Package ‘prognosticROC’

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Type Package

Title Prognostic ROC curves for evaluating the predictive capacity of a binary test

Version 0.6

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Description This package contains functions to assess prognostic ROC curve . The user enters herself/him the survival according to the model she/he choose or she/he enters individual survival data. The area under the prognostic ROC curve is assessed by using the trapezoidal rules. The extrapolated area (when survival curves do not reach 0) are performed by assuming pessimist, optimist and non-informative situation.

License GPL (>=2)

LazyLoad yes

Depends splines, survival

Imports splines, survival

URL www.r-project.org, www.divat.fr

R topics documented:

`prognosticROC-package` *Prognostic ROC curves*

Description

This package computes prognostic ROC curves.

Details

The separation between two survival curves represents the magnitude of the association between the intervention and the time-to-event. A statistical test can determine the statistical significance of the difference but does not quantify its magnitude. The purpose of the prognostic ROC curve is to represent this uncertainty: the AUC is the probability that the time-to-event is improved in one arm compared to the other. This package is designed for computing such prognostic ROC curve with confidence intervals obtained by bootstrap resampling (from individual data only).

Package:	prognosticROC
Type:	Package
Version:	0.6
Date:	2013-07-04
License:	GPL (>=2)
LazyLoad:	yes

AggregatedPROC	Compute prognostic ROC curve based on survival function already determined by the user (parametric model, Kaplan-Meier curve, weighted estimations,...)
IndividualPROC	Compute prognostic ROC curve based on individual data, survival function are determined by the Kaplan-Meier estimator, confidence intervals are obtained by bootstrap

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References

Combescure C, Perneger TV, Weber DC, Daures JP and Foucher Y. Prognostic ROC curves for censored time-to-event endpoints: a method for representing the overall discriminative capacity of binary markers. Manuscript submitted.

See Also

URL: http://www.divat.fr

`AggregatedPROC` *Prognostic ROC curve based on survival probabilities already computed*

Description

The user enters the survival according to the model she/he chooses. The area under the prognostic ROC curve is assessed by using the trapezoidal rules. The extrapolated areas (when survival curves do not reach 0) are performed by assuming pessimist, optimist and non-informative situation.

Usage

```
AggregatedPROC(Time.LR, Surv.LR, Time.HR, Surv.HR)
```

Arguments

`Time.LR`	A numeric vector with the survival times in the low risk group.
`Surv.LR`	A numeric vector with the survival probabilities corresponding to `Time.LR`
`Time.HR`	A numeric vector with the survival times in the high risk group.
`Surv.HR`	A numeric vector with the survival probabilities corresponding to `Time.HR`.

Details

The maximum prognostic time is the minimum between the maximum of `Time.LR` and the maximum of `Time.HR`.

Value

`max.time`	This is the maximum prognostic time used for the analysis
`table`	This data frame presents the different time cut-offs associated with the coordinates of the ROC curves.
`auc`	This data frame presents the different estimations of the area under the prognostic ROC curve: the lower bound, the pessimist, the non-informative, the optimist and the upper bound.

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Examples

```
# example of two survival curves using exponential distributions
time.hr <- seq(0, 600, by=5)
time.lr <- seq(0, 500, by=2)
surv.hr <- exp(-0.005*time.hr)
surv.lr <- exp(-0.003*time.lr)

# Illustration of both survival curves
plot(time.hr, surv.hr, xlab="Time (in days)",
 ylab="Patient survival", lwd=2, type="l")
lines(time.lr, surv.lr, lty=2, col=2, lwd=2)
legend("topright", c("High-Risk Group", "Low-Risk Group"), lwd=2,
 col=1:2, lty=1:2)

# Computation of the prognostic ROC curve
proc.result <- AggregatedPROC(time.lr, surv.lr, time.hr, surv.hr)

# Representation of the prognostic ROC curve
plot(proc.result$table$x, proc.result$table$y, type="l",
 lwd=2, xlim=c(0,1), ylim=c(0,1),
 xlab="1-Survival in the low risk group",
 ylab="1-Survival in the high risk group")
abline(c(0,0), c(1,1), lty=2)

# The pessimist value of the area under the curve
proc.result$auc$pessimist
```

`IndividualPROC` *Prognostic ROC curve based on individual data*

Description

The user enters individual survival data. The area under the prognostic ROC curve is assessed by using the trapezoidal rules. The extrapolated areas (when survival curves do not reach 0) are performed by assuming pessimist, optimist and non-informative situation. The confidence intervals are obtained by non-parametric bootstrapping.

Usage

```
IndividualPROC(times, failures, variable, B)
```

Arguments

`times`	A numeric vector with the follow up times.
`failures`	A numeric vector with the event indicator (0=right censored, 1=event).
`variable`	A numeric vector with the result of the binary test (only two groups). The variable equals 1 for the high risk group and 0 for the low risk group.
`B`	The number of bootstrap samples to compute the confidence intervals. The default value is 0, which corresponds to no confidence interval computation.

Details

The maximum prognostic time is the minimum between the two last observed times of failure in both groups.

Value

`max.time`	This is the maximum prognostic time used for the analysis
`table`	This data frame presents the different time cut-offs associated with the coordinates of the ROC curves.
`auc`	This data frame presents the different estimations of the area under the prognostic ROC curve: the lower bound, the pessimist, the non-informative, the optimist and the upper bound.
`CI.95`	This data frame presents the 95 percentage confidence intervals of the area under the prognostic ROC curve: the lower bound, the pessimist, the non-informative, the optimist and the upper bound.
`auc.boot`	This data frame presents the different estimations of the area under the prognostic ROC curve for each of the `B` bootstrap samples: the lower bound, the pessimist, the non-informative, the optimist and the upper bound.

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Examples

```
####################################################################
# example of two samples with different exponential distributions #
####################################################################

n1 <- 200
n2 <- 350
grp  <- c(rep(1, n1), rep(0, n2))
time.evt <- c(rexp(n1, rate = 1.2), rexp(n2, rate = 0.5))
time.cen <- rexp(n1+n2, rate = 0.2)
time <- pmin(time.evt, time.cen)
evt  <- 1*(time.evt < time.cen)

# Illustration of both survival curves
surv.temp <- survfit(Surv(time, evt) ~ grp)
plot(surv.temp, lty = 2:3)

# Computation of the prognostic ROC curve
proc.result <- IndividualPROC(time, evt, grp, B=1000)

# Representation of the prognostic ROC curve
```

```
plot(proc.result$table$x, proc.result$table$y, type="l",
 lwd=2, xlim=c(0,1), ylim=c(0,1),
 xlab="1-Survival in the low risk group",
 ylab="1-Survival in the high risk group")
abline(c(0,0), c(1,1), lty=2)

# The corresponding 95% CI of the pessimist value
proc.result$CI.95$pessimist


################################################################
# example of two samples with closed exponential distributions #
################################################################

n1 <- 200
n2 <- 350
grp  <- c(rep(1, n1), rep(0, n2))
time.evt <- c(rexp(n1, rate = 1.11), rexp(n2, rate = 1.09))
time.cen <- rexp(n1+n2, rate = 0.2)
time <- pmin(time.evt, time.cen)
evt  <- 1*(time.evt < time.cen)

plot(survfit(Surv(time, evt) ~ grp) , lty = 2:3)

proc.result <- IndividualPROC(time, evt, grp, B=1000)

# The 95% CI of the non informative value by bootstrap
proc.result$CI.95$noninformative

# The 90% CI of the non informative value by bootstrap
quantile(proc.result$auc.boot$noninformative, probs=c(0.05, 0.95))
```

Index