for the healthy population, $Y_{\bar{D}} = X\beta_{\bar{D}} + \sigma_{\bar{D}}\varepsilon_{\bar{D}}$, is assumed, such that

$$S_{X\bar{D}}(y) = S_{\bar{D}}\left(\frac{y - X\beta_{\bar{D}}}{\sigma_{\bar{D}}}\right)$$

where $S_{\bar{D}}$ is the survival function of $\varepsilon_{\bar{D}}$. In line with the assumptions made about the distribution of $\varepsilon_{\bar{D}}$, estimators will be referred to as: (a) "normal", where gaussian error is assumed, i.e., $S_{\bar{D}}(y) = 1 - \Phi(y)$; and, (b) "empirical", where no assumption is made about the distribution (in this case, the survival function $S_{\bar{D}}$ is empirically estimated on the basis of standardised residuals).

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

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

```

library(ROCRegression)
data(elas)
#####
# Direct parametric ROC-GLM (PROCGLM): Covariate age
#####
fit.roc.procglm <- ROCreg(method = "PROCGLM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas)

summary(fit.roc.procglm)

# Change the ROC model (binormal vs bilogistic)
fit.roc.procglm <- ROCreg(method = "PROCGLM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas,
control=controlROCreg(ROC.model="logistic"))

summary(fit.roc.procglm)

# Change the cardinality of the set of false positive fractions
fit.roc.procglm <- ROCreg(method = "PROCGLM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas,
control=controlROCreg(card.T=50))

summary(fit.roc.procglm)

#####
# Direct semiparametric ROC-GLM (SROCGLM): Covariate age
#####
fit.roc.srocglm <- ROCreg(method = "SROCGLM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas, se.fit=TRUE)

summary(fit.roc.srocglm)

# Change the estimator of the conditional survival function
fit.roc.srocglm <- ROCreg(method = "SROCGLM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas, se.fit=TRUE,
control=controlROCreg(est.surv="empirical"))

summary(fit.roc.srocglm)

```

controlROCregData

*Setting ROC regression prediction and plot defaults***Description**

Used to set parameters controlling the behaviour of `ROCregData()`.

Usage

```
controlROCCregData(cat.cont = NULL, card.cont = 50)
```

Arguments

`cat.cont` an optional list. If there are categorical covariates, a list of length equal to the number of combined levels of the categorical covariates. The components of the list are named lists with the values of the continuous covariate(s) where the ROC curve will be estimated. If there are no categorical covariates, a named list with the values of the continuous covariate(s). With the default, `NULL`, these values are computed internally taking into account the argument `card.cont`.

`card.cont` an optional numeric vector with the number of values of each continuous covariate where the ROC curve will be estimated. Atomic values are recycled. The default, 50, is used when `cat.cont` is `NULL`.

Details

The value returned by this function is used as the control argument of the functions `ROCCregData`, `predict.ROCCreg` and `plot.ROCCreg`.

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

See Also

[ROCCregData](#), [predict.ROCCreg](#), [plot.ROCCreg](#)

Examples

```
library(ROCRegression)
data(elas)
#####
# Induced semiparametric model (SM): Covariate age
#####
fit.roc.sm <- ROCCreg(method = "SM", model = c("~age", "~age"),
  group = "status", tag.healthy = 0, marker = "elas", data = elas)

newdata <- ROCCregData(fit.roc.sm, control=controlROCCregData(card.cont=10))
summary(newdata)

plot(fit.roc.sm, data=newdata)
```

elas

Leukocyte Elastase Data

Description

The `elas` data set was obtained from the Cardiology Service at the Hospital General de Galicia (Santiago de Compostela, Spain). This study was conducted to evaluate the clinical usefulness of leukocyte elastase determination in the diagnosis of coronary artery disease (CAD).

Usage

```
data(elas)
```

Format

A data frame with 141 observations on the following 6 variables.

