

Package ‘eventglm’

November 10, 2020

Type Package

Title Regression Models for Event History Outcomes

Version 1.0.2

Date 2020-11-07

Description A user friendly, easy to understand way of doing event history regression for marginal estimands of interest, including the cumulative incidence and the restricted mean survival, using the pseudo observation framework for estimation. For a review of the methodology, see Andersen and Pohar Perme (2010) <doi:10.1177/0962280209105020>. The interface uses the well known formulation of a generalized linear model and allows for features including plotting of residuals, the use of sampling weights, and corrected variance estimation.

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URL <https://sachsmc.github.io/eventglm/>

BugReports <https://github.com/sachsmc/eventglm/issues/>

Encoding UTF-8

LazyData true

Suggests testthat, prodlim, knitr, rmarkdown, rio, data.table

RoxygenNote 7.1.1

Imports survival, sandwich, stats

Depends R (>= 2.10)

VignetteBuilder knitr

NeedsCompilation yes

Author Michael C Sachs [aut, cre],
Erin E Gabriel [aut],
Morten Overgaard [ctb] (Corrected variance calculation),
Thomas A Gerds [ctb] (Fast computation of leave one out cumulative incidence),
Terry Therneau [ctb] (Restricted mean computation)

Maintainer Michael C Sachs <sachsmc@gmail.com>

Repository CRAN

Date/Publication 2020-11-10 10:30:02 UTC

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colon	<i>Chemotherapy for Stage B/C colon cancer</i>
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Description

These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are only one record per patient for the death outcome (or censoring). This is redistributed from the survival package, with a small modification to include only the death outcome.

Usage

colon

Format

A data frame with 929 rows and 17 variables:

id id

study 1 for all patients

rx Treatment - Obs(ervation), Lev(amisole), Lev(amisole)+5-FU

sex 1=male

age in years

obstruct obstruction of colon by tumour

perfor perforation of colon

adhere adherence to nearby organs

nodes number of lymph nodes with detectable cancer

time days until death or censoring

status censoring status

differ differentiation of tumour (1=well, 2=moderate, 3=poor)

extent Extent of local spread (1=submucosa, 2=muscle, 3=serosa, 4=contiguous structures)

surg time from surgery to registration (0=short, 1=long)

node4 more than 4 positive lymph nodes

etype event type: 1=recurrence,2=death

event event indicator: censored, death

See Also

[colon](#)

confint.pseudoglm

Confidence Intervals for pseudoglm Model Parameters

Description

Computes Wald confidence intervals for one or more parameters in a fitted model. Users can specify the type of variance estimate used, with the default being the robust sandwich variance estimator.

Usage

```
## S3 method for class 'pseudoglm'  
confint(object, parm, level = 0.95, type = "robust", ...)
```

Arguments

object	A fitted model object from cumincglm or rmeanglm
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required.
type	The type of variance estimate to use, see vcov.pseudoglm
...	Not used

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as $(1-\text{level})/2$ and $1 - (1-\text{level})/2$ in

Examples

```
cumincipcw <- cumincglm(survival::Surv(etime, event) ~ age + sex,
  time = 200, cause = "pcm", link = "identity",
  model.censoring = "independent", data = mgus2)
confint(cumincipcw)
```

 cumincglm

Generalized linear models for cumulative incidence

Description

Using pseudo observations for the cumulative incidence, this function then runs a generalized linear model and estimates the parameters representing contrasts in the cumulative incidence at a particular time (specified by the `time` argument) across covariate values. The link function can be "identity" for estimating differences in the cumulative incidence, "log" for estimating ratios, and any of the other link functions supported by [quasi](#).

Usage

```
cumincglm(
  formula,
  time,
  cause = 1,
  link = "identity",
  model.censoring = "independent",
  formula.censoring = NULL,
  ipcw.method = "binder",
  data,
  weights,
  subset,
```

```

na.action,
offset,
control = list(...),
model = FALSE,
x = TRUE,
y = TRUE,
singular.ok = TRUE,
contrasts = NULL,
...
)

