Package ‘mets’

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Type Package

Title Analysis of Multivariate Event Times

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Description Implementation of various statistical models for multivariate event history data <doi:10.1007/s10985-013-9244-x>. Including multivariate cumulative incidence models <doi:10.1002/sim.6016>, and bivariate random effects probit models (Liability models) <doi:10.1016/j.csda.2015.01.014>. Modern methods for survival analysis, including regression modelling (Cox, Fine-Gray, Ghosh-Lin, Binomial regression) with fast computation of influence functions.

License GPL (>= 2)

LazyLoad yes

URL `https://kkholst.github.io/mets/`

BugReports `https://github.com/kkholst/mets/issues`

Depends R (>= 3.5)

Imports Rcpp, compiler, lava (>= 1.8.0), methods, mvtnorm, numDeriv, splines, survival (>= 2.43-1), timereg (>= 1.9.4)

Suggests cmprsk, cowplot, ggplot2, icenReg, knitr, mets, optimx, prodlim, rmarkdown, tinytest (>= 1.4.1), ucminf

VignetteBuilder knitr

ByteCompile yes

LinkingTo Rcpp, RcppArmadillo, mvtnorm

Encoding UTF-8

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NeedsCompilation yes

Repository CRAN

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Contents

`aalenfrailty` *Aalen frailty model*

Description

Additive hazards model with (gamma) frailty

Usage

```
aalenfrailty(time, status, X, id, theta, B = NULL, ...)
```

Arguments

`time`	Time variable
`status`	Status variable (0,1)
`X`	Covariate design matrix
`id`	cluster variable
`theta`	list of thetas (returns score evaluated here), or starting point for optimization (defaults to magic number 0.1)
`B`	(optional) Cumulative coefficients (update theta by fixing B)
`...`	Additional arguments to lower level functions

Details

Aalen frailty model

Value

Parameter estimates

Author(s)

Klaus K. Holst

Examples

```
library("timereg")
dd <- simAalenFrailty(5000)
f <- ~1##+x
X <- model.matrix(f,dd) ## design matrix for non-parametric terms
system.time(out<-timereg::aalen(update(f,Surv(time,status)~.),dd,n.sim=0,robust=0))
dix <- which(dd$status==1)
t1 <- system.time(bb <- .Call("Bhat",as.integer(dd$status),
                              X,0.2,as.integer(dd$id),NULL,NULL,
                              PACKAGE="mets"))
spec <- 1
##plot(out,spec=spec)
```

```
## plot(dd$time[dix],bb$B2[,spec],col="red",type="s",
##      ylim=c(0,max(dd$time)*c(beta0,beta)[spec]))
## abline(a=0,b=c(beta0,beta)[spec])
##'

## Not run:
thetas <- seq(0.1,2,length.out=10)
Us <- unlist(aalenfrailty(dd$time,dd$status,X,dd$id,as.list(thetas)))
##plot(thetas,Us,type="l",ylim=c(-.5,1)); abline(h=0,lty=2); abline(v=theta,lty=2)
op <- aalenfrailty(dd$time,dd$status,X,dd$id)
op

## End(Not run)
```

`aalenMets` *Fast additive hazards model with robust standard errors*

Description

Fast Lin-Ying additive hazards model with a possibly stratified baseline. Robust variance is default variance with the summary.

Usage

```
aalenMets(formula, data = data, no.baseline = FALSE, ...)
```

Arguments

`formula`	formula with 'Surv' outcome (see `coxph`)
`data`	data frame
`no.baseline`	to fit model without baseline hazard
`...`	Additional arguments to phreg

Details

influence functions (iid) will follow numerical order of given cluster variable so ordering after $id will give iid in order of data-set.

Author(s)

Thomas Scheike

Examples

```
data(bmt); bmt$time <- bmt$time+runif(408)*0.001
out <- aalenMets(Surv(time,cause==1)~tcell+platelet+age,data=bmt)
summary(out)

## out2 <- timereg::aalen(Surv(time,cause==1)~const(tcell)+const(platelet)+const(age),data=bmt)
## summary(out2)
```

`ACTG175` *ACTG175, block randmized study from speff2trial package*

Description

Data from speff2trial

Format

Randomized study

Source

Hammer et al. 1996, speff2trial package.

Examples

```
data(ACTG175)
```

`back2timereg` *Convert to timereg object*

Description

convert to timereg object

Usage

```
back2timereg(obj)
```

Arguments

`obj`	no use

Author(s)

Thomas Scheike

`base1cumhaz` *rate of CRBSI for HPN patients of Copenhagen*

Description

rate of CRBSI for HPN patients of Copenhagen

Source

Estimated data

`base44cumhaz` *rate of Occlusion/Thrombosis complication for catheter of HPN patients of Copenhagen*

Description

rate of Occlusion/Thrombosis complication for catheter of HPN patients of Copenhagen

Source

Estimated data

`base4cumhaz` *rate of Mechanical (hole/defect) complication for catheter of HPN patients of Copenhagen*

Description

rate of Mechanical (hole/defect) complication for catheter of HPN patients of Copenhagen

Source

Estimated data

`basehazplot.phreg` *Plotting the baselines of stratified Cox*

Description

Plotting the baselines of stratified Cox

Usage

```
basehazplot.phreg(
  x,
  se = FALSE,
  time = NULL,
  add = FALSE,
  ylim = NULL,
  xlim = NULL,
  lty = NULL,
  col = NULL,
  lwd = NULL,
  legend = TRUE,
  ylab = NULL,
  xlab = NULL,
  polygon = TRUE,
  level = 0.95,
  stratas = NULL,
  robust = FALSE,
  conf.type = c("plain", "log"),
  ...
)
```

Arguments

`x`	phreg object
`se`	to include standard errors
`time`	to plot for specific time variables
`add`	to add to previous plot
`ylim`	to give ylim
`xlim`	to give xlim
`lty`	to specify lty of components
`col`	to specify col of components
`lwd`	to specify lwd of components
`legend`	to specify col of components
`ylab`	to specify ylab
`xlab`	to specify xlab

`polygon`	to get standard error in shaded form
`level`	of standard errors
`stratas`	wich strata to plot
`robust`	to use robust standard errors if possible
`conf.type`	"plain" or "log" transformed
`...`	Additional arguments to lower level funtions

Author(s)

Klaus K. Holst, Thomas Scheike

Examples

```
data(TRACE)
dcut(TRACE) <- ~.
out1 <- phreg(Surv(time,status==9)~vf+chf+strata(wmicat.4),data=TRACE)

par(mfrow=c(2,2))
plot(out1)
plot(out1,stratas=c(0,3))
plot(out1,stratas=c(0,3),col=2:3,lty=1:2,se=TRUE)
plot(out1,stratas=c(0),col=2,lty=2,se=TRUE,polygon=FALSE)
plot(out1,stratas=c(0),col=matrix(c(2,1,3),1,3),lty=matrix(c(1,2,3),1,3),se=TRUE,polygon=FALSE)
```

`bicomprisk` *Estimation of concordance in bivariate competing risks data*

Description

Estimation of concordance in bivariate competing risks data

Usage

```
bicomprisk(
  formula,
  data,
  cause = c(1, 1),
  cens = 0,
  causes,
  indiv,
  strata = NULL,
  id,
  num,
  max.clust = 1000,
  marg = NULL,
  se.clusters = NULL,
  wname = NULL,
```

```
  prodlim = FALSE,
  messages = TRUE,
  model,
  return.data = 0,
  uniform = 0,
  conservative = 1,
  resample.iid = 1,
  ...
)
```

Arguments

`formula`	Formula with left-hand-side being a `Event` object (see example below) and the left-hand-side specying the covariate structure
`data`	Data frame
`cause`	Causes (default (1,1)) for which to estimate the bivariate cumulative incidence
`cens`	The censoring code
`causes`	causes
`indiv`	indiv
`strata`	Strata
`id`	Clustering variable
`num`	num
`max.clust`	max number of clusters in timereg::comp.risk call for iid decompostion, max.clust=NULL uses all clusters otherwise rougher grouping.
`marg`	marginal cumulative incidence to make stanard errors for same clusters for subsequent use in casewise.test()
`se.clusters`	to specify clusters for standard errors. Either a vector of cluster indices or a column name in `data`. Defaults to the `id` variable.
`wname`	name of additonal weight used for paired competing risks data.
`prodlim`	prodlim to use prodlim estimator (Aalen-Johansen) rather than IPCW weighted estimator based on comp.risk function.These are equivalent in the case of no covariates. These esimators are the same in the case of stratified fitting.
`messages`	Control amount of output
`model`	Type of competing risk model (default is Fine-Gray model "fg", see comp.risk).
`return.data`	Should data be returned (skipping modeling)
`uniform`	to compute uniform standard errors for concordance estimates based on resampling.
`conservative`	for conservative standard errors, recommended for larger data-sets.
`resample.iid`	to return iid residual processes for further computations such as tests.
`...`	Additional arguments to timereg::comp.risk function

Author(s)

Thomas Scheike, Klaus K. Holst

References

Scheike, T. H.; Holst, K. K. & Hjelmborg, J. B. Estimating twin concordance for bivariate competing risks twin data Statistics in Medicine, Wiley Online Library, 2014 , 33 , 1193-204

Examples

```
library("timereg")

## Simulated data example
prt <- simnordic.random(2000,delayed=TRUE,ptrunc=0.7,
      cordz=0.5,cormz=2,lam0=0.3)
## Bivariate competing risk, concordance estimates
p11 <- bicomprisk(Event(time,cause)~strata(zyg)+id(id),data=prt,cause=c(1,1))

p11mz <- p11$model$"MZ"
p11dz <- p11$model$"DZ"
par(mfrow=c(1,2))
## Concordance
plot(p11mz,ylim=c(0,0.1));
plot(p11dz,ylim=c(0,0.1));

## entry time, truncation weighting
### other weighting procedure
prtl <-  prt[!prt$truncated,]
prt2 <- ipw2(prtl,cluster="id",same.cens=TRUE,
     time="time",cause="cause",entrytime="entry",
     pairs=TRUE,strata="zyg",obs.only=TRUE)

prt22 <- fast.reshape(prt2,id="id")

prt22$event <- (prt22$cause1==1)*(prt22$cause2==1)*1
prt22$timel <- pmax(prt22$time1,prt22$time2)
ipwc <- timereg::comp.risk(Event(timel,event)~-1+factor(zyg1),
  data=prt22,cause=1,n.sim=0,model="rcif2",times=50:90,
  weights=prt22$weights1,cens.weights=rep(1,nrow(prt22)))

p11wmz <- ipwc$cum[,2]
p11wdz <- ipwc$cum[,3]
lines(ipwc$cum[,1],p11wmz,col=3)
lines(ipwc$cum[,1],p11wdz,col=3)
```

`BinAugmentCifstrata` *Augmentation for Binomial regression based on stratified NPMLE Cif (Aalen-Johansen)*

Description

Computes the augmentation term for each individual as well as the sum

$$A = \int_0^t H(u,X) \frac{1}{S^*(u,s)} \frac{1}{G_c(u)} dM_c(u)$$

with

$$H(u,X) = F_1^*(t,s) - F_1^*(u,s)$$

using a KM for

$$G_c(t)$$

and a working model for cumulative baseline related to

$$F_1^*(t,s)$$

and

$$s$$

is strata,

$$S^*(t,s) = 1 - F_1^*(t,s) - F_2^*(t,s)$$

.

Usage

```
BinAugmentCifstrata(
  formula,
  data = data,
  cause = 1,
  cens.code = 0,
  km = TRUE,
  time = NULL,
  weights = NULL,
  offset = NULL,
  ...
)
```

Arguments

`formula`	formula with 'Event', strata model for CIF given by strata, and strataC specifies censoring strata
`data`	data frame
`cause`	of interest
`cens.code`	code of censoring
`km`	to use Kaplan-Meier
`time`	of interest
`weights`	weights for estimating equations
`offset`	offsets for logistic regression
`...`	Additional arguments to binreg function.

Details

Standard errors computed under assumption of correct

$$G_c(s)$$

model.

Author(s)

Thomas Scheike

Examples

```
data(bmt)
dcut(bmt,breaks=2) <- ~age
out1<-BinAugmentCifstrata(Event(time,cause)~platelet+agecat.2+
  strata(platelet,agecat.2),data=bmt,cause=1,time=40)
summary(out1)

out2<-BinAugmentCifstrata(Event(time,cause)~platelet+agecat.2+
    strata(platelet,agecat.2)+strataC(platelet),data=bmt,cause=1,time=40)
summary(out2)
```

`binomial.twostage` *Fits Clayton-Oakes or bivariate Plackett (OR) models for binary data using marginals that are on logistic form. If clusters contain more than two times, the algoritm uses a compososite likelihood based on all pairwise bivariate models.*

Description

The pairwise pairwise odds ratio model provides an alternative to the alternating logistic regression (ALR).

Usage

```
binomial.twostage(
  margbin,
  data = parent.frame(),
  method = "nr",
  detail = 0,
  clusters = NULL,
  silent = 1,
  weights = NULL,
  theta = NULL,
  theta.des = NULL,
  var.link = 0,
  var.par = 1,
```

```
    var.func = NULL,
    iid = 1,
    notaylor = 1,
    model = "plackett",
    marginal.p = NULL,
    beta.iid = NULL,
    Dbeta.iid = NULL,
    strata = NULL,
    max.clust = NULL,
    se.clusters = NULL,
    numDeriv = 0,
    random.design = NULL,
    pairs = NULL,
    dim.theta = NULL,
    additive.gamma.sum = NULL,
    pair.ascertained = 0,
    case.control = 0,
    no.opt = FALSE,
    twostage = 1,
    beta = NULL,
    ...
  )
```

Arguments

`margbin`	Marginal binomial model
`data`	data frame
`method`	Scoring method "nr", for lava NR optimizer
`detail`	Detail
`clusters`	Cluster variable
`silent`	Debug information
`weights`	Weights for log-likelihood, can be used for each type of outcome in 2x2 tables.
`theta`	Starting values for variance components
`theta.des`	design for dependence parameters, when pairs are given the indeces of the theta-design for this pair, is given in pairs as column 5
`var.link`	Link function for variance
`var.par`	parametrization
`var.func`	when alternative parametrizations are used this function can specify how the paramters are related to the λ_j's.
`iid`	Calculate i.i.d. decomposition when iid>=1, when iid=2 then avoids adding the uncertainty for marginal paramters for additive gamma model (default).
`notaylor`	Taylor expansion
`model`	model
`marginal.p`	vector of marginal probabilities

`beta.iid`	iid decomposition of marginal probability estimates for each subject, if based on GLM model this is computed.
`Dbeta.iid`	derivatives of marginal model wrt marginal parameters, if based on GLM model this is computed.
`strata`	strata for fitting: considers only pairs where both are from same strata
`max.clust`	max clusters
`se.clusters`	clusters for iid decomposition for roubst standard errors
`numDeriv`	uses Fisher scoring aprox of second derivative if 0, otherwise numerical derivatives
`random.design`	random effect design for additive gamma model, when pairs are given the indeces of the pairs random.design rows are given as columns 3:4
`pairs`	matrix with rows of indeces (two-columns) for the pairs considered in the pairwise composite score, useful for case-control sampling when marginal is known.
`dim.theta`	dimension of theta when pairs and pairs specific design is given. That is when pairs has 6 columns.
`additive.gamma.sum`	this is specification of the lamtot in the models via a matrix that is multiplied onto the parameters theta (dimensions=(number random effects x number of theta parameters), when null then sums all parameters. Default is a matrix of 1's
`pair.ascertained`	if pairs are sampled only when there are events in the pair i.e. Y1+Y2>=1.
`case.control`	if data is case control data for pair call, and here 2nd column of pairs are probands (cases or controls)
`no.opt`	for not optimizing
`twostage`	default twostage=1, to fit MLE use twostage=0
`beta`	is starting value for beta for MLE version
`...`	for NR of lava

Details

The reported standard errors are based on a cluster corrected score equations from the pairwise likelihoods assuming that the marginals are known. This gives correct standard errors in the case of the Odds-Ratio model (Plackett distribution) for dependence, but incorrect standard errors for the Clayton-Oakes types model (that is also called "gamma"-frailty). For the additive gamma version of the standard errors are adjusted for the uncertainty in the marginal models via an iid deomposition using the iid() function of lava. For the clayton oakes model that is not speicifed via the random effects these can be fixed subsequently using the iid influence functions for the marginal model, but typically this does not change much.

For the Clayton-Oakes version of the model, given the gamma distributed random effects it is assumed that the probabilities are indpendent, and that the marginal survival functions are on logistic form

$$logit(P(Y=1|X)) = \alpha + x^T \beta$$

therefore conditional on the random effect the probability of the event is

$$logit(P(Y=1|X,Z)) = exp(-Z \cdot Laplace^{-1}(lamtot, lamtot, P(Y=1|x)))$$

Can also fit a structured additive gamma random effects model, such the ACE, ADE model for survival data:

Now random.design specificies the random effects for each subject within a cluster. This is a matrix of 1's and 0's with dimension n x d. With d random effects. For a cluster with two subjects, we let the random.design rows be v_1 and v_2. Such that the random effects for subject 1 is

$$v_1^T (Z_1, ..., Z_d)$$

, for d random effects. Each random effect has an associated parameter $(\lambda_1, ..., \lambda_d)$. By construction subjects 1's random effect are Gamma distributed with mean $\lambda_j / v_1^T \lambda$ and variance $\lambda_j / (v_1^T \lambda)^2$. Note that the random effect $v_1^T (Z_1, ..., Z_d)$ has mean 1 and variance $1/(v_1^T \lambda)$. It is here asssumed that $lamtot = v_1^T \lambda$ is fixed over all clusters as it would be for the ACE model below.

The DEFAULT parametrization uses the variances of the random effecs (var.par=1)

$$\theta_j = \lambda_j / (v_1^T \lambda)^2$$

For alternative parametrizations (var.par=0) one can specify how the parameters relate to λ_j with the function

Based on these parameters the relative contribution (the heritability, h) is equivalent to the expected values of the random effects $\lambda_j / v_1^T \lambda$

Given the random effects the probabilities are independent and on the form

$$logit(P(Y = 1|X)) = exp(-Laplace^{-1}(lamtot, lamtot, P(Y = 1|x)))$$

with the inverse laplace of the gamma distribution with mean 1 and variance lamtot.

The parameters $(\lambda_1, ..., \lambda_d)$ are related to the parameters of the model by a regression construction $pard$ (d x k), that links the d λ parameters with the (k) underlying θ parameters

$$\lambda = theta.des\theta$$

here using theta.des to specify these low-dimension association. Default is a diagonal matrix.

Author(s)

Thomas Scheike

References

Two-stage binomial modelling

Examples

```
data(twinstut)
twinstut0 <- subset(twinstut, tvparnr<4000)
twinstut <- twinstut0
twinstut$binstut <- (twinstut$stutter=="yes")*1
theta.des <- model.matrix( ~-1+factor(zyg),data=twinstut)
margbin <- glm(binstut~factor(sex)+age,data=twinstut,family=binomial())
bin <- binomial.twostage(margbin,data=twinstut,var.link=1,
         clusters=twinstut$tvparnr,theta.des=theta.des,detail=0)
```

```
summary(bin)

twinstut$cage <- scale(twinstut$age)
theta.des <- model.matrix( ~-1+factor(zyg)+cage,data=twinstut)
bina <- binomial.twostage(margbin,data=twinstut,var.link=1,
         clusters=twinstut$tvparnr,theta.des=theta.des)
summary(bina)

theta.des <- model.matrix( ~-1+factor(zyg)+factor(zyg)*cage,data=twinstut)
bina <- binomial.twostage(margbin,data=twinstut,var.link=1,
         clusters=twinstut$tvparnr,theta.des=theta.des)
summary(bina)

 ## Reduce Ex.Timings
## refers to zygosity of first subject in eash pair : zyg1
## could also use zyg2 (since zyg2=zyg1 within twinpair's))
out <- easy.binomial.twostage(stutter~factor(sex)+age,data=twinstut,
                          response="binstut",id="tvparnr",var.link=1,
                    theta.formula=~-1+factor(zyg1))
summary(out)

## refers to zygosity of first subject in eash pair : zyg1
## could also use zyg2 (since zyg2=zyg1 within twinpair's))
desfs<-function(x,num1="zyg1",num2="zyg2")
    c(x[num1]=="dz",x[num1]=="mz",x[num1]=="os")*1

out3 <- easy.binomial.twostage(binstut~factor(sex)+age,
      data=twinstut,response="binstut",id="tvparnr",var.link=1,
      theta.formula=desfs,desnames=c("mz","dz","os"))
summary(out3)


### use of clayton oakes binomial additive gamma model
###########################################################
 ## Reduce Ex.Timings
data <- simbinClaytonOakes.family.ace(10000,2,1,beta=NULL,alpha=NULL)
margbin <- glm(ybin~x,data=data,family=binomial())
margbin

head(data)
data$number <- c(1,2,3,4)
data$child <- 1*(data$number==3)

### make ace random effects design
out <- ace.family.design(data,member="type",id="cluster")
out$pardes
head(out$des.rv)

bints <- binomial.twostage(margbin,data=data,
     clusters=data$cluster,detail=0,var.par=1,
     theta=c(2,1),var.link=0,
     random.design=out$des.rv,theta.des=out$pardes)
summary(bints)
```

```
data <- simbinClaytonOakes.twin.ace(10000,2,1,beta=NULL,alpha=NULL)
out  <- twin.polygen.design(data,id="cluster",zygname="zygosity")
out$pardes
head(out$des.rv)
margbin <- glm(ybin~x,data=data,family=binomial())

bintwin <- binomial.twostage(margbin,data=data,
     clusters=data$cluster,var.par=1,
     theta=c(2,1),random.design=out$des.rv,theta.des=out$pardes)
summary(bintwin)
concordanceTwinACE(bintwin)
```

`binreg` *Binomial Regression for censored competing risks data*

Description

Simple version of comp.risk function of timereg for just one time-point thus fitting the model

$$P(T \leq t, \epsilon = 1|X) = expit(X^T beta)$$

Usage

```
binreg(
  formula,
  data,
  cause = 1,
  time = NULL,
  beta = NULL,
  type = c("II", "I"),
  offset = NULL,
  weights = NULL,
  cens.weights = NULL,
  cens.model = ~+1,
  se = TRUE,
  kaplan.meier = TRUE,
  cens.code = 0,
  no.opt = FALSE,
  method = "nr",
  augmentation = NULL,
  outcome = c("cif", "rmst"),
  model = "exp",
  Ydirect = NULL,
  ...
)
```

Arguments

`formula`	formula with outcome (see `coxph`)
`data`	data frame
`cause`	cause of interest (numeric variable)
`time`	time of interest
`beta`	starting values
`type`	"II" adds augmentation term, and "I" classic binomial regression
`offset`	offsets for partial likelihood
`weights`	for score equations
`cens.weights`	censoring weights
`cens.model`	only stratified cox model without covariates
`se`	to compute se's based on IPCW
`kaplan.meier`	uses Kaplan-Meier for IPCW in contrast to exp(-Baseline)
`cens.code`	gives censoring code
`no.opt`	to not optimize
`method`	for optimization
`augmentation`	to augment binomial regression
`outcome`	can do CIF regression "cif"=F(t|X), "rmst"=E(min(T, t) | X) , or "rmst-cause"=E(I(epsilon==cause) (t - mint(T,t))) | X)
`model`	possible exp model for E(min(T, t) | X)=exp(X^t beta) , or E(I(epsilon==cause) (t - mint(T,t))) | X)=exp(X^t beta)
`Ydirect`	use this Y instead of outcome constructed inside the program (e.g. I(T< t, epsilon=1)), then uses IPCW vesion of the Y, set outcome to "rmst" to fit using the model specified by model
`...`	Additional arguments to lower level funtions

Details

Based on binomial regresion IPCW response estimating equation:

$$X(\Delta^{ipcw}(t)I(T \leq t, \epsilon = 1) - expit(X^T beta)) = 0$$

where

$$\Delta^{ipcw}(t) = I((min(t, T) < C)/G_c(min(t, T)-)$$

is IPCW adjustment of the response

$$Y(t) = I(T \leq t, \epsilon = 1)$$

.

(type="I") sovlves this estimating equation using a stratified Kaplan-Meier for the censoring distribution. For (type="II") the default an additional censoring augmentation term

$$X \int E(Y(t)|T > s)/G_c(s) d\hat{M}_c$$

is added.

logitIPCW instead considers

$$XI(min(T_i,t) < G_i)/G_c(min(T_i,t))(I(T \leq t, \epsilon = 1) - expit(X^T beta)) = 0$$

a standard logistic regression with weights that adjust for IPCW.

The variance is based on the squared influence functions that are also returned as the iid component. naive.var is variance under known censoring model.

Censoring model may depend on strata (cens.model=~strata(gX)).

Author(s)

Thomas Scheike

Examples

```
library(mets)
data(bmt); bmt$time <- bmt$time+runif(408)*0.001
# logistic regresion with IPCW binomial regression
out <- binreg(Event(time,cause)~tcell+platelet,bmt,time=50)
summary(out)

predict(out,data.frame(tcell=c(0,1),platelet=c(1,1)),se=TRUE)

outs <- binreg(Event(time,cause)~tcell+platelet,bmt,time=50,cens.model=~strata(tcell,platelet))
summary(outs)

## glm with IPCW weights
outl <- logitIPCW(Event(time,cause)~tcell+platelet,bmt,time=50)
summary(outl)

##########################################
### risk-ratio of different causes #######
##########################################
data(bmt)
bmt$id <- 1:nrow(bmt)
bmt$status <- bmt$cause
bmt$strata <- 1
bmtdob <- bmt
bmtdob$strata <-2
bmtdob <- dtransform(bmtdob,status=1,cause==2)
bmtdob <- dtransform(bmtdob,status=2,cause==1)
###
bmtdob <- rbind(bmt,bmtdob)
dtable(bmtdob,cause+status~strata)

cif1 <- cif(Event(time,cause)~+1,bmt,cause=1)
cif2 <- cif(Event(time,cause)~+1,bmt,cause=2)
bplot(cif1)
bplot(cif2,add=TRUE,col=2)
```

```
cifs1 <- binreg(Event(time,cause)~tcell+platelet+age,bmt,cause=2,time=50)
cifs2 <- binreg(Event(time,cause)~tcell+platelet+age,bmt,cause=2,time=50)
summary(cifs1)
summary(cifs2)

cifdob <- binreg(Event(time,status)~-1+factor(strata)+
 tcell*factor(strata)+platelet*factor(strata)+age*factor(strata)
 +cluster(id),bmtdob,cause=1,time=50,cens.model=~strata(strata)+cluster(id))
summary(cifdob)

riskratio <- function(p) {
  Z <- rbind(c(1,0,1,1,0,0,0,0), c(0,1,1,1,0,1,1,0))
  lp <- c(Z %*% p)
  p <- lava::expit(lp)
  return(p[1]/p[2])
}

lava::estimate(cifdob,f=riskratio)
```

`binregATE` *Average Treatment effect for censored competing risks data using Binomial Regression*

Description

Under the standard causal assumptions we can estimate the average treatment effect E(Y(1) - Y(0)). We need Consistency, ignorability (Y(1), Y(0) indep A given X), and positivity.

Usage

```
binregATE(
  formula,
  data,
  cause = 1,
  time = NULL,
  beta = NULL,
  treat.model = ~+1,
  cens.model = ~+1,
  offset = NULL,
  weights = NULL,
  cens.weights = NULL,
  se = TRUE,
  type = c("II", "I"),
  kaplan.meier = TRUE,
  cens.code = 0,
  no.opt = FALSE,
  method = "nr",
```

```
  augmentation = NULL,
  outcome = c("cif", "rmst"),
  model = "exp",
  Ydirect = NULL,
  ...
)
```

Arguments

`formula`	formula with outcome (see `coxph`)
`data`	data frame
`cause`	cause of interest
`time`	time of interest
`beta`	starting values
`treat.model`	logistic treatment model given covariates
`cens.model`	only stratified cox model without covariates
`offset`	offsets for partial likelihood
`weights`	for score equations
`cens.weights`	censoring weights
`se`	to compute se's with IPCW adjustment, otherwise assumes that IPCW weights are known
`type`	"II" adds augmentation term, and "I" classic binomial regression
`kaplan.meier`	uses Kaplan-Meier for IPCW in contrast to exp(-Baseline)
`cens.code`	gives censoring code
`no.opt`	to not optimize
`method`	for optimization
`augmentation`	for augment binomial regression
`outcome`	can do CIF regression "cif"=F(t|X), "rmst"=E(min(T, t) | X) , or E(I(epsilon==cause) (t - mint(T,t))) | X) depending on the number of the number of causes.
`model`	exp or linear model for E(min(T, t) | X)=exp(X^t beta), or E(I(epsilon==cause) (t - mint(T,t))) | X)=exp(X^t beta)
`Ydirect`	use this outcome Y with IPCW vesion
`...`	Additional arguments to lower level funtions

Details

The first covariate in the specification of the competing risks regression model must be the treatment variable that should be coded as a factor. If the factor has more than two levels then it uses the mlogit for propensity score modelling. If there are no censorings this is the same as ordinary logistic regression modelling.

Estimates the ATE using the the standard binary double robust estimating equations that are IPCW censoring adjusted. Rather than binomial regression we also consider a IPCW weighted version of standard logistic regression logitIPCWATE.

Author(s)

Thomas Scheike

Examples

```
data(bmt)
dfactor(bmt)  <-  ~.

brs <- binregATE(Event(time,cause)~tcell.f+platelet+age,bmt,time=50,cause=1,
  treat.model=tcell.f~platelet+age)
summary(brs)

brsi <- binregATE(Event(time,cause)~tcell.f+tcell.f*platelet+tcell.f*age,bmt,time=50,cause=1,
  treat.model=tcell.f~platelet+age)
summary(brsi)
```

`binregCasewise` *Estimates the casewise concordance based on Concordance and marginal estimate using binreg*

Description

Estimates the casewise concordance based on Concordance and marginal estimate using binreg

Usage

```
binregCasewise(concbreg, margbreg, zygs = c("DZ", "MZ"), newdata = NULL, ...)
```

Arguments

`concbreg`	Concordance
`margbreg`	Marginal estimate
`zygs`	order of zygosity for estimation of concordance and casewise.
`newdata`	to give instead of zygs.
`...`	to pass to estimate function

Details

Uses cluster iid for the two binomial-regression estimates standard errors better than those of casewise that are often conservative.

Author(s)

Thomas Scheike

Examples

```
data(prt)
prt <- force.same.cens(prt,cause="status")

dd <- bicompriskData(Event(time, status)~strata(zyg)+id(id), data=prt, cause=c(2, 2))
newdata <- data.frame(zyg=c("DZ","MZ"),id=1)

## concordance
bcif1 <- binreg(Event(time,status)~-1+factor(zyg)+cluster(id), data=dd,
                time=80, cause=1, cens.model=~strata(zyg))
pconc <- predict(bcif1,newdata)

## marginal estimates
mbcif1 <- binreg(Event(time,status)~cluster(id), data=prt, time=80, cause=2)
mc <- predict(mbcif1,newdata)
mc

cse <- binregCasewise(bcif1,mbcif1)
cse
```

`binregG` *G-estimator for binomial regression model (Standardized estimates)*

Description

Computes G-estimator

$$\hat{F}(t, A = a) = n^{-1} \sum_i \hat{F}(t, A = a, Z_i)$$

. Assumes that the first covariate is A. Gives influence functions of these risk estimates and SE's are based on these. If first covariate is a factor then all contrast are computed, and if continuous then considered covariate values are given by Avalues.

