

Package ‘pseudo’

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Title Pseudo - observations

Version 1.0

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Description Various functions for computing pseudo-observations for censored data regression

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Depends KMSurv, geepack

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pseudoci	<i>Pseudo-observations for the cumulative incidence function</i>
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Description

Computes pseudo-observations for modeling competing risks based on the cumulative incidence function.

Usage

```
pseudoci(time,event, tmax)
```

Arguments

time	the follow up time.
event	the status indicator: 0=alive, 1=dead (risk 1), 2= dead (risk 2).
tmax	a vector of time points at which the pseudo-observations are to be computed. If missing, the pseudo-observations are reported at each event time.

Details

The function calculates the pseudo-observations for the cumulative incidence function for each individual and each risk at all the required time points. The pseudo-observations can be used for fitting a regression model with a generalized estimating equation.

Value

A data frame. The first two columns contain the follow up time and the status indicator as given by the user. The following columns present the pseudo-observations for each of the risks at all the required (sorted) time points.

References

Klein J.P., Gerster M., Andersen P.K., Tarima S.: "SAS and R Functions to Compute Pseudo-values for Censored Data Regression." *Department of Biostatistics, University of Copenhagen*, research report 07/11.

See Also

[pseudomean](#), [pseudosurv](#)

Examples

```
library(KMsurv)
data(bmt)

#calculate the pseudo-observations
cutoffs <- c(50,105,170,280,530)
bmt$icr <- bmt$d1 + bmt$d3
pseudo <- pseudoci(time=bmt$t2,event=bmt$icr,tmax=cutoffs)

#rearrange the data, use only pseudo-observations for relapse
rel_mask <- c(-1,50,-1,105,-1,170,-1,280,-1,530)
b <- NULL
for(j in 3:ncol(pseudo)){
  b <- rbind(b,cbind(bmt,pseudo = pseudo[,j],
    tpseudo = rel_mask[j-2],id=1:nrow(bmt)))
}
b <- b[order(b$id),]
b <- b[b$tpseudo != -1,]

# fit the model
library(geepack)
```

```

fit <- geese(pseudo ~ as.factor(tpseudo) + as.factor(group) + as.factor(z8) +
z1 - 1, data =b, id=id, jack = TRUE, scale.fix=TRUE, family=gaussian,
mean.link = "cloglog", corstr="independence")

#The results using the AJ variance estimate
cbind(mean = round(fit$beta,4), SD = round(sqrt(diag(fit$vbeta.ajs)),4),
Z = round(fit$beta/sqrt(diag(fit$vbeta.ajs)),4),
PVal = round(2-2*pnorm(abs(fit$beta/sqrt(diag(fit$vbeta.ajs))))),4))

```

pseudomean

Pseudo-observations for the restricted mean

Description

Computes pseudo-observations for modeling survival function based on the restricted mean.

Usage

```
pseudomean(time,event, tmax)
```

Arguments

time	the follow up time.
event	the status indicator: 0=alive, 1=dead.
tmax	the maximum cut-off point for the restricted mean. If missing or larger than the maximum follow up time, it is replaced by the maximum follow up time.

Details

The function calculates the pseudo-observations for the restricted mean survival for each individual at prespecified time-points. The pseudo-observations can be used for fitting a regression model with a generalized estimating equation.

Value

A data frame. The first two columns contain the follow up time and the status indicator as given by the user. The third column presents the computed pseudo-observations.

References

Klein J.P., Gerster M., Andersen P.K., Tarima S.: "SAS and R Functions to Compute Pseudo-values for Censored Data Regression." *Department of Biostatistics, University of Copenhagen*, research report 07/11.

See Also

[pseudosurv](#), [pseudoci](#)

Examples

```

library(KMsurv)
data(bmt)

#compute the pseudo-observations:
pseudo = pseudomean(time=bmt$t2, event=bmt$d3, tmax=2000)

#arrange the data
a <- cbind(bmt, pseudo = pseudo$psumean, id=1:nrow(bmt))

#fit a regression model for the mean time

library(geepack)
summary(fit <- geese(pseudo ~ z1 + as.factor(z8) + as.factor(group),
  data = a, id=id, jack = TRUE, family=gaussian,
  corstr="independence", scale.fix=FALSE))

#rearrange the output
round(cbind(mean = fit$beta, SD = sqrt(diag(fit$vbeta.ajs)),
  Z = fit$beta/sqrt(diag(fit$vbeta.ajs)), PVal =
  2-2*pnorm(abs(fit$beta/sqrt(diag(fit$vbeta.ajs))))), 4)

```

pseudosurv

Pseudo-observations for the Kaplan-Meier estimate

Description

Computes pseudo-observations for modeling survival function based on the Kaplan-Meier estimator.

Usage

```
pseudosurv(time, event, tmax)
```

Arguments

time	the follow up time.
event	the status indicator: 0=alive, 1=dead.
tmax	a vector of time points at which the pseudo-observations are to be computed. If missing, the pseudo-observations are reported at each event time.

Details

The function calculates the pseudo-observations for the value of the survival function at prespecified time-points for each individual. The pseudo-observations can be used for fitting a regression model with a generalized estimating equation.

Value

A data frame. The first two columns contain the follow up time and the status indicator as given by the user. The following columns present the pseudo-observations for each of the required (sorted) time points.

References

Klein J.P., Gerster M., Andersen P.K., Tarima S.: "SAS and R Functions to Compute Pseudo-values for Censored Data Regression." *Department of Biostatistics, University of Copenhagen*, research report 07/11.

See Also

[pseudomean](#), [pseudoci](#)

Examples

```
library(KMsurv)
data(bmt)

#calculate the pseudo-observations
cutoffs <- c(50,105,170,280,530)
pseudo <- pseudosurv(time=bmt$t2,event=bmt$d3,tmax=cutoffs)

#rearrange the data
b <- NULL
for(j in 3:ncol(pseudo)){
  b <- rbind(b,cbind(bmt,pseudo=pseudo[,j],tpseudo=cutoffs[j-2],
    id=1:nrow(bmt)))
}
b <- b[order(b$id),]

#fit a Cox model using GEE
library(geepack)
summary(fit <- geese(pseudo~as.factor(tpseudo)+as.factor(group)+
  as.factor(z8)+z1,data=b,scale.fix=TRUE,family=gaussian,
  jack=TRUE, mean.link="cloglog",corstr="independence"))

#The results using the AJ variance estimate
round(cbind(mean = fit$beta,SD = sqrt(diag(fit$vbeta.ajs)),
  Z = fit$beta/sqrt(diag(fit$vbeta.ajs)),PVal =
  2-2*pnorm(abs(fit$beta/sqrt(diag(fit$vbeta.ajs))))),4)
```

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