Package ‘frailtypack’

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Title General Frailty Models: Shared, Joint and Nested Frailty Models with Prediction; Evaluation of Failure-Time Surrogate Endpoints

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Imports statmod, nlme

LazyLoad no

Description The following several classes of frailty models using a penalized likelihood estimation on the hazard function but also a parametric estimation can be fit using this R package:

1) A shared frailty model (with gamma or log-normal frailty distribution) and Cox proportional hazard model. Clustered and recurrent survival times can be studied.
2) Additive frailty models for proportional hazard models with two correlated random effects (intercept random effect with random slope).
3) Nested frailty models for hierarchically clustered data (with 2 levels of clustering) by including two iid gamma random effects.
4) Joint frailty models in the context of the joint modelling for recurrent events with terminal event for clustered data or not. A joint frailty model for two semi-competing risks and clustered data is also proposed.
5) Joint general frailty models in the context of the joint modelling for recurrent events with terminal event data with two independent frailty terms.
6) Joint Nested frailty models in the context of the joint modelling for recurrent events with terminal event, for hierarchically clustered data (with two levels of clustering) by including two iid gamma random effects.
7) Multivariate joint frailty models for two types of recurrent events and a terminal event.
8) Joint models for longitudinal data and a terminal event.
9) Trivariate joint models for longitudinal data, recurrent events and a terminal event.
10) Joint frailty models for the validation of surrogate endpoints in multiple randomized clinical trials with failure-time endpoints.
Prediction values are available (for a terminal event or for a new recurrent event). Left-truncated (not for Joint model), right-censored data, interval-censored data (only for Cox proportional hazard and shared frailty model) and strata are allowed. In each model, the random effects have the gamma or normal distribution. Now, you can also consider time-varying covariates effects in Cox, shared and joint frailty models (1-5). The package includes concordance measures for Cox proportional hazards models and for shared frailty models.

License  GPL (>= 2.0)

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VignetteBuilder  knitr

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Description

Frailtypack fits several classes of frailty models using a penalized likelihood estimation on the hazard function but also a parametric estimation. 1) A shared frailty model and Cox proportional hazard model. Clustered and recurrent survival times can be studied. 2) Additive frailty models for proportional hazard models with two correlated random effects (intercept random effect with random slope). 3) Nested frailty models for hierarchically clustered data (with 2 levels of clustering) by including two iid gamma random effects. 4) Joint frailty models in the context of joint modelling for recurrent events with terminal event for clustered data or not. A joint frailty model for two semi-competing risks for clustered data is also proposed. 5) Joint General frailty models in the context of a joint modelling for recurrent events with terminal event data with two independent frailty terms. 6) Joint Nested frailty models in the context of joint modelling for recurrent events with terminal event, for hierarchically clustered data (with two levels of clustering) by including two iid gamma random effects. 7) Multivariate joint frailty models for two types of recurrent events and a terminal event. 8) Joint models for longitudinal data and a terminal event. 9) Trivariate joint models for longitudinal data, recurrent events and a terminal event. Prediction values are available. Left truncated (not for the joint models), right-censored data, interval-censored data (only for Cox proportional hazard and shared frailty model) and strata are allowed. In each model, the random effects have the gamma or normal distribution. Now, you can also consider time-varying effect covariates in Cox, shared and joint frailty models. The package includes concordance measures for Cox proportional hazards models and for shared frailty models. 10) Joint frailty models for the validation of surrogate endpoints in multiple randomized clinical trials with failure-time endpoints. This model includes a shared individual-level random effect, a shared trial random-effect associated with the hazard risks and a correlated random effects-by-trial interaction.

Details

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Author(s)

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References


Examples

```r
# Not run:

### Additive model with 1 covariate ---###

data(dataAdditive)
modAdd <- additivePenal(Surv(t1,t2,event)~
cluster(group)+var1+slope(var1),
correlation=TRUE,data=dataAdditive,
n.knots=8,kappa=10000,hazard="Splines")

### Joint model (recurrent and terminal events) with 2 covariates ---###

data(readmission)
modJoint.gap <- frailtyPenal(Surv(time,event)~
cluster(id)+sex+dukes+charlson+terminal(death),
formula.terminalEvent=sex+dukes+charlson,
data=readmission,n.knots=10,kappa=c(100,100),
recurrentAG=FALSE,hazard="Splines")

### General Joint model (recurrent and terminal events) with 2 covariates ---###
data(readmission)
```
modJoint.general <- frailtyPenal(Surv(time,event) ~ cluster(id) + dukes + charlson + sex + chemo + terminal(death),
formula.terminalEvent = ~ dukes + charlson + sex + chemo,
data = readmission, jointGeneral = TRUE, n.knots = 8,
kappa = c(2.11e+08, 9.53e+11))

##### Nested model (or hierarchical model) with 2 covariates ######

data(dataNested)
modClu <- frailtyPenal(Surv(t1,t2,event) ~
cluster(group)+subcluster(subgroup)+cov1+cov2,
data=dataNested,n.knots=8,kappa=50000,hazard="Splines")

##### Joint Nested Frailty model ######

#-- here is generated cluster (30 clusters)
readmissionNested <- transform(readmission,group=id%30+1)

modJointNested_Splines <- frailtyPenal(formula = Surv(t.start, t.stop, event) ~
subcluster(id) + cluster(group) + dukes + terminal(death),
formula.terminalEvent = ~dukes, data = readmissionNested, recurrentAG = TRUE, n.knots = 8, kappa = c(9.55e+9, 1.41e+12), initialize = TRUE)

modJointNested_Weib <- frailtyPenal(formula = Surv(t.start, t.stop, event) ~
subcluster(id) + cluster(group) + dukes + terminal(death), formula.terminalEvent = ~dukes, hazard = (~Weibull), data = readmissionNested, recurrentAG = TRUE, initialize = FALSE)

Joint-GapSpline <- frailtyPenal(formula = Surv(time, event) ~
subcluster(id) + cluster(group) + dukes + terminal(death),
formula.terminalEvent = ~dukes, data = readmissionNested, recurrentAG = FALSE, n.knots = 8, kappa = c(9.55e+9, 1.41e+12), initialize = TRUE, init.Alpha = 1.091, Ksi = "None")

##### Semiparametric Shared model ######

data(readmission)
sha.sp <- frailtyPenal(Surv(t.start,t.stop,event) ~
sex+dukes+charlson+cluster(id),data=readmission, n.knots=6,kappa=5000,recurrentAG=TRUE, cross.validation=TRUE,hazard="Splines")

##### Parametric Shared model ######

data(readmission)
sha.p <- frailtyPenal(Surv(t.start,t.stop,event) ~
cluster(id)+sex+dukes+charlson,
 data=readmission, recurrentAG=TRUE, hazard="Piecewise-per",nb.int=6)

##### Joint model for longitudinal ######

##### data and a terminal event ######

data(colorectal)
data(colorectalLongi)

# Survival data preparation - only terminal events
colorectalSurv <- subset(colorectal, new.lesions == 0)

model.weib.RE <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, colorectalSurv, data.Longi = colorectalLongi, random = c("1", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, hazard = "Weibull")

### Trivariate joint model for longitudinal ----
### data, recurrent and terminal events ----

data(colorectal)
data(colorectalLongi)

# (computation takes around 40 minutes)

model.spli.RE <- trivPenal(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + who.PS + terminal(state), formula.terminalEvent = age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, data = colorectal, data.Longi = colorectalLongi, random = c("1", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, recurrentAG = TRUE, n.knots = 6, kappa = c(0.01, 2), method.GH = "Pseudo-adaptive", n.nodes = 7, init.B = c(-0.07, -0.13, -0.16, -0.17, 0.42, # recurrent events covariates -0.23, -0.1, -0.09, -0.12, 0.8, -0.23, # terminal event covariates 3.02, -0.30, 0.05, -0.63, -0.02, -0.29, 0.11, 0.74)) # biomarker covariates

### Surrogacy evaluation based on generated data with a combination of Monte Carlo and classical Gaussian Hermite integration. 
### (Computation takes around 5 minutes)

# Generation of data to use
data.sim <- jointSurrSimul(n.obs = 600, n.trial = 30, cens.adm = 549.24, alpha = 1.5, theta = 3.5, gamma = 2.5, zeta = 1, sigma.s = 0.7, sigma.t = 0.7, rsqrt = 0.8, betas = -1.25, betat = -1.25, full.data = 0, random.generator = 1, seed = 0, nb.reject.data = 0)

# Joint surrogate model estimation
joint.surro.sim.MCGH <- jointSurrPenal(data = data.sim, int.method = 2, nb.mc = 300, nb.gh = 20)

## End(Not run)
Description

Fit an additive frailty model using a semiparametric penalized likelihood estimation or a parametric estimation. The main issue in a meta-analysis study is how to take into account the heterogeneity between trials and between the treatment effects across trials. Additive models are proportional hazard model with two correlated random trial effects that act either multiplicatively on the hazard function or in interaction with the treatment, which allows studying for instance meta-analysis or multicentric datasets. Right-censored data are allowed, but not the left-truncated data. A stratified analysis is possible (maximum number of strata = 2). This approach is different from the shared frailty models.

In an additive model, the hazard function for the $j$th subject in the $i$th trial with random trial effect $u_i$ as well as the random treatment-by-trial interaction $v_i$ is:

$$
\lambda_{ij}(t|u_i, v_i) = \lambda_0(t) \exp(u_i + v_i X_{ij1} + \sum_{k=1}^{p} \beta_k X_{ijk})
$$

where

$$
cov(u_i, v_i) = \rho \sigma \tau
$$

$$
u_i \sim N(0, \sigma^2), v_i \sim N(0, \tau^2)
$$

Usage

```
additivePenal(formula, data, correlation = FALSE, recurrentAG = FALSE, cross.validation = FALSE, n.knots, kappa, maxit = 350, hazard = "Splines", nb.int, LIMparam = 1e-4, LIMlogl = 1e-4, LIMderiv = 1e-3, print.times = TRUE)
```

Arguments

- `formula` a formula object, with the response on the left of a `~` operator, and the terms on the right. The response must be a survival object as returned by the 'Surv' function like in survival package. The `slope()` function is required. Interactions are possible using `*` or `:`.
- `data` a 'data.frame' with the variables used in 'formula'.
- `correlation` Logical value. Are the random effects correlated? If so, the correlation coefficient is estimated. The default is FALSE.
- `recurrentAG` Always FALSE for additive models (left-truncated data are not allowed).
- `cross.validation` Logical value. Is cross validation procedure used for estimating smoothing parameter in the penalized likelihood estimation? If so a search of the smoothing parameter using cross validation is done, with kappa as the seed. The cross validation is not implemented for two strata. The default is FALSE.
- `n.knots` integer giving the number of knots to use. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. Number of knots must be between 4 and 20. (See Note)
kappa positive smoothing parameter in the penalized likelihood estimation. In a strati-
fied additive model, this argument must be a vector with kappas for both strata.
The coefficient kappa of the integral of the squared second derivative of hazard
function in the fit. To obtain an initial value for kappa, a solution is to fit the
corresponding shared frailty model using cross validation (see cross.validation).
We advise the user to identify several possible tuning parameters, note their de-
faults and look at the sensitivity of the results to varying them. Value required.
(See Note)

maxit maximum number of iterations for the Marquardt algorithm. Default is 350
hazard Type of hazard functions: "Splines" for semiparametric hazard functions with
the penalized likelihood estimation, "Piecewise-per" for piecewise constant haz-
ards functions using percentile, "Piecewise-equi" for piecewise constant hazard
functions using equidistant intervals, "Weibull" for parametric Weibull func-
tions. Default is "Splines".

nb.int Number of intervals (between 1 and 20) for the parametric hazard functions
("Piecewise-per", "Piecewise-equi").
LIMparam Convergence threshold of the Marquardt algorithm for the parameters (see De-
tails), $10^{-4}$ by default.
LIMlogl Convergence threshold of the Marquardt algorithm for the log-likelihood (see De-
tails), $10^{-4}$ by default.
LIMderiv Convergence threshold of the Marquardt algorithm for the gradient (see Details),
$10^{-3}$ by default.
print.times a logical parameter to print iteration process. Default is TRUE.

Details

The estimated parameter are obtained by maximizing the penalized log-likelihood or by a simple
log-likelihood (in the parametric case) using the robust Marquardt algorithm (Marquardt,1963).
The parameters are initialized with values obtained with Cox proportional hazard model. The itera-
tions are stopped when the difference between two consecutive loglikelihoods was small ($<10^{-4}$),
the estimated coefficients were stable (consecutive values $<10^{-4}$), and the gradient small enough
($<10^{-3}$). To be sure of having a positive function at all stages of the algorithm, the spline co-
efficients were reparametrized to be positive at each stage. The variance space of the two random
effects is reduced, so the variances are positive, and the correlation coefficient values are constrained
to be between -1 and 1. The marginal log-likelihood depends on integrations that are approximated
by using the Laplace integration technique with a first order approximation. The smoothing pa-
rameter can be fixed or estimated by maximizing likelihood cross-validation criterion. The usual
squared Wald statistic was modified to a mixture of two $\chi^2$ distribution to get significance test for
the variance of the random effects.

INITIAL VALUES

The splines and the regression coefficients are initialized to 0.1. An adjusted Cox model is fitted, it
provides new initial values for the splines coefficients and the regression coefficients. The variances
of the frailties are initialized to 0.1. Then an additive frailty model with independent frailties is
fitted. At last, an additive frailty model with correlated frailties is fitted.
Value

An additive model or more generally an object of class 'additivePenal'. Methods defined for 'additivePenal' objects are provided for print, plot and summary.

b sequence of the corresponding estimation of the splines coefficients, the random effects variances and the regression coefficients.
call The code used for fitting the model.
coef the regression coefficients.
cov covariance between the two frailty terms \( \text{cov}(u_i, v_i) \)
cross.Val Logical value. Is cross validation procedure used for estimating the smoothing parameters in the penalized likelihood estimation?
correlation Logical value. Are the random effects correlated?
DoF degrees of freedom associated with the "kappa".
formula the formula part of the code used for the model.
groups the maximum number of groups used in the fit.
kappa A vector with the smoothing parameters in the penalized likelihood estimation corresponding to each baseline function as components.
loglikPenal the complete marginal penalized log-likelihood in the semiparametric case.
loglik the marginal log-likelihood in the parametric case.
n the number of observations used in the fit.
n.events the number of events observed in the fit.
n.iter number of iterations needed to converge.
n.knots number of knots for estimating the baseline functions.
n.strat number of stratum.
rho the corresponding correlation coefficient for the two frailty terms.
sigma2 Variance for the random intercept (the random effect associated to the baseline hazard functions).
tau2 Variance for the random slope (the random effect associated to the treatment effect across trials).
varH the variance matrix of all parameters before positivity constraint transformation (Sigma2, Tau2, the regression coefficients and the spline coefficients). Then after, the delta method is needed to obtain the estimated variance parameters.
varHIH the robust estimation of the variance matrix of all parameters (Sigma2, Tau2, the regression coefficients and the spline coefficients).
varSigma2 The variance of the estimates of "sigma2".
varTau2 The variance of the estimates of "tau2".
varcov Variance of the estimates of "cov".
x matrix of times where both survival and hazard functions are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times.
1am array (dim=3) of hazard estimates and confidence bands.
surv: array (dim=3) of baseline survival estimates and confidence bands.

type.of.hazard: Type of hazard functions (0: "Splines", 1: "Piecewise", 2: "Weibull").

type.of.Piecewise: Type of Piecewise hazard functions (1: "percentile", 0: "equidistant").

nbintervR: Number of intervals (between 1 and 20) for the parametric hazard functions ("Piecewise-per", "Piecewise-equi").

npar: number of parameters.

nvar: number of explanatory variables.

noVar: indicator of explanatory variable.

LCV: the approximated likelihood cross-validation criterion in the semiparametric case (with H minus the converged Hessian matrix, and l(.) the full log-likelihood).

\[
LCV = \frac{1}{n} \left( \text{trace} \left( H^{-1} H \right) - l(.) \right)
\]

AIC: the Akaike information Criterion for the parametric case.

\[
AIC = \frac{1}{n} (np - l(.) )
\]

n.knots.temp: initial value for the number of knots.

shape.weib: shape parameter for the Weibull hazard function.

scale.weib: scale parameter for the Weibull hazard function.

martingale.res: martingale residuals for each cluster.

desfrailty.pred: empirical Bayes prediction of the first frailty term.

frailty.pred2: empirical Bayes prediction of the second frailty term.

linear.pred: linear predictor: uses simply "Beta'X + u_i + v_i * X_1" in the additive Fraiity models.

global.chisq: a vector with the values of each multivariate Wald test.

dof.chisq: a vector with the degree of freedom for each multivariate Wald test.

global.chisq.test: a binary variable equals to 0 when no multivariate Wald is given, 1 otherwise.

p.global.chisq: a vector with the p_values for each global multivariate Wald test.

names.factor: Names of the "as.factor" variables.

Xlevels: vector of the values that factor might have taken.

contrasts: type of contrast for factor variable.

beta_p.value: p_values of the Wald test for the estimated regression coefficients.

**Note**

"kappa" and "n.knots" are the arguments that the user have to change if the fitted model does not converge. "n.knots" takes integer values between 4 and 20. But with n.knots=20, the model would take a long time to converge. So, usually, begin first with n.knots=7, and increase it step by step until it converges. "kappa" only takes positive values. So, choose a value for kappa (for instance 10000), and if it does not converge, multiply or divide this value by 10 or 5 until it converges.
References


See Also

`slope`

Examples

```r
## Not run:
### Additive model with 1 covariate

data(dataAdditive)

modAdd <- additivePenal(Surv(t1,t2,event)-cluster(group)+
  var1+slope(var1),correlation=TRUE,data=dataAdditive,
  n.knots=8, kappa=10000)

#-- Var1 is boolean as a treatment variable

## End(Not run)
```

---

### `bcos` *Breast Cosmesis Data*

**Description**

The often used data set for interval-censored data, described and given in full in Finkelstein and Wolfe (1985). It involves 94 breast cancer patients who were randomized to either radiation therapy with chemotherapy or radiation therapy alone. The outcome is time until the onset of breast retraction which is interval-censored between the last clinic visit before the event was observed and the first visit when the event was observed. Patients without breast retraction were right-censored.

**Usage**

`data(bcos)`
**Format**

A data frame with 94 observations and 3 variables:

- **left**  left end point of the breast retraction interval
- **right**  right end point of the breast retraction interval
- **treatment**  type of treatment received

**Source**


---

<table>
<thead>
<tr>
<th>cluster</th>
<th>Identify clusters</th>
</tr>
</thead>
</table>

**Description**

This is a special function used in the context of the models for grouped data. It identifies correlated groups of observations defined by using 'cluster' function, and is used of 'frailtyPenal' formula for fitting univariate and joint models.

**Usage**

```r
cluster(x)
```

**Arguments**

- **x**  A character, factor, or numeric variable which is supposed to indicate the variable group

**Value**

- **x**  A variable identified as a cluster

**See Also**

- frailtyPenal

**Examples**

```r
## Not run:
data(readmission)
modSha <- frailtyPenal(Surv(time,event)-as.factor(dukes)+cluster(id),
n.knots=10,kappa=10000,data=readmission,hazard="Splines")
```
Cmeasures

Description

Compute concordance probability estimation for Cox proportional hazard or shared frailty models in case of grouped data (Mauguen et al. 2012). Concordance is given at different levels of comparison, taking into account the cluster membership: between-groups, within-groups and an overall measure, being a weighted average of the previous two. Can also compute the c-index (Harrell et al. 1996) at these three levels. It is possible to exclude tied pairs from concordance estimation (otherwise, account for 1/2).

Usage

Cmeasures(fitc, ties = 1, marginal = 0, cindex = 0, Nboot = 0, tau = 0, data.val)

Arguments

fitc
A frailtyPenal object, for a shared frailty model. If the fit is a Cox model, no clustering membership is taken into account and only marginal concordance probability estimation is provided. Only an overall measure is given, where all patients are compared two by two. If a counting process formulation is used to performed the fit, with 't.start' and 't.stop', the gap-times (t.stop-t.start) are used in the concordance estimation.

ties
Indicates if the tied pairs on prediction value must be included (ties=1) or excluded (ties=0) from the concordance estimation. Default is ties=1. When included, tied pairs account for 1/2 in the concordance.

marginal
Indicates if the concordance based on marginal predictions must be given (marginal=1) in addition to conditional ones or not (marginal=0). Marginal predictions do not include the frailty estimation in the linear predictor computation: uses "Beta’X" instead of "Beta’X + log z_i". Default is marginal=0.

cindex
Indicates if the c-index (Harrell et al. 1996) must be computed (cindex=1) in addition to the concordance probability estimation or not (cindex=0). C-index is also given at the three comparison levels (between, within and overall). Default is cindex=0.
Cmeasures

Nboot
Number of bootstrap resamplings to compute standard-error of the concordances measures, as well as a percentile 95% confidence interval. Nboot=0 indicates no bootstrap procedure. Maximum admitted is 1000. Minimum admitted is 2. Default is 0. Resampling is done at the group level. If Cox model is used, resampling is done at individual level.

tau
Time used to limit the interval on which the concordance is estimated. Note that the survival function for the underlying censoring time distribution needs to be positive at tau. If tau=0, the maximum of the observed event times is used. Default is tau=0.

data.val
A dataframe. It is possible to specify a different dataset than the one used in the model input in the argument 'fitc'. This new dataset will be a validation population and the function will compute new concordance measures from the parameters estimated on the development population. In this case for conditional measures, the frailties are a posteriori predicted. The two datasets must have the same covariates with the same coding without missing data.

Value

call
The shared frailty model evaluated.

Frailty
Logical value. Was model with frailties fitted.

frequencies
Numbers of patients, events and groups used to fit the model.

npairs
Number of pairs of subjects, between-groups, within-groups and over all the population. If cindex=1, number of comparable (useable) pairs also available.

Nboot
Number of bootstrap resamplings required.

ties
A binary, indicating if the tied pairs on prediction were used to compute the concordance.

CPEcond
Values of Gonen & Heller’s measure (conditional). If Nboot>0, give SE, the standard-error of the parameters evaluated by bootstrap, IC.low and IC.high, the lower and upper bounds of the percentile confidence interval evaluated by bootstrap (2.5% and 97.5% percentiles).

Cunocond
Values of Uno’s measure (conditional). If Nboot>0, give SE, the standard-error of the parameters evaluated by bootstrap, IC.low and IC.high, the lower and upper bounds of the percentile confidence interval evaluated by bootstrap (2.5% and 97.5% percentiles).

marginal
A binary, indicating if the marginal values were computed.

CPEmarg
Values of Gonen & Heller’s measure (marginal), if marginal=1. If Nboot>0, give SE, the standard-error of the parameters evaluated by bootstrap, IC.low and IC.high, the lower and upper bounds of the percentile confidence interval evaluated by bootstrap (2.5% and 97.5% percentiles).

Cunomarg
Values of Uno’s measure (marginal), if marginal=1. If Nboot>0, give SE, the standard-error of the parameters evaluated by bootstrap, IC.low and IC.high, the lower and upper bounds of the percentile confidence interval evaluated by bootstrap (2.5% and 97.5% percentiles).

cindex
A binary, indicating if the c-indexes were computed.
cindexcond  Values of the C-index of Harrell (conditional). If Nboot>0, give SE, the standard-error of the parameters evaluated by bootstrap, IC.low and IC.high, the lower and upper bounds of the percentile confidence interval evaluated by bootstrap (2.5% and 97.5% percentiles).

cindexmarg  Values of the C-index of Harrell (marginal), if marginal=1. If Nboot>0, give SE, the standard-error of the parameters evaluated by bootstrap, IC.low and IC.high, the lower and upper bounds of the percentile confidence interval evaluated by bootstrap (2.5% and 97.5% percentiles).

References


See Also

`print.Cmeasures.frailtyPenal`

Examples

```r
## Not run:
#-- load data
data(readmission)

#-- a frailtypenal fit
fit <- frailtypenal(Surv(time,event)=cluster(id)+dukes+charlson+chemo,data=readmission,cross.validation=FALSE, n.knots=10,kappa=1,hazard="Splines")

#-- a Cmeasures call
fit.Cmeasures <- Cmeasures(fit)
fit.Cmeasures.noties <- Cmeasures(fit, ties=0)
fit.Cmeasures.marginal <- Cmeasures(fit, marginal=1)
fit.Cmeasures.cindex <- Cmeasures(fit, cindex=1)

#-- a short summary
fit.Cmeasures
fit.Cmeasures.noties
fit.Cmeasures.marginal
fit.Cmeasures.cindex
```
**Description**

Randomly chosen 150 patients from the follow-up of the FFCD 2000-05 multicenter phase III clinical trial originally including 410 patients with metastatic colorectal cancer randomized into two therapeutic strategies: combination and sequential. The dataset contains times of observed appearances of new lesions censored by a terminal event (death or right-censoring) with baseline characteristics (treatment arm, age, WHO performance status and previous resection).

**Usage**

data(colorectal)

**Format**

This data frame contains the following columns:

- **id**: identification of each subject. Repeated for each recurrence
- **time0**: start of interval (0 or previous recurrence time)
- **time1**: recurrence or censoring time
- **new.lesions**: Appearance of new lesions status. 0: censored or no event, 1: new lesions
- **treatment**: To which treatment arm a patient was allocated? 1: sequential (S); 2: combination (C)
- **age**: Age at baseline: 1: <50 years, 2: 50-69 years, 3: >69 years
- **who.PS**: WHO performance status at baseline: 1: status 0, 2: status 1, 3: status 2
- **prev.resection**: Previous resection of the primary tumor? 0: No, 1: Yes
- **state**: death indicator. 0: alive, 1: dead
- **gap.time**: interocurrence time or censoring time

**Note**

We thank the Federation Francophone de Cancerologie Digestive and Gustave Roussy for sharing the data of the FFCD 2000-05 trial supported by an unrestricted Grant from Sanofi.

**References**

<table>
<thead>
<tr>
<th>colorectalLongi</th>
<th>Follow-up of metastatic colorectal cancer patients: longitudinal measurements of tumor size</th>
</tr>
</thead>
</table>

**Description**

Randomly chosen 150 patients from the follow-up of the FFCD 2000-05 multicenter phase III clinical trial originally including 410 patients with metastatic colorectal cancer randomized into two therapeutic strategies: combination and sequential. The dataset contains measurements of tumor size (left-censored sums of the longest diameters of target lesions; transformed using Box-Cox) with baseline characteristics (treatment arm, age, WHO performance status and previous resection).

**Usage**

data(colorectalLongi)

**Format**

This data frame contains the following columns:

- **id** identification of each subject. Repeated for each recurrence
- **year** time of visit counted in years from baseline
- **tumor.size** Individual longitudinal measurement of transformed (Box-Cox with parameter 0.3) sums of the longest diameters, left-censored due to a detection limit (threshold $s = -3.33$).
- **treatment** To which treatment arm a patient was allocated? 1: sequential (S); 2: combination (C)
- **age** Age at baseline: 1: <50 years, 2: 50-69 years, 3: >69 years
- **who.PS** WHO performance status at baseline: 1: status 0, 2: status 1, 3: status 2
- **prev.resection** Previous resection of the primate tumor? 0: No, 1: Yes

**Note**

We thank the Federation Francophone de Cancerologie Digestive and Gustave Roussy for sharing the data of the FFCD 2000-05 trial supported by an unrestricted Grant from Sanofi.

**References**

dataAdditive

Simulated data as a gathering of clinical trials databases

Description

This contains simulated samples of 100 clusters with 100 subjects in each cluster, like a gathering of clinical trials databases. Two correlated centred gaussian random effects are generated with the same variance fixed at 0.3 and the covariance at -0.2. The regression coefficient $\beta$ is fixed at -0.11. The percentage of right-censored data is around 30 percent which are generated from a uniform distribution on [1,150]. The baseline hazard function is considered as a simple Weibull.

Usage

data(dataAdditive)

Format

This data frame contains the following columns:

- **group** identification variable
- **t1** start of interval (=0, because left-truncated data are not allowed)
- **t2** end of interval (death or censoring time)
- **event** censoring status (0:alive, 1:death, as a censoring indicator)
- **var1** dichotomous covariate (=0 or 1, as a treatment variable)
- **var2** dichotomous covariate (=0 or 1, as a treatment variable)

Source


dataMultiv

Simulated data for two types of recurrent events and a terminal event

Description

This contains a simulated sample of 800 subjects and 1652 observations. This dataset can be used to illustrate how to fit a joint multivariate frailty model. Two gaussian correlated random effects were generated with mean 0, variances 0.5 and a correlation coefficient equals to 0.5. The coefficients $\alpha_1$ and $\alpha_2$ were fixed to 1. The three baseline hazard functions followed a Weibull distribution and right censoring was fixed at 5.
Usage
dataNCC

dataMultiv

Format
This data frame contains the following columns:

PATIENT identification of patient
obs number of observation for a patient
TIME0 start of interval
TIME1 end of interval (death or censoring time)
INDICREC recurrent of type 1 status (0:no, 1:yes)
INDICMETA recurrent of type 2 status (0:no, 1:yes)
INDICDEATH censoring status (0: alive, 1: death)
v1 dichotomous covariate (0,1)
v2 dichotomous covariate (0,1)
v3 dichotomous covariate (0,1)
TIMEGAP time to event

Description
This contains a simulated sample of 819 subjects and 1510 observations. This dataset can be used to illustrate how to fit a joint frailty model for data from nested case-control studies.

Usage
dataNCC

data(datancc)

Format
This data frame contains the following columns:
id identification of patient
cov1 dichotomous covariate (0,1)
cov2 dichotomous covariate (0,1)
t.start start of interval
t.stop end of interval (death or censoring time)
gaptime time to event
event recurrent event status (0:no, 1:yes)
**dataNested**

- **deathdays**: time of terminal event (death or right-censoring)
- **death**: censoring status (0: alive, 1: death)
- **ncc.wts**: weights for NCC design

---

**Simulated data with two levels of grouping**

**Description**

This contains a simulated sample of 400 observations which allow establishing 20 clusters with 4 subgroups and 5 subjects in each subgroup, in order to obtain two levels of grouping. This data set is useful to illustrate how to fit a nested model. Two independent gamma frailty parameters with a variance fixed at 0.1 for the cluster effect and at 0.5 for the subcluster effect were generated. Independent survival times were generated from a simple Weibull baseline risk function. The percentage of censoring data was around 30 per cent. The right-censoring variables were generated from a uniform distribution on [1, 36] and a left-truncating variable was generated with a uniform distribution on [0, 10]. Observations were included only if the survival time is greater than the truncated time.

**Usage**

```r
data(dataNested)
```

**Format**

This data frame contains the following columns:

- **group**: group identification variable
- **subgroup**: subgroup identification variable
- **t1**: start of interval (0 or truncated time)
- **t2**: end of interval (death or censoring time)
- **event**: censoring status (0: alive, 1: death)
- **cov1**: dichotomous covariate (0, 1)
- **cov2**: dichotomous covariate (0, 1)

**Source**

Data Description

Advanced Ovarian Cancer dataset

This dataset combines the data that were collected in four double-blind randomized clinical trials in advanced ovarian cancer. In these trials, the objective was to examine the efficacy of cyclophosphamide plus cisplatin (CP) versus cyclophosphamide plus adriamycin plus cisplatin (CAP) to treat advanced ovarian cancer. The candidate surrogate endpoint $S$ is progression-free survival time, defined as the time (in years) from randomization to clinical progression of the disease or death. The true endpoint $T$ is survival time, defined as the time (in years) from randomization to death of any cause.

Usage

data(dataOvarian)

Format

This data frame contains the following columns:

- **patientID**: The identification number of a patient
- **trialID**: The center in which a patient was treated
- **trt**: The treatment indicator, coded as $0 = \text{cyclophosphamide plus cisplatin (CP)}$ and $1 = \text{cyclophosphamide plus adriamycin plus cisplatin (CAP)}$
- **timeS**: The candidate surrogate (progression-free survival)
- **statusS**: Censoring indicator for Progression-free survival
- **timeT**: The true endpoint (survival time)
- **statusT**: Censoring indicator for survival time

Source

**Description**

This function computes the difference of two EPOCE estimates (CVPOL and MPOL) and its 95% tracking interval between two joint models estimated using frailtyPenal, longiPenal or trivPenal. Difference in CVPOL is computed when the EPOCE was previously estimated on the same dataset as used for estimation (using an approximated cross-validation), and difference in MPOL is computed when the EPOCE was previously estimated on an external dataset.

**Usage**

```r
Diffepoce(epoce1, epoce2)
```

**Arguments**

- `epoce1`: a first object inheriting from class epoce.
- `epoce2`: a second object inheriting from class epoce.

**Details**

From the EPOCE estimates and the individual contributions to the prognostic observed log-likelihood obtained with epoce function on the same dataset from two different estimated joint models, the difference of CVPOL (or MPOL) and its 95% tracking interval is computed. The 95% tracking interval is: \( \Delta(\text{CVPOL}) \pm qnorm(0.975) \times \sqrt{\text{VARIANCE}} \) for an external dataset \( \Delta(\text{MPOL}) \pm qnorm(0.975) \times \sqrt{\text{VARIANCE}} \) for the dataset used in frailtyPenal, longiPenal or trivPenal where \( \Delta(\text{CVPOL}) \) (or \( \Delta(\text{MPOL}) \)) is the difference of CVPOL (or MPOL) of the two joint models, and \( \text{VARIANCE} \) is the empirical variance of the difference of individuals contributions to the prognostic observed log-likelihoods of the two joint models.

The estimators of EPOCE from arguments `epoce1` and `epoce2` must have been computed on the same dataset and with the `pred.times`.

**Value**

- `new.data`: a boolean which is FALSE if computation is done on the same data as for estimation, and TRUE otherwise
- `pred.times`: time or vector of times used in the function
- `DEPOCE`: the difference between the two MPOL or CVPOL for each time
- `TIlinf`: lower confidence band for the difference
- `TIlsup`: upper confidence band for the difference
References


Examples

```r
## Not run:
# Example for joint frailty models
data(readmission)

# first joint frailty model
joint1 <- frailtyPenal(Surv(t.start, t.stop, event) ~ cluster(id) +
                      dukes + charlson + sex + chemo + terminal(death),
                      formula.terminalEvent = ~ dukes + charlson + sex + chemo,  
                      data = readmission, n.knots = 8, kappa = c(2.11e+08, 9.53e+11),
                      recurrentAG=TRUE)

# second joint frailty model without dukes nor charlson as covariates
joint2 <- frailtyPenal(Surv(t.start, t.stop, event) ~ cluster(id) +
                      sex + chemo + terminal(death),
                      formula.terminalEvent = ~ sex + chemo, 
                      data = readmission, n.knots = 8, kappa = c(2.11e+08, 9.53e+11),
                      recurrentAG=TRUE)

temps <- c(200, 500, 800, 1100)

# computation of estimators of EPOCE for the two models
epoce1 <- epoce(joint1, temps)
epoce2 <- epoce(joint2, temps)

# computation of the difference
diff <- Diffepeoce(epoce1, epoce2)
print(diff)
plot(diff)

# Example for joint models with a biomarker
data(colorectal)
data(colorectallongi)

# Survival data preparation - only terminal events
colorectalSurv <- subset(colorectal, new.lesions == 0)

# first joint model for a biomarker and a terminal event
modLongi <- longiPenal(Surv(time0, time1, state) ~ age +
treatment + who.PS, tumor.size ~ year*treatment + age +
who.PS, colorectalSurv, data.Longi = colorectallongi,)
```
Estimators of the Expected Prognostic Observed Cross-Entropy (EPOCE) for evaluating predictive accuracy of joint models.