`elas` Leukocyte elastase. Numeric vector

`status` True disease status (presence/absence of coronary artery disease). Numeric vector (0=absence, 1=presence)

`gender` Gender of patient. Factor with levels Male Female

`age` Age of patient. Numeric vector

`CADgroup` a factor with levels complex-lesion simple-lesion. Only for CAD-group patients.

`bmi` Body Mass Index (BMI) of patient. Numeric vector

`angor` Angina pectoris. Factor with levels Yes No

Source

Amaro, A., Gude, F., Gonzalez-Juanatey, R., Iglesias, C., Fernandez-Vazquez, F., Garcia-Acuna, J. and Gil, M. (1995). Plasma leukocyte elastase concentration in angiographically diagnosed coronary artery disease. *European Heart Journal* **16**, 615–622.

References

Amaro, A., Gude, F., Gonzalez-Juanatey, R., Iglesias, C., Fernandez-Vazquez, F., Garcia-Acuna, J. and Gil, M. (1995). Plasma leukocyte elastase concentration in angiographically diagnosed coronary artery disease. *European Heart Journal* **16**, 615–622.

plot.ROCreg

Default ROC regression model plotting

Description

Plots the ROC curve, and, optionally, AUC, Youden Index and optimal threshold, from a [ROCreg](#) object. The suitable type of graphic is chosen according to the number and nature of the covariates.

Usage

```
## S3 method for class 'ROCreg'
plot(x, data = NULL, step.p = 0.02, accuracy = NULL,
     AUC.calc = c("simpson", "integrate"), control = controlROCregData(),
     ask = TRUE, ...)
```

Arguments

x	an object of class ROCreg as produced by ROCreg().
data	an optional data frame or an object produced by predict.ROCreg() containing the values of covariates at which the ROC curve will be plotted. If not supplied, ROCregData() is called.
step.p	a numeric value, defaulting to 0.02. ROC curve values are calculated for false positive fractions in the sequence 0, step.p, 2*step.p, ..., 1.
accuracy	a character vector indicating which of AUC ("AUC"), Youden index ("YI") and/or optimal threshold ("TH") should be added as annotations to the plot.
AUC.calc	a character string specifying the integration method for computing the AUC.
control	the output of the function controlROCregData(), its value is used only when the data argument is NULL.
ask	a logical value. If TRUE, the default, the user is asked for confirmation, before a new figure is drawn.
...	further arguments passed to or from other methods.

Value

An object of class predict.ROCreg as produced by predict.ROCreg().

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

See Also

[ROCreg](#), [predict.ROCreg](#), [ROCregData](#), [controlROCregData](#)

Examples

```
library(ROCRegression)
data(elas)
#####
# Induced semiparametric model (SM): Covariate agee
#####
fit.roc.sm <- ROCreg(method = "SM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas)

df.pred <- data.frame(age=seq(min(elas$age), max(elas$age), l=100))
pred <- predict(fit.roc.sm, newdata=df.pred)

# Example 1
plot(fit.roc.sm, accuracy="AUC")
# Example 2
plot(fit.roc.sm, data = df.pred, accuracy="AUC")
# Example 3
plot(fit.roc.sm, data = pred, accuracy="AUC")
# Notice that, in the last example, the AUC is not plotted
# since it was not asked in the call to the function predict
```

predict.ROCreg	<i>Prediction from fitted ROC regression models</i>
----------------	---

Description

Computes the ROC curve at the values of the covariates supplied in the data argument. Optionally, accuracy measures, such as AUC or Youden Index (YI) can be obtained, and also a YI-based optimal threshold.

Usage

```
## S3 method for class 'ROCreg'
predict(object, newdata = NULL, step.p = 0.02, accuracy = NULL,
AUC.calc = c("simpson", "integrate"), control = controlROCregData(), ...)
```

Arguments

object	an object of class ROCreg as produced by ROCreg()
newdata	optional data frame containing the values of the covariates at which ROC curve will be computed. If not supplied, the function ROCregData() is used to build a default dataset.
step.p	a numeric value, defaulting to 0.02. ROC curve values are calculated for false positive fractions in the sequence 0, step.p, 2*step.p, ..., 1.
accuracy	a character vector indicating which of AUC ("AUC"), Youden index ("YI") and/or optimal threshold ("TH") should be also computed.
AUC.calc	a character string specifying the integration method for computing the AUC.
control	the output of the function controlROCreg().
...	further arguments passed to or from other methods. Not implemented.

