

# Package: eha (via r-universe)

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**Title** Event History Analysis

**Description** Parametric proportional hazards fitting with left truncation and right censoring for common families of distributions, piecewise constant hazards, and discrete models. Parametric accelerated failure time models for left truncated and right censored data. Proportional hazards models for tabular and register data. Sampling of risk sets in Cox regression, selections in the Lexis diagram, bootstrapping. Broström (2022) <[doi:10.1201/9780429503764](https://doi.org/10.1201/9780429503764)>.

**BugReports** <https://github.com/goranbrostrom/eha/issues>

**License** GPL (>= 2)

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**ByteCompile** yes

**URL** <https://ehar.se/r/eha/>

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**Imports** stats, graphics, survival (>= 3.0)

**NeedsCompilation** yes

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**Suggests** knitr, rmarkdown, bookdown

**VignetteBuilder** knitr, utils

**Repository** <https://goranbrostrom.r-universe.dev>

**RemoteUrl** <https://github.com/goranbrostrom/eha>

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eha-package*eha: Event History Analysis*

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## Description

Parametric proportional hazards fitting with left truncation and right censoring for common families of distributions, piecewise constant hazards, and discrete models. Parametric accelerated failure time models for left truncated and right censored data. Proportional hazards models for tabular and register data. Sampling of risk sets in Cox regression, selections in the Lexis diagram, bootstrapping. Broström (2022) [doi:10.1201/9780429503764](https://doi.org/10.1201/9780429503764).

## Details

Eha enhances the recommended **survival** package in several ways, see the description. The main applications in mind are demography and epidemiology. For standard Cox regression analysis the function `coxph` in **survival** is still recommended. The function `coxreg` in **eha** in fact calls `coxph` for the standard kind of analyses.

## Author(s)

**Maintainer:** Göran Broström <[goran.brostrom@umu.se](mailto:goran.brostrom@umu.se)>

Other contributors:

- Jianming Jin [contributor]

## References

Broström, G. (2012). *Event History Analysis with R*, Chapman and Hall/CRC Press, Boca Raton, FL.

## See Also

Useful links:

- <https://ehar.se/r/eha/>
- Report bugs at <https://github.com/goranbrostrom/eha/issues>

aftreg

*Accelerated Failure Time Regression***Description**

The accelerated failure time model with parametric baseline hazard(s). Allows for stratification with different scale and shape in each stratum, and left truncated and right censored data.

**Usage**

```
aftreg(
  formula = formula(data),
  data = parent.frame(),
  na.action = getOption("na.action"),
  dist = "weibull",
  init,
  shape = 0,
  id,
  param = c("lifeAcc", "lifeExp"),
  control = list(eps = 1e-08, maxiter = 20, trace = FALSE),
  singular.ok = TRUE,
  model = FALSE,
  x = FALSE,
  y = 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.
data	a data.frame in which to interpret the variables named in the formula.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
dist	Which distribution? Default is "weibull", with the alternatives "gompertz", "ev", "loglogistic" and "lognormal". A special case like the exponential can be obtained by choosing "weibull" in combination with shape = 1.
init	vector of initial values of the iteration. Default initial value is zero for all variables.
shape	If positive, the shape parameter is fixed at that value. If zero or negative, the shape parameter is estimated. Stratification is now regarded as a meaningful option even if shape is fixed.
id	If there are more than one spell per individual, it is essential to keep spells together by the id argument. This allows for time-varying covariates.

param	Which parametrization should be used? The <code>lifeAcc</code> uses the parametrization given in the vignette, while the <code>lifeExp</code> uses the same as in the <code>survreg</code> function.
control	a list with components <code>eps</code> (convergence criterion), <code>maxiter</code> (maximum number of iterations), and <code>trace</code> (logical, debug output if TRUE). You can change any component without mention the other(s).
singular.ok	Not used.
model	Not used.
x	Return the design matrix in the model object?
y	Return the response in the model object?

### Details

The parameterization is different from the one used by `survreg`, when `param = "lifeAcc"`. The result is then true acceleration of time. Then the model is

$$S(t; a, b, \beta, z) = S_0((t / \exp(b - z\beta))^{\exp(a)})$$

where  $S_0$  is some standardized survivor function. The baseline parameters  $a$  and  $b$  are log shape and log scale, respectively. This is for the default parametrization. With the `lifeExp` parametrization, some signs are changed:

$$b - z\beta$$

is changed to

$$b + z\beta$$

. For the Gompertz distribution, the base parametrization is canonical, a necessity for consistency with the shape/scale paradigm (this is new in 2.3).

### Value

A list of class "aftreg" with components

coefficients	Fitted parameter estimates.
var	Covariance matrix of the estimates.
loglik	Vector of length two; first component is the value at the initial parameter values, the second componet is the maximized value.
score	The score test statistic (at the initial value).
linear.predictors	The estimated linear predictors.
means	Means of the columns of the design matrix.
w.means	Weighted (against exposure time) means of covariates; weighted relative frequencies of levels of factors.
n	Number of spells in indata (possibly after removal of cases with NA's).
n.events	Number of events in data.
terms	Used by extractor functions.

assign	Used by extractor functions.
wald.test	The Wald test statistic (at the initial value).
y	The Surv vector.
isF	Logical vector indicating the covariates that are factors.
covars	The covariates.
ttr	Total Time at Risk.
levels	List of levels of factors.
formula	The calling formula.
call	The call.
method	The method.
convergence	Did the optimization converge?
fail	Did the optimization fail? (Is NULL if not).
pfixed	TRUE if shape was fixed in the estimation.
param	The parametrization.

**Author(s)**

Göran Broström

**See Also**[coxreg](#), [phreg](#), [survreg](#)**Examples**

```
data(mort)
aftreg(Surv(enter, exit, event) ~ ses, param = "lifeExp", data = mort)
```

aftreg.fit

*Parametric proportional hazards regression***Description**

This function is called by [aftreg](#), but it can also be directly called by a user.

**Usage**

```
aftreg.fit(X, Y, dist, param, strata, offset, init, shape, id, control, pfixed)
```

**Arguments**

X	The design (covariate) matrix.
Y	A survival object, the response.
dist	Which baseline distribution?
param	Which parametrization?
strata	A stratum variable.
offset	Offset.
init	Initial regression parameter values.
shape	If positive, a fixed value of the shape parameter in the distribution. Otherwise, the shape is estimated.
id	See corresponding argument to <a href="#">aftreg</a> .
control	Controls convergence and output.
pfixed	A logical indicating fixed shape parameter(s).

**Details**

See [aftreg](#) for more detail.

**Value**

coefficients	Estimated regression coefficients plus estimated scale and shape coefficients, sorted by strata, if present.
df	Degrees of freedom; No. of regression parameters.
var	Variance-covariance matrix
loglik	Vector of length 2. The first component is the maximized loglikelihood with only scale and shape in the model, the second the final maximum.
conver	TRUE if convergence
fail	TRUE if failure
iter	Number of Newton-Raphson iterates.
n.strata	The number of strata in the data.

**Author(s)**

Göran Broström

**See Also**

[aftreg](#)



---

age.window	<i>Age cut of survival data</i>
------------	---------------------------------

---

**Description**

For a given age interval, each spell is cut to fit into the given age interval.

**Usage**

```
age.window(dat, window, surv = c("enter", "exit", "event"))
```

**Arguments**

dat	Input data frame. Must contain survival data.
window	Vector of length two; the age interval.
surv	Vector of length three giving the names of the central variables in 'dat'.

**Details**

The window must be in the order (begin, end)

**Value**

A data frame of the same form as the input data frame, but 'cut' as desired. Intervals exceeding window[2] will be given event = 0. If the selection gives an empty result, NULL is returned, with no warning.

**Author(s)**

Göran Broström

**See Also**

[cal.window](#), [coxreg](#), [aftreg](#)

**Examples**

```
dat <- data.frame(enter = 0, exit = 5.731, event = 1, x = 2)
window <- c(2, 5.3)
dat.trim <- age.window(dat, window)
```

---

`cal.window`*Calendar time cut of survival data*

---

**Description**

For a given time interval, each spell is cut so that it fully lies in the given time interval

**Usage**

```
cal.window(dat, window, surv = c("enter", "exit", "event", "birthdate"))
```

**Arguments**

<code>dat</code>	Input data frame. Must contain survival data and a birth date.
<code>window</code>	Vector of length two; the time interval
<code>surv</code>	Vector of length four giving the names of the central variables in 'dat'.

**Details**

The window must be in the order (begin, end)

**Value**

A data frame of the same form as the input data frame, but 'cut' as desired. Intervals exceeding `window[2]` will be given `event = 0`

**Author(s)**

Göran Broström

**See Also**

[age.window](#), [coxreg](#), [aftreg](#)

**Examples**

```
dat <- data.frame(enter = 0, exit = 5.731, event = 1,
  birthdate = 1962.505, x = 2)
window <- c(1963, 1965)
dat.trim <- cal.window(dat, window)
```

---

check.dist	<i>Graphical goodness-of-fit test</i>
------------	---------------------------------------

---

## Description

Comparison of the cumulative hazards functions for a semi-parametric and a parametric model.

## Usage

```
check.dist(sp, pp, main = NULL, col = 1:2, lty = 1:2, printLegend = TRUE)
```

## Arguments

sp	An object of type "coxreg", typically output from <a href="#">coxreg</a>
pp	An object of type "phreg", typically output from <a href="#">phreg</a>
main	Header for the plot. Default is distribution and "cumulative hazard function"
col	Line colors. should be NULL (black lines) or of length 2
lty	line types.
printLegend	Should a legend be printed? Default is TRUE.

## Details

For the moment only a graphical comparison. The arguments sp and pp may be swapped.

## Value

No return value.

## Author(s)

Göran Broström

## See Also

[coxreg](#) and [phreg](#).

## Examples

```
data(mort)
oldpar <- par(mfrow = c(2, 2))
fit.cr <- coxreg(Surv(enter, exit, event) ~ ses, data = mort)
fit.w <- phreg(Surv(enter, exit, event) ~ ses, data = mort)
fit.g <- phreg(Surv(enter, exit, event) ~ ses, data = mort,
  dist = "gompertz")
fit.ev <- phreg(Surv(enter, exit, event) ~ ses, data = mort,
  dist = "ev")
check.dist(fit.cr, fit.w)
```

```
check.dist(fit.cr, fit.g)
check.dist(fit.cr, fit.ev)
par(oldpar)
```

---

check.surv

---

*Check the integrity of survival data.*


---

## Description

Check that exit occurs after enter, that spells from an individual do not overlap, and that each individual experiences at most one event.

## Usage

```
check.surv(enter, exit, event, id = NULL, eps = 1e-08)
```

## Arguments

enter	Left truncation time.
exit	Time of exit.
event	Indicator of event. Zero means 'no event'.
id	Identification of individuals.
eps	The smallest allowed spell length or overlap.

## Details

Interval lengths must be strictly positive.

## Value

A vector of id's for the insane individuals. Of zero length if no errors.

## Author(s)

Göran Broström

## See Also

[join.spells](#), [coxreg](#), [aftreg](#)

## Examples

```
xx <- data.frame(enter = c(0, 1), exit = c(1.5, 3), event = c(0, 1), id =
c(1,1))
check.surv(xx$enter, xx$exit, xx$event, xx$id)
```

---

child

*Child mortality, Skellefteå, Sweeden 1850–1900.*


---

**Description**

Children born in Skellefteå, Sweden, 1850-1884, are followed fifteen years or until death or out-migration.

**Usage**

```
data(child)
```

**Format**

A data frame with 26855 children born 1850-1884.

id An identification number.

m.id Mother's id.

sex Sex.

socBranch Working branch of family (father).

birthdate Birthdate.

enter Start age of follow-up, always zero.

exit Age of departure, either by death or emigration.

event Type of departure, death = 1, right censoring = 0.

illeg Born out of marriage ("illegitimate")?

m.age Mother's age.

**Details**

The Skellefteå region is a large region in the northern part of Sweden.

**Source**

Data originate from the Centre for Demographic and Ageing Research, Umeå University, Umeå, Sweden, <https://www.umu.se/en/centre-for-demographic-and-ageing-research/>.

**Examples**

```
fit <- coxreg(Surv(enter, exit, event) ~ sex + socBranch, data = child, coxph = TRUE)
summary(fit)
```

---

compHaz*Graphical comparison of cumulative hazards*

---

**Description**

Comparison of the estimated baseline cumulative hazards functions for two survival models.

**Usage**

```
compHaz(  
  fit1,  
  fit2,  
  main = NULL,  
  lty = 1:2,  
  col = c("red", "blue"),  
  printLegend = TRUE  
)
```

**Arguments**

fit1	An object of type "coxreg", "phreg", or other output from survival fitters.
fit2	An object of type "coxreg", "phreg", or other output from survival fitters.
main	Header for the plot. Default is NULL.
lty	line types.
col	Line colors. should be NULL (black lines) or of length 2.
printLegend	Should a legend be printed? Default is TRUE.

**Value**

No return value.

**Author(s)**

Göran Broström

**See Also**

[hazards](#), [coxreg](#), and [phreg](#).

**Examples**