```

Arguments

formula	A formula specifying the model. The left hand side must be a Surv object specifying a right censored survival or competing risks outcome. The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For competing risks, the event variable will be a factor, whose first level is treated as censoring. The right hand side is the usual linear combination of covariates.
time	Numeric constant specifying the time at which the cumulative incidence or survival probability effect estimates are desired.
cause	Numeric or character constant specifying the cause indicator of interest.
link	Link function for the cumulative incidence regression model.
model.censoring	Type of model for the censoring distribution. Options are "stratified", which computes the pseudo-observations stratified on a set of categorical covariates, "aareg" for Aalen's additive hazards model, and "coxph" for Cox's proportional hazards model. With those options, we assume that the time to event and event indicator are conditionally independent of the censoring time, and that the censoring model is correctly specified. If "independent", we assume completely independent censoring, i.e., that the time to event and covariates are independent of the censoring time. the censoring time is independent of the covariates in the model.
formula.censoring	A one sided formula (e.g., $\sim x_1 + x_2$) specifying the model for the censoring distribution. If NULL, uses the same mean model as for the outcome.
ipcw.method	Which method to use for calculation of inverse probability of censoring weighted pseudo observations. "binder" the default, uses the number of observations as the denominator, while the "hajek" method uses the sum of the weights as the denominator.
data	Data frame in which all variables of formula can be interpreted.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process.

na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> . Another possible value is NULL, no action. Value <code>na.exclude</code> can be useful.
offset	this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <code>model.offset</code> .
control	a list of parameters for controlling the fitting process. This is passed to <code>glm.control</code> .
model	a logical value indicating whether model frame should be included as a component of the returned value.
x	logical value indicating whether the model matrix used in the fitting process should be returned as components of the returned value.
y	logical value indicating whether the response vector (pseudo-observations) used in the fitting process should be returned as components of the returned value.
singular.ok	logical; if FALSE a singular fit is an error.
contrasts	an optional list. See the contrasts.arg of <code>model.matrix.default</code> .
...	Other arguments passed to <code>glm.fit</code>

Value

A pseudoglm object, with its own methods for print, summary, and vcov. It inherits from glm, so predict and other glm methods are supported.

Examples

```
cumincipcw <- cumincglm(Surv(etime, event) ~ age + sex,
  time = 200, cause = "pcm", link = "identity",
  model.censoring = "independent", data = mgus2)
# stratified on only the categorical covariate
cumincipw2 <- cumincglm(Surv(etime, event) ~ age + sex,
  time = 200, cause = "pcm", link = "identity",
  model.censoring = "stratified",
  formula.censoring = ~ sex, data = mgus2)
```

Description

A user friendly, easy to understand way of doing event history regression for marginal estimands of interest, including the cumulative incidence and the restricted mean survival, using the pseudo observation framework for estimation. The interface uses the well known formulation of a generalized linear model and allows for features including plotting of residuals, the use of sampling weights, and corrected variance estimation.

get_pseudo_cuminc *Utility to get jackknife pseudo observations of cumulative incidence*

Description

Utility to get jackknife pseudo observations of cumulative incidence

Usage

```
get_pseudo_cuminc(marginal.estimate, time, cause, mr)
```

Arguments

marginal.estimate	
time	A survfit object with no covariates
cause	Time at which to calculate the obs
mr	which cause
	Model response of the survival object

Value

A vector of pseudo-observations

get_pseudo_rmean *Utility to get jackknife pseudo observations of restricted mean*

Description

Utility to get jackknife pseudo observations of restricted mean

Usage

```
get_pseudo_rmean(marginal.estimate, time, cause, mr)
```

Arguments

marginal.estimate	
time	A survfit object with no covariates
cause	Time at which to calculate the obs
mr	which cause
	Model response of the survival object

Value

A vector of pseudo-observations

`jackknife.competing.risks2`

Compute jackknife pseudo-observations of the cause-specific cumulative incidence for competing risks

Description

Compute jackknife pseudo-observations of the cause-specific cumulative incidence for competing risks

Usage

```
jackknife.competing.risks2(object, times, cause, mr)
```

Arguments

<code>object</code>	A survfit object, with competing events
<code>times</code>	Times at which the cumulative incidence is computed, must be length 1
<code>cause</code>	Value indicating for which cause the cumulative incidence is to be computed, it must match one of the values available in object (see example)
<code>mr</code>	Model response, the result of a call to Surv, or a matrix with two columns: "time" (observed follow up time) and "status" (0 = censored, 1, ..., k = event types)

Value

A vector of jackknifed pseudo-observations of the cause-specific cumulative incidence at time times

Examples

```
sfit.cuminc <- survival::survfit(survival::Surv(etime, event) ~ 1, data = mgus2)
mrs <- with(mgus2, Surv(etime, event))
pseudo.obs <- jackknife.competing.risks2(sfit.cuminc, times = 200, cause = "pcm", mrs)
mean(pseudo.obs)
# agrees with
summary(sfit.cuminc, times = 200)
```

jackknife.survival2 *Compute jackknife pseudo-observations of the survival function*

