Package 'modelROC'

June 25, 2021

Title Model Based ROC Analysis

Version 1.0

Description The ROC curve method is one of the most important and commonly used
methods for model accuracy assessment, which is one of the most important elements
of model evaluation.
The 'modelROC' package is a model-based ROC assessment tool, which directly works
for ROC analysis of regression results for logistic regression of binary variables,
including the glm() and lrm() commands, and COX regression for survival analysis,
including the cph() and coxph() commands.
The most important feature of 'modelROC' is that both the model and the independent
variables can be analysed simultaneously, and for survival analysis
multiple time points and area under the curve analysis are supported.
Still, flexible visualisation is possible with the 'ggplot2' package.
Reference are Kelly H. Zou (1998) <doi:10.1002/(sici)1097-
0258(19971015)16:19%3C2143::aid-sim655%3E3.0.co;2-3> and
P J Heagerty (2000) <doi:10.1111/j.0006-341x.2000.00337.x>.

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Encoding UTF-8

RoxygenNote 7.1.1

Depends ggplot2

Imports do, tmcn, ROCit, survivalROC

Suggests ggDCA, rms

NeedsCompilation no

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R topics documented:

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auc   *auc for model*

Description

auc for model

Usage

```
auc(...)

## S3 method for class 'cph'
auc(..., model = NULL, x = NULL, method = c("NNE", "KM"))

## S3 method for class 'coxph'
auc(..., model = NULL, x = NULL, method = c("NNE", "KM"))
```

Arguments

...	one or more fit
model	can be logical or characters. FALSE means no model TP and FP, characters mean model names.
x	can be logical or characters. TRUE means all x variable in regression will be calculated. One or more characters will be calculated only.
method	NNE or KM

Value

auc dataframe

one auc_coxph for cox regression. model means model names,

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ggplot   *Plot for ROC curve*

Description

Plot for ROC curve

Usage

```
## S3 method for class 'auc_coxph'
ggplot(
  data,
  mapping,
  color = NULL,
  lwd = 1.05,
  grid.space = 2,
  ncol = NULL,
  ...,
  environment = parent.frame()
)

## S3 method for class 'roc_coxph'
ggplot(
  data,
  mapping,
  color = NULL,
  lwd = 1.05,
  grid.space = 2,
  rank = FALSE,
  ncol = NULL,
  ...,
  environment = parent.frame()
)

## S3 method for class 'roc_logit'
ggplot(
  data,
  mapping,
  color = NULL,
  lwd = 1.05,
  grid.space = 2,
  rank = FALSE,
  ...,
  environment = parent.frame()
)
```

Arguments

`data`	resultes of roc() function
`mapping`	ignore
`color`	one or more colors
`lwd`	logical or integers
`grid.space`	space between grids, default is 2
`ncol`	number of column for grid plot
`...`	ignore
`environment`	ignore
`rank`	rank by AUC

Value

a ggplot picture.