Description

This function computes estimators of the Expected Prognostic Observed Cross-Entropy (EPOCE) for evaluating the predictive accuracy of joint models using frailtyPenal, longiPenal, trivPenal or trivPenalNL. On the same data as used for estimation of the joint model, this function computes both the Mean Prognosis Observed Loss (MPOL) and the Cross-Validated Prognosis Observed Loss (CVPOL), two estimators of EPOCE. The latter corrects the MPOL estimate for over-optimism by approximated cross-validation. On external, this function only computes MPOL.

Usage

epoce(fit, pred.times, newdata = NULL, newdata.Longi = NULL)
Arguments

fit A jointPenal, longiPenal, trivPenal or trivPenalNL object.
pred.times Time or vector of times to compute epoce.
newdata Optional. In case of joint models obtained with frailtyPenal, trivPenal or
trivPenalNL. For models inheriting from trivPenal or trivPenalNL class, if
newdata is given, newdata.Longi must be given as well. When missing, the
data used for estimating the fit are used, and CVPOL and MPOL are computed
(internal validation). When newdata is specified, only MPOL is computed on
this new dataset (external validation). The new dataset and the dataset used
in the estimation must have the same covariates with the same coding without
missing data.
newdata.Longi Optional. In case of joint models obtained with longiPenal, trivPenal or
trivPenalNL. For models inheriting from longiPenal, if the newdata.Longi
is given, newdata must be NULL, but for models from trivPenal or trivPenalNL
class, if newdata.Longi is given, newdata must be provided as well. The two
datasets newdata and newdata.Longi must include the information concerning
the same patients with the same characteristics and the appropriate data on fol-
low up (recurrences for newdata and longitudinal measurements for newdata.Longi).

Value

data name of the data used to compute epoce
new.data a boolean which is FALSE if computation is done on the same data as for esti-
mation, and TRUE otherwise
pred.times time or vector of times used in the function
mpol values of MPOL for each pred.times
cvpol values of CVPOL for each pred.times
IndivContrib all the contributions to the log-likelihood for each pred.times
AtRisk number of subject still at risk for each pred.times

References

by estimating differences of expected conditional Kullback-Leibler risks. *Biometrics*, 68(2), 380-
387.

Examples

```r
## Not run:

#############################################################
#### EPOCE on a joint frailty model ####
#############################################################

data(readmission)
```
modJoint.gap <- frailtyPenal(Surv(t.start, t.stop, event) ~ cluster(id) +
dukes + charlson + sex + chemo + terminal(death),
formula.terminalEvent = ~ dukes + charlson + sex + chemo,
data = readmission, n.knots = 8, kappa =c(2.11e+08, 9.53e+11),
recurrentAG=TRUE)

# computation on the same dataset
temps <- c(200, 500, 800, 1100)
epoke <- epoce(modJoint.gap, temps)

print(epoce)
plot(epoce, type = "cvpol")

# computation on a new dataset
# here a sample of readmission with the first 50 subjects
s <- readmission[1:100,]
epoke <- epoce(modJoint.gap, temps, newdata=s)

print(epoce)
plot(epoce, type = "cvpol")

******************************************************************************
EPOCE on a joint model for a biomarker and a terminal event
******************************************************************************
data(colorectal)
data(colorectallongi)

# Survival data preparation - only terminal events
colorectalSurv <- subset(colorectal, new.lesions == 0)

modLongi <- longiPenal(Surv(time0, time1, state) ~ age +
treatment + who.PS, tumor.size ~ year*treatment + age +
who.PS, colorectalSurv, data.Longi =colorectallongi,
random = c("1", "year"), id = "id", link = "Random-effects",
left.censoring = -3.33, hazard = "Weibull",
method.GH = "Pseudo-adaptive")

# computation on the same dataset
time <- c(1, 1.5, 2, 2.5)
epoke <- epoce(modLongi, time)

print(epoce)
plot(epoce, type = "cvpol")

# computation on a new dataset
# here a sample of colorectal data with the first 50 subjects
s <- subset(colorectal, new.lesions == 0 & id%in%1:50)
s.Longi <- subset(colorectallongi, id%in%1:50)
epoke <- epoce(modLongi, time, newdata = s, newdata.Longi = s.Longi)
print(epoce)
plot(epoce, type = "cvpol")

--------------------------------------------------------------------------------
#### EPOCE on a joint model for a biomarker, ####
#### recurrent events and a terminal event ####
--------------------------------------------------------------------------------
data(colorectal)
data(colorectallongi)

# Linear model for the biomarker
# (computation takes around 30 minutes)
model.trivPenalNL <- trivPenal(Surv(gap.time, new.lesions) ~ cluster(id) + age + treatment + who.PS + prev.resection + terminal(state),
formula.terminalEvent =~ age + treatment + who.PS + prev.resection,
tumor.size ~ year * treatment + age + who.PS, data = colorectal,
data.Longi = colorectallongi, random = c("1", "year"), id = "id",
link = "Random-effects", left.censoring = -3.33, recurrentAG = FALSE,
hazard = "Weibull", method.GH="Pseudo-adaptive", n.nodes=7)

# computation on the same dataset
time <- c(1, 1.5, 2, 2.5)
epoce <- epoce(model.trivPenalNL, time)
print(epoce)
plot(epoce, type = "cvpol")

# computation on a new dataset
# here a sample of colorectal data with the first 100 subjects
s <- subset(colorectal, id%in%1:100)
s.Longi <- subset(colorectallongi, id%in%1:100)
# (computation takes around 10 minutes)
epoce <- epoce(model.trivPenalNL, time, newdata = s, newdata.Longi = s.Longi)

print(epoce)
plot(epoce, type = "cvpol")

# Non-linear model for the biomarker

# No information on dose - creation of a dummy variable
colorectallongi$dose <- 1

# (computation can take around 40 minutes)
model.trivPenalNL <- trivPenal(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + terminal(state), formula.terminalEvent =~ age + treatment, biomarker = "tumor.size",
formula.KG =~ 1, formula.KD ~ treatment, dose = "dose", time.biomarker = "year",
data = colorectal, data.Longi = colorectallongi, random = c("y0", "KG"), id = "id",
init.B = c(-0.22, -0.16, -0.35, -0.19, 0.04, -0.41, 0.23), init.Alpha = 1.86,
event2


describe event2

Description

This is a special function used in the context of multivariate frailty model with two types of recurrent events and a terminal event (e.g., censoring variable related to both recurrent events). It contains the indicator of the recurrent event of type 2, normally 0=no event, 1=event, and is used on the right hand side of a formula of a `multivPenal` object. Using event2() in a formula implies that a multivariate frailty model for two types of recurrent events and a terminal event is fitted.

Usage

`event2(x)`

Arguments

`x`  
A numeric variable but should be a boolean which equals 1 if the subject has experienced an event of type 2 and 0 if not.

Value

`x`  
an indicator for an event of type 2

See Also

`multivPenal`
fit a shared, joint or nested frailty model

**Description**

**Shared Frailty model**

Fit a shared gamma or log-normal frailty model using a semiparametric Penalized Likelihood estimation or parametric estimation on the hazard function. Left-truncated, right-censored data, interval-censored data and strata (up to 6 levels) are allowed. It allows to obtain a non-parametric smooth hazard of survival function. This approach is different from the partial penalized likelihood approach of Therneau et al.

The hazard function, conditional on the frailty term $\omega_i$, of a shared gamma frailty model for the $j^{th}$ subject in the $i^{th}$ group:

$$
\lambda_{ij}(t|\omega_i) = \lambda_0(t)\omega_i \exp(\beta^{'Z}_{ij})
$$

$$
\omega_i \sim \Gamma \left( \frac{1}{\theta}, \frac{1}{\theta} \right) \quad E(\omega_i) = 1 \quad Var(\omega_i) = \theta
$$

where $\lambda_0(t)$ is the baseline hazard function, $\beta$ the vector of the regression coefficient associated to the covariate vector $Z_{ij}$ for the $j^{th}$ individual in the $i^{th}$ group.

Otherwise, in case of a shared log-normal frailty model, we have for the $j^{th}$ subject in the $i^{th}$ group:

$$
\lambda_{ij}(t|\eta_i) = \lambda_0(t) \exp(\eta_i + \beta^{'Z}_{ij})
$$

$$
\eta_i \sim N(0, \sigma^2)
$$

From now on, you can also consider time-varying effects covariates in your model, see timedep function for more details.

**Joint Frailty model**

Fit a joint either with gamma or log-normal frailty model for recurrent and terminal events using a penalized likelihood estimation on the hazard function or a parametric estimation. Right-censored data and strata (up to 6 levels) for the recurrent event part are allowed. Left-truncated data is not possible. Joint frailty models allow studying, jointly, survival processes of recurrent and terminal events, by considering the terminal event as an informative censoring.

There is two kinds of joint frailty models that can be fitted with frailtyPenal:

- The first one (Rondeau et al. 2007) includes a common frailty term to the individuals ($\omega_i$) for the two rates which will take into account the heterogeneity in the data, associated with unobserved covariates. The frailty term acts differently for the two rates ($\omega_i$ for the recurrent rate and $\omega^*_i$ for the death rate). The covariates could be different for the recurrent rate and death rate.

For the $j^{th}$ recurrence ($j = 1, ..., n_i$) and the $i^{th}$ subject ($i = 1, ..., G$), the joint gamma frailty model for recurrent event hazard function $r_{ij}(\cdot)$ and death rate $\lambda_i(\cdot)$ is:
{ \begin{align*} r_{ij}(t|\omega_i) & = \omega_i r_0(t) \exp(\beta_1^i Z_i(t)) \quad \text{(Recurrent)} \\ \lambda_{ij}(t|\omega_i) & = \omega_i^\alpha \lambda_0(t) \exp(\beta_2^i Z_i(t)) \quad \text{(Death)} \end{align*} }

where \( r_0(t) \) (resp. \( \lambda_0(t) \)) is the recurrent (resp. terminal) event baseline hazard function, \( \beta_1 \) (resp. \( \beta_2 \)) the regression coefficient vector, \( Z_i(t) \) the covariate vector. The random effects of frailties \( \omega_i \sim \Gamma(\frac{1}{\gamma}, \frac{1}{\theta}) \) and are iid.

The joint log-normal frailty model will be:

{ \begin{align*} r_{ij}(t|\eta_i) & = r_0(t) \exp(\eta_i + \beta_1^i Z_{ij}(t)) \quad \text{(Time to event)} \\ \lambda_{ij}(t|\eta_i) & = \lambda_0(t) \exp(\alpha \eta_i + \beta_2^i Z_{ij}(t)) \quad \text{(Death)} \end{align*} }

where \( \eta_i \sim N(0, \sigma^2) \)

- The second one (Rondeau et al. 2011) is quite similar but the frailty term is common to the individuals from a same group. This model is useful for the joint modelling two clustered survival outcomes. This joint models have been developed for clustered semi-competing events. The follow-up of each of the two competing outcomes stops when the event occurs. In this case, \( j \) is for the subject and \( i \) for the cluster.

{ \begin{align*} r_{ij}(t|u_i) & = u_i r_0(t) \exp(\beta_1^i Z_{ij}(t)) \quad \text{(Time to event)} \\ \lambda_{ij}(t|u_i) & = u_i^\alpha \lambda_0(t) \exp(\beta_2^i Z_{ij}(t)) \quad \text{(Death)} \end{align*} }

It should be noted that in these models it is not recommended to include \( \alpha \) parameter as there is not enough information to estimate it and thus there might be convergence problems.

In case of a log-normal distribution of the frailties, we will have:

{ \begin{align*} r_{ij}(t|v_i) & = r_0(t) \exp(v_i + \beta_1^i Z_{ij}(t)) \quad \text{(Time to event)} \\ \lambda_{ij}(t|v_i) & = \lambda_0(t) \exp(\alpha v_i + \beta_2^i Z_{ij}(t)) \quad \text{(Death)} \end{align*} }

where \( v_i \sim N(0, \sigma^2) \)

This joint frailty model can also be applied to clustered recurrent events and a terminal event (example on "readmission" data below).

From now on, you can also consider time-varying effects covariates in your model, see timedep function for more details.

There is a possibility to use a weighted penalized maximum likelihood approach for nested case-control design, in which risk set sampling is performed based on a single outcome (Jazic et al., Submitted).

General Joint Frailty model Fit a general joint frailty model for recurrent and terminal events considering two independent frailty terms. The frailty term \( u_i \) represents the unobserved association between recurrences and death. The frailty term \( v_i \) is specific to the recurrent event rate. Thus, the general joint frailty model is:

{ \begin{align*} r_{ij}(t|u_i, v_i) & = r_0(t) \exp(\beta_1^i Z_{ij}(t) + v_i) \quad \text{(Time to event)} \\ \lambda_{ij}(t|u_i, v_i) & = \lambda_0(t) \exp(\alpha v_i + \beta_2^i Z_{ij}(t)) \quad \text{(Death)} \end{align*} }

where \( v_i \sim N(0, \sigma^2) \)
Joint nested frailty model

Data should be ordered according to cluster and subcluster

Fit a joint frailty model using a Penalized Likelihood on the hazard function or using a parametric estimation. Nested frailty models allow survival studies for hierarchically clustered data by including two iid gamma random effects. Left-truncated and right-censored data are allowed. Stratification analysis is allowed (maximum of strata = 2).

The hazard function conditional on the two frailties \( v_i \) and \( w_{ij} \) for the \( k^{th} \) individual of the \( j^{th} \) subgroup of the \( i^{th} \) group is:

\[
\begin{align*}
\lambda_{ijk}(t|v_i, w_{ij}) &= \lambda_0(t)\exp(\beta'X_{ijk}) \\
v_i &\sim \Gamma\left(\frac{1}{\alpha}, \frac{1}{\alpha}\right) \text{ i.i.d. } E(v_i) = 1 \text{ Var}(v_i) = \alpha \\
w_{ij} &\sim \Gamma\left(\frac{1}{\eta}, \frac{1}{\eta}\right) \text{ i.i.d. } E(w_{ij}) = 1 \text{ Var}(w_{ij}) = \eta
\end{align*}
\]

where \( \lambda_0(t) \) is the baseline hazard function, \( X_{ijk} \) denotes the covariate vector and \( \beta \) the corresponding vector of regression parameters.

Joint Nested Frailty Model

Fit a joint model for recurrent and terminal events using a penalized likelihood on the hazard functions or a parametric estimation. Right-censored data are allowed but left-truncated data and stratified analysis are not allowed.

Joint nested frailty models allow studying, jointly, survival processes of recurrent and terminal events for hierarchically clustered data, by considering the terminal event as an informative censoring and by including two iid gamma random effects.

The joint nested frailty model includes two shared frailty terms, one for the subgroup \( (u_{fi}) \) and one for the group \( (w_f) \) into the hazard functions. This random effects account the heterogeneity in the data, associated with unobserved covariates. The frailty terms act differently for the two rates \( (u_{fi}, w_f^\xi \text{ for recurrent rate and } u_{fi}^{\eta}, w_f^\eta \text{ for the terminal event rate}) \). The covariates could be different for the recurrent rate and death rate.

For the \( j^{th} \) recurrence \( (j = 1, \ldots, n_i) \) of the \( i^{th} \) individual \( (i = 1, \ldots, m_f) \) of the \( f^{th} \) group \( (f = 1, \ldots, n) \), the joint nested gamma frailty model for recurrent event hazard function \( r_{fij}(\cdot) \) and for terminal event hazard function \( \lambda_{fi} \) is:

\[
\begin{align*}
\{ r_{fij}(t|\omega_f, u_{fi}, X_{fij}) &= r_0(t)u_{fi}\omega_f^\xi \exp(\beta'X_{fij}) \quad \text{(Recurrent)} \\
\lambda_{fi}(t|\omega_f, u_{fi}, X_{fij}) &= \lambda_0(t)u_{fi}^{\eta}\omega_f \exp(\gamma'X_{fi}) \quad \text{(Death)}
\end{align*}
\]

where \( r_0(t) \) (resp. \( \lambda_0(t) \)) is the recurrent (resp. terminal) event baseline hazard function, \( \beta \) (resp. \( \gamma \)) the regression coefficient vector, \( X_{fij}(t) \) the covariates vector. The random effects are

\[ \omega_f \sim \Gamma\left(\frac{1}{\eta}, \frac{1}{\eta}\right) \]
and

\[ u_{fi} \sim \Gamma \left( \frac{1}{\theta}, \frac{1}{\theta} \right) \]

Usage


Arguments

formula a formula object, with the response on the left of a \( \sim \) operator, and the terms on the right. The response must be a survival object as returned by the 'Surv' function like in survival package. In case of interval-censored data, the response must be an object as returned by the 'SurvIC' function from this package. Interactions are possible using * or ::.

formula.terminalEvent only for joint and joint nested frailty models : a formula object, only requires terms on the right to indicate which variables are modelling the terminal event. Interactions are possible using * or ::.

data a 'data.frame' with the variables used in 'formula'.

recurrentAG Logical value. Is Andersen-Gill model fitted? If so indicates that recurrent event times with the counting process approach of Andersen and Gill is used. This formulation can be used for dealing with time-dependent covariates. The default is FALSE.

cross.validation Logical value. Is cross validation procedure used for estimating smoothing parameter in the penalized likelihood estimation? If so a search of the smoothing parameter using cross validation is done, with kappa as the seed. The cross validation is not implemented for several strata, neither for interval-censored data. The cross validation has been implemented for a Cox proportional hazard model, with no covariates. The default is FALSE.

jointGeneral Logical value. Does the model include two independent random effects? If so, this will fit a general joint frailty model with an association between the recurrent events and a terminal event (explained by the variance \( \theta \)) and an association amongst the recurrent events (explained by the variance \( \eta \)).

n.knots integer giving the number of knots to use. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. We estimate I or M-splines of order 4. When the user set a number of knots equals to k (n.knots=k) then the number of interior knots is (k-2) and the number of splines is (k-2)+order. Number of knots must be between 4 and 20. (See Note)
kappa
positive smoothing parameter in the penalized likelihood estimation. In a stratified shared model, this argument must be a vector with kappas for both strata. In a stratified joint model, this argument must be a vector with kappas for both strata for recurrent events plus one kappa for terminal event. The coefficient kappa of the integral of the squared second derivative of hazard function in the fit (penalized log likelihood). To obtain an initial value for kappa, a solution is to fit the corresponding shared frailty model using cross validation (See cross.validation). We advise the user to identify several possible tuning parameters, note their defaults and look at the sensitivity of the results to varying them. Value required. (See Note).

maxit
maximum number of iterations for the Marquardt algorithm. Default is 300

hazard
Type of hazard functions: "Splines" for semiparametric hazard functions using equidistant intervals or "Splines-per" using percentile with the penalized likelihood estimation, "Piecewise-per" for piecewise constant hazard function using percentile (not available for interval-censored data), "Piecewise-equi" for piecewise constant hazard function using equidistant intervals, "Weibull" for parametric Weibull functions. Default is "Splines". In case of jointGeneral = TRUE or if a joint nested frailty model is fitted, only hazard = "Splines" can be chosen.

nb.int
Number of time intervals (between 1 and 20) for the parametric hazard functions ("Piecewise-per", "Piecewise-equi"). In a joint model, you need to specify a number of time interval for both recurrent hazard function and the death hazard function (vector of length 2).

RandDist
Type of random effect distribution: "Gamma" for a gamma distribution, "LogN" for a log-normal distribution. Default is "Gamma". Not implemented for nested model. If jointGeneral = TRUE or if a joint nested frailty model is fitted, the log-normal distribution cannot be chosen.

betaknots
Number of inner knots used for the estimation of B-splines. Default is 1. See 'timedep' function for more details. Not implemented for nested and joint nested frailty models.

betaorder
Order of the B-splines. Default is cubic B-splines (order = 3). See 'timedep' function for more details. Not implemented for nested and joint nested frailty models.

initialize
Logical value, only for joint nested frailty models. Option TRUE indicates fitting an appropriate standard joint frailty model (without group effect, only the subgroup effect) to provide initial values for the joint nested model. Default is TRUE.

init.B
A vector of initial values for regression coefficients. This vector should be of the same size as the whole vector of covariates with the first elements for the covariates related to the recurrent events and then to the terminal event (interactions in the end of each component). Default is 0.1 for each (for Cox and shared model) or 0.5 (for joint and joint nested frailty models).

init.Theta
Initial value for variance of the frailties.

init.Alpha
Only for joint and joint nested frailty models: initial value for parameter alpha.

Alpha
Only for joint and joint nested frailty model: input "None" so as to fit a joint model without the parameter alpha.
**frailtyPenal**

init.Ksi  
Only for joint nested frailty model: initial value for parameter $\xi$.

Ksi  
Only for joint nested frailty model: input "None" indicates a joint nested frailty model without the parameter $\xi$.

init.Eta  
Only for general joint and joint nested frailty models: initial value for the variance $\eta$ of the frailty $v_i$ (general joint model) and of the frailty $\omega_i$ (joint nested frailty model).

LIMparam  
Convergence threshold of the Marquardt algorithm for the parameters (see Details), $10^{-3}$ by default.

LIMlogl  
Convergence threshold of the Marquardt algorithm for the log-likelihood (see Details), $10^{-3}$ by default.

LIMderiv  
Convergence threshold of the Marquardt algorithm for the gradient (see Details), $10^{-3}$ by default.

print.times  
a logical parameter to print iteration process. Default is TRUE.

**Details**

Typical usages are for a Cox model

```r
frailtyPenal(Surv(time, event) ~ var1+var2, data, ...)
```

for a shared model

```r
frailtyPenal(Surv(time, event) ~ cluster(group)+var1+var2, data, ...)
```

for a joint model

```r
frailtyPenal(Surv(time, event) ~ cluster(group)+var1+var2+ var3+terminal(death), formula.terminalEvent=~ var1+var4, data, ...)
```

for a joint model for clustered data

```r
frailtyPenal(Surv(time, event) ~ cluster(group)+num.id(group2)+ var1+var2+var3+terminal(death), formula.terminalEvent=~ var1+var4, data, ...)
```

for a joint model for data from nested case-control studies

```r
frailtyPenal(Surv(time, event) ~ cluster(group)+num.id(group2)+ var1+var2+var3+terminal(death)+wts(wts.ncc), formula.terminalEvent=~var1+var4, data, ...)
```

for a nested model

```r
frailtyPenal(Surv(time, event) ~ cluster(group)+subcluster(sbgroup)+ var1+var2, data, ...)
```

for a joint nested frailty model
frailtyPenal(Surv(time, event)~cluster(group)+subcluster(sbgroup)+
var1+var2++terminal(death), formula.terminalEvent=~var1+var4, data, ...)

The estimated parameter are obtained using the robust Marquardt algorithm (Marquardt, 1963) which is a combination between a Newton-Raphson algorithm and a steepest descent algorithm. The iterations are stopped when the difference between two consecutive log-likelihoods was small ($< 10^{-3}$), the estimated coefficients were stable (consecutive values ($< 10^{-3}$), and the gradient small enough ($< 10^{-3}$). When frailty parameter is small, numerical problems may arise. To solve this problem, an alternative formula of the penalized log-likelihood is used (see Rondeau, 2003 for further details). Cubic M-splines of order 4 are used for the hazard function, and I-splines (integrated M-splines) are used for the cumulative hazard function.

The inverse of the Hessian matrix is the variance estimator and to deal with the positivity constraint of the variance component and the spline coefficients, a squared transformation is used and the standard errors are computed by the $\Delta$-method (Knight & Xekalaki, 2000). The smooth parameter can be chosen by maximizing a likelihood cross validation criterion (Joly and other, 1998). The integrations in the full log likelihood were evaluated using Gaussian quadrature. Laguerre polynomials with 20 points were used to treat the integrations on $[0, \infty[$.

INITIAL VALUES

The splines and the regression coefficients are initialized to 0.1. In case of shared model, the program fits, firstly, an adjusted Cox model to give new initial values for the splines and the regression coefficients. The variance of the frailty term $\theta$ is initialized to 0.1. Then, a shared frailty model is fitted.

In case of a joint frailty model, the splines and the regression coefficients are initialized to 0.5. The program fits an adjusted Cox model to have new initial values for the regression and the splines coefficients. The variance of the frailty term $\theta$ and the coefficient $\alpha$ associated in the death hazard function are initialized to 1. Then, it fits a joint frailty model.

In case of a general joint frailty model we need to initialize the jointGeneral logical value to TRUE.

In case of a nested model, the program fits an adjusted Cox model to provide new initial values for the regression and the splines coefficients. The variances of the frailties are initialized to 0.1. Then, a shared frailty model with covariates with only subgroup frailty is fitted to give a new initial value for the variance of the subgroup frailty term. Then, a shared frailty model with covariates and only group frailty terms is fitted to give a new initial value for the variance of the group frailties. In a last step, a nested frailty model is fitted.

In case of a joint nested model, the splines and the regression coefficients are initialized to 0.5 and the variances of the frailty terms $\eta$ and $\xi$ are initialized to 1. If the option 'initialize' is TRUE, the program fits a joint frailty model to provide initial values for the splines, covariates coefficients, variance $\theta$ of the frailty terms and $\alpha$. The variances of the second frailty term ($\eta$) and the second coefficient $\xi$ are initialized to 1. Then, a joint nested frailty model is fitted.

NCC DESIGN

It is possible to fit a joint frailty model for data from nested case-control studies using the approach of weighted penalized maximum likelihood. For this model, only splines can be used for baseline hazards and no time-varying effects of covariates can be included. To accommodate the nested case-control design, the formula for the recurrent events should simply include the special term wts(wts.ncc), where wts.ncc refers to a column of prespecified weights in the data set for every observation. For details, see Jazic et al., Submitted (available on request from the package authors).
Value

The following components are included in a 'frailtyPenal' object for each model.

- **b**: sequence of the corresponding estimation of the coefficients for the hazard functions (parametric or semiparametric), the random effects variances and the regression coefficients.
- **call**: The code used for the model.
- **formula**: the formula part of the code used for the model.
- **coef**: the regression coefficients.
- **crossVal**: Logical value. Is cross validation procedure used for estimating the smoothing parameters in the penalized likelihood estimation?
- **DoF**: Degrees of freedom associated with the "kappa".
- **groups**: the maximum number of groups used in the fit.
- **kappa**: A vector with the smoothing parameters in the penalized likelihood estimation corresponding to each baseline function as components.
- **loglikPenal**: the complete marginal penalized log-likelihood in the semiparametric case.
- **loglik**: the marginal log-likelihood in the parametric case.
- **n**: the number of observations used in the fit.
- **n.events**: the number of events observed in the fit.
- **n.iter**: number of iterations needed to converge.
- **n.knots**: number of knots for estimating the baseline functions in the penalized likelihood estimation.
- **n.strat**: number of stratum.
- **varH**: the variance matrix of all parameters before positivity constraint transformation. Then, the delta method is needed to obtain the estimated variance parameters. That is why some variances don’t match with the printed values at the end of the model.
- **varHIH**: the robust estimation of the variance matrix of all parameters.
- **x**: matrix of times where both survival and hazard function are estimated. By default `seq(0,max(time),length=99)`, where time is the vector of survival times.
- **lam**: array (dim=3) of hazard estimates and confidence bands.
- **surv**: array (dim=3) of baseline survival estimates and confidence bands.
- **nbintervR**: Number of intervals (between 1 and 20) for the parametric hazard functions ("Piecewise-per", "Piecewise-equi").
- **npar**: number of parameters.
- **nvar**: number of explanatory variables.
- **LCV**: the approximated likelihood cross-validation criterion in the semiparametric case (with $H$ minus the converged Hessian matrix, and $l(.)$ the full log-likelihood).

\[
LCV = \frac{1}{n} \left( \text{trace}(H^{-1}H) - l(.) \right)
\]
AIC: the Akaike information Criterion for the parametric case.
\[ AIC = \frac{1}{n} (np - l(.) ) \]

n.knots.temp: initial value for the number of knots.
shape.weib: shape parameter for the Weibull hazard function.
scale.weib: scale parameter for the Weibull hazard function.
martingale.res: martingale residuals for each cluster.
martingaleCox: martingale residuals for observation in the Cox model.
Frailty: Logical value. Was model with frailties fitted?
frailty.pred: empirical Bayes prediction of the frailty term (i.e., using conditional posterior distributions).
frailty.var: variance of the empirical Bayes prediction of the frailty term (only for gamma frailty models).
frailty.sd: standard error of the frailty empirical Bayes prediction (only for gamma frailty models).
global_chisq: a vector with the values of each multivariate Wald test.
dof_chisq: a vector with the degree of freedom for each multivariate Wald test.
global_chisqN.test: a binary variable equals to 0 when no multivariate Wald is given, 1 otherwise.
p.global_chisq: a vector with the p_values for each global multivariate Wald test.
names.factor: Names of the "as.factor" variables.
xlevels: vector of the values that factor might have taken.
contrasts: type of contrast for factor variable.
beta_p.value: p-values of the Wald test for the estimated regression coefficients.

The following components are specific to shared models.
equidistant: Indicator for the intervals used the estimation of baseline hazard functions (for splines or piecewise-constant functions): 1 for equidistant intervals; 0 for intervals using percentile (note: equidistant = 2 in case of parametric estimation using Weibull distribution).
intcens: Logical value. Indicator if a joint frailty model with interval-censored data was fitted.
theta: variance of the gamma frailty parameter \( \text{Var}(\omega_i) \)
sigma2: variance of the log-normal frailty parameter \( \text{Var}(\eta_i) \)
linear.pred: linear predictor: uses simply "Beta'X" in the cox proportional hazard model or "Beta'X + log w_i" in the shared gamma frailty models, otherwise uses "Beta'X + w_i" for log-normal frailty distribution.
BetaTpsMat: matrix of time varying-effects and confidence bands (the first column used for abscissa of times)
theta_p.value: p-value of the Wald test for the estimated variance of the gamma frailty.
sigma2_p.value  p-value of the Wald test for the estimated variance of the log-normal frailty.

The following components are specific to joint models.

intcens Logical value. Indicator if a joint frailty model with interval-censored data was fitted.

theta variance of the gamma frailty parameter (\(Var(\omega_i)\)) or (\(Var(u_i)\))

sigma2 variance of the log-normal frailty parameter (\(Var(\eta_i)\)) or (\(Var(v_i)\))

eta variance of the second gamma frailty parameter in general joint frailty models (\(Var(\nu_i)\))

indic_alpha indicator if a joint frailty model with \(\alpha\) parameter was fitted

alpha the coefficient \(\alpha\) associated with the frailty parameter in the terminal hazard function.

nbintervR Number of intervals (between 1 and 20) for the recurrent parametric hazard functions ("Piecewise-per", "Piecewise-equi").

nbintervDC Number of intervals (between 1 and 20) for the death parametric hazard functions ("Piecewise-per", "Piecewise-equi").

nvar A vector with the number of covariates of each type of hazard function as components.

nvarRec number of recurrent explanatory variables.

nvarEnd number of death explanatory variables.

noVar1 indicator of recurrent explanatory variables.

noVar2 indicator of death explanatory variables.

xR matrix of times where both survival and hazard function are estimated for the recurrent event. By default seq(0,max(time),length=99), where time is the vector of survival times.

xD matrix of times for the terminal event.

lamR array (dim=3) of hazard estimates and confidence bands for recurrent event.

lamD the same value as lamR for the terminal event.

survR array (dim=3) of baseline survival estimates and confidence bands for recurrent event.

survD the same value as survR for the terminal event.

martingale.res martingale residuals for each cluster (recurrent).

martingaledeath.res martingale residuals for each cluster (death).

linear.pred linear predictor: uses "Beta'X + log w_i" in the gamma frailty model, otherwise uses "Beta'X + eta_i" for log-normal frailty distribution

lineardeath.pred linear predictor for the terminal part: "Beta'X + alpha.log w_i" for gamma, "Beta'X + alpha.eta_i" for log-normal frailty distribution

Xlevels vector of the values that factor might have taken for the recurrent part.

contrasts type of contrast for factor variable for the recurrent part.
Xlevels2  vector of the values that factor might have taken for the death part.

contrasts2  type of contrast for factor variable for the death part.

BetaTpsMat  matrix of time varying-effects and confidence bands for recurrent event (the first column used for abscissa of times of recurrence)

BetaTpsMatDc  matrix of time varying-effects and confidence bands for terminal event (the first column used for abscissa of times of death)

alpha.p.value  p-value of the Wald test for the estimated $\alpha$.

ncc  Logical value whether nested case-control design with weights was used for the joint model.

The following components are specific to **nested** models.

alpha  variance of the cluster effect ($Var(v_i)$)

eta  variance of the subcluster effect ($Var(w_{ij})$)

subgroups  the maximum number of subgroups used in the fit.

frailty.pred.group  empirical Bayes prediction of the frailty term by group.

frailty.pred.subgroup  empirical Bayes prediction of the frailty term by subgroup.

linear.pred  linear predictor: uses "Beta'X + log v_i.w_ij".

subgbyg  subgroup by group.

n.strat  A vector with the number of covariates of each type of hazard function as components.

alpha.p.value  p-value of the Wald test for the estimated variance of the cluster effect.

eta.p.value  p-value of the Wald test for the estimated variance of the subcluster effect.

The following components are specific to **joint nested frailty** models.

theta  variance of the subcluster effect ($Var(u_{fi})$)

eta  variance of the cluster effect ($Var(\omega_f)$)

alpha  the power coefficient $\alpha$ associated with the frailty parameter ($u_{fi}$) in the terminal event hazard function.

ksi  the power coefficient $\xi$ associated with the frailty parameter ($\omega_f$) in the recurrent event hazard function.

indic.alpha  indicator if a joint frailty model with $\alpha$ parameter was fitted or not.

indic.ksi  indicator if a joint frailty model with $\xi$ parameter was fitted or not.

frailty.fam.pred  empirical Bayes prediction of the frailty term by family.

eta.p.value  p-value of the Wald test for the estimated variance of the cluster effect.

alpha.p.value  p-value of the Wald test for the estimated power coefficient $\alpha$.

ksi.p.value  p-value of the Wald test for the estimated power coefficient $\xi$. 
Note

From a prediction aim, we recommend you to input a data sorted by the group variable with numerical numbers from 1 to n (number of groups). In case of a nested model, we recommend you to input a data sorted by the group variable then sorted by the subgroup variable both with numerical numbers from 1 to n (number of groups) and from 1 to m (number or subgroups). "kappa" and "n.knots" are the arguments that the user have to change if the fitted model does not converge. "n.knots" takes integer values between 4 and 20. But with n.knots=20, the model would take a long time to converge. So, usually, begin first with n.knots=7, and increase it step by step until it converges. "kappa" only takes positive values. So, choose a value for kappa (for instance 10000), and if it does not converge, multiply or divide this value by 10 or 5 until it converges.