Usage

```
binregG(x, data, Avalues = c(0, 1), varname = NULL)
```

Arguments

`x`	binreg object
`data`	data frame for risk averaging
`Avalues`	values to compare for first covariate A
`varname`	if given then averages for this variable, default is first variable

Author(s)

Thomas Scheike

Examples

```
data(bmt); bmt$time <- bmt$time+runif(408)*0.001
bmt$event <- (bmt$cause!=0)*1

b1 <- binreg(Event(time,cause)~age+tcell+platelet,bmt,cause=1,time=50)
sb1 <- binregG(b1,bmt,Avalues=c(0,1,2))
summary(sb1)
```

`binregTSR` *2 Stage Randomization for Survival Data or competing Risks Data*

Description

Under two-stage randomization we can estimate the average treatment effect E(Y(i,j)) of treatment regime (i,j). The estimator can be agumented in different ways: using the two randomizations and the dynamic censoring augmetatation. The treatment's must be given as factors.

Usage

```
binregTSR(
  formula,
  data,
  cause = 1,
  time = NULL,
  cens.code = 0,
  response.code = NULL,
  augmentR0 = NULL,
  treat.model0 = ~+1,
  augmentR1 = NULL,
  treat.model1 = ~+1,
  augmentC = NULL,
  cens.model = ~+1,
  estpr = c(1, 1),
  response.name = NULL,
  offset = NULL,
  weights = NULL,
  cens.weights = NULL,
  beta = NULL,
  kaplan.meier = TRUE,
  no.opt = FALSE,
  method = "nr",
  augmentation = NULL,
  outcome = c("cif", "rmst", "rmst-cause"),
  model = "exp",
  Ydirect = NULL,
  return.dataw = 0,
  pi0 = 0.5,
```

```
    pi1 = 0.5,
    cens.time.fixed = 1,
    outcome.iid = 1,
    meanCs = 0,
    ...
  )
```

Arguments

`formula`	formula with outcome (see `coxph`)
`data`	data frame
`cause`	cause of interest
`time`	time of interest
`cens.code`	gives censoring code
`response.code`	code of status of survival data that indicates a response at which 2nd randomization is performed
`augmentR0`	augmentation model for 1st randomization
`treat.model0`	logistic treatment model for 1st randomization
`augmentR1`	augmentation model for 2nd randomization
`treat.model1`	logistic treatment model for 2ndrandomization
`augmentC`	augmentation model for censoring
`cens.model`	stratification for censoring model based on observed covariates
`estpr`	estimate randomization probabilities using model
`response.name`	can give name of response variable, otherwise reads this as first variable of treat.model1
`offset`	not implemented
`weights`	not implemented
`cens.weights`	can be given
`beta`	starting values
`kaplan.meier`	for censoring weights, rather than exp cumulative hazard
`no.opt`	not implemented
`method`	not implemented
`augmentation`	not implemented
`outcome`	can be c("cif","rmst","rmst-cause")
`model`	not implemented, uses linear regression for augmentation
`Ydirect`	use this Y instead of outcome constructed inside the program (e.g. I(T< t, epsilon=1)), see binreg for more on this
`return.dataw`	to return weighted data for all treatment regimes
`pi0`	set up known randomization probabilities
`pi1`	set up known randomization probabilities

`cens.time.fixed`	to use time-dependent weights for censoring estimation using weights
`outcome.iid`	to get iid contribution from outcome model (here linear regression working models).
`meanCs`	(0) indicates that censoring augmentation is centered by CensAugment.times/n
`...`	Additional arguments to lower level funtions

Details

The solved estimating eqution is

$$(I(min(T_i,t) < G_i)/G_c(min(T_i,t))I(T \leq t, \epsilon = 1) - AUG_0 - AUG_1 + AUG_C - p(i,j)) = 0$$

where using the covariates from augmentR0

$$AUG_0 = \frac{A_0(i) - \pi_0(i)}{\pi_0(i)} X_0 \gamma_0$$

and using the covariates from augmentR1

$$AUG_1 = \frac{A_0(i)}{\pi_0(i)} \frac{A_1(j) - \pi_1(j)}{\pi_1(j)} X_1 \gamma_1$$

and the censoring augmentation is

$$AUG_C = \int_0^t \gamma_c(s)^T (e(s) - \bar{e}(s)) \frac{1}{G_c(s)} dM_c(s)$$

where

$$\gamma_c(s)$$

is chosen to minimize the variance given the dynamic covariates specified by augmentC.

In the observational case, we can use propensity score modelling and outcome modelling (using linear regression).

Standard errors are estimated using the influence function of all estimators and tests of differences can therefore be computed subsequently.

Author(s)

Thomas Scheike

Examples

```
ddf <- mets:::gsim(200,covs=1,null=0,cens=1,ce=2)

bb <- binregTSR(Event(entry,time,status)~+1+cluster(id),ddf$datat,time=2,cause=c(1),
        cens.code=0,treat.model0=A0.f~+1,treat.model1=A1.f~A0.f,
        augmentR1=~X11+X12+TR,augmentR0=~X01+X02,
        augmentC=~A01+A02+X01+X02+A11t+A12t+X11+X12+TR,
        response.code=2)
summary(bb)
```

`biprobit` *Bivariate Probit model*

Description

Bivariate Probit model

Usage

```
biprobit(
  x,
  data,
  id,
  rho = ~1,
  num = NULL,
  strata = NULL,
  eqmarg = TRUE,
  indep = FALSE,
  weights = NULL,
  weights.fun = function(x) ifelse(any(x <= 0), 0, max(x)),
  randomeffect = FALSE,
  vcov = "robust",
  pairs.only = FALSE,
  allmarg = !is.null(weights),
  control = list(trace = 0),
  messages = 1,
  constrain = NULL,
  table = pairs.only,
  p = NULL,
  ...
)
```

Arguments

`x`	formula (or vector)
`data`	data.frame
`id`	The name of the column in the dataset containing the cluster id-variable.
`rho`	Formula specifying the regression model for the dependence parameter
`num`	Optional name of order variable
`strata`	Strata
`eqmarg`	If TRUE same marginals are assumed (exchangeable)
`indep`	Independence
`weights`	Weights
`weights.fun`	Function defining the bivariate weight in each cluster

`randomeffect`	If TRUE a random effect model is used (otherwise correlation parameter is estimated allowing for both negative and positive dependence)
`vcov`	Type of standard errors to be calculated
`pairs.only`	Include complete pairs only?
`allmarg`	Should all marginal terms be included
`control`	Control argument parsed on to the optimization routine. Starting values may be parsed as '`start`'.
`messages`	Control amount of messages shown
`constrain`	Vector of parameter constraints (NA where free). Use this to set an offset.
`table`	Type of estimation procedure
`p`	Parameter vector p in which to evaluate log-Likelihood and score function
`...`	Optional arguments

Examples

```
data(prt)
prt0 <- subset(prt,country=="Denmark")
a <- biprobit(cancer~1+zyg, ~1+zyg, data=prt0, id="id")
b <- biprobit(cancer~1+zyg, ~1+zyg, data=prt0, id="id",pairs.only=TRUE)
predict(b,newdata=lava::Expand(prt,zyg=c("MZ")))
predict(b,newdata=lava::Expand(prt,zyg=c("MZ","DZ")))

 ## Reduce Ex.Timings
n <- 2e3
x <- sort(runif(n, -1, 1))
y <- rmvn(n, c(0,0), rho=cbind(tanh(x)))>0
d <- data.frame(y1=y[,1], y2=y[,2], x=x)
dd <- fast.reshape(d)

a <- biprobit(y~1+x,rho=~1+x,data=dd,id="id")
summary(a, mean.contrast=c(1,.5), cor.contrast=c(1,.5))
with(predict(a,data.frame(x=seq(-1,1,by=.1))), plot(p00~x,type="l"))

pp <- predict(a,data.frame(x=seq(-1,1,by=.1)),which=c(1))
plot(pp[,1]~pp$x, type="l", xlab="x", ylab="Concordance", lwd=2, xaxs="i")
lava::confband(pp$x,pp[,2],pp[,3],polygon=TRUE,lty=0,col=lava::Col(1))

pp <- predict(a,data.frame(x=seq(-1,1,by=.1)),which=c(9)) ## rho
plot(pp[,1]~pp$x, type="l", xlab="x", ylab="Correlation", lwd=2, xaxs="i")
lava::confband(pp$x,pp[,2],pp[,3],polygon=TRUE,lty=0,col=lava::Col(1))
with(pp, lines(x,tanh(-x),lwd=2,lty=2))

xp <- seq(-1,1,length.out=6); delta <- mean(diff(xp))
a2 <- biprobit(y~1+x,rho=~1+I(cut(x,breaks=xp)),data=dd,id="id")
pp2 <- predict(a2,data.frame(x=xp[-1]-delta/2),which=c(9)) ## rho
lava::confband(pp2$x,pp2[,2],pp2[,3],center=pp2[,1])
```

```
## Time
## Not run:
    a <- biprobit.time(cancer~1, rho=~1+zyg, id="id", data=prt, eqmarg=TRUE,
                       cens.formula=Surv(time,status==0)~1,
                       breaks=seq(75,100,by=3),fix.censweights=TRUE)

    a <- biprobit.time2(cancer~1+zyg, rho=~1+zyg, id="id", data=prt0, eqmarg=TRUE,
                       cens.formula=Surv(time,status==0)~zyg,
                       breaks=100)

   #a1 <- biprobit.time2(cancer~1, rho=~1, id="id", data=subset(prt0,zyg=="MZ"), eqmarg=TRUE,
    #                   cens.formula=Surv(time,status==0)~1,
    #                   breaks=100,pairs.only=TRUE)

   #a2 <- biprobit.time2(cancer~1, rho=~1, id="id", data=subset(prt0,zyg=="DZ"), eqmarg=TRUE,
    #                    cens.formula=Surv(time,status==0)~1,
    #                    breaks=100,pairs.only=TRUE)

## End(Not run)
```

`blocksample` *Block sampling*

Description

Sample blockwise from clustered data

Usage

```
blocksample(data, size, idvar = NULL, replace = TRUE, ...)
```

Arguments

`data`	Data frame
`size`	Size of samples
`idvar`	Column defining the clusters
`replace`	Logical indicating wether to sample with replacement
`...`	additional arguments to lower level functions

Details

Original id is stored in the attribute 'id'

Value

`data.frame`

Author(s)

Klaus K. Holst

Examples

```
d <- data.frame(x=rnorm(5), z=rnorm(5), id=c(4,10,10,5,5), v=rnorm(5))
(dd <- blocksample(d,size=20,~id))
attributes(dd)$id

## Not run:
blocksample(data.table::data.table(d),1e6,~id)

## End(Not run)


d <- data.frame(x=c(1,rnorm(9)),
               z=rnorm(10),
               id=c(4,10,10,5,5,4,4,5,10,5),
               id2=c(1,1,2,1,2,1,1,1,1,2),
               v=rnorm(10))
dsample(d,~id, size=2)
dsample(d,.~id+id2)
dsample(d,x+z~id|x>0,size=5)
```

`bmt` *The Bone Marrow Transplant Data*

Description

Bone marrow transplant data with 408 rows and 5 columns.

Format

The data has 408 rows and 5 columns.

cause a numeric vector code. Survival status. 1: dead from treatment related causes, 2: relapse , 0: censored.

time a numeric vector. Survival time.

platelet a numeric vector code. Plalelet 1: more than 100 x 10^9 per L, 0: less.

tcell a numeric vector. T-cell depleted BMT 1:yes, 0:no.

age a numeric vector code. Age of patient, scaled and centered ((age-35)/15).

Source

Simulated data

References

NN

Examples

```
data(bmt)
names(bmt)
```

Bootphreg *Wild bootstrap for Cox PH regression*

Description

wild bootstrap for uniform bands for Cox models

Usage

```
Bootphreg(
  formula,
  data,
  offset = NULL,
  weights = NULL,
  B = 1000,
  type = c("exp", "poisson", "normal"),
  ...
)
```

Arguments

`formula`	formula with 'Surv' outcome (see `coxph`)
`data`	data frame
`offset`	offsets for cox model
`weights`	weights for Cox score equations
`B`	bootstraps
`type`	distribution for multiplier
`...`	Additional arguments to lower level funtions

Author(s)

Klaus K. Holst, Thomas Scheike

References

Wild bootstrap based confidence intervals for multiplicative hazards models, Dobler, Pauly, and Scheike (2018),

Examples

```
n <- 100
x <- 4*rnorm(n)
time1 <- 2*rexp(n)/exp(x*0.3)
time2 <- 2*rexp(n)/exp(x*(-0.3))
status <- ifelse(time1<time2,1,2)
time <- pmin(time1,time2)
rbin <- rbinom(n,1,0.5)
cc <-rexp(n)*(rbin==1)+(rbin==0)*rep(3,n)
status <- ifelse(time < cc,status,0)
time  <- ifelse(time < cc,time,cc)
data <- data.frame(time=time,status=status,x=x)

b1 <- Bootphreg(Surv(time,status==1)~x,data,B=1000)
b2 <- Bootphreg(Surv(time,status==2)~x,data,B=1000)
c1 <- phreg(Surv(time,status==1)~x,data)
c2 <- phreg(Surv(time,status==2)~x,data)

### exp to make all bootstraps positive
out <- pred.cif.boot(b1,b2,c1,c2,gplot=0)

cif.true <- (1-exp(-out$time))*.5
with(out,plot(time,cif,ylim=c(0,1),type="l"))
lines(out$time,cif.true,col=3)
with(out,plotConfRegion(time,band.EE,col=1))
with(out,plotConfRegion(time,band.EE.log,col=3))
with(out,plotConfRegion(time,band.EE.log.o,col=2))
```

`bptwin` *Liability model for twin data*

Description

Liability-threshold model for twin data

Usage

```
bptwin(
  x,
  data,
  id,
  zyg,
  DZ,
  group = NULL,
  num = NULL,
  weights = NULL,
  weights.fun = function(x) ifelse(any(x <= 0), 0, max(x)),
  strata = NULL,
```

```
  messages = 1,
  control = list(trace = 0),
  type = "ace",
  eqmean = TRUE,
  pairs.only = FALSE,
  samecens = TRUE,
  allmarg = samecens & !is.null(weights),
  stderr = TRUE,
  robustvar = TRUE,
  p,
  indiv = FALSE,
  constrain,
  varlink,
  ...
)
```

Arguments

`x`	Formula specifying effects of covariates on the response.
`data`	`data.frame` with one observation pr row. In addition a column with the zygosity (DZ or MZ given as a factor) of each individual much be specified as well as a twin id variable giving a unique pair of numbers/factors to each twin pair.
`id`	The name of the column in the dataset containing the twin-id variable.
`zyg`	The name of the column in the dataset containing the zygosity variable.
`DZ`	Character defining the level in the zyg variable corresponding to the dyzogitic twins.
`group`	Optional. Variable name defining group for interaction analysis (e.g., gender)
`num`	Optional twin number variable
`weights`	Weight matrix if needed by the chosen estimator (IPCW)
`weights.fun`	Function defining a single weight each individual/cluster
`strata`	Strata
`messages`	Control amount of messages shown
`control`	Control argument parsed on to the optimization routine. Starting values may be parsed as '`start`'.
`type`	Character defining the type of analysis to be performed. Should be a subset of "acde" (additive genetic factors, common environmental factors, dominant genetic factors, unique environmental factors).
`eqmean`	Equal means (with type="cor")?
`pairs.only`	Include complete pairs only?
`samecens`	Same censoring
`allmarg`	Should all marginal terms be included
`stderr`	Should standard errors be calculated?
`robustvar`	If TRUE robust (sandwich) variance estimates of the variance are used

`p`	Parameter vector p in which to evaluate log-Likelihood and score function
`indiv`	If TRUE the score and log-Likelihood contribution of each twin-pair
`constrain`	Development argument
`varlink`	Link function for variance parameters
`...`	Additional arguments to lower level functions

Author(s)

Klaus K. Holst

See Also

`twinlm`, `twinlm.time`, `twinlm.strata`, `twinsim`

Examples

```
data(twinstut)
b0 <- bptwin(stutter~sex,
             data=droplevels(subset(twinstut,zyg%in%c("mz","dz"))),
             id="tvparnr",zyg="zyg",DZ="dz",type="ae")
summary(b0)
```

`calgb8923` *CALGB 8923, twostage randomization SMART design*

Description

Data from CALGB 8923

Format

Data from smart design id: id of subject status : 1-death, 2-response for second randomization, 0-censoring A0 : treament at first randomization A1 : treament at second randomization At.f : treament given at record (A0 or A1) TR : time of response sex : 0-males, 1-females consent: 1 if agrees to 2nd randomization, censored if not R: 1 if response trt1: A0 trt2: A1

Source

https://github.com/ycchao/code_Joint_model_SMART

Examples

```
data(calgb8923)
```

`casewise` *Estimates the casewise concordance based on Concordance and marginal estimate using prodlim but no testing*

Description

.. content for description (no empty lines) ..

Usage

```
casewise(conc, marg, cause.marg)
```

Arguments

`conc`	Concordance
`marg`	Marginal estimate
`cause.marg`	specififes which cause that should be used for marginal cif based on prodlim

Author(s)

Thomas Scheike

Examples

```
 ## Reduce Ex.Timings
library(prodlim)
data(prt);
prt <- force.same.cens(prt,cause="status")

### marginal cumulative incidence of prostate cancer##'
outm <- prodlim(Hist(time,status)~+1,data=prt)

times <- 60:100
cifmz <- predict(outm,cause=2,time=times,newdata=data.frame(zyg="MZ")) ## cause is 2 (second cause)
cifdz <- predict(outm,cause=2,time=times,newdata=data.frame(zyg="DZ"))

### concordance for MZ and DZ twins
cc <- bicomprisk(Event(time,status)~strata(zyg)+id(id),data=prt,cause=c(2,2),prodlim=TRUE)
cdz <- cc$model$"DZ"
cmz <- cc$model$"MZ"

cdz <- casewise(cdz,outm,cause.marg=2)
cmz <- casewise(cmz,outm,cause.marg=2)

plot(cmz,ci=NULL,ylim=c(0,0.5),xlim=c(60,100),legend=TRUE,col=c(3,2,1))
par(new=TRUE)
plot(cdz,ci=NULL,ylim=c(0,0.5),xlim=c(60,100),legend=TRUE)
summary(cdz)
summary(cmz)
```

`casewise.test` *Estimates the casewise concordance based on Concordance and marginal estimate using timereg and performs test for independence*

Description

Estimates the casewise concordance based on Concordance and marginal estimate using timereg and performs test for independence

Usage

```
casewise.test(conc, marg, test = "no-test", p = 0.01)
```

Arguments

`conc`	Concordance
`marg`	Marginal estimate
`test`	Type of test for independence assumption. "conc" makes test on concordance scale and "case" means a test on the casewise concordance
`p`	check that marginal probability is greater at some point than p

Details

Uses cluster based conservative standard errors for marginal and sometimes only the uncertainty of the concordance estimates. This works prettey well, alternatively one can use also the funcions Casewise for a specific time point

Author(s)

Thomas Scheike

Examples

```
 ## Reduce Ex.Timings
library("timereg")
data("prt",package="mets");
prt <- force.same.cens(prt,cause="status")

prt <- prt[which(prt$id %in% sample(unique(prt$id),7500)),]
### marginal cumulative incidence of prostate cancer
times <- seq(60,100,by=2)
outm <- timereg::comp.risk(Event(time,status)~+1,data=prt,cause=2,times=times)

cifmz <- predict(outm,X=1,uniform=0,resample.iid=1)
cifdz <- predict(outm,X=1,uniform=0,resample.iid=1)

### concordance for MZ and DZ twins
cc <- bicomprisk(Event(time,status)~strata(zyg)+id(id),
```

```
                 data=prt,cause=c(2,2))
cdz <- cc$model$"DZ"
cmz <- cc$model$"MZ"

### To compute casewise cluster argument must be passed on,
###  here with a max of 100 to limit comp-time
outm <- timereg::comp.risk(Event(time,status)~+1,data=prt,
                 cause=2,times=times,max.clust=100)
cifmz <- predict(outm,X=1,uniform=0,resample.iid=1)
cc <- bicomprisk(Event(time,status)~strata(zyg)+id(id),data=prt,
                cause=c(2,2),se.clusters=outm$clusters)
cdz <- cc$model$"DZ"
cmz <- cc$model$"MZ"

cdz <- casewise.test(cdz,cifmz,test="case") ## test based on casewise
cmz <- casewise.test(cmz,cifmz,test="conc") ## based on concordance

plot(cmz,ylim=c(0,0.7),xlim=c(60,100))
par(new=TRUE)
plot(cdz,ylim=c(0,0.7),xlim=c(60,100))

slope.process(cdz$casewise[,1],cdz$casewise[,2],iid=cdz$casewise.iid)

slope.process(cmz$casewise[,1],cmz$casewise[,2],iid=cmz$casewise.iid)
```

`cif` *Cumulative incidence with robust standard errors*

Description

Cumulative incidence with robust standard errors

Usage

```
cif(formula, data = data, cause = 1, cens.code = 0, death.code = NULL, ...)
```

Arguments

`formula`	formula with 'Event' outcome and strata (only!)
`data`	data frame
`cause`	NULL looks at all, otherwise specify which cause to consider
`cens.code`	censoring code "0" is default, and death is cens.code!=0
`death.code`	alternative to cens.code give codes of death
`...`	Additional arguments to lower level funtions

Author(s)

Thomas Scheike

Examples

```
data(bmt)
bmt$cluster <- sample(1:100,408,replace=TRUE)
out1 <- cif(Event(time,cause)~+1,data=bmt,cause=1)
out2 <- cif(Event(time,cause)~+1+cluster(cluster),data=bmt,cause=1)

par(mfrow=c(1,2))
plot(out1,se=TRUE)
plot(out2,se=TRUE)
```

`cifreg` *CIF regression*

Description

CIF logistic-link for propodds=1 default and CIF Fine-Gray (cloglog) regression for propodds=NULL. The FG model can also be called using the cifregFG function that has propodds=NULL.

Usage

```
cifreg(
  formula,
  data,
  propodds = 1,
  cause = 1,
  cens.code = 0,
  no.codes = NULL,
  ...
)
```

Arguments

`formula`	formula with 'Event' outcome
`data`	data frame
`propodds`	to fit logit link model, and propodds=NULL to fit Fine-Gray model
`cause`	of interest
`cens.code`	code of censoring
`no.codes`	certain event codes to be ignored when finding competing causes
`...`	Additional arguments to recreg

Details

For FG model:

$$\int (X - E) Y_1(t) w(t) dM_1$$

is computed and summed over clusters and returned multiplied with inverse of second derivative as iid.naive. Here

$$w(t) = G(t)(I(T_i \wedge t < C_i)/G_c(T_i \wedge t))$$

and

$$E(t) = S_1(t)/S_0(t)$$

and

$$S_j(t) = \sum X_i^j Y_{i1}(t) w_i(t) \exp(X_i^T \beta)$$

.

The iid decomposition of the beta's, however, also have a censoring term that is also is computed and added (still scaled with inverse second derivative)

$$\int (X - E) Y_1(t) w(t) dM_1 + \int q(s)/p(s) dM_c$$

and returned as the iid

For logistic link standard errors are slightly to small since uncertainty from recursive baseline is not considered, so for smaller data-sets it is recommended to use the prop.odds.subdist of timereg that is also more efficient due to use of different weights for the estimating equations. Alternatively, one can also bootstrap the standard errors.

Author(s)

Thomas Scheike

Examples

```
## data with no ties
library(mets)
data(bmt,package="timereg")
bmt$time <- bmt$time+runif(nrow(bmt))*0.01
bmt$id <- 1:nrow(bmt)

## logistic link  OR interpretation
or=cifreg(Event(time,cause)~tcell+platelet+age,data=bmt,cause=1)
summary(or)
par(mfrow=c(1,2))
plot(or)
nd <- data.frame(tcell=c(1,0),platelet=0,age=0)
por <- predict(or,nd)
plot(por)

## Fine-Gray model
fg=cifregFG(Event(time,cause)~tcell+platelet+age,data=bmt,cause=1)
summary(fg)
plot(fg)
```

```
nd <- data.frame(tcell=c(1,0),platelet=0,age=0)
pfg <- predict(fg,nd,se=1)
plot(pfg,se=1)

## not run to avoid timing issues
## gofFG(Event(time,cause)~tcell+platelet+age,data=bmt,cause=1)

sfg <- cifregFG(Event(time,cause)~strata(tcell)+platelet+age,data=bmt,cause=1)
summary(sfg)
plot(sfg)

### predictions with CI based on iid decomposition of baseline and beta
### these are used in the predict function above
fg <- cifregFG(Event(time,cause)~tcell+platelet+age,data=bmt,cause=1)
Biid <- IIDbaseline.cifreg(fg,time=20)
pfg1 <- FGprediid(Biid,nd)
pfg1
```

`ClaytonOakes` *Clayton-Oakes model with piece-wise constant hazards*

Description

Clayton-Oakes frailty model

Usage

```
ClaytonOakes(
  formula,
  data = parent.frame(),
  cluster,
  var.formula = ~1,
  cuts = NULL,
  type = "piecewise",
  start,
  control = list(),
  var.invlink = exp,
  ...
)
```

Arguments

`formula`	formula specifying the marginal proportional (piecewise constant) hazard structure with the right-hand-side being a survival object (Surv) specifying the entry time (optional), the follow-up time, and event/censoring status at follow-up. The clustering can be specified using the special function `cluster` (see example below).
`data`	Data frame

`cluster`	Variable defining the clustering (if not given in the formula)
`var.formula`	Formula specifying the variance component structure (if not given via the cluster special function in the formula) using a linear model with log-link.
`cuts`	Cut points defining the piecewise constant hazard
`type`	when equal to `two.stage`, the Clayton-Oakes-Glidden estimator will be calculated via the `timereg` package
`start`	Optional starting values
`control`	Control parameters to the optimization routine
`var.invlink`	Inverse link function for variance structure model
`...`	Additional arguments

Author(s)

Klaus K. Holst

Examples

```
set.seed(1)
d <- subset(simClaytonOakes(500,4,2,1,stoptime=2,left=2),truncated)
e <- ClaytonOakes(survival::Surv(lefttime,time,status)~x+cluster(~1,cluster),
                  cuts=c(0,0.5,1,2),data=d)
e

d2 <- simClaytonOakes(500,4,2,1,stoptime=2,left=0)
d2$z <- rep(1,nrow(d2)); d2$z[d2$cluster%in%sample(d2$cluster,100)] <- 0
## Marginal=Cox Proportional Hazards model:
## ts <- ClaytonOakes(survival::Surv(time,status)~timereg::prop(x)+cluster(~1,cluster),
##                    data=d2,type="two.stage")
## Marginal=Aalens additive model:
## ts2 <- ClaytonOakes(survival::Surv(time,status)~x+cluster(~1,cluster),
##                     data=d2,type="two.stage")
## Marginal=Piecewise constant:
e2 <- ClaytonOakes(survival::Surv(time,status)~x+cluster(~-1+factor(z),cluster),
                   cuts=c(0,0.5,1,2),data=d2)
e2


e0 <- ClaytonOakes(survival::Surv(time,status)~cluster(~-1+factor(z),cluster),
                   cuts=c(0,0.5,1,2),data=d2)
##ts0 <- ClaytonOakes(survival::Surv(time,status)~cluster(~1,cluster),
##                    data=d2,type="two.stage")
##plot(ts0)
plot(e0)

e3 <- ClaytonOakes(survival::Surv(time,status)~x+cluster(~1,cluster),cuts=c(0,0.5,1,2),
                   data=d,var.invlink=identity)
e3
```

`cluster.index` *Finds subjects related to same cluster*

Description

Finds subjects related to same cluster

Usage

```
cluster.index(
  clusters,
  index.type = FALSE,
  num = NULL,
  Rindex = 0,
  mat = NULL,
  return.all = FALSE,
  code.na = NA
)
```

Arguments

`clusters`	list of indeces
`index.type`	if TRUE then already list of integers of index.type
`num`	to get numbering according to num-type in separate columns
`Rindex`	index starts with 1, in C is it is 0
`mat`	to return matrix of indeces
`return.all`	return all arguments
`code.na`	how to code missing values

Author(s)

Klaus Holst, Thomas Scheike

References

Cluster indeces

See Also

familycluster.index familyclusterWithProbands.index

Examples

```
i<-c(1,1,2,2,1,3)
d<- cluster.index(i)
print(d)

type<-c("m","f","m","c","c","c")
d<- cluster.index(i,num=type,Rindex=1)
print(d)
```

`concordanceCor` *Concordance Computes concordance and casewise concordance*

Description

Concordance for Twins

Usage

```
concordanceCor(
  object,
  cif1,
  cif2 = NULL,
  messages = TRUE,
  model = NULL,
  coefs = NULL,
  ...
)
```

Arguments

`object`	Output from the cor.cif, rr.cif or or.cif function
`cif1`	Marginal cumulative incidence
`cif2`	Marginal cumulative incidence of other cause (cause2) if it is different from cause1
`messages`	To print messages
`model`	Specfifies wich model that is considered if object not given.
`coefs`	Specfifies dependence parameters if object is not given.
`...`	Extra arguments, not used.

Details

The concordance is the probability that both twins have experienced the event of interest and is defined as

$$cor(t) = P(T_1 \leq t, \epsilon_1 = 1, T_2 \leq t, \epsilon_2 = 1)$$

Similarly, the casewise concordance is

$$casewise(t) = \frac{cor(t)}{P(T_1 \leq t, \epsilon_1 = 1)}$$

that is the probability that twin "2" has the event given that twins "1" has.

Author(s)

Thomas Scheike

References

Estimating twin concordance for bivariate competing risks twin data Thomas H. Scheike, Klaus K. Holst and Jacob B. Hjelmborg, Statistics in Medicine 2014, 1193-1204

Estimating Twin Pair Concordance for Age of Onset. Thomas H. Scheike, Jacob V B Hjelmborg, Klaus K. Holst, 2015 in Behavior genetics DOI:10.1007/s10519-015-9729-3

`cor.cif` *Cross-odds-ratio, OR or RR risk regression for competing risks*

Description

Fits a parametric model for the log-cross-odds-ratio for the predictive effect of for the cumulative incidence curves for T_1 experiencing cause i given that T_2 has experienced a cause k :

$$\log(COR(i|k)) = h(\theta, z_1, i, z_2, k, t) =_{default} \theta^T z =$$

with the log cross odds ratio being

$$COR(i|k) = \frac{O(T_1 \leq t, cause_1 = i | T_2 \leq t, cause_2 = k)}{O(T_1 \leq t, cause_1 = i)}$$

the conditional odds divided by the unconditional odds, with the odds being, respectively

$$O(T_1 \leq t, cause_1 = i | T_2 \leq t, cause_1 = k) = \frac{P_x(T_1 \leq t, cause_1 = i | T_2 \leq t, cause_2 = k)}{P_x((T_1 \leq t, cause_1 = i)^c | T_2 \leq t, cause_2 = k)}$$

and

$$O(T_1 \leq t, cause_1 = i) = \frac{P_x(T_1 \leq t, cause_1 = i)}{P_x((T_1 \leq t, cause_1 = i)^c)}.$$

Here B^c is the complement event of B, P_x is the distribution given covariates (x are subject specific and z are cluster specific covariates), and $h()$ is a function that is the simple identity $\theta^T z$ by default.