```
fit.cr <- coxreg(Surv(enter, exit, event) ~ sex, data = oldmort)  
fit.w <- phreg(Surv(enter, exit, event) ~ sex, data = oldmort)  
compHaz(fit.cr, fit.w)
```

---

coxfunk*Loglikelihood function (partial likelihood) of a Cox regression*

---

**Description**

Calculates minus the log likelihood function and its first and second order derivatives for data from a Cox regression model. It is used by coxreg if the argument coxph = FALSE

**Usage**

```
coxfunk(beta, X, offset, rs, what = 2)
```

**Arguments**

beta	Regression parameters
X	The design (covariate) matrix.
offset	Offset.
rs	Risk set created by risksets(..., collate_sets = TRUE)
what	what = 0 means only loglikelihood, 1 means score vector as well, 2 loglikelihood, score and hessian.

**Details**

Note that the function returns log likelihood, score vector and minus hessian, i.e. the observed information. The model is

**Value**

A list with components

loglik	The log likelihood.
dloglik	The score vector. Nonzero if what >= 1
d2loglik	The hessian. Nonzero if ord >= 2

**Author(s)**

Göran Broström

**See Also**

[coxreg](#)

coxreg

*Cox regression***Description**

Performs Cox regression with some special attractions, especially *sampling of risksets* and *the weird bootstrap*.

**Usage**

```
coxreg(formula = formula(data), data = parent.frame(), weights,
subset, t.offset, na.action = getOption("na.action"), init = NULL, method =
c("efron", "breslow", "mppl", "ml"), control = list(eps = 1e-08, maxiter =
25, trace = FALSE), singular.ok = TRUE, model = FALSE, center = NULL, x =
FALSE, y = TRUE, hazards = NULL, boot = FALSE, efrac = 0, geometric = FALSE,
rs = NULL, frailty = NULL, max.survs = NULL, coxph = 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.
data	a data.frame in which to interpret the variables named in the formula.
weights	Case weights; time-fixed or time-varying.
subset	An optional vector specifying a subset of observations to be used in the fitting process.
t.offset	Case offsets; time-varying.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
init	vector of initial values of the iteration. Default initial value is zero for all variables.
method	Method of treating ties, "efron" (default), "breslow", "mppl" (maximum partial partial likelihood), or "ml" (maximum likelihood).
control	a list with components eps (convergence criterion), maxiter (maximum number of iterations), and silent (logical, controlling amount of output). You can change any component without mention the other(s).
singular.ok	Not used
model	Not used
center	deprecated. See Details.
x	Return the design matrix in the model object?
y	return the response in the model object?
hazards	deprecated. Was: Calculate baseline hazards? Default is TRUE. Calculating hazards is better done separately, after fitting. In most cases.



boot	Number of boot replicates. Defaults to FALSE, no boot samples.
efrac	Upper limit of fraction failures in 'mopl'.
geometric	If TRUE, forces an 'ml' model with constant riskset probability. Default is FALSE.
rs	Risk set?
frailty	Grouping variable for frailty analysis. Not in use (yet).
max.survs	Sampling of risk sets? If given, it should be (the upper limit of) the number of survivors in each risk set.
coxph	Logical, defaults to TRUE. Determines if standard work should be passed to <a href="#">coxph</a> via entry points.

### Details

The default method, efron, and the alternative, breslow, are both the same as in [coxph](#) in package survival. The methods mopl and ml are maximum likelihood, discrete-model, based.

### Value

A list of class c("coxreg", "coxph") with components

coefficients	Fitted parameter estimates.
var	Covariance matrix of the estimates.
loglik	Vector of length two; first component is the value at the initial parameter values, the second component is the maximized value.
score	The score test statistic (at the initial value).
linear.predictors	The estimated linear predictors.
residuals	The martingale residuals.
hazards	The estimated baseline hazards, calculated at the value zero of the covariates (rather, columns of the design matrix). Is a list, with one component per stratum. Each component is a matrix with two columns, the first contains risk times, the second the corresponding hazard atom.
means	Means of the columns of the design matrix corresponding to covariates, if center = TRUE. Columns corresponding to factor levels give a zero in the corresponding position in means. If center = FALSE, means are all zero.
w.means	Weighted (against exposure time) means of covariates; weighted relative frequencies of levels of factors.
n	Number of spells in indata (possibly after removal of cases with NA's).
n.events	Number of events in data.
terms	Used by extractor functions.
assign	Used by extractor functions.
y	The Surv vector.
isF	Logical vector indicating the covariates that are factors.

covars	The covariates.
ttr	Total Time at Risk.
levels	List of levels of factors.
formula	The calling formula.
bootstrap	The (matrix of) bootstrap replicates, if requested on input. It is up to the user to do whatever desirable with this sample.
call	The call.
method	The method.
n.strata	Number of strata.
convergence	Did the optimization converge?
fail	Did the optimization fail? (Is NULL if not).

### Warning

The use of `rs` is dangerous, see note. It can however speed up computing time considerably for huge data sets.

### Note

This function starts by creating risksets, if no riskset is supplied via `rs`, with the aid of [risksets](#). Supplying output from `risksets` via `rs` fails if there are any NA's in the data! Note also that it depends on stratification, so `rs` contains information about stratification. Giving another strata variable in the formula is an error. The same is ok, for instance to supply stratum interactions.

### Author(s)

Göran Broström

### References

Broström, G. and Lindkvist, M. (2008). Partial partial likelihood. Communications in Statistics: Simulation and Computation 37:4, 679-686.

### See Also

[coxph](#), [risksets](#)

### Examples

```
dat <- data.frame(time= c(4, 3,1,1,2,2,3),
                  status=c(1,1,1,0,1,1,0),
                  x=     c(0, 2,1,1,1,0,0),
                  sex=   c(0, 0,0,0,1,1,1))
coxreg( Surv(time, status) ~ x + strata(sex), data = dat) #stratified model
# Same as:
rs <- risksets(Surv(dat$time, dat$status), strata = dat$sex)
coxreg( Surv(time, status) ~ x, data = dat, rs = rs) #stratified model
```

coxreg.fit

*Cox regression***Description**

Called by `coxreg`, but a user can call it directly.

**Usage**

```
coxreg.fit(
  X,
  Y,
  rs,
  weights,
  t.offset = NULL,
  strats,
  offset,
  init,
  max.survs,
  method = "efron",
  boot = FALSE,
  efrac = 0,
  calc.martres = TRUE,
  control,
  verbose = TRUE,
  calc.hazards = NULL,
  center = NULL
)
```

**Arguments**

<code>X</code>	The design matrix.
<code>Y</code>	The survival object.
<code>rs</code>	The risk set composition. If absent, calculated.
<code>weights</code>	Case weights; time-fixed or time-varying.
<code>t.offset</code>	Case offset; time-varying.
<code>strats</code>	The stratum variable. Can be absent.
<code>offset</code>	Offset. Can be absent.
<code>init</code>	Start values. If absent, equal to zero.
<code>max.survs</code>	Sampling of risk sets? If so, gives the maximum number of survivors in each risk set.
<code>method</code>	Either "efron" (default) or "breslow".
<code>boot</code>	Number of bootstrap replicates. Defaults to FALSE, no bootstrapping.
<code>efrac</code>	Upper limit of fraction failures in 'mppl'.

calc.martres	Should martingale residuals be calculated?
control	See <a href="#">coxreg</a>
verbose	Should Warnings about convergence be printed?
calc.hazards	Deprecated. See <a href="#">coxreg</a> .
center	Deprecated. See <a href="#">coxreg</a> .

### Details

rs is dangerous to use when NA's are present.

### Value

A list with components

coefficients	Estimated regression parameters.
var	Covariance matrix of estimated coefficients.
loglik	First component is value at init, second at maximum.
score	Score test statistic, at initial value.
linear.predictors	Linear predictors.
residuals	Martingale residuals.
hazard	Estimated baseline hazard. At value zero of design variables.
means	Means of the columns of the design matrix.
bootstrap	The bootstrap replicates, if requested on input.
conver	TRUE if convergence.
f.conver	TRUE if variables converged.
fail	TRUE if failure.
iter	Number of performed iterations.

### Note

It is the user's responsibility to check that indata is sane.

### Author(s)

Göran Broström

### See Also

[coxreg](#), [risksets](#)

## Examples

```
X <- as.matrix(data.frame(
  x=      c(0, 2,1,4,1,0,3),
  sex=    c(1, 0,0,0,1,1,1)))
time <- c(1,2,3,4,5,6,7)
status <- c(1,1,1,0,1,1,0)
stratum <- rep(1, length(time))

coxreg.fit(X, Surv(time, status), strats = stratum, max.survs = 6,
  control = list(eps=1.e-4, maxiter = 10, trace = FALSE))
```

---

coxreg2

Cox regression

---

## Description

Performs Cox regression with some special attractions, especially *sampling of risksets* and *the weird bootstrap*.

## Usage

```
coxreg2(formula = formula(data), data = parent.frame(), weights,
subset, t.offset, na.action = getOption("na.action"), init = NULL, method =
c("efron", "breslow", "mppl", "ml"), control = list(eps = 1e-08, maxiter =
25, trace = FALSE), singular.ok = TRUE, model = FALSE, center = NULL, x =
FALSE, y = TRUE, hazards = NULL, boot = FALSE, efrac = 0, geometric = FALSE,
rs = NULL, frailty = NULL, max.survs = NULL, coxph = 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.
data	a data.frame in which to interpret the variables named in the formula.
weights	Case weights; time-fixed or time-varying.
subset	An optional vector specifying a subset of observations to be used in the fitting process.
t.offset	Case offsets; time-varying.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
init	vector of initial values of the iteration. Default initial value is zero for all variables.
method	Method of treating ties, "efron" (default), "breslow", "mppl" (maximum partial partial likelihood), or "ml" (maximum likelihood).

<code>control</code>	a list with components <code>eps</code> (convergence criterion), <code>maxiter</code> (maximum number of iterations), and <code>silent</code> (logical, controlling amount of output). You can change any component without mention the other(s).
<code>singular.ok</code>	Not used
<code>model</code>	Not used
<code>center</code>	deprecated. See Details.
<code>x</code>	Return the design matrix in the model object?
<code>y</code>	return the response in the model object?
<code>hazards</code>	deprecated. Was: Calculate baseline hazards? Default is TRUE. Calculating hazards is better done separately, after fitting. In most cases.
<code>boot</code>	Number of boot replicates. Defaults to FALSE, no boot samples.
<code>efrac</code>	Upper limit of fraction failures in 'mppl'.
<code>geometric</code>	If TRUE, forces an 'ml' model with constant riskset probability. Default is FALSE.
<code>rs</code>	Risk set?
<code>frailty</code>	Grouping variable for frailty analysis. Not in use (yet).
<code>max.survs</code>	Sampling of risk sets? If given, it should be (the upper limit of) the number of survivors in each risk set.
<code>coxph</code>	Logical, defaults to TRUE. Determines if standard work should be passed to <a href="#">coxph</a> via entry points.

## Details

The default method, `efron`, and the alternative, `breslow`, are both the same as in [coxph](#) in package `survival`. The methods `mppl` and `ml` are maximum likelihood, discrete-model, based.

## Value

A list of class `c("coxreg", "coxph")` with components

<code>coefficients</code>	Fitted parameter estimates.
<code>var</code>	Covariance matrix of the estimates.
<code>loglik</code>	Vector of length two; first component is the value at the initial parameter values, the second component is the maximized value.
<code>score</code>	The score test statistic (at the initial value).
<code>linear.predictors</code>	The estimated linear predictors.
<code>residuals</code>	The martingale residuals.
<code>hazards</code>	The estimated baseline hazards, calculated at the value zero of the covariates (rather, columns of the design matrix). Is a list, with one component per stratum. Each component is a matrix with two columns, the first contains risk times, the second the corresponding hazard atom.

means	Means of the columns of the design matrix corresponding to covariates, if center = TRUE. Columns corresponding to factor levels give a zero in the corresponding position in means. If center = FALSE, means are all zero.
w.means	Weighted (against exposure time) means of covariates; weighted relative frequencies of levels of factors.
n	Number of spells in indata (possibly after removal of cases with NA's).
n.events	Number of events in data.
terms	Used by extractor functions.
assign	Used by extractor functions.
y	The Surv vector.
isF	Logical vector indicating the covariates that are factors.
covars	The covariates.
ttr	Total Time at Risk.
levels	List of levels of factors.
formula	The calling formula.
bootstrap	The (matrix of) bootstrap replicates, if requested on input. It is up to the user to do whatever desirable with this sample.
call	The call.
method	The method.
n.strata	Number of strata.
convergence	Did the optimization converge?
fail	Did the optimization fail? (Is NULL if not).

### Warning

The use of `rs` is dangerous, see note. It can however speed up computing time considerably for huge data sets.

### Note

This function starts by creating risksets, if no riskset is supplied via `rs`, with the aid of [risksets](#). Supplying output from `risksets` via `rs` fails if there are any NA's in the data! Note also that it depends on stratification, so `rs` contains information about stratification. Giving another strata variable in the formula is an error. The same is ok, for instance to supply stratum interactions.

### Author(s)

Göran Broström

### References

Broström, G. and Lindkvist, M. (2008). Partial partial likelihood. Communications in Statistics: Simulation and Computation 37:4, 679-686.

**See Also**[coxph](#), [risksets](#)**Examples**