References


See Also

survic, cluster, subcluster, terminal, num.id, timedep
Examples

```r
## Not run:

```coproportional hazard model (SHARED without frailties)```
```estimated with penalized likelihood```
```data(kidney)
frailtyPenal(Surv(time,status)-sex+age,
n.knots=12,kappa=10000,data=kidney)
```-shared frailty model
```frailtyPenal(Surv(time,status)-cluster(id)+sex+age,
n.knots=12,kappa=10000,data=kidney)
```-- with an initialisation of regression coefficients
```frailtyPenal(Surv(time,status)-cluster(id)+sex+age,
n.knots=12,kappa=10000,data=kidney,init.B=c(-1.44,0))
```-- with truncated data
```data(nested)
frailtyPenal(Surv(t1,t2,event) ~ cluster(group),
data=dataNested,n.knots=10,kappa=10000,
cross.validation=TRUE,recurrentAG=FALSE)
```-- stratified analysis
```data(readmission)
frailtyPenal(Surv(time,event)-cluster(id)+dukes+strata(sex),
n.knots=10,kappa=c(10000,10000),data=readmission)
```-- recurrentAG=TRUE
```frailtyPenal(Surv(t.start,t.stop,event)-cluster(id)+sex+dukes+
charlson,data=readmission,n.knots=6,kappa=1e5,recurrentAG=TRUE)
```-- cross.validation=TRUE
```frailtyPenal(Surv(t.start,t.stop,event)-cluster(id)+sex+dukes+
charlson,data=readmission,n.knots=6,kappa=5000,recurrentAG=TRUE,
cross.validation=TRUE)
```-- log-normal distribution
```frailtyPenal(Surv(t.start,t.stop,event)-cluster(id)+sex+dukes+
charlson,data=readmission,n.knots=6,kappa=5000,recurrentAG=TRUE,
RandDist="LogN")
```
frailtyPenal

### Joint Frailty model (recurrent and terminal events) ###

```r
data(readmission)
#-- Gap-time
modJoint.gap <- frailtyPenal(Surv(time,event)~cluster(id)+sex+dukes+charlson+ terminal(death), formula.terminalEvent = sex+dukes+charlson, 
data=readmission,n.knots=14,kappa=c(9.55e+9,1.41e+12), 
recurrentAG=FALSE)

#-- Calendar time
modJoint.calendar <- frailtyPenal(Surv(t.start,t.stop,event)~cluster(id)+ 
sex+dukes+charlson+terminal(death), formula.terminalEvent = sex+ 
dukes+charlson, data=readmission,n.knots=10,kappa=c(9.55e9,1.41e12), 
recurrentAG=TRUE)

#-- without alpha parameter
modJoint.gap <- frailtyPenal(Surv(time,event)~cluster(id)+sex+dukes+charlson+ 
terminal(death), formula.terminalEvent = sex+dukes+charlson, 
data=readmission,n.knots=10,kappa=c(9.55e9,1.41e12), 
recurrentAG=FALSE,Alpha="None")

#-- log-normal distribution
modJoint.log <- frailtyPenal(Surv(t.start,t.stop,event)~cluster(id)+sex+ 
dukes+charlson+terminal(death), formula.terminalEvent = sex+ 
dukes+charlson, data=readmission,n.knots=10,kappa=c(9.55e9,1.41e12), 
recurrentAG=TRUE, RandDist="LogN")

### Joint frailty model for NCC data ###

data(dataNCC)
modJoint.ncc <- frailtyPenal(Surv(t.start,t.stop,event)~cluster(id)+cov1+ 
cov2+terminal(death)+wts(ncc.wts), formula.terminalEvent = cov1+cov2, 
data=dataNCC,n.knots=8,kappa=c(1.6e+10, 5.0e+03), recurrentAG=TRUE, RandDist="LogN")

### Joint Frailty model for clustered data ###

#-- here is generated cluster (5 clusters)
readmission <- transform(readmission,group=id%%5+1)

#-- exclusion all recurrent events --
#-- to obtain framework of semi-competing risks --
readmission2 <- subset(readmission, (t.start == 0 & event == 1) | event == 0)

joi.clus.gap <- frailtyPenal(Surv(time,event)~cluster(group)+ 
num.id(id)+dukes+charlson+sex+chemo+terminal(death), 
formula.terminalEvent = dukes+charlson+sex+chemo, 
data=readmission2,recurrentAG=FALSE, n.knots=8, 
kappa=c(1.e+10,1.e+10) ,Alpha="None")

### General Joint model (recurrent and terminal events)
with 2 covariates ---####

data(readmission)
modJoint.general <- frailtyPenal(Surv(time,event) ~ cluster(id) + dukes + charlson + sex + chemo + terminal(death),
formula.terminalEvent = ~ dukes + charlson + sex + chemo,
data = readmission, jointGeneral = TRUE, n.knots = 8,
kappa = c(2.11e+08, 9.53e+11))

#### Nested Frailty model ####

##### WARNING ######
# Data should be ordered according to cluster and subcluster

data(dataNested)
modClu <- frailtyPenal(Surv(t1,t2,event)~cluster(group)+
subcluster(subgroup)+cov1+cov2,data=dataNested,
n.knots=8,kappa=50000)

modClu.str <- frailtyPenal(Surv(t1,t2,event)~cluster(group)+
subcluster(subgroup)+cov1+strata(cov2),data=dataNested,
n.knots=8,kappa=c(50000,50000))

##### Joint Nested Frailty model ######

#-- here is generated cluster (30 clusters)
readmissionNested <- transform(readmission,group=id%%30+1)

modJointNested_Splines <- frailtyPenal(formula = Surv(t.start, t.stop, event) ~ subcluster(id) + cluster(group) + dukes + terminal(death),
formula.terminalEvent = ~dukes, data = readmissionNested, recurrentAG = TRUE, n.knots = 8, kappa = c(9.55e+9, 1.41e+12), initialize = TRUE)

modJointNested_Weib <- frailtyPenal(Surv(t.start, t.stop,event)~subcluster(id) + cluster(group)+dukes+ terminal(death),formula.terminalEvent=~dukes, hazard = ('Weibull'), data=readmissionNested,recurrentAG=TRUE, initialize = FALSE)

JoinE_GapSpline <- frailtyPenal(formula = Surv(time, event) ~ subcluster(id) + cluster(group) + dukes + terminal(death),
formula.terminalEvent = ~dukes, data = readmissionNested, recurrentAG = FALSE, n.knots = 8, kappa = c(9.55e+9, 1.41e+12), initialize = TRUE, init.Alpha = 1.091, Ksi = "None")

## End(Not run)
Description

This meta-analysis was carried out by the GASTRIC (Global Advanced/Adjuvant Stomach Tumor Research international Collaboration) group, using individual data on patients with curatively resected gastric cancer. Data from all published randomized trials, with a patient recruitment end date before 2004, and comparing adjuvant chemotherapy with surgery alone for resectable gastric cancers, were searched electronically. The candidate surrogate endpoint \( S \) was Disease-free survival time, defined as the time (in days) to relapse, second cancer or dead from any cause. The true endpoint \( T \) was the overall survival time, defined as the time (in days) from randomization to death of any cause or to the last follow-up.

Usage

data(gastadj)

Format

This data frame contains the following columns:

- **trialID**: The trial in which the patient was treated
- **patientID**: The identification number of a patient
- **trt**: The treatment indicator, coded as 0 = Control and 1 = Experimental
- **timeS**: The candidate surrogate (progression-free survival in days)
- **statusS**: Censoring indicator for progression-free survival (0 = alive and progression-free, 1 = with progression or dead)
- **timeT**: The true endpoint (overall survival time in days)
- **statusT**: Censoring indicator for survival time (0 = alive, 1 = dead)

Source


---

**hazard**

*Hazard function.*

Description

Let \( t \) be a continuous variable, we determine the value of the hazard function to \( t \) after run fit.

Usage

hazard(t, ObjFrailty)
jointSurroPenal

Arguments

- **t**: time for hazard function.
- **ObjFrailty**: an object from the frailtypack fit.

Value

return the value of hazard function in t.

Examples

```r
## Not run:

#-- a fit Shared
data(readmission)
fit.shared <- frailtyPenal(Surv(time,event)~dukes+cluster(id)+
strata(sex),n.knots=10,kappa=c(10000,10000),data=readmission)

#-- calling survival
hazard(20,fit.shared)

## End(Not run)
```

---

**jointSurroPenal**

*Fit the one-step Joint surrogate model for the evaluation of a candidate surrogate endpoint*

**Description**

**Joint Frailty Surrogate model definition**

Fit the one-step Joint surrogate model for the evaluation of a candidate surrogate endpoint, with different integration methods on the random effects, using a semiparametric penalized likelihood estimation. This approach extends that of Burzykowski et al. (2001) by including in the same joint frailty model the individual-level and the trial-level random effects.

For the \( j^{th} \) subject \((j=1, \ldots, n_i)\) of the \( i^{th} \) trial \((i=1, \ldots, G)\), the joint surrogate model is defined as follows:

\[
\begin{align*}
\lambda_{S,ij}(t|\omega_{ij}, u_i, v_{S,i}, Z_{ij1}) &= \lambda_{0S}(t) \exp(\omega_{ij} + u_i + v_{S,i} Z_{ij1} + \beta_S Z_{ij1}) \\
\lambda_{T,ij}(t|\omega_{ij}, u_i, v_{T,i}, Z_{ij1}) &= \lambda_{0T}(t) \exp(\zeta \omega_{ij} + \alpha u_i + v_{T,i} Z_{ij1} + \beta_T Z_{ij1})
\end{align*}
\]

where,

\[
\omega_{ij} \sim N(0, \theta), u_i \sim N(0, \gamma), \omega_{ij} \perp u_i, u_i \perp v_{S,i}, u_i \perp v_{T,i}
\]
and 

$$(v_S, v_T)^T \sim \mathcal{N}(0, \Sigma_v)$$

with

$$\Sigma_v = \begin{pmatrix} \sigma_{vS}^2 & \sigma_{vST} \\ \sigma_{vST} & \sigma_{vT}^2 \end{pmatrix}$$

In this model, $\lambda_{0S}(t)$ is the baseline hazard function associated with the surrogate endpoint and $\beta_S$ the fixed treatment effect (or log-hazard ratio); $\lambda_{0T}(t)$ is the baseline hazard function associated with the true endpoint and $\beta_T$ the fixed treatment effect. $\omega_{ij}$ is a shared individual-level frailty that serve to take into account the heterogeneity in the data at the individual level; $u_i$ is a shared frailty effect associated with the baseline hazard function that serve to take into account the heterogeneity between trials of the baseline hazard function, associated with the fact that we have several trials in this meta-analytical design. The power parameters $\zeta$ and $\alpha$ distinguish both individual and trial-level heterogeneities between the surrogate and the true endpoint. $v_S$ and $v_T$ are two correlated random effects treatment-by-trial interactions. $Z_{ij1}$ represents the treatment arm to which the patient has been randomized.

**Surrogacy evaluation**

We proposed new definitions of Kendall’s $\tau$ and coefficient of determination as individual-level and trial-level association measurements, to evaluate a candidate surrogate endpoint (Soefu et al., 2018). The formulations are given below.

**Individual-level surrogacy**

To measure the strength of association between $S_{ij}$ and $T_{ij}$ after adjusting the marginal distributions for the trial and the treatment effects, as show in Soefu et al.(2018), we use the Kendall’s $\tau$ define by:

$$\tau = 2 \int_{u_i} \int_{\omega_{ij}} \int_{\omega_{ij}'} \left\{ \frac{\exp(\omega_{ij} + u_i + \zeta u_i') + \exp(\omega_{ij'} + u_i + \zeta u_i')}{(\exp(\omega_{ij'} + u_i) + \exp(\omega_{ij'} + u_i'))(\exp(\zeta u_i' + \alpha u_i) + \exp(\zeta u_i + \alpha u_i'))} \right\} \frac{1}{\sqrt{2\pi\theta}} \exp \left[ -\frac{1}{2} \frac{\omega_{ij}^2}{\theta} \right] \frac{1}{\sqrt{2\pi\gamma}} \exp \left[ -\frac{1}{2} \frac{u_i^2}{\gamma} \right] d\omega_{ij}' du_i' - 1$$

where $\theta, \zeta, \alpha$ and $\gamma$ are estimated using the joint surrogate model defined previously. Kendall’s $\tau$ is the difference between the probability of concordance and the probability of discordance of two realizations of $S_{ij}$ and $T_{ij}$. It belongs to the interval [-1,1] and assumes a zero value when $S_{ij}$ and $T_{ij}$ are independent. We estimate Kendall’s $\tau$ using Monte-Carlo or Gaussian Hermite quadrature integration methods. Its confidence interval is estimated using parametric bootstrap.

**Trial-level surrogacy**

The key motivation for validating a surrogate endpoint is to be able to predict the effect of treatment on the true endpoint, based on the observed effect of treatment on the surrogate endpoint. As shown by Buyse et al. (2000), the coefficient of determination obtains from the covariance matrix $\Sigma_v$ of the random effects treatment-by-trial interaction can be used to evaluate underlined prediction, and therefore as surrogacy evaluation measurement at trial-level. It is defined by:

$$R^2_{\text{trial}} = \frac{\sigma_{vST}^2}{\sigma_{vS}^2 \sigma_{vT}^2}$$
The SEs of $R^2_{trial}$ is calculated using the Delta-method. We also propose $R^2_{trial}$ and 95% CI computed using the parametric bootstrap. The use of delta-method can lead to confidence limits violating the [0,1], as noted by (Burzykowski et al., 2001). However, using other methods would not significantly alter the findings of the surrogacy assessment.

Usage

```r
jointSurroPenal(data, maxit=40, indice.zeta = 1,
indice.alpha = 1, frail.base = 1, n.knots = 6,
LIMparam = 0.001, LIMlogl = 0.001, LIMderiv = 0.001,
nb.mc = 300, nb.gh = 32, nb.gh2 = 20, adaptatif = 0,
int.method = 2, nb.iterPGH = 5, nb.MC.kendall = 10000,
Nboot.kendall = 1000, true.init.val = 0,
theta.init = 1, sigma.ss.init = 0.5, sigma.tt.init = 0.5,
sigma.st.init = 0.48, gamma.init = 0.5, alpha.init = 1,
zeta.init = 1, betas.init = 0.5, betat.init = 0.5, scale = 1,
random.generator = 1, kappa.use = 4, random = 0,
random.nb.sim = 0, seed = 0, init.kappa = NULL, nb.decimal = 4,
print.times = TRUE, print.itter=FALSE)
```

Arguments

- `data` A data.frame containing at least 7 variables intitled:
  - `patientID`: A numeric, that represents the patient’s identifier, must be unique;
  - `trialID`: A numeric, that represents the trial in which each patient was randomized;
  - `times`: The follow up time associated with the surrogate endpoint;
  - `statusS`: The event indicator associated with the surrogate endpoint. Normally 0 = no event, 1 = event;
  - `timeT`: The follow up time associated with the true endpoint;
  - `statusT`: The event indicator associated with the true endpoint. Normally 0 = no event, 1 = event;
  - `trt`: The treatment indicator for each patient, with 1 = treated, 0 = untreated.

- `maxit` maximum number of iterations for the Marquardt algorithm. Default is 40.

- `indice.zeta` A binary, indicates whether the power’s parameter $\zeta$ should be estimated (1) or not (0). If 0, $\zeta$ will be set to 1 during estimation. The default is 1. This parameter can be seted to 0 in case of convergence and identification issues.

- `indice.alpha` A binary, indicates whether the power’s parameter $\alpha$ should be estimated (1) or not (0). If 0, $\alpha$ will be set to 1 during estimation. The default is 1.

- `frail.base` Considered the heterogeneity between trial on the baseline risk (1), using the shared cluster specific frailties ($u_i$), or not (0). The default is 1.

- `n.knots` integer giving the number of knots to use. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. We estimate I or M-splines of order 4. When the user set a number of knots equals to k (n.knots=k) then the
number of interior knots is (k-2) and the number of splines is (k-2)+order. Number of knots must be between 4 and 20. (See frailtyPenal for more details).

LIMparam Convergence threshold of the Marquardt algorithm for the parameters, 10\(-3\) by default (See frailtyPenal for more details).

LIMlogl Convergence threshold of the Marquardt algorithm for the log-likelihood, 10\(-3\) by default (See frailtyPenal for more details).

LIMderiv Convergence threshold of the Marquardt algorithm for the gradient, 10\(-3\) by default (See frailtyPenal for more details).

nb.mc Number of samples considered in the Monte-Carlo integration. Required in case int.method is equals to 0, 2 or 4. A value between 100 and 300 most often gives good results. However, beyond 300, the program takes a lot of time to estimate the parameters. The default is 300.

nb.gh Number of nodes for the Gaussian-Hermite quadrature. It can be chosen among 5, 7, 9, 12, 15, 20 and 32. The default is 32.

nb.gh2 Number of nodes for the Gauss-Hermite quadrature used to re-estimate the model, in case of non-convergence, defined as previously. The default is 20.

adaptatif A binary, indicates whether the pseudo adaptive Gaussian-Hermite quadrature (1) or the classical Gaussian-Hermite quadrature (0) is used. The default is 0.

int.method A numeric, indicates the integration method: 0 for Monte carlo, 1 for Gaussian-Hermite quadrature, 2 for a combination of both Gaussian-Hermite quadrature to integrate over the individual-level random effects and Monte carlo to integrate over the trial-level random effects, 4 for a combination of both Monte carlo to integrate over the individual-level random effects and Gaussian-Hermite quadrature to integrate over the trial-level random effects. The default is 2.

nb.iterPGH Number of iterations before the re-estimation of the posterior random effects, in case of the two-steps pseudo-adaptive Gaussian-hermite quadrature. If set to 0 there is no re-estimation”. The default is 5.

nb.MC.kendall Number of generated points used with the Monte-Carlo to estimate integrals in the Kendall’s \(\tau\) formulation. Better to use at least 4000 points for stable results. The default is 10000.

nboot.kendall Number of samples considered in the parametric bootstrap to estimate the confidence interval of the Kendall’s \(\tau\). The default is 1000.

true.init.val Numerical value. Indicates if the given initial values to parameters (0) should be considered. If set to 2, \(\alpha\) and \(\gamma\) are initialised using two separated shared frailty model (see frailtyPenal for more details); \(\sigma^2_{vS}, \sigma^2_{vT}\) and \(\sigma^2_{vST}\) are fixed by the user or the default values; \(\zeta, \theta, \beta_S\) and \(\beta_T\) are initialized using a classical joint frailty model, considering individual level random effects. If the joint frailty model is faced to convergence issues, \(\beta_S\) and \(\beta_T\) are initialized using two shared frailty models. In all others scenarios, if the simplified model does not converge, default given parameters values are used. Initial values for spline’s associated parameters are fixed to 0.5. The default for this argument is 0.

theta.init Initial values for \(\theta\), required if true.init.val is set to 0 or 2. The default is 1.

sigma.ss.init Initial values for \(\sigma^2_{vS}\), required if true.init.val is set to 0 or 2. The default is 0.5.
sigma.tt.init  Initial values for $\sigma^2_{\nu_T}$, required if true.init.val is set to 0 or 2. The default is 0.5.

sigma.st.init  Initial values for $\sigma_{\nu_{ST}}$, required if true.init.val is set to 0 or 2. The default is 0.48.

gamma.init  Initial values for $\gamma$, required if true.init.val is set to 0 or 2. The default is 0.5.

alpha.init  Initial values for $\alpha$, required if true.init.val is set to 0 or 2. The default is 1.

zeta.init  Initial values for $\zeta$, required if true.init.val is set to 0 or 2. The default is 1.

betas.init  Initial values for $\beta_S$, required if true.init.val is set to 0 or 2. The default is 0.5.

betat.init  Initial values for $\beta_T$, required if true.init.val is set to 0 or 2. The default is 0.5.

scale  A numeric that allows to rescale the survival times, to avoid numerical problems in case of some convergence issues. If no change is need the argument is set to 1, the default value. eg: 365 aims to convert days to years “.

random.generator  Random number generator to use by the Fortran compiler, 1 for the intrinsec subroutine Random_number and 2 for the subroutine unirann(). The default is 1. In case of convergence problem with int.method set to 0, 2 or 4, that requires integration by Monte-Carlo, user could change the random numbers generator.

kappa.use  A numeric, that indicates how to manage the smoothing parameters $k_1$ and $k_2$ in case of convergence issues. If it is set to 1, the given smoothing parameters or those obtained by cross-validation are used. If it is set to 3, the associated smoothing parameters are successively divided by 10, in case of convergence issues until 5 times. If it is set to 4, the management of the smoothing parameter is as in case 1, follows by the successive division as described in case 3 and preceded by the changing of the number of nodes for the Gauss-Hermite quadrature. The default is 4.

random  A binary that says if we reset the random number generation with a different environment at each call (1) or not (0). If it is set to 1, we use the computer clock as seed. In the last case, it is not possible to reproduce the generated datasets”. The default is 0. Required if random.generator is set to 1.

random.nb.sim  If random is set to 1, a binary that indicates the number of generations that will be made.

seed  The seed to use for data (or samples) generation. required if random is set to 0. The default is 0.

init.kappa  smoothing parameter used to penalized the log-likelihood. By default (init.kappa = NULL) the values used are obtian by cross-validation.

nb.decimal  Number of decimal required for results presentation.

print.times  a logical parameter to print estimation time. Default is TRUE.

print.itter  a logical parameter to print iteration process. Default is FALSE.
Details

The estimated parameter are obtained using the robust Marquardt algorithm (Marquardt, 1963) which is a combination between a Newton-Raphson algorithm and a steepest descent algorithm. The iterations are stopped when the difference between two consecutive log-likelihoods was small ($< 10^{-3}$), the estimated coefficients were stable (consecutive values ($< 10^{-3}$), and the gradient small enough ($< 10^{-3}$), by default. Cubic M-splines of order 4 are used for the hazard function, and I-splines (integrated M-splines) are used for the cumulative hazard function.

The inverse of the Hessian matrix is the variance estimator and to deal with the positivity constraint of the variance component and the spline coefficients, a squared transformation is used and the standard errors are computed by the $\Delta$-method (Knight & Xekalaki, 2000). The smooth parameter can be chosen by maximizing a likelihood cross validation criterion (Joly and other, 1998).

We proposed based on the joint surrogate model a new definition of the Kendall’s $\tau$. Moreover, distinct numerical integration methods are available to approximate the integrals in the marginal log-likelihood.

Non-convergence case management procedure

Special attention must be given to initializing model parameters, the choice of the number of spline knots, the smoothing parameters and the number of quadrature points to solve convergence issues. We first initialized parameters using the user’s desired strategy, as specified by the option true.init.val. When numerical or convergence problems are encountered, with kappa.use set to 4, the model is fitted again using a combination of the following strategies: vary the number of quadrature point (nb. gh to nb. gh2 or nb. gh2 to nb. gh) in case of the use of the Gaussian Hermite quadrature integration (see int.method); divided or multiplied the smoothing parameters ($k_1$, $k_2$) by 10 or 100 according to their preceding values, or used parameter vectors obtained during the last iteration (with a modification of the number of quadrature points and smoothing parameters). Using this strategy, we usually obtained during simulation the rejection rate less than 3%. A sensitivity analysis was conducted without this strategy, and similar results were obtained on the converged samples, with about a 23% rejection rate.

Value

This function return an object of class jointSurroPenal with elements:

- **EPS**: A vector containing the obtained convergence thresholds with the Marquardt algorithm, for the parameters, the log-likelihood and for the gradient;
- **b**: A vector containing estimates for the splines parameter’s, the power’s parameter $\zeta$ (if indice.zeta is set to 1), the standard error of the shared individual-level frailty $\omega_{ij}$ ($\theta$), elements of the lower triangular matrix (L) from the Cholesky decomposition such that $\Sigma = LL^T$, with $\Sigma$ the covariances of the random effects $(v_S, v_T)$, the coefficient $\alpha$ (if indice.alpha is set to 1), the standard error of the random effect $u_i$ and the regression coefficients $\beta_S$ and $\beta_T$;
- **varH**: The variance matrix of all parameters in b (before positivity constraint transformation for the variance of the measurement error, for which the delta method is used);
- **varH.t**: The robust estimation of the variance matrix of all parameters in b;
- **loglikPenal**: The complete marginal penalized log-likelihood;
the approximated likelihood cross-validation criterion in the semiparametric case (with $H$ minus the converged Hessian matrix, and $l(.)$ the full log-likelihood).

$$LCV = \frac{1}{n}(\text{trace}(H^{-1}_{pl} H) - l(.));$$

- **LCV** vector of times for surrogate endpoint where both survival and hazard function are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times;
- **lamS** array (dim = 3) of hazard estimates and confidence bands, for surrogate endpoint;
- **survS** array (dim = 3) of baseline survival estimates and confidence bands, for surrogate endpoint;
- **XT** vector of times for true endpoint where both survival and hazard function are estimated. By default seq(0, max(time), length = 99), where time is the vector of survival times;
- **lamT** array (dim = 3) of hazard estimates and confidence bands, for true endpoint;
- **survT** array (dim = 3) of baseline survival estimates and confidence bands, for true endpoint;
- **n.iter** number of iterations needed to converge;
- **theta** Estimate for $\theta$;
- **gamma** Estimate for $\gamma$;
- **alpha** Estimate for $\alpha$;
- **zeta** Estimate for $\zeta$;
- **sigma.s** Estimate for $\sigma_S$;
- **sigma.t** Estimate for $\sigma_T$;
- **sigma.st** Estimate for $\sigma_{ST}$;
- **beta.s** Estimate for $\beta_S$;
- **beta.t** Estimate for $\beta_T$;
- **ui** A binary, that indicates if the heterogeneity between trial on the baseline risk has been Considered (1), using the shared cluster specific frailties ($u_i$), or not (0);
- **ktau** The Kendall’s $\tau$ with the correspondant 95 % CI computed using the parametric bootstrap;
- **R2.boot** The $R^2_{trial}$ with the correspondant 95 % CI computed using the parametric bootstrap;
- **Coefficients** The estimates with the corresponding standard errors and the 95 % CI
- **kappa** Positive smoothing parameters used for convergence. These values could be different to initial values if kappa.use is set to 3 or 4;
- **scale** The value used to rescale the survival times

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References


See Also

jointSurrSimul, summary.jointSurroPenal, jointSurroPenalSimul

Examples

# Generation of data to use
data.sim <- jointSurrSimul(n.obs=600, n.trial = 30, cens.adm=549.24,
alpha = 1.5, theta = 3.5, gamma = 2.5, zeta = 1, sigma.s = 0.7,
sigma.t = 0.7, rsqrt = 0.8, betas = -1.25, betat = -1.25,
full.data = 0, random.generator = 1, seed = 0, nb.reject.data = 0)

## Not run:
# Surrogacy evaluation based on generated data with a combination of Monte Carlo
# and classical Gaussian Hermite integration.*
# (Computation takes around 5 minutes)
joint.surro.sim.MCGH <- jointSurroPenal(data = data.sim, int.method = 2,
  nb.mc = 300, nb.gh = 20)

# Surrogacy evaluation based on generated data with a combination of Monte Carlo
# and Pseudo-adaptive Gaussian Hermite integration.
# (Computation takes around 4 minutes)
joint.surro.sim.MCPGH <- jointSurroPenal(data = data.sim, int.method = 2,
  nb.mc = 300, nb.gh = 20, adaptatif = 1)

# Results
summary(joint.surro.sim.MCGH)
summary(joint.surro.sim.MCPGH)

# Data from the advanced ovarian cancer randomized clinical trials.
# Joint surrogate model with \text{\textbackslash zeta} fixed to \text{\textbackslash code{1}}, 8 nodes spline
# and the rescaled survival time.

data(dataOvarian)
# (Computation takes around 13 minutes)
joint.surro.oar <- jointSurroPenal(data = dataOvarian, n.knots = 8,
  init.kappa = c(2000,1000), indice.alpha = 0, nb.mc = 200,
  scale = 1/365)
# results
summary(joint.surro.ovar)

# data from the adjuvant chemotherapy and resectable gastric cancer
meta-analyses:
# Joint surrogate model with initial values for the parameters and the
# smoothing parameters, and sample for the Monte-Carlo integration
# generated by the subroutine \code{uniran}.
# (Computation takes around 14 minutes)

data(gastadj)
joint.surro.gast <- jointSurroPenal(data = gastadj, nb.mc = 100, nb.gh = 20,
indice.zeta = 0, indice.alpha = 0, n.knots = 10,
random.generator = 2, init.kappa = c(3677000000,1002518452))

# results
summary(joint.surro.gast)

## End(Not run)

---

**jointSurroPenalSimul**

Simulation studies based on the one-step Joint surrogate model for the evaluation of a candidate surrogate endpoint

---

**Description**

This function aims to allow simulation studies, based on the joint frailty surrogate model, described in `jointSurroPenal`

**Usage**

```
jointSurroPenalSimul(maxit=40, indice.zeta = 1,
indice.alpha = 1, frail.base = 1, n.knots = 6, nb.dataset = 1,
nbSubSimul=1000, ntrialSimul=30, LIMparam = 0.001,
LIMlogl = 0.001, LIMderiv = 0.001, nb.mc = 300, nb.gh = 32,
nb.gh2 = 20, adaptatif = 0, int.method = 2, nb.iterPGH = 5,
nb.MC.kendall = 10000, nboot.kendall = 1000, true.init.val = 0,
theta.init = 1, sigma.ss.init = 0.5, sigma.tt.init = 0.5,
sigma.st.init = 0.48, gamma.init = 0.5, alpha.init = 1,
zeta.init = 1, betas.init = 0.5, betat.init = 0.5,
random.generator = 1, equi.subj.trial = 1, prop.subj.trial = NULL,
equi.subj.trt = 1, prop.subj.trt = NULL,
theta2 = 3.5, zeta = 1, gamma.ui = 2.5, alpha.ui = 1,
betas = -1.25, betat = -1.25, lambdas = 1.8, nus = 0.0045,
lambdat = 3, nut = 0.0025, time.cens = 549, R2 = 0.81,
sigma.s = 0.7, sigma.t = 0.7, kappa.use = 4, random = 0,
random.nb.sim = 0, seed = 0, init.kappa = NULL,
nb.decimal = 4, print.times = TRUE, print.itter=FALSE)
```
Arguments

maxit maximum number of iterations for the Marquardt algorithm. Default is 40.
indice.zeta A binary, indicates whether the power’s parameter $\zeta$ should be estimated (1) or not (0). If 0, $\zeta$ will be set to 1 during estimation. The default is 1. This parameter can be set to 0 in case of identification issues.
indice.alpha A binary, indicates whether the power’s parameter $\alpha$ should be estimated (1) or not (0). If 0, $\alpha$ will be set to 1 during estimation. The default is 1.
frail.base Consider the heterogeneous between trial on the baseline risk (1), using the shared cluster specific frailties ($u_i$), or not (0). The default is 1.
n.knots integer giving the number of knots to use. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. We estimate I or M-splines of order 4. When the user set a number of knots equals to k (n.knots=k) then the number of interior knots is (k-2) and the number of splines is (k-2)+order. Number of knots must be between 4 and 20. (See frailtypenal for more details).
nb.dataset Number of dataset to analyze. The default is 1.
nbSubSimul Number of subjects.
ntrialSimul Number of trials.
LIMparam Convergence threshold of the Marquardt algorithm for the parameters, $10^{-3}$ by default (See frailtypenal for more details).
LIMlogl Convergence threshold of the Marquardt algorithm for the log-likelihood, $10^{-3}$ by default (See frailtypenal for more details).
LIMderiv Convergence threshold of the Marquardt algorithm for the gradient, $10^{-3}$ by default (See frailtypenal for more details).
nb.mc Number of samples considered in the Monte-Carlo integration. Required in case int.method is equals to 0, 2 or 4. A value between 100 and 300 most often gives good results. However, beyond 300, the program takes a lot of time to estimate the parameters. The default is 300.
nb.gh Number of nodes for the Gaussian-Hermite quadrature. It can be chosen among 5, 7, 9, 12, 15, 20 and 32. The default is 32.
nb.gh2 Number of nodes for the Gauss-Hermite quadrature used to re-estimate the model, in case of non-convergence, defined as previously. The default is 20.
adapatif A binary, indicates whether the pseudo adaptive Gaussian-Hermite quadrature (1) or the classical Gaussian-Hermite quadrature (0) is used. The default is 0.
int.method A numeric, indicates the integration method: 0 for Monte Carlo, 1 for Gaussian-Hermite quadrature, 2 for a combination of both Gaussian-Hermite quadrature to integrate over the individual-level random effects and Monte Carlo to integrate over the trial-level random effects, 4 for a combination of both Monte Carlo to integrate over the individual-level random effects and Gaussian-Hermite quadrature to integrate over the trial-level random effects. The default is 2.
nb.iterPGH Number of iterations before the re-estimation of the posterior random effects, in case of the two-steps pseudo-adaptive Gaussian-Hermite quadrature. If set to 0 there is no re-estimation”. The default is 5.
jointSurroPenalSimul

nb.MC.kendall Number of generated points used with the Monte-Carlo to estimate integrals in the Kendall’s $\tau$ formulation. Better to use at least 4000 points for stable results. The default is 10000.

nboot.kendall Number of samples considered in the parametric bootstrap to estimate the confidence interval of the Kendall’s $\tau$. The default is 1000.

true.init.val Numerical value. Indicates if the real parameter values (1), or the given initial values to parameters (0) should be considered. If set to 2, $\alpha$ and $\gamma$ are initialised using two separated shared frailty model (see frailtyPenal for more details); $\sigma^2_v$, $\sigma^2_p$ and $\sigma_{vST}$ are fixed using the default initial values given by the user; $\zeta$, $\theta$, $\beta_S$ and $\beta_T$ are initialized using a classical joint frailty model, considering individual level random effects. If the joint frailty model is faced to convergence issues, $\beta_S$ and $\beta_T$ are initialized using two shared frailty models. In all others scenarios, if the simplified model does not converge, default given parameters values are used. Initial values for spline’s associated parameters are fixed to PNU. The default for this argument is 0.

theta.init Initial values for $\theta$, required if true.init.val is set to 0 or 2. The default is 1.

sigma.ss.init Initial values for $\sigma^2_v$, required if true.init.val is set to 0 or 2. The default is 0.5.

sigma.tt.init Initial values for $\sigma^2_p$, required if true.init.val is set to 0 or 2. The default is 0.5.

sigma.st.init Initial values for $\sigma_{vST}$, required if true.init.val is set to 0 or 2. The default is 0.48.

gamma.init Initial values for $\gamma$, required if true.init.val is set to 0 or 2. The default is 0.5.

alpha.init Initial values for $\alpha$, required if true.init.val is set to 0 or 2. The default is 1.

zeta.init Initial values for $\zeta$, required if true.init.val is set to 0 or 2. The default is 1.

betas.init Initial values for $\beta_S$, required if true.init.val is set to 0 or 2. The default is 0.5.

betat.init Initial values for $\beta_T$, required if true.init.val is set to 0 or 2. The default is 0.5.

random.generator Random number generator to use by the Fortran compiler, 1 for the intrinsec subroutine Random_number and 2 for the subroutine uniran(). The default is 1.

equi.subj.trial A binary, that indicates if the same proportion of subjects per trial should be considered in the process of data generation (1) or not (0). In case of different trial sizes, fill in prop.subj.trial the proportions of subjects to be considered per trial. The default is 1.

prop.subj.trial Vector of the proportions of subjects to consider per trial. Requires if equi.subj.trial is different to 1. The size of this vector is equal to the number of trials.

equi.subj.trt Indicates if the same proportion of treated subjects per trial should be considered (1) or not (0). If 0, fill in prop.subj.trt the proportions of treated subjects to be considered per trial. The default is 1.
prop.subj.trt Vector of the proportions of treated subjects to consider per trial. Requires if equi.subj.trt is different to 0.5. The size of this vector is equal to the number of trials.

theta2 True value for $\theta$. The default is 3.5.

zeta True value for $\zeta$ in case of simulation. The default is 1.

gamma.ui True value for $\gamma$ in case of simulation. The default is 2.5.

alpha.ui True value for $\alpha$ in case of simulation. The default is 1.

betas True value for $\beta_S$ in case of simulation. The default is $-1.25$.

betat True value for $\beta_T$ in case of simulation. The default is $-1.25$.

lambdas Desired scale parameter for the Weibull distribution associated with the Surrogate endpoint. The default is 1.8.

nus Desired shape parameter for the Weibull distribution associated with the Surrogate endpoint. The default is 0.0045.

lambdat Desired scale parameter for the Weibull distribution associated with the True endpoint. The default is 3.

nut Desired shape parameter for the Weibull distribution associated with the True endpoint. The default is 0.0025.

time.cens Censorship time. The default is 549, for about 40% of censored subjects.

