Package 'MRsurv'

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Type Package

Title A multiplicative-regression model for relative survival.

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Description This package contains functions, data and examples to compute a multiplicative-
regression model for relative survival.

License GPL (>= 2)

LazyLoad yes

Depends survival, mvtnorm

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

NeedsCompilation no

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R topics documented:

MRsurv-package   *Multiplicative-regression model for relative survival.*

Description

This package computes multiplicative-regression model for relative survival.

Details

Relative survival models are traditionally used in the evaluation of mortality related to chronic diseases, taking into account the expected mortality of general population (life table by gender, calendar year and age). Here, we propose here an adaptation of a multiplicative-regression model for relative survival to study the heterogeneity of risk factors between two groups of patients. These developments were motivated by the analysis of factors associated with the time to graft failure (return-to-dialysis or patient death) in second kidney transplant recipients compared to first kidney transplant recipients. The parameters' estimation is based on partial likelihood maximization and Monte-Carlo simulations associated with bootstrap re-sampling yields to obtain the corresponding standard deviations.

Package:	MRsurv
Type:	Package
Version:	0.2
Date:	2013-10-31
License:	GPL (>=2)
LazyLoad:	yes

MRsurvival	Compute a MRS model to compare the risk factors between a reference and a relative population.
FTR.data	These data were extracted from the DIVAT data bank for first kidney transplant recipients (reference group).
STR.data	These data were extracted from the DIVAT data bank for second kidney transplant recipients (relative group).

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References

Andersen P, Borch-Johnsen K, Deckert T, Green A, Hougaard P, Keiding N, Kreiner S. A cox regression model for the relative mortality and its application to diabetes mellitus survival data. Biometrics Dec 1985; 41(4):921-932.

K. Trebern-Launay, M. Giral, J. Dantal and Y. Foucher. Comparison of the risk factors effects between two populations: two alternative approaches illustrated by the analysis of first and second kidney transplant recipients. BMC Med Res Methodol. 2013 Aug 6;13:102.

See Also

URL: http://www.divat.fr

| FTR.data | *These data were extracted from the DIVAT data bank for first kidney transplant recipients.* |

Description

Data were extracted from the DIVAT cohort. It corresponds to the reference sample constituted by first transplant recipients (FTR).

Usage

```
data(FTR.data)
```

Format

A data frame with the 4 following variables.

Tps.Evt This numeric vector provides the post-transplantation time (in days).

Evt This numeric vector provides the indicator of graft failure at the end of the follow-up (1 for failure and 0 for right censoring).

ageR2cl This numeric vector provides the recipient age at transplantation (1 for older than 55 years and 0 otherwise).

sexeR This numeric vector provides the recipient gender (1 for men and 0 for women).

Details

First transplant recipients (FTR) constituted the reference group. Recipients older than 18 years at the date of transplantation between 1996 and 2010 were selected from the French DIVAT (www.divat.fr/en) multicentric prospective cohort. Only recipients with a maintenance therapy with calcineurin inhibitors, mammalian target of rapamycin inhibitors or belatacept, in addition to mycophenolic acid and steroid were included. Simultaneous transplantations were excluded. Two explicative variables are proposed: recipient age at transplantation and recipient gender.

References

K. Trebern-Launay, M. Giral, J. Dantal and Y. Foucher. Comparison of the risk factors effects between two populations: two alternative approaches illustrated by the analysis of first and second kidney transplant recipients. BMC Med Res Methodol. 2013 Aug 6;13:102.

Examples

```
data(FTR.data)

# Compute a Cox PH model with both explicative variables
cox.FTR<-coxph(Surv(Tps.Evt/365.24, Evt) ~ ageR2cl + sexeR, data=FTR.data)
summary(cox.FTR)
```

MRsurvival	*Multiplicative-regression model to compare the risk factors between a reference and relative populations.*

Description

Compute a MRS model to compare the risk factors between a reference and a relative population.

Usage

```
MRsurvival(time.ref, status.ref, cov.rel, data.rel, cox.ref, cov.ref, init, B)
```

Arguments

time.ref	The column name of the data frame data.rel, in which the time of follow-up of each individual is collected.
status.ref	The column name of the data frame data.rel, in which the indicator of event at the end of follow-up is collected (1 if the event is observed and 0 if right censoring).
cov.rel	The column(s) name(s) of the data frame declared in data.rel in order to declare the explicative variable included in the multiplicative relative model.
data.rel	A data frame with the variables (columns) of the individuals (raw) of the relative sample.
cox.ref	The results of the Cox model performed in the reference sample, i.e an object obtained by the coxph function.
cov.ref	The column(s) name(s) of the data frame data.rel in order to declare the explicative variable corresponding to those included in the Cox model cox.ref. Please, note that the order of these variables is important and have to be similar with the order in cox.ref.
init	A vector with the same length than cov.rel with the initial values for the parameters to be optimized.
B	The number of iterations of the bootstrap resampling.

