Package 'xhaz'

October 14, 2022

Title Excess Hazard Modelling Considering Inappropriate Mortality
Rates

Version 2.0.1

Description Fits relative survival regression models with or without proportional excess haz-
ards and with the additional possibility to correct for background mortality by one or more param-
eter(s). These models are relevant when the observed mortality in the studied group is not compa-
rable to that of the general population or in population-based studies where the available life ta-
bles used for net survival estimation are insufficiently stratified. In the latter case, the pro-
posed model by Touraine et al. (2020) <doi:10.1177/0962280218823234> can be used. The user can also fit a model that re-
lax the proportional expected hazards assumption considered in the Touraine et al. excess haz-
ard model. This extension was proposed by Mba et al. (2020) <doi:10.1186/s12874-020-01139-
z> to allow non-proportional effects of the additional variable on the general population mortal-
ity. In non-population-based studies, researchers can identify non-
comparability source of bias in terms of expected mortality of selected individuals. A pro-
posed excess hazard model correcting this selection bias is presented in Goun-
gounga et al. (2019) <doi:10.1186/s12874-019-0747-3>.

License AGPL (>= 3)

Depends R (>= 3.5.0), statmod, stats, survival

Imports gtools, numDeriv, optimParallel, splines, stringr, survexp.fr

Suggests knitr, rmarkdown, spelling, testthat (>= 2.1.0)

VignetteBuilder knitr

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Language en-US

NeedsCompilation no

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R **topics documented:**

AIC.bsplines   *Akaike's An Information Criterion for excess hazard model with base-line hazard following a B-splines functions*

Description

Calculates the Akaike's 'An Information Criterion' for fitted models from xhaz.

Usage

```
## S3 method for class 'bsplines'
AIC(object, ..., k = 2)
```

Arguments

object	a fitted model object obtained from xhaz function
...	optionally more fitted model objects obtained from xhaz function
k	numeric, the penalty per parameter to be used; the default k = 2 is the classical AIC.

Value

the value corresponds to the AIC calculated from the total log-likelihood of the fitted model if just one object is provided. If multiple objects are provided, a data.frame with columns corresponding to the objects and rows representing the number of parameters in the model (df) and the AIC

Examples

```
library("xhaz")

#Giorgi et al model: baseline excess hazard is a quadratic Bsplines
#                    function with two interior knots and allow here a
#                    linear and proportional effects for the covariates on
#                    baseline excess hazard.
levels(simuData$sex) <- c("male", "female")

fitphBS <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                data = simuData,
                ratetable = survexp.us,
                interval = c(0, NA, NA, 6),
                rmap = list(age = 'age', sex = 'sex', year = 'date'),
                baseline = "bsplines", pophaz = "classic")

fitphBS
AIC(fitphBS)
```

AIC.constant	*Akaike's An Information Criterion for excess hazard model with base-line hazard following a piecewise constant function*

Description

Calculates the Akaike's 'An Information Criterion' for fitted models from xhaz.

Usage

```
## S3 method for class 'constant'
AIC(object, ..., k = 2)
```

Arguments

object	a fitted model object obtained from xhaz function
...	optionally more fitted model objects obtained from xhaz function
k	numeric, the penalty per parameter to be used; the default k = 2 is the classical AIC.

Value

the value corresponds to the AIC calculated from the total log-likelihood of the fitted model if just one object is provided. If multiple objects are provided, a data.frame with columns corresponding to the objects and rows representing the number of parameters in the model (df) and the AIC

Examples

```
library("xhaz")

# Esteve et al. model: baseline excess hazard is a piecewise function
#                      linear and proportional effects for the covariates on
#                      baseline excess hazard.

levels(simuData$sex) <- c("male", "female")

set.seed(1980)
simuData2 <- simuData[sample(nrow(simuData), size = 500), ]

fit.estv2 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                  data = simuData2,
                  ratetable = survexp.us,
                  interval = c(0, NA, NA, NA, NA, NA, 6),
                  rmap = list(age = 'age', sex = 'sex', year = 'date'),
                  baseline = "constant", pophaz = "classic")


fit.estv2

AIC(fit.estv2)
```

| anova.bsplines | *anova.bsplines function used for likelihood-ratio Test of two models from xhaz function* |

Description

This function compute an analysis of deviance table for two excess hazard models fitted using xhaz R package.

Usage

```
## S3 method for class 'bsplines'
anova(object, ..., test = "LRT")
```

Arguments

`object`	an object of class bsplines
`...`	an object of class bsplines
`test`	a character string. The appropriate test is a likelihood-ratio test, all other choices result in Not yet implemented test.

Value

An object of class `anova` inheriting from class `matrix`. The different columns contain respectively the degrees of freedom and the log-likelihood values of the two nested models, the degree of freedom of the chi-square statistic, the chi-square statistic and the p-value of the likelihood ratio test.

Note

As expected, the comparison between two or more models by anova or more excess hazard models will only be valid if they are fitted to the same dataset, and if the compared models are nested. This may be a problem if there are missing values.