R2 Desired $R^2_{trial}$. The default is 0.81.

sigma.s True value for $\sigma_S^2$. The default is 0.7.

sigma.t True value for $\sigma_T^2$. The default is 0.7.

kappa.use A numeric, that indicates how to manage the smoothing parameters $k_1$ and $k_2$ in case of convergence issues. If it is set to 0, the first smoothing parameters that allowed convergence on the first dataset is used for all simulations. If it is set to 1, a smoothing parameter is estimated by cross-validation for each dataset generated. If it is set to 2, the same process for choosing kappas as in case 1 is used, but in case of convergence issue, the first smoothing parameters that allowed convergence among the three previous that have worked is used. If it is set to 3, the associated smoothing parameters are successively divided by 10, in case of convergence issues until 5 times. If it is set to 4, the management of the smoothing parameters is as in case 2, preceded by the successive division described in case 3 and by the changing of the number of nodes for the Gauss-Hermite quadrature. The default is 4.

random A binary that says if we reset the random number generation with a different environment at each call (1) or not (0). If it is set to 1, we use the computer clock as seed. In the last case, it is not possible to reproduce the generated datasets”. The default is 0. Required if random.generator is set to 1.

random.nb.sim If random is set to 1, a binary that indicates the number of generations that will be made, equal to nb.dataset in this case.

seed The seed to use for data generation. Required if random is set to 0. The default is 0.

init.kappa smoothing parameter used to penalized the log-likelihood. By default (init.kappa = NULL) the values used are obtain by cross-validation.
jointSurroPenalSimul

- **nb.decimal**: Number of decimal required for results presentation.
- **print.times**: a logical parameter to print estimation time. Default is TRUE.
- **print.itter**: a logical parameter to print iteration process. Default is FALSE.

**Details**

The estimated parameter are obtained using the robust Marquardt algorithm (Marquardt, 1963) which is a combination between a Newton-Raphson algorithm and a steepest descent algorithm. The iterations are stopped when the difference between two consecutive log-likelihoods was small ($< 10^{-3}$), the estimated coefficients were stable (consecutive values ($< 10^{-3}$), and the gradient small enough ($< 10^{-3}$), by default. Cubic M-splines of order 4 are used for the hazard function, and I-splines (integrated M-splines) are used for the cumulative hazard function.

The inverse of the Hessian matrix is the variance estimator and to deal with the positivity constraint of the variance component and the spline coefficients, a squared transformation is used and the standard errors are computed by the $\Delta$-method (Knight & Xekalaki, 2000). The smooth parameter can be chosen by maximizing a likelihood cross validation criterion (Joly and other, 1998).

We proposed based on the joint surrogate model a new definition of the Kendall’s $\tau$. Moreover, distinct numerical integration methods are available to approximate the integrals in the marginal log-likelihood.

**Non-convergence case management procedure**

Special attention must be given to initializing model parameters, the choice of the number of spline knots, the smoothing parameters and the number of quadrature points to solve convergence issues. We first initialized parameters using the user's desired strategy, as specified by the option `true.init.val`. When numerical or convergence problems are encountered, with `kappa.use` set to 4, the model is fitted again using a combination of the following strategies: vary the number of quadrature point (nb. gh to nb. gh2 or nb. gh2 to nb. gh) in case of the use of the Gaussian Hermite quadrature integration (see `int.method`); divided or multiplied the smoothing parameters ($k_1$, $k_2$) by 10 or 100 according to their preceding values, or used parameter vectors obtained during the last iteration (with a modification of the number of quadrature points and smoothing parameters). Using this strategy, we usually obtained during simulation the rejection rate less than 3%. A sensitivity analysis was conducted without this strategy, and similar results were obtained on the converged samples, with about a 23% rejection rate.

**Value**

This function return an object of class `jointSurroPenalSimul` with elements:

- **theta2**: True value for $\theta$;
- **zeta**: true value for $\zeta$;
- **gamma.ui**: true value for $\gamma$;
- **alpha.ui**: true value for $\alpha$;
- **sigma.s**: true value for $\sigma_s$;
- **sigma.t**: true value for $\sigma_T$;
- **sigma.st**: true value for $\sigma_{ST}$;
- **betas**: true value for $\beta_s$;
Betat  true value for $\beta_T$;
R2  true value for $R^2_{trial}$;

nb.subject  total number of subjects used;
nb.trials  total number of trials used;
nb.simul  number of simulated datasets;
nb.gh  number of nodes for the Gaussian-Hermite quadrature;
nb.gh2  number of nodes for the Gauss-Hermite quadrature used to re-estimate the model, in case of non-convergence;
nb.mc  number of samples considered in the Monte-Carlo integration;
kappa.use  a numeric, that indicates how to manage the smoothing parameters $k_1$ and $k_2$ in case of convergence issues;
n.knots  number of knots used for splines;
int.method  integration method used;
n.iter  mean number of iterations needed to converge;
dataTkendall  a matrix with nb.dataset line(s) and three columns, of the estimates of Kendall’s $\tau$ and theirs confidence intervals using the parametric bootstrap. All non-convergence cases are represented by a line of 0;
dataR2boot  a matrix with nb.dataset line(s) and three columns, of the estimates of $R^2_{trial}$ and theirs confidence intervals using the parametric bootstrap. All non-convergence cases are represented by a line of 0.
dataParamEstim  a dataframe including all estimates with the associated standard errors, for all simulation. All non-convergence cases are represented by a line of 0;

Author(s)

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References


See Also

jointSurroPenal, summary.jointSurroPenalSimul, jointSurrSimul

Examples

## Not run:
# Surrogacy model evaluation performance study based on 10 generated data
# (Computation takes around 30 minutes)
# To realize a simulation study on 100 samples or more (as required), use
# nb.dataset = 100
jointSimul <- jointSurroPenalSimul(nb.dataset = 10, nbSubSimul = 600,
ntrialSimul = 30, LIMparam = 0.001, LIMlogl = 0.001,
LIMderiv = 0.001, nb.mc = 200, nb.gh = 20,
nb.gh2 = 32, true.init.val = 1, print.itter = F)

# results
summary(jointSimul, d = 3, R2.boot = 1) # bootstrap
summary(jointSimul, d = 3, R2.boot = 0) # Delta-method

## End(Not run)

---

**jointSurroTKendall**  
*Kendall’s τ estimation using numerical integration methods*

### Description

This function estimates the Kendall’s τ based on the joint surrogate model described in *jointSurroPenal* (Soeuf et al., 2018), for the evaluation of a candidate surrogate endpoints, at the individual-level. We used the Monte-carlo and the gaussian Hermite quadrature methods for numerical integration. In case of Gaussian Hermite quadrature, it is better to choose at least 20 quadrature nodes for better results. The actual value of nodes used is the maximum between 20 and nb.gh

### Usage

```r
jointSurroTKendall(object = NULL, theta, gamma, alpha = 1, zeta = 1,
sigma.v = matrix(rep(0, 4), 2, 2), int.method = 0,
nb.MC.kendall = 10000, nb.gh = 32, random.generator = 1,
random = 0, random.nb.sim = 0, seed = 0, ui = 1)
```

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An object inheriting from jointSurroPenal class. The default is NULL</td>
</tr>
<tr>
<td>theta</td>
<td>Variance of the individual-level random effect, ω_{ij}. Required if object is set to NULL</td>
</tr>
<tr>
<td>gamma</td>
<td>Variance of the trial-level random effect associated with the baseline risk, u_i. Required if object is set to NULL. The default is 3.5.</td>
</tr>
<tr>
<td>alpha</td>
<td>Power parameter associated with u_i. Required if object is set to NULL. The default is 1</td>
</tr>
<tr>
<td>zeta</td>
<td>Power parameter associated with ω_{ij}. Required if object is set to NULL. The default is 1</td>
</tr>
<tr>
<td>sigma.v</td>
<td>Covariance matrix of the random effects treatment-by-trial interaction (v_{S_i}, v_{T_i})</td>
</tr>
<tr>
<td>int.method</td>
<td>A numeric, indicates the integration method: 0 for Monte carlo and 1 for Gaussian-Hermite quadrature. The default is 0</td>
</tr>
</tbody>
</table>
**jointSurroTKendall**

- **nb.MC.kendall**: Number of generated points used with the Monte-Carlo to estimate integrals in the Kendall’s τ formulation. Better to use at least 4000 points for stable results. The default is 10000.

- **nb.gh**: Number of nodes for the Gaussian-Hermite quadrature. The default is 32.

- **random.generator**: Random number generator to use by the Fortran compiler, 1 for the intrinsic subroutine Random_number and 2 for the subroutine uni ran(). The default is 1.

- **random**: A binary that says if we reset the random number generation with a different environment at each call (1) or not (0). If it is set to 1, we use the computer clock as a seed. In the last case, it is not possible to reproduce the generated datasets. The default is 0.

- **random.nb.sim**: If random is set to 1, a binary that indicates the number of generations that will be made.

- **seed**: The seed to use for data (or samples) generation. required if random is set to 0. The default is 0.

- **ui**: A binary, indicates whether one considered trial random effect associated with the baseline risk (1) or not (0). The default is 1.

**Value**

This function return the estimated Kendall’s τ

**Author(s)**

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**References**


**See Also**

jointSurrSimul, summary.jointSurrPenal

**Examples**

```r
tau1 <- jointSurroTKendall(theta = 3.5, gamma = 2.5, nb.gh = 32)
tau2 <- jointSurroTKendall(theta = 1, gamma = 0.8, alpha = 1, zeta = 1, nb.gh = 32)

#------Kendall's \(\tau\) from a joint surrogate model ------#

data.sim <- jointSurrSimul(n.obs=400, n.trial = 20, cens.adm=549,
alpha = 1.5, theta = 3.5, gamma = 2.5, zeta = 1,
sigma.s = 0.7, sigma.t = 0.7, rsqrt = 0.8, betas = -1.25,
betat = -1.25, full.data = 0, random.generator = 1,
seed = 0, nb.reject.data = 0)
```
JointSurrSimul

Generate survival times for two endpoints using the joint frailty surrogate model

Description

date are generated from the one-step joint surrogate model (see JointSurrPenal for more details)

Usage

JointSurrSimul(n.obs = 600, n.trial = 30, cens.adm = 549.24, alpha = 1.5, theta = 3.5, gamma = 2.5, zeta = 1, sigma.s = 0.7, sigma.t = 0.7, rsqrt = 0.8, betas = -1.25, betat = -1.25, frailt.base = 1, lambda.S = 1.8, nu.S = 0.0045, lambda.T = 3, nu.T = 0.0025, ver = 1, typeOf = 1, equi.subj.trial = 1, equi.subj.trt = 1, prop.subj.trial = NULL, prop.subj.trt = NULL, full.data = 0, random.generator = 1, random = 0, random.nb.sim = 0, seed = 0, nb.reject.data = 0)

Arguments

n.obs Number of considered subjects. The default is 600.
n.trial Number of considered trials. The default is 30.
cens.adm Censorship time. The default is 549, for about 40% of censored subjects.
alpha Fixed value for $\alpha$. The default is 1.5.
theta Fixed value for $\theta$. The default is 3.5.
gamma Fixed value for $\gamma$. The default is 2.5.
zeta Fixed value for $\zeta$. The default is 1.
sigma.s Fixed value for $\sigma_S^2$. The default is 0.7.
sigma.t Fixed value for $\sigma_T^2$. The default is 0.7.
rsqrt Desired level of correlation between $v_S$ and $v_T$. $R_{\text{trial}}^2 = rsqrt^2$. The default is 0.8.
betas Fixed value for $\beta_S$. The default is -1.25.
Fixed value for $\beta_T$. The default is $-1.25$.

Considered the heterogeneity on the baseline risk (1) or not (0). The default is 1.

Desired scale parameter for the Weibull distribution associated with the Surrogate endpoint. The default is 1.8.

Desired shape parameter for the Weibull distribution associated with the Surrogate endpoint. The default is 0.0045.

Desired scale parameter for the Weibull distribution associated with the True endpoint. The default is 3.

Desired shape parameter for the Weibull distribution associated with the True endpoint. The default is 0.0025.

Number of covariates. For surrogate evaluation, we just considered one covariate, the treatment arm.

Type of joint model used for data generation: 0 = classical joint model with a shared individual frailty effect (Rondeau, 2007), 1 = joint surrogate model with shared frailty effects $u_i$ and $\omega_{ij}$, and two correlated random effects treatment-by-trial interaction ($v_{Si}$, $v_{Ti}$) as described in Sofeu et al. (2018).

A binary variable that indicates if the same proportion of subjects should be included per trial (1) or not (0). If 0, the proportions of subject per trial are required in parameter prop.subj.trial.

A binary variable that indicates if the same proportion of subjects is randomized per trial (1) or not (0). If 0, the proportions of subject per trial are required in parameter prop.subj.trt.

The proportions of subjects per trial. Requires if equi.subj.trial=0.

The proportions of randomized subject per trial. Requires if equi.subj.trt=0.

Specified if you wan the function to return the full dataset (1), including the random effects, or the restrictive dataset (0) with 7 columns required for the function jointSurroPenal.

Random number generator to use by the Fortran compiler, 1 for the intrinsic subroutine Random_number and 2 for the subroutine uniran(). The default is 1.

A binary that says if we reset the random number generation with a different environment at each call (1) or not (0). If it is set to 1, we use the computer clock as seed. In the last case, it is not possible to reproduce the generated datasets”. The default is 0. Required if random.generator is set to 1.

required if random.generator is set to 1, and if random is set to 1.

The seed to use for data (or samples) generation. Required if random.generator is set to 1. Must be a positive value. If negative, the program do not account for seed. The default is 0.
nb.reject.data  Number of generation to reject before the considered dataset. This parameter is required when data generation is for simulation. With a fixed parameter and random.generator set to 1, all generated data are the same. By varying this parameter, different datasets are obtained during data generations. The default value is 0, in case of one dataset.

Details

We just considered in this generation, the Gaussian random effects. If the parameter full.data is set to 1, this function return a list containing several parameters, including the generated random effects. The desired individual level correlation (Kendall’s $\tau$) depend on the values of $\alpha$, $\theta$, $\gamma$ and $\zeta$.

Value

This function return if the parameter full.data is set to 0, a data.frame with columns:

- **patientID**: A numeric, that represents the patient’s identifier, must be unique;
- **trialID**: A numeric, that represents the trial in which each patient was randomized;
- **trt**: The treatment indicator for each patient, with 1 = treated, 0 = untreated;
- **times**: The follow-up time associated with the surrogate endpoint;
- **statusS**: The event indicator associated with the surrogate endpoint. Normally 0 = no event, 1 = event;
- **timeT**: The follow-up time associated with the true endpoint;
- **statusT**: The event indicator associated with the true endpoint. Normally 0 = no event, 1 = event;

If the argument full.data is set to 1, additional columns corresponding to random effects $\omega_{ij}$, $u_i$, $v_{Si}$ and $v_{Ti}$ are returned. Note that $u_i$, $v_{Si}$ and $v_{Ti}$ are returned if typeof is set to 1.

Author(s)

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References


See Also

jointSurSimul
Examples

data.sim <- jointSurrSimul(n.obs = 600, n.trial = 30, cens.adm = 549.24, alpha = 1.5,
theta = 3.5, gamma = 2.5, zeta = 1, sigma.s = 0.7, sigma.t = 0.7,
rsqrt = 0.8, betas = -1.25, betat = -1.25, full.data = 0,
random.generator = 1, seed = 0, nb.reject.data = 0)

longiPenal  Fit a Joint Model for Longitudinal Data and a Terminal Event

Description

Fit a joint model for longitudinal data and a terminal event using a semiparametric penalized likelihood estimation or a parametric estimation on the hazard function.

The longitudinal outcomes $y_i(t_{ik})$ ($k = 1, \ldots, n_i, i = 1, \ldots, N$) for $N$ subjects are described by a linear mixed model and the risk of the terminal event is represented by a proportional hazard risk model. The joint model is constructed assuming that the processes are linked via a latent structure (Wulfsohn and Tsiatsis 1997):

$$ \begin{align*}
    y_i(t_{ik}) &= X_{Li}(t_{ik})^\top \beta_L + Z_i(t_{ik})^\top b_i + \epsilon_i(t_{ik}) \quad \text{(Longitudinal)} \\
    \lambda_i(t|b_i) &= \lambda_0(t) \exp(X_{Ti}(t)\beta_T + h(b_i, \beta_L, Z_i(t), X_{Li}(t))^\top \eta_T) \quad \text{(Terminal)}
\end{align*} $$

where $X_{Li}(t)$ and $X_{Ti}$ are vectors of fixed effects covariates and $\beta_L$ and $\beta_T$ are the associated coefficients. Measurements errors $\epsilon_i(t_{ik})$ are iid normally distributed with mean 0 and variance $\sigma^2$. The random effects $b_i = (b_{0i}, \ldots, b_{qi})^\top \sim N(0, B_1)$ are associated to covariates $Z_i(t)$ and independent from the measurement error. The relationship between the two processes is explained via $h(b_i, \beta_L, Z_i(t), X_{Li}(t))$ with coefficients $\eta_T$. Two forms of the function $h(\cdot)$ are available: the random effects $b_i$ and the current biomarker level $m_i(t) = X_{Li}(t_{ik})^\top \beta_L + Z_i(t_{ik})^\top b_i$.

We consider that the longitudinal outcome can be a subject to a quantification limit, i.e. some observations, below a level of detection $s$ cannot be quantified (left-censoring).

Usage

longiPenal(formula, formula.LongitudinalData, data, data.Longi,

Arguments

formula a formula object, with the response on the left of a $\sim$ operator, and the terms on the right. The response must be a survival object as returned by the 'Surv' function like in survival package. Interactions are possible using * or :.
a formula object, only requires terms on the right to indicate which variables are modelling the longitudinal outcome. It must follow the standard form used for linear mixed-effects models. Interactions are possible using * or :.

data

a 'data.frame' with the variables used in formula.

data.LongitudinalData

a 'data.frame' with the variables used in formula.LongitudinalData.

random

Names of variables for the random effects of the longitudinal outcome. Maximum 3 random effects are possible at the moment. The random intercept is chosen using "1".

id

Name of the variable representing the individuals.

intercept

Logical value. Is the fixed intercept of the biomarker included in the mixed-effects model? The default is TRUE.

link

Type of link function for the dependence between the biomarker and death: "Random-effects" for the association directly via the random effects of the biomarker, "Current-level" for the association via the true current level of the biomarker. The option "Current-level" can be chosen only if the biomarker random effects are associated with the intercept and time (following this order). The default is "Random-effects".

left.censoring

Is the biomarker left-censored below a threshold $s$? The default is FALSE, ie. no left-censoring. In case of a left-censored biomarker, this argument must be equal to the threshold $s$.

n.knots

Integer giving the number of knots to use. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. We estimate I or M-splines of order 4. When the user set a number of knots equals to k (n.knots=k) then the number of interior knots is (k-2) and the number of splines is (k-2)+order. Number of knots must be between 4 and 20. (See Note in frailtyPenal function)

kappa

Positive smoothing parameter in the penalized likelihood estimation. The coefficient kappa of the integral of the squared second derivative of hazard function in the fit (penalized log likelihood). To obtain an initial value for kappa, a solution is to fit the corresponding Cox model using cross validation (See cross-validation in function frailtyPenal). We advise the user to identify several possible tuning parameters, note their defaults and look at the sensitivity of the results to varying them.

maxit

Maximum number of iterations for the Marquardt algorithm. The default is 350.

hazard

Type of hazard functions: "Splines" for semiparametric hazard functions using equidistant intervals or "Splines-per" using percentile with the penalized likelihood estimation, "Weibull" for the parametric Weibull functions. The default is "Splines".

init.B

Vector of initial values for regression coefficients. This vector should be of the same size as the whole vector of covariates with the first elements for the covariates related to the terminal event and then for the covariates related to the biomarker (interactions in the end of each component). Default is 0.5 for each.

init.Random

Initial value for variance of the elements of the matrix of the distribution of the random effects. Default is 0.5 for each element.
Initial values for regression coefficients for the link function. Default is 0.5 for each.

Method for the Gauss-Hermite quadrature: "Standard" for the standard non-adaptive Gaussian quadrature, "Pseudo-adaptive" for the pseudo-adaptive Gaussian quadrature and "HRMSYM" for the algorithm for the multivariate non-adaptive Gaussian quadrature (see Details). The default is "Standard".

Number of nodes for the Gauss-Hermite quadrature. They can be chosen among 5, 7, 9, 12, 15, 20 and 32. The default is 9.

Convergence threshold of the Marquardt algorithm for the parameters (see Details of frailtyPenal function), $10^{-3}$ by default.

Convergence threshold of the Marquardt algorithm for the log-likelihood (see Details of frailtyPenal function), $10^{-3}$ by default.

Convergence threshold of the Marquardt algorithm for the gradient (see Details of frailtyPenal function), $10^{-3}$ by default.

a logical parameter to print iteration process. The default is TRUE.

Typical usage for the joint model

longiPenal(Surv(time,event)~var1+var2, biomarker ~ var1+var2, data, data.Longi, ...)

The method of the Gauss-Hermite quadrature for approximations of the multidimensional integrals, i.e. length of random is 2, can be chosen among the standard, non-adaptive, pseudo-adaptive in which the quadrature points are transformed using the information from the fitted mixed-effects model for the biomarker (Rizopoulos 2012) or multivariate non-adaptive procedure proposed by Genz et al. 1996 and implemented in FORTRAN subroutine HRMSYM. The choice of the method is important for estimations. The standard non-adaptive Gauss-Hermite quadrature ("Standard") with a specific number of points gives accurate results but can be time consuming. The non-adaptive procedure ("HRMSYM") offers advantageous computational time but in case of datasets in which some individuals have few repeated observations (biomarker measures or recurrent events), this method may be moderately unstable. The pseudo-adaptive quadrature uses transformed quadrature points to center and scale the integrand by utilizing estimates of the random effects from an appropriate linear mixed-effects model. This method enables using less quadrature points while preserving the estimation accuracy and thus lead to a better computational time.

NOTE. Data frames data and data.Longi must be consistent. Names and types of corresponding covariates must be the same, as well as the number and identification of individuals.

The following components are included in a 'longiPenal' object for each model:

The sequence of the corresponding estimation of the coefficients for the hazard functions (parametric or semiparametric), the random effects variances and the regression coefficients.

The code used for the model.
formula
The formula part of the code used for the terminal event part of the model.
formula.LongitudinalData
The formula part of the code used for the longitudinal part of the model.
coef
The regression coefficients (first for the terminal event and then for the biomarker.
groups
The number of groups used in the fit.
kappa
The value of the smoothing parameter in the penalized likelihood estimation corresponding to the baseline hazard function for the terminal event.
logLikPenal
The complete marginal penalized log-likelihood in the semiparametric case.
logLik
The marginal log-likelihood in the parametric case.
n.measurements
The number of biomarker observations used in the fit.
max_rep
The maximal number of repeated measurements per individual.
n.deaths
The number of events observed in the fit.
n.iter
The number of iterations needed to converge.
n.knots
The number of knots for estimating the baseline hazard function in the penalized likelihood estimation.
n.strat
The number of stratum.
varH
The variance matrix of all parameters (before positivity constraint transformation for the variance of the measurement error, for which the delta method is used).
varHIH
The robust estimation of the variance matrix of all parameters.
xD
The vector of times where both survival and hazard function of the terminal event are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times.
\lambda D
The array (dim=3) of baseline hazard estimates and confidence bands (terminal event).
survD
The array (dim=3) of baseline survival estimates and confidence bands (terminal event).
typeof
The type of the baseline hazard functions (0:"Splines", "2:Weibull").
npar
The number of parameters.
nvar
The vector of number of explanatory variables for the terminal event and biomarker.
nvarEnd
The number of explanatory variables for the terminal event.
nvarY
The number of explanatory variables for the biomarker.
noVarEnd
The indicator of absence of the explanatory variables for the terminal event.
noVarY
The indicator of absence of the explanatory variables for the biomarker.
LCV
The approximated likelihood cross-validation criterion in the semiparametric case (with H minus the converged Hessian matrix, and l(.) the full log-likelihood).

\[ LCV = \frac{1}{n} (\text{trace}(H^{-1}pl H) - l(.)) \]
AIC

The Akaike information Criterion for the parametric case.

\[ AIC = \frac{1}{n}(np - l(.) \right) \]

n.knots.temp

The initial value for the number of knots.

shape.weib

The shape parameter for the Weibull hazard function.

scale.weib

The scale parameter for the Weibull hazard function.

martingaledeath.res

The martingale residuals for each individual.

conditional.res

The conditional residuals for the biomarker (subject-specific):

\[ R_i^{(m)} = y_i - X_i^\top \hat{\beta} \]

marginal.res

The marginal residuals for the biomarker (population averaged):

\[ R_i^{(c)} = y_i - X_i^\top \hat{\beta} \]

marginal.chol.res

The Cholesky marginal residuals for the biomarker:

\[ R_i^{(m)} = U_i^{(m)} R_i^{(m)} \]

conditional.st.res

The standardized conditional residuals for the biomarker.

marginal.st.res

The standardized marginal residuals for the biomarker.

random.effects.pred

The empirical Bayes predictions of the random effects (ie. using conditional posterior distributions).

pred.y.marg

The marginal predictions of the longitudinal outcome.

pred.y.cond

The conditional (given the random effects) predictions of the longitudinal outcome.

lineardeath.pred

The linear predictor for the terminal part.

global.chisq.d

The vector with values of each multivariate Wald test for the terminal part.

dof.chisq.d

The vector with degrees of freedom for each multivariate Wald test for the terminal part.

global.chisq.test.d

The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the terminal part).

p.global.chisq.d

The vector with the p_values for each global multivariate Wald test for the terminal part.

global.chisq

The vector with values of each multivariate Wald test for the longitudinal part.

dof.chisq

The vector with degrees of freedom for each multivariate Wald test for the longitudinal part.
global_chisq.test
The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the longitudinal part).

p.global_chisq
The vector with the p_values for each global multivariate Wald test for the longitudinal part.

names.factordc
The names of the "as.factor" variables for the terminal part.

names.factor
The names of the "as.factor" variables for the longitudinal part.

intercept
The logical value. Is the fixed intercept included in the linear mixed-effects model?

B1
The variance matrix of the random effects for the longitudinal outcome.

ResidualSE
The standard deviation of the measurement error.

eta
The regression coefficients for the link function.

ne_re
The number of random effects used in the fit.

names.re
The names of variables for the random effects.

link
The name of the type of the link function.

eta_p.value
p-values of the Wald test for the estimated regression coefficients for the link function.

beta_p.value
p-values of the Wald test for the estimated regression coefficients.

leftCensoring
The logical value. Is the longitudinal outcome left-censored?

leftCensoring.threshold
For the left-censored biomarker, the value of the left-censoring threshold used for the fit.

prop.censored
The fraction of observations subjected to the left-censoring.

methodGH
The Gaussian quadrature method used in the fit.

n.nodes
The number of nodes used for the Gaussian quadrature in the fit.

References


multivPenal

See Also

plot.longiPenal, print.longiPenal, summary.longiPenal

Examples

### Not run:

#### Joint model for longitudinal data and a terminal event

```r
data(colorectal)
data(colorectalLongi)

# Survival data preparation - only terminal events
colorectalSurv <- subset(colorectal, new.lesions == 0)

# Baseline hazard function approximated with splines
# Random effects as the link function

model.spli.RE <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, colorectalSurv, data.Longi = colorectalLongi, random = c("1", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, n.knots = 7, kappa = 2)

# Weibull baseline hazard function
# Current level of the biomarker as the link function

model.weib.CL <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, colorectalSurv, data.Longi = colorectalLongi, random = c("1", "year"), id = "id", link = "Current-level", left.censoring = -3.33, hazard = "Weibull")
```

## End(Not run)

---

**multivPenal**

*Fit a multivariate frailty model for two types of recurrent events and a terminal event.*

**Description**

Fit a multivariate frailty model for two types of recurrent events with a terminal event using a penalized likelihood estimation on the hazard function or a parametric estimation. Right-censored data are allowed. Left-truncated data and stratified analysis are not possible. Multivariate frailty models allow studying, with a joint model, three survival dependent processes for two types of recurrent events and a terminal event. Multivariate joint frailty models are applicable in mainly two
settings. First, when focus is on the terminal event and we wish to account for the effect of previous endogenous recurrent event. Second, when focus is on a recurrent event and we wish to correct for informative censoring.

The multivariate frailty model for two types of recurrent events with a terminal event is (in the calendar or time-to-event timescale):

\[
\begin{align*}
  r^{(1)}_i(t|u_i, v_i) &= r^{(1)}_0(t) \exp(\beta_1^1 Z_i(t) + u_i) \\
  r^{(2)}_i(t|u_i, v_i) &= r^{(2)}_0(t) \exp(\beta_2^2 Z_i(t) + v_i) \\
  \lambda_i(t|u_i, v_i) &= \lambda_0(t) \exp(\beta_3^3 Z_i(t) + \alpha_1 u_i + \alpha_2 v_i)
\end{align*}
\]

where \( r^{(l)}_0(t), l \in 1, 2 \) and \( \lambda_0(t) \) are respectively the recurrent and terminal event baseline hazard functions, and \( \beta_1, \beta_2, \beta_3 \) the regression coefficient vectors associated with \( Z_i(t) \) the covariate vector. The covariates could be different for the different event hazard functions and may be time-dependent. We consider that death stops new occurrences of recurrent events of any type, hence given \( t > D \), \( dN^{R(l)}_*(t), l \in 1, 2 \) takes the value 0. Thus, the terminal and the two recurrent event processes are not independent or even conditional upon frailties and covariates. We consider the hazard functions of recurrent events among individuals still alive. Components in the above multivariate frailty model are linked together by two Gaussian and correlated random effects \( u_i, v_i \):

\[
(u_i, v_i)^T \sim \mathcal{N}(0, \Sigma_{uv}), \text{with}
\]

\[\Sigma_{uv} = \begin{pmatrix} \theta_1 & \rho \sqrt{\theta_1 \theta_2} \\ \rho \sqrt{\theta_1 \theta_2} & \theta_2 \end{pmatrix}\]

Dependencies between these three types of event are taken into account by two correlated random effects and parameters \( \theta_1, \theta_2 \) the variance of the random effects and \( \alpha_1, \alpha_2 \) the coefficients for these random effects into the terminal event part. If \( \alpha_1 \) and \( \theta_1 \) are both significantly different from 0, then the recurrent events of type 1 and death are significantly associated (the sign of the association is the sign of \( \alpha_1 \)). If \( \alpha_2 \) and \( \theta_2 \) are both significantly different from 0, then the recurrent events of type 2 and death are significantly associated (the sign of the association is the sign of \( \alpha_2 \)). If \( \rho \), the correlation between the two random effects, is significantly different from 0, then the recurrent events of type 1 and the recurrent events of type 2 are significantly associated (the sign of the association is the sign of \( \rho \)).

**Usage**

```
multivPenal(formula, formula.Event2, formula.terminalEvent, data, initialize = TRUE, recurrentAG = FALSE, n.knots, kappa, maxit = 350, hazard = "Splines", nb.int, print.times = TRUE)
```

**Arguments**

- **formula** a formula object, with the response for the first recurrent event on the left of a \( \sim \) operator, and the terms on the right. The response must be a survival object as returned by the ‘Surv’ function like in survival package. Interactions are possible using * or :.

- **formula.Event2** a formula object, with the response for the second recurrent event on the left of a \( \sim \) operator, and the terms on the right. The response must be a survival object as returned by the ‘Surv’ function like in survival package. Interactions are possible using * or :.
formula.terminalEvent

a formula object, with the response for the terminal event on the left of a ∼ operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function like in survival package.

data

a 'data.frame' with the variables used in `formula`, `formula.Event2` and `formula.terminalEvent`.

initialize

Logical value to initialize regression coefficients and baseline hazard functions parameters. When the estimation is semi-parametric with splines, this initialization produces also values for smoothing parameters (by cross validation). When initialization is requested, the program first fit two shared frailty models (for the two types of recurrent events) and a Cox proportional hazards model (for the terminal event). Default is TRUE.

recurrentAG

Logical value. Is Andersen-Gill model fitted? If so indicates that recurrent event times with the counting process approach of Andersen and Gill is used. This formulation can be used for dealing with time-dependent covariates. The default is FALSE.

n.knots

integer vector of length 3 (for the three outcomes) giving the number of knots to use. First is for the recurrent of type 1, second is for the recurrent of type 2 and third is for the terminal event hazard function. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. Number of knots must be between 4 and 20. (See Note)

kappa

vector of length 3 (for the three outcomes) for positive smoothing parameters in the penalized likelihood estimation. First is for the recurrent of type 1, second is for the recurrent of type 2 and third is for the terminal event hazard function. The coefficient kappa of the integral of the squared second derivative of hazard function in the fit (penalized log likelihood). Initial values for the kappas can be obtained with the option "initialize=TRUE". We advise the user to identify several possible tuning parameters, note their defaults and look at the sensitivity of the results to varying them. Value required.(See Note)

maxit

maximum number of iterations for the Marquardt algorithm. Default is 350.

hazard

Type of hazard functions: "Splines" for semi-parametric hazard functions with the penalized likelihood estimation, "Piecewise-per" for piecewise constant hazard function using percentile, "Piecewise-equi" for piecewise constant hazard function using equidistant intervals, "Weibull" for parametric Weibull function. Default is "Splines".

nb.int

An integer vector of length 3 (for the three outcomes). First is the Number of intervals (between 1 and 20) for the recurrent of type 1 parametric hazard functions ("Piecewise-per", "Piecewise-equi"). Second is the Number of intervals (between 1 and 20) for the recurrent of type 2 parametric hazard functions ("Piecewise-per", "Piecewise-equi"). Third is Number of intervals (between 1 and 20) for the death parametric hazard functions ("Piecewise-per", "Piecewise-equi")

print.times

a logical parameter to print iteration process. Default is TRUE.
**Value**

Parameters estimates of a multivariate joint frailty model, more generally a 'multivPenal' object. Methods defined for 'multivPenal' objects are provided for print, plot and summary. The following components are included in a 'multivPenal' object for multivariate Joint frailty models.