```

dat <- data.frame(time= c(4, 3,1,1,2,2,3),
                  status=c(1,1,1,0,1,1,0),
                  x=     c(0, 2,1,1,1,0,0),
                  sex=   c(0, 0,0,0,1,1,1))
coxreg( Surv(time, status) ~ x + strata(sex), data = dat) #stratified model
# Same as:
rs <- risksets(Surv(dat$time, dat$status), strata = dat$sex)
coxreg( Surv(time, status) ~ x, data = dat, rs = rs) #stratified model

```

cro

*Creates a minimal representation of a data frame.***Description**

Given a data frame with a defined response variable, this function creates a unique representation of the covariates in the data frame, vector (matrix) of responses, and a pointer vector, connecting the responses with the corresponding covariates.

**Usage**

```
cro(dat, response = 1)
```

**Arguments**

dat	A data frame
response	The column(s) where the response resides.

**Details**

The rows in the data frame are converted to text strings with `paste` and compared with `match`.

**Value**

A list with components

y	The response.
covar	A data frame with unique rows of covariates.
keys	Pointers from y to covar, connecting each response with its covariate vector.

**Note**

This function is based on suggestions by Anne York and Brian Ripley.



**Author(s)**

Göran Broström

**See Also**[match](#), [paste](#)**Examples**

```
dat <- data.frame(y = c(1.1, 2.3, 0.7), x1 = c(1, 0, 1), x2 = c(0, 1, 0))
cro(dat)
```

EV

*The EV Distribution***Description**

Density, distribution function, quantile function, hazard function, cumulative hazard function, and random generation for the EV distribution with parameters shape and scale.

**Usage**

```
dEV(x, shape = 1, scale = 1, log = FALSE)
pEV(q, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)
qEV(p, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)
hEV(x, shape = 1, scale = 1, log = FALSE)
HEV(x, shape = 1, scale = 1, log.p = FALSE)
rEV(n, shape = 1, scale = 1)
```

**Arguments**

shape, scale	shape and scale parameters, both defaulting to 1.
lower.tail	logical; if TRUE (default), probabilities are $P(X \leq x)$ , otherwise, $P(X > x)$ .
x, q	vector of quantiles.
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$ , the length is taken to be the number required.
log, log.p	logical; if TRUE, probabilities p are given as $\log(p)$ .

**Details**

The EV distribution with scale parameter  $a$  and shape parameter  $\sigma$  has hazard function given by

$$h(x) = (b/\sigma)(x/\sigma)^{b-1} \exp(-(x/\sigma)^b)$$

for  $x \geq 0$ .

**Value**

dEV gives the density, pEV gives the distribution function, qEV gives the quantile function, hEV gives the hazard function, HEV gives the cumulative hazard function, and rEV generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

---

 fert

---

*Marital fertility nineteenth century*


---

**Description**

Birth intervals for married women with at least one birth, 19th northern Sweden

**Usage**

```
data(fert)
```

**Format**

A data frame with 12169 observations the lengths (in years) of birth intervals for 1859 married women with at least one birth. The first interval (`parity = 0`) is the interval from marriage to first birth.

`id` Personal identification number for mother.

`parity` Time order of birth interval for the present mother. The interval with `parity = 0` is the first, from marriage to first birth.

`age` The age of mother at start of interval.

`year` The calendar year at start of interval.

`next.ivl` The length of the coming time interval.

`event` An indicator for whether the `next.ivl` ends in a new birth (`event = 1`) or is right censored (`event = 0`). Censoring occurs when the woman ends her fertility period within her first marriage (marriage dissolution or reaching the age of 48).

`prev.ivl` The length of the previous time interval. May be used as explanatory variable in a Cox regression of birth intervals.

`ses` Socio-economic status, a factor with levels lower, upper, farmer, and unknown.

`parish` The Skelleftea region consists of three parishes, Jorn, Norsjo, and Skelleftea.

**Details**

The data set contain clusters of dependent observations defined by mother's id.

**Source**

Data is coming from The Demographic Data Base, Umea University, Umea, Sweden.

## References

<https://www.umu.se/enheten-for-demografi-och-aldrandeforskning/>

## Examples

```
data(fert)
fit <- coxreg(Surv(next.ivl, event) ~ ses + prev.ivl, data = fert, subset =
  (parity == 1))
summary(fit)
```

---

frail.fit	<i>Frailty experiment</i>
-----------	---------------------------

---

## Description

Utilizing GLMM models: Experimental, not exported (yet).

## Usage

```
frail.fit(X, Y, rs, strats, offset, init, max.survs, frailty, control)
```

## Arguments

X	design matrix
Y	survival object
rs	output from <a href="#">risksets</a>
strats	strata
offset	offset
init	start values
max.survs	for sampling of riskset survivors
frailty	grouping variable
control	control of optimization

---

`geome.fit`*Constant intensity discrete time proportional hazards*

---

**Description**

This function is called from `coxreg`. A user may call it directly.

**Usage**

```
geome.fit(X, Y, rs, strats, offset, init, max.survs, method = "ml", control)
```

**Arguments**

<code>X</code>	The design matrix
<code>Y</code>	Survival object
<code>rs</code>	risk set produced by <a href="#">risksets</a>
<code>strats</code>	Stratum indicator
<code>offset</code>	Offset
<code>init</code>	Initial values
<code>max.survs</code>	Maximal survivors
<code>method</code>	"ml", always, i.e., this argument is ignored.
<code>control</code>	See <code>coxreg</code> .

**Value**

See the code.

**Note**

Nothing special  
`coxreg` is a defunct function

**Author(s)**

Göran Broström

**References**

See [coxreg](#).

**See Also**

[coxreg](#)

**Description**

Density, distribution function, quantile function, hazard function, cumulative hazard function, and random generation for the Gompertz distribution with parameters shape and scale.

**Usage**

```
dgompertz(x, shape = 1, scale = 1, rate, log = FALSE,
param = c("default", "canonical", "rate"))
pgompertz(q, shape = 1, scale = 1, rate, lower.tail = TRUE, log.p = FALSE,
param = c("default", "canonical", "rate"))
qgompertz(p, shape = 1, scale = 1, rate, lower.tail = TRUE, log.p = FALSE,
param = c("default", "canonical", "rate"))
hgompertz(x, shape = 1, scale = 1, rate, log = FALSE,
param = c("default", "canonical", "rate"))
Hgompertz(x, shape = 1, scale = 1, rate, log.p = FALSE,
param = c("default", "canonical", "rate"))
rgompertz(n, shape = 1, scale = 1, rate,
param = c("default", "canonical", "rate"))
```

**Arguments**

shape, scale	shape and scale parameters, both defaulting to 1.
rate	the rate parameter for that parametrization, replaces scale.
lower.tail	logical; if TRUE (default), probabilities are $P(X \leq x)$ , otherwise, $P(X > x)$ .
param	default or canonical or rate.
x, q	vector of quantiles.
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$ , the length is taken to be the number required.
log, log.p	logical; if TRUE, probabilities p are given as $\log(p)$ .

**Details**

The Gompertz distribution with scale parameter  $a$  and shape parameter  $\sigma$  has hazard function given by

$$h(x) = a \exp(x/\sigma)$$

for  $x \geq 0$ . If `param = "canonical"`, then then  $a \rightarrow a/b$ , so that  $b$  is a true scale parameter (for any fixed  $a$ ), and  $b$  is an 'AFT parameter'. If `param = "rate"`, then  $b \rightarrow 1/b$ .

**Value**

dgompertz gives the density, pgompertz gives the distribution function, qgompertz gives the quantile function, hgompertz gives the hazard function, Hgompertz gives the cumulative hazard function, and rgompertz generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

---

hazards	<i>Get baseline hazards atoms from fits from</i>
---------	--

---

**Description**

Get baseline hazards atoms from fits from

**Usage**

```
hazards(x, cum = TRUE, ...)
```

**Arguments**

x	A reg object.
cum	Logical: Should the cumulative hazards be returned?
...	Additional arguments for various methods.

**Value**

A list where each component is a two-column matrix representing hazard atoms from one stratum. The first column is event time, and the second column is the corresponding hazard atom.

---

HiscoHisclass	<i>HISCO to HISCLASS transformation</i>
---------------	---

---

**Description**

HISCO to HISCLASS transformation

**Usage**

```
HiscoHisclass(hisco, status = NULL, relation = NULL, urban = NULL,
debug = FALSE)
```

**Arguments**

hisco	Hisco codes to be transformed to hisclass.
status	Optional standard description of status.
relation	Relation between owner of occupation and self.
urban	Logical, "Is residence in an urban area?"
debug	Logical, prints intermediate values if TRUE.

**Value**

A vector of hisclass codes, same length as input hisco.

**Author(s)**

Göran Broström with translation and modification of a Stata do.

**References**

Van Leeuwen, M. and Maas, I. (2011). HISCLASS. A Historical International Social Class Scheme. Leuven University Press.

---

import_strata	<i>strata function imported from survival</i>
---------------	---

---

**Description**

This function is imported from the survival package. See [strata](#).

---

import_Surv	<i>Surv function imported from survival</i>
-------------	---

---

**Description**

This function is imported from the survival package. See [Surv](#).

---

infants

*Infant mortality and maternal death, Sweeden 1821–1894.*


---

### Description

Matched data on infant mortality, from seven parishes in Sweden, 1821–1894.

### Usage

```
data(infants)
```

### Format

A data frame with 80 rows and five variables.

**stratum** Triplet No. Each triplet consist of one infant whose mother died (a case), and two controls, i.e, infants whose mother did not die. Matched on covariates below.

**enter** Age (in days) of case when its mother died.

**exit** Age (in days) at death or right censoring (at age 365 days).

**event** Follow-up ends with death (1) or right censoring (0).

**mother** dead for cases, alive for controls.

**age** Mother's age at infant's birth.

**sex** The infant's sex.

**parish** Birth parish, either Nedertornea or not Nedertornea.

**civst** Civil status of mother, married or unmarried.

**ses** Socio-economic status of mother, either farmer or not farmer.

**year** Year of birth of the infant.

### Details

From 5641 first-born in seven Swedish parishes 1820-1895, from Fleninge in the very south to Nedertorneå in the very north, those whose mother died during their first year of life were selected, in all 35 infants. To each of them, two controls were selected by matching on the given covariates.

### Source

Data originate from The Demographic Data Base, Umeå University, Umeå, Sweden, <https://www.umu.se/enheten-for-demografi-och-aldrandeforskning/>.

### References

Broström, G. (1987). The influence of mother's death on infant mortality: A case study in matched data survival analysis. *Scandinavian Journal of Statistics* 14, 113-123.



**Examples**

```
data(infants)
fit <- coxreg(Surv(enter, exit, event) ~ strata(stratum) + mother, data = infants)
fit
fit.w <- phreg(Surv(enter, exit, event) ~ mother + parish + ses, data = infants)
summary(fit.w) ## Weibull proportional hazards model.
```

---

join.spells

*Straighten up a survival data frame*


---

**Description**

Unnecessary cut spells are glued together, overlapping spells are "polished", etc.

**Usage**

```
join.spells(dat, strict = FALSE, eps = 1e-08)
```

**Arguments**

dat	A data frame with names enter, exit, event, id.
strict	If TRUE, nothing is changed if errors in spells (non-positive length, overlapping intervals, etc.) are detected. Otherwise (the default), bad spells are removed, with "earlier life" having higher priority.
eps	Tolerance for equality of two event times. Should be kept small.

**Details**

In case of overlapping intervals (i.e., a data error), the appropriate id's are returned if strict is TRUE.

**Value**

A data frame with the same variables as the input, but individual spells are joined, if possible (identical covariate values, and adjacent time intervals).

**Author(s)**

Göran Broström

**References**

Therneau, T.M. and Grambsch, P.M. (2000). *Modeling Survival Data: Extending the Cox model*. Springer.

**See Also**

[coxreg](#), [aftreg](#), [check.surv](#)

---

Loglogistic

*The Loglogistic Distribution*


---

**Description**

Density, distribution function, quantile function, hazard function, cumulative hazard function, and random generation for the Loglogistic distribution with parameters shape and scale.

**Usage**

```
dllogis(x, shape = 1, scale = 1, log = FALSE)
pllogis(q, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)
qllogis(p, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)
hllogis(x, shape = 1, scale = 1, prop = 1, log = FALSE)
Hllogis(x, shape = 1, scale = 1, prop = 1, log.p = FALSE)
rllogis(n, shape = 1, scale = 1)
```

**Arguments**

shape, scale	shape and scale parameters, both defaulting to 1.
lower.tail	logical; if TRUE (default), probabilities are $P(X \leq x)$ , otherwise, $P(X > x)$ .
x, q	vector of quantiles.
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$ , the length is taken to be the number required.
log, log.p	logical; if TRUE, probabilities p are given as $\log(p)$ .
prop	proportionality constant in the extended Loglogistic distribution.

**Details**

The Loglogistic distribution with scale parameter  $a$  and shape parameter  $\sigma$  has hazard function given by

$$h(x) = (b/\sigma)(x/\sigma)^{b-1} \exp(-(x/\sigma)^b)$$

for  $x \geq 0$ .

**Value**

dllogis gives the density, pllogis gives the distribution function, qllogis gives the quantile function, hllogis gives the hazard function, Hllogis gives the cumulative hazard function, and rllogis generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

**Description**

Density, distribution function, quantile function, hazard function, cumulative hazard function, and random generation for the Lognormal distribution with parameters shape and scale.

**Usage**