Value

A list of class predict.ROCreg containing the following components:

data	a data frame whose rows are the different combinations of covariate values at which ROC curve (and, optionally, accuracy measures) has been computed.
ROC	a matrix whose rows are the computed ROC curve values for the different combinations of covariate values given by the corresponding rows of data. In each row, the ROC values are computed at the sequence of false positive fractions determined by the argument step.p.
AUC	a numeric vector of computed AUC values. Absent if "AUC" is not an element of the argument accuracy.
YI	a numeric vector of computed Youden index values. Absent if "YI" is not an element of the argument accuracy.
TH	a numeric vector of computed optimal threshold values. Absent if "TH" is not an element of the argument accuracy.
step.p	the value of the argument step.p used in the call.
control	the value of the argument control used in the call.

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

See Also

[ROCreg](#), [ROCregData](#), [controlROCregData](#)

Examples

```
library(ROCRegression)
data(elas)
#####
# Induced semiparametric model (SM): Covariate age
#####
fit.roc.sm <- ROCreg(method = "SM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas)

df.pred <- data.frame(age=seq(min(elas$age), max(elas$age),l=100))

# Example 1
pred <- predict(fit.roc.sm, newdata=df.pred)
names(pred)
# Example 2
pred <- predict(fit.roc.sm, newdata=df.pred, accuracy=c("AUC", "YI"))
names(pred)
# Example 3
pred <- predict(fit.roc.sm, accuracy=c("AUC", "YI"))
names(pred)
plot(fit.roc.sm, data=pred)
```

print.ROCreg

Print method for ROCreg objects

Description

Default print method for objects fitted with ROCreg. A short summary with the call to the ROCreg() function, the ROC regression method and the coefficient estimates is printed.

Usage

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

Arguments

x an object of class ROCreg as produced by ROCreg().
... further arguments passed to or from other methods.

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

See Also

[ROCreg](#), [summary.ROCreg](#)

Examples

```
library(ROCRegression)
data(elas)
#####
# Induced semiparametric model (SM): Covariate age
#####
fit.roc.sm <- ROCreg(method = "SM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data =elas)

fit.roc.sm

print(fit.roc.sm)
```

ROCreg	<i>ROC regression model fitting</i>
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Description

Fits a ROC regression model with a vector of continuous and/or categorical covariates, and their possible interactions. Various approaches to regression analysis of ROC curves have been implemented, including the "normal" method of Faraggi (2003), the "semiparametric" method of Pepe (1998), the "parametric ROC-GLM" method of Alonzo and Pepe (2002) and the "Semiparametric ROC-GLM" method of Cai (2004).

Usage

```
ROCreg(method = c("NM", "SM", "PROCGLM", "SROCGLM"), model, group,
tag.healthy, marker = NULL, data, se.fit = FALSE, na.action = na.omit,
control = controlROCreg())
```

Arguments

method	a character string specifying which method is used: "NM" (normal method), "SM" (semiparametric method), "PROCGLM" (parametric ROC-GLM method) or "SROCGLM" (semiparametric ROC-GLM method).
model	right-hand formula(s) giving the model(s) to be fitted. For induced methodology (that is "NM" and "SM" models), the first formula is the regression model for the healthy population, and the second one for the diseased population. As regard direct methodology ("PROCGLM" and "SROCGLM" models), the first formula is the regression model for the healthy population, while the second one is the ROC regression model. Atomic values are also valid, being recycled. See details.
group	a character string with the name of the variable that distinguishes healthy from diseased individuals.
tag.healthy	the value codifying the healthy individuals in the variable group.
marker	a character string with the name of the diagnostic test variable.