Usage

```
cor.cif(
  cif,
  data,
  cause = NULL,
  times = NULL,
  cause1 = 1,
  cause2 = 1,
  cens.code = NULL,
  cens.model = "KM",
  Nit = 40,
  detail = 0,
  clusters = NULL,
  theta = NULL,
  theta.des = NULL,
  step = 1,
  sym = 0,
  weights = NULL,
  par.func = NULL,
  dpar.func = NULL,
  dimpar = NULL,
  score.method = "nlminb",
  same.cens = FALSE,
  censoring.weights = NULL,
  silent = 1,
  ...
)
```

Arguments

`cif`	a model object from the timereg::comp.risk function with the marginal cumulative incidence of cause1, i.e., the event of interest, and whose odds the comparision is compared to the conditional odds given cause2
`data`	a data.frame with the variables.
`cause`	specifies the causes related to the death times, the value cens.code is the censoring value. When missing it comes from marginal cif.
`times`	time-vector that specifies the times used for the estimating euqations for the cross-odds-ratio estimation.
`cause1`	specificies the cause considered.
`cause2`	specificies the cause that is conditioned on.
`cens.code`	specificies the code for the censoring if NULL then uses the one from the marginal cif model.
`cens.model`	specified which model to use for the ICPW, KM is Kaplan-Meier alternatively it may be "cox"
`Nit`	number of iterations for Newton-Raphson algorithm.
`detail`	if 0 no details are printed during iterations, if 1 details are given.

`clusters`	specifies the cluster structure.
`theta`	specifies starting values for the cross-odds-ratio parameters of the model.
`theta.des`	specifies a regression design for the cross-odds-ratio parameters.
`step`	specifies the step size for the Newton-Raphson algorithm.
`sym`	specifies if symmetry is used in the model.
`weights`	weights for estimating equations.
`par.func`	parfunc
`dpar.func`	dparfunc
`dimpar`	dimpar
`score.method`	"nlminb", can also use "nr".
`same.cens`	if true then censoring within clusters are assumed to be the same variable, default is independent censoring.
`censoring.weights`	these probabilities are used for the bivariate censoring dist.
`silent`	1 to suppress output about convergence related issues.
`...`	Not used.

Details

The OR dependence measure is given by

$$OR(i,k) = \log(\frac{O(T_1 \leq t, cause_1 = i | T_2 \leq t, cause_2 = k)}{O(T_1 \leq t, cause_1 = i) | T_2 \leq t, cause_2 = k)}$$

This measure is numerically more stabile than the COR measure, and is symetric in i,k.

The RR dependence measure is given by

$$RR(i,k) = \log(\frac{P(T_1 \leq t, cause_1 = i, T_2 \leq t, cause_2 = k)}{P(T_1 \leq t, cause_1 = i) P(T_2 \leq t, cause_2 = k)}$$

This measure is numerically more stabile than the COR measure, and is symetric in i,k.

The model is fitted under symmetry (sym=1), i.e., such that it is assumed that T_1 and T_2 can be interchanged and leads to the same cross-odd-ratio (i.e. $COR(i|k) = COR(k|i)$), as would be expected for twins or without symmetry as might be the case with mothers and daughters (sym=0).

$h()$ may be specified as an R-function of the parameters, see example below, but the default is that it is simply $\theta^T z$.

Value

returns an object of type 'cor'. With the following arguments:

`theta`	estimate of proportional odds parameters of model.
`var.theta`	variance for gamma.
`hess`	the derivative of the used score.
`score`	scores at final stage.
`score`	scores at final stage.
`theta.iid`	matrix of iid decomposition of parametric effects.

Author(s)

Thomas Scheike

References

Cross odds ratio Modelling of dependence for Multivariate Competing Risks Data, Scheike and Sun (2012), Biostatistics.

A Semiparametric Random Effects Model for Multivariate Competing Risks Data, Scheike, Zhang, Sun, Jensen (2010), Biometrika.

Examples

```
 ## Reduce Ex.Timings
library("timereg")
data(multcif);
multcif$cause[multcif$cause==0] <- 2
zyg <- rep(rbinom(200,1,0.5),each=2)
theta.des <- model.matrix(~-1+factor(zyg))

times=seq(0.05,1,by=0.05) # to speed up computations use only these time-points
add <- timereg::comp.risk(Event(time,cause)~+1+cluster(id),data=multcif,cause=1,
               n.sim=0,times=times,model="fg",max.clust=NULL)
add2 <- timereg::comp.risk(Event(time,cause)~+1+cluster(id),data=multcif,cause=2,
               n.sim=0,times=times,model="fg",max.clust=NULL)

out1 <- cor.cif(add,data=multcif,cause1=1,cause2=1)
summary(out1)

out2 <- cor.cif(add,data=multcif,cause1=1,cause2=1,theta.des=theta.des)
summary(out2)

##out3 <- cor.cif(add,data=multcif,cause1=1,cause2=2,cif2=add2)
##summary(out3)
###########################################################
# investigating further models using parfunc and dparfunc
###########################################################
set.seed(100)
prt<-simnordic.random(2000,cordz=2,cormz=5)
prt$status <-prt$cause
table(prt$status)

times <- seq(40,100,by=10)
cifmod <- timereg::comp.risk(Event(time,cause)~+1+cluster(id),data=prt,
                    cause=1,n.sim=0,
                    times=times,conservative=1,max.clust=NULL,model="fg")
theta.des <- model.matrix(~-1+factor(zyg),data=prt)

parfunc <- function(par,t,pardes)
{
par <- pardes %*% c(par[1],par[2]) +
       pardes %*% c( par[3]*(t-60)/12,par[4]*(t-60)/12)
```

```
par
}
head(parfunc(c(0.1,1,0.1,1),50,theta.des))

dparfunc <- function(par,t,pardes)
{
dpar <- cbind(pardes, t(t(pardes) * c( (t-60)/12,(t-60)/12)) )
dpar
}
head(dparfunc(c(0.1,1,0.1,1),50,theta.des))

names(prt)
or1 <- or.cif(cifmod,data=prt,cause1=1,cause2=1,theta.des=theta.des,
              same.cens=TRUE,theta=c(0.6,1.1,0.1,0.1),
              par.func=parfunc,dpar.func=dparfunc,dimpar=4,
              score.method="nr",detail=1)
summary(or1)

 cor1 <- cor.cif(cifmod,data=prt,cause1=1,cause2=1,theta.des=theta.des,
                 same.cens=TRUE,theta=c(0.5,1.0,0.1,0.1),
                 par.func=parfunc,dpar.func=dparfunc,dimpar=4,
                 control=list(trace=TRUE),detail=1)
summary(cor1)

### piecewise contant OR model
gparfunc <- function(par,t,pardes)
{
cuts <- c(0,80,90,120)
grop <- diff(t<cuts)
paru  <- (pardes[,1]==1) * sum(grop*par[1:3]) +
    (pardes[,2]==1) * sum(grop*par[4:6])
paru
}

dgparfunc <- function(par,t,pardes)
{
cuts <- c(0,80,90,120)
grop <- diff(t<cuts)
par1 <- matrix(c(grop),nrow(pardes),length(grop),byrow=TRUE)
parmz <- par1* (pardes[,1]==1)
pardz <- (pardes[,2]==1) * par1
dpar <- cbind( parmz,pardz)
dpar
}
head(dgparfunc(rep(0.1,6),50,theta.des))
head(gparfunc(rep(0.1,6),50,theta.des))

or1g <- or.cif(cifmod,data=prt,cause1=1,cause2=1,
               theta.des=theta.des, same.cens=TRUE,
               par.func=gparfunc,dpar.func=dgparfunc,
               dimpar=6,score.method="nr",detail=1)
summary(or1g)
names(or1g)
```

```
head(or1g$theta.iid)
```

`count.history` *Counts the number of previous events of two types for recurrent events processes*

Description

Counts the number of previous events of two types for recurrent events processes

Usage

```
count.history(
  data,
  status = "status",
  id = "id",
  types = 1:2,
  names.count = "Count",
  lag = TRUE,
  multitype = FALSE
)
```

Arguments

`data`	data-frame
`status`	name of status
`id`	id
`types`	types of the events (code) related to status
`names.count`	name of Counts, for example Count1 Count2 when types=c(1,2)
`lag`	if true counts previously observed, and if lag=FALSE counts up to know
`multitype`	if multitype then count number of types also when types=c(1,2) for example

Author(s)

Thomas Scheike

Examples

```
########################################
## getting some rates to mimick
########################################

data(base1cumhaz)
data(base4cumhaz)
data(drcumhaz)
```

```
dr <- drcumhaz
base1 <- base1cumhaz
base4 <- base4cumhaz

######################################################################
### simulating simple model that mimicks data
### now with two event types and second type has same rate as death rate
######################################################################

rr <- simRecurrentII(1000,base1,base4,death.cumhaz=dr)
rr <-  count.history(rr)
dtable(rr,~"Count*"+status,level=1)
```

`daggregate` *aggregating for for data frames*

Description

aggregating for for data frames

Usage

```
daggregate(
  data,
  y = NULL,
  x = NULL,
  subset,
  ...,
  fun = "summary",
  regex = mets.options()$regex,
  missing = FALSE,
  remove.empty = FALSE,
  matrix = FALSE,
  silent = FALSE,
  na.action = na.pass,
  convert = NULL
)
```

Arguments

`data`	data.frame
`y`	name of variable, or formula, or names of variables on data frame.
`x`	name of variable, or formula, or names of variables on data frame.
`subset`	subset expression
`...`	additional arguments to lower level functions
`fun`	function defining aggregation

`regex`	interpret x,y as regular expressions
`missing`	Missing used in groups (x)
`remove.empty`	remove empty groups from output
`matrix`	if TRUE a matrix is returned instead of an array
`silent`	suppress messages
`na.action`	How model.frame deals with 'NA's
`convert`	if TRUE try to coerce result into matrix. Can also be a user-defined function

Examples

```
data("sTRACE")
daggregate(iris, "^.e.al", x="Species", fun=cor, regex=TRUE)
daggregate(iris, Sepal.Length+Petal.Length ~Species, fun=summary)
daggregate(iris, log(Sepal.Length)+I(Petal.Length>1.5) ~ Species,
                 fun=summary)
daggregate(iris, "*Length*", x="Species", fun=head)
daggregate(iris, "^.e.al", x="Species", fun=tail, regex=TRUE)
daggregate(sTRACE, status~ diabetes, fun=table)
daggregate(sTRACE, status~ diabetes+sex, fun=table)
daggregate(sTRACE, status + diabetes+sex ~ vf+I(wmi>1.4), fun=table)
daggregate(iris, "^.e.al", x="Species",regex=TRUE)
dlist(iris,Petal.Length+Sepal.Length ~ Species |Petal.Length>1.3 & Sepal.Length>5,
            n=list(1:3,-(3:1)))
daggregate(iris, I(Sepal.Length>7)~Species | I(Petal.Length>1.5))
daggregate(iris, I(Sepal.Length>7)~Species | I(Petal.Length>1.5),
                 fun=table)

dsum(iris, .~Species, matrix=TRUE, missing=TRUE)

par(mfrow=c(1,2))
data(iris)
drename(iris) <- ~.
daggregate(iris,'sepal*'~species|species!="virginica",fun=plot)
daggregate(iris,'sepal*'~I(as.numeric(species))|I(as.numeric(species))!=1,fun=summary)

dnumeric(iris) <- ~species
daggregate(iris,'sepal*'~species.n|species.n!=1,fun=summary)
```

`Dbvn` *Derivatives of the bivariate normal cumulative distribution function*

Description

Derivatives of the bivariate normal cumulative distribution function

Usage

```
Dbvn(p,design=function(p,...) {
     return(list(mu=cbind(p[1],p[1]),
               dmu=cbind(1,1),
               S=matrix(c(p[2],p[3],p[3],p[4]),ncol=2),
               dS=rbind(c(1,0,0,0),c(0,1,1,0),c(0,0,0,1)))  )},
     Y=cbind(0,0))
```

Arguments

`p`	Parameter vector
`design`	Design function with defines mean, derivative of mean, variance, and derivative of variance with respect to the parameter p
`Y`	column vector where the CDF is evaluated

Author(s)

Klaus K. Holst

`dby` *Calculate summary statistics grouped by*

Description

Calculate summary statistics grouped by variable

Usage

```
dby(
  data,
  INPUT,
  ...,
  ID = NULL,
  ORDER = NULL,
  SUBSET = NULL,
  SORT = 0,
  COMBINE = !REDUCE,
  NOCHECK = FALSE,
  ARGS = NULL,
  NAMES,
  COLUMN = FALSE,
  REDUCE = FALSE,
  REGEX = mets.options()$regex,
  ALL = TRUE
)
```

Arguments

`data`	Data.frame
`INPUT`	Input variables (character or formula)
`...`	functions
`ID`	id variable
`ORDER`	(optional) order variable
`SUBSET`	(optional) subset expression
`SORT`	sort order (id+order variable)
`COMBINE`	If TRUE result is appended to data
`NOCHECK`	No sorting or check for missing data
`ARGS`	Optional list of arguments to functions (...)
`NAMES`	Optional vector of column names
`COLUMN`	If TRUE do the calculations for each column
`REDUCE`	Reduce number of redundant rows
`REGEX`	Allow regular expressions
`ALL`	if FALSE only the subset will be returned

Details

Calculate summary statistics grouped by

dby2 for column-wise calculations

Author(s)

Klaus K. Holst and Thomas Scheike

Examples

```
n <- 4
k <- c(3,rbinom(n-1,3,0.5)+1)
N <- sum(k)
d <- data.frame(y=rnorm(N),x=rnorm(N),
   id=rep(seq(n),k),num=unlist(sapply(k,seq))
)
d2 <- d[sample(nrow(d)),]

dby(d2, y~id, mean)
dby(d2, y~id + order(num), cumsum)

dby(d,y ~ id + order(num), dlag)
dby(d,y ~ id + order(num), dlag, ARGS=list(k=1:2))
dby(d,y ~ id + order(num), dlag, ARGS=list(k=1:2), NAMES=c("l1","l2"))

dby(d, y~id + order(num), mean=mean, csum=cumsum, n=length)
dby(d2, y~id + order(num), a=cumsum, b=mean, N=length,
```

```
  l1=function(x) c(NA,x)[-length(x)]
)

dby(d, y~id + order(num), nn=seq_along, n=length)
dby(d, y~id + order(num), nn=seq_along, n=length)

d <- d[,1:4]
dby(d, x<0) <- list(z=mean)
d <- dby(d, is.na(z), z=1)

f <- function(x) apply(x,1,min)
dby(d, y+x~id, min=f)

dby(d,y+x~id+order(num), function(x) x)

f <- function(x) { cbind(cumsum(x[,1]),cumsum(x[,2]))/sum(x)}
dby(d, y+x~id, f)

## column-wise
a <- d
dby2(a, mean, median, REGEX=TRUE) <- '^[y|x]'~id
a
## wildcards
dby2(a,'y*'+'x*'~id,mean)


## subset
dby(d, x<0) <- list(z=NA)
d
dby(d, y~id|x>-1, v=mean,z=1)
dby(d, y+x~id|x>-1, mean, median, COLUMN=TRUE)

dby2(d, y+x~id|x>0, mean, REDUCE=TRUE)

dby(d,y~id|x<0,mean,ALL=FALSE)

a <- iris
a <- dby(a,y=1)
dby(a,Species=="versicolor") <- list(y=2)
```

---

dcor *summary, tables, and correlations for data frames*

Description

summary, tables, and correlations for data frames

Usage

```
dcor(data, y = NULL, x = NULL, use = "pairwise.complete.obs", ...)
```

Arguments

`data`	if x is formula or names for data frame then data frame is needed.
`y`	name of variable, or fomula, or names of variables on data frame.
`x`	possible group variable
`use`	how to handle missing values
`...`	Optional additional arguments

Author(s)

Klaus K. Holst and Thomas Scheike

Examples

```
data("sTRACE",package="timereg")
dt<- sTRACE
dt$time2 <- dt$time^2
dt$wmi2 <- dt$wmi^2
head(dt)

dcor(dt)

dcor(dt,~time+wmi)
dcor(dt,~time+wmi,~vf+chf)
dcor(dt,time+wmi~vf+chf)

dcor(dt,c("time*","wmi*"),~vf+chf)
```

`dcut` *Cutting, sorting, rm (removing), rename for data frames*

Description

Cut variables, if breaks are given these are used, otherwise cuts into using group size given by probs, or equispace groups on range. Default is equally sized groups if possible

Usage

```
dcut(
  data,
  y = NULL,
  x = NULL,
  breaks = 4,
  probs = NULL,
  equi = FALSE,
  regex = mets.options()$regex,
  sep = NULL,
  na.rm = TRUE,
```

```
  labels = NULL,
  all = FALSE,
  ...
)
```

Arguments

`data`	if x is formula or names for data frame then data frame is needed.
`y`	name of variable, or fomula, or names of variables on data frame.
`x`	name of variable, or fomula, or names of variables on data frame.
`breaks`	number of breaks, for variables or vector of break points,
`probs`	groups defined from quantiles
`equi`	for equi-spaced breaks
`regex`	for regular expressions.
`sep`	seperator for naming of cut names.
`na.rm`	to remove NA for grouping variables.
`labels`	to use for cut groups
`all`	to do all variables, even when breaks are not unique
`...`	Optional additional arguments

Author(s)

Klaus K. Holst and Thomas Scheike

Examples

```
data("sTRACE",package="timereg")
sTRACE$age2 <- sTRACE$age^2
sTRACE$age3 <- sTRACE$age^3

mm <- dcut(sTRACE,~age+wmi)
head(mm)

mm <- dcut(sTRACE,catage4+wmi4~age+wmi)
head(mm)

mm <- dcut(sTRACE,~age+wmi,breaks=c(2,4))
head(mm)

mm <- dcut(sTRACE,c("age","wmi"))
head(mm)

mm <- dcut(sTRACE,~.)
head(mm)

mm <- dcut(sTRACE,c("age","wmi"),breaks=c(2,4))
head(mm)
```

```
gx <- dcut(sTRACE$age)
head(gx)


## Removes all cuts variables with these names wildcards
mm1 <- drm(mm,c("*.2","*.4"))
head(mm1)

## wildcards, for age, age2, age4 and wmi
head(dcut(mm,c("a*","?m*")))

## with direct asignment
drm(mm) <- c("*.2","*.4")
head(mm)

dcut(mm) <- c("age","*m*")
dcut(mm) <- ageg1+wmig1~age+wmi
head(mm)

############################
## renaming
############################

head(mm)
drename(mm, ~Age+Wmi) <- c("wmi","age")
head(mm)
mm1 <- mm

## all names to lower
drename(mm1) <- ~.
head(mm1)

## A* to lower
mm2 <-  drename(mm,c("A*","W*"))
head(mm2)
drename(mm) <- "A*"
head(mm)

dd <- data.frame(A_1=1:2,B_1=1:2)
funn <- function(x) gsub("_",".",x)
drename(dd) <- ~.
drename(dd,fun=funn) <- ~.
names(dd)
```

`dermalridges` *Dermal ridges data (families)*

Description

Data on dermal ridge counts in left and right hand in (nuclear) families

Format

Data on 50 families with ridge counts in left and right hand for moter, father and each child. Family id in 'family' and gender and child number in 'sex' and 'child'.

Source

Sarah B. Holt (1952). Genetics of dermal ridges: bilateral asymmetry in finger ridge-counts. Annals of Eugenics 17 (1), pp.211–231. DOI: 10.1111/j.1469-1809.1952.tb02513.x

Examples

```
data(dermalridges)
fast.reshape(dermalridges,id="family",varying=c("child.left","child.right","sex"))
```

`dermalridgesMZ` *Dermal ridges data (monozygotic twins)*

Description

Data on dermal ridge counts in left and right hand in (nuclear) families

Format

Data on dermal ridge counts (left and right hand) in 18 monozygotic twin pairs.

Source

Sarah B. Holt (1952). Genetics of dermal ridges: bilateral asymmetry in finger ridge-counts. Annals of Eugenics 17 (1), pp.211–231. DOI: 10.1111/j.1469-1809.1952.tb02513.x

Examples

```
data(dermalridgesMZ)
fast.reshape(dermalridgesMZ,id="id",varying=c("left","right"))
```

`diabetes` *The Diabetic Retinopathy Data*

Description

The data was colleceted to test a laser treatment for delaying blindness in patients with dibetic retinopathy. The subset of 197 patiens given in Huster et al. (1989) is used.

Format

This data frame contains the following columns:

id a numeric vector. Patient code.

agedx a numeric vector. Age of patient at diagnosis.

time a numeric vector. Survival time: time to blindness or censoring.

status a numeric vector code. Survival status. 1: blindness, 0: censored.

trteye a numeric vector code. Random eye selected for treatment. 1: left eye 2: right eye.

treat a numeric vector. 1: treatment 0: untreated.

adult a numeric vector code. 1: younger than 20, 2: older than 20.

Source

Huster W.J. and Brookmeyer, R. and Self. S. (1989) MOdelling paired survival data with covariates, Biometrics 45, 145-56.

Examples

```
data(diabetes)
names(diabetes)
```

`divide.conquer` *Split a data set and run function*

Description

Split a data set and run function

Usage

```
divide.conquer(func = NULL, data, size, splits, id = NULL, ...)
```

Arguments

`func`	called function
`data`	data-frame
`size`	size of splits
`splits`	number of splits (ignored if size is given)
`id`	optional cluster variable
`...`	Additional arguments to lower level functions

Author(s)

Thomas Scheike, Klaus K. Holst

Examples

```
## avoid dependency on timereg
## library(timereg)
## data(TRACE)
## res <- divide.conquer(prop.odds,TRACE,
##       formula=Event(time,status==9)~chf+vf+age,n.sim=0,size=200)
```

`divide.conquer.timereg`

Split a data set and run function from timereg and aggregate

Description

Split a data set and run function of cox-aalen type and aggregate results

Usage

```
divide.conquer.timereg(func = NULL, data, size, ...)
```

Arguments

`func`	called function
`data`	data-frame
`size`	size of splits
`...`	Additional arguments to lower level functions

Author(s)

Thomas Scheike, Klaus K. Holst

Examples

```
## library(timereg)
## data(TRACE)
## a <- divide.conquer.timereg(prop.odds,TRACE,
##                            formula=Event(time,status==9)~chf+vf+age,n.sim=0,size=200)
## coef(a)
## a2 <- divide.conquer.timereg(prop.odds,TRACE,
##                            formula=Event(time,status==9)~chf+vf+age,n.sim=0,size=500)
## coef(a2)
##
##if (interactive()) {
##par(mfrow=c(1,1))
##plot(a,xlim=c(0,8),ylim=c(0,0.01))
##par(new=TRUE)
##plot(a2,xlim=c(0,8),ylim=c(0,0.01))
##}
```

`dlag` *Lag operator*

Description

Lag operator

Usage

```
dlag(data, x, k = 1, combine = TRUE, simplify = TRUE, names, ...)
```

Arguments

`data`	data.frame or vector
`x`	optional column names or formula
`k`	lag (vector of integers)
`combine`	combine results with original data.frame
`simplify`	Return vector if possible
`names`	optional new column names
`...`	additional arguments to lower level functions

Examples

```
d <- data.frame(y=1:10,x=c(10:1))
dlag(d,k=1:2)
dlag(d,~x,k=0:1)
dlag(d$x,k=1)
dlag(d$x,k=-1:2, names=letters[1:4])
```

---

doubleFGR *Double CIF Fine-Gray model with two causes*

Description

Estimation based on derived hazards and recursive estimating equations. fits two parametrizations 1)

$$F_1(t,X) = 1 - \exp(-\exp(X^T\beta)\Lambda_1(t))$$

and

$$F_2(t,X_2) = 1 - \exp(-\exp(X_2^T\beta_2)\Lambda_2(t))$$

or restricted version 2)

$$F_1(t,X) = 1 - \exp(-\exp(X^T\beta)\Lambda_1(t))$$

and

$$F_2(t,X_2,X) = (1 - \exp(-\exp(X_2^T\beta_2)\Lambda_2(t)))(1 - F_1(\infty,X))$$

Usage

```
doubleFGR(formula, data, offset = NULL, weights = NULL, X2 = NULL, ...)
```

Arguments

`formula`	formula with 'Event'
`data`	data frame
`offset`	offsets for cox model
`weights`	weights for Cox score equations
`X2`	specifies the regression design for second CIF model
`...`	Additional arguments to lower level funtions

Author(s)

Thomas Scheike

Examples

```
res <- 0
data(bmt)
bmt$age2 <- bmt$age
newdata <- bmt[1:19,]
if (interactive()) par(mfrow=c(5,3))

## same X1 and X2
pr2 <- doubleFGR(Event(time,cause)~age+platelet,data=bmt,restrict=res)
if (interactive()) {
  bplotdFG(pr2,cause=1)
  bplotdFG(pr2,cause=2,add=TRUE)
```

```
}
pp21 <- predictdFG(pr2,newdata=newdata)
pp22 <- predictdFG(pr2,newdata=newdata,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}
pp21 <- predictdFG(pr2)
pp22 <- predictdFG(pr2,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}

pr2 <- doubleFGR(Event(time,cause)~strata(platelet),data=bmt,restrict=res)
if (interactive()) {
  bplotdFG(pr2,cause=1)
  bplotdFG(pr2,cause=2,add=TRUE)
}
pp21 <- predictdFG(pr2,newdata=newdata)
pp22 <- predictdFG(pr2,,newdata=newdata,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}
pp21 <- predictdFG(pr2)
pp22 <- predictdFG(pr2,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}

## different X1 and X2
pr2 <- doubleFGR(Event(time,cause)~age+platelet+age2,data=bmt,X2=3,restrict=res)
if (interactive()) {
  bplotdFG(pr2,cause=1)
  bplotdFG(pr2,cause=2,add=TRUE)
}
pp21 <- predictdFG(pr2,newdata=newdata)
pp22 <- predictdFG(pr2,newdata=newdata,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}
pp21 <- predictdFG(pr2)
pp22 <- predictdFG(pr2,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}

### uden X1
pr2 <- doubleFGR(Event(time,cause)~age+platelet,data=bmt,X2=1:2,restrict=res)
```

```
if (interactive()) {
  bplotdFG(pr2,cause=1)
  bplotdFG(pr2,cause=2,add=TRUE)
}
pp21 <- predictdFG(pr2,newdata=newdata)
pp22 <- predictdFG(pr2,newdata=newdata,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}
pp21 <- predictdFG(pr2)
p22 <- predictdFG(pr2,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}

### without X2
pr2 <- doubleFGR(Event(time,cause)~age+platelet,data=bmt,X2=0,restrict=res)
if (interactive()) {
  bplotdFG(pr2,cause=1)
  bplotdFG(pr2,cause=2,add=TRUE)
}
pp21 <- predictdFG(pr2,newdata=newdata)
pp22 <- predictdFG(pr2,newdata=newdata,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}
pp21 <- predictdFG(pr2)
pp22 <- predictdFG(pr2,cause=2)
if (interactive()) {
  plot(pp21)
  plot(pp22,add=TRUE,col=2)
}
```

`dprint` *list, head, print, tail*

Description

listing for data frames

Usage

```
dprint(data, y = NULL, n = 0, ..., x = NULL)
```

Arguments

`data`	if x is formula or names for data frame then data frame is needed.
`y`	name of variable, or fomula, or names of variables on data frame.
`n`	Index of observations to print (default c(1:nfirst, n-nlast:nlast)
`...`	Optional additional arguments (nfirst,nlast, and print options)
`x`	possible group variable

Author(s)

Klaus K. Holst and Thomas Scheike

Examples

```
m <- lava::lvm(letters)
d <- lava::sim(m, 20)

dlist(d,~a+b+c)
dlist(d,~a+b+c|a<0 & b>0)
## listing all :
dlist(d,~a+b+c|a<0 & b>0,n=0)
dlist(d,a+b+c~I(d>0)|a<0 & b>0)
dlist(d,.~I(d>0)|a<0 & b>0)
dlist(d,~a+b+c|a<0 & b>0, nlast=0)
dlist(d,~a+b+c|a<0 & b>0, nfirst=3, nlast=3)
dlist(d,~a+b+c|a<0 & b>0, 1:5)
dlist(d,~a+b+c|a<0 & b>0, -(5:1))
dlist(d,~a+b+c|a<0 & b>0, list(1:5,50:55,-(5:1)))
dprint(d,a+b+c ~ I(d>0) |a<0 & b>0, list(1:5,50:55,-(5:1)))
```

`drcumhaz` *Rate for leaving HPN program for patients of Copenhagen*

Description

Rate for leaving HPN program for patients of Copenhagen

Source

Estimated data

`dreg` *Regression for data frames with dutility call*

Description

Regression for data frames with dutility call

Usage

```
dreg(
  data,
  y,
  x = NULL,
  z = NULL,
  x.oneatatime = TRUE,
  x.base.names = NULL,
  z.arg = c("clever", "base", "group", "condition"),
  fun. = lm,
  summary. = summary,
  regex = FALSE,
  convert = NULL,
  doSummary = TRUE,
  special = NULL,
  equal = TRUE,
  test = 1,
  ...
)
```

Arguments

`data`	data frame
`y`	name of variable, or fomula, or names of variables on data frame.
`x`	name of variable, or fomula, or names of variables on data frame.
`z`	name of variable, or fomula, or names of variables on data frame.
`x.oneatatime`	x's one at a time
`x.base.names`	base covarirates
`z.arg`	what is Z, c("clever","base","group","condition"), clever decides based on type of Z, base means that Z is used as fixed baseline covaraites for all X, group means the analyses is done based on groups of Z, and condition means that Z specifies a condition on the data
`fun.`	function lm is default
`summary.`	summary to use
`regex`	regex
`convert`	convert

`doSummary`	doSummary or not
`special`	special's
`equal`	to do pairwise stuff
`test`	development argument
`...`	Additional arguments for fun

Author(s)