```
hlnorm(x, meanlog = 0, sdlog = 1, shape = 1 / sdlog, scale = exp(meanlog),
prop = 1, log = FALSE)
Hlnorm(x, meanlog = 0, sdlog = 1, shape = 1 / sdlog, scale = exp(meanlog),
prop = 1, log.p = FALSE)
```

**Arguments**

x	vector of quantiles.
meanlog	mean in the Normal distribution.
sdlog, shape	sdlog is standard deviation in the Normal distribution, shape = 1/sdlog.
scale	is exp(meanlog).
prop	proportionality constant in the extended Lognormal distribution.
log, log.p	logical; if TRUE, probabilities p are given as log(p).

**Details**

The Lognormal distribution with scale parameter  $a$  and shape parameter  $\sigma$  has hazard function given by

$$h(x) = (b/\sigma)(x/\sigma)^{b-1} \exp(-(x/\sigma)^b)$$

for  $x \geq 0$ .

**Value**

dlnorm gives the density, plnorm gives the distribution function, qlnorm gives the quantile function, hlnorm gives the hazard function, Hlnorm gives the cumulative hazard function, and rlnorm generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

---

`logrank`*The Log-rank test*

---

**Description**

Performs the log-rank test on survival data, possibly stratified.

**Usage**

```
logrank(Y, group, data = parent.frame())
```

**Arguments**

<code>Y</code>	a survival object as returned by the <a href="#">Surv</a> function.
<code>group</code>	defines the groups to be compared. Coerced to a factor.
<code>data</code>	a <code>data.frame</code> in which to interpret the variables.

**Value**

A list of class `logrank` with components

<code>test.statistic</code>	The logrank (score) test statistic.
<code>df</code>	The degrees of freedom of the test statistic.
<code>p.value</code>	The p value of the test.
<code>hazards</code>	A list of two-column matrices, describing event times and corresponding hazard atoms in each stratum (class <code>'hazdata'</code> ).
<code>call</code>	The call

**Note**

The test is performed by fitting a Cox regression model and reporting its score test. With tied data, this might be slightly different from the true logrank test, but the difference is unimportant in practice.

**Author(s)**

Göran Broström

**See Also**

[coxreg](#), [print.logrank](#).

**Examples**

```
fit <- logrank(Y = Surv(enter, exit, event), group = civ,  
data = oldmort[oldmort$region == "town", ])  
fit
```

---

`logrye`*Rye prices, Scania, southern Sweden, 1801-1894.*

---

**Description**

The data consists of yearly rye prices from 1801 to 1894. Logged and detrended, so the time series is supposed to measure short term fluctuations in rye prices.

**Usage**

```
data(scania)
```

**Format**

A data frame with 94 observations in two columns on the following 2 variables.

`year` The year the price is recorded.

`foodprices` Detrended log rye prices.

**Details**

The Scanian area in southern Sweden was during the 19th century a mainly rural area.

**Source**

The Scanian Economic Demographic Database.

**References**

Jörberg, L. (1972). A History of Prices in Sweden 1732-1914, CWK Gleerup, Lund.

**Examples**

```
data(logrye)
summary(logrye)
```

ltx

*LaTeX printing of regression results.***Description**

This (generic) function prints the LaTeX code of the results of a fit from [coxreg](#), [phreg](#), [tpchreg](#), or [aftreg](#), similar to what `xtable` does for fits from other functions.

**Usage**

```
ltx(
  x,
  caption = NULL,
  label = NULL,
  dr = NULL,
  digits = max(options()$digits - 4, 3),
  ...
)
```

**Arguments**

<code>x</code>	The output from a call to <code>coxreg</code> , <code>tpchreg</code> , or <code>aftreg</code>
<code>caption</code>	A suitable caption for the table.
<code>label</code>	A label used in the LaTeX code.
<code>dr</code>	Output from a <code>drop1</code> call.
<code>digits</code>	Number of digits to be printed.
<code>...</code>	Not used.

**Details**

The result is a printout which is (much) nicer than the standard printed output from `glm` and friends,

**Value**

LaTeX code version of the results from a run with [coxreg](#), [phreg](#), [phreg](#), or [aftreg](#).

**Note**

For printing confidence limits, use [ltx2](#).

**Author(s)**

Göran Broström.

**See Also**

[ltx2](#), [coxreg](#), [phreg](#), [phreg](#), and [aftreg](#).

## Examples

```
data(oldmort)
fit <- coxreg(Surv(enter, exit, event) ~ civ + sex, data = oldmort)
dr <- drop1(fit, test = "Chisq")
ltx(fit, dr = dr, caption = "A test example.", label = "tab:test1")
```

---

ltx2

*LaTeX alternative printing of regression results.*


---

## Description

This (generic) function prints the LaTeX code of the results of a fit from [coxreg](#), [phreg](#), [tpchreg](#), or [aftreg](#).

## Usage

```
ltx2(
  x,
  caption = NULL,
  label = NULL,
  dr = NULL,
  digits = max(options()$digits - 4, 4),
  conf = 0.95,
  keep = NULL,
  ...
)
```

## Arguments

<code>x</code>	The output from a call to <code>coxreg</code> , <code>tpchreg</code> , or <code>aftreg</code>
<code>caption</code>	A suitable caption for the table.
<code>label</code>	A label used in the LaTeX code.
<code>dr</code>	Output from a <code>drop1</code> call.
<code>digits</code>	Number of digits to be printed.
<code>conf</code>	Confidence intervals level.
<code>keep</code>	Number of covariates to present.
<code>...</code>	Not used.

## Value

LaTeX code version of the results from a run with [coxreg](#), [phreg](#), [phreg](#), [aftreg](#).

**Note**

Resulting tables contain estimated hazard ratios and confidence limits instead of regression coefficients and standard errors as in [ltx](#).

**Author(s)**

Göran Broström.

**See Also**

[xtable](#), [coxreg](#), [phreg](#), [phreg](#), [aftreg](#), and [ltx](#).

**Examples**

```
data(oldmort)
fit <- coxreg(Surv(enter, exit, event) ~ sex, data = oldmort)
ltx2(fit, caption = "A test example.", label = "tab:test1")
```

---

make.communal

---

*Put communals in "fixed" data frame*


---

**Description**

Given an ordinary data frame suitable for survival analysis, and a data frame with "communal" time series, this function includes the communal covariates as fixed, by the "cutting spells" method.

**Usage**

```
make.communal(
  dat,
  com.dat,
  communal = TRUE,
  start,
  period = 1,
  lag = 0,
  surv = c("enter", "exit", "event", "birthdate"),
  tol = 1e-04,
  fortran = TRUE
)
```

**Arguments**

dat	A data frame containing interval specified survival data and covariates, of which one must give a "birth date", the connection between duration and calendar time
com.dat	Data frame with communal covariates. They must have the same start year and periodicity, given by start and lag.



communal	Boolean; if TRUE, then it is a true communal (default), otherwise a fixed. The first component is the first year (start date in decimal form), and the second component is the period length. The third is lag and the fourth is scale.
start	Start date in decimal form.
period	Period length. Defaults to one.
lag	The lag of the effect. Defaults to zero.
surv	Character vector of length 4 giving the names of interval start, interval end, event indicator, birth date, in that order. These names must correspond to names in dat
tol	Largest length of an interval considered to be of zero length. The cutting sometimes produces zero length intervals, which we want to discard.
fortran	If TRUE, then a Fortran implementation of the function is used. This is the default. This possibility is only for debugging purposes. You should of course get identical results with the two methods.

### Details

The main purpose of this function is to prepare a data file for use with [coxreg](#), [aftreg](#), and [coxph](#).

### Value

The return value is a data frame with the same variables as in the combination of dat and com.dat. Therefore it is an error to have common name(s) in the two data frames.

### Note

Not very vigorously tested.

### Author(s)

Göran Broström

### See Also

[coxreg](#), [aftreg](#), [coxph](#), [cal.window](#)

### Examples

```
dat <- data.frame(enter = 0, exit = 5.731, event = 1,
  birthdate = 1962.505, x = 2)
## Birth date: July 2, 1962 (approximately).
com.dat <- data.frame(price = c(12, 3, -5, 6, -8, -9, 1, 7))
dat.com <- make.communal(dat, com.dat, start = 1962.000)
```

**Description**

Density, distribution function, quantile function, hazard function, cumulative hazard function, and random generation for the Gompertz-Makeham distribution with parameters shape and scale.

**Usage**

```
dmakeham(x, shape = c(1, 1), scale = 1, log = FALSE)
pmakeham(q, shape = c(1, 1), scale = 1, lower.tail = TRUE, log.p = FALSE)
qmakeham(p, shape = c(1, 1), scale = 1, lower.tail = TRUE, log.p = FALSE)
hmakeham(x, shape = c(1, 1), scale = 1, log = FALSE)
Hmakeham(x, shape = c(1, 1), scale = 1, log.p = FALSE)
rmakeham(n, shape = c(1, 1), scale = 1)
```

**Arguments**

shape	A vector, default value c(1, 1).
scale	defaulting to 1.
lower.tail	logical; if TRUE (default), probabilities are $P(X \leq x)$ , otherwise, $P(X > x)$ .
x, q	vector of quantiles.
p	vector of probabilities.
n	number of observations. If length(n) > 1, the length is taken to be the number required.
log, log.p	logical; if TRUE, probabilities p are given as log(p).

**Details**

The Gompertz-Makeham distribution with shape parameter  $a$  and scale parameter  $\sigma$  has hazard function given by

$$h(x) = a[2] + a[1] \exp(x/\sigma)$$

for  $x \geq 0$ .

**Value**

dmakeham gives the density, pmakeham gives the distribution function, qmakeham gives the quantile function, hmakeham gives the hazard function, Hmakeham gives the cumulative hazard function, and rmakeham generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

---

male.mortality	<i>Male mortality in ages 40-60, nineteenth century</i>
----------------	---

---

**Description**

Males born in the years 1800-1820 and surviving at least 40 years in the parish Skellefteå in northern Sweden are followed from their fortieth birthday until death or the sixtieth birthday, whichever comes first.

**Usage**

```
data(male.mortality)
```

**Format**

A data frame with 2058 observations on the following 6 variables.

`id` Personal identification number.

`enter` Start of duration. Measured in years since the fortieth birthday.

`exit` End of duration. Measured in years since the fortieth birthday.

`event` a logical vector indicating death at end of interval.

`birthdate` The birthdate in decimal form.

`ses` Socio-economic status, a factor with levels lower, upper

**Details**

The interesting explanatory covariate is `ses` (socioeconomic status), which is a time-varying covariate. This explains why several individuals are represented by more than one record each. Left truncation and right censoring are introduced this way.

**Note**

This data set is also known, and accessible, as `mort`.

**Source**

Data is coming from The Demographic Data Base, Umea University, Umeå, Sweden.

**References**

<https://www.umu.se/enheten-for-demografi-och-aldrandeforskning/>

**Examples**

```
data(male.mortality)
fit <- coxreg(Surv(enter, exit, event) ~ ses, data = male.mortality)
summary(fit)
```

---

mlreg	<i>ML proportional hazards regression</i>
-------	---

---

## Description

Maximum Likelihood estimation of proportional hazards models. Is deprecated, use `coxreg` instead.

## Usage