<code>data</code>	a data frame containing all needed variables.
<code>se.fit</code>	a logical value. If TRUE, inference on the coefficients of the ROC curve is performed.
<code>na.action</code>	a function that indicates the behaviour when the data contains NA's.
<code>control</code>	output of the <code>controlROCRreg</code> function.

Details

Continuous biomarkers are often used to discriminate between diseased and healthy populations. The ROC curve is a widely used tool for characterizing the marker accuracy. To account for covariates that might influence the test accuracy, various ROC regression methodologies have been proposed in the statistical literature: the induced methodology (Pepe, 1998; Faraggi, 2003) and the direct methodology (Alonzo and Pepe, 2002; Cai, 2004).

Induced ROC methodology assumes that the test result Y , in both healthy (\bar{D}) and diseased (D) populations separately, can be expressed as a regression model on covariates X :

$$Y_{\bar{D}} = X\beta_{\bar{D}} + \sigma_{\bar{D}}\varepsilon_{\bar{D}}$$

$$Y_D = X\beta_D + \sigma_D\varepsilon_D$$

In this setting, the covariate-specific ROC curve can be expressed as:

$$ROC_X(t) = S_D(X\beta + \alpha S_{\bar{D}}^{-1}(t))$$

where $\beta = \frac{\beta_{\bar{D}} - \beta_D}{\sigma_D}$, $\alpha = \frac{\sigma_{\bar{D}}}{\sigma_D}$, and S_D and $S_{\bar{D}}$ are the survival functions of ε_D and $\varepsilon_{\bar{D}}$ respectively. In this package we have implemented two methods that differ in their assumptions about the distribution of errors ε_D and $\varepsilon_{\bar{D}}$, namely: (a) the Normal Method ("NM"), which assumes Gaussian errors; and (b) the Semiparametric Method ("SM"), where the distributions of the errors are not specified. In the Normal Method ("NM") the covariate-specific ROC curve follows the so-called binormal model, and it is usually expressed as $ROC_X(t) = \Phi(-X\beta + \alpha\Phi^{-1}(t))$.

In contrast to induced methodology, in direct methodology the effect of the covariates is evaluated directly on the ROC curve, within the framework of the generalised linear models (GLMs). In this methodology, the general form of the ROC curve is given by the following regression model:

$$ROC_X(t) = g(X\beta + h(t))$$

where g is a known link function and h is an unknown monotonic increasing function. Different proposals for h have been suggested in the literature: in Alonzo and Pepe (2002) a parametric form is specified (Parametric ROC-GLM Method, "PROCGLM"); in Cai (2004) it remains unspecified (Semiparametric ROC-GLM Method, "SROCGLM").

Value

A list with the following components:

<code>call</code>	the matched call.
<code>method</code>	the value of the argument method used in the call.
<code>group</code>	the value of the argument group used in the call.
<code>marker</code>	the value of the argument marker used in the call.
<code>control</code>	value of the argument control used in the call.
<code>group</code>	a character vector with the names of the covariates used in the fit.

<code>se.fit</code>	the value of the argument <code>se.fit</code> used in the call.
<code>data</code>	the original supplied data argument.
<code>ROC.fit</code>	a list with the details of the fitted ROC. Its specific components depend on the method used.

Note

For "NM" method approximate confidence intervals and p-values based on the distribution of the parameter estimates of the induced ROC are given (Rodríguez-Alvarez et al. 2010). For "SM", "PROCGLM" and "SROCGLM" methods bootstrap techniques are used to compute the standard errors of the parameter estimates. In this case, the data must be resampled in accordance with the study design (see [controlROCRreg](#)).