Author(s)

Juste Goungounga, Robert Darlin Mba, Nathalie Grafféo and Roch Giorgi

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

Giorgi R, Abrahamowicz M, Quantin C, Bolard P, Esteve J, Gouvernet J, Faivre J. A relative survival regression model using B-spline functions to model non-proportional hazards. Statistics in Medicine 2003; 22: 2767-84. (PubMed)

See Also

`xhaz`, `summary.bsplines`, `print.constant`

Examples

```
# load the data set in the package

library("survival")
library("numDeriv")
library("survexp.fr")
library("statmod")

data("dataCancer", package = "xhaz")   # load the data set in the package

fit.phBS <- xhaz(
      formula = Surv(obs_time_year, event) ~ ageCentre + immuno_trt,
      data = dataCancer,
      ratetable = survexp.fr::survexp.fr,
      interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
      rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
      baseline = "bsplines", pophaz  = "classic")



fit.nphBS <- xhaz(
      formula = Surv(obs_time_year, event) ~ ageCentre + qbs(immuno_trt),
      data = dataCancer,
      ratetable = survexp.fr::survexp.fr,
      interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
      rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
      baseline = "bsplines", pophaz  = "classic")

anova(fit.phBS, fit.nphBS)
```

---

anova.constant	*anova.constant function used for likelihood-ratio Test of two models from xhaz function*

Description

This function compute an analysis of deviance table for two excess hazard models fitted using xhaz R package.

Usage

```
## S3 method for class 'constant'
anova(object, ..., test = "LRT")
```

Arguments

`object`	an object of class constant
`...`	an object of class constant
`test`	a character string. The appropriate test is a likelihood-ratio test, all other choices result in Not yet implemented test.

Value

An object of class `anova` inheriting from class `matrix`. The different columns contain respectively the degrees of freedom and the log-likelihood values of the two nested models, the degree of freedom of the chi-square statistic, the chi-square statistic and the p-value of the likelihood ratio test.

Note

As expected, the comparison between two or more models by anova or more excess hazard models will only be valid if they are fitted to the same dataset, and if the compared models are nested. This may be a problem if there are missing values.

Author(s)

Juste Goungounga, Robert Darlin Mba, Nathalie Grafféo and Roch Giorgi

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

Giorgi R, Abrahamowicz M, Quantin C, Bolard P, Esteve J, Gouvernet J, Faivre J. A relative survival regression model using B-spline functions to model non-proportional hazards. Statistics in Medicine 2003; 22: 2767-84. (PubMed)

See Also

xhaz, summary.bsplines, print.constant

Examples

```
# load the data set in the package
library("survival")
library("numDeriv")
library("survexp.fr")


data("dataCancer")    # load the data set in the package

fit.ph <- xhaz(
      formula = Surv(obs_time_year, event) ~ ageCentre + immuno_trt,
      data = dataCancer,
      ratetable = survexp.fr::survexp.fr,
      interval = c(0, NA, NA, NA, max(dataCancer$obs_time_year)),
      rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
      baseline = "constant", pophaz  = "classic")



fit.ph2 <- xhaz(
      formula = Surv(obs_time_year, event) ~ ageCentre ,
      data = dataCancer,
      ratetable = survexp.fr::survexp.fr,
      interval = c(0, NA, NA, NA, max(dataCancer$obs_time_year)),
      rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
      baseline = "constant", pophaz  = "classic")

  anova(fit.ph2, fit.ph)
```

BIC.bsplines	*Bayesian Information Criterion for excess hazard model with baseline hazard following a B-splines functions*

Description

Calculates the Bayesian Information Criterion' for fitted models from xhaz.

Usage

```
## S3 method for class 'bsplines'
BIC(object, ...)
```

Arguments

object	a fitted model object obtained from xhaz function
...	optionally more fitted model objects obtained from xhaz function

Value

the value corresponds to the BIC calculated from the total log-likelihood of the fitted model if just one object is provided. If multiple objects are provided, a data.frame with columns corresponding to the objects and rows representing the number of parameters in the model (df) and the BIC.

Examples

```
library("xhaz")

#Giorgi et al model: baseline excess hazard is a quadratic Bsplines
#                     function with two interior knots and allow here a
#                     linear and proportional effects for the covariates on
#                     baseline excess hazard.
levels(simuData$sex) <- c("male", "female")

fitphBS <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                data = simuData,
                ratetable = survexp.us,
                interval = c(0, NA, NA, 6),
                rmap = list(age = 'age', sex = 'sex', year = 'date'),
                baseline = "bsplines", pophaz = "classic")

fitphBS
BIC(fitphBS)
```

BIC.constant	*Bayesian Information Criterion for excess hazard model with baseline hazard following a piecewise constant function*

Description

Calculates the Bayesian Information Criterion' for fitted models from xhaz.

Usage

```
## S3 method for class 'constant'
BIC(object, ...)
```

Arguments

object   a fitted model object obtained from xhaz function

...   optionally more fitted model objects obtained from xhaz function

Value

the value corresponds to the BIC calculated from the total log-likelihood of the fitted model if just one object is provided. If multiple objects are provided, a data.frame with columns corresponding to the objects and rows representing the number of parameters in the model (df) and the BIC.

Examples

```
library("xhaz")

# Esteve et al. model: baseline excess hazard is a piecewise function
#                      linear and proportional effects for the covariates on
#                      baseline excess hazard.

levels(simuData$sex) <- c("male", "female")

set.seed(1980)
simuData2 <- simuData[sample(nrow(simuData), size = 500), ]
fit.estv2 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                  data = simuData2,
                  ratetable = survexp.us,
                  interval = c(0, NA, NA, NA, NA, NA, 6),
                  rmap = list(age = 'age', sex = 'sex', year = 'date'),
                  baseline = "constant", pophaz = "classic")


fit.estv2

BIC(fit.estv2)
```

---

dataCancer	*Simulated data with cause death information with non comparability bias in term of individuals expected hazard*

Description

Simulated data

Usage

```
data(dataCancer)
```

Format

This dataset contains the following variables:

obs_time Follow-up time (months)

obs_time_year Follow-up time (years)

event Vital status

age Age at diagnosis

agegrp "<30" , "30_60" and ">=60" age groups

ageCentre centered age at diagnosis

sexx Sex(Female,Male).

immuno_trt Treatment group

year_date date of diagnosis.