```
mlreg(
  formula = formula(data),
  data = parent.frame(),
  na.action = getOption("na.action"),
  init = NULL,
  method = c("ML", "MPPL"),
  control = list(eps = 1e-08, maxiter = 10, n.points = 12, trace = FALSE),
  singular.ok = TRUE,
  model = FALSE,
  center = TRUE,
  x = FALSE,
  y = TRUE,
  boot = FALSE,
  geometric = FALSE,
  rs = NULL,
  frailty = NULL,
  max.survs = NULL
)
```

## Arguments

<code>formula</code>	a formula object, with the response on the left of a <code>~</code> operator, and the terms on the right. The response must be a survival object as returned by the <code>Surv</code> function.
<code>data</code>	a <code>data.frame</code> in which to interpret the variables named in the formula.
<code>na.action</code>	a missing-data filter function, applied to the <code>model.frame</code> , after any subset argument has been used. Default is <code>options()\$na.action</code> .
<code>init</code>	vector of initial values of the iteration. Default initial value is zero for all variables.
<code>method</code>	Method of treating ties, "ML", the default, means pure maximum likelihood, i.e, data are treated as discrete. The choice "MPPL" implies that risk sets with no tied events are treated as in ordinary Cox regression. This is a cameleont that adapts to data, part discrete and part continuous.
<code>control</code>	a list with components <code>eps</code> (convergence criterion), <code>maxiter</code> (maximum number of iterations), and <code>silent</code> (logical, controlling amount of output). You can change any component without mention the other(s).

singular.ok	Not used.
model	Not used.
center	Should covariates be centered? Default is TRUE
x	Return the design matrix in the model object?
y	return the response in the model object?
boot	No. of bootstrap replicates. Defaults to FALSE, i.e., no bootstrapping.
geometric	If TRUE, the intensity is assumed constant within strata.
rs	Risk set? If present, speeds up calculations considerably.
frailty	A grouping variable for frailty analysis. Full name is needed.
max.survs	Sampling of risk sets?

### Details

Method ML performs a true discrete analysis, i.e., one parameter per observed event time. Method MPPL is a compromise between the discrete and continuous time approaches; one parameter per observed event time with multiple events. With no ties in data, an ordinary Cox regression (as with [coxreg](#)) is performed.

### Value

A list of class `c("mlreg", "coxreg", "coxph")` with components

coefficients	Fitted parameter estimates.
var	Covariance matrix of the estimates.
loglik	Vector of length two; first component is the value at the initial parameter values, the second component is the maximized value.
score	The score test statistic (at the initial value).
linear.predictors	The estimated linear predictors.
residuals	The martingale residuals.
hazard	The estimated baseline hazard.
means	Means of the columns of the design matrix.
w.means	Weighted (against exposure time) means of covariates; weighted relative frequencies of levels of factors.
n	Number of spells in indata (possibly after removal of cases with NA's).
events	Number of events in data.
terms	Used by extractor functions.
assign	Used by extractor functions.
wald.test	The Walt test statistic (at the initial value).
y	The Surv vector.
isF	Logical vector indicating the covariates that are factors.
covars	The covariates.

ttr	Total Time at Risk.
levels	List of levels of factors.
formula	The calling formula.
call	The call.
bootstrap	The bootstrap sample, if requested on input.
sigma	Present if a frailty model is fitted. Equals the estimated frailty standard deviation.
sigma.sd	The standard error of the estimated frailty standard deviation.
method	The method.
convergence	Did the optimization converge?
fail	Did the optimization fail? (Is NULL if not).

### Warning

The use of `rs` is dangerous, see note above. It can however speed up computing time.

### Note

This function starts by creating risksets, if no riskset is supplied via `rs`, with the aid of [risksets](#). This latter mechanism fails if there are any NA's in the data! Note also that it depends on stratification, so `rs` contains information about stratification. Giving another strata variable in the formula is an error. The same is ok, for instance to supply stratum interactions.

Note further that `mlreg` is deprecated. [coxreg](#) should be used instead.

### Author(s)

Göran Broström

### References

Broström, G. (2002). Cox regression; Ties without tears. *Communications in Statistics: Theory and Methods* **31**, 285–297.

### See Also

[coxreg](#), [risksets](#)

### Examples

```
dat <- data.frame(time= c(4, 3,1,1,2,2,3),
                  status=c(1,1,1,0,1,1,0),
                  x=     c(0, 2,1,1,1,0,0),
                  sex=    c(0, 0,0,0,1,1,1))
mlreg( Surv(time, status) ~ x + strata(sex), data = dat) #stratified model
# Same as:
rs <- risksets(Surv(dat$time, dat$status), strata = dat$sex)
mlreg( Surv(time, status) ~ x, data = dat, rs = rs) #stratified model
```

---

`mort`*Male mortality in ages 40-60, nineteenth century*

---

**Description**

Males born in the years 1800-1820 and surviving at least 40 years in the parish Skellefteå in northern Sweden are followed from their fortieth birthday until death or the sixtieth birthday, whichever comes first.

**Usage**

```
data(mort)
```

**Format**

A data frame with 2058 observations on the following 6 variables.

`id` Personal identification number.

`enter` Start of duration. Measured in years since the fortieth birthday.

`exit` End of duration. Measured in years since the fortieth birthday.

`event` a logical vector indicating death at end of interval.

`birthdate` The birthdate in decimal form.

`ses` Socio-economic status, a factor with levels lower, upper

**Details**

The interesting explanatory covariate is `ses` (socioeconomic status), which is a time-varying covariate. This explains why several individuals are represented by more than one record each. Left truncation and right censoring are introduced this way.

**Note**

This data set is also known, and accessible, as `male.mortality`

**Source**

Data is coming from The Demographic Data Base, Umea University, Umeå, Sweden.

**References**

<https://www.umu.se/enheten-for-demografi-och-aldrandeforskning/>

**Examples**

```
data(mort)
fit <- coxreg(Surv(enter, exit, event) ~ ses, data = mort)
summary(fit)
```

---

oe	Create an oe object
----	---------------------

---

### Description

Create an *oe* ("occurrence/exposure") object, used as a response variable in a model formula specifically in [tpchreg](#).

### Usage

```
oe(count, exposure)
```

### Arguments

count	Number of events, a non-negative integer-valued vector.
exposure	exposure time corresponding to count. A positive numeric vector.

### See Also

[tpchreg](#).

---

oldmort	Old age mortality, Sundsvall, Sweden, 1860-1880.
---------	--

---

### Description

The data consists of old age life histories from 1 January 1860 to 31 december 1880, 21 years. Only (parts of) life histories above age 60 is considered.

### Usage

```
data(oldmort)
```

### Format

A data frame with 6508 observations from 4603 persons on the following 13 variables.

id	Identification number.
enter	Start age for the interval.
exit	Stop age for the interval.
event	Indicator of death; equals TRUE if the person died at the end of the interval, FALSE otherwise.
birthdate	Birthdate as a real number (i.e., "1765-06-27" is 1765.490).
m.id	Mother's identification number.
f.id	Father's identification number.



sex Gender, a factor with levels male female  
 civ Civil status, a factor with levels unmarried married widow  
 ses.50 Socio-economic status at age 50, a factor with levels middle unknown upper farmer lower  
 birthplace a factor with levels parish region remote  
 imr.birth Infant mortality rate at birth in the region of birth  
 region Subregion of Sundsvall, a factor with levels town industry rural

## Details

The Sundsvall area in mid-Sweden was during the 19th century a fast growing forest industry. At the end of the century, it was one of the largest sawmill area in Europe. The town Sundsvall is fast growing part of the region and center for the commerce.

## Source

The Demographic Data Base, Umeå University, Sweden.

## References

Edvinsson, S. (2000). The Demographic Data Base at Umeå University: A resource for historical studies. In Hall, McKaa, and Thorvaldsen (eds), "Handbook of International Historical Microdata for Population Research", Minnesota Population Center, Minneapolis.

## Examples

```
data(oldmort)
summary(oldmort)
## maybe str(oldmort) ; plot(oldmort) ...
```

---

Pch

*The Piecewise Constant Hazards distribution.*

---

## Description

Density, distribution function, quantile function, hazard function, cumulative hazard function, mean, and random generation for the Piecewise Constant Hazards (pch) distribution.

## Usage

```
ppch(q, cuts, levels, lower.tail = TRUE, log.p = FALSE)
dpch(x, cuts, levels, log = FALSE)
hpch(x, cuts, levels, log = FALSE)
Hpch(x, cuts, levels, log.p = FALSE)
qpch(p, cuts, levels, lower.tail = TRUE, log.p = FALSE)
mpch(cuts, levels)
rpch(n, cuts, levels)
```

**Arguments**

<code>cuts</code>	Vector of cut points defining the intervals where the hazard function is constant.
<code>levels</code>	Vector of levels (values of the hazard function).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P(X \leq x)$ , otherwise, $P(X > x)$ .
<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$ .
<code>n</code>	number of observations. If $\text{length}(n) > 1$ , the length is taken to be the number required.

**Details**

The pch distribution has a hazard function that is piecewise constant on intervals defined by cut-points

$$0 < c_1 < \dots < c_n < \infty, n \geq 0$$

If  $n = 0$ , this reduces to an exponential distribution.

**Value**

`dpch` gives the density, `ppch` gives the distribution function, `qpch` gives the quantile function, `hpch` gives the hazard function, `Hpch` gives the cumulative hazard function, `mpch` gives the mean, and `rpch` generates random deviates.

**Note**

the parameter `levels` must have length at least 1, and the number of cut points must be one less than the number of levels.

---

pchreg

*Piecewise Constant Proportional Hazards Regression*

---

**Description**

Proportional hazards model with piecewise constant baseline hazard(s). Allows for stratification and left truncated and right censored data.

**Usage**

```
pchreg(
  formula = formula(data),
  data = parent.frame(),
  na.action = getOption("na.action"),
  cuts = NULL,
  init,
  control = list(eps = 1e-08, maxiter = 20, trace = FALSE),
```

```

    singular.ok = TRUE,
    model = FALSE,
    x = FALSE,
    y = 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.
data	a data.frame in which to interpret the variables named in the formula.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
cuts	Specifies the points in time where the hazard function jumps. If omitted, an exponential model is fitted.
init	vector of initial values of the iteration. Default initial value is zero for all variables.
control	a list with components eps (convergence criterion), maxiter (maximum number of iterations), and silent (logical, controlling amount of output). You can change any component without mention the other(s).
singular.ok	Not used.
model	Not used.
x	Return the design matrix in the model object?
y	Return the response in the model object?

### Value

A list of class "pchreg" with components

coefficients	Fitted parameter estimates.
cuts	Cut points (NULL if no cut points).
hazards	The estimated constant levels.
var	Covariance matrix of the estimates.
loglik	Vector of length two; first component is the value at the initial parameter values, the second component is the maximized value.
score	The score test statistic (at the initial value).
linear.predictors	The estimated linear predictors.
means	Means of the columns of the design matrix, except those columns corresponding to a factor level. Otherwise all zero.
w.means	Weighted (against exposure time) means of covariates; weighted relative frequencies of levels of factors.
n	Number of spells in indata (possibly after removal of cases with NA's).

n.events	Number of events in data.
terms	Used by extractor functions.
assign	Used by extractor functions.
wald.test	The Wald test statistic (at the initial value).
y	The Surv vector.
isF	Logical vector indicating the covariates that are factors.
covars	The covariates.
ttr	Total Time at Risk.
levels	List of levels of factors.
formula	The calling formula.
call	The call.
method	The method.
convergence	Did the optimization converge?
fail	Did the optimization fail? (Is NULL if not).

### Author(s)

Göran Broström

### See Also

[phreg](#), [coxreg](#), [link{aftreg}](#).

### Examples

```
## Not run:
dat <- age.window(oldmort, c(60, 80))
fit <- pchreg(Surv(enter, exit, event) ~ ses.50 + sex,
data = dat, cuts = seq(60, 80, by = 4))
summary(fit)

fit.cr <- coxreg(Surv(enter, exit, event) ~ ses.50 + sex, data = dat)
check.dist(fit.cr, fit, main = "Cumulative hazards")

## End(Not run)
```

---

perstat	<i>Period statistics</i>
---------	--------------------------

---

**Description**

Calculates occurrence / exposure rates for time periods given by period and for ages given by age.

**Usage**

```
perstat(surv, period, age = c(0, 200))
```

**Arguments**

surv	An (extended) surv object (4 columns with enter, exit, event, birthdate)
period	A vector of dates (in decimal form)
age	A vector of length 2; lowest and highest age

**Value**

A list with components

events	No. of events in each time period.
exposure	Exposure times in each period.
intensity	events / exposure

**Author(s)**

Göran Broström

**See Also**

[piecewise](#)

---

phfunc	<i>Loglikelihood function of a proportional hazards regression</i>
--------	--

---

**Description**

Calculates minus the log likelihood function and its first and second order derivatives for data from a Weibull regression model.

**Usage**

```
phfunc(
  beta = NULL,
  lambda,
  p,
  X = NULL,
  Y,
  offset = rep(0, length(Y)),
  ord = 2,
  pfixed = FALSE,
  dist = "weibull"
)
```

**Arguments**

beta	Regression parameters
lambda	The scale paramater
p	The shape parameter
X	The design (covariate) matrix.
Y	The response, a survival object.
offset	Offset.
ord	ord = 0 means only loglikelihood, 1 means score vector as well, 2 loglikelihood, score and hessian.
pfixed	Logical, if TRUE the shape parameter is regarded as a known constant in the calculations, meaning that it is not considered in the partial derivatives.
dist	Which distribution? The default is "weibull", with the alternatives "loglogistic" and "lognormal".

**Details**

Note that the function returns log likelihood, score vector and minus hessian, i.e. the observed information. The model is

$$S(t; p, \lambda, \beta, z) = S_0((t/\lambda)^p) e^{(z\beta)}$$

**Value**

A list with components

f	The log likelihood. Present if ord >= 0
fp	The score vector. Present if ord >= 1
fpp	The negative of the hessian. Present if ord >= 2

**Author(s)**

Göran Broström

**See Also**[phreg](#)

phreg

*Parametric Proportional Hazards Regression***Description**

Proportional hazards model with parametric baseline hazard(s). Allows for stratification with different scale and shape in each stratum, and left truncated and right censored data.