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

References

- Alonzo, T.A. and Pepe M.S. (2002). Distribution-free ROC analysis using binary regression techniques. *Biostatistics* **3**, 421–432.
- Faraggi, D. (2003). Adjusting receiver operating characteristic curves and related indices for covariates. *The Statistician* **52**, 179–192.
- Cai, T. (2004). Semi-parametric ROC regression analysis with placement values. *Biostatistics* **5**, 45–60.
- Pepe, M.S. (1998). Three approaches to regression analysis of receiver operating characteristic curves for continuous test results. *Biometrics* **54**, 124–135.
- Rodríguez-Alvarez, M.X., Tahoces, P.G., Cadarso-Suarez, C. and Lado, M.J. (2011). Comparative study of ROC regression techniques. Applications for the computer-aided diagnostic system in breast cancer detection. *Computational Statistics and Data Analysis*, **55**, 888–902.

See Also

[controlROCRreg](#), [summary.ROCRreg](#)

Examples

```
library(ROCRegression)
data(elas)
#####
# marker: elas
# group: status
# covariates:
# age
# gender
# bmi
# angor
# CADgroup (disease-specific)
#####

#####
# Induced semiparametric model (SM): Covariate age
#####
```

```

fit.roc.sm <- ROCreg(method = "SM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas)

summary(fit.roc.sm)

plot(fit.roc.sm, accuracy="AUC")

# Inference on the coefficients of the ROC curve
fit.roc.sm <- ROCreg(method = "SM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas, se.fit = TRUE)

summary(fit.roc.sm)

#####
# Direct semiparametric ROC-GLM (SROCGLM): Covariate age
#####
fit.roc.srocglm <- ROCreg(method = "SROCGLM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas, se.fit=TRUE)

summary(fit.roc.srocglm)

plot(fit.roc.srocglm, accuracy="AUC")

#####
# Induced semiparametric model (SM): CADgroup (disease-specific covariate)
#####
fit.roc.sm <- ROCreg(method = "SM", model = c("~1", "~CADgroup"),
group = "status", tag.healthy = 0, marker = "elas", data = elas, se.fit=TRUE)

summary(fit.roc.sm)

plot(fit.roc.sm, accuracy="AUC")

```

ROCregAUCci

Computes the AUC and confidence intervals

Description

Computes the AUC and corresponding pointwise confidence intervals.

Usage

```

ROCregAUCci(method, model, group, tag.healthy, marker, data,
control = controlROCreg(), newdata = NULL, conf = 0.95)

```

Arguments

method	a character string specifying which method is used: "NM" (normal method), "SM" (semiparametric method), "PROCGLM" (parametric ROC-GLM method) or "SROCGLM" (semiparametric ROC-GLM method).
model	right-hand formula(s) giving the model(s) to be fitted. For induced methodology (that is, "NM" and "SM" models), the first formula is the regression model

for the healthy population, and the second one for the diseased population. As regard direct methodology ("PROCGLM" and "SROCGLM" models), the first formula is the regression model for the healthy population, while the second one is the ROC regression model. Atomic values are also valid, being recycled. See details.

group	a character string with the name of the variable that distinguishes healthy from diseased individuals.
tag.healthy	the value codifying the healthy individuals in the variable group.
marker	a character string with the name of the diagnostic test variable.
data	a data frame representing the data and containing all needed variables.
control	output of the controlROCreg function.
newdata	an optional data frame or an object produced by <code>predict.ROCreg()</code> containing the values of covariates at which the ROC curve will be plotted. If not supplied, <code>ROCregData()</code> is called.
conf	a numeric value, defaulting to 0.95, with the level of the confidence interval.

Details

The confidence intervals for the "NM" model are calculated based on Faraggi's results (Faraggi 2003), whereas the bootstrap percentile method is used for the rest of the ROC regression methods.

Value

A list with the following components:

call	the matched call.
data	a data frame whose rows are the different combinations of covariate values at which the AUC has been computed.
AUC	a numeric vector of computed AUC values.
AUC.l1	a numeric vector of computed confidence lower limit of AUC values.
AUC.u1	a numeric vector of computed confidence upper limit of AUC values.