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

Examples

```
data(dataCancer)
summary(dataCancer)
```

---

duplicate   *duplicate function*

Description

Duplicate data for survival analysis in the context of competing risks, where an individual can experience only one of alternative events, using the Lunn & McNeil (Biometrics, 1995) approaches. Duplication of data proceeds as follows: Suppose that we study J distinct types of events. Each observation concerning a given subject is duplicated J times, with one row for each type of event. In addition, (J-1) dummy variables are created, each indicating the type of event in relation with that observation (delta.j=1 if the event of type j is the observed one and 0 otherwise). Since, for a given subject, only the first occurring event is considered, the status indicator equals 1 for that event and 0 for all the others. In the case of a censored observation (dropout or administrative censoring), the same principle applies also: duplication of each subject's data is made J times with (J-1) dummy variables and a status indicator equal to 0 for all observations.

Usage

```
duplicate(status, event, data)
```

Arguments

status	the censoring status indicator (numeric vector), 0=alive, 1=dead.
event	the indicator of the event type (numeric vector). By default, the event==0 acts as the censoring indicator.
data	a data frame containing the data to duplicate.

Value

A data.frame containing the duplicated data with the new dummy variables, named `delta.number_of_the_event`, indicating the type of event.

Author(s)

Roch Giorgi

References

Lunn M and McNeil D. Applying Cox regression to competing risks. Biometrics 1995;51:524-532 (PubMed)

Examples

```
## Create the simplest test data set
data1 <- data.frame(futime = c(1, 2, 5, 2, 1, 7, 3, 4, 8, 8),
                    fustat = c(0, 1, 1, 1, 0, 0, 1, 0, 1, 1),
                    firstevent = c(0, 2, 1, 2, 0, 0, 1, 0, 2, 2),
                    x = c(1, 0, 0, 1, 0, 1, 1, 1, 0, 0))

## Duplicate data1 with firstevent == 0 as the censoring indicator.
dupli.data <- duplicate(status=fustat, event=firstevent, data=data1)


data2 <- data.frame(futime = c(10, 2, 7, 3, 4, 9, 13, 2, 5, 9),
                    fustat = c(0, 1, 1, 1, 0, 0, 1, 0, 1, 1),
                    firstevent = c(3, 2, 1, 2, 3, 3, 1, 3, 2, 2),
                    x = c(1, 0, 0, 1, 0, 1, 1, 1, 0, 0))


## Duplicate data1 with firstevent == 3 as the censoring indicator.

dupli.data <- duplicate(status = fustat,
                        event = firstevent == 3,
                        data = data2)


# Joint modeling
coxph(Surv(futime, fustat) ~ delta.2 + x + delta.2:(x), data = dupli.data)

coxph(Surv(futime, fustat) ~ delta.1 + x + delta.1:(x), data = dupli.data)
```

exphaz *exphaz function*

Description

Calculate the expected hazard and survival.

Usage

```
exphaz(
  formula = formula(data),
  data = sys.parent(),
  ratetable,
  rmap = list(age = NULL, sex = NULL, year = NULL),
  ratedata = sys.parent(),
  only_ehazard = TRUE,
  subset,
  na.action,
  scale = 365.2425
)
```

Arguments

formula	a formula object of the [Surv](#) function 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 (time in first and status in second).
data	a data frame in which to interpret the variables named in the formula
ratetable	a rate table stratified by age, sex, year (if missing, ratedata is used)
rmap	a list that maps data set names to the ratetable names.
ratedata	a data frame of the hazards mortality in general population.
only_ehazard	a boolean argument (by default, only_ehazard=TRUE). If TRUE, the cumulative population hazard is not provided.
subset	an expression indicating which subset of the rows in data should be used in the fit. All observations are included by default
na.action	a missing-data filter function. The default is na.fail, which returns an error if any missing values are found. An alternative is na.exclude, which deletes observations that contain one or more missing values.
scale	a numeric argument specifying if the ratetable contains death rates per day (default scale = 365.2425) or death rates per year (scale = 1).

Value

An object of class `list` containing the following components:

ehazard	expected hazard calculated from the matching `ratetable`.
ehazardInt	cumulative expected hazard calculated from the matching `ratetable`. if `only_ehazard=TRUE`, this quantity is not provided.
dateDiag	date of diagnosis

Note

`Time` is OBLIGATORY in YEARS.

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

Examples

```
library(survexp.fr)
library(xhaz)
fit.haz <- exphaz(
                formula = Surv(obs_time_year, event) ~ 1,
                data = dataCancer,
                ratetable = survexp.fr, only_ehazard = TRUE,
                rmap = list(age = 'age', sex = 'sexx', year = 'year_date')
)
```

---

plot.bsplines   *plot.bsplines*

Description

to plot the log hazard ratio functions for non-proportional hazards model

Usage

```
## S3 method for class 'bsplines'
plot(
  x,
  cov,
  conf.int = TRUE,
  baseline = FALSE,
  xrange,
  yrange,
  xlegend,
  ylegend,
  glegend,
  xaxs = NULL,
  add = FALSE,
  col = 1,
  lty = 1,
  lwd = 1,
  ...
)
```