Details

We proposed here an adaptation of a multiplicative-regression model for relative survival to study the heterogeneity of risk factors between two groups of patients. Estimation of parameters is based on partial likelihood maximization and Monte-Carlo simulations associated with bootstrap re-sampling yields to obtain the corresponding standard deviations. The expected hazard ratios are obtained by using a PH Cox model.

Value

`matrix.coef`	A matrix containing the parameters estimations at each of the B iterations.
`estim.coef`	A numerical vector containing the mean of the previous estimation
`lower95.coef`	A numerical vector containing the lower bounds of the 95% confidence intervals.
`upper95.coef`	A numerical vector containing the upper bounds of the 95% confidence intervals.

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References

Andersen P, Borch-Johnsen K, Deckert T, Green A, Hougaard P, Keiding N, Kreiner S. A cox regression model for the relative mortality and its application to diabetes mellitus survival data. Biometrics Dec 1985; 41(4):921-932.

K. Trebern-Launay, M. Giral, J. Dantal and Y. Foucher. Comparison of the risk factors effects between two populations: two alternative approaches illustrated by the analysis of first and second kidney transplant recipients. BMC Med Res Methodol. 2013 Aug 6;13:102.

Examples

```
# import and attach both samples
data(FTR.data)
data(STR.data)

# We reduce the dimension to save time for this example (CRAN policies)
STR.data <- STR.data[1:100,]

# Compute the Cox model in the reference sample (FTR)
cox.FTR<-coxph(Surv(Tps.Evt, Evt)~ ageR2cl + sexeR, data=FTR.data)
summary(cox.FTR)


# Compute the multiplicative relative model (STR)
mrs.STR <- MRsurvival(time.ref="Tps.Evt", status.ref="Evt",
 cov.rel=c("ageR2cl", "Tattente2cl"),
 data.rel=STR.data, cox.ref=cox.FTR, cov.ref=c("ageR2cl", "sexeR"),
 init=c(0,0), B=5)
  # Of course, choose B>>5 for real applications
```

```
# The values at each iteration
mrs.STR$matrix.coef

# The parameters estimations (mean of the values)
mrs.STR$estim.coef
apply(mrs.STR$matrix.coef, FUN="mean", MARGIN=2)

# The 95% confidence intervals
cbind(mrs.STR$lower95.coef, mrs.STR$upper95.coef)
```

STR.data   *These data were extracted from the DIVAT data bank for second kidney*
                                transplant recipients.

Description

Data were extracted from the DIVAT cohort. It corresponds to the relative sample constituted by second transplant recipients (STR).

Usage

```
data(FTR.data)
```

Format

A data frame with the 6 following variables.

Tps.Evt This numeric vector provides the post transplantation time (in days).

Evt This vector provides the indicators of graft failure at the end of the follow-up (1 for failures and 0 for right censoring).

ageR2cl This numeric vector provides the recipient age at transplantation (1 for older than 55 years and 0 otherwise).

sexeR This numeric vector provides the recipient gender (1 for men and 0 for women).

ageD2cl This numeric vector provides the donor age (1 for older than 55 years and 0 otherwise).

Tattente2cl This numeric vector provides the waiting time in dialysis between the two consecutive transplantations (1 for more than 3 years and 0 otherwise).

Details

Second transplant recipients (STR) constituted the relative group of interest. Recipients older than 18 years at the date of transplantation between 1996 and 2010 were selected from the French DIVAT (www.divat.fr/en) multicentric prospective cohort. Only recipients with a maintenance therapy with calcineurin inhibitors, mammalian target of rapamycin inhibitors or belatacept, in addition to mycophenolic acid and steroid were included. Simultaneous transplantations were excluded. Two explicative variables are common with the reference group: recipient age at transplantation and recipient gender. Two explicative variables are specific to STR: donor age and waiting time in dialysis between the two consecutive transplantations.

References

K. Trebern-Launay, M. Giral, J. Dantal and Y. Foucher. Comparison of the risk factors effects between two populations: two alternative approaches illustrated by the analysis of first and second kidney transplant recipients. BMC Med Res Methodol. 2013 Aug 6;13:102.

Examples

```
data(STR.data)

# The number of patients in the relative group.
dim(STR.data)

# Compute a Cox PH model
cox.STR<-coxph(Surv(Tps.Evt/365.24, Evt) ~ ageR2cl + Tattente2cl, data=STR.data)
summary(cox.STR)
```

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