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

References

Faraggi, D. (2003). Adjusting receiver operating characteristic curves and related indices for co-variates. *The Statistician* **52**, 179–192.

See Also

[ROCreg](#), [ROCregData](#)

Examples

```
library(ROCRegression)
data(elas)
#####
# Induced semiparametric model (SM): Covariate age
#####
fit.auc.sm <- ROCregAUCci(method = "SM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas)

plot(fit.auc.sm$data$age, fit.auc.sm$AUC, xlab="Age", ylab="AUC",
ylim=c(0,1), type="l", lwd=2)
lines(fit.auc.sm$data$age, fit.auc.sm$AUC.ll, lty=2)
lines(fit.auc.sm$data$age, fit.auc.sm$AUC.ul, lty=2)
abline(h=0.5, col="grey")
```

ROCCregData

*Default dataset for prediction or plotting***Description**

Selects an adequate set of points from the original data to be used as a default dataset for obtaining predictions or plots.

Usage

```
ROCCregData(ROCCreg, control = controlROCCregData())
```

Arguments

ROCCreg	an object of class ROCCreg as produced by ROCCreg()
control	output of the function controlROCCregData()

Value

a data frame containing selected values of all needed covariates.

Author(s)

Maria Xose Rodriguez-Alvarez and Ignacio Lopez de Ullibarri

See Also

[ROCCreg](#), [plot.ROCCreg](#), [predict.ROCCreg](#), [controlROCCregData](#)

Examples

```
library(ROCRegression)
data(elas)
#####
# Induced semiparametric model (SM): Covariate age
#####
fit.roc.sm <- ROCreg(method = "SM", model = c("~age", "~age"),
group = "status", tag.healthy = 0, marker = "elas", data = elas)
```

```
newdata <- ROCregData(fit.roc.sm, control=controlROCregData(card.cont=10))
summary(newdata)

plot(fit.roc.sm, data=newdata)
```

summary.ROCreg

*Summary method for ROCreg objects***Description**

Produces a summary of a ROCreg object. The call to the ROCreg() function, the ROC regression method and the coefficient estimates are printed. If the ROCreg was called with argument `se.fit = TRUE`, standard errors, confidence intervals and p-values of the coefficient estimates are also printed.

Usage

```
## S3 method for class 'ROCreg'
summary(object, conf = 0.95, ndigits = 4, ...)
```

Arguments

<code>object</code>	an object of class ROCreg as produced by ROCreg().
<code>conf</code>	a numeric value, defaulting to 0.95, with the level of the confidence interval of the parameters.
<code>ndigits</code>	the number of digits to use when printing confidence intervals and p-values. By default is 4.
<code>...</code>	further arguments passed to or from other methods. Not yet implemented.

Details

The function summary.ROCreg produces a list of summary information for a fitted ROCreg object. The result depends on the two arguments `method` and `se.fit` of the ROCreg() function used in the fitting process.

Note

The function summary.ROCreg also provides the confidence interval and p-value for the ROC parameter associated with the false positive fraction (except for the "SROCGLM" method). For the "NM" method, since this parameter is the quotient of standard deviations, the null hypothesis considered is $H_0 : \frac{\sigma_{\bar{D}}}{\sigma_D} = 1$. For the other methods, the null hypothesis is $H_0 : \alpha = 0$.

Author(s)

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References

Rodriguez-Alvarez, M.X., Tahoces, P.G., Cadarso-Suarez, C. and Lado, M.J. (2011). Comparative study of ROC regression techniques. Applications for the computer-aided diagnostic system in breast cancer detection. *Computational Statistics and Data Analysis*, **55**, 888–902.

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

```
library(ROCRegression)
data(elas)
#####
# Induced semiparametric model (SM): Covariate age
#####
fit.roc.sm <- ROCreg(method = "SM", model = c("~age", "~age"),
  group = "status", tag.healthy = 0, marker = "elas", data = elas, se.fit = TRUE)

summary(fit.roc.sm)

summary(fit.roc.sm, conf=0.80)
```

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