- `b` sequence of the corresponding estimation of the splines coefficients, the random effects variances, the coefficients of the frailties and the regression coefficients.
- `call` The code used for fitting the model.
- `n` the number of observations used in the fit.
- `groups` the number of subjects used in the fit.
- `n.events` the number of recurrent events of type 1 observed in the fit.
- `n.events2` the number of the recurrent events of type 2 observed in the fit.
- `n.deaths` the number of deaths observed in the fit.
- `loglikPenal` the complete marginal penalized log-likelihood in the semi-parametric case.
- `loglik` the marginal log-likelihood in the parametric case.
- `LCV` the approximated likelihood cross-validation criterion in the semi parametric case (with \( H \) minus the converged Hessian matrix, and \( l(.) \) the full log-likelihood.

\[
LCV = \frac{1}{n} \left( \text{trace}(H^{-1}H) - l(.) \right)
\]

- `AIC` the Akaike information Criterion for the parametric case.

\[
AIC = \frac{1}{n} (np - l(.))
\]

- `theta1` variance of the frailty parameter for recurrences of type 1 (\( \text{Var}(u_i) \))
- `theta2` variance of the frailty parameter for recurrences of type 2 (\( \text{Var}(v_i) \))
- `alpha1` the coefficient associated with the frailty parameter \( u_i \) in the terminal hazard function.
- `alpha2` the coefficient associated with the frailty parameter \( v_i \) in the terminal hazard function.
- `rho` the correlation coefficient between \( u_i \) and \( v_i \)
- `npar` number of parameters.
- `coef` the regression coefficients.
- `nvar` A vector with the number of covariates of each type of hazard function as components.
- `varH` the variance matrix of all parameters before positivity constraint transformation (theta, the regression coefficients and the spline coefficients). Then, the delta method is needed to obtain the estimated variance parameters.
- `varHIH` the robust estimation of the variance matrix of all parameters (theta, the regression coefficients and the spline coefficients).
formula the formula part of the code used for the model for the recurrent event.
formula.Event2 the formula part of the code used for the model for the second recurrent event.
formula.terminalEvent the formula part of the code used for the model for the terminal event.
x1 vector of times for hazard functions of the recurrent events of type 1 are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times.
lam1 matrix of hazard estimates and confidence bands for recurrent events of type 1.
xSu1 vector of times for the survival function of the recurrent event of type 1.
surv1 matrix of baseline survival estimates and confidence bands for recurrent events of type 1.
x2 vector of times for the recurrent event of type 2 (see x1 value).
lam2 the same value as lam1 for the recurrent event of type 2.
xSu2 vector of times for the survival function of the recurrent event of type 2.
surv2 the same value as surv1 for the recurrent event of type 2.
xEnd vector of times for the terminal event (see x1 value).
lamEnd the same value as lam1 for the terminal event.
xSuEnd vector of times for the survival function of the terminal event.
survEnd the same value as surv1 for the terminal event.
type.of.Piecewise Type of Piecewise hazard functions (1:"percentile", 0:"equidistant").
n.iter number of iterations needed to converge.
type.of.hazard Type of hazard functions (0:"Splines", 1:"Piecewise", 2:"Weibull").
n.knots a vector with number of knots for estimating the baseline functions.
kappa a vector with the smoothing parameters in the penalized likelihood estimation corresponding to each baseline function as components.
n.knots.temp initial value for the number of knots.
zi splines knots.
time knots for Piecewise hazard function for the recurrent event of type 1.
timedc knots for Piecewise hazard function for the terminal event.
time2 knots for Piecewise hazard function for the recurrent event of type 2.
noVar indicator vector for recurrent, death and recurrent 2 explanatory variables.
nvarRec number of the recurrent of type 1 explanatory variables.
nvarEnd number of death explanatory variables.
nvarRec2 number of the recurrent of type 2 explanatory variables.
nbintervR Number of intervals (between 1 and 20) for the the recurrent of type 1 parametric hazard functions ("Piecewise-per", "Piecewise-equ").
nbintervDC Number of intervals (between 1 and 20) for the death parametric hazard functions ("Piecewise-per", "Piecewise-equ").
nbintervR2
istop
shape.weib
scale.weib
martingale.res
martingale2.res
martingaleddeath.res
frailty.pred
frailty2.pred
frailty.var
frailty2.var
frailty.corr
linear.pred
linear2.pred
lineardeath.pred
global_chisq
dof_chisq
global_chisq.test
p.global_chisq
names.factor
global_chisq2
dof_chisq2
global_chisq.test2
p.global_chisq2
names.factor2
global_chisq_d

Number of intervals (between 1 and 20) for the recurrent of type 2 parametric hazard functions ("Piecewise-per", "Piecewise-equi").

Vector of the convergence criteria.

shape parameters for the Weibull hazard function.

scale parameters for the Weibull hazard function.

martingale residuals for each cluster (recurrent of type 1).

martingale residuals for each cluster (recurrent of type 2).

martingale residuals for each cluster (death).

empirical Bayes prediction of the first frailty term.

empirical Bayes prediction of the second frailty term.

variance of the empirical Bayes prediction of the first frailty term.

variance of the empirical Bayes prediction of the second frailty term.

Correlation between the empirical Bayes prediction of the two frailty.

linear predictor: uses Beta’X + ui in the multivariate frailty models.

linear predictor: uses Beta’X + vi in the multivariate frailty models.

linear predictor for the terminal part form the multivariate frailty models: Beta’X + alpha1 ui + alpha2 vi

Recurrent event of type 1: a vector with the values of each multivariate Wald test.

Recurrent event of type 1: a vector with the degree of freedom for each multivariate Wald test.

Recurrent event of type 1: a binary variable equals to 0 when no multivariate Wald is given, 1 otherwise.

Recurrent event of type 1: a vector with the p-values for each global multivariate Wald test.

Recurrent event of type 1: Names of the "as.factor" variables.

Recurrent event of type 2: a vector with the values of each multivariate Wald test.

Recurrent event of type 2: a vector with the degree of freedom for each multivariate Wald test.

Recurrent event of type 2: a binary variable equals to 0 when no multivariate Wald is given, 1 otherwise.

Recurrent event of type 2: a vector with the p_values for each global multivariate Wald test.

Recurrent event of type 2: Names of the "as.factor" variables.

Terminal event: a vector with the values of each multivariate Wald test.
**dof_chisq_d**  
Terminal event: a vector with the degree of freedom for each multivariate Wald test.

**global_chisq_d**  
Terminal event: a binary variable equals to 0 when no multivariate Wald is given, 1 otherwise.

**p.global_chisq_d**  
Terminal event: a vector with the p-values for each global multivariate Wald test.

**names.factordc**  
Terminal event: Names of the "as.factor" variables.

### Note

"kappa" (kappa[1], kappa[2] and kappa[3]) and "n.knots" (n.knots[1], n.knots[2] and n.knots[3]) are the arguments that the user has to change if the fitted model does not converge. "n.knots" takes integer values between 4 and 20. But with n.knots=20, the model will take a long time to converge. So, usually, begin first with n.knots=7, and increase it step by step until it converges. "kappa" only takes positive values. So, choose a value for kappa (for instance 10000), and if it does not converge, multiply or divide this value by 10 or 5 until it converges. Moreover, it may be useful to change the value of the initialize argument.

### References


### See Also

terminal.event2, print.multivPenal, summary.multivPenal, plot.multivPenal

### Examples

```r
## Not run:

### Multivariate Frailty model ----
data(dataMultiv)

# (computation takes around 60 minutes)
modMultiv.spli <- multivPenal(Surv(TIMEGAP, INDICREC) ~ cluster(PATIENT) + v1 + v2 +
event2(INDICMETA) + terminal(INDICDEATH), formula.Event2 = ~ v1 + v2 + v3,
formula.terminalEvent = ~ v1, data = dataMultiv, n.knots = c(8, 8, 8),
kappa = c(1, 1, 1), initialize = FALSE)

print(modMultiv.spli)

modMultiv.weib <- multivPenal(Surv(TIMEGAP, INDICREC) ~ cluster(PATIENT) + v1 + v2 +
event2(INDICMETA) + terminal(INDICDEATH), formula.Event2 = ~ v1 + v2 + v3,
formula.terminalEvent = ~ v1, data = dataMultiv, hazard = "Weibull")
```
num.id

Identify individuals in Joint model for clustered data

Description

This is a special function used in addition to the `cluster()` function in the context of survival joint models for clustered data. This function identifies subject index. It is used on the right hand side of a 'frailtyPenal' formula. Using `num.id()` in a formula implies that a joint frailty model for clustered data is fitted (Rondeau et al. 2011).

Usage

`num.id(x)`

Arguments

`x` A character or numeric variable which is supposed to indicate the variable identifying individuals

References


See Also

`frailtyPenal`
Examples

```r
## Not run:

data(readmission)
#-- here is generated cluster (5 clusters)
readmission <- transform(readmission, group=id%%5+1)

#-- exclusion all recurrent events --#
#-- to obtain framework of semi-competing risks --#
readmission2 <- subset(readmission, (t.start == 0 & event == 1) | event == 0)

joi.clus.gap <- frailtyPenal(Surv(time, event)-cluster(group)+
num.id(id)+dukes+charlson+sex+chemo+terminal(death),
formula.terminalEvent=dukes+charlson+sex+chemo,
data=readmission2, recurrentAG=FALSE, n.knots=8,
kappa=c(1.e+10,1.e+10), Alpha="None")

## End(Not run)
```

plot.Diffepoce

Plot difference of EPOCE estimators between two joint frailty models.

Description

Plots values of the difference of two Cross-Validated Prognosis Observed Loss (CVPOL) computed with two joint frailty models. Confidence intervals are allowed.

Usage

```r
## S3 method for class 'Diffepoce'
plot(x, conf.bands=TRUE, xlab = "Time", ylab = "EPOCE difference", ...)
```

Arguments

- **x**: An object inheriting from Diffepoce class.
- **conf.bands**: Logical value. Determines whether confidence intervals will be plotted. The default is FALSE.
- **xlab**: Label of x-axis. Default is "Time".
- **ylab**: Label of y-axis. Default is "EPOCE difference".
- **...**: Other unused arguments.
Value

Print one plot with one curve and its confidence interval.

See Also

diffepoce

plot.epoce

Plot values of estimators of the Expected Prognostic Observed Cross-Entropy (EPOCE).

Description

Plots values of estimators MPOL and CVPOL for evaluating EPOCE. No confidence interval.

Usage

```r
## S3 method for class 'epoce'
plot(x, type = "cvpol", pos.legend = "topright", cex.legend = 0.7,
     xlab = "Time", ylab = "Epoce", ...)
```

Arguments

- `x`: An object inheriting from epoce class
- `type`: Type of estimator to plot. If new dataset was used only mpol can be plotted ("mpol"), otherwise mpol and cvpol can be plotted ("mpol" and "cvpol", default is "cvpol").
- `pos.legend`: The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright".
- `cex.legend`: size of the legend. Default is 0.7.
- `xlab`: Label of x-axis. Default is "Time".
- `ylab`: Label of y-axis. Default is "Epoce".
- `...`: Other unused arguments.

Value

Print a curve of the estimator of EPOCE using time points defined in epoce.

See Also

epoke
Description

Plots estimated baseline survival and hazard functions from an object of class 'frailtyPenal'. Confidence bands are allowed.

Usage

```r
## S3 method for class 'frailtyPenal'
plot(x, type.plot = "Hazard", conf.bands=TRUE,
pos.legend = "topright", cex.legend=0.7, main, color=2, Xlab = "Time", Ylab
= "Hazard function", ...)
```

Arguments

- `x`: A shared frailty model, i.e. a frailtyPenal class object (output from calling frailtyPenal function).
- `type.plot`: a character string specifying the type of curve. Possible value are "Hazard", or "Survival". The default is "Hazard". Only the first letters are required, e.g "Haz", "Su"
- `conf.bands`: Logical value. Determines whether confidence bands will be plotted. The default is to do so.
- `pos.legend`: The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright"
- `cex.legend`: character expansion factor *relative* to current `par("cex")`. Default is 0.7
- `main`: title of plot
- `color`: color of the curve (integer)
- `Xlab`: Label of x-axis. Default is "Time"
- `Ylab`: Label of y-axis. Default is "Hazard function"
- `...`: other unused arguments

Value

Print a plot of a shared frailty model.

See Also

frailtyPenal
Examples

```r
## Not run:
data(readmission)

### Shared frailty model
modSha <- frailtyPenal(Surv(time,event)-as.factor(dukes)+cluster(id),
n.knots=10,kappa=10000,data=readmission,hazard="Splines")
plot(modSha,type="surv",conf=FALSE)

### Cox proportional hazard model
modCox <- frailtyPenal(Surv(time,event)-as.factor(dukes),n.knots=10,
kappa=10000,data=readmission,hazard="Splines")
plot(modCox)

## no confidence bands
plot(modSha,conf.bands=FALSE)
plot(modCox,conf.bands=FALSE)

## End(Not run)
```

---

plot.jointNestedPenal  *Plot method for a joint nested frailty model.*

Description

Plots estimated baseline survival and hazard functions of a joint nested frailty model (output from an object of class 'jointNestedPenal' for joint nested frailty models) for each type of event (terminal or recurrent). Confidence bands are allowed.

Usage

```r
## S3 method for class 'jointNestedPenal'
plot(x, event = "Both", type.plot = "Hazard",
conf.bands = FALSE, pos.legend="topleft", cex.legend = 0.7, ylim, main,
color = 2, xlab = "Time", ylab = "Hazard function", ...)
```
Arguments

- **x**: A joint nested model, i.e. an object of class `jointNestedPenal` for joint nested frailty model (output from calling `frailtyPenal` function).

- **event**: a character string specifying the type of curve. Possible value are "Terminal", "Recurrent", or "Both". The default is "Both".

- **type.plot**: a character string specifying the type of curve. Possible value are "Hazard", or "Survival". The default is "Hazard". Only the first letters are required, e.g "Haz", "Su"

- **conf.bands**: logical value. Determines whether confidence bands will be plotted. The default is to do so.

- **pos.legend**: The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright"

- **cex.legend**: character expansion factor *relative* to current `par("cex")`. Default is 0.7

- **ylim**: y-axis limits

- **main**: plot title

- **color**: curve color (integer)

- **xlab**: Label of x-axis. Default is "Time"

- **ylab**: Label of y-axis. Default is "Hazard function"

- **...**: other unused arguments

Value

Print a plot of the baseline survival or hazard functions for each type of event or both with the confidence bands or not (conf.bands argument)

See Also

- `frailtyPenal`

Examples

```r
## Not run:

#-- here is generated cluster (30 clusters)
readmissionNested <- transform(readmission,group=id%%30+1)

# Baseline hazard function approximated with splines with calendar-timescale
model.spli.AG <- frailtyPenal(formula = Surv(t.start, t.stop, event) ~ subcluster(id) + cluster(group) + dukes + terminal(death), formula.terminalEvent = ~dukes, data = readmissionNested, recurrentAG = TRUE, n.knots = 8, kappa = c(9.55e+9, 1.41e+12), initialize = TRUE)
```
# Plot the estimated baseline hazard function with the confidence intervals
plot(model.spli.AG)

# Plot the estimated baseline hazard function with the confidence intervals
plot(model.spli.RE, type = "Survival")

## End(Not run)

---

**plot.jointPenal**

*Plot Method for a Joint frailty model.*

**Description**

Plots estimated baseline survival and hazard functions of a joint frailty model (output from an object of class 'JointPenal' for joint frailty models) for each type of event (terminal or recurrent). Confidence bands are allowed.

**Usage**

```r
## S3 method for class 'jointPenal'
plot(x, event = "Both", type.plot = "Hazard", conf.bands = FALSE, pos.legend="topright", cex.legend = 0.7, ylim, main, color = 2, xlab = "Time", ylab = "Hazard function", ...)
```

**Arguments**

- `x` A joint model, i.e. an object of class frailtyPenal for Joint frailty model (output from calling frailtyPenal function).
- `event` a character string specifying the type of curve. Possible value are "Terminal", "Recurrent", or "Both". The default is "Both".
- `type.plot` a character string specifying the type of curve. Possible value are "Hazard", or "Survival". The default is "Hazard". Only the first letters are required, e.g "Haz", "Su"
- `conf.bands` logical value. Determines whether confidence bands will be plotted. The default is to do so.
- `pos.legend` The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright"
- `cex.legend` character expansion factor *relative* to current `par("cex")`. Default is 0.7
- `ylim` y-axis limits
- `main` plot title
- `color` curve color (integer)
- `Xlab` Label of x-axis. Default is "Time"
- `Ylab` Label of y-axis. Default is "Hazard function"
- `...` other unused arguments
Value

Print a plot of the baseline survival or hazard functions for each type of event or both with the confidence bands or not (conf.bands argument)

See Also

frailtyPenal

Examples

## Not run:

data(readmission)

##-- Gap-time
modJoint.gap <- frailtyPenal(Surv(time,event)-cluster(id)+sex+dukes+charlson+terminal(death),formula.terminalEvent=-sex+dukes+charlson,
data=readmission,n.knots=14,kappa=c(100,100))

##-- It takes around 1 minute to converge --#
plot(modJoint.gap,type.plot="Haz",event="recurrent",conf.bands=TRUE)
plot(modJoint.gap,type.plot="Haz",event="terminal",conf.bands=TRUE)
plot(modJoint.gap,type.plot="Haz",event="both",conf.bands=TRUE)

plot(modJoint.gap,type.plot="Su",event="recurrent",conf.bands=TRUE)
plot(modJoint.gap,type.plot="Su",event="terminal",conf.bands=TRUE)
plot(modJoint.gap,type.plot="Su",event="both",conf.bands=TRUE)

## End(Not run)
Usage

```r
## S3 method for class 'jointSurroPenal'
plot(x, type.plot = "Hazard", conf.bands=TRUE,
pos.legend = "topright", cex.legend=0.7, main, Xlab = "Time", Ylab = "Baseline hazard function", xmin = 0, xmax = NULL, ylim = c(0,1), endpoint = 2,
scale = 1, ...)
```

Arguments

- **x**: An object inheriting from `jointSurroPenal` class (output from calling `jointSurroPenal` function).
- **type.plot**: A character string specifying the type of curve. Possible values are "Hazard", or "Survival". The default is "Hazard". Only the first letters are required, e.g "Haz", "Su".
- **conf.bands**: Logical value. Determines whether confidence bands will be plotted. The default is to do so.
- **pos.legend**: The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right", and "center". The default is "topright".
- **cex.legend**: Character expansion factor *relative* to current `par("cex")`. Default is 0.7.
- **main**: Title of plot.
- **Xlab**: Label of x-axis. Default is "Time".
- **Ylab**: Label of y-axis. Default is "Baseline hazard function".
- **xmin**: Minimum value for x-axis, the default is 0.
- **xmax**: Maximum value for x-axis, the default is NULL.
- **ylim**: Range of y-axis. Default is from 0 to 1.
- **endpoint**: A binary that indicates the endpoint to represent. 0 for the surrogate endpoint, 1 for the true endpoint, and 2 for both surrogate endpoint and true endpoint. The default is 2.
- **scale**: A numeric that allows to rescale the survival times. If no change is needed the argument is set to 1, the default value. E.g: 1/365 aims to convert days to years.
- **...**: other unused arguments.

Value

Print a plot of the baseline survival or hazard functions for each type of event or both with the confidence bands or not (conf.bands argument)

See Also

`jointSurroPenal`
Examples

```r
## Not run:

### Joint surrogate model -----
### evaluation of surrogate endpoints---

data(dataOvarian)
joint.surro.ovar <- jointSurroPenal(data = dataOvarian, n.knots = 8,
               init.kappa = c(2000,1000), indice.alpha = 0, nb.mc = 200,
               scale = 1/365)

# Baseline Hazards functions for both the surrogate endpoint
# and the true endpoint
plot(joint.surro.ovar,endpoint = 2,type.plot = "Haz", conf.bands = T)

# Baseline survival functions for both the surrogate endpoint
# and the true endpoint
plot(joint.surro.ovar,endpoint = 2,type.plot = "Su", conf.bands = T)

## End(Not run)
```

## plot.longiPenal

*Plot Method for a joint model for longitudinal data and a terminal event.*

Description

Plots estimated baseline survival and hazard functions for a terminal outcome from an object of class 'longiPenal'. Confidence bands are allowed.

Usage

```r
## S3 method for class 'longiPenal'
plot(x, type.plot = "Hazard", conf.bands=TRUE,
pos.legend= "topright", cex.legend=0.7, main, color, Xlab = "Time", Ylab =
"Hazard function", ...)
```

Arguments

- `x` A joint model for longitudinal outcome and a terminal event, i.e. a longiPenal class object (output from calling longiPenal function).
@plot.longiPenal

**type.plot**
a character string specifying the type of curve for the terminal event. Possible value are "Hazard", or "Survival". The default is "Hazard". Only the first words are required, e.g "Haz", "Su"

**conf.bands**
Logical value. Determines whether confidence bands will be plotted. The default is to do so.

**pos.legend**
The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright"

**cex.legend**
character expansion factor *relative* to current \( \text{par('cex')} \). Default is 0.7

**main**
title of plot

**color**
color of the curve (integer)

**xlab**
Label of x-axis. Default is "Time"

**ylab**
Label of y-axis. Default is "Hazard function"

... other unused arguments

**Value**
Print a plot for the terminal event of the joint model for a longitudinal and survival data.

**See Also**

`longiPenal`

**Examples**

```r
## Not run:
### Joint model for longitudinal data and a terminal event ---###

data(colorectal)
data(colorectallongi)

data(colorectalSurv)
data(colorectallongi)

# Survival data preparation - only terminal events
colorectalSurv <- subset(colorectal, new.lesions == 0)

# Baseline hazard function approximated with splines
# Random effects as the link function

model.sul.RE <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year + treatment + age + who.PS, colorectalSurv, data.Longi = colorectallongi, random = c("1", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, n.knots = 7, kappa = 2)

pdf(file = "~/home/agarebi/etudiants/all10/newpack/test/plot_longi.pdf")

# Plot the estimated baseline hazard function with the confidence intervals
plot(model.sul.RE)
```
# Plot the estimated baseline hazard function with the confidence intervals
plot(model.spli.RE, type = "Survival")

## End(Not run)

---

**plot.multivPenal**  
*Plot Method for a multivariate frailty model.*

**Description**

Plots of estimated baseline survival and hazard functions of a multivariate frailty model (output from an object of class 'multivPenal' for multivariate frailty models) for each type of event (recurrent, terminal and second recurrent). Confidence intervals are allowed.

**Usage**

```r
## S3 method for class 'multivPenal'
plot(x, event = "Both", type.plot = "Hazard",
conf.bands = FALSE, pos.legend = "topright", cex.legend = 0.7, ylim, main,
color1="red", color2="blue", colorEnd="green", Xlab = "Time", Ylab = "Hazard function",
...)```

**Arguments**

- `x`: A joint multivariate model, i.e. an object of class `multivPenal` (output from calling `multivPenal` function).
- `event`: A character string specifying the type of outcome. Possible value are "Terminal", "Recurrent", "Recurrent2", or "Both". The default is "Both".
- `type.plot`: A character string specifying the type of curve. Possible value are "Hazard", or "Survival". The default is "Hazard". Only the first words are required, e.g. "Haz", "Su"
- `conf.bands`: logical value. Determines whether confidence intervals will be plotted. The default is to do so.
- `pos.legend`: The location of the legend can be specified by setting this argument to a single keyword from the list "bottom", "bottomright", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright".
- `cex.legend`: character expansion factor *relative* to current `par("cex")`. Default is 0.7
- `ylim`: y-axis limits
- `main`: plot title
- `color1`: curve color for recurrent event of type 1 (integer or color name in quotation marks)
- `color2`: curve color for recurrent event of type 2 (integer or color name in quotation marks)
plot.nestedPenal

Value

Print a plot of the baseline survival or hazard functions for each type of event or both with the confidence intervals or not (conf.bands argument)

See Also

multivPenal

Description

Plots estimated baseline survival and hazard functions (output from an object of class 'NestedPenal' for nested frailty models and an object of class 'additivePenal' object for additive frailty model). Confidence bands are allowed.

Usage

```r
# S3 method for class 'nestedPenal'
plot(x, type.plot="Hazard", conf.bands=TRUE,
pos.legend="topright", cex.legend=0.7, main, color=2, Xlab = "Time", Ylab = "Hazard function", ...)
# S3 method for class 'additivePenal'
plot(x, type.plot="Hazard", conf.bands=TRUE,
pos.legend="topright", cex.legend=0.7, main, color=2, Xlab = "Time", Ylab = "Hazard function", ...)
```

Arguments

- `x`: A nested model, i.e. an object of class frailtyPenal for Nested frailty models (output from calling frailtyPenal function), or a fitted additive frailty model (output from calling additivePenal).
- `type.plot`: a character string specifying the type of curve. Possible value are "Hazard", or "Survival". The default is "Hazard". Only the first words are required, e.g "Haz", "Su"
- `conf.bands`: logical value. Determines whether confidence bands will be plotted. The default is to do so.
pos.legend The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright".
cex.legend character expansion factor relative to current par("cex"). Default is 0.7
main plot title
color curve color (integer)
xlab Label of x-axis. Default is "Time"
ylab Label of y-axis. Default is "Hazard function"
... Other graphical parameters like those in plot.frailtyPenal

Value
Print a plot of the baseline survival or hazard functions with the confidence bands or not (conf.bands argument)

See Also
frailtyPenal

Examples

## Not run:

data(dataNested)
modNested <- frailtyPenal(Surv(t1,t2,event)~cluster(group)+
subcluster(subgroup)+cov1+cov2, data=dataNested, n.knots=8, kappa=50000, hazard="Splines")
plot(modNested, conf.bands=FALSE)

data(dataAdditive)
modAdd <- additivePenal(Surv(t1,t2,event)~cluster(group)+var1+slope(var1),
correlation=TRUE, data=dataAdditive, n.knots=8, kappa=862, hazard="Splines")

## 'var1' is boolean as a treatment variable
plot(modAdd)

## End(Not run)
plot.predFrailty  

Plot predictions using a Cox or a shared frailty model.

Description

Plots predicted probabilities of event. Confidence intervals are allowed.

Usage

```r
## S3 method for class 'predFrailty'
plot(x, conf.bands=FALSE, pos.legend="topright",
     cex.legend=0.7, ylim=c(0,1), Xlab = "Time t", Ylab, ...)
```

Arguments

- `x`: An object from the 'prediction' function, i.e. a `predFrailty` class object.
- `conf.bands`: Logical value. Determines whether confidence intervals will be plotted. The default is FALSE.
- `pos.legend`: The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright".
- `cex.legend`: size of the legend. Default is 0.7.
- `ylim`: range of y-axis. Default is from 0 to 1.
- `Xlab`: Label of x-axis. Default is "Time t".
- `Ylab`: Label of y-axis.
- `...`: Other unused arguments.

Value

Print one plot with as many curves as the number of profiles.

plot.predJoint  

Plot predictions using a joint frailty model.

Description

Plots predicted probabilities of terminal event. Confidence intervals are allowed.

Usage

```r
## S3 method for class 'predJoint'
plot(x, conf.bands=FALSE, relapses=TRUE, pos.legend="topright",
     cex.legend=0.7, ylim=c(0,1), Xlab = "Time t", Ylab = "Prediction probability of event", ...)
```
Arguments

x  An object from the 'prediction' function, more generally a predJoint class object.

conf.bands Logical value. Determines whether confidence intervals will be plotted. The default is FALSE.

relapses Logical value. Determines whether observed recurrent events will be plotted. The default is TRUE.

pos.legend The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright".

cex.legend size of the legend. Default is 0.7

ylim range of y-axis. Default is from 0 to 1

xlab Label of x-axis. Default is "Time t"

ylab Label of y-axis. Default is "Prediction probability of event"

... Other unused arguments

Value

Print as many plots as the number of subjects.

plot.predLongi  Plot predictions using a joint model for longitudinal data and a terminal event or a trivariate joint model for longitudinal data, recurrent events and a terminal event.

Description

Plots predicted probabilities of the event. Confidence intervals are allowed.

Usage

## S3 method for class 'predLongi'
plot(x, conf.bands=FALSE, pos.legend="topright", cex.legend=0.7, ylim=c(0,1), xlab = "Time t", ylab, ...)

Arguments

x  An object inheriting from predLongi.

conf.bands Logical value. Determines whether confidence intervals will be plotted. The default is FALSE.

pos.legend The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright".

cex.legend size of the legend. Default is 0.7.
**plot.trivPenal**

Method for a trivariate joint model for longitudinal data, recurrent events and a terminal event.

**Description**

Plots estimated baseline survival and hazard functions of a joint model (output from an object of class 'trivPenal') for each type of event (terminal or recurrent). Confidence bands are allowed.

**Value**

Print one plot with as many curves as the number of profiles.

```r
# S3 method for class 'trivPenal'
plot(x, event = "Both", type.plot = "Hazard", conf.bands = TRUE, pos.legend="topright", cex.legend = 0.7, ylim, main, color = 2, xlab = "Time", ylab = "Hazard function", ...)
```

**Arguments**

- `x`: A joint model, an object of class trivPenal.
- `event`: a character string specifying the type of curve. Possible value are "Terminal", "Recurrent", or "Both". The default is "Both".
- `type.plot`: a character string specifying the type of curve. Possible value are "Hazard", or "Survival". The default is "Hazard". Only the first words are required, e.g. "Haz", "Su"
- `conf.bands`: logical value. Determines whether confidence bands will be plotted. The default is to do so.
- `pos.legend`: The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright"
- `cex.legend`: character expansion factor *relative* to current 'par("cex")'. Default is 0.7
- `ylim`: y-axis limits
- `main`: plot title
- `color`: curve color (integer)
- `xlab`: Label of x-axis. Default is "Time"
- `ylab`: Label of y-axis. Default is "Hazard function"
- `...`: Other unused arguments
Print a plot of the baseline survival or hazard functions for each type of event or both with the confidence bands or not (conf.bands argument)

See Also

trivPenal

Examples

```r
## Not run:
####--- Trivariate joint model for longitudinal data, ---####
####--- recurrent events and a terminal event ---####

data(colorectal)
data(colorectalLongi)

# Weibull baseline hazard function
# Random effects as the link function, Gap timescale
# (computation takes around 30 minutes)
model.weib.RE.gap <- trivPenal(Surv(gap.time, new.lesions) ~ cluster(id) + age + treatment + who.PS + prev.resection + terminal(state),
formula.terminalEvent =~ age + treatment + who.PS + prev.resection,
tumor.size ~ year * treatment + age + who.PS, data = colorectal,
data.Longi = colorectalLongi, random = c("1", "year"), id = "id",
link = "Random-effects", left.censoring = -3.33, recurrentAG = FALSE,
hazard = "Weibull", method.GH="Pseudo-adaptive", n.nodes = 7)

plot(model.weib.RE.gap)
plot(model.weib.RE.gap, type = "survival")

## End(Not run)
```

**plot.trivPenalNL**  
*Plot Method for a Non-Linear Trivariate Joint Model for Recurrent Events and a Terminal Event with a Biomarker Described with an ODE.*

### Description

Plots estimated baseline survival and hazard functions of a joint model (output from an object of class 'trivPenalNL') for each type of event (terminal or recurrent). Confidence bands are allowed.

### Usage

```r
## S3 method for class 'trivPenalNL'
plot(x, event = "Both", type.plot = "Hazard", conf.bands = FALSE, pos.legend="topright", cex.legend = 0.7, ylim, main, color = 2,
Xlab = "Time", Ylab = "Hazard function", ...)
```
Arguments

x       A joint model, an object of class trivPenalNL.
event   a character string specifying the type of curve. Possible value are "terminal", "recurrent", or "both". The default is "both".
type.plot a character string specifying the type of curve. Possible value are "Hazard", or "survival". The default is "hazard". Only the first words are required, e.g "haz", "su"
conf.bands logical value. Determines whether confidence bands will be plotted. The default is to do so.
pos.legend The location of the legend can be specified by setting this argument to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". The default is "topright"
cex.legend character expansion factor *relative* to current `par("cex")`. Default is 0.7
ylim     y-axis limits
main     plot title
color    curve color (integer)
Xlab     Label of x-axis. Default is "Time"
Ylab     Label of y-axis. Default is "Hazard function"
...      other unused arguments

Value

Print a plot of the baseline survival or hazard functions for each type of event or both with the confidence bands or not (conf.bands argument)

See Also

trivPenalNL

Examples

```r
## Not run:
###--- Trivariate joint model for longitudinal data, ---###
###--- recurrent events and a terminal event ---###
data(colorectal)
data(colorectalLongi)