**Usage**

```
phreg(
  formula = formula(data),
  data = parent.frame(),
  na.action = getOption("na.action"),
  dist = "weibull",
  cuts = NULL,
  init,
  shape = 0,
  param = c("canonical", "rate"),
  control = list(eps = 1e-08, maxiter = 20, trace = FALSE),
  singular.ok = TRUE,
  model = FALSE,
  x = FALSE,
  y = 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.
data	a data.frame in which to interpret the variables named in the formula.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
dist	Which distribution? Default is "weibull", with the alternatives "ev" (Extreme value), "gompertz", "pch" (piecewise constant hazards function), "loglogistic" and "lognormal". A special case like the exponential can be obtained by choosing "weibull" in combination with shape = 1, or "pch" without cuts.
cuts	Only used with dist = "pch". Specifies the points in time where the hazard function jumps. If omitted, an exponential model is fitted.
init	vector of initial values of the iteration. Default initial value is zero for all variables.

shape	If positive, the shape parameter is fixed at that value (in each stratum). If zero or negative, the shape parameter is estimated. If more than one stratum is present in data, each stratum gets its own estimate. Only relevant for the Weibull and Extreme Value distributions.
param	Applies only to the Gompertz distribution: "canonical" is defined in the description of the <a href="#">Gompertz</a> distribution; "rate" transforms scale to 1/log(scale), giving the same parametrization as in Stata and SAS. The latter thus allows for a negative rate, or a "cure" (Gompertz) model. The default is "canonical"; if this results in extremely large scale and/or shape estimates, consider trying "rate".
control	a list with components eps (convergence criterion), maxiter (maximum number of iterations), and silent (logical, controlling amount of output). You can change any component without mention the other(s).
singular.ok	Not used.
model	Not used.
x	Return the design matrix in the model object?
y	Return the response in the model object?

## Details

The parameterization is the same as in [coxreg](#) and [coxph](#), but different from the one used by [survreg](#) (which is not a proportional hazards modelling function). The model is

$$S(t; a, b, \beta, z) = S_0((t/b)^a)^{\exp((z - \text{mean}(z))\beta)}$$

where  $S_0$  is some standardized survivor function.

## Value

A list of class `c("phreg", "coxreg")` with components

coefficients	Fitted parameter estimates.
cuts	Cut points for the "pch" distribution. NULL otherwise.
hazards	The estimated constant levels in the case of the "pch" distribution. NULL otherwise.
var	Covariance matrix of the estimates.
loglik	Vector of length two; first component is the value at the initial parameter values, the second component is the maximized value.
score	The score test statistic (at the initial value).
linear.predictors	The estimated linear predictors.
means	Means of the columns of the design matrix, except those columns corresponding to a factor level. Otherwise all zero.
w.means	Weighted (against exposure time) means of covariates; weighted relative frequencies of levels of factors.
n	Number of spells in indata (possibly after removal of cases with NA's).



n.events	Number of events in data.
terms	Used by extractor functions.
assign	Used by extractor functions.
wald.test	The Wald test statistic (at the initial value).
y	The Surv vector.
isF	Logical vector indicating the covariates that are factors.
covars	The covariates.
ttr	Total Time at Risk.
levels	List of levels of factors.
formula	The calling formula.
call	The call.
method	The method.
convergence	Did the optimization converge?
fail	Did the optimization fail? (Is NULL if not).
pfixed	TRUE if shape was fixed in the estimation.

### Warning

The lognormal and loglogistic distributions are included on an experimental basis for the moment. Use with care, results may be unreliable!

The gompertz distribution has an exponentially increasing hazard function under the canonical parametrization. This may cause instability in the convergence of the fitting algorithm in the case of near-exponential data. It may be resolved by using `param = "rate"`.

### Note

The lognormal and loglogistic baseline distributions are extended to a three-parameter family by adding a "proportionality" parameter (multiplying the baseline hazard function). The log of the estimated parameter turns up as '(Intercept)' in the printed output. The reason for this extension is that the standard lognormal and loglogistic distributions are not closed under proportional hazards.

### Author(s)

Göran Broström

### See Also

[coxreg](#), [check.dist](#), [link{aftreg}](#).

**Examples**

```
data(mort)
fit <- phreg(Surv(enter, exit, event) ~ ses, data = mort)
fit
plot(fit)
fit.cr <- coxreg(Surv(enter, exit, event) ~ ses, data = mort)
check.dist(fit.cr, fit)
```

phreg.fit

*Parametric proportional hazards regression***Description**

This function is called by [phreg](#), but it can also be directly called by a user.

**Usage**

```
phreg.fit(X, Y, dist, strata, offset, init, shape, control)
```

**Arguments**

X	The design (covariate) matrix.
Y	A survival object, the response.
dist	Which baseline distribution?
strata	A stratum variable.
offset	Offset.
init	Initial regression parameter values.
shape	If positive, a fixed value of the shape parameter in the distribution. Otherwise, the shape is estimated.
control	Controls convergence and output.

**Details**

See [phreg](#) for more detail.

**Value**

coefficients	Estimated regression coefficients plus estimated scale and shape coefficients, sorted by strata, if present.
var	Variance-covariance matrix
loglik	Vector of length 2. The first component is the maximized loglikelihood with only scale and shape in the model, the second the final maximum.
score	Score test statistic at initial values

linear.predictors	Linear predictors for each interval.
means	Means of the covariates
conver	TRUE if convergence
fail	TRUE if failure
iter	Number of Newton-Raphson iterates.
n.strata	The number of strata in the data.

**Author(s)**

Göran Broström

**See Also**[phreg](#)


---

piecewise	<i>Piecewise hazards</i>
-----------	--------------------------

---

**Description**

Calculate piecewise hazards, no. of events, and exposure times in each interval indicated by cutpoints.

**Usage**

```
piecewise(enter, exit, event, cutpoints)
```

**Arguments**

enter	Left interval endpoint
exit	Right interval endpoint
event	Indicator of event
cutpoints	Vector of cutpoints

**Details**

Exact calculation.

**Value**

A list with components

events	Vector of number of events
exposure	Vector of total exposure time
intensity	Vector of hazards, $\text{intensity} == \text{events} / \text{exposure}$

**Author(s)**

Göran Broström

**See Also**[perstat](#)

plot.aftreg

*Plots output from an AFT regression***Description**

Just a simple plot of the hazard (cumulative hazard, density, survival) functions for each stratum.

**Usage**

```
## S3 method for class 'aftreg'
plot(
  x,
  fn = c("haz", "cum", "den", "sur"),
  main = NULL,
  xlim = NULL,
  ylim = NULL,
  xlab = "Duration",
  ylab = "",
  col,
  lty,
  printLegend = TRUE,
  new.data = x$means,
  ...
)
```

**Arguments**

x	A aftreg object
fn	Which functions should be plotted! Default is all. They will scroll by, so you have to take care of explicitly what you want to be produced. See, eg, par(mfrow = ...)
main	Header for the plot
xlim	x limits
ylim	y limits
xlab	x label
ylab	y label
col	Colors?

lty	Line types?
printLegend	Should legend be printed? Default is yes.
new.data	At which covariate values?
...	Extra parameters passed to 'plot'

**Details**

The plot is drawn at the mean values of the covariates, by default.

**Value**

No return value.

**Author(s)**

Göran Broström

**See Also**

[aftreg](#)

**Examples**

```
y <- rlllogis(40, shape = 1, scale = 1)
x <- rep(c(1,1,2,2), 10)
fit <- aftreg(Surv(y, rep(1, 40)) ~ x, dist = "loglogistic")
plot(fit)
```

---

plot.coxreg

*Plot method for coxreg objects*


---

**Description**

A plot of a baseline function of a coxreg fit is produced, one curve for each stratum. A wrapper for plot.survfit in [survival](#).

**Usage**

```
## S3 method for class 'coxreg'
plot(
  x,
  fn = c("cum", "surv", "log", "loglog"),
  conf.int = FALSE,
  fig = TRUE,
  xlim = NULL,
  ylim = NULL,
  main = NULL,
```

```

    xlab = "Duration",
    ylab = "",
    col = 1,
    lty = 1,
    printLegend = TRUE,
    ...
)

```

### Arguments

x	A coxreg object
fn	What should be plotted? Default is "cumhaz", and the other choices are "surv", "log", and "loglog".
conf.int	logical or a value like 0.95 (default for one curve).
fig	logical. If TRUE the plot is actually drawn, otherwise only the coordinates of the curve(s) are returned.
xlim	Start and end of the x axis.
ylim	Start and end of the y axis.
main	A headline for the plot
xlab	Label on the x axis.
ylab	Label on the y axis.
col	Color of the curves. Defaults to 'black'.
lty	Line type(s).
printLegend	Either a logical or a text string; if TRUE, a legend is printed at a default place, if FALSE, no legend is printed. Otherwise, if a text string, it should be one of "bottomleft", "bottomright", "topleft", etc., see <a href="#">legend</a> for all possible choices.
...	Other parameters to pass to the plot.

### Value

An object of class `hazdata` containing the coordinates of the curve(s).

---

plot.hazdata	<i>Plots of hazdata objects.</i>
--------------	----------------------------------

---

### Description

Baseline hazards estimates.

**Usage**

```
## S3 method for class 'hazdata'
plot(
  x,
  strata = NULL,
  fn = c("cum", "surv", "log", "loglog"),
  fig = TRUE,
  xlim = NULL,
  ylim = NULL,
  main = NULL,
  xlab = "",
  ylab = "",
  col = "black",
  lty = 1,
  printLegend = TRUE,
  ...
)
```

**Arguments**

<code>x</code>	A hazdata object, typically the 'hazards' element in the output from <code>link{coxreg}</code> with <code>method = "ml"</code> or <code>method = "mopl"</code> or <code>coxph = FALSE</code> .
<code>strata</code>	Stratum names if there are strata present.
<code>fn</code>	Which type of plot? Allowed values are "cum" (or "cumhaz"), "surv" (or "sur"), "log", or "loglog". The last two plots the cumulative hazards on a log (y) scale or a log-log (xy) scale, respectively.
<code>fig</code>	Should a plot actually be produced? Default is TRUE.
<code>xlim</code>	Horizontal plot limits. If NULL, calculated by the function.
<code>ylim</code>	Vertical plot limits. If NULL, set to <code>c(0, 1)</code> for a plot of the survival function.
<code>main</code>	A heading for the plot.
<code>xlab</code>	Label on the x axis.
<code>ylab</code>	Label on the y-axis.
<code>col</code>	Color of the lines. May be a vector of length equal to No. of strata.
<code>lty</code>	Line type(s). May be a vector of length equal to No. of strata.
<code>printLegend</code>	Logical or character; should a legend be produced? Defaults to TRUE. If character, it should be one of <code>bottomleft</code> , <code>bottomright</code> , etc, see <a href="#">legend</a> .
<code>...</code>	Anything that <code>plot.default</code> likes...

**Details**

It is also possible to have as first argument an object of type "coxreg", given that it contains a component of type "hazdata".

**Value**

A list where the elements are two-column matrices, one for each stratum in the model. The first column contains risktimes, and the second the y coordinates for the requested curve(s).

**Note**

x is a list where each element is a two-column matrix. The first column contains failure times, and the second column contains the corresponding 'hazard atoms'.

**Author(s)**

Göran Broström

**Examples**

```
time0 <- numeric(50)
group <- c(rep(0, 25), rep(1, 25))
x <- runif(50, -0.5, 0.5)
time1 <- rexp( 50, exp(group) )
event <- rep(1, 50)
fit <- coxreg(Surv(time0, time1, event) ~ x + strata(group), method = "ml")
plot(fit$hazards, col = 1:2, fn = "surv", xlab = "Duration")
## Same result as:
## plot(fit, col = 1:2, fn = "sur", xlab = "Duration")
```

---

plot.logrank

*Plots of hazdata objects.*


---

**Description**

Baseline hazards estimates.

**Usage**

```
## S3 method for class 'logrank'
plot(
  x,
  fn = c("cum", "surv", "log", "loglog"),
  xlim = NULL,
  ylim = NULL,
  main = NULL,
  xlab = "",
  ylab = "",
  col = "black",
  lty = 1,
  printLegend = TRUE,
  ...
)
```



**Arguments**

<code>x</code>	A logrank object, typically the 'hazards' element in the output from <code>link{logrank}</code> .
<code>fn</code>	Which type of plot? Allowed values are "cum" (or "cumhaz"), "surv" (or "sur"), "log", or "loglog". The last two plots the cumulative hazards on a log (y) scale or a log-log (xy) scale, respectively.
<code>xlim</code>	Horizontal plot limits. If NULL, calculated by the function.
<code>ylim</code>	Vertical plot limits. If NULL, set to <code>c(0, 1)</code> for a plot of the survival function.
<code>main</code>	A heading for the plot.
<code>xlab</code>	Label on the x axis.
<code>ylab</code>	Label on the y-axis.
<code>col</code>	Color of the lines. May be a vector of length equal to No. of strata.
<code>lty</code>	Line type(s). May be a vector of length equal to No. of strata.
<code>printLegend</code>	Logical or character; should a legend be produced? Defaults to TRUE. If character, it should be one of <code>bottomleft</code> , <code>bottomright</code> , etc, see <a href="#">legend</a> .
<code>...</code>	Anything that <code>plot.default</code> likes...

**Details**

It is also possible to have as first argument an object of type "coxreg", given that it contains a component of type "hazdata".

**Value**

A list where the elements are two-column matrices, one for each stratum in the model. The first column contains risktimes, and the second the y coordinates for the requested curve(s).

**Note**

`x` is a list where each element is a two-column matrix. The first column contains failure times, and the second column contains the corresponding 'hazard atoms'.

**Author(s)**

Göran Broström

**Examples**