Klaus K. Holst, Thomas Scheike

Examples

```
##'
data(iris)
dat <- iris
drename(dat) <- ~.
names(dat)
set.seed(1)
dat$time <- runif(nrow(dat))
dat$time1 <- runif(nrow(dat))
dat$status <- rbinom(nrow(dat),1,0.5)
dat$S1 <- with(dat, Surv(time,status))
dat$S2 <- with(dat, Surv(time1,status))
dat$id <- 1:nrow(dat)

mm <- dreg(dat, "*.length"~"*.width"|I(species=="setosa" & status==1))
mm <- dreg(dat, "*.length"~"*.width"|species+status)
mm <- dreg(dat, "*.length"~"*.width"|species)
mm <- dreg(dat, "*.length"~"*.width"|species+status,z.arg="group")

 ## Reduce Ex.Timings
y <- "S*"~"*.width"
xs <- dreg(dat, y, fun.=phreg)
## xs <- dreg(dat, y, fun.=survdiff)

y <- "S*"~"*.width"
xs <- dreg(dat, y, x.oneatatime=FALSE, fun.=phreg)

## under condition
y <- S1~"*.width"|I(species=="setosa" & sepal.width>3)
xs <- dreg(dat, y, z.arg="condition", fun.=phreg)
xs <- dreg(dat, y, fun.=phreg)

## under condition
y <- S1~"*.width"|species=="setosa"
xs <- dreg(dat, y, z.arg="condition", fun.=phreg)
xs <- dreg(dat, y, fun.=phreg)

## with baseline  after |
y <- S1~"*.width"|sepal.length
xs <- dreg(dat, y, fun.=phreg)
```

```
## by group by species, not working
y <- S1~"*.width"|species
ss <- split(dat, paste(dat$species, dat$status))

xs <- dreg(dat, y, fun.=phreg)

## species as base, species is factor so assumes that this is grouping
y <- S1~"*.width"|species
xs <- dreg(dat, y, z.arg="base", fun.=phreg)

##  background var after | and then one of x's at at time
y <- S1~"*.width"|status+"sepal*"
xs <- dreg(dat, y, fun.=phreg)

##  background var after | and then one of x's at at time
##y <- S1~"*.width"|status+"sepal*"
##xs <- dreg(dat, y, x.oneatatime=FALSE, fun.=phreg)
##xs <- dreg(dat, y, fun.=phreg)

##  background var after | and then one of x's at at time
##y <- S1~"*.width"+factor(species)
##xs <- dreg(dat, y, fun.=phreg)
##xs <- dreg(dat, y, fun.=phreg, x.oneatatime=FALSE)

y <- S1~"*.width"|factor(species)
xs <- dreg(dat, y, z.arg="base", fun.=phreg)

y <- S1~"*.width"|cluster(id)+factor(species)
xs <- dreg(dat, y, z.arg="base", fun.=phreg)
xs <- dreg(dat, y, z.arg="base", fun.=survival::coxph)

## under condition with groups
y <- S1~"*.width"|I(sepal.length>4)
xs <- dreg(subset(dat, species=="setosa"), y,z.arg="group",fun.=phreg)

## under condition with groups
y <- S1~"*.width"+I(log(sepal.length))|I(sepal.length>4)
xs <- dreg(subset(dat, species=="setosa"), y,z.arg="group",fun.=phreg)

y <- S1~"*.width"+I(dcut(sepal.length))|I(sepal.length>4)
xs <- dreg(subset(dat,species=="setosa"), y,z.arg="group",fun.=phreg)

ff <- function(formula,data,...) {
 ss <- survfit(formula,data,...)
 kmplot(ss,...)
 return(ss)
}

if (interactive()) {
dcut(dat) <- ~"*.width"
y <- S1~"*.4"|I(sepal.length>4)
par(mfrow=c(1, 2))
```

```
xs <- dreg(dat, y, fun.=ff)
}
```

`drelevel` *relev levels for data frames*

Description

levels shows levels for variables in data frame, relevel relevels a factor in data.frame

Usage

```
drelevel(
  data,
  y = NULL,
  x = NULL,
  ref = NULL,
  newlevels = NULL,
  regex = mets.options()$regex,
  sep = NULL,
  overwrite = FALSE,
  ...
)
```

Arguments

`data`	if x is formula or names for data frame then data frame is needed.
`y`	name of variable, or fomula, or names of variables on data frame.
`x`	name of variable, or fomula, or names of variables on data frame.
`ref`	new reference variable
`newlevels`	to combine levels of factor in data frame
`regex`	for regular expressions.
`sep`	seperator for naming of cut names.
`overwrite`	to overwrite variable
`...`	Optional additional arguments

Author(s)

Klaus K. Holst and Thomas Scheike

Examples

```
data(mena)
dstr(mena)
dfactor(mena)  <- ~twinnum
dnumeric(mena) <- ~twinnum.f

dstr(mena)

mena2 <- drelevel(mena,"cohort",ref="(1980,1982]")
mena2 <- drelevel(mena,~cohort,ref="(1980,1982]")
mena2 <- drelevel(mena,cohortII~cohort,ref="(1980,1982]")
dlevels(mena)
dlevels(mena2)
drelevel(mena,ref="(1975,1977]")  <-  ~cohort
drelevel(mena,ref="(1980,1982]")  <-  ~cohort
dlevels(mena,"coh*")
dtable(mena,"coh*",level=1)

### level 1 of zyg as baseline for new variable
drelevel(mena,ref=1) <- ~zyg
drelevel(mena,ref=c("DZ","[1973,1975]")) <- ~ zyg+cohort
drelevel(mena,ref=c("DZ","[1973,1975]")) <- zygdz+cohort.early~ zyg+cohort
### level 2 of zyg and cohort as baseline for new variables
drelevel(mena,ref=2) <- ~ zyg+cohort
dlevels(mena)

##################### combining factor levels with newlevels argument

dcut(mena,labels=c("I","II","III","IV")) <- cat4~agemena
dlevels(drelevel(mena,~cat4,newlevels=1:3))
dlevels(drelevel(mena,ncat4~cat4,newlevels=3:2))
drelevel(mena,newlevels=3:2) <- ncat4~cat4
dlevels(mena)

dlevels(drelevel(mena,nca4~cat4,newlevels=list(c(1,4),2:3)))

drelevel(mena,newlevels=list(c(1,4),2:3)) <- nca4..2 ~ cat4
dlevels(mena)

drelevel(mena,newlevels=list("I-III"=c("I","II","III"),"IV"="IV")) <- nca4..3 ~ cat4
dlevels(mena)

drelevel(mena,newlevels=list("I-III"=c("I","II","III"))) <- nca4..4 ~ cat4
dlevels(mena)

drelevel(mena,newlevels=list(group1=c("I","II","III"))) <- nca4..5 ~ cat4
dlevels(mena)

drelevel(mena,newlevels=list(g1=c("I","II","III"),g2="IV")) <- nca4..6 ~ cat4
dlevels(mena)
```

`dsort` *Sort data frame*

Description

Sort data according to columns in data frame

Usage

```
dsort(data, x, ..., decreasing = FALSE, return.order = FALSE)
```

Arguments

`data`	Data frame
`x`	variable to order by
`...`	additional variables to order by
`decreasing`	sort order (vector of length x)
`return.order`	return order

Value

data.frame

Examples

```
data(data="hubble",package="lava")
dsort(hubble, "sigma")
dsort(hubble, hubble$sigma,"v")
dsort(hubble,~sigma+v)
dsort(hubble,~sigma-v)

## with direct asignment
dsort(hubble) <- ~sigma-v
```

`dspline` *Simple linear spline*

Description

Constructs simple linear spline on a data frame using the formula syntax of dutils that is adds (x-cuti)* (x>cuti) to the data-set for each knot of the spline. The full spline is thus given by x and spline variables added to the data-set.

Usage

```
dspline(
  data,
  y = NULL,
  x = NULL,
  breaks = 4,
  probs = NULL,
  equi = FALSE,
  regex = mets.options()$regex,
  sep = NULL,
  na.rm = TRUE,
  labels = NULL,
  all = FALSE,
  ...
)
```

Arguments

`data`	if x is formula or names for data frame then data frame is needed.
`y`	name of variable, or fomula, or names of variables on data frame.
`x`	name of variable, or fomula, or names of variables on data frame.
`breaks`	number of breaks, for variables or vector of break points,
`probs`	groups defined from quantiles
`equi`	for equi-spaced breaks
`regex`	for regular expressions.
`sep`	seperator for naming of cut names.
`na.rm`	to remove NA for grouping variables.
`labels`	to use for cut groups
`all`	to do all variables, even when breaks are not unique
`...`	Optional additional arguments

Author(s)

Thomas Scheike

Examples

```
data(TRACE)
TRACE <- dspline(TRACE,~wmi,breaks=c(1,1.3,1.7))
cca <- survival::coxph(Surv(time,status==9)~age+vf+chf+wmi,data=TRACE)
cca2 <- survival::coxph(Surv(time,status==9)~age+wmi+vf+chf+
                         wmi.spline1+wmi.spline2+wmi.spline3,data=TRACE)
anova(cca,cca2)

nd <- data.frame(age=50,vf=0,chf=0,wmi=seq(0.4,3,by=0.01))
nd <- dspline(nd,~wmi,breaks=c(1,1.3,1.7))
```

```
pl <- predict(cca2,newdata=nd)
plot(nd$wmi,pl,type="l")
```

`dtable` *tables for data frames*

Description

tables for data frames

Usage

```
dtable(
  data,
  y = NULL,
  x = NULL,
  ...,
  level = -1,
  response = NULL,
  flat = TRUE,
  total = FALSE,
  prop = FALSE,
  summary = NULL
)
```

Arguments

`data`	if x is formula or names for data frame then data frame is needed.
`y`	name of variable, or fomula, or names of variables on data frame.
`x`	name of variable, or fomula, or names of variables on data frame.
`...`	Optional additional arguments
`level`	1 for all marginal tables, 2 for all 2 by 2 tables, and null for the full table, possible versus group variable
`response`	For level=2, only produce tables with columns given by 'response' (index)
`flat`	produce flat tables
`total`	add total counts/proportions
`prop`	Proportions instead of counts (vector of margins)
`summary`	summary function

Author(s)

Klaus K. Holst and Thomas Scheike

Examples

```
data("sTRACE",package="timereg")

dtable(sTRACE,~status)
dtable(sTRACE,~status+vf)
dtable(sTRACE,~status+vf,level=1)
dtable(sTRACE,~status+vf,~chf+diabetes)

dtable(sTRACE,c("*f*","status"),~diabetes)
dtable(sTRACE,c("*f*","status"),~diabetes, level=2)
dtable(sTRACE,c("*f*","status"),level=1)

dtable(sTRACE,~"*f*"+status,level=1)
dtable(sTRACE,~"*f*"+status+I(wmi>1.4)|age>60,level=2)
dtable(sTRACE,"*f*"+status~I(wmi>0.5)|age>60,level=1)
dtable(sTRACE,status~dcut(age))

dtable(sTRACE,~status+vf+sex|age>60)
dtable(sTRACE,status+vf+sex~+1|age>60, level=2)
dtable(sTRACE,.~status+vf+sex|age>60,level=1)
dtable(sTRACE,status+vf+sex~diabetes|age>60)
dtable(sTRACE,status+vf+sex~diabetes|age>60, flat=FALSE)

dtable(sTRACE,status+vf+sex~diabetes|age>60, level=1)
dtable(sTRACE,status+vf+sex~diabetes|age>60, level=2)

dtable(sTRACE,status+vf+sex~diabetes|age>60, level=2, prop=1, total=TRUE)
dtable(sTRACE,status+vf+sex~diabetes|age>60, level=2, prop=2, total=TRUE)
dtable(sTRACE,status+vf+sex~diabetes|age>60, level=2, prop=1:2, summary=summary)
```

`dtransform` *Transform that allows condition*

Description

Defines new variables under condition for data frame

Usage

```
dtransform(data, ...)
```

Arguments

`data`	is data frame
`...`	new variable definitions including possible if condition

Examples

```
data(mena)

xx <- dtransform(mena,ll=log(agemena)+twinnum)

xx <- dtransform(mena,ll=log(agemena)+twinnum,agemena<15)
xx <- dtransform(xx  ,ll=100+agemena,ll2=1000,agemena>15)
dsummary(xx,ll+ll2~I(agemena>15))
```

---

easy.binomial.twostage

Fits two-stage binomial for describing depdendence in binomial data using marginals that are on logistic form using the binomial.twostage funcion, but call is different and easier and the data manipulation is build into the function. Useful in particular for family design data.

Description

If clusters contain more than two times, the algoritm uses a compososite likelihood based on the pairwise bivariate models.

Usage

```
easy.binomial.twostage(
  margbin = NULL,
  data = parent.frame(),
  method = "nr",
  response = "response",
  id = "id",
  Nit = 60,
  detail = 0,
  silent = 1,
  weights = NULL,
  control = list(),
  theta = NULL,
  theta.formula = NULL,
  desnames = NULL,
  deshelp = 0,
  var.link = 1,
  iid = 1,
  step = 1,
  model = "plackett",
  marginal.p = NULL,
  strata = NULL,
  max.clust = NULL,
  se.clusters = NULL
)
```

Arguments

`margbin`	Marginal binomial model
`data`	data frame
`method`	Scoring method
`response`	name of response variable in data frame
`id`	name of cluster variable in data frame
`Nit`	Number of iterations
`detail`	Detail for more output for iterations
`silent`	Debug information
`weights`	Weights for log-likelihood, can be used for each type of outcome in 2x2 tables.
`control`	Optimization arguments
`theta`	Starting values for variance components
`theta.formula`	design for depedence, either formula or design function
`desnames`	names for dependence parameters
`deshelp`	if 1 then prints out some data sets that are used, on on which the design function operates
`var.link`	Link function for variance
`iid`	Calculate i.i.d. decomposition
`step`	Step size
`model`	model
`marginal.p`	vector of marginal probabilities
`strata`	strata for fitting
`max.clust`	max clusters used for i.i.d. decompostion
`se.clusters`	clusters for iid decomposition for roubst standard errors

Details

The reported standard errors are based on the estimated information from the likelihood assuming that the marginals are known. This gives correct standard errors in the case of the plackett distribution (OR model for dependence), but incorrect for the clayton-oakes types model. The OR model is often known as the ALR model. Our fitting procedures gives correct standard errors due to the ortogonality and is fast.

Examples

```
data(twinstut)
twinstut0 <- subset(twinstut, tvparnr<4000)
twinstut <- twinstut0
twinstut$binstut <- (twinstut$stutter=="yes")*1
theta.des <- model.matrix( ~-1+factor(zyg),data=twinstut)
margbin <- glm(binstut~factor(sex)+age,data=twinstut,family=binomial())
bin <- binomial.twostage(margbin,data=twinstut,var.link=1,
        clusters=twinstut$tvparnr,theta.des=theta.des,detail=0,
```

```
                 method="nr")
summary(bin)
lava::estimate(coef=bin$theta,vcov=bin$var.theta,f=function(p) exp(p))

twinstut$cage <- scale(twinstut$age)
theta.des <- model.matrix( ~-1+factor(zyg)+cage,data=twinstut)
bina <- binomial.twostage(margbin,data=twinstut,var.link=1,
         clusters=twinstut$tvparnr,theta.des=theta.des,detail=0)
summary(bina)

theta.des <- model.matrix( ~-1+factor(zyg)+factor(zyg)*cage,data=twinstut)
bina <- binomial.twostage(margbin,data=twinstut,var.link=1,
         clusters=twinstut$tvparnr,theta.des=theta.des)
summary(bina)

out <- easy.binomial.twostage(stutter~factor(sex)+age,data=twinstut,
                              response="binstut",id="tvparnr",var.link=1,
          theta.formula=~-1+factor(zyg1))
summary(out)

## refers to zygosity of first subject in eash pair : zyg1
## could also use zyg2 (since zyg2=zyg1 within twinpair's))
## do not run t save time
# desfs <- function(x,num1="zyg1",namesdes=c("mz","dz","os"))
#     c(x[num1]=="mz",x[num1]=="dz",x[num1]=="os")*1
#
#out3 <- easy.binomial.twostage(binstut~factor(sex)+age,
#                                data=twinstut, response="binstut",id="tvparnr",
#                                var.link=1,theta.formula=desfs,
#                                desnames=c("mz","dz","os"))
#summary(out3)

 ## Reduce Ex.Timings
n <- 1000
set.seed(100)
dd <- simBinFam(n,beta=0.3)
binfam <- fast.reshape(dd,varying=c("age","x","y"))
## mother, father, children  (ordered)
head(binfam)

########### ########### ########### ########### ########### ###########
####  simple analyses of binomial family data
########### ########### ########### ########### ########### ###########
desfs <- function(x,num1="num1",num2="num2")
{
     pp <- 1*(((x[num1]=="m")*(x[num2]=="f"))|(x[num1]=="f")*(x[num2]=="m"))
     pc <- (x[num1]=="m" | x[num1]=="f")*(x[num2]=="b1" | x[num2]=="b2")*1
     cc <- (x[num1]=="b1")*(x[num2]=="b1" | x[num2]=="b2")*1
     c(pp,pc,cc)
}

ud <- easy.binomial.twostage(y~+1,data=binfam,
     response="y",id="id",
```

```
     theta.formula=desfs,desnames=c("pp","pc","cc"))
summary(ud)

udx <- easy.binomial.twostage(y~+x,data=binfam,
     response="y",id="id",
     theta.formula=desfs,desnames=c("pp","pc","cc"))
summary(udx)

########### ########### ########### ########### ########### ###########
####  now allowing parent child POR to be different for mother and father
########### ########### ########### ########### ########### ###########

desfsi <- function(x,num1="num1",num2="num2")
{
    pp <- (x[num1]=="m")*(x[num2]=="f")*1
    mc <- (x[num1]=="m")*(x[num2]=="b1" | x[num2]=="b2")*1
    fc <- (x[num1]=="f")*(x[num2]=="b1" | x[num2]=="b2")*1
    cc <- (x[num1]=="b1")*(x[num2]=="b1" | x[num2]=="b2")*1
    c(pp,mc,fc,cc)
}

udi <- easy.binomial.twostage(y~+1,data=binfam,
     response="y",id="id",
     theta.formula=desfsi,desnames=c("pp","mother-child","father-child","cc"))
summary(udi)

##now looking to see if interactions with age or age influences marginal models
##converting factors to numeric to make all involved covariates numeric
##to use desfai2 rather then desfai that works on binfam

nbinfam <- binfam
nbinfam$num <- as.numeric(binfam$num)
head(nbinfam)

desfsai <- function(x,num1="num1",num2="num2")
{
    pp <- (x[num1]=="m")*(x[num2]=="f")*1
### av age for pp=1 i.e parent pairs
    agepp <- ((as.numeric(x["age1"])+as.numeric(x["age2"]))/2-30)*pp
    mc <- (x[num1]=="m")*(x[num2]=="b1" | x[num2]=="b2")*1
    fc <- (x[num1]=="f")*(x[num2]=="b1" | x[num2]=="b2")*1
    cc <- (x[num1]=="b1")*(x[num2]=="b1" | x[num2]=="b2")*1
    agecc <- ((as.numeric(x["age1"])+as.numeric(x["age2"]))/2-12)*cc
    c(pp,agepp,mc,fc,cc,agecc)
}

desfsai2 <- function(x,num1="num1",num2="num2")
{
    pp <- (x[num1]==1)*(x[num2]==2)*1
    agepp <- (((x["age1"]+x["age2"]))/2-30)*pp ### av age for pp=1 i.e parent pairs
    mc <- (x[num1]==1)*(x[num2]==3 | x[num2]==4)*1
    fc <- (x[num1]==2)*(x[num2]==3 | x[num2]==4)*1
    cc <- (x[num1]==3)*(x[num2]==3 | x[num2]==4)*1
```

```
    agecc <- ((x["age1"]+x["age2"])/2-12)*cc ### av age for children
    c(pp,agepp,mc,fc,cc,agecc)
}

udxai2 <- easy.binomial.twostage(y~+x+age,data=binfam,
     response="y",id="id",
     theta.formula=desfsai,
     desnames=c("pp","pp-age","mother-child","father-child","cc","cc-age"))
summary(udxai2)
```

`Effbinreg` *Efficient IPCW for binary data*

Description

Simple version of comp.risk function of timereg for just one time-point thus fitting the model

$$E(T \leq t|X) = expit(X^T beta)$$

Usage

```
Effbinreg(
  formula,
  data,
  cause = 1,
  time = NULL,
  beta = NULL,
  offset = NULL,
  weights = NULL,
  cens.weights = NULL,
  cens.model = ~+1,
  se = TRUE,
  kaplan.meier = TRUE,
  cens.code = 0,
  no.opt = FALSE,
  method = "nr",
  augmentation = NULL,
  h = NULL,
  MCaugment = NULL,
  ...
)
```

Arguments

`formula`	formula with outcome (see coxph)
`data`	data frame
`cause`	cause of interest

`time`	time of interest
`beta`	starting values
`offset`	offsets for partial likelihood
`weights`	for score equations
`cens.weights`	censoring weights
`cens.model`	only stratified cox model without covariates
`se`	to compute se's based on IPCW
`kaplan.meier`	uses Kaplan-Meier for IPCW in contrast to exp(-Baseline)
`cens.code`	gives censoring code
`no.opt`	to not optimize
`method`	for optimization
`augmentation`	to augment binomial regression
`h`	h for estimating equation
`MCaugment`	iid of h and censoring model
`...`	Additional arguments to lower level funtions
`model`	exp or linear

Details

Based on binomial regresion IPCW response estimating equation:

$$X(\Delta(T \leq t)/G_c(T_i-) - expit(X^T beta)) = 0$$

for IPCW adjusted responses.

Based on binomial regresion IPCW response estimating equation:

$$h(X)X(\Delta(T \leq t)/G_c(T_i-) - expit(X^T beta)) = 0$$

for IPCW adjusted responses where h is given as an argument together with iid of censoring with h. By using appropriately the h argument we can also do the efficient IPCW estimator estimator this works the prepsurv and prepcif for survival or competing risks data. In this case also the censoring martingale should be given for variance calculation and this also comes out of the prepsurv or prepcif functions. (Experimental version at this stage).

Variance is based on

$$\sum w_i^2$$

also with IPCW adjustment, and naive.var is variance under known censoring model.

Censoring model may depend on strata.

Author(s)

Thomas Scheike

`EVaddGam` *Relative risk for additive gamma model*

Description

Computes the relative risk for additive gamma model at time 0

Usage

```
EVaddGam(theta, x1, x2, thetades, ags)
```

Arguments

`theta`	theta
`x1`	x1
`x2`	x2
`thetades`	thetades
`ags`	ags

Author(s)

Thomas Scheike

References

Eriksson and Scheike (2015), Additive Gamma frailty models for competing risks data, Biometrics (2015)

Examples

```
lam0 <- c(0.5,0.3)
pars <- c(1,1,1,1,0,1)
## genetic random effects, cause1, cause2 and overall
parg <- pars[c(1,3,5)]
## environmental random effects, cause1, cause2 and overall
parc <- pars[c(2,4,6)]

## simulate competing risks with two causes with hazards 0.5 and 0.3
## ace for each cause, and overall ace
out <- simCompete.twin.ace(10000,parg,parc,0,2,lam0=lam0,overall=1,all.sum=1)

## setting up design for running the model
mm <- familycluster.index(out$cluster)
head(mm$familypairindex,n=10)
pairs <- matrix(mm$familypairindex,ncol=2,byrow=TRUE)
tail(pairs,n=12)
#
kinship <- (out[pairs[,1],"zyg"]=="MZ")+ (out[pairs[,1],"zyg"]=="DZ")*0.5
```

```
# dout <- make.pairwise.design.competing(pairs,kinship,
#          type="ace",compete=length(lam0),overall=1)
# head(dout$ant.rvs)
## MZ
# dim(dout$theta.des)
# dout$random.design[,,1]
## DZ
# dout$theta.des[,,nrow(pairs)]
# dout$random.design[,,nrow(pairs)]
#
# thetades <- dout$theta.des[,,1]
# x <- dout$random.design[,,1]
# x
##EVaddGam(rep(1,6),x[1,],x[3,],thetades,matrix(1,18,6))

# thetades <- dout$theta.des[,,nrow(out)/2]
# x <- dout$random.design[,,nrow(out)/2]
##EVaddGam(rep(1,6),x[1,],x[4,],thetades,matrix(1,18,6))
```

`evalTerminal` *Evaluates piece constant covariates at min(D,t) where D is a terminal event*

Description

returns X(min(D,t)) and min(D,t) and their ratio. for censored observation 0. to use with the IPCW models implemented.

Usage

```
evalTerminal(formula, data = data, death.code = 2, time = NULL)
```

Arguments

`formula`	formula with 'Event' outcome and X to evaluate at min(D,t)
`data`	data frame
`death.code`	codes for death (terminating event, 2 default)
`time`	for evaluation

Author(s)

Thomas Scheike

`Event` *Event history object*

Description

Constructur for Event History objects

Usage

```
Event(time, time2 = TRUE, cause = NULL, cens.code = 0, ...)
```

Arguments

`time`	Time
`time2`	Time 2
`cause`	Cause
`cens.code`	Censoring code (default 0)
`...`	Additional arguments

Details

... content for details

Value

Object of class Event (a matrix)

Author(s)

Klaus K. Holst and Thomas Scheike

Examples

```
t1 <- 1:10
t2 <- t1+runif(10)
ca <- rbinom(10,2,0.4)
(x <- Event(t1,t2,ca))
```

`event.split` *event.split (SurvSplit).*

Description

contstructs start stop formulation of event time data after a variable in the data.set. Similar to SurvSplit of the survival package but can also split after random time given in data frame.

Usage

```
event.split(
  data,
  time = "time",
  status = "status",
  cuts = "cuts",
  name.id = "id",
  name.start = "start",
  cens.code = 0,
  order.id = TRUE,
  time.group = FALSE
)
```

Arguments

`data`	data to be split
`time`	time variable.
`status`	status variable.
`cuts`	cuts variable or numeric cut (only one value)
`name.id`	name of id variable.
`name.start`	name of start variable in data, start can also be numeric "0"
`cens.code`	code for the censoring.
`order.id`	order data after id and start.
`time.group`	make variable "before"."cut" that keeps track of wether start,stop is before (1) or after cut (0).

Author(s)

Thomas Scheike

Examples

```
set.seed(1)
d <- data.frame(event=round(5*runif(5),2),start=1:5,time=2*1:5,
status=rbinom(5,1,0.5),x=1:5)
d
```

```
d0 <- event.split(d,cuts="event",name.start=0)
d0

dd <- event.split(d,cuts="event")
dd
ddd <- event.split(dd,cuts=3.5)
ddd
event.split(ddd,cuts=5.5)

### successive cutting for many values
dd <- d
for  (cuts in seq(2,3,by=0.3)) dd <- event.split(dd,cuts=cuts)
dd

###########################################################################
### same but for situation with multiple events along the time-axis
###########################################################################
d <- data.frame(event1=1:5+runif(5)*0.5,start=1:5,time=2*1:5,
status=rbinom(5,1,0.5),x=1:5,start0=0)
d$event2 <- d$event1+0.2
d$event2[4:5] <- NA
d

d0 <- event.split(d,cuts="event1",name.start="start",time="time",status="status")
d0
###
d00 <- event.split(d0,cuts="event2",name.start="start",time="time",status="status")
d00
```

`eventpois` *Extract survival estimates from lifetable analysis*

Description

Summary for survival analyses via the ’lifetable’ function

Usage

```
eventpois(
  object,
  ...,
  timevar,
  time,
  int.len,
  confint = FALSE,
  level = 0.95,
  individual = FALSE,
  length.out = 25
)
```

Arguments

`object`	glm object (poisson regression)
`...`	Contrast arguments
`timevar`	Name of time variable
`time`	Time points (optional)
`int.len`	Time interval length (optional)
`confint`	If TRUE confidence limits are supplied
`level`	Level of confidence limits
`individual`	Individual predictions
`length.out`	Length of time vector

Details

Summary for survival analyses via the 'lifetable' function

Author(s)

Klaus K. Holst

`EventSplit2` *Event split with two time-scales, time and gaptime*

Description

Cuts time for two time-scales, as event.split

Usage

```
EventSplit2(
  data,
  time = "time",
  status = "status",
  entry = "start",
  cuts = "cuts",
  name.id = "id",
  gaptime = NULL,
  gaptime.entry = NULL,
  cuttime = c("time", "gaptime"),
  cens.code = 0,
  order.id = TRUE
)
```

Arguments

`data`	data to be split
`time`	time variable.
`status`	status variable.
`entry`	name of entry variable.
`cuts`	cuts variable or numeric cut (only one value)
`name.id`	name of id variable.
`gaptime`	gaptime variable.
`gaptime.entry`	name of entry variable for gaptime.
`cuttime`	to cut after time or gaptime
`cens.code`	code for the censoring.
`order.id`	order data after id and start.