# Weibull baseline hazard function
# Random effects as the link function, Gap timescale
# (computation takes around 30 minutes)
model.weib.RE.gap <- trivPenal(Surv(gap.time, new.lesions) ~ cluster(id) + age + treatment + who.PS + prev.resection + terminal(state),
formula.terminalEvent = ~ age + treatment + who.PS + prev.resection,
tumor.size ~ year * treatment + age + who.PS, data = colorectal,
```
prediction

Prediction probabilities for Cox proportional hazard, Shared, Joint frailty models, Joint models for longitudinal data and a terminal event and Trivariate joint model for longitudinal data, recurrent events and a terminal event (linear and non-linear).

Description

For Cox proportional hazard model
A predictive probability of event between t and horizon time t+w, with w the window of prediction.

\[ P(t, t+w) = \frac{S_i(t) - S_i(t+w)}{S_i(t)} = 1 - \left( \frac{S_0(t+w)}{S_0(t)} \right)^{\exp(\beta'Z_i)} \]

For Gamma Shared Frailty model for clustered (not recurrent) events
Two kinds of predictive probabilities can be calculated:
- a conditional predictive probability of event between t and horizon time t+w, i.e. given a specific group

\[ P^{\text{cond}}(t, t+w) = \frac{S_{ij}(t|u_i) - S_{ij}(t+w|u_i)}{S_{ij}(t|u_i)} = 1 - \left( \frac{S_0(t+w)}{S_0(t)} \right)^{u_i \exp(\beta'Z_{ij})} \]

- a marginal predictive probability of event between t and horizon time t+w, i.e. averaged over the population

\[ P^{\text{mar}}(t, t+w) = 1 - \left( \frac{1 + \theta H_0(t) \exp(\beta'Z_{ij})}{1 + \theta H_0(t+w) \exp(\beta'Z_{ij})} \right)^{1/\theta} \]

For Gaussian Shared Frailty model for clustered (not recurrent) events
Two kinds of predictive probabilities can be calculated:
- a conditional predictive probability of event between t and horizon time t+w, i.e. given a specific group and given a specific Gaussian random effect \( \eta \)

\[ P^{\text{cond}}(t, t+w) = \frac{S_{ij}(t|\eta_i) - S_{ij}(t+w|\eta_i)}{S_{ij}(t|\eta_i)} = 1 - \left( \frac{S_0(t+w)}{S_0(t)} \right)^{\exp(\eta_i + \beta'Z_{ij})} \]
- A marginal predictive probability of event between $t$ and horizon time $t+w$, i.e. averaged over the population

$$
P^\text{marg}(t, t+w) = \frac{\int_{-\infty}^{+\infty} (S_{ij}(t|\eta_i) - S_{ij}(t + w|\eta_i)) g(\eta) d\eta}{\int_{-\infty}^{+\infty} S_{ij}(t) g(\eta) d\eta}
$$

For Gamma Shared Frailty model for recurrent events

Two kinds of predictive probabilities can be calculated:

- A marginal predictive probability of event between $t$ and horizon time $t+w$, i.e. averaged over the population.

$$
P^\text{marg}(t, t+w) = \frac{\int_{0}^{+\infty} (S_{i(j+1)}(t|u_i) - S_{ij}(t + w|u_i)) \cdot (u_i)^j S_{ij}(X_{ij}|u_i) g(u) du}{\int_{0}^{+\infty} S_{i(j+1)}(t|u_i) (u_i)^j S_{ij}(X_{ij}|u_i)) g(u) du}
$$

- A conditional predictive probability of event between $t$ and horizon time $t+w$, i.e. given a specific individual.

This prediction method is the same as the conditional gamma prediction method applied for clustered events (see formula $P^\text{cond}$ before).

For Gaussian Shared Frailty model for recurrent events

Two kinds of predictive probabilities can be calculated:

- A marginal predictive probability of event between $t$ and horizon time $t+w$, i.e. averaged over the population.

$$
P^\text{marg}(t, t+w) = \frac{\int_{0}^{+\infty} (S_{i(j+1)}(t|\eta_i) - S_{ij}(t + w|\eta_i)) \cdot \exp(J\eta_i) S_{ij}(X_{ij}|\eta_i) g(\eta) d\eta}{\int_{0}^{+\infty} S_{i(j+1)}(t|\eta_i) \exp(J\eta_i) S_{ij}(X_{ij}|\eta_i)) g(\eta) d\eta}
$$

- A conditional predictive probability of event between $t$ and horizon time $t+w$, i.e. given a specific individual.

This prediction method is the same as the conditional Gaussian prediction method applied for clustered events (see formula $P^\text{cond}$ before).

It is possible to compute all these predictions in two ways on a scale of times:

- either you want a cumulative probability of developing the event between $t$ and $t+w$ (with $t$ fixed, but with a varying window of prediction $w$);
- either you want at a specific time the probability to develop the event in the next $w$ (i.e. for a varying prediction time $t$, but for a fixed window of prediction). See Details.

For Joint Frailty model

Prediction for two types of event can be calculated: for a terminal event or for a new recurrent event, knowing patient’s characteristics.

- Prediction of death knowing patients’ characteristics:
It is to predict the probability of death in a specific time window given the history of patient $i$ before the time of prediction $t$. The history $H_{i,l}^{J}$, ($l = 1, 2$) is the information on covariates before time $t$, but also the number of recurrences and the time of occurrences. Three types of marginal probabilities are computed:

- a prediction of death between $t$ and $t+w$ given that the patient had exactly $J$ recurrences ($H_{i,l}^{J,1}$) before $t$

$$\begin{align*}
P^1(t, t+w) &= P(D_i \leq t+w | D_i > t, H_{i,l}^{J,1}) = \frac{\int_0^\infty [S_i^D(t) - S_i^D(t+w)] S_{i,j+1}^R(t) g(u) du}{\int_0^\infty S_i^D(t)(u_i)^J S_{i,j+1}^R(t) g(u) du_i}
\end{align*}$$

- a prediction of death between $t$ and $t+w$ given that the patient had at least $J$ recurrences ($H_{i,l}^{J,2}$) before $t$

$$\begin{align*}
P^2(t, t+w) &= P(D_i \leq t+w | D_i > t, H_{i,l}^{J,2}) = \frac{\int_0^\infty [S_i^D(t) - S_i^D(t+w)] S_{i,j}^R(X_{ij}) g(u) du_i}{\int_0^\infty S_i^D(t)(u_i)^J S_{i,j}^R(X_{ij}) g(u) du_i}
\end{align*}$$

- a prediction of death between $t$ and $t+w$ considering the recurrence history only in the parameters estimation. It corresponds to the average probability of death between $t$ and $t+w$ for a patient with these given characteristics.

$$\begin{align*}
P^3(t, t+w) &= P(D_i \leq t+w | D_i > t) = \frac{\int_0^\infty [S_i^D(t) - S_i^D(t+w)] g(u) du_i}{\int_0^\infty S_i^D(t) g(u) du_i}
\end{align*}$$

- Prediction of risk of a new recurrent event knowing patients’ characteristics:

It is to predict the probability of a new recurrent event in a specific time window given the history of patient $i$ before the time of prediction $t$. The history $H_{i,l}^{J}$ is the information on covariates before time $t$, but also the number of recurrences and the time of occurrences. The marginal probability computed is a prediction of a new recurrent event between $t$ and $t+w$ given that the patient had exactly $J$ recurrences ($H_{i,l}^{J}$) before $t$:

$$\begin{align*}
P^R(t, t+w) &= P(X_{i,(j+1)} \leq t+w | X_{i,(j+1)} > t, D_i > t, H_{i,l}^{J}) = \\
\frac{\int_0^\infty [S_{i,j+1}^R(t) - S_{i,j+1}^R(t+w)] S_i^D(t) g(u) du_i}{\int_0^\infty S_{i,j+1}^R(t) S_i^D(t)(u_i)^J S_{i,j+1}^R(X_{ij}) g(u) du_i}
\end{align*}$$

It is possible to compute all these predictions in two ways: - either you want a cumulative probability of developing the event between $t$ and $t+w$ (with $t$ fixed, but with a varying window of prediction $w$); - either you want at a specific time the probability to develop the event in the next $w$ (ie, for a varying prediction time $t$, but for a fixed window of prediction). See Details.

With Gaussian frailties ($\eta$), the same expressions are used but with $u_i^J$ replaced by $\exp(J \eta_i)$ and $g(\eta)$ corresponds to the Gaussian distribution.

For Joint Nested Frailty models

Prediction of the probability of developing a terminal event between $t$ and $t+w$ for subject $i$ who survived by time $t$ based on the visiting and disease histories of their own and other family members observed by time $t$. 


Let \( Y_{f_i}^R(t) \) be the history of subject \( i \) in family \( f \), before time \( t \), which includes all the recurrent events and covariate information. For disease history, let \( T_{f_i}^D(t) = \min(T_{f_i}, t) \) be the observed time to an event before \( t \); \( \delta_{f_i}^D(t) \) the disease indicator by time \( t \) and \( X_{f_i}^D(t) \) the covariate information observed up to time \( t \). We define the family history of subject \( i \) in family \( f \) by
\[
H_{f(-i)}(t) = \{ Y_{f_i}^R(t), T_{f_i}^D(t), \delta_{f_i}^D(t), X_{f_i}^D(t), \forall l \in \{1, ..., i - 1, i + 1, ..., m_f \} \}
\]
which includes the visiting and disease history of all subjects except for subject \( i \) in family \( f \) as well as their covariate information by time \( t \).

The prediction probability can be written as :
\[
P(T_{f_i}^D < t + s | T_{f_i}^D > t, Y_i(t), H_{(f-i)}(t)) =
\]
\[
\int \int P(t < T_{f_i}^D < t + s | X_{f_i}^D, \omega_{f_i}) P(Y_i(t)|X_{f_i}^R(t), \omega_i) P(H_{f(-i)}(t)|X_{f(-i)}(t), \omega_{f_i}) \| g_u g_{\omega f}
\]
\[
\int \int P(T_{f_i}^D > t | X_{f_i}^D, \omega_{f_i}) P(Y_i(t)|X_{f_i}^R(t), \omega_i) P(H_{f(-i)}(t)|X_{f(-i)}(t), \omega_{f_i}) \| g_u g_{\omega f}
\]

**For Joint models for longitudinal data and a terminal event**

The predicted probabilities are calculated in a specific time window given the history of biomarker measurements before the time of prediction \( t (Y_i(t)) \). The probabilities are conditional also on covariates before time \( t \) and that the subject was at risk at \( t \). The marginal predicted probability of the terminal event is
\[
P(t, t+w) = P(D_i \leq t+w | D_i > t, Y_i(t)) = \int_0^\infty [S_i^D(t) - S_i^D(t+w)] f(Y_i(t)\|X_{L_i}, b_i) f(b_i) db_i
\]
\[
\int_0^\infty S_i^D(t) f(Y_i(t)\|X_{L_i}, b_i) f(b_i) db_i
\]

These probabilities can be calculated in several time points with fixed time of prediction \( t \) and varying window \( w \) or with fixed window \( w \) and varying time of prediction \( t \). See Details for an example of how to construct time windows.

**For Trivariate joint models for longitudinal data, recurrent events and a terminal event**

The predicted probabilities are calculated in a specific time window given the history of biomarker measurements \( Y_i(t) \) and recurrences \( H_i^{J,1} \) (complete history of recurrences with known \( J \) number of observed events) before the time of prediction \( t \). The probabilities are conditional also on covariates before time \( t \) and that the subject was at risk at \( t \). The marginal predicted probability of the terminal event is
\[
P(t, t+w) = P(D_i \leq t+w | D_i > t, H_i^{J,1}, Y_i(t)) =
\]
\[
\int_0^\infty \int_0^\infty [S_i^{D}(t) - S_i^{D}(t+w)] \exp(J(v_i+g(t)^\top \eta_{R})) S_i^R(t) f(Y_i(t)\|X_{L_i}, b_i) f(u_i) du_i
\]
\[
\int_0^\infty S_i^{D}(t) \exp(J(v_i+g(t)^\top \eta_{R})) S_i^R(t) f(Y_i(t)\|X_{L_i}, b_i) f(u_i) du_i
\]

The biomarker history can be represented using a linear (trivPenal) or non-linear mixed-effects model (trivPenalNL).

These probabilities can be calculated in several time points with fixed time of prediction \( t \) and varying window \( w \) or with fixed window \( w \) and varying time of prediction \( t \). See Details for an example of how to construct time windows.
**Usage**

```r
prediction(fit, data, data.Longi, t, window, event="Both", conditional = FALSE, MC.sample=0, individual)
```

**Arguments**

- `fit` A frailtyPenal, jointPenal, longiPenal, trivPenal or trivPenalNL object.
- `data` Data frame for the prediction. See Details.
- `data.Longi` Data frame for the prediction used for joint models with longitudinal data. See Details.
- `t` Time or vector of times for prediction.
- `window` Window or vector of windows for prediction.
- `event` Only for joint and shared models. The type of event you want to predict: "Terminal" for a terminal event, "Recurrent" for a recurrent event or "Both". Default value is "Both". For joint nested model, only 'Terminal' is allowed. In a shared model, if you want to predict a new recurrent event then the argument "Recurrent" should be use. If you want to predict a new event from clustered data, do not use this option.
- `conditional` Only for prediction method applied on shared models. Provides distinction between the conditional and marginal prediction methods. Default is FALSE.
- `MC.sample` Number of samples used to calculate confidence bands with a Monte-Carlo method (with a maximum of 1000 samples). If MC.sample=0 (default value), no confidence intervals are calculated.
- `individual` Only for joint nested model. Vector of individuals (of the same family) you want to make prediction.

**Details**

To compute predictions with a prediction time t fixed and a variable window:

```r
prediction(fit, datapred, t=10, window=seq(1,10,by=1))
```

Otherwise, you can have a variable prediction time and a fixed window.

```r
prediction(fit, datapred, t=seq(10,20,by=1), window=5)
```

Or fix both prediction time t and window.

```r
prediction(fit, datapred, t=10, window=5)
```

The data frame building is an important step. It will contain profiles of patient on which you want to do predictions. To make predictions on a Cox proportional hazard or a shared frailty model, only covariates need to be included. You have to distinguish between numerical and categorical variables (factors). If we fit a shared frailty model with two covariates sex (factor) and age (numeric), here is the associated data frame for three profiles of prediction.
prediction

datapred <- data.frame(sex=0, age=0) datapred$sex <- as.factor(datapred$sex) levels(datapred$sex)<- c(1,2) datapred[1,] <- c(1,40) # man, 40 years old datapred[2,] <- c(2,45) # woman, 45 years old datapred[3,] <- c(1,60) # man, 60 years old

Time-dependent covariates: In the context of time-dependent covariate, the last previous value of the covariate is used before the time t of prediction.

It should be noted, that in a data frame for both marginal and conditional prediction on a shared frailty model for clustered data, the group must be specified. In the case of marginal predictions this can be any number as it does not influence predictions. However, for conditional predictions, the group must be also included in the data set used for the model fitting. The conditional predictions apply the empirical Bayes estimate of the frailty from the specified cluster. Here, three individuals belong to group 5.

datapred <- data.frame(group=0, sex=0, age=0) datapred$sex <- as.factor(datapred$sex) levels(datapred$sex)<- c(1,2) datapred[1,] <- c(5,1,40) # man, 40 years old (cluster 5) datapred[2,] <- c(5,2,45) # woman, 45 years old (cluster 5) datapred[3,] <- c(5,1,60) # man, 60 years old (cluster 5)

To use the prediction function on joint frailty models and trivariate joint models, the construction will be a little bit different. In these cases, the prediction for the terminal event takes into account covariates but also history of recurrent event times for a patient. You have to create a data frame with the relapse times, the indicator of event, the cluster variable and the covariates. Relapses occurring after the prediction time may be included but will be ignored for the prediction. A joint model with calendar-timescale need to be fitted with Surv(start,stop,event), relapse times correspond to the "stop" variable and indicators of event correspond to the "event" variable (if event=0, the relapse will not be taken into account). For patients without relapses, all the values of "event" variable should be set to 0. Finally, the same cluster variable name needs to be in the joint model and in the data frame for predictions ("id" in the following example). For instance, we observe relapses of a disease and fit a joint model adjusted for two covariates sex (1:male 2:female) and chemo (treatment by chemotherapy 1:no 2:yes). We describe 3 different profiles of prediction all treated by chemotherapy: 1) a man with four relapses at 100, 200, 300 and 400 days, 2) a man with only one relapse at 1000 days, 3) a woman without relapse.

datapred <- data.frame(time=0, event=0, id=0, sex=0, chemo=0) datapred$sex <- as.factor(datapred$sex) levels(datapred$sex)<- c(1,2) datapred$chemo <- as.factor(datapred$chemo) levels(datapred$chemo)<- c(1,2) datapred[1,] <- c(100,1,1,1,2) # first relapse of the patient 1 datapred[2,] <- c(200,1,1,1,2) # second relapse of the patient 1 datapred[3,] <- c(300,1,1,1,2) # third relapse of the patient 1 datapred[4,] <- c(400,1,1,1,2) # fourth relapse of the patient 1 datapred[5,] <- c(1000,1,2,1,2) # one relapse at 1000 days for patient 2 datapred[6,] <- c(100,0,3,2,2) # patient 3 did not relapse

The data can also be the dataset used to fit the joint model. In this case, you will obtain as many prediction rows as patients.
Finally, for the predictions using joint models for longitudinal data and a terminal event and trivariate joint models, a data frame with the history of the biomarker measurements must be provided. It must include data on measurements (values and time points), cluster variable and covariates. Measurements taken after the prediction time may be included but will be ignored for the prediction. The same cluster variable name must be in the data frame, in the data frame used for the joint model and in the data frame with the recurrent event and terminal event times. For instance, we observe two patients and each one had 5 tumor size measurements (patient 1 had an increasing tumor size and patient 2, decreasing). The joint model used for the predictions was adjusted on sex (1: male, 2: female), treatment (1: sequential arm, 2: combined arm), WHO baseline performance status (1: 0 status, 2: 1 status, 3: 2 status) and previous resection of the primate tumor (0: no, 1: yes). The data frame for the biomarker measurements can be:

```r
datapredj_longi <- data.frame(id = 0, year = 0, tumor.size =
0, treatment = 0, age = 0, who.PS = 0, prev.resection = 0)
datapredj_longi$treatment <- as.factor(datapredj_longi$treatment)
levels(datapredj_longi$treatment) <- 1:2
datapredj_longi$age <- as.factor(datapredj_longi$age)
levels(datapredj_longi$age) <- 1:3
datapredj_longi$who.PS <- as.factor(datapredj_longi$who.PS)
levels(datapredj_longi$who.PS) <- 1:3
datapredj_longi$prev.resection <- as.factor (datapredj_longi$prev.resection)
levels(datapredj_longi$prev.resection) <- 1:2
# patient 1: increasing tumor size
datapredj_longi[1,] <- c(1, 0,1.2,2,1,1,1) datapredj_longi[2,] <-
c(1,0.3,1.4,2,1,1,1) datapredj_longi[3,] <- c(1,0.6,1.9,2,1,1,1)
datapredj_longi[4,] <- c(1,0.2,5,2,1,1,1) datapredj_longi[5,] <-
c(1,1.5,3,9,2,1,1,1)

# patient 2: decreasing tumor size
datapredj_longi[6,] <- c(2, 0,1.2,2,1,1,1) datapredj_longi[7,] <- c(2,0.3,0.7,2,1,1,1) datapredj_longi[8,] <-
c(2,0.5,0.3,2,1,1,1) datapredj_longi[9,] <- c(2,0.7,0.1,2,1,1,1)
datapredj_longi[10,] <- c(2,0.9,0.1,2,1,1,1)
```

**Value**

The following components are included in a 'predFrailty' object obtained by using prediction function for Cox proportional hazard and shared frailty model.

<table>
<thead>
<tr>
<th>Component</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>npred</td>
<td>Number of individual predictions</td>
</tr>
<tr>
<td>x.time</td>
<td>A vector of prediction times of interest (used for plotting predictions): vector of prediction times t if fixed window. Otherwise vector of prediction times t+w</td>
</tr>
<tr>
<td>window</td>
<td>Prediction window or vector of prediction windows</td>
</tr>
<tr>
<td>pred</td>
<td>Predictions estimated for each profile</td>
</tr>
<tr>
<td>(icproba</td>
<td>Logical value. Were confidence intervals estimated?</td>
</tr>
<tr>
<td>predlow</td>
<td>Lower limit of Monte-Carlo confidence interval for each prediction</td>
</tr>
<tr>
<td>predhigh</td>
<td>Upper limit of Monte-Carlo confidence interval for each prediction</td>
</tr>
<tr>
<td>type</td>
<td>Type of prediction probability (marginal or conditional)</td>
</tr>
<tr>
<td>group</td>
<td>For conditional probability, the list of group on which you make predictions</td>
</tr>
</tbody>
</table>
The following components are included in a 'predJoint' object obtained by using prediction function for joint frailty model.

npred Number of individual predictions
x.time A vector of prediction times of interest (used for plotting predictions): vector of prediction times \( t \) if fixed window. Otherwise vector of prediction times \( t+w \)
window Prediction window or vector of prediction windows
group Id of each patient
pred1 Estimation of probability of type 1: exactly \( j \) recurrences
pred2 Estimation of probability of type 2: at least \( j \) recurrences
pred3 Estimation of probability of type 3
pred1_rec Estimation of prediction of relapse
icproba Logical value. Were confidence intervals estimated?
predlow1 Lower limit of Monte-Carlo confidence interval for probability of type 1
predhigh1 Upper limit of Monte-Carlo confidence interval for probability of type 1
predlow2 Lower limit of Monte-Carlo confidence interval for probability of type 2
predhigh2 Upper limit of Monte-Carlo confidence interval for probability of type 2
predlow3 Lower limit of Monte-Carlo confidence interval for probability of type 3
predhigh3 Upper limit of Monte-Carlo confidence interval for probability of type 3
predhigh1_rec Upper limit of Monte-Carlo confidence interval for prediction of relapse
predlow1_rec Lower limit of Monte-Carlo confidence interval for prediction of relapse

The following components are included in a 'predLongi' object obtained by using prediction function for joint models with longitudinal data.

npred Number of individual predictions
x.time A vector of prediction times of interest (used for plotting predictions): vector of prediction times \( t \) if fixed window. Otherwise vector of prediction times \( t+w \)
window Prediction window or vector of prediction windows
group Id of each patient
pred Estimation of probability
icproba Logical value. Were confidence intervals estimated?
predLow Lower limit of Monte-Carlo confidence intervals
predHigh Upper limit of Monte-Carlo confidence intervals
trivariate Logical value. Are the prediction calculated from the trivariate model?
References


Examples

```r
## Not run:

#########################################################################
#### prediction on a COX or SHARED frailty model ####
#########################################################################

data(readmission)
#-- here is a generated cluster (31 clusters of 13 subjects)
readmission <- transform(readmission, group=id%%3+1)

#-- we compute predictions of death
#-- we extract last row of each subject for the time of death
readmission <- aggregate(readmission, by=list(readmission$id),
                         FUN=function(x){x[length(x)][,,-1]})

###-- predictions on a Cox proportional hazard model --##
cox <- frailtyPenal(Surv(t.stop, death) ~ sex + dukes,
                      n.knots=10, kappa=10000, data=readmission)

#-- construction of the data frame for predictions
datapred <- data.frame(sex=0, dukes=0)
datapred$sex <- as.factor(datapred$sex)
levels(datapred$sex) <- c(1, 2)
datapred$dukes <- as.factor(datapred$dukes)
levels(datapred$dukes) <- c(1, 2, 3)
datapred[1,] <- c(1, 2) # man, dukes 2
datapred[2,] <- c(2, 3) # woman, dukes 3

#-- prediction of death for two patients between 100 and 100+w,
#-- with w in (50, 100, ..., 1900)
pred.cox <- prediction(cox, datapred, t=100, window=seq(50, 1900, 50))
plot(pred.cox)

#-- prediction of death for two patients between t and t+100,
#-- with t in (100, 150, ..., 1500)
```
pred.cox2 <- prediction(cox, datapred, t=seq(100, 1500, 50), window=400)
plot(pred.cox2)

#-- predictions on a shared frailty model for clustered data --#
sha <- frailtyPenal(Surv(t.stop, death) ~ cluster(group) + sex + dukes,
n.knots=10, kappa=10000, data=readmission)

#-- marginal prediction # a group must be specified but it does not influence the results # in the marginal predictions setting
datapred$group[1:2] <- 1
pred.sha.marg <- prediction(sha, datapred, t=100, window=seq(50, 1900, 50))
plot(pred.sha.marg)

#-- conditional prediction, given a specific cluster (group=5)
datapred$group[1:2] <- 5
pred.sha.cond <- prediction(sha, datapred, t=100, window=seq(50, 1900, 50),
conditional = TRUE)
plot(pred.sha.cond)

#-- marginal prediction of a recurrent event, on a shared frailty model data(readmission)
datapred <- data.frame(t.stop=0, event=0, id=0, sex=0, dukes=0)
datapred$sex <- as.factor(datapred$sex)
levels(datapred$sex)<- c(1,2)
datapred$dukes <- as.factor(datapred$dukes)
levels(datapred$dukes)<- c(1,2,3)
datapred[1,] <- c(100,1,1,1,2) # man, dukes 2, 3 recurrent events
datapred[2,] <- c(200,1,1,1,2)
datapred[3,] <- c(300,1,1,1,2)
datapred[4,] <- c(350,0,2,1,2) # man, dukes 2 0 recurrent event

#-- Shared frailty model with gamma distribution
sha <- frailtyPenal(Surv(t.stop, event) ~ cluster(id) + sex + dukes, n.knots=10,
kappa=10000, data=readmission)
pred.sha.rec.marg <- prediction(sha, datapred, t=200, window=seq(50, 1900, 50),
event = 'Recurrent', MC.sample=100)
plot(pred.sha.rec.marg, conf.bands=TRUE)

#-- conditional prediction of a recurrent event, on a shared frailty model
pred.sha.rec.cond <- prediction(sha, datapred, t=200, window=seq(50, 1900, 50),
event = 'Recurrent', conditional = TRUE, MC.sample=100)
plot(pred.sha.rec.cond, conf.bands=TRUE)

#---------------------------------------------------------
# prediction on a JOINT frailty model #
#---------------------------------------------------------
data(readmission)
prediction

##-- predictions of death on a joint model --##
`joi <- frailtyPenal(Surv(t.start,t.stop,event),cluster(id)
+sex+dukes+terminal(death),formula.terminalEvent=sex
+dukes,data=readmission,n.knots=10,kappa=c(100,100),recurrentAG=TRUE)`

##-- construction of the data frame for predictions
`datapredj <- data.frame(t.stop=0,event=0,id=0,sex=0,dukes=0)`
`datapredj$sex <- as.factor(datapredj$sex)`
`levels(datapredj$sex) <- c(1,2)`
`datapredj$dukes <- as.factor(datapredj$dukes)`
`levels(datapredj$dukes) <- c(1,2,3)`
`datapredj[1,] <- c(100,1,1,1,2)`
`datapredj[2,] <- c(200,1,1,1,2)`
`datapredj[3,] <- c(300,1,1,1,2)`
`datapredj[4,] <- c(400,1,1,1,2)`
`datapredj[5,] <- c(500,1,2,1,2)`

##-- prediction of death between 100 and 100+500 given relapses
`pred.joint0 <- prediction(joi,datapredj,t=100,window=500,event = "Terminal")
print(pred.joint0)`

##-- prediction of death between 100 and 100+w given relapses
# (with confidence intervals)
`pred.joint <- prediction(joi,datapredj,t=100,window=seq(50,1500,50),
event = "Terminal",MC.sample=100)
plot(pred.joint,conf.bands=TRUE)`
`# each y-value of the plot corresponds to the prediction between [100,x]`

##-- prediction of death between t and t+500 given relapses
`pred.joint2 <- prediction(joi,datapredj,t=seq(100,1000,50),
window=500, event = "Terminal")
plot(pred.joint2)`
`# each y-value of the plot corresponds to the prediction between [x,x+500],
# or in the next 500`

##-- prediction of relapse between 100 and 100+w given relapses
# (with confidence intervals)
`pred.joint <- prediction(joi,datapredj,t=100,window=seq(50,1500,50),
event = "Recurrent",MC.sample=100)
plot(pred.joint,conf.bands=TRUE)`
`# each y-value of the plot corresponds to the prediction between [100,x]`

##-- prediction of relapse and death between 100 and 100+w given relapses
# (with confidence intervals)
`pred.joint <- prediction(joi,datapredj,t=100,window=seq(50,1500,50),
event = "Both",MC.sample=100)
plot(pred.joint,conf.bands=TRUE)`
`# each y-value of the plot corresponds to the prediction between [100,x]`

########################################################################
### prediction on a JOINT model for longitudinal data and a terminal event ###
########################################################################
data(colorectal)
data(colorectalLongi)

# Survival data preparation - only terminal events
colorectalSurv <- subset(colorectal, new.lesions == 0)

#-- construction of the data-frame for predictions
#-- biomarker observations
datapredj_longi <- data.frame(id = 0, year = 0, tumor.size = 0, treatment = 0,
    age = 0, who.PS = 0, prev.resection = 0)
datapredj_longi$treatment <- as.factor(datapredj_longi$treatment)
levels(datapredj_longi$treatment) <- 1:2
datapredj_longi$age <- as.factor(datapredj_longi$age)
levels(datapredj_longi$age) <- 1:3
datapredj_longi$who.PS <- as.factor(datapredj_longi$who.PS)
levels(datapredj_longi$who.PS) <- 1:3
datapredj_longi$prev.resection <- as.factor(datapredj_longi$prev.resection)
levels(datapredj_longi$prev.resection) <- 1:2

# patient 1: increasing tumor size
datapredj_longi[1,] <- c(1, 0,1.2 ,2,1,1)
datapredj_longi[2,] <- c(1,0.3,1,4,2,1,1)
datapredj_longi[3,] <- c(1,0.6,1,9,2,1,1)
datapredj_longi[4,] <- c(1,0.9,2,5,2,1,1)
datapredj_longi[5,] <- c(1,1.5,3,9,2,1,1)

# patient 2: decreasing tumor size
datapredj_longi[6,] <- c(2, 0,1.2 ,2,1,1)
datapredj_longi[7,] <- c(2,0.3,0,7,2,1,1)
datapredj_longi[8,] <- c(2,0.5,0,3,2,1,1)
datapredj_longi[9,] <- c(2,0.7,0,1,2,1,1)
datapredj_longi[10,] <- c(2,0.9,0,1,2,1,1)

#-- terminal event
datapredj <- data.frame(id = 0, treatment = 0, age = 0, who.PS = 0,
    prev.resection = 0)
datapredj$treatment <- as.factor(datapredj$treatment)
levels(datapredj$treatment) <- 1:2
datapredj$age <- as.factor(datapredj$age)
levels(datapredj$age) <- 1:3
datapredj$who.PS <- as.factor(datapredj$who.PS)
datapredj$prev.resection <- as.factor(datapredj$prev.resection)
levels(datapredj$prev.resection) <- 1:2
levels(datapredj$who.PS) <- 1:3
datapredj[1,] <- c(1,2,1,1,1)
datapredj[2,] <- c(2,2,1,1,1)

model.spli.CL <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS ,
    colorectalSurv, data.Longi = colorectalLongi, random = c("1", "year"),
    id = "id", link = "Current-level", left.censoring = -3.33, n.knots = 6, kappa = 1)
prediction

```r
#-- prediction of death between 1 year and 1+2 given history of the biomarker
pred_jointLongi0 <- prediction(model.sp1i.CL, datapredj, datapredj_longi,
t = 1, window = 2)
print(pred_jointLongi0)

#-- prediction of death between 1 year and 1+w given history of the biomarker
pred_jointLongi <- prediction(model.sp1i.CL, datapredj, datapredj_longi,
t = 1, window = seq(0.5, 2.5, 0.2), MC.sample = 100)
plot(pred_jointLongi, conf.bands = TRUE)
# each y-value of the plot corresponds to the prediction between [1,x]

#-- prediction of death between t and t+0.5 given history of the biomarker
pred_jointLongi2 <- prediction(model.sp1i.CL, datapredj, datapredj_longi,
t = seq(1, 2.5, 0.5), window = 0.5, MC.sample = 100)
plot(pred_jointLongi2, conf.bands = TRUE)
# each y-value of the plot corresponds to the prediction between [x,x+0.5]
# or in the next 0.5

############################################################
###-- Warning! You can compute this prediction method with ONLY ONE family
###-- by dataset of prediction.
###-- Please make sure your data frame contains a column for individuals AND a
###-- column for the reference number of the family chosen.

data(readmission)
readmissionNested <- transform(readmission, group=id%%30+1)

#-- construction of the data frame for predictions :
#-- family 5 was selected for the prediction
DataPred <- readmissionNested[which(readmissionNested$group==5),]

#-- Fitting the model
modJointNested_Splines <-
frailtyPenal(formula = Surv(t.start, t.stop, event)~subcluster(id)+
cluster(group) + dukes + terminal(death), formula.terminalEvent
=dukes, data = readmissionNested, recurrentAG = TRUE,n.knots = 8,
kappa = c(9.55e+9, 1.41e+12), initialize = TRUE)

#-- Compute prediction over the individuals 274 and 4 of the family 5
predRead <- prediction(modJointNested_Splines, data=DataPred, t=500,
window=seq(100,1500,200), conditional=FALSE, individual = c(274, 4))

############################################################
###-- prediction on TRIVARIATE JOINT model (linear and non-linear) ###--

#--
data(colorectal)
data(colorectalLongi)
```
#-- construction of the data frame for predictions
#-- history of recurrences and terminal event
datapredj <- data.frame(time0 = 0, time1 = 0, new.lesions = 0, id = 0, 
treatment = 0, age = 0, who.PS = 0, prev.resection = 0)
datapredj$treatment <- as.factor(datapredj$treatment)
levels(datapredj$treatment) <- 1:2
datapredj$age <- as.factor(datapredj$age)
levels(datapredj$age) <- 1:3
datapredj$who.PS <- as.factor(datapredj$who.PS)
levels(datapredj$who.PS) <- 1:3
datapredj$prev.resection <- as.factor(datapredj$prev.resection)
levels(datapredj$prev.resection) <- 1:2

datapredj[1,] <- c(0, 0.4, 1, 1, 2, 1, 1, 1)
datapredj[2,] <- c(0.4, 1.2, 1, 2, 1, 1, 1, 1)
datapredj[3,] <- c(0.5, 1, 2, 2, 1, 1, 1, 1)

#-- Linear trivariate joint model
# (computation takes around 40 minutes)
model.trivPenal <- trivPenal(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + who.PS + terminal(state),
formula.terminalEvent = age + treatment + who.PS + prev.resection,
tumor.size ~ year * treatment + age + who.PS, 
data = colorectal,
data.Longi = colorectalLongi, random = c("1", "year"), id = "id",
link = "Random-effects", left.censoring = -3.33, recurrentAG = TRUE,
n.knots = 6, kappa = c(0.01, 2), method.GH = "Pseudo-adaptive",
n.nodes = 7, init.B = c(-0.07, -0.13, -0.16, -0.17, 0.42, #recurrent events covarates
-0.23, -0.1, -0.09, -0.12, 0.8, -0.23, #terminal event covarates
3.02, -0.30, 0.05, -0.63, -0.02, -0.29, 0.11, 0.74)) #biomarker covarates

#-- prediction of death between 1 year and 1+2
pred.jointTri0 <- prediction(model.trivPenal, datapredj, datapredj_longi, t = 1, window = 2)
print(pred.jointTri0)

#-- prediction of death between 1 year and 1+w
pred.jointTri < prediction(model.trivPenal, datapredj, datapredj_longi, t = 1, window = seq(0.5, 2.5, 0.2), MC.sample = 100)
plot(pred.jointTri, conf.bands = TRUE)

#-- prediction of death between t and t+0.5
pred.jointTri2 <- prediction(model.trivPenal, datapredj, datapredj_longi, t = seq(1, 2.5, 0.5), window = 0.5, MC.sample = 100)
plot(pred.jointTri2, conf.bands = TRUE)

########################################################################

# No information on dose - creation of a dummy variable
colorectalLongi$Dose <- 1

# (computation can take around 40 minutes)
model.trivPenalNL <- trivPenalNL(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + terminal(state), formula.terminalEvent = ~ age + treatment, biomarker = "tumor.size", formula.KG = 1, formula.KD = treatment, dose = "dose", time.biomarker = "year", data = colorectal, data.Longi = colorectallongi, random = c("y0", "KG"), id = "id", init.B = c(-0.22, -0.16, -0.35, -0.19, 0.04, -0.41, 0.23), init.Alpha = 1.86, init.Eta = c(0.5, 0.57, 0.5, 2.34), init.Biomarker = c(1.24, 0.81, 1.07, -1.53), recurrentAG = TRUE, n.knots = 5, kappa = c(0.01, 2), method.GH = "Pseudo-adaptive")

#-- prediction of death between 1 year and 1+2
pred.jointTrNL0 <- prediction(model.trivPenalNL, datapredj, datapredj_longi, t = 1, window = 2)
print(pred.jointTrNL0)

#-- prediction of death between 1 year and 1+w
pred.jointTrNL <- prediction(model.trivPenalNL, datapredj, datapredj_longi, t = 1, window = seq(0.5, 2.5, 0.2), MC.sample = 100)
plot(pred.jointTrNL, conf.bands = TRUE)

#-- prediction of death between t and t+0.5
pred.jointTrNL2 <- prediction(model.trivPenalNL, datapredj, datapredj_longi, t = seq(2, 3, 0.2), window = 0.5, MC.sample = 100)
plot(pred.jointTrNL2, conf.bands = TRUE)

## End(Not run)

---

### print.additivePenal

**Print a Short Summary of parameter estimates of an additive frailty model**

#### Description

Prints a short summary of the parameter estimates of an additive frailty model or more generally of an 'additivePenal' object

#### Usage