Description

Compute jackknife pseudo-observations of the survival function

Usage

```
jackknife.survival2(object, times, mr)
```

Arguments

object	A survfit object, with a single event (no competing risks)
times	Times at which the survival is computed, must be length 1
mr	Model response, the result of a call to Surv, or a matrix with two columns: "time" (observed follow up time) and "status" (0 = censored, 1 = event)

Value

A vector of jackknifed estimates of survival at time times

Examples

```
sfit.surv <- survival::survfit(survival::Surv(time, status) ~ 1, data = colon)
mrs <- with(colon, Surv(time, status))
pseudo.obs <- jackknife.survival2(sfit.surv, times = 1000, mrs)
mean(pseudo.obs)
# agrees with
summary(sfit.surv, times = 1000)
```

leaveOneOut.competing.risks

Compute jackknife pseudo-observations of the cause-specific cumulative incidence for competing risks

Description

This version computes them for all times up to times, for the restricted mean lifetime lost

Usage

```
leaveOneOut.competing.risks(object, times, cause, mr)
```

Arguments

object	A survfit object, with competing events
times	Times at which the cumulative incidence is computed, must be length 1
cause	Value indicating for which cause the cumulative incidence is to be computed, it must match one of the values available in object (see example)
mr	Model response, the result of a call to Surv, or a matrix with two columns: "time" (observed follow up time) and "status" (0 = censored, 1, ..., k = event types)

Value

A vector of jackknifed values of the cause-specific cumulative incidence at time times

Examples

```
sfit.cuminc <- survival::survfit(survival::Surv(etime, event) ~ 1, data = mgus2)
mrs <- with(mgus2, Surv(etime, event))
jackvals <- leaveOneOut.competing.risks(sfit.cuminc, times = 200, cause = "pcm", mrs)
```

leaveOneOut.competing.risks2

Compute jackknife pseudo-observations of the cause-specific cumulative incidence for competing risks

Description

Compute jackknife pseudo-observations of the cause-specific cumulative incidence for competing risks

Usage

```
leaveOneOut.competing.risks2(object, times, cause, mr)
```

Arguments

object	A survfit object, with competing events
times	Times at which the cumulative incidence is computed, must be length 1
cause	Value indicating for which cause the cumulative incidence is to be computed, it must match one of the values available in object (see example)
mr	Model response, the result of a call to Surv, or a matrix with two columns: "time" (observed follow up time) and "status" (0 = censored, 1, ..., k = event types)

Value

A vector of jackknifed values of the cause-specific cumulative incidence at time times

Examples

```
sfit.cuminc <- survival::survfit(survival::Surv(etime, event) ~ 1, data = mgus2)
mrs <- with(mgus2, Surv(etime, event))
jackvals <- leaveOneOut.competing.risks2(sfit.cuminc, times = 200, cause = "pcm", mrs)
```

leaveOneOut.survival *Compute leave one out jackknife contributions of the survival function*

Description

For each subject, the survival function is recomputed leaving that subject out. This one does the calculation for all observed times, for calculation of the restricted mean

Usage

```
leaveOneOut.survival(object, times, mr)
```

Arguments

object	A survfit object, with a single event (no competing risks)
times	Compute values at observed times up to and including this time
mr	Model response, the result of a call to Surv, or a matrix with two columns: "time" (observed follow up time) and "status" (0 = censored, 1 = event)

Value

A vector of jackknifed values of survival at time times

Examples

```
sfit.surv <- survival::survfit(survival::Surv(time, status) ~ 1, data = colon)
mrs <- with(colon, Surv(time, status))
jackvals <- leaveOneOut.survival(sfit.surv, 1000, mrs)
```

`leaveOneOut.survival2` *Compute leave one out jackknife contributions of the survival function*

Description

For each subject, the survival function is recomputed leaving that subject out. This is the workhorse for `jackknife.survival2` and will generally not be called by the user.