Author(s)

Thomas Scheike

Examples

```
rr  <- data.frame(time=c(500,1000),start=c(0,500),status=c(1,1),id=c(1,1))
rr$gaptime <-  rr$time-rr$start
rr$gapstart <- 0

rr1 <- EventSplit2(rr,cuts=600,cuttime="time",  gaptime="gaptime",gaptime.entry="gapstart")
rr2 <- EventSplit2(rr1,cuts=100,cuttime="gaptime",gaptime="gaptime",gaptime.entry="gapstart")

dlist(rr1,start-time+status+gapstart+gaptime~id)
dlist(rr2,start-time+status+gapstart+gaptime~id)
```

`familycluster.index` *Finds all pairs within a cluster (family)*

Description

Finds all pairs within a cluster (family)

Usage

```
familycluster.index(clusters, index.type = FALSE, num = NULL, Rindex = 1)
```

Arguments

`clusters`	list of indeces
`index.type`	argument of cluster index
`num`	num
`Rindex`	index starts with 1 in R, and 0 in C

Author(s)

Klaus Holst, Thomas Scheike

References

Cluster indeces

See Also

cluster.index familyclusterWithProbands.index

Examples

```
i<-c(1,1,2,2,1,3)
d<- familycluster.index(i)
print(d)
```

`familyclusterWithProbands.index`

Finds all pairs within a cluster (famly) with the proband (case/control)

Description

second column of pairs are the probands and the first column the related subjects

Usage

```
familyclusterWithProbands.index(
  clusters,
  probands,
  index.type = FALSE,
  num = NULL,
  Rindex = 1
)
```

Arguments

`clusters`	list of indeces giving the clusters (families)
`probands`	list of 0,1 where 1 specifices which of the subjects that are probands
`index.type`	argument passed to other functions
`num`	argument passed to other functions
`Rindex`	index starts with 1, in C is it is 0

Author(s)

Klaus Holst, Thomas Scheike

References

Cluster indeces

See Also

familycluster.index cluster.index

Examples

```
i<-c(1,1,2,2,1,3)
p<-c(1,0,0,1,0,1)
d<- familyclusterWithProbands.index(i,p)
print(d)
```

`fast.approx` *Fast approximation*

Description

Fast approximation

Usage

```
fast.approx(
  time,
  new.time,
  equal = FALSE,
  type = c("nearest", "right", "left"),
  sorted = FALSE,
  ...
)
```

Arguments

`time`	Original ordered time points
`new.time`	New time points
`equal`	If TRUE a list is returned with additional element
`type`	Type of matching, nearest index, nearest greater than or equal (right), number of elements smaller than y otherwise the closest value above new.time is returned.
`sorted`	Set to true if new.time is already sorted
`...`	Optional additional arguments

Author(s)

Klaus K. Holst

Examples

```
id <- c(1,1,2,2,7,7,10,10)
fast.approx(unique(id),id)

t <- 0:6
n <- c(-1,0,0.1,0.9,1,1.1,1.2,6,6.5)
fast.approx(t,n,type="left")
```

`fast.pattern` *Fast pattern*

Description

Fast pattern

Usage

```
fast.pattern(x, y, categories = 2, ...)
```

Arguments

`x`	Matrix (binary) of patterns. Optionally if `y` is also passed as argument, then the pattern matrix is defined as the elements agreeing in the two matrices.
`y`	Optional matrix argument with same dimensions as `x` (see above)
`categories`	Default 2 (binary)
`...`	Optional additional arguments

Author(s)

Klaus K. Holst

Examples

```
X <- matrix(rbinom(100,1,0.5),ncol=4)
fast.pattern(X)

X <- matrix(rbinom(100,3,0.5),ncol=4)
fast.pattern(X,categories=4)
```

`fast.reshape` *Fast reshape*

Description

Fast reshape/tranpose of data

Usage

```
fast.reshape(
  data,
  varying,
  id,
  num,
  sep = "",
  keep,
  idname = "id",
  numname = "num",
  factor = FALSE,
  idcombine = TRUE,
  labelnum = FALSE,
  labels,
  regex = mets.options()$regex,
  dropid = FALSE,
  ...
)
```

Arguments

`data`	data.frame or matrix
`varying`	Vector of prefix-names of the time varying variables. Optional for Long->Wide reshaping.
`id`	id-variable. If omitted then reshape Wide->Long.
`num`	Optional number/time variable
`sep`	String seperating prefix-name with number/time
`keep`	Vector of column names to keep
`idname`	Name of id-variable (Wide->Long)
`numname`	Name of number-variable (Wide->Long)

`factor`	If true all factors are kept (otherwise treated as character)
`idcombine`	If TRUE and `id` is vector of several variables, the unique id is combined from all the variables. Otherwise the first variable is only used as identifier.
`labelnum`	If TRUE varying variables in wide format (going from long->wide) are labeled 1,2,3,... otherwise use 'num' variable. In long-format (going from wide->long) varying variables matching 'varying' prefix are only selected if their postfix is a number.
`labels`	Optional labels for the number variable
`regex`	Use regular expressions
`dropid`	Drop id in long format (default FALSE)
`...`	Optional additional arguments

Author(s)

Thomas Scheike, Klaus K. Holst

Examples

```
m <- lava::lvm(c(y1,y2,y3,y4)~x)
d <- lava::sim(m,5)
d
fast.reshape(d,"y")
fast.reshape(fast.reshape(d,"y"),id="id")

##### From wide-format
(dd <- fast.reshape(d,"y"))
## Same with explicit setting new id and number variable/column names
## and seperator "" (default) and dropping x
fast.reshape(d,"y",idname="a",timevar="b",sep="",keep=c())
## Same with 'reshape' list-syntax
fast.reshape(d,list(c("y1","y2","y3","y4")),labelnum=TRUE)

##### From long-format
fast.reshape(dd,id="id")
## Restrict set up within-cluster varying variables
fast.reshape(dd,"y",id="id")
fast.reshape(dd,"y",id="id",keep="x",sep=".")

#####
x <- data.frame(id=c(5,5,6,6,7),y=1:5,x=1:5,tv=c(1,2,2,1,2))
x
(xw <- fast.reshape(x,id="id"))
(xl <- fast.reshape(xw,c("y","x"),idname="id2",keep=c()))
(xl <- fast.reshape(xw,c("y","x","tv")))
(xw2 <- fast.reshape(xl,id="id",num="num"))
fast.reshape(xw2,c("y","x"),idname="id")

### more generally:
### varying=list(c("ym","yf","yb1","yb2"), c("zm","zf","zb1","zb2"))
### varying=list(c("ym","yf","yb1","yb2")))
```

```
##### Family cluster example
d <- mets:::simBinFam(3)
d
fast.reshape(d,var=”y”)
fast.reshape(d,varying=list(c(”ym”,”yf”,”yb1”,”yb2”)))

d <- lava::sim(lava::lvm(~y1+y2+ya),10)
d
(dd <- fast.reshape(d,”y”))
fast.reshape(d,”y”,labelnum=TRUE)
fast.reshape(dd,id=”id”,num=”num”)
fast.reshape(dd,id=”id”,num=”num”,labelnum=TRUE)
fast.reshape(d,c(a=”y”),labelnum=TRUE) ## New column name


##### Unbalanced data
m <- lava::lvm(c(y1,y2,y3,y4)~ x+z1+z3+z5)
d <- lava::sim(m,3)
d
fast.reshape(d,c(”y”,”z”))

##### not-varying syntax:
fast.reshape(d,-c(”x”))

##### Automatically define varying variables from trailing digits
fast.reshape(d)

##### Prostate cancer example
data(prt)
head(prtw <- fast.reshape(prt,”cancer”,id=”id”))
ftable(cancer1~cancer2,data=prtw)
rm(prtw)
```

`FG_AugmentCifstrata` *Augmentation for Fine-Gray model based on stratified NPMLE Cif (Aalen-Johansen)*

Description

Computes the augmentation term for each individual as well as the sum

$$A(\beta) = \int H(t, X, \beta) \frac{F_2^*(t, s)}{S^*(t, s)} \frac{1}{G_c(t)} dM_c$$

with

$$H(t, X, \beta) = \int_t^\infty (X - E(\beta, t)) G_c(t) d\Lambda_1^* i(t, s)$$

using a KM for

$$G_c(t)$$

and a working model for cumulative baseline related to

$$F_1^*(t,s)$$

and

$$s$$

is strata,

$$S^*(t,s) = 1 - F_1^*(t,s) - F_2^*(t,s)$$

, and

$$E(\beta^p, t)$$

is given. Assumes that no strata for baseline of ine-Gay model that is augmented.

Usage

```
FG_AugmentCifstrata(
  formula,
  data = data,
  E = NULL,
  cause = NULL,
  cens.code = 0,
  km = TRUE,
  case.weights = NULL,
  weights = NULL,
  offset = NULL,
  ...
)
```

Arguments

`formula`	formula with 'Event', strata model for CIF given by strata, and strataC specifies censoring strata
`data`	data frame
`E`	from FG-model
`cause`	of interest
`cens.code`	code of censoring
`km`	to use Kaplan-Meier
`case.weights`	weights for FG score equations (that follow dN_1)
`weights`	weights for FG score equations
`offset`	offsets for FG model
`...`	Additional arguments to lower level funtions

Details

After a couple of iterations we end up with a solution of

$$\int (X - E(\beta))Y_1(t)w(t)dM_1 + A(\beta)$$

the augmented FG-score.

Standard errors computed under assumption of correct

$$G_c$$

model.

Author(s)

Thomas Scheike

Examples

```
set.seed(100)
rho1 <- 0.2; rho2 <- 10
n <- 400
beta=c(0.0,-0.1,-0.5,0.3)
dats <- simul.cifs(n,rho1,rho2,beta,rc=0.2)
dtable(dats,~status)
dsort(dats) <- ~time
fg <- cifreg(Event(time,status)~Z1+Z2,data=dats,cause=1,propodds=NULL)
summary(fg)

fgaugS <- FG_AugmentCifstrata(Event(time,status)~Z1+Z2+strata(Z1,Z2),data=dats,cause=1,E=fg$E)
summary(fgaugS)
fgaugS2 <- FG_AugmentCifstrata(Event(time,status)~Z1+Z2+strata(Z1,Z2),data=dats,cause=1,E=fgaugS$E)
summary(fgaugS2)
```

`ghaplos` *ghaplos haplo-types for subjects of haploX data*

Description

ghaplos haplo-types for subjects of haploX data

Source

Simulated data

`glm_IPTW` *IPTW GLM, Inverse Probaibilty of Treatment Weighted GLM*

Description

Fits GLM model with treatment weights

$$w(A) = \sum_a I(A=a)/P(A=a|X)$$

, computes standard errors via influence functions that are returned as the IID argument. Propensity scores are fitted using either logistic regression (glm) or the multinomial model (mlogit) when more than two categories for treatment. The treatment needs to be a factor and is identified on the rhs of the "treat.model".

Usage

```
glm_IPTW(
  formula,
  data,
  treat.model = NULL,
  family = binomial(),
  id = NULL,
  weights = NULL,
  estpr = 1,
  pi0 = 0.5,
  ...
)
```

Arguments

`formula`	for glm
`data`	data frame for risk averaging
`treat.model`	propensity score model (binary or multinomial)
`family`	of glm (logistic regression)
`id`	cluster id for standard errors
`weights`	may be given, and then uses weights*w(A) as the weights
`estpr`	to estimate propensity scores and get infuence function contribution to uncertainty
`pi0`	fixed simple weights
`...`	arguments for glm call

Details

Also works with cluster argument.

Author(s)

Thomas Scheike

`gof.phreg` *GOF for Cox PH regression*

Description

Cumulative score process residuals for Cox PH regression p-values based on Lin, Wei, Ying resampling.

Usage

```
## S3 method for class 'phreg'
gof(object, n.sim = 1000, silent = 1, robust = NULL, ...)
```

Arguments

`object`	is phreg object
`n.sim`	number of simulations for score processes
`silent`	to show timing estimate will be produced for longer jobs
`robust`	to control wether robust dM_i(t) or dN_i are used for simulations
`...`	Additional arguments to lower level funtions

Author(s)

Thomas Scheike and Klaus K. Holst

Examples

```
library(mets)
data(sTRACE)

m1 <- phreg(Surv(time,status==9)~vf+chf+diabetes,data=sTRACE)
gg <- gof(m1)
gg
par(mfrow=c(1,3))
plot(gg)

m1 <- phreg(Surv(time,status==9)~strata(vf)+chf+diabetes,data=sTRACE)
## to get Martingale ~ dN based simulations
gg <- gof(m1)
gg

## to get Martingale robust simulations, specify cluster in  call
sTRACE$id <- 1:500
m1 <- phreg(Surv(time,status==9)~vf+chf+diabetes+cluster(id),data=sTRACE)
```

```
gg <- gof(m1)
gg

m1 <- phreg(Surv(time,status==9)~strata(vf)+chf+diabetes+cluster(id),data=sTRACE)
gg <- gof(m1)
gg
```

`gofG.phreg` *Stratified baseline graphical GOF test for Cox covariates in PH regression*

Description

Looks at stratified baseline in Cox model and plots all baselines versus each other to see if lines are straight, with 50 resample versions under the assumptiosn that the stratified Cox is correct

Usage

```
gofG.phreg(x, sim = 0, silent = 1, lm = TRUE, ...)
```

Arguments

`x`	phreg object
`sim`	to simulate som variation from cox model to put on graph
`silent`	to keep it absolutely silent
`lm`	addd line to plot, regressing the cumulatives on each other
`...`	Additional arguments to lower level funtions

Author(s)

Thomas Scheike and Klaus K. Holst

Examples

```
data(tTRACE)

m1 <- phreg(Surv(time,status==9)~strata(vf)+chf+wmi,data=tTRACE)
m2 <- phreg(Surv(time,status==9)~vf+strata(chf)+wmi,data=tTRACE)
par(mfrow=c(2,2))

gofG.phreg(m1)
gofG.phreg(m2)

bplot(m1,log="y")
bplot(m2,log="y")
```

`gofM.phreg` *GOF for Cox covariates in PH regression*

Description

Cumulative residuals after model matrix for Cox PH regression p-values based on Lin, Wei, Ying resampling.

Usage

```
gofM.phreg(
  formula,
  data,
  offset = NULL,
  weights = NULL,
  modelmatrix = NULL,
  n.sim = 1000,
  silent = 1,
  ...
)
```

Arguments

`formula`	formula for cox regression
`data`	data for model
`offset`	offset
`weights`	weights
`modelmatrix`	matrix for cumulating residuals
`n.sim`	number of simulations for score processes
`silent`	to keep it absolutely silent, otherwise timing estimate will be prduced for longer jobs.
`...`	Additional arguments to lower level funtions

Details

That is, computes

$$U(t) = \int_0^t M^t d\hat{M}$$

and resamples its asymptotic distribution.

This will show if the residuals are consistent with the model. Typically, M will be a design matrix for the continous covariates that gives for example the quartiles, and then the plot will show if for the different quartiles of the covariate the risk prediction is consistent over time (time x covariate interaction).

Author(s)

Thomas Scheike and Klaus K. Holst

Examples

```
library(mets)
data(TRACE)
set.seed(1)
TRACEsam <- blocksample(TRACE,idvar="id",replace=FALSE,100)

dcut(TRACEsam)  <- ~.
mm <- model.matrix(~-1+factor(wmicat.4),data=TRACEsam)
m1 <- gofM.phreg(Surv(time,status==9)~vf+chf+wmi,data=TRACEsam,modelmatrix=mm)
summary(m1)
if (interactive()) {
par(mfrow=c(2,2))
plot(m1)
}

m1 <- gofM.phreg(Surv(time,status==9)~strata(vf)+chf+wmi,data=TRACEsam,modelmatrix=mm)
summary(m1)

## cumulative sums in covariates, via design matrix mm
mm <- cumContr(TRACEsam$wmi,breaks=10,equi=TRUE)
m1 <- gofM.phreg(Surv(time,status==9)~strata(vf)+chf+wmi,data=TRACEsam,
  modelmatrix=mm,silent=0)
summary(m1)
```

`gofZ.phreg` *GOF for Cox covariates in PH regression*

Description

That is, computes

$$U(z,\tau) = \int_0^\tau M(z)^t d\hat{M}$$

and resamples its asymptotic distribution.

Usage

```
gofZ.phreg(
  formula,
  data,
  vars = NULL,
  offset = NULL,
  weights = NULL,
  breaks = 50,
```

```
  equi = FALSE,
  n.sim = 1000,
  silent = 1,
  ...
)
```

Arguments

`formula`	formula for cox regression
`data`	data for model
`vars`	which variables to test for linearity
`offset`	offset
`weights`	weights
`breaks`	number of breaks for cumulatives in covarirate direction
`equi`	equidistant breaks or not
`n.sim`	number of simulations for score processes
`silent`	to keep it absolutely silent, otherwise timing estimate will be prduced for longer jobs.
`...`	Additional arguments to lower level funtions

Details

This will show if the residuals are consistent with the model evaulated in the z covariate. M is here chosen based on a grid (z_1, ..., z_m) and the different columns are $I(Z_i \leq z_l)$. for $l = 1, ..., m$. The process in z is resampled to find extreme values. The time-points of evuluation is by default 50 points, chosen as 2

The p-value is valid but depends on the chosen grid. When the number of break points are high this will give the orginal test of Lin, Wei and Ying for linearity, that is also computed in the timereg package.

Author(s)

Thomas Scheike and Klaus K. Holst

Examples

```
library(mets)
data(TRACE)
set.seed(1)
TRACEsam <- blocksample(TRACE,idvar="id",replace=FALSE,100)

## cumulative sums in covariates, via design matrix mm
 ## Reduce Ex.Timings
m1 <- gofZ.phreg(Surv(time,status==9)~strata(vf)+chf+wmi+age,data=TRACEsam)
summary(m1)
plot(m1,type="z")
```

`Grandom.cif` *Additive Random effects model for competing risks data for polygenetic modelling*

Description

Fits a random effects model describing the dependence in the cumulative incidence curves for subjects within a cluster. Given the gamma distributed random effects it is assumed that the cumulative incidence curves are indpendent, and that the marginal cumulative incidence curves are on additive form

$$P(T \leq t, cause = 1|x, z) = P_1(t, x, z) = 1 - exp(-x^T A(t) - tz^T \beta)$$

Usage

```
Grandom.cif(
  cif,
  data,
  cause = NULL,
  cif2 = NULL,
  times = NULL,
  cause1 = 1,
  cause2 = 1,
  cens.code = NULL,
  cens.model = "KM",
  Nit = 40,
  detail = 0,
  clusters = NULL,
  theta = NULL,
  theta.des = NULL,
  weights = NULL,
  step = 1,
  sym = 0,
  same.cens = FALSE,
  censoring.weights = NULL,
  silent = 1,
  var.link = 0,
  score.method = "nr",
  entry = NULL,
  estimator = 1,
  trunkp = 1,
  admin.cens = NULL,
  random.design = NULL,
  ...
)
```

Arguments

`cif`	a model object from the timereg::comp.risk function with the marginal cumulative incidence of cause2, i.e., the event that is conditioned on, and whose odds the comparision is made with respect to
`data`	a data.frame with the variables.
`cause`	specifies the causes related to the death times, the value cens.code is the censoring value.
`cif2`	specificies model for cause2 if different from cause1.
`times`	time points
`cause1`	cause of first coordinate.
`cause2`	cause of second coordinate.
`cens.code`	specificies the code for the censoring if NULL then uses the one from the marginal cif model.
`cens.model`	specified which model to use for the ICPW, KM is Kaplan-Meier alternatively it may be "cox"
`Nit`	number of iterations for Newton-Raphson algorithm.
`detail`	if 0 no details are printed during iterations, if 1 details are given.
`clusters`	specifies the cluster structure.
`theta`	specifies starting values for the cross-odds-ratio parameters of the model.
`theta.des`	specifies a regression design for the cross-odds-ratio parameters.
`weights`	weights for score equations.
`step`	specifies the step size for the Newton-Raphson algorith.m
`sym`	1 for symmetri and 0 otherwise
`same.cens`	if true then censoring within clusters are assumed to be the same variable, default is independent censoring.
`censoring.weights`	Censoring probabilities
`silent`	debug information
`var.link`	if var.link=1 then var is on log-scale.
`score.method`	default uses "nlminb" optimzer, alternatively, use the "nr" algorithm.
`entry`	entry-age in case of delayed entry. Then two causes must be given.
`estimator`	estimator
`trunkp`	gives probability of survival for delayed entry, and related to entry-ages given above.
`admin.cens`	Administrative censoring
`random.design`	specifies a regression design of 0/1's for the random effects.
`...`	extra arguments.

Details

We allow a regression structure for the indenpendent gamma distributed random effects and their variances that may depend on cluster covariates.

random.design specificies the random effects for each subject within a cluster. This is a matrix of 1's and 0's with dimension n x d. With d random effects. For a cluster with two subjects, we let the random.design rows be v_1 and v_2. Such that the random effects for subject 1 is

$$v_1^T (Z_1, ..., Z_d)$$

, for d random effects. Each random effect has an associated parameter $(\lambda_1, ..., \lambda_d)$. By construction subjects 1's random effect are Gamma distributed with mean $\lambda_1/v_1^T \lambda$ and variance $\lambda_1/(v_1^T \lambda)^2$. Note that the random effect $v_1^T (Z_1, ..., Z_d)$ has mean 1 and variance $1/(v_1^T \lambda)$.

The parameters $(\lambda_1, ..., \lambda_d)$ are related to the parameters of the model by a regression construction $pard$ (d x k), that links the d λ parameters with the (k) underlying θ parameters

$$\lambda = pard\theta$$

Value

returns an object of type 'random.cif'. With the following arguments:

`theta`	estimate of parameters of model.
`var.theta`	variance for gamma.
`hess`	the derivative of the used score.
`score`	scores at final stage.
`theta.iid`	matrix of iid decomposition of parametric effects.

Author(s)

Thomas Scheike

References

A Semiparametric Random Effects Model for Multivariate Competing Risks Data, Scheike, Zhang, Sun, Jensen (2010), Biometrika.

Cross odds ratio Modelling of dependence for Multivariate Competing Risks Data, Scheike and Sun (2013), Biostatitistics.

Scheike, Holst, Hjelmborg (2014), LIDA, Estimating heritability for cause specific hazards based on twin data

Examples

```
## Reduce Ex.Timings
d <- simnordic.random(5000,delayed=TRUE,
      cordz=1.0,cormz=2,lam0=0.3,country=TRUE)
times <- seq(50,90,by=10)
addm <- timereg::comp.risk(Event(time,cause)~-1+factor(country)+cluster(id),data=d,
times=times,cause=1,max.clust=NULL)
```

```
 ### making group indidcator
 mm <- model.matrix(~-1+factor(zyg),d)

 out1m<-random.cif(addm,data=d,cause1=1,cause2=1,theta=1,
   theta.des=mm,same.cens=TRUE)
 summary(out1m)

 ## this model can also be formulated as a random effects model
 ## but with different parameters
 out2m<-Grandom.cif(addm,data=d,cause1=1,cause2=1,
    theta=c(0.5,1),step=1.0,
    random.design=mm,same.cens=TRUE)
 summary(out2m)
 1/out2m$theta
 out1m$theta

 ####################################################################
 ################### ACE modelling of twin data #####################
 ####################################################################
 ### assume that zygbin gives the zygosity of mono and dizygotic twins
 ### 0 for mono and 1 for dizygotic twins. We now formulate and AC model
 zygbin <- d$zyg=="DZ"

 n <- nrow(d)
 ### random effects for each cluster
 des.rv <- cbind(mm,(zygbin==1)*rep(c(1,0)),(zygbin==1)*rep(c(0,1)),1)
 ### design making parameters half the variance for dizygotic components
 pardes <- rbind(c(1,0), c(0.5,0),c(0.5,0), c(0.5,0), c(0,1))

 outacem <-Grandom.cif(addm,data=d,cause1=1,cause2=1,
same.cens=TRUE,theta=c(0.35,0.15),
            step=1.0,theta.des=pardes,random.design=des.rv)
 summary(outacem)
```

`hapfreqs` *hapfreqs data set*

Description

hapfreqs data set

Source

Simulated data

`haplo.surv.discrete` *Discrete time to event haplo type analysis*

Description

Can be used for logistic regression when time variable is "1" for all id.

Usage

```
haplo.surv.discrete(
  X = NULL,
  y = "y",
  time.name = "time",
  Haplos = NULL,
  id = "id",
  desnames = NULL,
  designfunc = NULL,
  beta = NULL,
  no.opt = FALSE,
  method = "NR",
  stderr = TRUE,
  designMatrix = NULL,
  response = NULL,
  idhap = NULL,
  design.only = FALSE,
  covnames = NULL,
  fam = binomial,
  weights = NULL,
  offsets = NULL,
  idhapweights = NULL,
  ...
)
```

Arguments

`X`	design matrix data-frame (sorted after id and time variable) with id time response and desnames
`y`	name of response (binary response with logistic link) from X
`time.name`	to sort after time for X
`Haplos`	(data.frame with id, haplo1, haplo2 (haplotypes (h)) and p=P(h|G)) haplotypes given as factor.
`id`	name of id variale from X
`desnames`	names for design matrix
`designfunc`	function that computes design given haplotypes h=(h1,h2) x(h)
`beta`	starting values

`no.opt`	optimization TRUE/FALSE
`method`	NR, nlm
`stderr`	to return only estimate
`designMatrix`	gives response and designMatrix directly not implemented (mush contain: p, id, idhap)
`response`	gives response and design directly designMatrix not implemented
`idhap`	name of id-hap variable to specify different haplotypes for different id
`design.only`	to return only design matrices for haplo-type analyses.
`covnames`	names of covariates to extract from object for regression
`fam`	family of models, now binomial default and only option
`weights`	weights following id for GLM
`offsets`	following id for GLM
`idhapweights`	weights following id-hap for GLM (WIP)
`...`	Additional arguments to lower level funtions lava::NR optimizer or nlm

Details

Cycle-specific logistic regression of haplo-type effects with known haplo-type probabilities. Given observed genotype G and unobserved haplotypes H we here mix out over the possible haplotypes using that P(H|G) is provided.

$$S(t|x,G)) = E(S(t|x,H)|G) = \sum_{h \in G} P(h|G) S(t|z,h)$$

so survival can be computed by mixing out over possible h given g.

Survival is based on logistic regression for the discrete hazard function of the form

$$logit(P(T = t|T \geq t, x, h)) = \alpha_t + x(h)\beta$$

where x(h) is a regression design of x and haplotypes $h = (h_1, h_2)$

Likelihood is maximized and standard errors assumes that P(H|G) is known.

The design over the possible haplotypes is constructed by merging X with Haplos and can be viewed by design.only=TRUE

Author(s)

Thomas Scheike

Examples

```
## some haplotypes of interest
types <- c("DCGCGCTCACG","DTCCGCTGACG","ITCAGTTGACG","ITCCGCTGAGG")

## some haplotypes frequencies for simulations
data(hapfreqs)
```

```
www <-which(hapfreqs$haplotype %in% types)
hapfreqs$freq[www]

baseline=hapfreqs$haplotype[9]
baseline

designftypes <- function(x,sm=0) {# {{{
hap1=x[1]
hap2=x[2]
if (sm==0) y <- 1*( (hap1==types) | (hap2==types))
if (sm==1) y <- 1*(hap1==types) + 1*(hap2==types)
return(y)
}# }}}

tcoef=c(-1.93110204,-0.47531630,-0.04118204,-1.57872602,-0.22176426,-0.13836416,
0.88830288,0.60756224,0.39802821,0.32706859)

data(hHaplos)
data(haploX)

haploX$time <- haploX$times
Xdes <- model.matrix(~factor(time),haploX)
colnames(Xdes) <- paste("X",1:ncol(Xdes),sep="")
X <- dkeep(haploX,~id+y+time)
X <- cbind(X,Xdes)
Haplos <- dkeep(ghaplos,~id+"haplo*"+p)
desnames=paste("X",1:6,sep="")   # six X's related to 6 cycles
out <- haplo.surv.discrete(X=X,y="y",time.name="time",
         Haplos=Haplos,desnames=desnames,designfunc=designftypes)
names(out$coef) <- c(desnames,types)
out$coef
summary(out)
```

`haploX` *haploX covariates and response for haplo survival discrete survival*

Description

haploX covariates and response for haplo survival discrete survival

Source

Simulated data

`hfactioncpx12` *hfaction, subset of block randmized study HF-ACtion from WA package*

Description

Data from HF-action trial slightly modified from WA package, consisting of 741 nonischemic patients with baseline cardiopulmonary test duration less than or equal to 12 minutes.

Format

Randomized study status : 1-event, 2-death, 0-censoring treatment : 1/0

Source

WA package, Connor et al. 2009

Examples

```
data(hfactioncpx12)
```

`interval.logitsurv.discrete` *Discrete time to event interval censored data*

Description

$$logit(P(T > t|x)) = log(G(t)) + x\beta$$
$$P(T > t|x) = \frac{1}{1 + G(t)exp(x\beta)}$$

Usage

```
interval.logitsurv.discrete(
  formula,
  data,
  beta = NULL,
  no.opt = FALSE,
  method = "NR",
  stderr = TRUE,
  weights = NULL,
  offsets = NULL,
  exp.link = 1,
  increment = 1,
  ...
)
```

Arguments

`formula`	formula
`data`	data
`beta`	starting values
`no.opt`	optimization TRUE/FALSE
`method`	NR, nlm
`stderr`	to return only estimate
`weights`	weights following id for GLM
`offsets`	following id for GLM
`exp.link`	parametrize increments exp(alpha) > 0
`increment`	using increments dG(t)=exp(alpha) as parameters
`...`	Additional arguments to lower level funtions lava::NR optimizer or nlm

Details

This is thus also the cumulative odds model, since

$$P(T \leq t|x) = \frac{G(t)\exp(x\beta)}{1 + G(t)exp(x\beta)}$$

The baseline $G(t)$ is written as $cumsum(exp(\alpha))$ and this is not the standard parametrization that takes log of $G(t)$ as the parameters.