```r
## S3 method for class 'additivePenal'
print(x, digits = max(options()$digits - 4, 6), 
...)
```

#### Arguments

- `x` the result of a call to the additivePenal function
- `digits` number of digits to print
- `...` other unused arguments
Value
Print the parameter estimates of the survival or hazard functions.

See Also
additivePenal

print.Cmeasures
Print a short summary of results of 
Cmeasure function.

Description
Print a short summary of results of the concordance measure estimated by the Cmeasure function.

Usage
## S3 method for class 'Cmeasures'
print(x, ...)

Arguments

x a Cmeasures object.

... Other unused arguments

Value
Print concordance measures estimated.

See Also
Cmeasures

print.frailtyPenal
Print a Short Summary of parameter estimates of a shared frailty model

Description
Prints a short summary of parameter estimates of a 'frailtyPenal' object

Usage
## S3 method for class 'frailtyPenal'
print(x, digits = max(options()$digits - 4, 6),
   ...)
Arguments

x: the result of a call to the frailtyPenal function.
digits: number of digits to print.
...: other unused arguments.

Value

Print the parameter estimates of the survival or hazard functions.

See Also

frailtyPenal

Description

Prints a short summary of parameter estimates of a joint nested frailty model, or more generally an object of class 'jointNestedPenal' for joint nested frailty models.

Usage

## S3 method for class 'jointNestedPenal'
print(x, digits = max(options()$digits - 4, 6), ...)

Arguments

x: the result of a call to the jointNestedPenal function
digits: number of digits to print
...: other unused arguments

Value

Print, separately for each type of event (recurrent and terminal), the parameter estimates of the survival or hazard functions.

See Also

frailtyPenal
**print.jointPenal**

*Print a Short Summary of parameter estimates of a joint frailty model*

**Description**

Prints a short summary of parameter estimates of a joint frailty model, or more generally an object of class 'frailtyPenal' for joint frailty models.

**Usage**

```r
## S3 method for class 'jointPenal'
print(x, digits = max(options()$digits - 4, 6), ...)
```

**Arguments**

- `x`: the result of a call to the jointPenal function
- `digits`: number of digits to print
- `...`: other unused arguments

**Value**

Print, separately for each type of event (recurrent and terminal), the parameter estimates of the survival or hazard functions.

**See Also**

- `frailtyPenal`

---

**print.longiPenal**

*Print a Summary of parameter estimates of a joint model for longitudinal data and a terminal event*

**Description**

Prints a short summary of parameter estimates of a joint model for longitudinal data and a terminal event, an object inheriting from class 'longiPenal'.

**Usage**

```r
## S3 method for class 'longiPenal'
print(x, digits = max(options()$digits - 4, 6), ...)
```
Arguments

- x: an object inheriting from `longiPenal` class
- digits: number of digits to print
- ...: other unused arguments

Value

Print, separately for each part of the model (longitudinal and terminal) the parameter estimates and details on the estimation.

See Also

- `longiPenal`

print.multivPenal

Print a Short Summary of parameter estimates of a multivariate frailty model

Description

Prints a short summary of parameter estimates of a multivariate frailty model, or more generally an object of class 'multivPenal'.

Usage

```r
## S3 method for class 'multivPenal'
print(x, digits = max(options()$digits - 4, 6),
       ...)
```

Arguments

- x: the result of a call to the multivPenal function
- digits: number of digits to print
- ...: other unused arguments

Value

Print, separately for each type of event (recurrent1, recurrent2 and terminal), the parameter estimates of the survival or hazard functions.

See Also

- `multivPenal`
print.nestedPenal  

Print a Short Summary of parameter estimates of a nested frailty model

Description

Prints a short summary of parameter estimates of a nested frailty model

Usage

```r
## S3 method for class 'nestedPenal'
print(x, digits = max(options()$digits - 4, 6),
   ...)  
```

Arguments

- `x`: the result of a call to the frailtyPenal function for nested frailty models
- `digits`: number of digits to print
- `...`: other unused arguments

Value

- `n`: the number of observations used in the fit.
- `n.groups`: the maximum number of groups used in the fit
- `n.events`: the number of events observed in the fit
- `eta`: variance of the subcluster effect \( Var(w_{ij}) \)
- `theta`: variance of the cluster effect \( Var(v_i) \)
- `coef`: the coefficients of the linear predictor, which multiply the columns of the model matrix.
- `SE(H)`: the standard error of the estimates deduced from the variance matrix of theta and of the coefficients.
- `SE(HIH)`: the standard error of the estimates deduced from the robust estimation of the variance matrix of theta and of the coefficients.
- `p`: p-value

See Also

- `frailtyPenal`
print.prediction

Print a short summary of results of prediction function.

Description

Print a short summary of results of prediction function.

Usage

### S3 method for class 'predFrailty'
print(x, digits = 3, ...)

### S3 method for class 'predJoint'
print(x, digits = 3, ...)

### S3 method for class 'predLongi'
print(x, digits = 3, ...)

Arguments

- **x**: An object from the 'prediction' function, objects inheriting from predFrailty, predJoint and predLongi classes.
- **digits**: Number of digits to print
- **...**: Other unused arguments

Value

Print the probabilities estimated.

See Also

prediction

print.trivPenal

Print a Summary of parameter estimates of a joint model for longitudinal data, recurrent events and a terminal event

Description

Prints a short summary of parameter estimates of a joint model for longitudinal data, recurrent events and a terminal event, an object inheriting from class 'trivPenal'.

Usage

### S3 method for class 'trivPenal'
print(x, digits = max(options()$digits - 4, 6), ...)
print.trivPenalNL

Arguments

x an object inheriting from trivPenal class
digits number of digits to print
... other unused arguments

Value

Print, separately for each part of the model (longitudinal, recurrent and terminal) the parameter estimates and details on the estimation.

See Also

trivPenal

print.trivPenalNL

Print a Summary of parameter estimates of a non-linear trivariate joint model for longitudinal data, recurrent events and a terminal event

Description

Prints a short summary of parameter estimates of a non-linear trivariate joint model for longitudinal data, recurrent events and a terminal event, an object inheriting from class 'trivPenalNL'.

Usage

## S3 method for class 'trivPenalNL'
print(x, digits = max(options()$digits - 4, 6), ...)

Arguments

x an object inheriting from trivPenalNL class
digits number of digits to print
... other unused arguments

Value

Print, separately for each part of the model (biomarker growth, biomarker decline, recurrent events and terminal event) the parameter estimates and details on the estimation.

See Also

trivPenalNL
readmission

Rehospitalization colorectal cancer

Description

This contains rehospitalization times after surgery in patients diagnosed with colorectal cancer

Usage

data(readmission)

Format

This data frame contains the following columns:

- **id**: identification of each subject. Repeated for each recurrence
- **enum**: which readmission
- **t.start**: start of interval (0 or previous recurrence time)
- **t.stop**: recurrence or censoring time
- **time**: interocurrence or censoring time
- **event**: rehospitalization status. All event are 1 for each subject excepting last one that it is 0
- **chemo**: Did patient receive chemotherapy? 1: No; 2: Yes
- **sex**: gender: 1:Males 2:Females
- **dukes**: Dukes’ tumoral stage: 1:A-B; 2:C 3:D
- **charlson**: Comorbidity Charlson’s index. Time-dependent covariate. 0: Index 0; 1: Index 1-2; 3: Index >=3
- **death**: death indicator. 1:dead and 0:alive

Source

**slope**

*Identify variable associated with the random slope*

**Description**

This is a special function used in the context of survival additive models. It identifies the variable which is in interaction with the random slope \((v_i)\). Generally, this variable is the treatment variable. Using `interaction()` in a formula implies that an additive frailty model is fitted.

**Usage**

```r
slope(x)
```

**Arguments**

- `x` A factor, a character or a numerical variable

**Value**

- `x` The variable in interaction with the random slope

**Note**

It is necessary to specify which variable is in interaction with the random slope, even if only one explanatory variable is included in the model.

**See Also**

`additivePenal`

**Examples**

```r
## Not run:
data(dataAdditive)

##-- Additive with one covariate --##
modAdd1cov <- additivePenal(Surv(t1,t2,event)~cluster(group)+var1+slope(var1),data=dataAdditive,n.knots=8,kappa=10000,hazard="Splines")

##-- Additive with two covariates --##
set.seed(1234)
dataAdditive$var2 <- rbinom(nrow(dataAdditive),1,0.5)
modAdd2cov <- additivePenal(Surv(t1,t2,event)~cluster(group)+var1+
```
subcluster

Identify subclusters

Description

This is a special function used in the context of survival nested or joint nested models. It identifies correlated groups of observations within other groups defined by using 'cluster' function from 'survival' package, and is used on the right hand side of 'frailtyPenal' formula for fitting a nested or joint nested model. Using subcluster() in a formula implies that a nested or a joint nested frailty model is estimated.

Usage

subcluster(x)

Arguments

x

A character, factor, or numeric variable which is supposed to indicate the variable subgroup

Value

x

A variable identified as a subcluster

See Also

frailtyPenal
Examples

```r
# Not run:

data(dataNested)
modClu <- frailtyPenal(Surv(t1, t2, event) ~ cluster(group) +
                        subcluster(subgroup) + cov1 + cov2, data = dataNested,
                        n.knots = 8, kappa = c(50000, 50000), hazard = "Splines")

print(modClu)

#-- here is generated cluster (30 clusters)
readmissionNested <- transform(readmission, group = id %% 30 + 1)

modJointNested_Splines <- frailtyPenal(formula = Surv(t.start, t.stop, event) ~
                                                        subcluster(id) + cluster(group) + dukes +
                                                        terminal(death), formula.terminalEvent = ~dukes,
                                                        data = readmissionNested, recurrentAG = TRUE,
                                                        n.knots = 8, kappa = c(9.55e+9, 1.41e+12), initialize = TRUE)

# End(Not run)
```

summary.additivePenal  summary of parameter estimates of an additive frailty model

Description

This function returns hazard ratios (HR) and its confidence intervals

Usage

```r
# S3 method for class 'additivePenal'
summary(object, level = 0.95, len = 6, d = 2,
        lab = "hr", ...)
```

Arguments

- `object` output from a call to additivePenal.
- `level` significance level of confidence interval. Default is 95%.
- `len` the total field width. Default is 6.
- `d` the desired number of digits after the decimal point. Default of 6 digits is used.
- `lab` label of printed results.
- `...` other unused arguments.
**Value**

Prints HR and its confidence intervals for each covariate. Confidence level is allowed (level argument).

**See Also**

additivePenal

**Examples**

```r
## Not run:

data(dataAdditive)

modAdd <- additivePenal(Surv(t1,t2,event)-cluster(group)+var1+slope(var1),
correlation=TRUE,data=dataAdditive,n.knots=8,kappa=862,hazard="Splines")

#- 'var1' is boolean as a treatment variable.

summary(modAdd)

## End(Not run)
```

---

**summary.frailtyPenal**  
*summary of parameter estimates of a shared frailty model*

**Description**

This function returns hazard ratios (HR) and its confidence intervals.

**Usage**

```
## S3 method for class 'frailtyPenal'
summary(object, level = 0.95, len = 6, d = 2,
lab="hr", ...)
```

**Arguments**

- **object**: output from a call to frailtyPenal.
- **level**: significance level of confidence interval. Default is 95%.
- **len**: the total field width. Default is 6.
- **d**: the desired number of digits after the decimal point. Default of 6 digits is used.
- **lab**: label of printed results.
- **...**: other unused arguments.
summary.jointNestedPenal

**Value**

Prints HR and its confidence intervals. Confidence level is allowed (level argument).

**See Also**

frailtyPenal

**Examples**

```r
## Not run:

data(kidney)

###-- Shared frailty model --###
modSha <- frailtyPenal(Surv(time,status)~age+sex+cluster(id),
n.knots=8,kappa=10000,data=kidney,hazard="Splines")

###-- Cox proportional hazard model --###
modCox <- frailtyPenal(Surv(time,status)~age+sex,  
n.knots=8,kappa=10000,data=kidney,hazard="Splines")

#-- confidence interval at 95% level (default)
summary(modSha)
summary(modCox)

#-- confidence interval at 99% level
summary(modSha,level=0.99)
summary(modCox,level=0.99)

## End(Not run)
```

---

**summary.jointNestedPenal**

*summary of parameter estimates of a joint nested frailty model*

**Description**

This function returns hazard ratios (HR) and its confidence intervals.
summary.jointNestedPenal

Usage

## S3 method for class 'jointNestedPenal'
summary(object, level = 0.95, len = 6, d = 2, lab="hr", ...)

Arguments

- **object**: output from a call to frailtyPenal for joint nested models
- **level**: significance level of confidence interval. Default is 95%.
- **len**: the total field width. Default is 6.
- **d**: the desired number of digits after the decimal point. Default of 6 digits is used.
- **lab**: label of printed results.
- **...**: other unused arguments.

Value

Prints HR and its confidence intervals for each covariate. Confidence level is allowed (level argument).

See Also

- frailtyPenal

Examples

## Not run:

```r
#-- here is generated cluster (30 clusters)
readmissionNested <- transform(readmission, group=id%%30+1)

# Baseline hazard function approximated with splines with calendar-timescale

model.spli.AG <- frailtyPenal(formula = Surv(t.start, t.stop, event) ~ subcluster(id) + cluster(group) + dukes + terminal(death),
                              formula.terminalEvent = ~dukes, data = readmissionNested, recurrentAG = TRUE, n.knots = 8, kappa = c(0.55e+9, 1.41e+12),
                              initialize = TRUE)

summary(model.spli.AG)
```

## End(Not run)
summary.jointPenal  

summary of parameter estimates of a joint frailty model

Description

This function returns hazard ratios (HR) and its confidence intervals.

Usage

## S3 method for class 'jointPenal'
summary(object, level = 0.95, len = 6, d = 2, 
lab="hr", ...)

Arguments

object  
output from a call to frailtyPenal for joint models

level  
significance level of confidence interval. Default is 95%.

d  
the total field width. Default is 6.

d  
the desired number of digits after the decimal point. Default of 6 digits is used.

lab  
label of printed results.

...  
other unused arguments.

Value

Prints HR and its confidence intervals for each covariate. Confidence level is allowed (level argument).

See Also

frailtyPenal

Examples

## Not run:

data(readmission)

#-- gap-time
modJoint.gap <- frailtyPenal(Surv(time,event)~cluster(id)+sex+dukes+charlson+terminal(death),formula.terminalEvent=~sex+dukes+charlson,
data=readmission,n.knots=14,kappa=rep(9.55e+9,1.41e+12))

#-- calendar time
modJoint.calendar <- frailtyPenal(Surv(t.start,t.stop,event)~cluster(id)+
                            sex+dukes+charlson+terminal(death),formula.terminalEvent=~sex+dukes+charlson,
Short summary of the random effects parameters, the fixed treatment effects, and the surrogacy evaluation criteria estimated from a joint surrogate model

Description

This function returns the estimate of the coefficients and their standard error with p-values of the Wald test for the joint surrogate model, also hazard ratios (HR) and their confidence intervals for the fixed treatment effects, and finally an estimate of the surrogacy evaluation criterion (Kendall’s \( \tau \) and \( R^2_{trial} \)).

Usage

```r
## S3 method for class 'jointSurroPenal'
summary(object, d = 4, len = 3, int.method.kt = 0, nb.gh = 32, ...)
```

Arguments

- `object`: an object inheriting from `jointSurroPenal` class.
- `d`: The desired number of digits after the decimal point for parameters. The maximum of 4 digits is required for the estimates. Default of 3 digits is used.
- `len`: The desired number of digits after the decimal point for p-value and convergence criteria. Default of 4 digits is used.
- `int.method.kt`: A binary, indicates the integration method for Kendall’s \( \tau \) estimation: 0 for Monte Carlo, and 1 for Gaussian Hermite quadrature. The default is 0.
- `nb.gh`: Number of nodes for the Gaussian-Hermite quadrature. The default is 32 1 for Gaussian-Hermite quadrature.
- `...`: other unused arguments.
Value
For the variances parameters of the random effects, it prints the estimate of the coefficients with their standard error, Z-statistics and p-values of the Wald test. For the fixed treatment effects, it also prints HR and its confidence intervals for each covariate. For the surrogacy evaluation criteria, it prints the estimated Kendall’s $\tau$ with its 95% Confidence interval obtained by the parametric bootstrap, the estimated $R^2_{trial}(R2trial)$ with standard error and the 95% Confidence interval obtained by Delta-method, $R^2_{trial}(R2.boot)$ and its 95% Confidence interval obtained by the parametric bootstrap. We notice that, using the bootstrap, the standard error of the point estimate is not available. The other parameters displayed are: the penalized marginal log-likelihood, number of iterations, the LCV and the Convergence criteria.

Author(s)
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See Also
jointSurroPenal jointSurroTKendall

Examples

```r
###---Data generation---###
data.sim <- jointSurrSimul(n.obs=400, n.trial = 20, cens.adm=549,
alpha = 1.5, theta = 3.5, gamma = 2.5, zeta = 1,
sigma.s = 0.7, sigma.t = 0.7, rsqrt = 0.8, betas = -1.25,
betat = -1.25, full.data = 0, random.generator = 1,
seed = 0, nb.reject.data = 0)

## Not run:
###---Estimation---###
joint.surrogate <- jointSurroPenal(data = data.sim, nb.mc = 300,
nb.gh = 20, indice.alpha = 1, n.knots = 6)

summary(joint.surrogate)
summary(joint.surrogate, d = 4, len = 3, int.method.kt = 1, nb.gh = 25)

## End(Not run)
```
Description

This function returns the true value, the mean of the estimates, the empirical standard error, the mean of the estimated standard errors (Mean SE), and the percentage of coverate for model parameters.

Usage

```r
## S3 method for class 'jointSurroPenalSimul'
summary(object, d = 3, R2boot = 0, ...)
```

Arguments

- `object`: an object inheriting from `jointSurroPenalSimul` class.
- `d`: The desired number of digits after the decimal point. Default of 3.
- `R2boot`: A binary that specifies whether the confidence interval of \( R^2_{trial} \) should be computed using parametric bootstrap (1) or Delta-method (0). The default is 0.
- `...`: other unused arguments.

Value

For each parameter of the joint surrogate model, we print the true simulation value, the empirical standard error (empirical SE), the mean of the estimated standard errors (Mean SE), and the percentage of coverate (CP) for each model parameters. For the Kendall’s \( \tau \), the 95% Confidence interval is obtained by the parametric bootstrap. For \( R^2_{trial} \), the standard error is obtained by Delta-method and the 95% Confidence interval could be obtained by Delta-method or parametric bootstrap. We also display the total number of non-convergence case with the associated percentage (\( R : n(\%) \)), the mean number of iterations to reach convergence, and other estimation and simulation parameters.

Author(s)

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See Also

`jointSurroPenalSimul`

Examples

```r
# studies simulation
## Not run:
# Studies simulation
# (Computation takes around 11 hours)
joint.simul <- jointSurroPenalSimul(nb.dataset = 10, nbSubSimul=600, ntrialSimul=30, LIMparam = 0.001, LIMlogl = 0.001, LIMderiv = 0.001, nb.mc = 200, nb.gh = 20, nb.gh2 = 32, true.init.val = 1, print.itter=F)
```
summary.longiPenal

Short summary of fixed covariates estimates of a joint model for longitudinal data and a terminal event

Description

This function returns coefficients estimates and their standard error with p-values of the Wald test for the longitudinal outcome and hazard ratios (HR) and their confidence intervals for the terminal event.

Usage

```r
# S3 method for class 'longiPenal'
summary(object, level = 0.95, len = 6, d = 2,
lab=c("coef","hr"), ...)
```

Arguments

- **object**: an object inheriting from longiPenal class
- **level**: significance level of confidence interval. Default is 95%.
- **len**: the total field width for the terminal part. Default is 6.
- **d**: the desired number of digits after the decimal point. Default of 6 digits is used.
- **lab**: labels of printed results for the longitudinal outcome and the terminal event respectively.
- **...**: other unused arguments.

Value

For the longitudinal outcome it prints the estimates of coefficients of the fixed covariates with their standard error and p-values of the Wald test. For the terminal event it prints HR and its confidence intervals for each covariate. Confidence level is allowed (level argument).

See Also

longiPenal
Examples

### Not run:
#### Joint model for longitudinal data and a terminal event ---###

```r
data(colorectal)
data(colorectallongi)

# Survival data preparation - only terminal events
colorectalsurv <- subset(colorectal, new.lesions == 0)

# Baseline hazard function approximated with splines
# Random effects as the link function
model.spli.RE <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, colorectalsurv, data.Longi = colorectallongi, random = c("I", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, n.knots = 7, kappa = 2)

# Weibull baseline hazard function
# Current level of the biomarker as the link function
model.weib.CL <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, colorectalsurv, data.Longi = colorectallongi, random = c("I", "year"), id = "id", link = "Current-level", left.censoring = -3.33, hazard = "Weibull")

summary(model.spli.RE)
summary(model.weib.CL)

### End(Not run)
```

**summary.multivPenal**  
*summary of parameter estimates of a multivariate frailty model.*

**Description**

This function returns hazard ratio (HR) and its confidence intervals.

**Usage**

```r
## S3 method for class 'multivPenal'
summary(object, level = 0.95, len = 6, d = 2, lab = "hr", ...)
```
summary.nestedPenal

Arguments

object: output from a call to multivPenal for joint multivariate models.
level: significance level of confidence interval. Default is 95%.
len: the total field width. Default is 6.
d: the desired number of digits after the decimal point. Default of 6 digits is used.
lab: label of printed results.
... other unused arguments.

Value

Prints HR and its confidence intervals for each covariate. Confidence level is allowed (level argument).

See Also

multivPenal

summary.nestedPenal  summary of regression coefficient estimates of a nested frailty model

Description

This function returns hazard ratios (HR) and its confidence intervals for each regression coefficient.

Usage

## S3 method for class 'nestedPenal'
summary(object, level = 0.95, len = 6, d = 2,
lab="hr", ...)
See Also

frailtyPenal

Examples

```r
data(dataNested)

modNested <- frailtyPenal(Surv(t1,t2,event)~cluster(group)+
subcluster(subgroup)+cov1+cov2,data=dataNested,
n.knots=8,kappa=c(50000,50000),hazard="Splines")

#- It takes 90 minutes to converge (depends on processor)

summary(modNested)

# End(Not run)
```

summary.trivPenal  Short summary of fixed covariates estimates of a joint model for longitudinal data, recurrent events and a terminal event

Description

This function returns coefficients estimates and their standard error with p-values of the Wald test for the longitudinal outcome and hazard ratios (HR) and their confidence intervals for the terminal event.

Usage

```r
## S3 method for class 'trivPenal'
summary(object, level = 0.95, len = 6, d = 2,
lab=c("coef","hr"), ...)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>an object inheriting from trivPenal class</td>
</tr>
<tr>
<td>level</td>
<td>significance level of confidence interval. Default is 95%.</td>
</tr>
<tr>
<td>len</td>
<td>the total field width for the terminal part. Default is 6.</td>
</tr>
<tr>
<td>d</td>
<td>the desired number of digits after the decimal point. Default of 6 digits is used.</td>
</tr>
<tr>
<td>lab</td>
<td>labels of printed results for the longitudinal outcome and the terminal event respectively.</td>
</tr>
<tr>
<td>...</td>
<td>other unused arguments.</td>
</tr>
</tbody>
</table>
Value

For the longitudinal outcome it prints the estimates of coefficients of the fixed covariates with their standard error and p-values of the Wald test. For the terminal event it prints HR and its confidence intervals for each covariate. Confidence level is allowed (level argument).

See Also

trivPenal

Examples

## Not run:

### Trivariate joint model for longitudinal data, recurrent events and a terminal event

data(colorectal)
data(colorectallongi)

# Weibull baseline hazard function
# Random effects as the link function, Gap timescale
# (computation takes around 30 minutes)
model.weib.RE.gap <- trivPenal(Surv(gap.time, new.lesions) ~ cluster(id) + age + treatment + who.PS + prev.resection + terminal(state), formula.terminalEvent =~ age + treatment + who.PS + prev.resection, tumor.size = year * treatment + age + who.PS, data = colorectal, data.Longi = colorectallongi, random = c("1", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, recurrentAG = FALSE, hazard = "Weibull", method.GH="Pseudo-adaptive", n.nodes = 7)

summary(model.weib.RE.gap)

## End(Not run)
Usage

```r
## S3 method for class 'trivPenalNL'
summary(object, level = 0.95, len = 6, d = 2,
lab=c("coef","hr"), ...)
```

Arguments

- `object`: an object inheriting from `trivPenal` class
- `level`: significance level of confidence interval. Default is 95%.
- `len`: the total field width for the terminal part. Default is 6.
- `d`: the desired number of digits after the decimal point. Default of 6 digits is used.
- `lab`: labels of printed results for the longitudinal outcome and the terminal event respectively.
- `...`: other unused arguments.

Value

For the longitudinal outcome it prints the estimates of coefficients of the fixed covariates with their standard error and p-values of the Wald test (separately for the biomarker growth and decline). For the terminal event it prints HR and its confidence intervals for each covariate. Confidence level is allowed (level argument).

See Also

`trivPenalNL`

Examples

```r
## Not run:

###----- Trivariate joint model for longitudinal data, ---###
###----- recurrent events and a terminal event ---###

data(colorectal)
data(colorectallongi)

# Weibull baseline hazard function
# Random effects as the link function, Gap timescale
# (computation takes around 30 minutes)
model.weib.RE.gap <- trivPenal(Surv(gap.time, new.lesions) ~ cluster(id) + age + treatment + who.PS + prev.resection + terminal(state),
formula.terminalEvent =~ age + treatment + who.PS + prev.resection,
tumor.size ~ year * treatment + age + who.PS, data = colorectal,
data.Longi = colorectallongi, random = c("1", "year"), id = "id",
link = "Random-effects", left.censoring = -3.33, recurrentAG = FALSE,
hazard = "Weibull", method=G="Pseudo-adaptive", n.nodes = 7)
```
Create a survival object for interval censoring and possibly left truncated data

Description

This is a function used in case of interval-censoring as a response variable in a model formula only for Cox proportional hazard or shared frailty model. Sometimes, an unobserved event might occur in a time interval \([L, U]\). Recurrent argument gets invalid with the use of SurvIC. Note that this function used a Kronecker product which can suffer from computation issue when the number of subjects in each cluster is high. Time dependent variables are not allowed.

Usage

SurvIC(t0, lower, upper, event)

Arguments

t0 Truncation time for left truncated data only. To be ignored otherwise.
lower Starting time of the interval for interval-censored data. Time of right-censoring instead.
upper Ending time of the interval for interval-censored data. For right-censored data, lower and upper time must be equal (for numerical reason).
event Status indicator 0=right-censored, 1=interval-censored

Details

Typical usages are SurvIC(lower, upper, event) or SurvIC(t0, lower, upper, event)

Examples

## Not run:

data(bcos)
bcos$event <- ifelse(bcos$left!=bcos$right,1,0)

### Cox proportional hazard model with interval censoring ---###

cox.ic <- frailtyPenal(SurvIC(left, right, event)-treatment, 
data=bcos, n.knots=8, kappa=10000)
survival

### Shared model with interval censoring ###

```r
bcos$group <- c(rep(1:20,4),1:14)
sha.ic <- frailtyPenal(SurvIC(left,right,event)-cluster(group)+
treatment,data=bcos,n.knots=8,kappa=10000)
```

## End(Not run)

---

### survival

#### Survival function

**Description**

Let $t$ be a continuous variable, we determine the value of the survival function to $t$ after run fit.

**Usage**

```r
survival(t, ObjFrailty)
```

**Arguments**

- **t**: time for survival function.
- **ObjFrailty**: an object from the frailtypack fit.

**Value**

return the value of survival function in $t$.

**Examples**

```r
## Not run:

#-- a fit Shared
data(readmission)

fit.shared <- frailtyPenal(Surv(time,event)-dukes+cluster(id)+
strata(sex),n.knots=10,kappa=c(10000,10000),data=readmission)

#-- calling survival
survival(20,fit.shared)
```
## terminal

**Identify terminal indicator**

**Description**

This is a special function used in the context of recurrent event models with terminal event (e.g., censoring variable related to recurrent events). It contains the status indicator, normally 0=alive, 1=dead, and is used on the right hand side of a formula of a ‘frailtyPenal’, ‘longiPenal’ and ‘trivPenal’ functions. Using `terminal()` in a formula implies that a joint frailty model for recurrent events and terminal events is fitted.

**Usage**

```r
terminal(x)
```

**Arguments**

- `x` A numeric variable but should be a Boolean which equals 1 if the subject is dead and 0 if he is alive or censored, as a death indicator.

**Value**

- `x` A death indicator

**See Also**

- `frailtyPenal`

---

## timedep

**Identify time-varying effects**

**Description**

This is a special function used in the context of Cox models and shared and joint frailty models. It identifies time-varying effects of covariates in the model. It is used in ‘frailtyPenal’ on the right hand side of formula or of formula.terminalEvent.

When considering time-varying effects in a survival model, regression coefficients can be modeled with a linear combination of B-splines $B(t)$ with coefficients $\zeta$ of order $q$ with $m$ interior knots:

$$
\beta(t) = \sum_{j=-q+1}^{m} \zeta_j B_{j,q}(t)
$$
You can notice that a linear combination of B-splines of order 1 without any interior knots (0 interior knot) is the same as a model without time-varying effect (or with constant effect over time).

Statistical tests (likelihood ratio tests) can be done in order to know whether the time-dependent coefficients are significantly different from zero or to test whether a covariate has a time-dependent effect significantly different from zero or not. These tests are correct only with a parametric approach yet.

- Proportional Hazard assumption ?

Time-dependency of a covariate effect can be tested. We need to estimate $m + q$ parameters $\zeta_j$ for $j = -q + 1, \ldots, m$ for a time-varying coefficient. Only one ($q = 1, m = 0$) parameter is estimated for a constant effect. A global test is done.

$$H_0 : \beta(t) = \beta$$

The corresponding LR statistic has a $\chi^2$ distribution of degree $m + q - 1$.

- Significant association ?

We can also use a LR test to test whether a covariate has a significant effect on the hazard function. The null hypothesis is:

$$H_0 : \beta(t) = 0$$

For that we fit a model considering the covariate with a regression coefficient modeled using B-splines and a model without the covariate. Hence, the LR statistic has a $\chi^2$ distribution of degree $m + q$.

Usage
timedep(x)

Arguments

x A numerical or a factor variable that would have a time-varying effect on the event

Value

x A variable identified with a time-varying effect

References

Examples

```r
## Not run:
data(readmission)

##### Shared Frailty model with time-varying effect --####
sha.time <- frailtyPenal(Surv(time,event)-cluster(id)+dukes+charlson+
timedep(sex)+chemo,data=readmission,n=knots=8,kappa=1,
betaknots=3,betaorder=3)

## print results of the fit and the associated curves for the
## time-dependent effects
print(sha.time)

##### Joint Frailty model with time-varying effect --####
joj.time <- frailtyPenal(Surv(time,event)-cluster(id)+timedep(sex)+
chemo+terminal(death),formula.terminalEvent=timedep(sex)+chemo,
data=readmission,n=knots=8,kappa=c(1,1),betaknots=3,betaorder=3)

print(joj.time)

## End(Not run)
```

---

**trivPenal**

*Fit a Trivariate Joint Model for Longitudinal Data, Recurrent Events and a Terminal Event*

---

**Description**

Fit a trivariate joint model for longitudinal data, recurrent events and a terminal event using a semi-parametric penalized likelihood estimation or a parametric estimation on the hazard functions.

The longitudinal outcomes $y_{i}(t_{ik}) (k=1,...,n_i, i=1,...,N)$ for $N$ subjects are described by a linear mixed model and the risks of the recurrent and terminal events are represented by proportional hazard risk models. The joint model is constructed assuming that the processes are linked via a latent structure (Krol et al. 2015):

\[
\begin{align*}
\begin{cases}
    y_{i}(t_{ik}) = X_{Li}(t_{ik})^\top \beta_L + Z_{i}(t_{ik})^\top b_i + \epsilon_{i}(t_{ik}) & \text{(Longitudinal)} \\
    r_{ij}(t|b_i) = r_0(t) \exp(v_i + X_{Rij}(t) \beta_R + g(b_i, \beta_L, Z_{i}(t), X_{Li}(t))^\top \eta_R) & \text{(Recurrent)} \\
    \lambda_i(t|b_i) = \lambda_0(t) \exp(\alpha v_i + X_{Ti}(t) \beta_T + h(b_i, \beta_L, Z_{i}(t), X_{Li}(t))^\top \eta_T) & \text{(Terminal)}
\end{cases}
\end{align*}
\]

where $X_{Li}(t)$, $X_{Rij}(t)$ and $X_{Ti}(t)$ are vectors of fixed effects covariates and $\beta_L$, $\beta_R$ and $\beta_T$ are the associated coefficients. Measurements errors $\epsilon_{i}(t_{ik})$ are iid normally distributed with mean 0.
and variance $\sigma^2$. The random effects $b_i = (b_{i1}, \ldots, b_{iq_i})^T \sim \mathcal{N}(0, B_1)$ are associated to covariates $Z_i(t)$ and independent from the measurement error. The relationship between the biomarker and recurrent events is explained via $g(b_{i}, \beta_L, Z_i(t), X_{L_i}(t))$ with coefficients $\eta_R$ and between the biomarker and terminal event is explained via $h(b_{i}, \beta_L, Z_i(t), X_{L_i}(t))$ with coefficients $\eta_T$. Two forms of the functions $g(\cdot)$ and $h(\cdot)$ are available: the random effects $b_i$ and the current biomarker level $m_i(t) = X_{L_i}(t_{ik})^T \beta_L + Z_i(t_{ik})^T b_i$. The frailty term $v_i$ is gaussian with mean 0 and variance $\sigma_v$. Together with $b_i$ constitutes the random effects of the model:

$$u_i = \begin{pmatrix} b_i \\ v_i \end{pmatrix} \sim \mathcal{N} \left( 0, \begin{pmatrix} B_1 & 0 \\ 0 & \sigma_v^2 \end{pmatrix} \right).$$

We consider that the longitudinal outcome can be subject to a quantification limit, i.e. some observations below a level of detection $s$ cannot be quantified (left-censoring).