Usage

```
leaveOneOut.survival2(object, times, mr)
```

Arguments

<code>object</code>	A survfit object, with a single event (no competing risks)
<code>times</code>	Times at which the survival is computed, must be length 1
<code>mr</code>	Model response, the result of a call to <code>Surv</code> , or a matrix with two columns: "time" (observed follow up time) and "status" (0 = censored, 1 = event)

Value

A vector of jackknifed values of survival at time `times`

Examples

```
sfit.surv <- survival::survfit(survival::Surv(time, status) ~ 1, data = colon)
mrs <- with(colon, Surv(time, status))
jackvals <- leaveOneOut.survival2(sfit.surv, times = 1000, mrs)
```

`mgus2`

Monoclonal gammopathy data

Description

Natural history of 1341 sequential patients with monoclonal gammopathy of undetermined significance (MGUS). This is a superset of the `mgus` data, at a later point in the accrual process. This dataset is redistributed from the `survival` package with an added competing risks event indicator.

Usage

```
mgus2
```

Format

A data frame with 1384 observations on the following 10 variables.

id subject identifier
 age age at diagnosis, in years
 sex a factor with levels F M
 dxyr year of diagnosis
 hgb hemoglobin
 creat creatinine
 mspike size of the monoclonal serum spike
 ptime time until progression to a plasma cell malignancy (PCM) or last contact, in months
 pstat occurrence of PCM: 0=no, 1=yes
 futime time until death or last contact, in months
 death occurrence of death: 0=no, 1=yes
 etime time until either death, pcm, or last contact
 event factor indicating which event occurred first

See Also

[mgus2](#)

print.pseudoglm *Print method for pseudoglm*

Description

Print method for pseudoglm

Usage

```
## S3 method for class 'pseudoglm'
print(x, digits = max(3L, getOption("digits") - 3L), ...)
```

Arguments

x	A pseudoglm object, as returned by cumincglm or rmeanglm
digits	Number of significant digits
...	Not used

Value

x, invisibly

pseudo_rmst2 *Compute pseudo-observations for the restricted mean survival*

Description

Compute pseudo-observations for the restricted mean survival

Usage

```
pseudo_rmst2(sfit, jacks, times, tmax, type = "cuminc")
```

Arguments

sfit	A survfit object
jacks	A matrix of leave-one-out jackknife values, subjects in the rows, times in the columns
times	Times at which the survival is calculated
tmax	Max time
type	"cuminc" or "survival"

Value

A vector of pseudo observations for the restricted mean or lifetime lost

residuals.pseudoglm *Pseudo-observation scaled residuals*

Description

Computes residuals according to the recommendations of Pohar-Perme and Andersen (2009) <doi:10.1002/sim.3401>.

Usage

```
## S3 method for class 'pseudoglm'
residuals(object, type = NULL, ...)
```

Arguments

object	A pseudoglm object, as returned by cumincglm or rmeanglm
type	Either "scaled" (the default for cumulative incidence outcomes) or one of the types available in residuals.glm for restricted mean outcomes, with the default being "deviance".
...	Arguments passed on to residuals.glm .

Details

The scaled residuals are computed as

$$\hat{\epsilon}_i = \frac{\hat{E}(V_i) - \hat{Y}_i}{\sqrt{\hat{Y}_i(1 - \hat{Y}_i)}}$$

When the outcome is the cumulative incidence, the denominator corresponds to an estimate of the standard error of the conditional estimate of the outcome in the absence of censoring. For the restricted mean, no such rescaling is done and the computation is passed off to [residuals.glm](#).

Value

A numeric vector of residuals

References

Perme MP, Andersen PK. Checking hazard regression models using pseudo-observations. *Stat Med*. 2008;27(25):5309-5328. <doi:10.1002/sim.3401>

rmeanglm

Generalized linear models for the restricted mean survival

Description

Using pseudo observations for the restricted mean, or the restricted mean lifetime lost in the competing risks case, this function then runs a generalized linear model to estimate associations of the restricted mean/lifetime lost up to a particular time (specified by the `time` argument) with covariates. The link function can be "identity" for estimating differences in the restricted mean, "log" for estimating ratios, and any of the other link functions supported by [quasi](#).