Arguments

x	An object of class xhaz
cov	specify covariates for which a plot is required.
conf.int	a vector of logical values indicating whether (if TRUE) confidence intervals will be plotted. The default is to do so if the plot concerns only one curve.
baseline	a vector of logical values indicating whether (if baseline = TRUE) to plot the curve for the baseline group. Default is FALSE, except if cov is unspecified.
xrange	vector indicating the minimum and the maximum values of the x axis. By default, these values are automatically calculated for the first plot (i.e before the use of add argument).
yrange	vector indicating the minimum and the maximum values of the y axis. By default, these values are automatically calculated for the first plot (i.e before the use of add argument).
xlegend	value indicating the location of the legend over x axis. By default, location at the left of the plot.
ylegend	value indicating the location of the legend over y axis. By default, location at the top of the plot
glegend	vectors of names attributed to each lines of the excess hazard to be displayed in the plot. If (baseline = TRUE), glegend is "baseline".
xaxs	the x axis style, as listed in 'par'. Survival curves are traditionally drawn with the curve touching the bounding box on the left edge, but not touching it on the right edge. This corresponds to neither of the two standard S axis styles of "e" (neither touches) or "i" (both touch). If xaxis is missing or NULL the internal axis style is used (xaxs= i) but only after the right endpoint has been extended.

add	a logical value indicating whether to add the survival curves to the current plot (if add = TRUE). Default is FALSE.
col	a vector of integers specifying colors for each curve. The default value is 1.
lty	a vector of integers specifying line types for each curve. The default value is fixed by the number of covariates (plus 1 if baseline = TRUE).
lwd	a vector of numeric values for line widths. The default value is 1.
...	additional arguments affecting the plot function

Value

The return of this function produce graphics of log hazard ratio functions for non-proportional hazards model

Author(s)

Juste Goungounga, Robert Darlin Mba, Nathalie Grafféo and Roch Giorgi

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

Giorgi R, Abrahamowicz M, Quantin C, Bolard P, Esteve J, Gouvernet J, Faivre J. A relative survival regression model using B-spline functions to model non-proportional hazards. Statistics in Medicine 2003; 22: 2767-84. (PubMed)

Examples

```
# load the data set in the package
library("xhaz")
library("survexp.fr")

data("dataCancer", package = "xhaz")   # load the data set in the package

fit.nphBS <- xhaz(
      formula = Surv(obs_time_year, event) ~ ageCentre + qbs(immuno_trt),
      data = dataCancer,
      ratetable = survexp.fr,
```

```
        interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
        rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
        baseline = "bsplines", pophaz  = "classic")

plot(fit.nphBS, cov = "immuno_trt", col = "blue", baseline = FALSE)
```

---

plot.predxhaz   *plots of excess hazard and net Survival from an* predxhaz *object*

Description

Function to plot excess hazard or net survival

Usage

```
## S3 method for class 'predxhaz'
plot(x, what = "survival", ...)
```

Arguments

x	An object of class predxhaz
what	allow to choose between excess hazard (what="hazard") or net survival (what="survival").
...	additional arguments affecting the plot function

Value

The return of this function produce graphics of excess hazard or net survival, or time-dependent effects, when times.pts argument is provided in prediction call.

Author(s)

Juste Goungounga, Robert Darlin Mba, Nathalie Grafféo and Roch Giorgi

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

Examples

```
data("dataCancer")
# load the data set in the package
library("survival")
library("numDeriv")
library("survexp.fr")
data("simuData", package = "xhaz") # load the data sets 'simuData'

#define the levels of variable sex
levels(simuData$sex) <- c("male", "female")

# Esteve et al. model


fit.estv1 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                  data = simuData, ratetable = survexp.us,
                  interval = c(0, NA, NA, NA, NA, NA, max(simuData$time_year)),
                  rmap = list(age = 'age', sex = 'sex', year = 'date'),
                  baseline = "constant", pophaz = "classic")


predict_est <- predict(object = fit.estv1,
                       new.data = simuData,
                       times.pts = c(seq(0, 4, 0.1)),
                       baseline = TRUE)

plot(predict_est, what = "survival",
     xlab = "time since diagnosis (year)",
     ylab = "net survival", ylim = c(0, 1))
data("dataCancer", package = "xhaz")   # load the data set in the package

fit.phBS <- xhaz(
     formula = Surv(obs_time_year, event) ~ ageCentre + immuno_trt,
     data = dataCancer, ratetable = survexp.fr::survexp.fr,
     interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
     rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
     baseline = "bsplines", pophaz  = "classic")


predict_mod1 <- predict(object = fit.phBS, new.data = dataCancer,
                        times.pts = c(seq(0, 10, 0.1)), baseline = FALSE)

old.par <- par(no.readonly = TRUE)
par(mfrow = c(2, 1))


plot(predict_mod1, what = "survival",
     xlab = "time since diagnosis (year)",
     ylab = "net survival", ylim = c(0, 1))

plot(predict_mod1, what = "hazard",
```

```
    xlab = "time since diagnosis (year)",
    ylab = "excess hazard")

par(old.par)
```

---

predict.bsplines *Predictions of excess hazard and net Survival from a* bsplines *object*

Description

Function to predict excess hazard and net survival based on an object of class bsplines. The function allows the predictions at several time points but not exceeding the maximum time of follow-up from the baseline model.