Usage

```r
trivPenal(formula, formula.terminalEvent, formula.LongitudinalData, data, 
data.Longi, random, id, intercept = TRUE, link = "Random-effects", 
left.censoring = FALSE, recurrentAG = FALSE, n.knots, kappa, maxit = 300, 
print.times = TRUE)
```

Arguments

- `formula` a formula object, with the response on the left of a $\sim$ operator, and the terms on the right. The response must be a survival object as returned by the 'Surv' function like in survival package. Interactions are possible using * or :

- `formula.terminalEvent` A formula object, only requires terms on the right to indicate which variables are modelling the terminal event. Interactions are possible using * or :

- `formula.LongitudinalData` A formula object, only requires terms on the right to indicate which variables are modelling the longitudinal outcome. It must follow the standard form used for linear mixed-effects models. Interactions are possible using * or :

- `data` A 'data.frame' with the variables used in `formula`.

- `data.Longi` A 'data.frame' with the variables used in `formula.LongitudinalData`.

- `random` Names of variables for the random effects of the longitudinal outcome. Maximum 3 random effects are possible at the moment. The random intercept is chosen using "1".

- `id` Name of the variable representing the individuals.

- `intercept` Logical value. Is the fixed intercept of the biomarker included in the mixed-effects model? The default is TRUE.

- `link` Type of link functions for the dependence between the biomarker and death and between the biomarker and the recurrent events: "Random-effects" for the association directly via the random effects of the biomarker, "Current-level" for the association via the true current level of the biomarker. The option "Current-level"
can be chosen only if the biomarker random effects are associated with the intercept and time (following this order). The default is "Random-effects".

**left.censoring** Is the biomarker left-censored below a threshold $s$? If there is no left-censoring, the argument must be equal to FALSE, otherwise the value of the threshold must be given.

**recurrentAG** Logical value. Is Andersen-Gill model fitted? If so indicates that recurrent event times with the counting process approach of Andersen and Gill is used. This formulation can be used for dealing with time-dependent covariates. The default is FALSE.

**n.knots** Integer giving the number of knots to use. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. We estimate I or M-splines of order 4. When the user set a number of knots equals to $k$ (n.knots=$k$) then the number of interior knots is $(k-2)$ and the number of splines is $(k-2)$+order. Number of knots must be between 4 and 20. (See Note in frailtyPenal function)

**kappa** Positive smoothing parameters in the penalized likelihood estimation. The coefficient kappa of the integral of the squared second derivative of hazard function in the fit (penalized log likelihood). To obtain an initial value for kappa, a solution is to fit the corresponding Cox model using cross validation (See cross.validation in function frailtyPenal). We advise the user to identify several possible tuning parameters, note their defaults and look at the sensitivity of the results to varying them.

**maxit** Maximum number of iterations for the Marquardt algorithm. Default is 300

**hazard** Type of hazard functions: "Splines" for semiparametric hazard functions using equidistant intervals or "Splines-per" using percentile with the penalized likelihood estimation, "Weibull" for the parametric Weibull functions. The default is "Splines".

**init.B** Vector of initial values for regression coefficients. This vector should be of the same size as the whole vector of covariates with the first elements for the covariates related to the recurrent events, then to the terminal event and then to the biomarker (interactions in the end of each component). Default is 0.5 for each.

**init.Random** Initial value for variance of the elements of the matrix of the distribution of the random effects.

**init.Eta** Initial values for regression coefficients for the link functions, first for the recurrent events ($\eta_R$) and for the terminal event ($\eta_T$).

**init.Alpha** Initial value for parameter alpha

**method.GH** Method for the Gauss-Hermite quadrature: "Standard" for the standard non-adaptive Gaussian quadrature, "Pseudo-adaptive" for the pseudo-adaptive Gaussian quadrature and "HRMSYM" for the algorithm for the multivariate non-adaptive Gaussian quadrature (see Details). The default is "Standard".

**n.nodes** Number of nodes for the Gauss-Hermite quadrature. They can be chosen among 5, 7, 9, 12, 15, 20 and 32. The default is 9.

**LIMparam** Convergence threshold of the Marquardt algorithm for the parameters (see Details), $10^{-3}$ by default.
LIMlogl  Convergence threshold of the Marquardt algorithm for the log-likelihood (see Details), $10^{-3}$ by default.

LIMderiv  Convergence threshold of the Marquardt algorithm for the gradient (see Details), $10^{-3}$ by default.

print.times  a logical parameter to print iteration process. Default is TRUE.

Details

Typical usage for the joint model

```
trivPenal(Surv(time, event)~cluster(id) + var1 + var2 +
terminal(death), formula.terminalEvent =~ var1 + var3, biomarker ~
var1+var2, data, data.Longi, ...)
```

The method of the Gauss-Hermite quadrature for approximations of the multidimensional integrals, i.e. length of random is 2, can be chosen among the standard, non-adaptive, pseudo-adaptive in which the quadrature points are transformed using the information from the fitted mixed-effects model for the biomarker (Rizopoulos 2012) or multivariate non-adaptive procedure proposed by Genz et al. 1996 and implemented in FORTRAN subroutine HRMSYM. The choice of the method is important for estimations. The standard non-adaptive Gauss-Hermite quadrature ("Standard") with a specific number of points gives accurate results but can be time consuming. The non-adaptive procedure ("HRMSYM") offers advantageous computational time but in case of datasets in which some individuals have few repeated observations (biomarker measures or recurrent events), this method may be moderately unstable. The pseudo-adaptive quadrature uses transformed quadrature points to center and scale the integrand by utilizing estimates of the random effects from an appropriate linear mixed-effects model (this transformation does not include the frailty in the trivariate model, for which the standard method is used). This method enables using less quadrature points while preserving the estimation accuracy and thus lead to a better computational time.

NOTE. Data frames data and data.Longi must be consistent. Names and types of corresponding covariates must be the same, as well as the number and identification of individuals.

Value

The following components are included in a 'trivPenal' object for each model:

b  The sequence of the corresponding estimation of the coefficients for the hazard functions (parametric or semiparametric), the random effects variances and the regression coefficients.

call  The code used for the model.

formula  The formula part of the code used for the recurrent event part of the model.

formula.terminalEvent  The formula part of the code used for the terminal event part of the model.

formula.LongitudinalData  The formula part of the code used for the longitudinal part of the model.

coef  The regression coefficients (first for the recurrent events, then for the terminal event and then for the biomarker.

groups  The number of groups used in the fit.
The values of the smoothing parameters in the penalized likelihood estimation corresponding to the baseline hazard functions for the recurrent and terminal events.

The complete marginal penalized log-likelihood in the semiparametric case.

The marginal log-likelihood in the parametric case.

The number of biomarker observations used in the fit.

The maximal number of repeated measurements per individual.

The number of observations in 'data' (recurrent and terminal events) used in the fit.

The number of recurrent events observed in the fit.

The number of terminal events observed in the fit.

The number of iterations needed to converge.

The number of knots for estimating the baseline hazard function in the penalized likelihood estimation.

The number of stratum.

The variance matrix of all parameters (before positivity constraint transformation for the variance of the measurement error, for which the delta method is used).

The robust estimation of the variance matrix of all parameters.

The vector of times where both survival and hazard function of the recurrent events are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times.

The array (dim=3) of baseline hazard estimates and confidence bands (recurrent events).

The array (dim=3) of baseline survival estimates and confidence bands (recurrent events).

The vector of times where both survival and hazard function of the terminal event are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times.

The array (dim=3) of baseline hazard estimates and confidence bands.

The array (dim=3) of baseline survival estimates and confidence bands.

The type of the baseline hazard function (0:"Splines", "2:Weibull").

The number of parameters.

The vector of number of explanatory variables for the recurrent events, terminal event and biomarker.

The number of explanatory variables for the recurrent events.

The number of explanatory variables for the terminal event.

The number of explanatory variables for the biomarker.

The indicator of absence of the explanatory variables for the recurrent events.

The indicator of absence of the explanatory variables for the terminal event.
noVarY  The indicator of absence of the explanatory variables for the biomarker.

LCV  The approximated likelihood cross-validation criterion in the semiparametric case (with H minus the converged Hessian matrix, and l(.) the full log-likelihood).

\[ LCV = \frac{1}{n} \left( \text{trace}(H^{-1}) - l(.) \right) \]

AIC  The Akaike information Criterion for the parametric case.

\[ AIC = \frac{1}{n} (np - l(.)) \]

n.knots.temp  The initial value for the number of knots.

shape.weib  The shape parameter for the Weibull hazard functions (the first element for the recurrences and the second one for the terminal event).

scale.weib  The scale parameter for the Weibull hazard functions (the first element for the recurrences and the second one for the terminal event).

martingale.res  The martingale residuals related to the recurrences for each individual.

martingaled.eath.res  The martingale residuals related to the terminal event for each individual.

conditional.res  The conditional residuals for the biomarker (subject-specific):

\[ R_i^{(m)} = y_i - X_i^L \hat{\beta}_L - Z_i^L \hat{b}_i. \]

marginal.res  The marginal residuals for the biomarker (population averaged):

\[ R_i^{(c)} = y_i - X_i^L \hat{\beta}_L. \]

marginal_chol.res  The Cholesky marginal residuals for the biomarker:

\[ R_i^{(m)} = \hat{U}_i^{(m)} R_i^{(m)}, \]  
where $\hat{U}_i^{(m)}$ is an upper-triangular matrix obtained by the Cholesky decomposition of the variance matrix $V_R^{(m)} = \hat{V}_i - X_i^L(\sum_{i=1}^{N} X_i^L \hat{V}_i^{-1} X_i^L)^{-1} X_i^L$.

conditional_st.res  The standardized conditional residuals for the biomarker.

marginal_st.res  The standardized marginal residuals for the biomarker.

random.effects.pred  The empirical Bayes predictions of the random effects (ie. using conditional posterior distributions).

frailty.pred  The empirical Bayes predictions of the frailty term (ie. using conditional posterior distributions).

pred.y.marg  The marginal predictions of the longitudinal outcome.

pred.y.cond  The conditional (given the random effects) predictions of the longitudinal outcome.

linear.pred  The linear predictor for the recurrent events part.

lineardeath.pred  The linear predictor for the terminal event part.
- `global_chisqR`: The vector with values of each multivariate Wald test for the recurrent part.
- `dof_chisqR`: The vector with degrees of freedom for each multivariate Wald test for the recurrent part.
- `global_chisq.testR`: The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the recurrent part).
- `p.global_chisqR`: The vector with the p_values for each global multivariate Wald test for the recurrent part.
- `global_chisqT`: The vector with values of each multivariate Wald test for the terminal part.
- `dof_chisqT`: The vector with degrees of freedom for each multivariate Wald test for the terminal part.
- `global_chisq.testT`: The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the terminal part).
- `p.global_chisqT`: The vector with the p_values for each global multivariate Wald test for the terminal part.
- `global_chisqY`: The vector with values of each multivariate Wald test for the longitudinal part.
- `dof_chisqY`: The vector with degrees of freedom for each multivariate Wald test for the longitudinal part.
- `global_chisq.testY`: The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the longitudinal part).
- `p.global_chisqY`: The vector with the p_values for each global multivariate Wald test for the longitudinal part.
- `names.factorR`: The names of the "as.factor" variables for the recurrent part.
- `names.factorT`: The names of the "as.factor" variables for the terminal part.
- `names.factorY`: The names of the "as.factor" variables for the longitudinal part.
- `AG`: The logical value. Is Andersen-Gill model fitted?
- `intercept`: The logical value. Is the fixed intercept included in the linear mixed-effects model?
- `B1`: The variance matrix of the random effects for the longitudinal outcome.
- `sigma2`: The variance of the frailty term ($\sigma_v$).
- `alpha`: The coefficient $\alpha$ associated with the frailty parameter in the terminal hazard function.
- `ResidualSE`: The variance of the measurement error.
- `etaR`: The regression coefficients for the link function $g(\cdot)$.
- `etaT`: The regression coefficients for the link function $h(\cdot)$.
- `ne_re`: The number of random effects $b$ used in the fit.
- `names.re`: The names of variables for the random effects $b_i$. 
trivPenal

- **link**: The name of the type of the link functions.
- **leftCensoring**: The logical value. Is the longitudinal outcome left-censored?
- **leftCensoring.threshold**: For the left-censored biomarker, the value of the left-censoring threshold used for the fit.
- **prop.censored**: The fraction of observations subjected to the left-censoring.
- **methodGH**: The Gaussian quadrature method used in the fit.
- **n.nodes**: The number of nodes used for the Gaussian quadrature in the fit.
- **alpha_p.value**: p-value of the Wald test for the estimated coefficient $\alpha$.
- **sigma2_p.value**: p-value of the Wald test for the estimated variance of the frailty term ($\sigma_v$).
- **etaR_p.value**: p-values of the Wald test for the estimated regression coefficients for the link function $g(\cdot)$.
- **etaT_p.value**: p-values of the Wald test for the estimated regression coefficients for the link function $h(\cdot)$.
- **beta_p.value**: p-values of the Wald test for the estimated regression coefficients.

**Note**

It is recommended to initialize the parameter values using the results from the reduced models (for example, longiPenal for the longitudinal and terminal part and frailtyPenal for the recurrent part. See example.

**References**


**See Also**

`plot.trivPenal`, `print.trivPenal`, `summary.trivPenal`
Examples

## Not run:

```r
### Trivariate joint model for longitudinal data, ---###
### recurrent events and a terminal event ---###

data(colorectal)
data(colorectallongi)

# Parameter initialisation for covariates - longitudinal and terminal part

# Survival data preparation - only terminal events
colorectalsurv <- subset(colorectal, new.lesions == 0)
initial.longi <- longiPenal(Surv(time1, state) ~ age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, colorectalsurv, data.Longi = colorectallongi, random = c("1", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, n.knots = 6, kappa = 2, method.GH="Pseudo-adaptive", maxit=40, n.nodes=7)

# Parameter initialisation for covariates - recurrent part
initial.frailty <- frailtyPenal(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + who.PS, data = colorectal, recurrentAG = TRUE, RandDist = "LogN", n.knots = 6, kappa =2)

# Baseline hazard function approximated with splines
# Random effects as the link function, Calendar timescale
# (computation takes around 40 minutes)
model.spli.RE.cal <- trivPenal(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + who.PS + terminal(state), formula.terminalEvent <- age + treatment + who.PS + prev.resection, tumor.size ~ year * treatment + age + who.PS, data = colorectal, data.Longi = colorectallongi, random = c("1", "year"), id = "id", link = "Random-effects", left.censoring = -3.33, recurrentAG = TRUE, n.knots = 6, kappa=c(0.01, 2), method.GH="Standard", n.nodes = 7, init.B = c(-0.07, -0.13, -0.16, -0.17, 0.42, recurrent events covariates -0.16, -0.14, -0.14, 0.08, 0.86, -0.24, terminal event covariates 2.93, -0.28, -0.13, 0.17, -0.41, 0.23, 0.97, -0.61)) #biomarker covariates

# Weibull baseline hazard function
# Random effects as the link function, Gap timescale
# (computation takes around 30 minutes)
model.weib.RE.gap <- trivPenal(Surv(gap.time, new.lesions) ~ cluster(id) + age + treatment + who.PS + prev.resection + terminal(state),
```

```
Fit a Non-Linear Trivariate Joint Model for Recurrent Events and a Terminal Event with a Biomarker Described with an ODE Population Model

Description

Fit a non-linear trivariate joint model for a longitudinal biomarker, recurrent events and a terminal event using a semiparametric penalized likelihood estimation or a parametric estimation on the hazard functions.

The values \( y_i(t) \) for \( i = 1, \ldots, N \) for \( N \) subjects represent the individual evolution of the biomarker e.g. tumor size expressed as the sum of the longest diameters (SLD) of target lesions. The dynamics of the biomarker are described by an ordinary differential equation (ODE) that includes the effect of the natural net growth and the treatment effect:

\[
\begin{align*}
\frac{dy_i(t)}{dt} &= \exp(K_{G,0} + b_{G,i} + X_{G,i}(t)^T \beta_G)y_i(t) \\
&\quad - d_i \exp(K_{D,0} + b_{D,i} - t \times \exp(\lambda + b_{\lambda,i}) + X_{D,i}(t)^T \beta_D), \\
y_i(0) &= \exp(y_0 + b_{y_0,i})
\end{align*}
\]

The model includes the following parameters (using the interpretation of tumor dynamics): \( \exp(K_{G,0}) \) the constant tumor growth rate, \( \exp(K_{D,0}) \) the drug-induced tumor decline rate, \( \lambda \) resistance effect to drug (exponential tumor decay change with time), \( \exp(y_0) \) the initial level of the biomarker and \( d_i \) is the treatment concentration (e.g. dose). The random effects \( b_i^T = (b_{y_0,i}, b_{G,i}, b_{D,i}, b_{\lambda,i})^T \) are gaussian variables with a diagonal covariance matrix \( B_1 \). In the trivariate model we use the analytical solution of the equation with the population-based approach of the non-linear mixed effects model. We can also assume a transformation for the observations of the biomarker (one parameter Box-Cox transformation) and we include a gaussian measurement error, for individual \( i \) and observation \( k (k = 1, \ldots, n_i) \), \( \epsilon_{ik} \sim N(0, \sigma^2) \).

The risks of the recurrent \( r_{ij}(\cdot) \) the risk of the \( j \)-th event of the individual \( i \) and terminal events \( \lambda_i \) the risk of the event of the individual \( i \) are represented by proportional hazard risk models. The joint model is constructed assuming that the processes are linked via a latent structure and includes the non-linear mixed effects model for the longitudinal data:
\[
\begin{align*}
  y(t_{ik}) &= \exp[y_0 + b_{y,i} + t_{ik} \times \exp(KG + bG_i + XG_i(t)^\top \betaG)] \\
  &+ d_i \times \exp(KD + bD_i - \lambda - b\lambda_i + XD_i(t)^\top \betaD) \\
  &\times (\exp((\lambda + b\lambda_i)t_{ik}) - 1) + \epsilon_k \\
  r_{ij}(t|b_i) &= r_0(t) \exp(v_i + XR_{ij}(t)^\top \betaR + g(y_i(t))^\top \etaR) \\
  \lambda_i(t|b_i) &= \lambda_0(t) \exp(\alpha v_i + XT_i(t)^\top \betaT + h(y_i(t))^\top \etaT)
\end{align*}
\]

where \(XG_i(t), XD_i(t), XR_{ij}(t)\) and \(XT_i(t)\) are vectors of possible time-varying fixed effects covariates and \(\betaG, \betaD, \betaR\) and \(\betaT\) are the associated coefficients. The random effects \(b_i\) are independent from the measurement error. The relationship between the biomarker and recurrent events is explained via \(g(y_i(t))\) with coefficients \(\etaR\) and between the biomarker and terminal event is explained via \(h(y_i(t))\) with coefficients \(\etaT\). Currently, only one form of the functions \(g(\cdot)\) and \(h(\cdot)\) is available: the random effects \(b_i\). The frailty term \(v_i\) is gaussian with mean 0 and variance \(\sigma_v\). Together with \(b_i\) constitutes the random effects of the model:

\[
u_i = \begin{pmatrix} b_i \\ v_i \end{pmatrix} \sim \mathcal{N}\left(0, \begin{pmatrix} B_1 & 0 \\ 0 & \sigma_v^2 \end{pmatrix} \right)
\]

Any combination of the random effects \(b_i\), e.g. \(b_i = b_{y,i}\) or \(b_i = \{b_{G,i}, b_{D,i}, b\lambda_i\}\) can be chosen for the model.

We consider that the longitudinal outcome can be a subject to a quantification limit, i.e. some observations, below a level of detection \(s\) cannot be quantified (left-censoring).

**Usage**

\[
\]

**Arguments**

- **formula**
  a formula object, with the response on the left of a \(\sim\) operator, and the terms on the right. The response must be a survival object as returned by the 'Surv' function like in survival package. Interactions are possible using * or :.

- **formula.terminalEvent**
  A formula object, only requires terms on the right to indicate which variables are modelling the terminal event. Interactions are possible using * or :

- **biomarker**
  Name of the variable representing the longitudinal biomarker.

- **formula.KG**
  A formula object, only requires terms on the right to indicate which covariates related to the biomarker growth are included in the longitudinal sub-model. It must follow the standard form used for linear mixed-effects models. Interactions are possible using * or :.
A formula object, only requires terms on the right to indicate which covariates related to the biomarker drug-induced decline are included in the longitudinal sub-model. It must follow the standard form used for linear mixed-effects models. Interactions are possible using * or :.

dose
Name of the variable representing the drug concentration indicator.

time.biomarker
Name of the variable of times of biomarker measurements.

data
A 'data.frame' with the variables used in formula.

data.Longi
A 'data.frame' with the variables used in formula.KG, formula.KD, biomarker, dose, time.biomarker and id.

random
Names of parameters for which the random effects are included in the mixed model. The names must be chosen among "y0", "KG", "KD" and "lambda". Any combination of the mentioned names is allowed.

id
Name of the variable representing the individuals.

link
Type of link functions for the dependence between the biomarker and death and between the biomarker and the recurrent events: only "Random-effects" for the association directly via the random effects of the biomarker is allowed for the moment (option for a future extension).

BoxCox
Should the Box-Cox transformation be used for the longitudinal biomarker? If there is no transformation, the argument must be equal to FALSE, otherwise the Box-Cox parameter must be given, then the transformed values are $y^* = (y^\xi - 1)/\xi$, where $\xi$ is the Box-Cox parameter.

left censoring
Is the biomarker left-censored below a threshold $s$? If there is no left-censoring, the argument must be equal to FALSE, otherwise the value of the threshold must be given.

recurrentAG
Logical value. Is Andersen-Gill model fitted? If so indicates that recurrent event times with the counting process approach of Andersen and Gill is used. This formulation can be used for dealing with time-dependent covariates. The default is FALSE.

n.knots
Integer giving the number of knots to use. Value required in the penalized likelihood estimation. It corresponds to the (n.knots+2) splines functions for the approximation of the hazard or the survival functions. We estimate I or M-splines of order 4. When the user set a number of knots equals to k (n.knots=k) then the number of interior knots is (k-2) and the number of splines is (k-2)+order. Number of knots must be between 4 and 20. (See Note in frailtyPenal function)

kappa
Positive smoothing parameters in the penalized likelihood estimation. The coefficient kappa of the integral of the squared second derivative of hazard function in the fit (penalized log likelihood). To obtain an initial value for kappa, a solution is to fit the corresponding Cox model using cross validation (See cross.validation in function frailtyPenal). We advise the user to identify several possible tuning parameters, note their defaults and look at the sensitivity of the results to varying them.

maxit
Maximum number of iterations for the Marquardt algorithm. Default is 300

hazard
Type of hazard functions: "Splines" for semiparametric hazard functions using equidistant intervals or "Splines-per" using percentile with the penalized likelihood estimation, "Weibull" for the parametric Weibull functions. The default is "Splines".
init.B Vector of initial values for regression coefficients. This vector should be of the same size as the whole vector of covariates with the first elements for the covariates related to the recurrent events, then to the terminal event and then to the biomarker (interactions in the end of each component). Default is 0.5 for each.

init.Random Initial value for variance of the elements of the matrix of the distribution of the random effects.

init.Eta Initial values for regression coefficients for the link functions, first for the recurrent events ($\eta_R$) and for the terminal event ($\eta_T$).

init.Alpha Initial value for parameter alpha.

init.Biomarker Initial values for biomarker parameters: $y_0, K_{G,0}, K_{D,0}$ and $\lambda$ (using this order).

method.GH Method for the Gauss-Hermite quadrature: "Standard" for the standard non-adaptive Gaussian quadrature and "Pseudo-adaptive" for the pseudo-adaptive Gaussian quadrature (see Details). The default is "Standard". When the option "Pseudo-adaptive" is chosen, then a univariate model (non-linear mixed model for the biomarker) is fitted in order to obtain the estimations of the random effects $b_i$.

init.GH Only when the option "Pseudo-adaptive" of the argument method.GH is chosen. If TRUE, the estimations of the biomarker parameters ($y_0, K_{G,0}, K_{D,0}$ and $\lambda$), $\sigma_\epsilon$, $\beta_G$ and $\beta_D$ from the univariate mixed model are used as the initial values of the parameters related to the biomarker.

n.nodes Number of nodes for the Gauss-Hermite quadrature (from 5 to 32). The default is 9.

lim.param Convergence threshold of the Marquardt algorithm for the parameters (see Details), $10^{-3}$ by default.

lim.logl Convergence threshold of the Marquardt algorithm for the log-likelihood (see Details), $10^{-3}$ by default.

lim.deriv Convergence threshold of the Marquardt algorithm for the gradient (see Details), $10^{-3}$ by default.

print.times a logical parameter to print iteration process. Default is TRUE.

Details

Typical usage for the joint model

```r
trivPenalNL(Surv(time, event) ~ cluster(id) + var1 + var2 +
  terminal(death), formula.terminalEvent =~ var1 + var3, biomarker =
  "biomarker.name", dose = "dose.name", time.biomarker = "time", formula.KG ~
  var1, formula.KD ~ var2, data, data.Longi, ...)
```

The method of the Gauss-Hermite quadrature for approximations of the multidimensional integrals, i.e. \texttt{length}\ of \texttt{random} more than 2, can be chosen among the standard (non-adaptive) and pseudo-adaptive in which the quadrature points are transformed using the information from the fitted mixed-effects model for the biomarker (Rizopoulos 2012) or multivariate non-adaptive procedure proposed by Genz et al. 1996 and implemented in FORTRAN subroutine HRMSYM. The
choice of the method is important for estimations. The standard non-adaptive Gauss-Hermite
quadrature ("Standard") with a specific number of points gives accurate results but can be time
consuming. The pseudo-adaptive quadrature uses transformed quadrature points to center and scale
the integrand by utilizing estimates of the random effects from an appropriate non-linear mixed-
effects model (this transformation does not include the frailty in the trivariate model, for which the
standard method, with 20 quadrature points, is used). This method enables using less quadrature
points while preserving the estimation accuracy and thus lead to a better computational time.

NOTE. Data frames data and data.Longi must be consistent. Names and types of corresponding
covariates must be the same, as well as the number and identification of individuals.

**Value**

The following components are included in a 'trivPenalNL' object for each model:

- **b**
  The sequence of the corresponding estimation of the coefficients for the hazard
  functions (parametric or semiparametric), the random effects variances and the
  regression coefficients.

- **call**
  The code used for the model.

- **formula**
  The formula part of the code used for the recurrent event part of the model.

- **formula.terminalEvent**
  The formula part of the code used for the terminal event part of the model.

- **formula.KG**
  The formula part of the code used for the longitudinal part of the model, for the
  biomarker growth dynamics.

- **formula.KD**
  The formula part of the code used for the longitudinal part of the model, for the
  biomarker decline dynamics.

- **coef**
  The regression coefficients (first for the recurrent events, then for the terminal
  event, then for the biomarker growth and then for the biomarker decline.

- **groups**
  The number of groups used in the fit.

- **kappa**
  The values of the smoothing parameters in the penalized likelihood estimation
  corresponding to the baseline hazard functions for the recurrent and terminal
  events.

- **logLikPenal**
  The complete marginal penalized log-likelihood in the semiparametric case.

- **logLik**
  The marginal log-likelihood in the parametric case.

- **n.measurements**
  The number of biomarker observations used in the fit.

- **max_rep**
  The maximal number of repeated measurements per individual.

- **n**
  The number of observations in 'data' (recurrent and terminal events) used in the
  fit.

- **n.events**
  The number of recurrent events observed in the fit.

- **n.deaths**
  The number of terminal events observed in the fit.

- **n.iter**
  The number of iterations needed to converge.

- **n.knots**
  The number of knots for estimating the baseline hazard function in the penalized
  likelihood estimation.

- **n.strat**
  The number of stratum.
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varH
The variance matrix of all parameters (before positivity constraint transformation for the variance of the measurement error, for which the delta method is used).

varHIH
The robust estimation of the variance matrix of all parameters.

xR
The vector of times where both survival and hazard function of the recurrent events are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times.

lamR
The array (dim=3) of baseline hazard estimates and confidence bands (recurrent events).

survR
The array (dim=3) of baseline survival estimates and confidence bands (recurrent events).

xD
The vector of times where both survival and hazard function of the terminal event are estimated. By default seq(0,max(time),length=99), where time is the vector of survival times.

lamD
The array (dim=3) of baseline hazard estimates and confidence bands.

survD
The array (dim=3) of baseline survival estimates and confidence bands.

typeof
The type of the baseline hazard function (0:“Splines”, ”2:Weibull”).
npar
The number of parameters.
nvar
The vector of number of explanatory variables for the recurrent events, terminal event, biomarker growth and biomarker decline.
nvarRec
The number of explanatory variables for the recurrent events.
nvarEnd
The number of explanatory variables for the terminal event.
nvarKG
The number of explanatory variables for the biomarker growth.
nvarKD
The number of explanatory variables for the biomarker decline.
novarRec
The indicator of absence of the explanatory variables for the recurrent events.
novarEnd
The indicator of absence of the explanatory variables for the terminal event.
novarKG
The indicator of absence of the explanatory variables for the biomarker growth.
novarKD
The indicator of absence of the explanatory variables for the biomarker decline.
LCV
The approximated likelihood cross-validation criterion in the semiparametric case (with H minus the converged Hessian matrix, and l(.) the full log-likelihood).

\[ LCV = \frac{1}{n} \left( \text{trace}(H^{-1} H) - l(.) \right) \]

AIC
The Akaike information Criterion for the parametric case.

\[ AIC = \frac{1}{n} \left( np - l(.) \right) \]

n.knots.temp
The initial value for the number of knots.

shape.weib
The shape parameter for the Weibull hazard functions (the first element for the recurrences and the second one for the terminal event).

scale.weib
The scale parameter for the Weibull hazard functions (the first element for the recurrences and the second one for the terminal event).
random.effects.pred
The empirical Bayes predictions of the random effects (i.e., using conditional posterior distributions).

global_chisq.testR
The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the recurrent part).

global_chisq.testT
The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the terminal part).

global_chisq.testKG
The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the biomarker growth).

global_chisq.testKD
The binary variable equals to 0 when no multivariate Wald is given, 1 otherwise (for the biomarker decline).

ag
The logical value. Is Andersen-Gill model fitted?

b1
The variance matrix of the random effects for the longitudinal outcome.

sigmaR
The variance of the frailty term ($\sigma_v$).

alpha
The coefficient $\alpha$ associated with the frailty parameter in the terminal hazard function.

ResidualSE
The variance of the measurement error.

 etaR
The regression coefficients for the link function $g(\cdot)$.

detaT
The regression coefficients for the link function $h(\cdot)$.

ne_re
The number of random effects $b$ used in the fit.

names.re
The names of variables for the random effects $b_i$.

link
The name of the type of the link functions.

leftCensoring
The logical value. Is the longitudinal outcome left-censored?

leftCensoring.threshold
For the left-censored biomarker, the value of the left-censoring threshold used for the fit.

prop.censored
The fraction of observations subjected to the left-censoring.

methodGH
The Gaussian quadrature method used in the fit.

n.nodes
The number of nodes used for the Gaussian quadrature in the fit.

K_G0
Value of the estimate of the biomarker growth parameter.

K_D0
Value of the estimate of the biomarker decay parameter.

lambda
Value of the estimate of the biomarker resistance to drug.

y_0
Value of the estimate of the biomarker initial level.

biomarker
Name of the variable associated with the biomarker in the data.

time.biomarker
Name of the variable associated with the time of measurements of the biomarker in the data.

dose
Name of the variable associated with the drug concentration in the data.
BoxCox  The logical value. Is the BoxCox transformation applied for the biomarker?

BoxCox_parameter  The value of the BoxCox transformation parameter.

alpha_p.value  p-value of the Wald test for the estimated coefficient $\alpha$.

sigma2_p.value  p-value of the Wald test for the estimated variance of the frailty term ($\sigma_v$).

etaR_p.value  p-values of the Wald test for the estimated regression coefficients for the link function $g(\cdot)$.

etaT_p.value  p-values of the Wald test for the estimated regression coefficients for the link function $h(\cdot)$.

y_0_p.value  p-value of the Wald test for the estimated biomarker initial level.

K_G0_p.value  p-value of the Wald test for the estimated biomarker growth parameter.

K_D0_p.value  p-value of the Wald test for the estimated biomarker decay parameter.

lambda_p.value  p-value of the Wald test for the estimated biomarker resistance to drug.

beta_p.value  p-values of the Wald test for the estimated regression coefficients.

Note

It is recommended to initialize the parameter values using the results from a corresponding reduced model (frailtyPenal for the recurrent and terminal part). See example.

Estimations of models with more than three random effects can be very long.

References


See Also

plot.trivPenalNL, print.trivPenalNL, summary.trivPenalNL
### Examples

#### Not run:

```
### Non-linear trivariate joint model for longitudinal data, recrrenc events and a terminal event

data(colorectal)
data(colorectallongi)

# No information on dose - creation of a dummy variable
colorectallongi$dose <- 1

# Parameters initialisation - estimation of a simplified model
# with two random effects (a frailty term and a random effect
# related to biomarker growth (KG))
initial.model <- trivPenalNL(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + terminal(state), formula.terminalEvent =~ age + treatment, biomarker = "tumor.size", formula.KG = 1, formula.KD ~ treatment, dose = "dose", time.biomarker = "year", data = colorectal, data.Longi = colorectallongi, random = "KG", id = "id", recurrentAG = TRUE, n.knots = 5, kappa = c(0.01, 2), method.GH = "Pseudo-adaptive")

# Trivariate joint model with initial values for parameters
# (computation takes around 40 minutes)
model <- trivPenalNL(Surv(time0, time1, new.lesions) ~ cluster(id) + age + treatment + terminal(state), formula.terminalEvent =~ age + treatment, biomarker = "tumor.size", formula.KG = 1, formula.KD ~ treatment, dose = "dose", time.biomarker = "year", data = colorectal, data.Longi = colorectallongi, random = c("y0", "KG"), id = "id", init.B = c(-0.22, -0.16, -0.35, -0.19, 0.04, -0.41, 0.23), init.Alpha = 1.86, init.Eta = c(0.5, 0.57, 0.5, 2.34), init.Biomarker = c(1.24, 0.81, 1.07, -1.53), recurrentAG = TRUE, n.knots = 5, kappa = c(0.01, 2), method.GH = "Pseudo-adaptive")

```

#### End(Not run)

---

### wts

**Identify weights**

#### Description

This is a special function used in the context of the joint frailty models for data from nested case-control studies. It specifies weights defined by using `wts` function, and is used of `frailtyPenal` formula for fitting joint models.
Usage

wts(x)

Arguments

x  A numeric variable which is supposed to indicate the weights

Value

x  A variable identified as weights

See Also

frailtyPenal

Examples

## Not run:

data(dataNCC)
modJoint.ncc <- frailtyPenal(Surv(t.start,t.stop,event)~cluster(id)+cov1
+ cov2+terminal(death)+wts(ncc.wts), formula.terminalEvent=-cov1+cov2,
data=dataNCC,n.knots=8,kappa=c(1.6e+10, 5.0e+03),recurrantAG=TRUE, RandDist="LogN")

print(modJoint.ncc)

## End(Not run)
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