Usage

```
rmeanglm(
  formula,
  time,
  cause = 1,
  link = "identity",
  model.censoring = "independent",
  formula.censoring = NULL,
  ipcw.method = "binder",
  data,
  weights,
  subset,
  na.action,
  offset,
  control = list(...),
  model = FALSE,
```

```

x = TRUE,
y = TRUE,
singular.ok = TRUE,
contrasts = NULL,
...
)

```

Arguments

formula	A formula specifying the model. The left hand side must be a Surv object specifying a right censored survival or competing risks outcome. The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For competing risks, the event variable will be a factor, whose first level is treated as censoring. The right hand side is the usual linear combination of covariates.
time	Numeric constant specifying the time up to which the restricted mean effect estimates are desired.
cause	Numeric or character constant specifying the cause indicator of interest.
link	Link function for the restricted mean regression model.
model.censoring	Type of model for the censoring distribution. Options are "stratified", which computes the pseudo-observations stratified on a set of categorical covariates, "aareg" for Aalen's additive hazards model, and "coxph" for Cox's proportional hazards model. With those options, we assume that the time to event and event indicator are conditionally independent of the censoring time, and that the censoring model is correctly specified. If "independent", we assume completely independent censoring, i.e., that the time to event and covariates are independent of the censoring time. the censoring time is independent of the covariates in the model.
formula.censoring	A one sided formula (e.g., $\sim x_1 + x_2$) specifying the model for the censoring distribution. If NULL, uses the same mean model as for the outcome.
ipcw.method	Which method to use for calculation of inverse probability of censoring weighted pseudo observations. "binder" the default, uses the number of observations as the denominator, while the "hajek" method uses the sum of the weights as the denominator.
data	Data frame in which all variables of formula can be interpreted.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options , and is na.fail if that is unset. The 'factory-fresh' default is na.omit . Another possible value is NULL, no action. Value na.exclude can be useful.

offset	this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <code>model.offset</code> .
control	a list of parameters for controlling the fitting process. This is passed to <code>glm.control</code> .
model	a logical value indicating whether model frame should be included as a component of the returned value.
x	logical value indicating whether the model matrix used in the fitting process should be returned as components of the returned value.
y	logical value indicating whether the response vector (pseudo-observations) used in the fitting process should be returned as components of the returned value.
singular.ok	logical; if FALSE a singular fit is an error.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
...	Other arguments passed to <code>glm.fit</code>

Value

A pseudoglm object, with its own methods for print, summary, and vcov. It inherits from glm, so predict and other glm methods are supported.

Examples

```
cumincipcw <- rmeanglm(Surv(etime, event) ~ age + sex,
  time = 200, cause = "pcm", link = "identity",
  model.censoring = "independent", data = mgus2)
# stratified on only the categorical covariate
cumincipcw2 <- rmeanglm(Surv(etime, event) ~ age + sex,
  time = 200, cause = "pcm", link = "identity",
  model.censoring = "stratified",
  formula.censoring = ~ sex, data = mgus2)
```

summary.pseudoglm *Summary method*

Description

Summary method

Usage

```
## S3 method for class 'pseudoglm'
summary(
  object,
  correlation = FALSE,
  symbolic.cor = FALSE,
```

```

    type = "robust",
    ...
  )

```

Arguments

object	A pseudoglm object, as returned by cumincglm or rmeanglm
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
symbolic.cor	logical; If TRUE, print the correlations in a symbolic form rather than as numbers.
type	The method to use for variance estimation; one of "corrected", "robust", "naive", or "cluster"
...	Additional arguments passed to vcov.pseudoglm

Value

An object of class [summary.glm](#)

vcov.pseudoglm	<i>Compute covariance matrix of regression coefficient estimates</i>
----------------	--

Description

Compute covariance matrix of regression coefficient estimates

Usage

```

## S3 method for class 'pseudoglm'
vcov(object, type = "robust", ...)

```

Arguments

object	A pseudoglm object, as returned by cumincglm or rmeanglm .
type	The method to use for variance estimation; one of "corrected", "robust", "naive", or "cluster"
...	Arguments passed to vcovHC

Details

The "corrected" variance estimate is as described in Overgaard et al. (2017) <doi:10.1214/16-AOS1516>, with code adapted from Overgaard's Stata program. This method does not handle ties and only has marginal benefits in reasonable sample sizes. The default is "robust" which uses a sandwich estimator as implemented in the sandwich package. "cluster" is another option if you have clustered observations. Finally "naive" uses the same method as glm to compute the variance, and is known to be anti-conservative. The bootstrap is another recommended option that can be implemented using other tools; there is an example in the vignette.

Value

A numeric matrix containing the variance-covariance estimates

References

Overgaard, Morten; Parner, Erik Thorlund; Pedersen, Jan. Asymptotic theory of generalized estimating equations based on jack-knife pseudo-observations. *Ann. Statist.* 45 (2017), no. 5, 1988–2015. <doi:10.1214/16-AOS1516>.

See Also

[vcovHC](#)

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