```
fit <- logrank(Surv(enter, exit, event), group = civ, data = oldmort[oldmort$region == "town", ])
plot(fit)
```

plot.phreg

*Plots output from a phreg regression***Description**

Plot(s) of the hazard, density, cumulative hazards, and/or the survivor function(s) for each stratum.

**Usage**

```
## S3 method for class 'phreg'
plot(
  x,
  fn = c("haz", "cum", "den", "sur"),
  main = NULL,
  xlim = NULL,
  ylim = NULL,
  xlab = "Duration",
  ylab = "",
  col,
  lty,
  printLegend = TRUE,
  score = 1,
  fig = TRUE,
  ...
)
```

**Arguments**

x	A phreg object
fn	Which function should be plotted? Default is the hazard function(s).
main	Header for the plot
xlim	x limits
ylim	y limits
xlab	x label
ylab	y label
col	Color(s) for the curves. Defaults to black.
lty	Line type for the curve(s). Defaults to 1:(No. of strata).
printLegend	Logical, or character ("topleft", "bottomleft", "topright" or "bottomright"); if TRUE or character, a legend is added to the plot if the number of strata is two or more.
score	Multiplication factor for the hazard function.
fig	logical, should the graph be drawn? If FALSE, data is returned.
...	Extra parameters passed to 'plot' and 'lines'.

**Value**

No return value if fig = TRUE, otherwise the cumulative hazards function (coordinates), given fn = "cum".

**Note**

Reference hazard is given by the fit; zero for all covariates, and the reference category for factors.

**Author(s)**

Göran Broström

**See Also**

[phreg](#)

**Examples**

```
y <- rlllogis(40, shape = 1, scale = 1)
x <- rep(c(1,1,2,2), 10)
fit <- phreg(Surv(y, rep(1, 40)) ~ x, dist = "loglogistic")
plot(fit)
```

---

plot.tpchreg

*Plots output from a tpchreg regression*


---

**Description**

Plot(s) of the hazard, cumulative hazards, and/or the survivor function(s) for each stratum.

**Usage**

```
## S3 method for class 'tpchreg'
plot(
  x,
  fn = c("haz", "cum", "sur"),
  log = "",
  main = NULL,
  xlim = NULL,
  ylim = NULL,
  xlab = "Duration",
  ylab = "",
  col,
  lty,
  printLegend = TRUE,
  ...
)
```

**Arguments**

x	A tpchreg object
fn	Which functions should be plotted? Default is the hazard function.
log	character, "" (default), "y", or "xy".
main	Header for the plot
xlim	x limits
ylim	y limits
xlab	x label
ylab	y label
col	Color(s) for the curves. Defaults to black.
lty	Line type for the curve(s). Defaults to 1:(No. of strata).
printLegend	Logical, or character ("topleft", "bottomleft", "topright" or "bottomright"); if TRUE or character, a legend is added to the plot if the number of strata is two or more.
...	Extra parameters passed to 'plot' and 'lines'.

**Value**

No return value.

**Author(s)**

Göran Broström

**See Also**

[tpchreg](#)

---

plot.weibreg

*Plots output from a Weibull regression*


---

**Description**

Plot(s) of the hazard, density, cumulative hazards, and/or the survivor function(s) for each stratum.

**Usage**

```
## S3 method for class 'weibreg'
plot(
  x,
  fn = c("haz", "cum", "den", "sur"),
  main = NULL,
  xlim = NULL,
  ylim = NULL,
```

```
xlab = NULL,  
ylab = NULL,  
new.data = x$means,  
...  
)
```

### Arguments

x	A weibreg object
fn	Which functions should be plotted! Default is all. They will scroll by, so you have to take care explicitly what you want to be produced. See, eg, <code>par(mfrow = ...)</code>
main	Header for the plot
xlim	x limits
ylim	y limits
xlab	x label
ylab	y label
new.data	At which covariate values?
...	Extra parameters passed to 'plot'

### Details

The plot is drawn at the mean values of the covariates.

### Value

No return value

### Author(s)

Göran Broström

### See Also

[phreg](#), [weibreg](#)

### Examples

```
y <- rweibull(4, shape = 1, scale = 1)  
x <- c(1,1,2,2)  
fit <- weibreg(Surv(y, c(1,1,1,1)) ~ x)  
plot(fit)
```

plotHaz

*Graphical comparing of cumulative hazards***Description**

Comparison of the cumulative hazards functions for a semi-parametric and parametric models.

**Usage**

```
plotHaz(
  sp,
  pp,
  interval,
  main = NULL,
  xlab = "Time",
  ylab = "Cum. hazards",
  leglab,
  col = c("blue", "red"),
  lty = 1:2,
  ylim,
  log = "",
  printLegend = TRUE
)
```

**Arguments**

sp	An object of type "coxreg" or "phreg", typically output from <a href="#">coxreg</a> or <a href="#">phreg</a> .
pp	An object of type "coxreg" or "phreg", typically output from <a href="#">coxreg</a> or <a href="#">phreg</a> .
interval	Time interval for the plot, if missing, calculated from sp.
main	Header for the plot. Default is distribution and "cumulative hazard function"
xlab	Label on x axis (default "Time")
ylab	Label on y axis (default "Cum. Hazards")
leglab	Labels in legend.
col	Line colors. should be NULL (black lines) or of length 2
lty	line types.
ylim	Y limits for the plot.
log	Argument sent to plot, defaults to "".
printLegend	Should a legend be printed? Default is TRUE.

**Details**

For the moment only a graphical comparison. The arguments sp and pp may be swapped.

**Value**

No return value.

**Author(s)**

Göran Broström

**See Also**

[check.dist](#), [coxreg](#) and [phreg](#).

**Examples**

```
data(mort)
op <- par(mfrow = c(1, 2))
fit.cr <- coxreg(Surv(enter, exit, event) ~ ses, data = mort)
fit.w <- phreg(Surv(enter, exit, event) ~ ses, data = mort)
fit.g <- phreg(Surv(enter, exit, event) ~ ses, data = mort,
  dist = "gompertz")
plotHaz(fit.cr, fit.w, interval = c(0, 20), main = "Weibull")
plotHaz(fit.cr, fit.g, main = "Gompertz")
par(op)
```

---

print.aftreg

*Prints aftreg objects*


---

**Description**

The hazard, the cumulative hazard, the density, and the survivor baseline functions are plotted.

**Usage**

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

**Arguments**

x	A aftreg object
digits	Precision in printing
...	Not used.

**Value**

No value is returned.

**Note**

Doesn't work for threeway or higher order interactions. Use [print.coxph](#) in that case.

**Author(s)**

Göran Broström

**See Also**

[phreg](#), [print.coxph](#)

---

print.coxreg	<i>Prints coxreg objects</i>
--------------	------------------------------

---

**Description**

More "pretty-printing" than `print.coxph`, which is a fall-back for 'difficult' objects.

**Usage**

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

**Arguments**

<code>x</code>	A coxreg object, typically the result of running <code>coxreg</code>
<code>digits</code>	Output format.
<code>...</code>	Other arguments.

**Details**

Doesn't work with three-way and higher interactions, in which case `print.coxph` is used.

**Value**

No value is returned.

**Author(s)**

Göran Broström

**See Also**

[coxreg](#), [print.coxph](#)



---

print.logrank	<i>Prints logrank objects</i>
---------------	-------------------------------

---

**Description**

The result of logrank is printed

**Usage**

```
## S3 method for class 'logrank'  
print(x, digits = max(options())$digits - 4, 6), ...)
```

**Arguments**

x	A logrank object
digits	Precision in printing
...	Not used.

**Value**

The input is returned invisibly.

**Author(s)**

Göran Broström

**See Also**

[logrank](#), [coxreg](#)

---

print.phreg	<i>Prints phreg objects</i>
-------------	-----------------------------

---

**Description**

The hazard, the cumulative hazard, the density, and the survivor baseline functions are plotted.

**Usage**

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

**Arguments**

x	A phreg object
digits	Precision in printing
...	Not used.

**Value**

No value is returned.

**Note**

Doesn't work for threeway or higher order interactions. Use [print.coxph](#) in that case.

**Author(s)**

Göran Broström

**See Also**

[phreg](#), [print.coxph](#)

---

print.risksets	<i>Prints a summary of the content of a set of risk sets.</i>
----------------	---

---

**Description**

Given the output from risksets, summary statistics are given for it.

**Usage**

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

**Arguments**

x	An object of class 'risksets'.
...	Not used for the moment.

**Value**

No value is returned; the function prints summary statistics of risk sets.

**Note**

There is no `summary.risksets` yet. On the TODO list.

**Author(s)**

Göran Broström

**See Also**

risksets

**Examples**

```
rs <- with(mort, risksets(Surv(enter, exit, event)))
print(rs)
```

---

print.summary.aftreg    *Prints summary.aftreg objects*

---

**Description**

Prints summary.aftreg objects

**Usage**

```
## S3 method for class 'summary.aftreg'
print(x, digits = max(getOption("digits") - 3, 3), short = FALSE, ...)
```

**Arguments**

x	A summary.aftreg object, typically the result of running summary.aftreg, summary on a phreg object.
digits	Output format.
short	Logical: If TRUE, short output, only regression.
...	Other arguments.

**Value**

No value is returned.

**Author(s)**

Göran Broström

**See Also**[aftreg](#), [summary.aftreg](#)

---

print.summary.coxreg    *Prints summary.coxreg objects*

---

**Description**

Prints summary.coxreg objects

**Usage**

```
## S3 method for class 'summary.coxreg'  
print(x, digits = 3, short = FALSE, ...)
```

**Arguments**

x	A summary.coxreg object, typically the result of running summary.coxreg, summary on a coxreg object.
digits	Output format.
short	Logical, short or long (default) output?
...	Other arguments.

**Value**

No value is returned.

**Author(s)**

Göran Broström

**See Also**

[coxreg](#), [summary.coxreg](#)

---

print.summary.phreg    *Prints summary.phreg objects*

---

**Description**

Prints summary.phreg objects

**Usage**

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

**Arguments**

x	A summary.phreg object, typically the result of running summary.phreg, summary on a phreg object.
digits	Output format.
...	Other arguments.

**Value**

No value is returned.

**Author(s)**

Göran Broström

**See Also**

[phreg](#), [summary.phreg](#)

---

print.summary.tpchreg *Prints summary.tpchreg objects*

---

**Description**

Prints summary.tpchreg objects

**Usage**

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

**Arguments**

x	A summary.tpchreg object, typically the result of running summary.tpchreg, summary on a tpchreg object.
digits	Output format.
...	Other arguments.

**Value**

No value is returned.

**Author(s)**

Göran Broström

**See Also**

[tpchreg](#), [summary.tpchreg](#)

---

print.tpchreg	<i>Prints tpchreg objects</i>
---------------	-------------------------------

---

**Description**

More "pretty-printing"

**Usage**

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

**Arguments**

x	A tpchreg object, typically the result of running tpchreg
digits	Output format.
...	Other arguments.

**Details**

Doesn't work with three-way or higher interactions.

**Value**

No value is returned.

**Author(s)**

Göran Broström

**See Also**

[tpchreg](#), [print.coxreg](#)

---

print.weibreg	<i>Prints weibreg objects</i>
---------------	-------------------------------

---

**Description**

The hazard, the cumulative hazard, the density, and the survivor baseline functions are plotted.

**Usage**

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

**Arguments**

<code>x</code>	A weibreg object
<code>digits</code>	Precision in printing
<code>...</code>	Not used.

**Value**

No value is returned.

**Note**

Doesn't work for threeway or higher order interactions. Use [print.coxph](#) in that case.

**Author(s)**

Göran Broström

**See Also**

[weibreg](#), [print.coxph](#)

---

regtable	<i>Retrieves regression tables</i>
----------	------------------------------------

---

**Description**

Retrieves regression tables

**Usage**

```
regtable(x, digits = 3, short = TRUE, ...)
```

**Arguments**

<code>x</code>	A summary.XXreg object, typically the result of running <code>summary.XXreg</code> , summary on a XXreg object.
<code>digits</code>	Output format.
<code>short</code>	If TRUE, return only coefficients table.
<code>...</code>	Other arguments.

**Value**

A character data frame, ready to print in various formats.

**Note**

Should not be used if interactions present.

**Author(s)**

Göran Broström

**See Also**[coxreg](#), [summary.coxreg](#)

---

risksets*Finds the compositions and sizes of risk sets*

---

**Description**

Focus is on the risk set composition just prior to a failure.

**Usage**