Examples

```
library(ggDCA)
library(rms)
library(modelROC)
###  COX ----------

fit <- cph(Surv(time,status)~ANLN+CENPA+GPR182,LIRI)

####        one model, one time ####
#----          auc for model

r <- auc(fit,
         model='This is model') # one model
unique(r)
ggplot(r)

r <- auc(fit,
         model=TRUE)             # all model
unique(r)
ggplot(r)


#----           auc for x
r <- auc(fit,
         x='ANLN')              # one x
unique(r)
ggplot(r)

r <- auc(fit,
         x=c('ANLN','CENPA'))   # more x
unique(r)
ggplot(r)
```

```
r <- auc(fit,
         x=TRUE)                  # all x
unique(r)
ggplot(r)

r <- auc(fit,
         model=TRUE,             # one model
         x=TRUE)                 # all x
unique(r)
ggplot(r)

r <- auc(fit,
         model='Three Genes',    # specify model names
         x=TRUE)                 # all X
unique(r)
ggplot(r)



####       more models ####
fit2 <- cph(Surv(time,status)~ANLN+CENPA,LIRI)


r <- auc(fit,fit2,
         model=c('Three Genes','Two Genes'))            #
unique(r)
ggplot(r)



r <- auc(fit,fit2,
         model=TRUE,
         x=TRUE)
unique(r)
ggplot(r)

library(ggDCA)
library(rms)
fit <- lrm(status~ANLN+CENPA+GPR182,LIRI)
####        one model ####
pp <- roc(fit,
          model=TRUE) # one model
unique(pp)
ggplot(pp)

pp <- roc(fit,
          x='ANLN') # one x
unique(pp)
ggplot(pp)


pp <- roc(fit,
```

```
         x=c('ANLN','CENPA')) # more x
unique(pp)
ggplot(pp)


pp <- roc(fit,
          x=TRUE) # ALL x
unique(pp)
ggplot(pp)


pp <- roc(fit,
          model=TRUE, # one model
          x=TRUE) # ALL x
unique(pp)
ggplot(pp)

pp <- roc(fit,
          model='Three Genes', # specify model name
          x=TRUE) # ALL x
unique(pp)
ggplot(pp)

####        more model    ####

fit2 <- lrm(status~ANLN+CENPA,LIRI)
pp <- roc(fit,fit2,
          model=TRUE) # all model
unique(pp)
ggplot(pp)


pp <- roc(fit,fit2,
          model=c('Three Genes','Two Genes')) # specify model names
unique(pp)
ggplot(pp)

pp <- roc(fit,fit2,
          x=TRUE,                             # all x
          model=c('Three Genes','Two Genes')) # all model
unique(pp)
ggplot(pp)

### COX ----------

fit <- cph(Surv(time,status)~ANLN+CENPA+GPR182,LIRI)
range(LIRI$time)
####       one model, one time ####
#----          roc for model

pp <- roc(fit, times=1,
          model='This is model') # one model
unique(pp)
```

```
ggplot(pp)

pp <- roc(fit, times=1,
          model=TRUE)              # all model
unique(pp)
ggplot(pp)

#----              roc for x
pp <- roc(fit, times=1,
          x='ANLN')                # one x
unique(pp)
ggplot(pp)

pp <- roc(fit, times=1,
          x=c('ANLN','CENPA'))     # more x
unique(pp)
ggplot(pp)

pp <- roc(fit, times=1,
          x=TRUE)                  # all x
unique(pp)
ggplot(pp)

pp <- roc(fit, times=1,
          model=TRUE,              # one model
          x=TRUE)                  # all x
unique(pp)
ggplot(pp)

pp <- roc(fit, times=1,
          model='Three Genes',     # specify model names
          x=TRUE)                  # all X
unique(pp)
ggplot(pp)

####        one model, more time ####

pp <- roc(fit, times=c(1,2,3,4,5,6),
          model=TRUE)              # one model
unique(pp)
ggplot(pp)


pp <- roc(fit, times=c(1,2),
          x =  'ANLN')             # one x

unique(pp)
ggplot(pp)


pp <- roc(fit, times=c(1,2,3,4,5,6),
          x = c('ANLN','CENPA')) # more x
unique(pp)
```

```
ggplot(pp,ncol = 3)


pp <- roc(fit, times=c(1,2),
          model=TRUE,               # one model
          x = TRUE) # all x
unique(pp)
ggplot(pp)

####        more models, one time ####
fit2 <- cph(Surv(time,status)~ANLN+CENPA,LIRI)

pp <- roc(fit,fit2,times=1,
          x=TRUE,
          model=c('Three Genes','Two Genes'))            #
unique(pp)
ggplot(pp)
####         more models, more time ####
pp <- roc(fit,fit2,times=c(1,2),
          model=c('Three Genes','Two Genes'))            #
unique(pp)
ggplot(pp)

pp <- roc(fit,fit2,times=c(1,2),
          x=TRUE,
          model=c('Three Genes','Two Genes'))            #
unique(pp)
ggplot(pp)
```

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roc	*roc for model*

Description

roc for model

Usage

```
roc(...)

## S3 method for class 'cph'
roc(..., times = NULL, model = NULL, x = NULL, method = c("NNE", "KM"))

## S3 method for class 'coxph'
roc(..., times = NULL, model = NULL, x = NULL, method = c("NNE", "KM"))

## S3 method for class 'glm'
roc(
```

```
  ...,
  negref = 0,
  model = NULL,
  x = NULL,
  method = c("empirical", "binormal", "nonparametric")
)

## S3 method for class 'lrm'
roc(
  ...,
  negref = 0,
  model = NULL,
  x = NULL,
  method = c("empirical", "binormal", "nonparametric")
)
```

Arguments

`...`	one or more fit
`times`	one or more times for cox regression
`model`	can be logical or characters. FALSE means no model TP and FP, characters mean model names.
`x`	can be logical or characters. TRUE means all x variable in regression will be calculated. One or more characters will be calculated only.
`method`	NNE or KM
`negref`	negative reference for each model

Value

roc dataframe

one roc_coxph for cox regression. model means model names,

References

Heagerty PJ, Lumley T, Pepe MS. *Time-dependent ROC curves for censored survival data and a diagnostic marker.* Biometrics, 2000.

Pepe, Margaret Sullivan. *The statistical evaluation of medical tests for classification and prediction.* Medicine, 2003.

Zou, Kelly H., W. J. Hall, and David E. Shapiro. *Smooth non-parametric receiver operating characteristic (ROC) curves for continuous diagnostic tests.* Statistics in medicine 16, no. 19 (1997): 2143-2156.

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unique   *Extract data from roc() function*

Description

Extract data from roc() function

Usage

```
## S3 method for class 'roc_coxph'
unique(x, incomparables = FALSE, ...)

## S3 method for class 'roc_logit'
unique(x, incomparables = FALSE, ...)

## S3 method for class 'auc_coxph'
unique(x, incomparables = FALSE, ...)
```

Arguments

x	result of roc() function
incomparables	ignore
...	ignore

Value

a dataframe.

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