Usage

```
## S3 method for class 'bsplines'
predict(object, new.data = NULL, times.pts = NULL, baseline = TRUE, ...)
```

Arguments

object	an object of class bsplines
new.data	new.data where is covariates
times.pts	time in year scale to calculate the excess hazard. The default value is NULL. In this case, time variable must be provided in the new.data
baseline	default is survival baseline; put baseline = FALSE to estimate the net survival with covariates
...	additional arguments affecting the predictions of excess hazard and net survival

Value

An object of class predxhaz, which is a list of data.frame. Each element of the list contains the estimates of hazard and survival at a fixed time point. The return of this function can be used to produce graphics of excess hazard or net survival, when times.pts argument is provided. This object contains:

times.pts	the times value in year at which the excess hazard and or the net survival have been estimated
hazard	the excess hazard values based on the model of interest
survival	the net survival values based on the model of interest

Author(s)

Juste Goungounga, Robert Darlin Mba, Nathalie Grafféo and Roch Giorgi

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

See Also

xhaz, print.bsplines, print.constant

Examples

```
library("survival")
library("numDeriv")
library("survexp.fr")
library("splines")
data("dataCancer", package = "xhaz")   # load the data set in the package

fit.phBS <- xhaz(
        formula = Surv(obs_time_year, event) ~ ageCentre + immuno_trt,
        data = dataCancer, ratetable = survexp.fr,
        interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
        rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
        baseline = "bsplines", pophaz = "classic")


print(fit.phBS)


predicted <- predict(object = fit.phBS,
                     new.data = dataCancer[1:10,],
                     times.pts = c(seq(0,10,1)),
                     baseline = TRUE)


#a list of predicted hazard and survival at different time points
print(predicted)


#predicted hazard and survival at time points 10 years
```

```
print(predicted[[10]])
```

---

predict.constant   *Predictions of excess hazard and net Survival from an* constant *object*

Description

Function to predict excess hazard and net survival based on an object of class constant. The function allows the predictions at several time points but not exceeding the maximum time of follow-up from the baseline model.

Usage

```
## S3 method for class 'constant'
predict(object, new.data = NULL, times.pts = NULL, baseline = TRUE, ...)
```

Arguments

object	An object of class constant
new.data	new.data where is covariates
times.pts	time in year scale to calculate the excess hazard. The default value is NULL. In this case, time variable must be provided in the new.data
baseline	default is survival baseline; put baseline = FALSE to estimate the net survival with covariates
...	additional arguments affecting the predictions of excess hazard and net survival

Value

An object of class predxhaz. The return of this fonction can be used to produce graphics of excess hazard or net survival, when times.pts argument is provided. This object contains:

times.pts	the times value in year at which the excess hazard and or the net survival have been estimated
hazard	the excess hazard values based on the model of interest
survival	the net survival values based on the model of interest

Author(s)

Juste Goungounga, Robert Darlin Mba, Nathalie Grafféo and Roch Giorgi

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

See Also

xhaz, print.bsplines, print.constant

Examples

```
# load the data set in the package
library("xhaz")
library("numDeriv")

# load the data sets 'simuData

data("simuData", package = "xhaz")

#define the levels of variable sex
levels(simuData$sex) <- c("male", "female")

# Esteve et al. model

set.seed(1980)
simuData2 <- simuData[sample(nrow(simuData), size = 500), ]

fit.estv2 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                  data = simuData2,
                  ratetable = survexp.us,
                  interval = c(0, NA, NA, NA, NA, NA, 6),
                  rmap = list(age = 'age', sex = 'sex', year = 'date'),
                  baseline = "constant", pophaz = "classic")


predict_est <- predict(object = fit.estv2,
                       new.data = simuData2,
                       times.pts = c(seq(0, 4, 1)),
                       baseline = TRUE)
predict_est
```

---

print.bsplines   *A print.bsplines Function used to print a object of class* bsplines

---

Description

This function present the estimated coefficients for the excess hazard baseline coefficient and for the covariate effects

Usage

```
## S3 method for class 'bsplines'
print(x, digits = max(options()$digits - 4, 3), ...)
```

Arguments

x	an object of class bsplines
digits	minimal number of significant digits.
...	additionnal parameters which can be used in the print function

Value

Estimated parameters of the model in different scales for interpretation purposes.

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

See Also

xhaz, plot.predxhaz, print.constant

Examples

```
library("xhaz")
library("survival")
library("numDeriv")
library("survexp.fr")
library("splines")
data("dataCancer", package = "xhaz")   # load the data set in the package

fit.phBS <- xhaz(
                formula = Surv(obs_time_year, event) ~ ageCentre + immuno_trt,
                data = dataCancer, ratetable = survexp.fr,
                interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
                rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
                baseline = "bsplines", pophaz = "classic")

print(fit.phBS)
```

---

print.constant	*A print.constant Function used to print a object of class constant*

Description

This function present the estimated coefficients for the excess hazard baseline coefficient and for the covariate effects

Usage

```
## S3 method for class 'constant'
print(x, ci_type = "lognormal", digits = max(options()$digits - 4, 3), ...)
```

Arguments

x	an object of class xhaz.constant
ci_type	method for confidence intervals calculation
digits	minimal number of significant digits.
...	additionnal parameters which can be used in the print function

Value

Estimated parameters of the model in different scales for interpretation purposes.

See Also

xhaz, summary.constant, print.bsplines

Examples

```
library("numDeriv")
library("survexp.fr")

data("simuData","rescaledData", "dataCancer")
# load the data sets 'simuData', 'rescaledData' and 'dataCancer'.

# Esteve et al. model: baseline excess hazard is a piecewise function
#                      linear and proportional effects for the covariates on
#                      baseline excess hazard.

levels(simuData$sex) <- c("male", "female")
set.seed(1980)
simuData2 <- simuData[sample(nrow(simuData), size = 500), ]

fit.estv2 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                  data = simuData2,
                  ratetable = survexp.us,
                  interval = c(0, NA, NA, NA, NA, NA, 6),
                  rmap = list(age = 'age', sex = 'sex', year = 'date'),
                  baseline = "constant", pophaz = "classic")


print(fit.estv2)
```

---

print.predxhaz   *A print.predxhaz Function used to print a object of class predxhaz*

Description

This function present the print of the predict function

Usage

```
## S3 method for class 'predxhaz'
print(x, ...)
```

Arguments

x   an object of class predxhaz

...   other parameters used for print function

Value

an object of class data.frame containing the following components:

`times.pts`	The time at which the estimations of excess hazard and net survival are predicted
`hazard`	the predicted excess hazard at the fixed times
`survival`	the predicted net survival at the fixed times

Examples

```
library("xhaz")
library("survexp.fr")
library("splines")

data("dataCancer", package = "xhaz")   # load the data set in the package

fit.phBS <- xhaz(
        formula = Surv(obs_time_year, event) ~ ageCentre + immuno_trt,
        data = dataCancer, ratetable = survexp.fr,
        interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
        rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
        baseline = "bsplines", pophaz = "classic")


fit.phBS


predicted <- predict(object = fit.phBS,
                     new.data = dataCancer[1:10,],
                     times.pts = c(seq(0,10,1)),
                     baseline = TRUE)



#a list of predicted hazard and survival at different time points
print(predicted)


#predicted hazard and survival at time points 10 years
print(predicted[[10]])
```

---

qbs	*qbs function*

Description

a function indicating which covariates have a time-dependent effect in the formula.

Usage

```
qbs(x)
```

Arguments

x   a covariate to be considered in the xhaz formula with a time-dependant effect. Quadratic B-splines with two interior knots are used.

Value

No return value, called for side effects.

Examples

```
library("xhaz")
library("numDeriv")
library("survexp.fr")
library("splines")

fit.tdphBS <- xhaz(
              formula = Surv(obs_time_year, event) ~ ageCentre + qbs(immuno_trt),
              data = dataCancer, ratetable = survexp.fr,
              interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
              rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
              baseline = "bsplines", pophaz = "classic")

print(fit.tdphBS)
```

---

rescaledData	*Simulated data with cause death information with non comparability bias in term of individuals expected hazard*

Description

Simulated data

Usage

```
data(rescaledData)
```

Format

This dataset contains the following variables:

time Follow-up time (months)
status Vital status
age Age at diagnosis
age.c Centred age
sex Sex(Female,Male)
hormTh Treatment group variable
date date of diagnosis

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Examples

```
data(rescaledData)
summary(rescaledData)
```

---

simuData   *Simulated data with cause death information in long term follow-up*
                            setting without non comparability bias in term of individuals expected
                            hazard

Description

Simulated data

Usage

```
data(simuData)
```

Format

This dataset contains the following variables:

age Age at diagnosis
agec Centered age
sex Sex(Female,Male)
race Race
date date of diagnosis.
time Follow-up time (months)
time_year Follow-up time (years)
status Vital status

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Examples

```
data(simuData)
summary(simuData)
```

---

summary.bsplines	*A summary.bsplines Function used to print a object of class* bsplines

---

Description

This function present the estimated coefficients for the excess hazard baseline coefficient and for the covariate effects

Usage

```
## S3 method for class 'bsplines'
summary(object, ...)
```

Arguments

object	an object of class bsplines
...	additionnal parameters which can be used in the summary function

Value

Estimated parameters of the model in different scales for interpretation purposes.

References

Goungounga JA, Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. Correcting for misclassification and selection effects in estimating net survival in clinical trials. BMC Med Res Methodol. 2019 May 16;19(1):104. doi: 10.1186/s12874-019-0747-3. PMID: 31096911; PMCID: PMC6524224. (PubMed)

Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

See Also

xhaz, summary.bsplines, plot.bsplines

Examples

```
library("xhaz")
library("survival")
library("numDeriv")
library("survexp.fr")
library("splines")

data("dataCancer", package = "xhaz")   # load the data set in the package

fit.phBS <- xhaz(
              formula = Surv(obs_time_year, event) ~ ageCentre + immuno_trt,
              data = dataCancer, ratetable = survexp.fr,
              interval = c(0, NA, NA, max(dataCancer$obs_time_year)),
              rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
              baseline = "bsplines", pophaz = "classic")

summary(fit.phBS)
```

---

summary.constant	*A summary.constant Function used to print a object of class* `xhaz.constant`

Description

This function present the estimated coefficients for the excess hazard baseline coefficient and for the covariate effects

Usage

```
## S3 method for class 'constant'
summary(object, ci_type = "lognormal", ...)
```

Arguments

`object`	an object of class xhaz.constant
`ci_type`	method for confidence intervals calculation
`...`	additionnal parameters which can be used in the `print` function

Value

Estimated parameters of the model in different scales for interpretation purposes.

See Also

xhaz, summary.constant, print.bsplines

Examples

```
library("xhaz")
library("numDeriv")
data("simuData", package = "xhaz")    # load the data sets 'simuData'

# Esteve et al. model: baseline excess hazard is a piecewise function
#                      linear and proportional effects for the covariates on
#                      baseline excess hazard.

levels(simuData$sex) <- c("male", "female")

set.seed(1980)
simuData2 <- simuData[sample(nrow(simuData), size = 500), ]

fit.estv2 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                  data = simuData2,
                  ratetable = survexp.us,
                  interval = c(0, NA, NA, NA, NA, NA, 6),
                  rmap = list(age = 'age', sex = 'sex', year = 'date'),
                  baseline = "constant", pophaz = "classic")



summary(fit.estv2)
```

---

xhaz   *xhaz function*

Description

Fits the excess hazard models proposed by Esteve et al. (1990) doi:10.1002/sim.4780090506,
with the possibility to account for time dependent covariates. Fits also the non-proportional excess
hazard model proposed by Giorgi et al. (2005) doi:10.1002/sim.2400. In addition, fits excess
hazard models with possibility to rescale (Goungounga et al. (2019) doi:10.1186/s12874-019-0747-3)
or to correct the background mortality with a proportional (Touraine et al. (2020) doi:10.1177/
0962280218823234) or non-proportional (Mba et al. (2020) doi:10.1186/s12874-020-01139-z)
effect.