Input are intervals given by]t_l,t_r] where t_r can be infinity for right-censored intervals When truly discrete]0,1] will be an observation at 1, and]j,j+1] will be an observation at j+1

Likelihood is maximized:

$$\prod P(T_i > t_{il}|x) - P(T_i > t_{ir}|x)$$

Author(s)

Thomas Scheike

Examples

```
data(ttpd)
dtable(ttpd,~entry+time2)
out <- interval.logitsurv.discrete(Interval(entry,time2)~X1+X2+X3+X4,ttpd)
summary(out)

pred <- predictlogitSurvd(out,se=FALSE)
plotSurvd(pred)
```

---

ipw *Inverse Probability of Censoring Weights*

Description

Internal function. Calculates Inverse Probability of Censoring Weights (IPCW) and adds them to a data.frame

Usage

```
ipw(
  formula,
  data,
  cluster,
  same.cens = FALSE,
  obs.only = FALSE,
  weight.name = "w",
  trunc.prob = FALSE,
  weight.name2 = "wt",
  indi.weight = "pr",
  cens.model = "aalen",
  pairs = FALSE,
  theta.formula = ~1,
  ...
)
```

Arguments

`formula`	Formula specifying the censoring model
`data`	data frame
`cluster`	clustering variable
`same.cens`	For clustered data, should same censoring be assumed (bivariate probability calculated as mininum of the marginal probabilities)
`obs.only`	Return data with uncensored observations only
`weight.name`	Name of weight variable in the new data.frame
`trunc.prob`	If TRUE truncation probabilities are also calculated and stored in 'weight.name2' (based on Clayton-Oakes gamma frailty model)
`weight.name2`	Name of truncation probabilities
`indi.weight`	Name of individual censoring weight in the new data.frame
`cens.model`	Censoring model (default Aalens additive model)
`pairs`	For paired data (e.g. twins) only the complete pairs are returned (With pairs=TRUE)
`theta.formula`	Model for the dependence parameter in the Clayton-Oakes model (truncation only)
`...`	Additional arguments to censoring model

Author(s)

Klaus K. Holst

Examples

```
## Not run:
data("prt",package="mets")
prtw <- ipw(Surv(time,status==0)~country, data=prt[sample(nrow(prt),5000),],
            cluster="id",weight.name="w")
plot(0,type="n",xlim=range(prtw$time),ylim=c(0,1),xlab="Age",ylab="Probability")
count <- 0
for (l in unique(prtw$country)) {
    count <- count+1
    prtw <- prtw[order(prtw$time),]
    with(subset(prtw,country==l),
         lines(time,w,col=count,lwd=2))
}
legend("topright",legend=unique(prtw$country),col=1:4,pch=-1,lty=1)

## End(Not run)
```

---

ipw2 *Inverse Probability of Censoring Weights*

Description

Internal function. Calculates Inverse Probability of Censoring and Truncation Weights and adds them to a data.frame

Usage

```
ipw2(
  data,
  times = NULL,
  entrytime = NULL,
  time = "time",
  cause = "cause",
  same.cens = FALSE,
  cluster = NULL,
  pairs = FALSE,
  strata = NULL,
  obs.only = TRUE,
  cens.formula = NULL,
  cens.code = 0,
  pair.cweight = "pcw",
  pair.tweight = "ptw",
  pair.weight = "weights",
  cname = "cweights",
```

```
    tname = "tweights",
    weight.name = "indi.weights",
    prec.factor = 100,
    ...
  )
```

Arguments

`data`	data frame
`times`	possible time argument for speciying a maximum value of time tau=max(times), to specify when things are considered censored or not.
`entrytime`	nam of entry-time for truncation.
`time`	name of time variable on data frame.
`cause`	name of cause indicator on data frame.
`same.cens`	For clustered data, should same censoring be assumed and same truncation (bivariate probability calculated as mininum of the marginal probabilities)
`cluster`	name of clustering variable
`pairs`	For paired data (e.g. twins) only the complete pairs are returned (With pairs=TRUE)
`strata`	name of strata variable to get weights stratified.
`obs.only`	Return data with uncensored observations only
`cens.formula`	model for Cox models for truncation and right censoring times.
`cens.code`	censoring.code
`pair.cweight`	Name of weight variable in the new data.frame for right censorig of pairs
`pair.tweight`	Name of weight variable in the new data.frame for left truncation of pairs
`pair.weight`	Name of weight variable in the new data.frame for right censoring and left truncation of pairs
`cname`	Name of weight variable in the new data.frame for right censoring of individuals
`tname`	Name of weight variable in the new data.frame for left truncation of individuals
`weight.name`	Name of weight variable in the new data.frame for right censoring and left truncation of individuals
`prec.factor`	To let tied censoring and truncation times come after the death times.
`...`	Additional arguments to censoring model

Author(s)

Thomas Scheike

Examples

```
library("timereg")
set.seed(1)
d <- simnordic.random(5000,delayed=TRUE,ptrunc=0.7,
      cordz=0.5,cormz=2,lam0=0.3,country=FALSE)
d$strata <- as.numeric(d$country)+(d$zyg=="MZ")*4
```

```
times <- seq(60,100,by=10)
## c1 <- timereg::comp.risk(Event(time,cause)~1+cluster(id),data=d,cause=1,
##  model="fg",times=times,max.clust=NULL,n.sim=0)
## mm=model.matrix(~-1+zyg,data=d)
## out1<-random.cif(c1,data=d,cause1=1,cause2=1,same.cens=TRUE,theta.des=mm)
## summary(out1)
## pc1 <- predict(c1,X=1,se=0)
## plot(pc1)
##
## dl <- d[!d$truncated,]
## dl <- ipw2(dl,cluster="id",same.cens=TRUE,time="time",entrytime="entry",cause="cause",
##            strata="strata",prec.factor=100)
## cl <- timereg::comp.risk(Event(time,cause)~+1+
##  cluster(id),
##   data=dl,cause=1,model="fg",
##  weights=dl$indi.weights,cens.weights=rep(1,nrow(dl)),
##           times=times,max.clust=NULL,n.sim=0)
## pcl <- predict(cl,X=1,se=0)
## lines(pcl$time,pcl$P1,col=2)
## mm=model.matrix(~-1+factor(zyg),data=dl)
## out2<-random.cif(cl,data=dl,cause1=1,cause2=1,theta.des=mm,
##                 weights=dl$weights,censoring.weights=rep(1,nrow(dl)))
## summary(out2)
```

`km` *Kaplan-Meier with robust standard errors*

Description

Kaplan-Meier with robust standard errors Robust variance is default variance and obtained from the predict call

Usage

```
km(formula, data = data, ...)
```

Arguments

`formula`	formula with 'Surv' 'Event' outcome
`data`	data frame
`...`	Additional arguments to phreg

Author(s)

Thomas Scheike

Examples

```
library(mets)
data(sTRACE)
sTRACE$cluster <- sample(1:100,500,replace=TRUE)
out1 <- km(Surv(time,status==9)~strata(vf,chf),data=sTRACE)
out2 <- km(Surv(time,status==9)~strata(vf,chf)+cluster(cluster),data=sTRACE)

summary(out1,times=1:3)
summary(out2,times=1:3)

par(mfrow=c(1,2))
plot(out1,se=TRUE)
plot(out2,se=TRUE)
```

`lifecourse` *Life-course plot*

Description

Life-course plot for event life data with recurrent events

Usage

```
lifecourse(
  formula,
  data,
  id = "id",
  group = NULL,
  type = "l",
  lty = 1,
  col = 1:10,
  alpha = 0.3,
  lwd = 1,
  recurrent.col = NULL,
  recurrent.lty = NULL,
  legend = NULL,
  pchlegend = NULL,
  by = NULL,
  status.legend = NULL,
  place.sl = "bottomright",
  xlab = "Time",
  ylab = "",
  add = FALSE,
  ...
)
```

Arguments

`formula`	Formula (Event(start,slut,status) ~ ...)
`data`	data.frame
`id`	Id variable
`group`	group variable
`type`	Type (line 'l', stair 's', ...)
`lty`	Line type
`col`	Colour
`alpha`	transparency (0-1)
`lwd`	Line width
`recurrent.col`	col of recurrence type
`recurrent.lty`	lty's of of recurrence type
`legend`	position of optional id legend
`pchlegend`	point type legends
`by`	make separate plot for each level in 'by' (formula, name of column, or vector)
`status.legend`	Status legend
`place.sl`	Placement of status legend
`xlab`	Label of X-axis
`ylab`	Label of Y-axis
`add`	Add to existing device
`...`	Additional arguments to lower level arguments

Author(s)

Thomas Scheike, Klaus K. Holst

Examples

```
data = data.frame(id=c(1,1,1,2,2),start=c(0,1,2,3,4),slut=c(1,2,4,4,7),
                  type=c(1,2,3,2,3),status=c(0,1,2,1,2),group=c(1,1,1,2,2))
ll = lifecourse(Event(start,slut,status)~id,data,id="id")
ll = lifecourse(Event(start,slut,status)~id,data,id="id",recurrent.col="type")

ll = lifecourse(Event(start,slut,status)~id,data,id="id",group=~group,col=1:2)
op <- par(mfrow=c(1,2))
ll = lifecourse(Event(start,slut,status)~id,data,id="id",by=~group)
par(op)
legends=c("censored","pregnant","married")
ll = lifecourse(Event(start,slut,status)~id,data,id="id",group=~group,col=1:2,status.legend=legends)
```

`lifetable.matrix` *Life table*

Description

Create simple life table

Usage

```
## S3 method for class 'matrix'
lifetable(x, strata = list(), breaks = c(),
   weights=NULL, confint = FALSE, ...)

 ## S3 method for class 'formula'
lifetable(x, data=parent.frame(), breaks = c(),
   weights=NULL, confint = FALSE, ...)
```

Arguments

`x`	time formula (Surv) or matrix/data.frame with columns time,status or entry,exit,status
`strata`	strata
`breaks`	time intervals
`weights`	weights variable
`confint`	if TRUE 95% confidence limits are calculated
`...`	additional arguments to lower level functions
`data`	data.frame

Author(s)

Klaus K. Holst

Examples

```
library(timereg)
data(TRACE)

d <- with(TRACE,lifetable(Surv(time,status==9)~sex+vf,breaks=c(0,0.2,0.5,8.5)))
summary(glm(events ~ offset(log(atrisk))+factor(int.end)*vf + sex*vf,
           data=d,poisson))
```

`LinSpline` *Simple linear spline*

Description

Simple linear spline

Usage

```
LinSpline(x, knots, num = TRUE, name = "Spline")
```

Arguments

`x`	variable to make into spline
`knots`	cut points
`num`	to give names x1 x2 and so forth
`name`	name of spline expansion name.1 name.2 and so forth

Author(s)

Thomas Scheike

`logitSurv` *Proportional odds survival model*

Description

Semiparametric Proportional odds model, that has the advantage that

$$logit(S(t|x)) = \log(\Lambda(t)) + x\beta$$

so covariate effects give OR of survival.

Usage

```
logitSurv(formula, data, offset = NULL, weights = NULL, ...)
```

Arguments

`formula`	formula with 'Surv' outcome (see `coxph`)
`data`	data frame
`offset`	offsets for exp(x beta) terms
`weights`	weights for score equations
`...`	Additional arguments to lower level funtions

Details

This is equivalent to using a hazards model

$$Z\lambda(t)\exp(x\beta)$$

where Z is gamma distributed with mean and variance 1.

Author(s)

Thomas Scheike

References

The proportional odds cumulative incidence model for competing risks, Eriksson, Frank and Li, Jianing and Scheike, Thomas and Zhang, Mei-Jie, Biometrics, 2015, 3, 687–695, 71,

Examples

```
data(TRACE)
dcut(TRACE) <- ~.
out1 <- logitSurv(Surv(time,status==9)~vf+chf+strata(wmicat.4),data=TRACE)
summary(out1)
gof(out1)
plot(out1)
```

`mediatorSurv` *Mediation analysis in survival context*

Description

Mediation analysis in survival context with robust standard errors taking the weights into account via influence function computations. Mediator and exposure must be factors. This is based on numerical derivative wrt parameters for weighting. See vignette for more examples.

Usage

```
mediatorSurv(
  survmodel,
  weightmodel,
  data = data,
  wdata = wdata,
  id = "id",
  silent = TRUE,
  ...
)
```

Arguments

`survmodel`	with mediation model (binreg, aalenMets, phreg)
`weightmodel`	mediation model
`data`	for computations
`wdata`	weighted data expansion for computations
`id`	name of id variable, important for SE computations
`silent`	to be silent
`...`	Additional arguments to survival model

Author(s)

Thomas Scheike

Examples

```
n <- 400
dat <- kumarsimRCT(n,rho1=0.5,rho2=0.5,rct=2,censpar=c(0,0,0,0),
          beta = c(-0.67, 0.59, 0.55, 0.25, 0.98, 0.18, 0.45, 0.31),
    treatmodel = c(-0.18, 0.56, 0.56, 0.54),restrict=1)
dfactor(dat) <- dnr.f~dnr
dfactor(dat) <- gp.f~gp
drename(dat) <- ttt24~”ttt24*”
dat$id <- 1:n
dat$ftime <- 1

weightmodel <- fit <- glm(gp.f~dnr.f+preauto+ttt24,data=dat,family=binomial)
wdata <- medweight(fit,data=dat)

### fitting models with and without mediator
aaMss2 <- binreg(Event(time,status)~gp+dnr+preauto+ttt24+cluster(id),data=dat,time=50,cause=2)
aaMss22 <- binreg(Event(time,status)~dnr+preauto+ttt24+cluster(id),data=dat,time=50,cause=2)

### estimating direct and indirect effects (under strong strong assumptions)
aaMss <- binreg(Event(time,status)~dnr.f0+dnr.f1+preauto+ttt24+cluster(id),
                data=wdata,time=50,weights=wdata$weights,cause=2)
## to compute standard errors , requires numDeriv
library(numDeriv)
ll <- mediatorSurv(aaMss,fit,data=dat,wdata=wdata)
summary(ll)
## not run bootstrap (to save time)
## bll <- BootmediatorSurv(aaMss,fit,data=dat,k.boot=500)
```

`medweight` *Computes mediation weights*

Description

Computes mediation weights for either binary or multinomial mediators. The important part is that the influence functions can be obtained to compute standard errors.

Usage

```
medweight(
  fit,
  data = data,
  var = NULL,
  name.weight = "weights",
  id.name = "id",
  ...
)
```

Arguments

`fit`	either glm-binomial or mlogit (mets package)
`data`	data frame with data
`var`	is NULL reads mediator and exposure from formulae in the fit.
`name.weight`	name of weights
`id.name`	name of id variable, important for SE computations
`...`	Additional arguments to

Author(s)

Thomas Scheike

`melanoma` *The Melanoma Survival Data*

Description

The melanoma data frame has 205 rows and 7 columns. It contains data relating to survival of patients after operation for malignant melanoma collected at Odense University Hospital by K.T. Drzewiecki.

Format

This data frame contains the following columns:

no a numeric vector. Patient code.

status a numeric vector code. Survival status. 1: dead from melanoma, 2: alive, 3: dead from other cause.

days a numeric vector. Survival time.

ulc a numeric vector code. Ulceration, 1: present, 0: absent.

thick a numeric vector. Tumour thickness (1/100 mm).

sex a numeric vector code. 0: female, 1: male.

Source

Andersen, P.K., Borgan O, Gill R.D., Keiding N. (1993), *Statistical Models Based on Counting Processes*, Springer-Verlag.

Drzewiecki, K.T., Ladefoged, C., and Christensen, H.E. (1980), Biopsy and prognosis for cutaneous malignant melanoma in clinical stage I. Scand. J. Plast. Reconstru. Surg. 14, 141-144.

Examples

```
data(melanoma)
names(melanoma)
```

`mena` *Menarche data set*

Description

Menarche data set

Source

Simulated data

`mets.options` *Set global options for* `mets`

Description

Extract and set global parameters of `mets`.

Usage

```
mets.options(...)
```

Arguments

`...`	Arguments

Details

- `regex`: If TRUE character vectors will be interpreted as regular expressions (`dby`, `dcut`, ...)
- `silent`: Set to `FALSE` to disable various output messages

Value

`list` of parameters

Examples

```
## Not run:
mets.options(regex=TRUE)

## End(Not run)
```

`migr` *Migraine data*

Description

Migraine data

`mlogit` *Multinomial regression based on phreg regression*

Description

Fits multinomial regression model

$$P_i = \frac{\exp(X_i^\beta)}{\sum_{j=1}^K \exp(X_j^\beta)}$$

for

$$i = 1, .., K$$

where

$$\beta_1 = 0$$

, such that

$$\sum_j P_j = 1$$

using phreg function. Thefore the ratio

$$\frac{P_i}{P_1} = \exp(X_i^\beta)$$

Usage

```
mlogit(formula, data, offset = NULL, weights = NULL, fix.X = FALSE, ...)
```

Arguments

`formula`	formula with outcome (see `coxph`)
`data`	data frame
`offset`	offsets for partial likelihood
`weights`	for score equations
`fix.X`	to have same coefficients for all categories
`...`	Additional arguments to lower level funtions

Details

Coefficients give log-Relative-Risk relative to baseline group (first level of factor, so that it can reset by relevel command). Standard errors computed based on sandwhich form

$$DU^-1 \sum U_i^2 DU^-1$$

.

Can also get influence functions (possibly robust) via iid() function, response should be a factor.

Can fit cumulative odds model as a special case of interval.logitsurv.discrete

Author(s)

Thomas Scheike

Examples

```
data(bmt)
dfactor(bmt) <- cause1f~cause
drelevel(bmt,ref=3) <- cause3f~cause
dlevels(bmt)

mreg <- mlogit(cause1f~+1,bmt)
summary(mreg)

mreg <- mlogit(cause1f~tcell+platelet,bmt)
summary(mreg)

mreg3 <- mlogit(cause3f~tcell+platelet,bmt)
summary(mreg3)

## inverse information standard errors
lava::estimate(coef=mreg3$coef,vcov=mreg3$II)

## predictions based on seen response or not
newdata <- data.frame(tcell=c(1,1,1),platelet=c(0,1,1),cause1f=c("2","1","0"))
## all probabilities
predict(mreg,newdata,response=FALSE)
## only probability of seen response
predict(mreg,newdata)
```

`multcif` *Multivariate Cumulative Incidence Function example data set*

Description

Multivariate Cumulative Incidence Function example data set

Source

Simulated data

`np` *np data set*

Description

np data set

Source

Simulated data

`npc` *For internal use*

Description

For internal use

Author(s)

Klaus K. Holst

`phreg` *Fast Cox PH regression*

Description

Fast Cox PH regression Robust variance is default variance with the summary.

Usage

```
phreg(formula, data, offset = NULL, weights = NULL, ...)
```

Arguments

`formula`	formula with 'Surv' outcome (see `coxph`)
`data`	data frame
`offset`	offsets for Cox model
`weights`	weights for Cox score equations
`...`	Additional arguments to lower level funtions

Details

influence functions (iid) will follow numerical order of given cluster variable so ordering after $id will give iid in order of data-set.

Author(s)

Klaus K. Holst, Thomas Scheike

Examples

```
data(TRACE)
dcut(TRACE) <- ~.
out1 <- phreg(Surv(time,status==9)~vf+chf+strata(wmicat.4),data=TRACE)
## robust standard errors default
summary(out1)

par(mfrow=c(1,2))
plot(out1)

## computing robust variance for baseline
rob1 <- robust.phreg(out1)
plot(rob1,se=TRUE,robust=TRUE)

## taking iid decomposition of regression parameters
betaiiid <- lava::iid(out1)

## making iid decomposition of baseline at a specific time-point
Aiiid <- mets::IIDbaseline.phreg(out1,time=30)
```

`phregR` *Fast Cox PH regression and calculations done in R to make play and adjustments easy*

Description

Fast Cox PH regression with R implementation to play and adjust in R function: FastCoxPLstrataR

Usage

```
phregR(formula, data, offset = NULL, weights = NULL, ...)
```

Arguments

`formula`	formula with 'Surv' outcome (see `coxph`)
`data`	data frame
`offset`	offsets for cox model
`weights`	weights for Cox score equations
`...`	Additional arguments to lower level funtions

Details

Robust variance is default variance with the summary.

influence functions (iid) will follow numerical order of given cluster variable so ordering after $id will give iid in order of data-set.

Author(s)

Klaus K. Holst, Thomas Scheike

`phreg_IPTW` *IPTW Cox, Inverse Probaibilty of Treatment Weighted Cox regression*

Description

Fits Cox model with treatment weights

$$w(A) = \sum_a I(A = a)/\pi(a|X)$$

, where

$$\pi(a|X) = P(A = a|X)$$

. Computes standard errors via influence functions that are returned as the IID argument. Propensity scores are fitted using either logistic regression (glm) or the multinomial model (mlogit) when there are than treatment categories. The treatment needs to be a factor and is identified on the rhs of the "treat.model". Recurrent events can be considered with start,stop structure and then cluster(id) must be specified. Robust standard errors are computed in all cases.

Usage

```
phreg_IPTW(
  formula,
  data,
  treat.model = NULL,
  treat.var = NULL,
  weights = NULL,
  estpr = 1,
  pi0 = 0.5,
  se.cluster = NULL,
  ...
)
```

Arguments

`formula`	for phreg
`data`	data frame for risk averaging
`treat.model`	propensity score model (binary or multinomial)

`treat.var`	a 1/0 variable that indicates when treatment is given and the propensity score is computed
`weights`	may be given, and then uses weights*w(A) as the weights
`estpr`	(=1, default) to estimate propensity scores and get infuence function contribution to uncertainty
`pi0`	fixed simple weights
`se.cluster`	to compute GEE type standard errors when additional cluster structure is present
`...`	arguments for phreg call

Details

Time-dependent propensity score weights can also be computed when treat.var is used, it must be 1 at the time of first (A_0) and 2nd treatment (A_1), then uses weights

$$w_0(A_0) * w_1(A_1)^{t > T_r}$$

where

$$T_r$$

is time of 2nd randomization.

Author(s)

Thomas Scheike

Examples

```
library(mets)
data <- mets:::simLT(0.7,100,beta=0.3,betac=0,ce=1,betao=0.3)
dfactor(data) <- Z.f~Z
out <- phreg_IPTW(Surv(time,status)~Z.f,data=data,treat.model=Z.f~X)
summary(out)
```

`phreg_rct` *Lu-Tsiatis More Efficient Log-Rank for Randomized studies with baseline covariates*

Description

Efficient implementation of the Lu-Tsiatis improvement using baseline covariates, extended to competing risks and recurrent events. Results almost equivalent with the speffSurv function of the speff2trial function in the survival case. A dynamic censoring augmentation regression is also computed to gain even more from the censoring augmentation. Furhter, we also deal with twostage randomizations. The function was implemented to deal with recurrent events (start,stop) + cluster, and more examples in vignette.

Usage

```
phreg_rct(
  formula,
  data,
  cause = 1,
  cens.code = 0,
  typesR = c("R0", "R1", "R01"),
  typesC = c("C", "dynC"),
  weights = NULL,
  augmentR0 = NULL,
  augmentR1 = NULL,
  augmentC = NULL,
  treat.model = ~+1,
  RCT = TRUE,
  treat.var = NULL,
  km = TRUE,
  level = 0.95,
  cens.model = NULL,
  estpr = 1,
  pi0 = 0.5,
  base.augment = FALSE,
  return.augmentR0 = FALSE,
  mlogit = FALSE,
  ...
)
```

Arguments

`formula`	formula with 'Surv' or 'Event' outcome (see `coxph`) and treatment (randomization 0/1)
`data`	data frame
`cause`	to use for competing risks, recurrent events data
`cens.code`	to use for competing risks, recurrent events data
`typesR`	augmentations used for randomization
`typesC`	augmentations used for censoring
`weights`	weights for score equation
`augmentR0`	formula for the randomization augmentation (~age+sex)
`augmentR1`	formula for the randomization augmentation (~age+sex)
`augmentC`	formula for the censoring augmentation (~age+sex)
`treat.model`	propensity score model, default is ~+1, assuming RCT study
`RCT`	if false will use propensity score adjustment for marginal model
`treat.var`	in case of twostage randomization, this variable is 1 for the treatment times, if start,stop then default assumes that only one treatment at first record
`km`	use Kaplan-Meier for the censoring weights (stratified on treatment)

`level`	of confidence intervals
`cens.model`	default is censoring model ~strata(treatment) but any model can be used to make censoring martingales
`estpr`	estimates propensity scores
`pi0`	possible fixed propensity scores for randomizations
`base.augment`	TRUE to covariate augment baselines (only for R0 augmentation)
`return.augmentR0`	to return augmentation data
`mlogit`	if TRUE then forces use of this function for propensity scores, default for binary treatment is glm
`...`	Additional arguments to phreg function

Author(s)

Thomas Scheike

References

Lu, Tsiatis (2008), Improving the efficiency of the log-rank test using auxiliary covariates, Biometrika, 679–694

Scheike et al. (2024), WIP, Two-stage randomization for recurrent events,

Examples

```
## Lu, Tsiatis simulation
data <- mets:::simLT(0.7,100)
dfactor(data) <- Z.f~Z

out <- phreg_rct(Surv(time,status)~Z.f,data=data,augmentR0=~X,augmentC=~factor(Z):X)
summary(out)
```

`plack.cif` *plack Computes concordance for or.cif based model, that is Plackett random effects model*

Description

.. content for description (no empty lines) ..

Usage

```
plack.cif(cif1, cif2, object)
```

Arguments

`cif1`	Cumulative incidence of first argument.
`cif2`	Cumulative incidence of second argument.
`object`	or.cif object with dependence parameters.

Author(s)

Thomas Scheike

`plot.phreg` *Plotting the baselines of stratified Cox*

Description

Plotting the baselines of stratified Cox

Usage

```
## S3 method for class 'phreg'
plot(x, ...)
```

Arguments

`x`	phreg object
`...`	Additional arguments to baseplot funtion

Author(s)

Klaus K. Holst, Thomas Scheike

Examples

```
data(TRACE)
dcut(TRACE) <- ~.
out1 <- phreg(Surv(time,status==9)~vf+chf+strata(wmicat.4),data=TRACE)

par(mfrow=c(2,2))
plot(out1)
plot(out1,stratas=c(0,3))
plot(out1,stratas=c(0,3),col=2:3,lty=1:2,se=TRUE)
plot(out1,stratas=c(0),col=2,lty=2,se=TRUE,polygon=FALSE)
plot(out1,stratas=c(0),col=matrix(c(2,1,3),1,3),lty=matrix(c(1,2,3),1,3),se=TRUE,polygon=FALSE)
```

`pmvn` *Multivariate normal distribution function*

Description

Multivariate normal distribution function

Usage

```
pmvn(lower, upper, mu, sigma, cor = FALSE)
```

Arguments

`lower`	lower limits
`upper`	upper limits
`mu`	mean vector
`sigma`	variance matrix or vector of correlation coefficients
`cor`	if TRUE sigma is treated as standardized (correlation matrix)

Examples

```
lower <- rbind(c(0,-Inf),c(-Inf,0))
upper <- rbind(c(Inf,0),c(0,Inf))
mu <- rbind(c(1,1),c(-1,1))
sigma <- diag(2)+1
pmvn(lower=lower,upper=upper,mu=mu,sigma=sigma)
```

`predict.phreg` *Predictions from proportional hazards model*

Description

Predictions from proportional hazards model

Usage

```
## S3 method for class 'phreg'
predict(
  object,
  newdata,
  times = NULL,
  individual.time = FALSE,
  tminus = FALSE,
  se = TRUE,
  robust = FALSE,
```

```
  conf.type = "log",
  conf.int = 0.95,
  km = FALSE,
  ...
)
```

Arguments

`object`	phreg object
`newdata`	data.frame
`times`	Time where to predict variable, default is all time-points from the object sorted
`individual.time`	to use one (individual) time per subject, and then newdata and times have same length and makes only predictions for these individual times.
`tminus`	to make predictions in T- that is strictly before given times, useful for IPCW techniques
`se`	with standard errors and upper and lower confidence intervals.
`robust`	to get robust se's also default for most functions (uses robse.cumhaz otherwise se.cumhaz).
`conf.type`	transformation for suvival estimates, default is log
`conf.int`	significance level
`km`	to use Kaplan-Meier product-limit for baseline $$S_{s0}(t) = (1 - dA_{s0}(t))$$, otherwise take exp of cumulative baseline.
`...`	Additional arguments to plot functions

`predictRisk` *Risk predictions to work with riskRegression package*

Description

Risk predictions to work with riskRegression package

Usage

```
predictRisk(object, ...)
```

Arguments

`object`	phreg/binreg/cifreg object
`...`	additional arguments to lower level functions

Author(s)

Thomas Scheike

`predictRisk.binreg` *Risk predictions to work with riskRegression package*

Description

Risk predictions to work with riskRegression package

Usage

```
## S3 method for class 'binreg'
predictRisk(object, newdata, cause, times = NULL, ...)
```

Arguments

`object`	phreg/binreg/cifreg object
`newdata`	data.frame on which to make new predictions
`cause`	cause (cif) to predict
`times`	times for predictions
`...`	additional arguments to lower level functions

`print.casewise` *prints Concordance test*

Description

prints Concordance test

Usage

```
## S3 method for class 'casewise'
print(x, digits = 3, ...)
```

Arguments

`x`	output from casewise.test
`digits`	number of digits
`...`	Additional arguments to lower level functions

Author(s)

Thomas Scheike

---

prob.exceed.recurrent *Estimation of probability of more that k events for recurrent events process*

Description

Estimation of probability of more that k events for recurrent events process where there is terminal event, based on this also estimate of variance of recurrent events. The estimator is based on cumulative incidence of exceeding "k" events. In contrast the probability of exceeding k events can also be computed as a counting process integral, and this is implemented in prob.exceedRecurrent

Usage

```
prob.exceed.recurrent(
  formula,
  data,
  cause = 1,
  death.code = 2,
  cens.code = 0,
  exceed = NULL,
  marks = NULL,
  cifmets = TRUE,
  all.cifs = FALSE,
  ...
)
```

Arguments

`formula`	formula
`data`	data-frame
`cause`	of interest
`death.code`	for status
`cens.code`	censoring codes
`exceed`	values (if not given then all observed values)
`marks`	may be give for jump-times and then exceed values needs to be specified
`cifmets`	if true uses cif of mets package rather than prodlim
`all.cifs`	if true then returns list of all fitted objects in cif.exceed
`...`	Additional arguments to lower level funtions

Author(s)

Thomas Scheike

References

Scheike, Eriksson, Tribler (2019) The mean, variance and correlation for bivariate recurrent events with a terminal event, JRSS-C

Examples

```
data(hfactioncpx12)
dtable(hfactioncpx12,~status)

oo <- prob.exceed.recurrent(Event(entry,time,status)~cluster(id),
        hfactioncpx12,cause=1,death.code=2)
plot(oo)
```

`prt` *Prostate data set*

Description

Prostate data set

Source

Simulated data

`random.cif` *Random effects model for competing risks data*

Description

Fits a random effects model describing the dependence in the cumulative incidence curves for subjects within a cluster. Given the gamma distributed random effects it is assumed that the cumulative incidence curves are indpendent, and that the marginal cumulative incidence curves are on the form

$$P(T \leq t, cause = 1 | x, z) = P_1(t, x, z) = 1 - exp(-x^T A(t) exp(z^T \beta))$$

We allow a regression structure for the random effects variances that may depend on cluster covariates.

Usage

```
random.cif(
  cif,
  data,
  cause = NULL,
  cif2 = NULL,
  cause1 = 1,
  cause2 = 1,
  cens.code = NULL,
  cens.model = "KM",
  Nit = 40,
  detail = 0,
  clusters = NULL,
  theta = NULL,
  theta.des = NULL,
  sym = 1,
  step = 1,
  same.cens = FALSE,
  var.link = 0,
  score.method = "nr",
  entry = NULL,
  trunkp = 1,
  ...
)
```

Arguments

`cif`	a model object from the comp.risk function with the marginal cumulative incidence of cause2, i.e., the event that is conditioned on, and whose odds the comparision is made with respect to
`data`	a data.frame with the variables.
`cause`	specifies the causes related to the death times, the value cens.code is the censoring value.
`cif2`	specificies model for cause2 if different from cause1.
`cause1`	cause of first coordinate.
`cause2`	cause of second coordinate.
`cens.code`	specificies the code for the censoring if NULL then uses the one from the marginal cif model.
`cens.model`	specified which model to use for the ICPW, KM is Kaplan-Meier alternatively it may be "cox"
`Nit`	number of iterations for Newton-Raphson algorithm.
`detail`	if 0 no details are printed during iterations, if 1 details are given.
`clusters`	specifies the cluster structure.
`theta`	specifies starting values for the cross-odds-ratio parameters of the model.
`theta.des`	specifies a regression design for the cross-odds-ratio parameters.

`sym`	1 for symmetry 0 otherwise
`step`	specifies the step size for the Newton-Raphson algorith.m
`same.cens`	if true then censoring within clusters are assumed to be the same variable, default is independent censoring.
`var.link`	if var.link=1 then var is on log-scale.
`score.method`	default uses "nlminb" optimzer, alternatively, use the "nr" algorithm.
`entry`	entry-age in case of delayed entry. Then two causes must be given.
`trunkp`	gives probability of survival for delayed entry, and related to entry-ages given above.
`...`	extra arguments.

Value

returns an object of type 'cor'. With the following arguments:

`theta`	estimate of proportional odds parameters of model.
`var.theta`	variance for gamma.
`hess`	the derivative of the used score.
`score`	scores at final stage.
`score`	scores at final stage.
`theta.iid`	matrix of iid decomposition of parametric effects.

Author(s)

Thomas Scheike

References

A Semiparametric Random Effects Model for Multivariate Competing Risks Data, Scheike, Zhang, Sun, Jensen (2010), Biometrika.

Cross odds ratio Modelling of dependence for Multivariate Competing Risks Data, Scheike and Sun (2012), work in progress.

Examples

```
## Reduce Ex.Timings
d <- simnordic.random(5000,delayed=TRUE,cordz=0.5,cormz=2,lam0=0.3,country=TRUE)
times <- seq(50,90,by=10)
add1 <- timereg::comp.risk(Event(time,cause)~-1+factor(country)+cluster(id),data=d,
times=times,cause=1,max.clust=NULL)

### making group indidcator
mm <- model.matrix(~-1+factor(zyg),d)

out1<-random.cif(add1,data=d,cause1=1,cause2=1,theta=1,same.cens=TRUE)
summary(out1)
```

```
 out2<-random.cif(add1,data=d,cause1=1,cause2=1,theta=1,
   theta.des=mm,same.cens=TRUE)
 summary(out2)

########################################
##### 2 different causes
########################################

 add2 <- timereg::comp.risk(Event(time,cause)~-1+factor(country)+cluster(id),data=d,
                 times=times,cause=2,max.clust=NULL)
 out3 <- random.cif(add1,data=d,cause1=1,cause2=2,cif2=add2,sym=1,same.cens=TRUE)
 summary(out3) ## negative dependence

out4 <- random.cif(add1,data=d,cause1=1,cause2=2,cif2=add2,theta.des=mm,sym=1,same.cens=TRUE)
 summary(out4) ## negative dependence
```

---

rchaz *Simulation of Piecewise constant hazard model (Cox).*

Description

Simulates data from piecwise constant baseline hazard that can also be of Cox type. Censor data at highest value of the break points.

