Package ‘prognosticROC’

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Type Package
Title Prognostic ROC curves for evaluating the predictive capacity of a binary test
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Description Prognostic ROC curve is an alternative graphical approach to represent the discriminative capacity of the marker: a receiver operating characteristic (ROC) curve by plotting 1 minus the survival in the high-risk group against 1 minus the survival in the low-risk group. This package contains functions to assess prognostic ROC curve. The user can enter the survival according to a model previously estimated or the user can also enter individual survival data for estimating the prognostic ROC curve by using Kaplan-Meier estimator. The area under the curve (AUC) corresponds to the probability that a patient in the low-risk group has a longer lifetime than a patient in the high-risk group. The prognostic ROC curve provides complementary information compared to survival curves. The AUC is assessed by using the trapezoidal rules. When survival curves do not reach 0, the prognostic ROC curve is incomplete and the extrapolations of the AUC are performed by assuming pessimist, optimist and non-informative situations.
License GPL (>= 2)
LazyLoad yes
Depends splines, survival
NeedsCompilation no
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prognosticROC-package

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).

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Version: 0.7
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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


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

<table>
<thead>
<tr>
<th>Time.LR</th>
<th>A numeric vector with the survival times in the low risk group.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Surv.LR</td>
<td>A numeric vector with the survival probabilities corresponding to Time.LR</td>
</tr>
<tr>
<td>Time.HR</td>
<td>A numeric vector with the survival times in the high risk group.</td>
</tr>
<tr>
<td>Surv.HR</td>
<td>A numeric vector with the survival probabilities corresponding to Time.HR.</td>
</tr>
</tbody>
</table>

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.

Author(s)

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References

Examples

```r
# 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 <- aggregated.proc(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.
**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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**References**


**Examples**

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

n1 <- 200
n2 <- 200
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)
ev <- 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=50)
  # Use B>50 for real applications

# 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
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