Usage

```
xhaz(
  formula = formula(data),
  data = sys.parent(),
  ratetable,
  rmap = list(age = NULL, sex = NULL, year = NULL),
  baseline = c("constant", "bsplines"),
  pophaz = c("classic", "rescaled", "corrected"),
  only_ehazard = FALSE,
  add.rmap = NULL,
 add.rmap.cut = list(breakpoint = FALSE, cut = NA, probs = NULL, criterion = "BIC",
    print_stepwise = FALSE),
  interval,
  ratedata = sys.parent(),
  subset,
  na.action,
  init,
  control = list(eps = 1e-04, iter.max = 800, level = 0.95),
  optim = TRUE,
  scale = 365.2425,
  trace = 0,
  speedy = FALSE,
  nghq = 12,
  ...
)
```

Arguments

formula	a formula object of the function 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 (time in first and status in second).
data	a data frame in which to interpret the variables named in the formula
ratetable	a rate table stratified by age, sex, year (if missing, ratedata is used)
rmap	a list that maps data set names to the ratetable names.
baseline	an argument to specify the baseline hazard: if it follows a piecewise constant, baseline = "constant" is used and corresponds to the baseline in Esteve et al. model; if the baseline follows a quadratic b-splines, baseline = "bsplines" is used, corresponding to the baseline excess hazard in Giorgi et al model.
pophaz	indicates three possibles arguments in character: classic or rescaled and corrected. If pophaz = "classic" chosen, fits the model that do not require to rescale or to correct the background mortality (i.e. the Esteve et al. model or Giorgi et al. model); if pophaz = "rescaled" or pophaz = "corrected" chosen, fits the models that require to rescale or to correct the background mortality.
only_ehazard	a boolean argument (by default, only_ehazard=FALSE). If only_ehazard = TRUE, pophaz = "classic" must be provided and the total value of the log-likelihood will not account for the cumulative population hazard.

add.rmap	character that indicates the name in character of the additional demographic variable from data to be used for correction of the life table, in particular when one is in the presence of an insufficiently stratified life table (see Touraine et al. model). This argument is not used if pophaz = "classic" or pophaz = "rescaled".
add.rmap.cut	a list containing arguments to specify the modeling strategy for breakpoint positions, which allows a non-proportional effect of the correction term acting on the background mortality. By default list(breakpoint = FALSE), i.e. a proportional effect of the correction term acting on the background mortality is needed; in this case, all the other argument of the list are not working for the model specification;
	if list(breakpoint = TRUE, cut = c(70)), the chosen cut-point(s) is (are) the numeric value(s) proposed. If list(breakpoint = TRUE, cut = NA), there is the same number of breakpoints as the number of NA, with their possible positions specified as here by probs, i.e. list(breakpoint = TRUE, cut = NA, probs = seq(0, 1, 0.25)). That corresponds to a numeric vector of probabilities with values between 0 and 1 as in quantile function. criterion is used to choose the best model, using the AIC or the BIC (the default criterion). If needed, all the fitted models are printed by the user by adding in the list print_stepwise = FALSE.
interval	a vector indicating either the location of the year-scale time intervals for models with piecewise constant function, or the location of the knots for models with B-splines functions for their baseline hazard (see the appropriate specification in baseline argument). The first component of the vector is 0, and the last one corresponds to the maximum time fellow-up of the study.
ratedata	a data frame of the hazards mortality in general population.
subset	an expression indicating which subset of the data should be used in the modeling. All observations are included by default
na.action	as in the coxph function, a missing-data filter function.
init	a list of initial values for the parameters to estimate. For each elements of the list, give the name of the covariate followed by the vector of the fixed initials values
control	a list of control values used to control the optimization process. In this list, eps, is a convergence criteria (by default, eps=10^-4), iter.max is the maximum number of iteration (by default, iter.max=15), and level, is the level used for the confidence intervals (by default, level=0.95).
optim	a Boolean argument (by default, optim = FALSE). If optim = TRUE), the maximization algorithm uses the optim function
scale	a numeric argument to specify whether the life table contains death rates per day (default scale = 365.2425) or death rates per year (scale = 1).
trace	a Boolean argument, if trace = TRUE), tracing information on the progress of the optimization is produced
speedy	a Boolean argument, if speedy = TRUE, optimization is done in a parallel mode
nghq	number of nodes and weights for Gaussian quadrature
...	other parameters used with the xhaz function

Details

Use the Surv(time_start, time_stop, status) notation for time dependent covariate with the appropriate organization of the data set (see the help page of the Surv function)

Only two interior knots are possible for the model with B-splines functions to fit the baseline (excess) hazard. Determination of the intervals might be user's defined or automatically computed according to the quantile of the distribution of deaths. Use NA for an automatic determination (for example, interval = c(0, NA, NA, 5)).