Usage

```
rchaz(
  cumhazard,
  rr,
  n = NULL,
  entry = NULL,
  cum.hazard = TRUE,
  cause = 1,
  extend = FALSE
)
```

Arguments

`cumhazard`	cumulative hazard, or piece-constant rates for periods defined by first column of input.
`rr`	relative risk for simulations, alternatively when rr=1 specify n
`n`	number of simulation if rr not given
`entry`	delayed entry time for simuations.
`cum.hazard`	specifies wheter input is cumulative hazard or rates.
`cause`	name of cause
`extend`	to extend piecewise constant with constant rate. Default is average rate over time from cumulative (when TRUE), if numeric then uses given rate.

Details

For a piecewise linear cumulative hazard the inverse is easy to compute with and delayed entry x we compute

$$\Lambda^{-1}(\Lambda(x) + E/RR)$$

, where RR are the relative risks and E is exponential with mean 1. This quantity has survival function

$$P(T > t|T > x) = exp(-RR(\Lambda(t) - \Lambda(x)))$$

.

Author(s)

Thomas Scheike

Examples

```
chaz <-  c(0,1,1.5,2,2.1)
breaks <- c(0,10,   20,  30,   40)
cumhaz <- cbind(breaks,chaz)
n <- 10
X <- rbinom(n,1,0.5)
beta <- 0.2
rrcox <- exp(X * beta)

pctime <- rchaz(cumhaz,n=10)
pctimecox <- rchaz(cumhaz,rrcox,entry=runif(n))
```

`rchazC` *Piecewise constant hazard distribution*

Description

Piecewise constant hazard distribution

Usage

```
rchazC(base1, rr, entry)
```

Arguments

`base1`	baseline
`rr`	relative risk terms
`entry`	entry times for left truncation

`rcrisk` *Simulation of Piecewise constant hazard models with two causes (Cox).*

Description

Simulates data from piecwise constant baseline hazard that can also be of Cox type. Censor data at highest value of the break points for either of the cumulatives.

Usage

```
rcrisk(
  cumhaz1,
  cumhaz2,
  rr1,
  rr2,
  n = NULL,
  cens = NULL,
  rrc = NULL,
  extend = TRUE,
  ...
)
```

Arguments

`cumhaz1`	cumulative hazard of cause 1
`cumhaz2`	cumulative hazard of cause 1
`rr1`	number of simulations or vector of relative risk for simuations.
`rr2`	number of simulations or vector of relative risk for simuations.
`n`	number of simulation if rr not given
`cens`	to censor further , rate or cumumlative hazard
`rrc`	retlativ risk for censoring.
`extend`	to extend the cumulative hazards to largest end-point
`...`	arguments for rchaz

Author(s)

Thomas Scheike

Examples

```
data(bmt);
cox1 <- phreg(Surv(time,cause==1)~tcell+platelet,data=bmt)
cox2 <- phreg(Surv(time,cause==2)~tcell+platelet,data=bmt)
```

```
X1 <- bmt[,c("tcell","platelet")]
n <- 100
xid <- sample(1:nrow(X1),n,replace=TRUE)
Z1 <- X1[xid,]
Z2 <- X1[xid,]
rr1 <- exp(as.matrix(Z1) %*% cox1$coef)
rr2 <- exp(as.matrix(Z2) %*% cox2$coef)

d <-  rcrisk(cox1$cum,cox2$cum,rr1,rr2)
dd <- cbind(d,Z1)

scox1 <- phreg(Surv(time,status==1)~tcell+platelet,data=dd)
scox2 <- phreg(Surv(time,status==2)~tcell+platelet,data=dd)
par(mfrow=c(1,2))
plot(cox1); plot(scox1,add=TRUE)
plot(cox2); plot(scox2,add=TRUE)
cbind(cox1$coef,scox1$coef,cox2$coef,scox2$coef)
```

`recreg` *Recurrent events regression with terminal event*

Description

Fits Ghosh-Lin IPCW Cox-type model

Usage

```
recreg(
  formula,
  data,
  cause = 1,
  death.code = 2,
  cens.code = 0,
  cens.model = ~1,
  weights = NULL,
  offset = NULL,
  Gc = NULL,
  wcomp = NULL,
  marks = NULL,
  augmentation.type = c("lindyn.augment", "lin.augment"),
  ...
)
```

Arguments

`formula`	formula with 'Event' outcome
`data`	data frame

`cause`	of interest (1 default)
`death.code`	codes for death (terminating event, 2 default)
`cens.code`	code of censoring (0 default)
`cens.model`	for stratified Cox model without covariates
`weights`	weights for score equations
`offset`	offsets for model
`Gc`	censoring weights for time argument, default is to calculate these with a Kaplan-Meier estimator, should then give G_c(T_i-)
`wcomp`	weights for composite outcome, so when cause=c(1,3), we might have wcomp=c(1,2).
`marks`	a mark value can be specified, this is vector from the data-frame where the mark value can be found at all events
`augmentation.type`	of augmentation when augmentation model is given
`...`	Additional arguments to lower level funtions

Details

For Cox type model :

$$E(dN_1(t)|X) = \mu_0(t)dtexp(X^T\beta)$$

by solving Cox-type IPCW weighted score equations

$$\int (Z - E(t))w(t)dN_1(t)$$

where

$$w(t) = G(t)(I(T_i \wedge t < C_i)/G_c(T_i \wedge t))$$

and

$$E(t) = S_1(t)/S_0(t)$$

and

$$S_j(t) = \sum X_i^j w_i(t) \exp(X_i^T\beta)$$

.

The iid decomposition of the beta's are on the form

$$\int (Z - E)w(t)dM_1 + \int q(s)/p(s)dM_c$$

and returned as iid.

Events, deaths and censorings are specified via stop start structure and the Event call, that via a status vector and cause (code), censoring-codes (cens.code) and death-codes (death.code) indentifies these. See example and vignette.

Author(s)

Thomas Scheike

Examples

```
## data with no ties
library(mets)
data(hfactioncpx12)
hf <- hfactioncpx12
hf$x <- as.numeric(hf$treatment)
dd <- data.frame(treatment=levels(hf$treatment),id=1)

gl <- recreg(Event(entry,time,status)~treatment+cluster(id),data=hf,cause=1,death.code=2)
summary(gl)
pgl <- predict(gl,dd,se=1); plot(pgl,se=1)

## censoring stratified after treatment
gls <- recreg(Event(entry,time,status)~treatment+cluster(id),data=hf,
cause=1,death.code=2,cens.model=~strata(treatment))
summary(gls)

## IPCW at 2 years
ll2 <- recregIPCW(Event(entry,time,status)~treatment+cluster(id),data=hf,
cause=1,death.code=2,time=2,cens.model=~strata(treatment))
summary(ll2)
```

`recurrentMarginal` *Fast recurrent marginal mean when death is possible*

Description

Fast Marginal means of recurrent events using the Lin and Ghosh (2000) standard errors. Fitting two models for death and recurent events these are combined to prducte the estimator

$$\int_0^t S(u|x=0) dR(u|x=0)$$

the mean number of recurrent events, here

$$S(u|x=0)$$

is the probability of survival for the baseline group, and

$$dR(u|x=0)$$

is the hazard rate of an event among survivors for the baseline. Here

$$S(u|x=0)$$

is estimated by

$$exp(-\Lambda_d(u|x=0)$$

with

$$\Lambda_d(u|x=0)$$

being the cumulative baseline for death.

Usage

```
recurrentMarginal(formula, data, cause = 1, ..., death.code = 2)
```

Arguments

`formula`	with Event object
`data`	data frame for computation
`cause`	of interest (1 default)
`...`	Additional arguments to lower level funtions
`death.code`	codes for death (terminating event, 2 default)

Details

Assumes no ties in the sense that jump times needs to be unique, this is particularly so for the stratified version.

Author(s)

Thomas Scheike

References

Cook, R. J. and Lawless, J. F. (1997) Marginal analysis of recurrent events and a terminating event. Statist. Med., 16, 911–924. Ghosh and Lin (2002) Nonparametric Analysis of Recurrent events and death, Biometrics, 554–562.

Examples

```
library(mets)
data(hfactioncpx12)
hf <- hfactioncpx12
hf$x <- as.numeric(hf$treatment)

##  to fit non-parametric models with just a baseline
xr <- phreg(Surv(entry,time,status==1)~cluster(id),data=hf)
dr <- phreg(Surv(entry,time,status==2)~cluster(id),data=hf)
par(mfrow=c(1,3))
plot(dr,se=TRUE)
title(main="death")
plot(xr,se=TRUE)
### robust standard errors
rxr <-  robust.phreg(xr,fixbeta=1)
plot(rxr,se=TRUE,robust=TRUE,add=TRUE,col=4)

## marginal mean of expected number of recurrent events
## out <- recurrentMarginalPhreg(xr,dr)
## summary(out,times=1:5)

## marginal mean using formula
outN <- recurrentMarginal(Event(entry,time,status)~cluster(id),hf,cause=1,death.code=2)
```

```
plot(outN,se=TRUE,col=2,add=TRUE)
summary(outN,times=1:5)

########################################################################
###   with strata     ##################################################
########################################################################
out <- recurrentMarginal(Event(entry,time,status)~strata(treatment)+cluster(id),
                         data=hf,cause=1,death.code=2)
plot(out,se=TRUE,ylab="marginal mean",col=1:2)

summary(out,times=1:5)
```

`resmean.phreg` *Restricted mean for stratified Kaplan-Meier or Cox model with martingale standard errors*

Description

Restricted mean for stratified Kaplan-Meier or stratified Cox with martingale standard error. Standard error is computed using linear interpolation between standard errors at jump-times. Plots gives restricted mean at all times. Years lost can be computed based on this and decomposed into years lost for different causes using the cif.yearslost function that is based on integrating the cumulative incidence functions. One particular feature of these functions are that the restricted mean and years-lost are computed for all event times as functions and can be plotted/viewed. When times are given and beyond the last event time withn a strata the curves are extrapolated using the estimates of cumulative incidence.

Usage

```
resmean.phreg(x, times = NULL, covs = NULL, ...)
```

Arguments

`x`	phreg object
`times`	possible times for which to report restricted mean
`covs`	possible covariate for Cox model
`...`	Additional arguments to lower level funtions

Author(s)

Thomas Scheike

Examples

```
data(bmt); bmt$time <- bmt$time+runif(408)*0.001
out1 <- phreg(Surv(time,cause!=0)~strata(tcell,platelet),data=bmt)

rm1 <- resmean.phreg(out1,times=10*(1:6))
summary(rm1)
par(mfrow=c(1,2))
plot(rm1,se=1)
plot(rm1,years.lost=TRUE,se=1)

## years.lost decomposed into causes
drm1 <- cif.yearslost(Event(time,cause)~strata(tcell,platelet),data=bmt,times=10*(1:6))
par(mfrow=c(1,2)); plot(drm1,cause=1,se=1); plot(drm1,cause=2,se=1);
summary(drm1)
```

`resmeanATE` *Average Treatment effect for Restricted Mean for censored competing risks data using IPCW*

Description

Under the standard causal assumptions we can estimate the average treatment effect E(Y(1) - Y(0)). We need Consistency, ignorability (Y(1), Y(0) indep A given X), and positivity.

Usage

```
resmeanATE(formula, data, model = "exp", ...)
```

Arguments

`formula`	formula with 'Event' outcome
`data`	data-frame
`model`	possible exp model for relevant mean model that is exp(X^t beta)
`...`	Additional arguments to pass to binregATE

Details

The first covariate in the specification of the competing risks regression model must be the treatment effect that is a factor. If the factor has more than two levels then it uses the mlogit for propensity score modelling. We consider the outcome mint(T;tau) or I(epsion==cause1)(t- min(T;t)) that gives years lost due to cause "cause" depending on the number of causes. The default model is the exp(X^ beta) and otherwise a linear model is used.

Estimates the ATE using the the standard binary double robust estimating equations that are IPCW censoring adjusted.

Author(s)

Thomas Scheike

Examples

```
library(mets); data(bmt); bmt$event <- bmt$cause!=0; dfactor(bmt) <- tcell~tcell
out <- resmeanATE(Event(time,event)~tcell+platelet,data=bmt,time=40,treat.model=tcell~platelet)
summary(out)

out1 <- resmeanATE(Event(time,cause)~tcell+platelet,data=bmt,cause=1,time=40,
                   treat.model=tcell~platelet)
summary(out1)
```

`resmeanIPCW` *Restricted IPCW mean for censored survival data*

Description

Simple and fast version for IPCW regression for just one time-point thus fitting the model

$$E(min(T,t)|X) = exp(X^T beta)$$

or in the case of competing risks data

$$E(I(epsilon = 1)(t - min(T,t))|X) = exp(X^T beta)$$

thus given years lost to cause, see `binreg` for the arguments.

Usage

```
resmeanIPCW(formula, data, ...)
```

Arguments

`formula`	formula with outcome on Event form
`data`	data frame
`...`	Additional arguments to lower level funtions

Details

When the status is binary assumes it is a survival setting and default is to consider outcome Y=min(T,t), if status has more than two levels, then computes years lost due to the specified cause, thus using the response

$$Y = (t - min(T,t))I(status = cause)$$

Based on binomial regresion IPCW response estimating equation:

$$X(\Delta(min(T,t))Y/G_c(min(T,t)) - exp(X^T beta)) = 0$$

for IPCW adjusted responses. Here

$$\Delta(min(T,t)) = I(min(T,t) \leq C)$$

is indicator of being uncensored. Concretely, the uncensored observations at time t will count those with an event (of any type) before t and those with a censoring time at t or further out. One should therefore be a bit careful when data has been constructed such that some of the event times T are equivalent to t.

Can also solve the binomial regresion IPCW response estimating equation:

$$h(X)X(\Delta(min(T,t))Y/G_c(min(T,t)) - exp(X^T beta)) = 0$$

for IPCW adjusted responses where h is given as an argument together with iid of censoring with h.

By using appropriately the h argument we can also do the efficient IPCW estimator estimator.

Variance is based on

$$\sum w_i^2$$

also with IPCW adjustment, and naive.var is variance under known censoring model.

When Ydirect is given it solves :

$$X(\Delta(min(T,t))Ydirect/G_c(min(T,t)) - exp(X^T beta)) = 0$$

for IPCW adjusted responses.

The actual influence (type="II") function is based on augmenting with

$$X \int_0^t E(Y|T > s)/G_c(s) dM_c(s)$$

and alternatively just solved directly (type="I") without any additional terms.

Censoring model may depend on strata.

Author(s)

Thomas Scheike

Examples

```
data(bmt); bmt$time <- bmt$time+runif(nrow(bmt))*0.001
# E( min(T;t) | X ) = exp( a+b X) with IPCW estimation
out <- resmeanIPCW(Event(time,cause!=0)~tcell+platelet+age,bmt,
                time=50,cens.model=~strata(platelet),model="exp")
summary(out)

### same as Kaplan-Meier for full censoring model
bmt$int <- with(bmt,strata(tcell,platelet))
out <- resmeanIPCW(Event(time,cause!=0)~-1+int,bmt,time=30,
                             cens.model=~strata(platelet,tcell),model="lin")
estimate(out)
out1 <- phreg(Surv(time,cause!=0)~strata(tcell,platelet),data=bmt)
rm1 <- resmean.phreg(out1,times=30)
summary(rm1)

## competing risks years-lost for cause 1
```

```
out <- resmeanIPCW(Event(time,cause)~-1+int,bmt,time=30,cause=1,
                            cens.model=~strata(platelet,tcell),model="lin")
estimate(out)
## same as integrated cumulative incidence
rmc1 <- cif.yearslost(Event(time,cause)~strata(tcell,platelet),data=bmt,times=30)
summary(rmc1)
```

`rpch` *Piecewise constant hazard distribution*

Description

Piecewise constant hazard distribution

Usage

```
rpch(n, lambda = 1, breaks = c(0, Inf))
```

Arguments

`n`	sample size
`lambda`	rate parameters
`breaks`	time cut-points

`sim.cause.cox` *Simulation of cause specific from Cox models.*

Description

Simulates data that looks like fit from cause specific Cox models. Censor data automatically. When censoring is given in the list of causes this will give censoring that looks like the data. Covariates are drawn from data-set with replacement. This gives covariates like the data.

Usage

```
sim.cause.cox(coxs,n,data=NULL,cens=NULL,rrc=NULL,...)
```

Arguments

`coxs`	list of cox models.
`n`	number of simulations.
`data`	to extract covariates for simulations (draws from observed covariates).
`cens`	specifies censoring model, if NULL then only censoring for each cause at end of last event of this type. if "is.matrix" then uses cumulative. hazard given, if "is.scalar" then uses rate for exponential, and if not given then takes average rate of in simulated data from cox model. But censoring can also be given as a cause.
`rrc`	possible vector of relative risk for cox-type censoring.
`...`	arguments for rchaz, for example entry-time

Author(s)

Thomas Scheike

Examples

```
nsim <- 100; data(bmt)

cox1 <- phreg(Surv(time,cause==1)~strata(tcell)+platelet,data=bmt)
cox2 <- phreg(Surv(time,cause==2)~tcell+strata(platelet),data=bmt)
coxs <- list(cox1,cox2)
dd <- sim.cause.cox(coxs,nsim,data=bmt)
scox1 <- phreg(Surv(time,status==1)~strata(tcell)+platelet,data=dd)
scox2 <- phreg(Surv(time,status==2)~tcell+strata(platelet),data=dd)
cbind(cox1$coef,scox1$coef)
cbind(cox2$coef,scox2$coef)
par(mfrow=c(1,2))
plot(cox1); plot(scox1,add=TRUE);
plot(cox2); plot(scox2,add=TRUE);
```

`sim.cif` *Simulation of output from Cumulative incidence regression model*

Description

Simulates data that looks like fit from fitted cumulative incidence model

Usage

```
sim.cif(cif,n,data=NULL,Z=NULL,drawZ=TRUE,cens=NULL,rrc=NULL,cumstart=c(0,0),...)
```

Arguments

`cif`	output form prop.odds.subdist or ccr (cmprsk), can also call invsubdist with with cumulative and linear predictor
`n`	number of simulations.
`data`	to extract covariates for simulations (draws from observed covariates).
`Z`	to use these covariates for simulation rather than drawing new ones.
`drawZ`	to random sample from Z or not
`cens`	specifies censoring model, if "is.matrix" then uses cumulative hazard given, if "is.scalar" then uses rate for exponential, and if not given then takes average rate of in simulated data from cox model.
`rrc`	possible vector of relative risk for cox-type censoring.
`cumstart`	to start cumulatives at time 0 in 0.
`...`	arguments for invsubdist

Author(s)

Thomas Scheike

Examples

```
data(bmt)

scif <-  cifreg(Event(time,cause)~tcell+platelet+age,data=bmt,cause=1,prop=NULL)
summary(scif)
plot(scif)
################################################################
#  simulating several causes with specific cumulatives
################################################################

cif1 <-  cifreg(Event(time,cause)~tcell+age,data=bmt,cause=1,prop=NULL)
cif2 <-  cifreg(Event(time,cause)~tcell+age,data=bmt,cause=2,prop=NULL)
# dd <- sim.cifsRestrict(list(cif1,cif2),200,data=bmt)
dd <- sim.cifs(list(cif1,cif2),200,data=bmt)
scif1 <-  cifreg(Event(time,cause)~tcell+age,data=dd,cause=1)
scif2 <-  cifreg(Event(time,cause)~tcell+age,data=dd,cause=2)

par(mfrow=c(1,2))
plot(cif1); plot(scif1,add=TRUE,col=2)
plot(cif2); plot(scif2,add=TRUE,col=2)
```

`sim.cox` *Simulation of output from Cox model.*

Description

Simulates data that looks like fit from Cox model. Censor data automatically for highest value of the event times by using cumulative hazard.

Usage

```
sim.cox(cox,n,data=NULL,cens=NULL,rrc=NULL,entry=NULL,rr=NULL,Z=NULL,extend=TRUE,...)
```

Arguments

`cox`	output form coxph or cox.aalen model fitting cox model.
`n`	number of simulations.
`data`	to extract covariates for simulations (draws from observed covariates).
`cens`	specifies censoring model, if "is.matrix" then uses cumulative hazard given, if "is.scalar" then uses rate for exponential, and if not given then takes average rate of in simulated data from cox model.
`rrc`	possible vector of relative risk for cox-type censoring.
`entry`	delayed entry variable for simulation.

`rr`	possible vector of relative risk for cox model.
`Z`	possible covariates to use instead of sampling from data.
`extend`	to extend possible stratified baselines to largest end-point
`...`	arguments for rchaz, for example entry-time.

Author(s)

Thomas Scheike

Examples

```
data(sTRACE)
nsim <- 100
coxs <-  phreg(Surv(time,status==9)~strata(chf)+vf+wmi,data=sTRACE)
sim3 <- sim.phreg(coxs,nsim,data=sTRACE)
cc <-   phreg(Surv(time, status)~strata(chf)+vf+wmi,data=sim3)
cbind(coxs$coef,cc$coef)
plot(coxs,col=1); plot(cc,add=TRUE,col=2)
```

`simAalenFrailty` *Simulate from the Aalen Frailty model*

Description

Simulate observations from Aalen Frailty model with Gamma distributed frailty and constant intensity.

Usage

```
simAalenFrailty(
  n = 5000,
  theta = 0.3,
  K = 2,
  beta0 = 1.5,
  beta = 1,
  cens = 1.5,
  cuts = 0,
  ...
)
```

Arguments

`n`	Number of observations in each cluster
`theta`	Dependence paramter (variance of frailty)
`K`	Number of clusters

`beta0`	Baseline (intercept)
`beta`	Effect (log hazard ratio) of covariate
`cens`	Censoring rate
`cuts`	time cuts
`...`	Additional arguments

Author(s)

Klaus K. Holst

`simClaytonOakes` *Simulate from the Clayton-Oakes frailty model*

Description

Simulate observations from the Clayton-Oakes copula model with piecewise constant marginals.

Usage

```
simClaytonOakes(
  K,
  n,
  eta,
  beta,
  stoptime,
  lam = 1,
  left = 0,
  pairleft = 0,
  trunc.prob = 0.5,
  same = 0
)
```

Arguments

`K`	Number of clusters
`n`	Number of observations in each cluster
`eta`	variance
`beta`	Effect (log hazard ratio) of covariate
`stoptime`	Stopping time
`lam`	constant hazard
`left`	Left truncation
`pairleft`	pairwise (1) left truncation or individual (0)
`trunc.prob`	Truncation probability
`same`	if 1 then left-truncation is same also for univariate truncation

Author(s)

Thomas Scheike and Klaus K. Holst

---

simClaytonOakesWei *Simulate from the Clayton-Oakes frailty model*

Description

Simulate observations from the Clayton-Oakes copula model with Weibull type baseline and Cox marginals.

Usage

```
simClaytonOakesWei(
  K,
  n,
  eta,
  beta,
  stoptime,
  weiscale = 1,
  weishape = 2,
  left = 0,
  pairleft = 0
)
```

Arguments

`K`	Number of clusters
`n`	Number of observations in each cluster
`eta`	1/variance
`beta`	Effect (log hazard ratio) of covariate
`stoptime`	Stopping time
`weiscale`	weibull scale parameter
`weishape`	weibull shape parameter
`left`	Left truncation
`pairleft`	pairwise (1) left truncation or individual (0)

Author(s)

Klaus K. Holst

---

simMultistate *Simulation of illness-death model*

Description

Simulation of illness-death model

Usage

```
simMultistate(
  n,
  cumhaz,
  cumhaz2,
  death.cumhaz,
  death.cumhaz2,
  rr = NULL,
  rr2 = NULL,
  rd = NULL,
  rd2 = NULL,
  gap.time = FALSE,
  max.recurrent = 100,
  dependence = 0,
  var.z = 0.22,
  cor.mat = NULL,
  cens = NULL,
  ...
)
```

Arguments

`n`	number of id's
`cumhaz`	cumulative hazard of going from state 1 to 2.
`cumhaz2`	cumulative hazard of going from state 2 to 1.
`death.cumhaz`	cumulative hazard of death from state 1.
`death.cumhaz2`	cumulative hazard of death from state 2.
`rr`	relative risk adjustment for cumhaz
`rr2`	relative risk adjustment for cumhaz2
`rd`	relative risk adjustment for death.cumhaz
`rd2`	relative risk adjustment for death.cumhaz2
`gap.time`	if true simulates gap-times with specified cumulative hazard
`max.recurrent`	limits number recurrent events to 100

`dependence`	0:independence; 1:all share same random effect with variance var.z; 2:random effect exp(normal) with correlation structure from cor.mat; 3:additive gamma distributed random effects, z1= (z11+ z12)/2 such that mean is 1 , z2= (z11^cor.mat(1,2)+ z13)/2, z3= (z12^(cor.mat(2,3)+z13^cor.mat(1,3))/2, with z11 z12 z13 are gamma with mean and variance 1 , first random effect is z1 and for N1 second random effect is z2 and for N2 third random effect is for death
`var.z`	variance of random effects
`cor.mat`	correlation matrix for var.z variance of random effects
`cens`	rate of censoring exponential distribution
`...`	Additional arguments to lower level funtions

Details

simMultistate with different death intensities from states 1 and 2

Must give cumulative hazards on some time-range

Author(s)

Thomas Scheike

Examples

```
########################################
## getting some rates to mimick
########################################
data(base1cumhaz)
data(base4cumhaz)
data(drcumhaz)
dr <- drcumhaz
dr2 <- drcumhaz
dr2[,2] <- 1.5*drcumhaz[,2]
base1 <- base1cumhaz
base4 <- base4cumhaz
cens <- rbind(c(0,0),c(2000,0.5),c(5110,3))

iddata <- simMultistate(10000,base1,base1,dr,dr2,cens=cens)
dlist(iddata,.~id|id<3,n=0)

### estimating rates from simulated data
c0 <- phreg(Surv(start,stop,status==0)~+1,iddata)
c3 <- phreg(Surv(start,stop,status==3)~+strata(from),iddata)
c1 <- phreg(Surv(start,stop,status==1)~+1,subset(iddata,from==2))
c2 <- phreg(Surv(start,stop,status==2)~+1,subset(iddata,from==1))
###
par(mfrow=c(2,3))
bplot(c0)
lines(cens,col=2)
bplot(c3,main="rates 1-> 3 , 2->3”)
lines(dr,col=1,lwd=2)
lines(dr2,col=2,lwd=2)
```

```
###
bplot(c1,main="rate 1->2")
lines(base1,lwd=2)
###
bplot(c2,main="rate 2->1")
lines(base1,lwd=2)
```

`simRecurrentII` *Simulation of recurrent events data based on cumulative hazards II*

Description

Simulation of recurrent events data based on cumulative hazards

Usage

```
simRecurrentII(
  n,
  cumhaz,
  cumhaz2,
  death.cumhaz = NULL,
  r1 = NULL,
  r2 = NULL,
  rd = NULL,
  rc = NULL,
  gap.time = FALSE,
  max.recurrent = 100,
  dhaz = NULL,
  haz2 = NULL,
  dependence = 0,
  var.z = 0.22,
  cor.mat = NULL,
  cens = NULL,
  ...
)
```

Arguments

`n`	number of id's
`cumhaz`	cumulative hazard of recurrent events
`cumhaz2`	cumulative hazard of recurrent events of type 2
`death.cumhaz`	cumulative hazard of death
`r1`	potential relative risk adjustment of rate
`r2`	potential relative risk adjustment of rate
`rd`	potential relative risk adjustment of rate

`rc`	potential relative risk adjustment of rate
`gap.time`	if true simulates gap-times with specified cumulative hazard
`max.recurrent`	limits number recurrent events to 100
`dhaz`	rate for death hazard if it is extended to time-range of first event
`haz2`	rate of second cause if it is extended to time-range of first event
`dependence`	0:independence; 1:all share same random effect with variance var.z; 2:random effect exp(normal) with correlation structure from cor.mat; 3:additive gamma distributed random effects, z1= (z11+ z12)/2 such that mean is 1 , z2= (z11^cor.mat(1,2)+ z13)/2, z3= (z12^(cor.mat(2,3)+z13^cor.mat(1,3))/2, with z11 z12 z13 are gamma with mean and variance 1 , first random effect is z1 and for N1 second random effect is z2 and for N2 third random effect is for death
`var.z`	variance of random effects
`cor.mat`	correlation matrix for var.z variance of random effects
`cens`	rate of censoring exponential distribution
`...`	Additional arguments to lower level funtions

Details

Must give hazard of death and two recurrent events. Possible with two event types and their dependence can be specified but the two recurrent events need to share random effect. Based on drawing the from cumhaz and cumhaz2 and taking the first event rather the cumulative and then distributing it out. Key advantage of this is that there is more flexibility wrt random effects

Author(s)

Thomas Scheike

Examples

```
########################################
## getting some rates to mimick
########################################

data(base1cumhaz)
data(base4cumhaz)
data(drcumhaz)
dr <- drcumhaz
base1 <- base1cumhaz
base4 <- base4cumhaz

cor.mat <- corM <- rbind(c(1.0, 0.6, 0.9), c(0.6, 1.0, 0.5), c(0.9, 0.5, 1.0))

######################################################################
### simulating simple model that mimicks data
######################################################################
rr <- simRecurrent(5,base1,death.cumhaz=dr)
dlist(rr,.~id,n=0)
```

```
rr <- simRecurrent(10000,base1,death.cumhaz=dr)
par(mfrow=c(1,3))
showfitsim(causes=1,rr,dr,base1,base1)
######################################################################
### simulating simple model
### random effect for all causes (Z shared for death and recurrent)
######################################################################
rr <- simRecurrent(100,base1,death.cumhaz=dr,dependence=1,var.gamma=0.4)

######################################################################
### simulating simple model that mimicks data
### now with two event types and second type has same rate as death rate
######################################################################
set.seed(100)
rr <- simRecurrentII(10000,base1,base4,death.cumhaz=dr)
dtable(rr,~death+status)
par(mfrow=c(2,2))
showfitsim(causes=2,rr,dr,base1,base4)

set.seed(100)
cumhaz <- list(base1,base1,base4)
drl <- list(dr,base4)
rr <- simRecurrentIII(100,cumhaz,death.cumhaz=drl,dep=0)
dtable(rr,~death+status)
showfitsimIII(rr,cumhaz,drl)
```

---

simRecurrentTS *Simulation of recurrent events data based on cumulative hazards: Two-stage model*

Description

Simulation of recurrent events data based on cumulative hazards

Usage

```
simRecurrentTS(
  n,
  cumhaz,
  cumhaz2,
  death.cumhaz = NULL,
  nu = rep(1, 3),
  share1 = 0.3,
  vargamD = 2,
  vargam12 = 0.5,
  gap.time = FALSE,
  max.recurrent = 100,
  cens = NULL,
```

```
  ...
)
```

Arguments

`n`	number of id's
`cumhaz`	cumulative hazard of recurrent events
`cumhaz2`	cumulative hazard of recurrent events of type 2
`death.cumhaz`	cumulative hazard of death
`nu`	powers of random effects where nu > -1/shape
`share1`	how random effect for death splits into two parts
`vargamD`	variance of random effect for death
`vargam12`	shared random effect for N1 and N2
`gap.time`	if true simulates gap-times with specified cumulative hazard
`max.recurrent`	limits number recurrent events to 100
`cens`	rate of censoring exponential distribution
`...`	Additional arguments to lower level funtions

Details

Model is constructed such that marginals are on specified form by linear approximations of cumulative hazards that are on a specific form to make them equivalent to marginals after integrating out over survivors. Therefore E(dN_1 | D>t) = cumhaz, E(dN_2 | D>t) = cumhaz2, and hazard of death is death.cumhazard

Must give hazard of death and two recurrent events. Hazard of death is death.cumhazard two event types and their dependence can be specified but the two recurrent events need to share random effect.

