

# 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

**License** GPL-2

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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))
```

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pseudomean

*Pseudo-observations for the restricted mean*


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## 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)

```

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pseudosurv

*Pseudo-observations for the Kaplan-Meier estimate*


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**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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