Value

An object of class xhaz.constant or xhaz.bsplines, according to the type of functions chosen to fit the baseline hazard of model (see details for argument baseline). This object is a list containing the following components:

coefficients	estimates found for the model
varcov	the variance-covariance matrix
loglik	for the Estève et al. model: the log-likelihood of the null model, i.e without covariate, and the log-likelihood of the full model, i.e with all the covariates declared in the formula; for the Giorgi et al. model: the log-likelihood of the full model
cov.test	for the Esteve et al.model: the log-likelihood of the null model, i.e without covariate, and the log-likelihood of the full model, i.e with all the covariates declared in the formula; for the Giorgi et al. model: the log-likelihood of the full model
message	a character string returned by the optimizer see details in optim help page
convergence	an integer code as in optim when "L-BFGS-B" method is used.
n	the number of individuals in the dataset
n.events	the number of events in the dataset. Event are considered as death whatever the cause
level	the confidence level used
interval	the intervals used to split time for piecewise baseline excess hazard, or knots positions for Bsplines baseline
terms	the representation of the terms in the model
call	the function call based on model
pophaz	the assumption considered for the life table used in the excess hazard model
add.rmap	the additional variable for which the life table is not stratified
ehazardInt	the cumulative hazard of each individuals calculated from the ratetable used in the model
ehazard	the individual expected hazard values from the ratetable used to fit the model
data	the dataset used to run the model
time_elapsed	the time to run the model

Note

`time` is OBLIGATORY in YEARS.

Author(s)

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References

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Touraine C, Grafféo N, Giorgi R; CENSUR working survival group. More accurate cancer-related excess mortality through correcting background mortality for extra variables. Stat Methods Med Res. 2020 Jan;29(1):122-136. doi: 10.1177/0962280218823234. Epub 2019 Jan 23. PMID: 30674229. (PubMed)

Mba RD, Goungounga JA, Grafféo N, Giorgi R; CENSUR working survival group. Correcting inaccurate background mortality in excess hazard models through breakpoints. BMC Med Res Methodol. 2020 Oct 29;20(1):268. doi: 10.1186/s12874-020-01139-z. PMID: 33121436; PMCID: PMC7596976. (PubMed)

Giorgi R, Abrahamowicz M, Quantin C, Bolard P, Esteve J, Gouvernet J, Faivre J. A relative survival regression model using B-spline functions to model non-proportional hazards. Statistics in Medicine 2003; 22: 2767-84. (PubMed)

Examples

```
library("numDeriv")
library("survexp.fr")
library("splines")
library("statmod")
data("simuData","rescaledData", "dataCancer")
# load the data sets 'simuData', 'rescaledData' and 'dataCancer'.

# Esteve et al. model: baseline excess hazard is a piecewise function
#                      linear and proportional effects for the covariates on
#                      baseline excess hazard.

levels(simuData$sex) <- c("male", "female")

fit.estv1 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                  data = simuData,
                  ratetable = survexp.us,
                  interval = c(0, NA, NA, NA, NA, NA, 6),
                  rmap = list(age = 'age', sex = 'sex', year = 'date'),
                  baseline = "constant", pophaz = "classic")


fit.estv1
```

```
# Touraine et al. model: baseline excess hazard is a piecewise function
#                        with a linear and proportional effects for the
#                        covariates on the baseline excess hazard.
# An additionnal cavariate (here race) missing in the life table is
# considered by the model.


fit.corrected1 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                       data = simuData,
                       ratetable = survexp.us,
                       interval = c(0, NA, NA, NA, NA, NA, 6),
                       rmap = list(age = 'age', sex = 'sex', year = 'date'),
                       baseline = "constant", pophaz = "corrected",
                       add.rmap = "race")



fit.corrected1

# extension of Touraine et al model: baseline excess hazard is a piecewise
# constant function with a linear and proportional effects for the covariates
# on the baseline excess hazard.

# An additionnal cavariate (here race) missing in the life table is
# considered by the model with a breakpoint at 75 years

fit.corrected2 <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                       data = simuData,
                       ratetable = survexp.us,
                       interval = c(0, NA, NA, NA, NA, NA, 6),
                       rmap = list(age = 'age', sex = 'sex', year = 'date'),
                       baseline = "constant", pophaz = "corrected",
                       add.rmap = "race",
                        add.rmap.cut = list(breakpoint = TRUE, cut = 75))



fit.corrected2


#Giorgi et al model: baseline excess hazard is a quadratic Bsplines
#                    function with two interior knots and allow here a
#                    linear and proportional effects for the covariates on
#                    baseline excess hazard.


fitphBS <- xhaz(formula = Surv(time_year, status) ~ agec + race,
                data = simuData,
                ratetable = survexp.us,
                interval = c(0, NA, NA, 6),
                rmap = list(age = 'age', sex = 'sex', year = 'date'),
```

```
                          baseline = "bsplines", pophaz = "classic")

    fitphBS




# Application on `dataCancer`.
#Giorgi et al model: baseline excess hazard is a quadratic Bspline
#                    function with two interior knots and allow here a
#                    linear and proportional effect for the variable
#                    "immuno_trt" plus a non-proportional effect
#                    for the variable "ageCentre" on baseline excess hazard.


fittdphBS <- xhaz(formula = Surv(obs_time_year, event) ~ qbs(ageCentre) + immuno_trt,
                  data = dataCancer,
                  ratetable = survexp.fr,
                  interval = c(0, 0.5, 12, 15),
                  rmap = list(age = 'age', sex = 'sexx', year = 'year_date'),
                  baseline = "bsplines", pophaz = "classic")

fittdphBS




# Application on `rescaledData`.
# rescaled model: baseline excess hazard is a piecewise function with a
# linear and proportional effects for the covariates on baseline excess hazard.

# A scale parameter on the expected mortality of general population is
# considered to account for the non-comparability source of bias.

rescaledData$timeyear <- rescaledData$time/12
rescaledData$agecr <- scale(rescaledData$age, TRUE, TRUE)

fit.res <- xhaz(formula = Surv(timeyear, status) ~ agecr + hormTh,
                data = rescaledData,
                ratetable = survexp.fr,
                interval = c(0, NA, NA, NA, NA, NA, max(rescaledData$timeyear)),
                rmap = list(age = 'age', sex = 'sex', year = 'date'),
                baseline = "constant", pophaz = "rescaled")

 fit.res
```

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