Random effect for death Z.death=(Zd1+Zd2), Z1=(Zd1^nu1) Z12, Z2=(Zd2^nu2) Z12^nu3

$$Z.death = Zd1 + Zd2$$

gamma distributions

$$Zdj$$

gamma distribution with mean parameters (sharej), vargamD, share2=1-share1

$$Z12$$

gamma distribution with mean 1 and variance vargam12

Author(s)

Thomas Scheike

Examples

```
########################################
## getting some rates to mimick
########################################

data(base1cumhaz)
data(base4cumhaz)
data(drcumhaz)
dr <- drcumhaz
base1 <- base1cumhaz
base4 <- base4cumhaz

rr <- simRecurrentTS(1000,base1,base4,death.cumhaz=dr)
dtable(rr,~death+status)
showfitsim(causes=2,rr,dr,base1,base4)
```

`summary.cor` *Summary for dependence models for competing risks*

Description

Computes concordance and casewise concordance for dependence models for competing risks models of the type cor.cif, rr.cif or or.cif for the given cumulative incidences and the different dependence measures in the object.

Usage

```
## S3 method for class 'cor'
summary(object, marg.cif = NULL, marg.cif2 = NULL, digits = 3, ...)
```

Arguments

`object`	object from cor.cif rr.cif or or.cif for dependence between competing risks data for two causes.
`marg.cif`	a number that gives the cumulative incidence in one time point for which concordance and casewise concordance are computed.
`marg.cif2`	the cumulative incidence for cause 2 for concordance and casewise concordance are computed. Default is that it is the same as marg.cif.
`digits`	digits in output.
`...`	Additional arguments.

Value

prints summary for dependence model.

`casewise`	gives casewise concordance that is, probability of cause 2 (related to cif2) given that cause 1 (related to cif1) has occured.
`concordance`	gives concordance that is, probability of cause 2 (related to cif2) and cause 1 (related to cif1).
`cif1`	cumulative incidence for cause1.
`cif2`	cumulative incidence for cause1.

Author(s)

Thomas Scheike

References

Cross odds ratio Modelling of dependence for Multivariate Competing Risks Data, Scheike and Sun (2012), Biostatistics.

A Semiparametric Random Effects Model for Multivariate Competing Risks Data, Scheike, Zhang, Sun, Jensen (2010), Biometrika.

Examples

```
## library("timereg")
## data("multcif",package="mets") # simulated data
## multcif$cause[multcif$cause==0] <- 2
##
## times=seq(0.1,3,by=0.1) # to speed up computations use only these time-points
## add <- timereg::comp.risk(Event(time,cause)~+1+cluster(id),
##                           data=multcif,n.sim=0,times=times,cause=1)
###
## out1<-cor.cif(add,data=multcif,cause1=1,cause2=1,theta=log(2+1))
## summary(out1)
##
## pad <- predict(add,X=1,se=0,uniform=0)
## summary(out1,marg.cif=pad)
```

`summaryGLM` *Reporting OR (exp(coef)) from glm with binomial link and glm predictions*

Description

Reporting OR from glm with binomial link and glm predictions

Usage

```
summaryGLM(object, id = NULL, fun = NULL, ...)
```

Arguments

`object`	glm output
`id`	possible id for cluster corrected standard errors
`fun`	possible function for non-standard predictions based on object
`...`	arguments of estimate of lava for example level=0.95

Author(s)

Thomas Scheike

Examples

```
data(sTRACE)
sTRACE$id <- sample(1:100,nrow(sTRACE),replace=TRUE)

model <- glm(I(status==9)~sex+factor(diabetes)+age,data=sTRACE,family=binomial)
summaryGLM(model)
summaryGLM(model,id=sTRACE$id)

nd <- data.frame(sex=c(0,1),age=67,diabetes=1)
predictGLM(model,nd)
```

`survival.twostage` *Twostage survival model for multivariate survival data*

Description

Fits Clayton-Oakes or bivariate Plackett models for bivariate survival data using marginals that are on Cox form. The dependence can be modelled via

1. Regression design on dependence parameter.
2. Random effects, additive gamma model.

If clusters contain more than two subjects, we use a composite likelihood based on the pairwise bivariate models, for full MLE see twostageMLE.

The two-stage model is constructed such that given the gamma distributed random effects it is assumed that the survival functions are indpendent, and that the marginal survival functions are on Cox form (or additive form)

$$P(T > t|x) = S(t|x) = exp(-exp(x^T\beta)A_0(t))$$

One possibility is to model the variance within clusters via a regression design, and then one can specify a regression structure for the independent gamma distributed random effect for each cluster, such that the variance is given by

$$\theta = h(z_j^T\alpha)$$

where z is specified by theta.des, and a possible link function var.link=1 will will use the exponential link $h(x) = exp(x)$, and var.link=0 the identity link $h(x) = x$. The reported standard errors are based on the estimated information from the likelihood assuming that the marginals are known (unlike the twostageMLE and for the additive gamma model below).

Can also fit a structured additive gamma random effects model, such as the ACE, ADE model for survival data. In this case the random.design specificies the random effects for each subject within a cluster. This is a matrix of 1's and 0's with dimension n x d. With d random effects. For a cluster with two subjects, we let the random.design rows be v_1 and v_2. Such that the random effects for subject 1 is

$$v_1^T (Z_1, ..., Z_d)$$

, for d random effects. Each random effect has an associated parameter $(\lambda_1, ..., \lambda_d)$. By construction subjects 1's random effect are Gamma distributed with mean $\lambda_j / v_1^T \lambda$ and variance $\lambda_j / (v_1^T \lambda)^2$. Note that the random effect $v_1^T (Z_1, ..., Z_d)$ has mean 1 and variance $1/(v_1^T \lambda)$. It is here asssumed that $lamtot = v_1^T \lambda$ is fixed within clusters as it would be for the ACE model below.

Based on these parameters the relative contribution (the heritability, h) is equivalent to the expected values of the random effects: $\lambda_j / v_1^T \lambda$

The DEFAULT parametrization (var.par=1) uses the variances of the random effecs

$$\theta_j = \lambda_j / (v_1^T \lambda)^2$$

For alternative parametrizations one can specify how the parameters relate to λ_j with the argument var.par=0.

For both types of models the basic model assumptions are that given the random effects of the clusters the survival distributions within a cluster are independent and ' on the form

$$P(T > t | x, z) = exp(-Z \cdot Laplace^{-1}(lamtot, lamtot, S(t|x)))$$

with the inverse laplace of the gamma distribution with mean 1 and variance 1/lamtot.

The parameters $(\lambda_1, ..., \lambda_d)$ are related to the parameters of the model by a regression construction $pard$ (d x k), that links the d λ parameters with the (k) underlying θ parameters

$$\lambda = theta.des \theta$$

here using theta.des to specify these low-dimension association. Default is a diagonal matrix. This can be used to make structural assumptions about the variances of the random-effects as is needed for the ACE model for example.

The case.control option that can be used with the pair specification of the pairwise parts of the estimating equations. Here it is assumed that the second subject of each pair is the proband.

Usage

```
survival.twostage(
  margsurv,
  data = parent.frame(),
  method = "nr",
  detail = 0,
  clusters = NULL,
  silent = 1,
  weights = NULL,
  theta = NULL,
```

```
  theta.des = NULL,
  var.link = 1,
  baseline.iid = 1,
  model = "clayton.oakes",
  marginal.trunc = NULL,
  marginal.survival = NULL,
  strata = NULL,
  se.clusters = NULL,
  numDeriv = 1,
  random.design = NULL,
  pairs = NULL,
  dim.theta = NULL,
  numDeriv.method = "simple",
  additive.gamma.sum = NULL,
  var.par = 1,
  no.opt = FALSE,
  ...
)
```

Arguments

`margsurv`	Marginal model
`data`	data frame
`method`	Scoring method "nr", for lava NR optimizer
`detail`	Detail
`clusters`	Cluster variable
`silent`	Debug information
`weights`	Weights
`theta`	Starting values for variance components
`theta.des`	design for dependence parameters, when pairs are given the indeces of the theta-design for this pair, is given in pairs as column 5
`var.link`	Link function for variance: exp-link.
`baseline.iid`	to adjust for baseline estimation, using phreg function on same data.
`model`	model
`marginal.trunc`	marginal left truncation probabilities
`marginal.survival`	optional vector of marginal survival probabilities
`strata`	strata for fitting, see example
`se.clusters`	for clusters for se calculation with iid
`numDeriv`	to get numDeriv version of second derivative, otherwise uses sum of squared scores for each pair
`random.design`	random effect design for additive gamma model, when pairs are given the indeces of the pairs random.design rows are given as columns 3:4

`pairs`	matrix with rows of indeces (two-columns) for the pairs considered in the pairwise composite score, useful for case-control sampling when marginal is known.
`dim.theta`	dimension of the theta parameter for pairs situation.
`numDeriv.method`	uses simple to speed up things and second derivative not so important.
`additive.gamma.sum`	for two.stage=0, this is specification of the lamtot in the models via a matrix that is multiplied onto the parameters theta (dimensions=(number random effects x number of theta parameters), when null then sums all parameters.
`var.par`	is 1 for the default parametrization with the variances of the random effects, var.par=0 specifies that the λ_j's are used as parameters.
`no.opt`	for not optimizng
`...`	Additional arguments to maximizer NR of lava. and ascertained sampling

Author(s)

Thomas Scheike

References

Twostage estimation of additive gamma frailty models for survival data. Scheike (2019), work in progress

Shih and Louis (1995) Inference on the association parameter in copula models for bivariate survival data, Biometrics, (1995).

Glidden (2000), A Two-Stage estimator of the dependence parameter for the Clayton Oakes model, LIDA, (2000).

Measuring early or late dependence for bivariate twin data Scheike, Holst, Hjelmborg (2015), LIDA

Estimating heritability for cause specific mortality based on twins studies Scheike, Holst, Hjelmborg (2014), LIDA

Additive Gamma frailty models for competing risks data, Biometrics (2015) Eriksson and Scheike (2015),

Examples

```
data(diabetes)

# Marginal Cox model  with treat as covariate
margph <- phreg(Surv(time,status)~treat+cluster(id),data=diabetes)
### Clayton-Oakes, MLE
fitco1<-twostageMLE(margph,data=diabetes,theta=1.0)
summary(fitco1)

### Plackett model
mph <- phreg(Surv(time,status)~treat+cluster(id),data=diabetes)
fitp <- survival.twostage(mph,data=diabetes,theta=3.0,Nit=40,
               clusters=diabetes$id,var.link=1,model="plackett")
summary(fitp)
```

```
### Clayton-Oakes
fitco2 <- survival.twostage(mph,data=diabetes,theta=0.0,detail=0,
                 clusters=diabetes$id,var.link=1,model="clayton.oakes")
summary(fitco2)
fitco3 <- survival.twostage(margph,data=diabetes,theta=1.0,detail=0,
                 clusters=diabetes$id,var.link=0,model="clayton.oakes")
summary(fitco3)

### without covariates but with stratafied
marg <- phreg(Surv(time,status)~+strata(treat)+cluster(id),data=diabetes)
fitpa <- survival.twostage(marg,data=diabetes,theta=1.0,
                clusters=diabetes$id,model="clayton.oakes")
summary(fitpa)

fitcoa <- survival.twostage(marg,data=diabetes,theta=1.0,clusters=diabetes$id,
                 model="clayton.oakes")
summary(fitcoa)

### Piecewise constant cross hazards ratio modelling
########################################################

d <- subset(simClaytonOakes(2000,2,0.5,0,stoptime=2,left=0),!truncated)
udp <- piecewise.twostage(c(0,0.5,2),data=d,method="optimize",
                          id="cluster",timevar="time",
                          status="status",model="clayton.oakes",silent=0)
summary(udp)

 ## Reduce Ex.Timings
### Same model using the strata option, a bit slower
########################################################
## makes the survival pieces for different areas in the plane
##ud1=surv.boxarea(c(0,0),c(0.5,0.5),data=d,id="cluster",timevar="time",status="status")
##ud2=surv.boxarea(c(0,0.5),c(0.5,2),data=d,id="cluster",timevar="time",status="status")
##ud3=surv.boxarea(c(0.5,0),c(2,0.5),data=d,id="cluster",timevar="time",status="status")
##ud4=surv.boxarea(c(0.5,0.5),c(2,2),data=d,id="cluster",timevar="time",status="status")

## everything done in one call
ud <- piecewise.data(c(0,0.5,2),data=d,timevar="time",status="status",id="cluster")
ud$strata <- factor(ud$strata);
ud$intstrata <- factor(ud$intstrata)

## makes strata specific id variable to identify pairs within strata
## se's computed based on the id variable across strata "cluster"
ud$idstrata <- ud$id+(as.numeric(ud$strata)-1)*2000

marg2 <- timereg::aalen(Surv(boxtime,status)~-1+factor(num):factor(intstrata),
               data=ud,n.sim=0,robust=0)
tdes <- model.matrix(~-1+factor(strata),data=ud)
fitp2 <- survival.twostage(marg2,data=ud,se.clusters=ud$cluster,clusters=ud$idstrata,
                model="clayton.oakes",theta.des=tdes,step=0.5)
summary(fitp2)
```

```
### now fitting the model with symmetry, i.e. strata 2 and 3 same effect
ud$stratas <- ud$strata;
ud$stratas[ud$strata=="0.5-2,0-0.5"] <- "0-0.5,0.5-2"
tdes2 <- model.matrix(~-1+factor(stratas),data=ud)
fitp3 <- survival.twostage(marg2,data=ud,clusters=ud$idstrata,se.cluster=ud$cluster,
                model="clayton.oakes",theta.des=tdes2,step=0.5)
summary(fitp3)

### same model using strata option, a bit slower
fitp4 <- survival.twostage(marg2,data=ud,clusters=ud$cluster,se.cluster=ud$cluster,
                model="clayton.oakes",theta.des=tdes2,step=0.5,strata=ud$strata)
summary(fitp4)


 ## Reduce Ex.Timings
### structured random effects model additive gamma ACE
### simulate structured two-stage additive gamma ACE model
data <- simClaytonOakes.twin.ace(4000,2,1,0,3)
out <- twin.polygen.design(data,id="cluster")
pardes <- out$pardes
pardes
des.rv <- out$des.rv
head(des.rv)
aa <- phreg(Surv(time,status)~x+cluster(cluster),data=data,robust=0)
ts <- survival.twostage(aa,data=data,clusters=data$cluster,detail=0,
       theta=c(2,1),var.link=0,step=0.5,
       random.design=des.rv,theta.des=pardes)
summary(ts)
```

`survivalG` *G-estimator for Cox and Fine-Gray model*

Description

Computes G-estimator
$$\hat{S}(t, A=a) = n^{-1} \sum_i \hat{S}(t, A=a, Z_i)$$
for the Cox model based on phreg og the Fine-Gray model based on the cifreg function. Gives influence functions of these risk estimates and SE's are based on these. If first covariate is a factor then all contrast are computed, and if continuous then considered covariate values are given by Avalues.

Usage

```
survivalG(
  x,
  data,
```

```
  time = NULL,
  Avalues = c(0, 1),
  varname = NULL,
  same.data = TRUE,
  id = NULL
)
```

Arguments

`x`	phreg or cifreg object
`data`	data frame for risk averaging
`time`	for estimate
`Avalues`	values to compare for first covariate A
`varname`	if given then averages for this variable, default is first variable
`same.data`	assumes that same data is used for fitting of survival model and averaging.
`id`	might be given to link to data to iid decomposition of survival data, must be coded as 1,2,..,

Author(s)

Thomas Scheike

Examples

```
data(bmt); bmt$time <- bmt$time+runif(408)*0.001
bmt$event <- (bmt$cause!=0)*1
dfactor(bmt) <- tcell.f~tcell

fg1 <- cifreg(Event(time,cause)~tcell.f+platelet+age,bmt,cause=1,
             cox.prep=TRUE,propodds=NULL)
summary(survivalG(fg1,bmt,50))

ss <- phreg(Surv(time,event)~tcell.f+platelet+age,bmt)
summary(survivalG(ss,bmt,50))

ss <- phreg(Surv(time,event)~strata(tcell.f)+platelet+age,bmt)
summary(survivalG(ss,bmt,50))

sst <- survivalGtime(ss,bmt,n=50)
plot(sst)

fg1t <- survivalGtime(fg1,bmt,n=50)
plot(fg1t)
```

`test.conc` *Concordance test Compares two concordance estimates*

Description

.. content for description (no empty lines) ..

Usage

```
test.conc(conc1, conc2, same.cluster = FALSE)
```

Arguments

`conc1`	Concordance estimate of group 1
`conc2`	Concordance estimate of group 2
`same.cluster`	if FALSE then groups are independent, otherwise estimates are based on same data.

Author(s)

Thomas Scheike

`tetrachoric` *Estimate parameters from odds-ratio*

Description

Calculate tetrachoric correlation of probabilities from odds-ratio

Usage

```
tetrachoric(P, OR, approx = 0, ...)
```

Arguments

`P`	Joint probabilities or marginals (if OR is given)
`OR`	Odds-ratio
`approx`	If TRUE an approximation of the tetrachoric correlation is used
`...`	Additional arguments

Examples

```
tetrachoric(0.3,1.25) # Marginal p1=p2=0.3, OR=2
P <- matrix(c(0.1,0.2,0.2,0.5),2)
prod(diag(P))/prod(lava::revdiag(P))
##mets:::assoc(P)
tetrachoric(P)
or2prob(2,0.1)
or2prob(2,c(0.1,0.2))
```

`TRACE` *The TRACE study group of myocardial infarction*

Description

The TRACE data frame contains 1877 patients and is a subset of a data set consisting of approximately 6000 patients. It contains data relating survival of patients after myocardial infarction to various risk factors.

Format

This data frame contains the following columns:

id a numeric vector. Patient code.

status a numeric vector code. Survival status. 9: dead from myocardial infarction, 0: alive, 7: dead from other causes.

time a numeric vector. Survival time in years.

chf a numeric vector code. Clinical heart pump failure, 1: present, 0: absent.

diabetes a numeric vector code. Diabetes, 1: present, 0: absent.

vf a numeric vector code. Ventricular fibrillation, 1: present, 0: absent.

wmi a numeric vector. Measure of heart pumping effect based on ultrasound measurements where 2 is normal and 0 is worst.

sex a numeric vector code. 1: female, 0: male.

age a numeric vector code. Age of patient.

Details

sTRACE is a subsample consisting of 300 patients.

tTRACE is a subsample consisting of 1000 patients.

Source

The TRACE study group.

Jensen, G.V., Torp-Pedersen, C., Hildebrandt, P., Kober, L., F. E. Nielsen, Melchior, T., Joen, T. and P. K. Andersen (1997), Does in-hospital ventricular fibrillation affect prognosis after myocardial infarction?, European Heart Journal 18, 919–924.

Examples

```
data(TRACE)
names(TRACE)
```

`ttpd` *ttpd discrete survival data on interval form*

Description

ttpd discrete survival data on interval form

Source

Simulated data

`twin.clustertrunc` *Estimation of twostage model with cluster truncation in bivariate situation*

Description

Estimation of twostage model with cluster truncation in bivariate situation

Usage

```
twin.clustertrunc(
  survformula,
  data = parent.frame(),
  theta.des = NULL,
  clusters = NULL,
  var.link = 1,
  Nit = 10,
  final.fitting = FALSE,
  ...
)
```

Arguments

`survformula`	Formula with survival model aalen or cox.aalen, some limitiation on model specification due to call of fast.reshape (so for example interactions and * and : do not work here, expand prior to call)
`data`	Data frame
`theta.des`	design for dependence parameters in two-stage model
`clusters`	clustering variable for twins

`var.link`	exp link for theta
`Nit`	number of iteration
`final.fitting`	TRUE to do final estimation with SE and ... arguments for marginal models
`...`	Additional arguments to lower level functions

Author(s)

Thomas Scheike

Examples

```
library("timereg")
data(diabetes)
v <- diabetes$time*runif(nrow(diabetes))*rbinom(nrow(diabetes),1,0.5)
diabetes$v <- v

aout <- twin.clustertrunc(Surv(v,time,status)~1+treat+adult,
 data=diabetes,clusters="id")
aout$two        ## twostage output
par(mfrow=c(2,2))
plot(aout$marg) ## marginal model output

out <- twin.clustertrunc(Surv(v,time,status)~1+prop(treat)+prop(adult),
 data=diabetes,clusters="id")
out$two        ## twostage output
plot(out$marg) ## marginal model output
```

`twinbmi` *BMI data set*

Description

BMI data set

Format

Self-reported BMI-values on 11,411 subjects

tvparnr: twin id bmi: BMI (m/kg^2) age: Age gender: (male/female) zyg: zygosity, MZ:=mz, DZ(same sex):=dz, DZ(opposite sex):=os

---

`twinlm` *Classic twin model for quantitative traits*

Description

Fits a classical twin model for quantitative traits.

Usage

```
twinlm(
  formula,
  data,
  id,
  zyg,
  DZ,
  group = NULL,
  group.equal = FALSE,
  strata = NULL,
  weights = NULL,
  type = c("ace"),
  twinnum = "twinnum",
  binary = FALSE,
  ordinal = 0,
  keep = weights,
  estimator = NULL,
  constrain = TRUE,
  control = list(),
  messages = 1,
  ...
)
```

Arguments

`formula`	Formula specifying effects of covariates on the response
`data`	`data.frame` with one observation pr row. In addition a column with the zygosity (DZ or MZ given as a factor) of each individual much be specified as well as a twin id variable giving a unique pair of numbers/factors to each twin pair
`id`	The name of the column in the dataset containing the twin-id variable.
`zyg`	The name of the column in the dataset containing the zygosity variable
`DZ`	Character defining the level in the zyg variable corresponding to the dyzogitic twins. If this argument is missing, the reference level (i.e. the first level) will be interpreted as the dyzogitic twins
`group`	Optional. Variable name defining group for interaction analysis (e.g., gender)
`group.equal`	If TRUE marginals of groups are asummed to be the same
`strata`	Strata variable name

`weights`	Weights matrix if needed by the chosen estimator. For use with Inverse Probability Weights
`type`	Character defining the type of analysis to be performed. Can be a subset of "aced" (additive genetic factors, common environmental factors, unique environmental factors, dominant genetic factors). Other choices are: • "0" (or "sat"): Saturated model where twin 1 and twin 2 within each twin pair may have a different marginal distribution. • "1" (or "flex","zyg"): Within twin pairs the marginal distribution is the same, but the marginal distribution may differ between MZ and DZ twins. A free correlation structure within MZ and DZ twins. • "2" (or "u", "eqmarg"): All individuals have the same marginals but a free correlation structure within MZ and DZ twins. The default value is an additive polygenic model `type="ace"`.
`twinnum`	The name of the column in the dataset numbering the twins (1,2). If it does not exist in `data` it will automatically be created.
`binary`	If `TRUE` a liability model is fitted. Note that if the right-hand-side of the formula is a factor, character vector, og logical variable, then the liability model is automatically chosen (wrapper of the `bptwin` function).
`ordinal`	If non-zero (number of bins) a liability model is fitted.
`keep`	Vector of variables from `data` that are not specified in `formula`, to be added to data.frame of the SEM
`estimator`	Choice of estimator/model
`constrain`	Development argument
`control`	Control argument parsed on to the optimization routine
`messages`	Control amount of messages shown
`...`	Additional arguments parsed on to lower-level functions

Value

Returns an object of class `twinlm`.

Author(s)

Klaus K. Holst

See Also

`bptwin`, `twinlm.time`, `twinlm.strata`, `twinsim`

Examples

```
## Simulate data
set.seed(1)
d <- twinsim(1000,b1=c(1,-1),b2=c(),acde=c(1,1,0,1))
## E(y|z1,z2) = z1 - z2. var(A) = var(C) = var(E) = 1
```

```
## E.g to fit the data to an ACE-model without any confounders we simply write
ace <- twinlm(y ~ 1, data=d, DZ="DZ", zyg="zyg", id="id")
ace
## An AE-model could be fitted as
ae <- twinlm(y ~ 1, data=d, DZ="DZ", zyg="zyg", id="id", type="ae")
## LRT:
lava::compare(ae,ace)
## AIC
AIC(ae)-AIC(ace)
## To adjust for the covariates we simply alter the formula statement
ace2 <- twinlm(y ~ x1+x2, data=d, DZ="DZ", zyg="zyg", id="id", type="ace")
## Summary/GOF
summary(ace2)
 ## Reduce Ex.Timings
## An interaction could be analyzed as:
ace3 <- twinlm(y ~ x1+x2 + x1:I(x2<0), data=d, DZ="DZ", zyg="zyg", id="id", type="ace")
ace3
## Categorical variables are also supported
d2 <- transform(d,x2cat=cut(x2,3,labels=c("Low","Med","High")))
ace4 <- twinlm(y ~ x1+x2cat, data=d2, DZ="DZ", zyg="zyg", id="id", type="ace")
```

`twinsim` *Simulate twin data*

Description

Simulate twin data from a linear normal ACE/ADE/AE model.

Usage

```
twinsim(
  nMZ = 100,
  nDZ = nMZ,
  b1 = c(),
  b2 = c(),
  mu = 0,
  acde = c(1, 1, 0, 1),
  randomslope = NULL,
  threshold = 0,
  cens = FALSE,
  wide = FALSE,
  ...
)
```

Arguments

`nMZ`	Number of monozygotic twin pairs
`nDZ`	Number of dizygotic twin pairs

`b1`	Effect of covariates (labelled x1,x2,...) of type 1. One distinct covariate value for each twin/individual.
`b2`	Effect of covariates (labelled g1,g2,...) of type 2. One covariate value for each twin pair.
`mu`	Intercept parameter.
`acde`	Variance of random effects (in the order A,C,D,E)
`randomslope`	Logical indicating wether to include random slopes of the variance components w.r.t. x1,x2,...
`threshold`	Treshold used to define binary outcome y0
`cens`	Logical variable indicating whether to censor outcome
`wide`	Logical indicating if wide data format should be returned
`...`	Additional arguments parsed on to lower-level functions

Author(s)

Klaus K. Holst

See Also

`twinlm`

`twinstut` *Stutter data set*

Description

Based on nation-wide questionnaire answers from 33,317 Danish twins

Format

tvparnr: twin-pair id zyg: zygosity, MZ:=mz, DZ(same sex):=dz, DZ(opposite sex):=os stutter: stutter status (yes/no) age: age nr: number within twin-pair

`twostageMLE` *Twostage survival model fitted by pseudo MLE*

Description

Fits Clayton-Oakes clustered survival data using marginals that are on Cox form in the likelihood for the dependence parameter as in Glidden (2000). The dependence can be modelled via a

1. Regression design on dependence parameter.

We allow a regression structure for the indenpendent gamma distributed random effects and their variances that may depend on cluster covariates. So

$$\theta = h(z_j^T \alpha)$$

where z is specified by theta.des . The link function can be the exp when var.link=1

Usage

```
twostageMLE(
  margsurv,
  data = parent.frame(),
  theta = NULL,
  theta.des = NULL,
  var.link = 0,
  method = "NR",
  no.opt = FALSE,
  weights = NULL,
  se.cluster = NULL,
  ...
)
```

Arguments

`margsurv`	Marginal model from phreg
`data`	data frame
`theta`	Starting values for variance components
`theta.des`	design for dependence parameters, when pairs are given this is could be a (pairs) x (numer of parameters) x (max number random effects) matrix
`var.link`	Link function for variance if 1 then uses exp link
`method`	type of opitmizer, default is Newton-Raphson "NR"
`no.opt`	to not optimize, for example to get score and iid for specific theta
`weights`	cluster specific weights, but given with length equivalent to data-set, weights for score equations
`se.cluster`	specifies how the influence functions are summed before squared when computing the variance. Note that the id from the marginal model is used to construct MLE, and then these scores can be summed with the se.cluster argument.
`...`	arguments to be passed to optimizer

Author(s)

Thomas Scheike

References

Measuring early or late dependence for bivariate twin data Scheike, Holst, Hjelmborg (2015), LIDA

Twostage modelling of additive gamma frailty models for survival data. Scheike and Holst, working paper

Shih and Louis (1995) Inference on the association parameter in copula models for bivariate survival data, Biometrics, (1995).

Glidden (2000), A Two-Stage estimator of the dependence parameter for the Clayton Oakes model, LIDA, (2000).

Examples

```
data(diabetes)
dd <- phreg(Surv(time,status==1)~treat+cluster(id),diabetes)
oo <- twostageMLE(dd,data=diabetes)
summary(oo)

theta.des <- model.matrix(~-1+factor(adult),diabetes)

oo <-twostageMLE(dd,data=diabetes,theta.des=theta.des)
summary(oo)
```

`WA_recurrent` *While-Alive estimands for recurrent events*

Description

Considers the ratio of means

$$E(N(min(D,t)))/E(min(D,t))$$

and the the mean of the events per time unit

$$E(N(min(D,t))/min(D,t))$$

both based on IPCW etimation. RMST estimator equivalent to Kaplan-Meier based estimator.

Usage

```
WA_recurrent(
  formula,
  data,
  time = NULL,
  cens.code = 0,
```

```
  cause = 1,
  death.code = 2,
  trans = NULL,
  cens.formula = NULL,
  augmentR = NULL,
  augmentC = NULL,
  type = NULL,
  ...
)
```

Arguments

`formula`	Event formula first covariate on rhs must be a factor giving the treatment
`data`	data frame
`time`	for estimation
`cens.code`	of censorings
`cause`	of events
`death.code`	of terminal events
`trans`	possible power for mean of events per time-unit
`cens.formula`	censoring model, default is to use strata(treatment)
`augmentR`	covariates for model of mean ratio
`augmentC`	covariates for censoring augmentation
`type`	augmentation for call of binreg, when augmentC is given default is "I" and otherwise "II"
`...`	arguments for binregATE

Author(s)

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