```
risksets(  
  x,  
  strata = NULL,  
  max.survs = NULL,  
  members = TRUE,  
  collate_sets = FALSE  
)
```

**Arguments**

x	A Surv object.
strata	Stratum indicator.
max.survs	Maximum number of survivors in each risk set. If smaller than the 'natural number', survivors are sampled from the present ones. No sampling if missing.
members	If TRUE, all members of all risk sets are listed in the resulting list, see below.
collate_sets	logical. If TRUE, group information by risk sets in a list. Only if members = TRUE.

**Details**

If the input argument max.survs is left alone, all survivors are accounted for in all risk sets.

**Value**

A list with components (if collate\_sets = FALSE)

antrs	No. of risk sets in each stratum. The number of strata is given by length(antrs).
risktimes	Ordered distinct failure time points.
eventset	If 'members' is TRUE, a vector of pointers to events in each risk set, else NULL.



riskset	If 'members' is TRUE, a vector of pointers to the members of the risk sets, in order. The 'n.events' first are the events. If 'members' is FALSE, 'riskset' is NULL.
size	The sizes of the risk sets.
n.events	The number of events in each risk set.
sample_fraction	If 'members' is TRUE, the sampling fraction of survivors in each risk set.

**Note**

Can be used to "sample the risk sets".

**Author(s)**

Göran Broström

**See Also**

[table.events](#), [coxreg](#).

**Examples**

```
enter <- c(0, 1, 0, 0)
exit <- c(1, 2, 3, 4)
event <- c(1, 1, 1, 0)
risksets(Surv(enter, exit, event))
```

---

scania

*Old age mortality, Scania, southern Sweden, 1813-1894.*

---

**Description**

The data consists of old age life histories from 1 January 1813 to 31 december 1894. Only (parts of) life histories above age 50 is considered.

**Usage**

```
data(scania)
```

**Format**

A data frame with 1931 observations from 1931 persons on the following 9 variables.

id Identification number (enumeration).

enter Start age for the interval.

exit Stop age for the interval.

event Indicator of death; equals TRUE if the person died at the end of the interval, FALSE otherwise.

birthdate Birthdate as a real number (i.e., "1765-06-27" is 1765.490).

sex Gender, a factor with levels male female.

parish One of five parishes in Scania, coded 1, 2, 3, 4, 5. Factor.

ses Socio-economic status at age 50, a factor with levels upper and lower.

immigrant a factor with levels no region and yes.

## Details

The Scanian area in southern Sweden was during the 19th century a mainly rural area.

## Source

The Scanian Economic Demographic Database, Lund University, Sweden.

## References

<https://www.lusem.lu.se/organisation/research-centres/centre-economic-demography/cedpop-databases-ced>

## Examples

```
data(scania)
summary(scania)
```

---

summary.aftreg

*Prints aftreg objects*

---

## Description

Prints aftreg objects

## Usage

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

## Arguments

object	A aftreg object
...	Additional ...

## Author(s)

Göran Broström

**See Also**[print.coxreg](#)**Examples**

```
## The function is currently defined as
function (object, ...)
print(object)
```

---

summary.coxreg	<i>A summary of coxreg objects.</i>
----------------	-------------------------------------

---

**Description**

A summary of coxreg objects.

**Usage**

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

**Arguments**

object	A coxreg object
...	Additional ...

**Author(s)**

Göran Broström

**See Also**[print.coxreg](#)**Examples**

```
fit <- coxreg(Surv(enter, exit, event) ~ sex + civ, data = oldmort)
summary(fit)
```

---

summary.phreg	<i>A summary of phreg objects.</i>
---------------	------------------------------------

---

**Description**

A summary of phreg objects.

**Usage**

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

**Arguments**

object	A phreg object
...	Additional ...

**Author(s)**

Göran Broström

**See Also**

[print.phreg](#)

**Examples**

```
fit <- phreg(Surv(enter, exit, event) ~ sex + civ,  
data = oldmort[oldmort$region == "town", ])  
summary(fit)
```

---

summary.tpchreg	<i>Summary for tpchreg objects</i>
-----------------	------------------------------------

---

**Description**

Summary for tpchreg objects

**Usage**

```
## S3 method for class 'tpchreg'  
summary(object, ci = FALSE, level = 0.95, ...)
```

**Arguments**

object	A tpchreg object.
ci	Logical. If TRUE, confidence limits are given instead of se's.
level	Confidence level, used if ci.
...	Additional ...

**Author(s)**

Göran Broström

**See Also**

[tpchreg](#)

**Examples**

```
## The function is currently defined as
## function (object, ...)
```

---

summary.weibreg	<i>Prints a weibreg object</i>
-----------------	--------------------------------

---

**Description**

This is the same as [print.weibreg](#)

**Usage**

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

**Arguments**

object	A weibreg object
...	Additional ...

**Author(s)**

Göran Broström

**See Also**

[print.weibreg](#)

**Examples**

```
## The function is currently defined as
function (object, ...)
  print(object)
```

SurvSplit

*Split a survival object at specified durations.***Description**

Given a survival object, (a matrix with two or three columns) and a set of specified cut times, split each record into multiple subrecords at each cut time. The new survival object will be in 'counting process' format, with an enter time, exit time, and event status for each record.

**Usage**

```
SurvSplit(Y, cuts)
```

**Arguments**

Y	A survival object, a matrix with two or three columns.
cuts	The cut points, must be strictly positive and distinct.

**Value**

A list with components

Y	The new survival object with three columns, i.e., in 'counting process' form.
ivl	Interval No., starting from leftmost, (0, cuts[1]) or similar.
idx	Row number for original Y row.

**Note**

This function is used in [phreg](#) for the piecewise constant hazards model. It uses [age.window](#) for each interval.

**Author(s)**

Göran Broström

**See Also**

[survSplit](#), [age.window](#).

## Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##-- or do help(data=index) for the standard data sets.

## The function is currently defined as
function(Y, cuts){
  if (NCOL(Y) == 2) Y <- cbind(rep(0, NROW(Y)), Y)
  indat <- cbind(Y, 1:NROW(Y), rep(-1, NROW(Y)))
  colnames(indat) <- c("enter", "exit", "event", "idx", "ivl")
  n <- length(cuts)
  cuts <- sort(cuts)
  if ((cuts[1] <= 0) || (cuts[n] == Inf))
    stop("'cuts' must be positive and finite.")
  cuts <- c(0, cuts, Inf)
  n <- n + 1
  out <- list()
  indat <- as.data.frame(indat)
  for (i in 1:n){
    out[[i]] <- age.window(indat, cuts[i:(i+1)])
    out[[i]]$ivl <- i
    out[[i]] <- t(out[[i]])
  }
  Y <- matrix(unlist(out), ncol = 5, byrow = TRUE)
  colnames(Y) <- colnames(indat)
  list(Y = Y[, 1:3],
       ivl = Y[, 5],
       idx = Y[, 4]
  )
}
```

---

swedeaths

*Swedish death data, 1969-2020.*


---

## Description

A data frame containing data on the number of deaths by sex, age and year, Sweden 1969-2020.

## Usage

```
data(swedeaths)
```

## Format

A data frame with 5 variables and 10504 observations.

age Numerical with integer values 0-100, representing achieved age in years during the actual calendar year. The highest value, 100, represents ages 100 and above.

sex A factor with two levels, "women" and "men".

year Calendar year.

deaths Number of deaths by age, sex, and year.

id Created by the reshape procedure, see Details.

## Details

Data are downloaded from Statistics Sweden in the form of a csv file and in that process converted to a data frame. Variable names are translated from Swedish, and some of them are converted to factors. Each numeric column contains the number of deaths by sex and age. The original data set is in wide form and then converted to long format.

## Source

Statistics Sweden, <https://www.scb.se>.

## See Also

[swepop](#), [tpchreg](#)

## Examples

```
summary(swedeaths)
## maybe str(swedeaths) ...
```

---

swepop

*Swedish population data, 1969-2020.*

---

## Description

A data frame containing data on the population size by sex, age and year, Sweden 1969-2020.

## Usage

```
data(swepop)
```

## Format

A data frame with 5 variables and 10504 observations.

age Numerical with integer values 0-100, representing achieved age in years during the actual calendar year. The highest value, 100, represents ages 100 and above.

sex A factor with two levels, "women" and "men".

year Calendar year.

pop Average population by age, sex, and year.

**id** Created by the reshape procedure, see Details.



## Details

Data are downloaded from Statistics Sweden in the form of a csv file and converted to a data frame. Variable names are translated from Swedish, and some of them are converted to factors. The variable pop contains the average population by sex and age, calculated by taking the mean value of the population size at December 31 the previous year and December 31 the current year. The original data contain the sizes at the end of each year. The original data set is in wide format and converted to long format by reshape.

## Source

Statistics Sweden, <https://www.scb.se>.

## See Also

[swedeaths](#)

## Examples

```
summary(swepop)
## maybe str(swepop) ...
```

---

table.events	<i>Calculating failure times, risk set sizes and No. of events in each risk set</i>
--------------	---

---

## Description

From input data of the 'interval' type, with an event indicator, summary statistics for each risk set (at an event time point) are calculated.

## Usage

```
table.events(enter = rep(0, length(exit)), exit, event, strict = TRUE)
```

## Arguments

enter	Left truncation time point.
exit	End time point, an event or a right censoring.
event	Event indicator.
strict	If TRUE, then tabulating is not done after a time point where all individuals in a riskset failed.

## Value

A list with components

times	Ordered distinct event time points.
events	Number of events at each event time point.
riskset.sizes	Number at risk at each event time point.

**Author(s)**

Göran Broström

**See Also**[risksets](#)**Examples**

```
exit = c(1,2,3,4,5)
event = c(1,1,0,1,1)
table.events(exit = exit, event = event)
```

toBinary

---

*Transforms a "survival" data frame into a data frame suitable for binary (logistic) regression*

---

**Description**

The result of the transformation can be used to do survival analysis via logistic regression. If the cloglog link is used, this corresponds to a discrete time analogue to Cox's proportional hazards model.

**Usage**

```
toBinary(
  dat,
  surv = c("enter", "exit", "event"),
  strats,
  max.survs = NROW(dat)
)
```

**Arguments**

dat	A data frame with three variables representing the survival response. The default is that they are named enter, exit, and event
surv	A character vector with the names of the three variables representing survival.
strats	An eventual stratification variable.
max.survs	Maximal number of survivors per risk set. If set to a (small) number, survivors are sampled from the risk sets.

**Details**

toBinary calls risksets in the eha package.

**Value**

Returns a data frame expanded risk set by risk set. The three "survival variables" are replaced by a variable named `event` (which overwrites an eventual variable by that name in the input). Two more variables are created, `riskset` and `orig.row`.

<code>event</code>	Indicates an event in the corresponding risk set.
<code>riskset</code>	Factor (with levels 1, 2, ...) indicating risk set.
<code>risktime</code>	The 'risktime' (age) in the corresponding riskset.
<code>orig.row</code>	The row number for this item in the original data frame.

**Note**

The survival variables must be three. If you only have *exit* and *event*, create a third containing all zeros.

**Author(s)**

Göran Broström

**See Also**

[coxreg, glm.](#)

**Examples**

```
enter <- rep(0, 4)
exit <- 1:4
event <- rep(1, 4)
z <- rep(c(-1, 1), 2)
dat <- data.frame(enter, exit, event, z)
binDat <- toBinary(dat)
dat
binDat
coxreg(Surv(enter, exit, event) ~ z, method = "ml", data = dat)
## Same as:
summary(glm(event ~ z + riskset, data = binDat, family = binomial(link = cloglog)))
```

---

toDate

*Convert time in years since "0000-01-01" to a date.*

---

**Description**

This function uses `as.Date` and a simple linear transformation.

**Usage**

```
toDate(times)
```

**Arguments**

times                    a vector of durations

**Value**

A vector of dates as character strings of the type "1897-05-21".

**Author(s)**

Göran Broström

**See Also**

[toDate](#)

**Examples**

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##-- or do help(data=index) for the standard data sets.
toDate(1897.357)
```

---

toTime

*Calculate duration in years from "0000-01-01" to a given date*

---

**Description**

Given a vector of dates, the output is a vector of durations in years since "0000-01-01".

**Usage**

```
toTime(dates)
```

**Arguments**

dates                    A vector of dates in character form or of class Date

**Value**

A vector of durations, as described above.

**Author(s)**

Göran Broström

**See Also**

[toDate](#)

## Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##-- or do help(data=index) for the standard data sets.

toTime(c("1897-05-16", "1901-11-21"))
```

---

toTpch	<i>Transform survival data to tabular form</i>
--------	--

---

## Description

Transform a "survival data frame" to tabular form aggregating number of events and exposure time by time intervals and covariates.

## Usage

```
toTpch(formula, data, cuts, enter = "enter", exit = "exit",
event = "event", episode = "age")
```

## Arguments

formula	A model formula.
data	A data frame with survival data.
cuts	An ordered, non-negative vector of time points at which a hazard function changes value. Note that data are left truncated at cuts[1] (the smallest value) and right censored at c[n], where n is the length of cuts and cuts[n] == max(cuts).
enter	Character string with the name of the variable representing left truncation values.
exit	Character string with the name of the event/censoring time variable.
event	Character string with the name of the event indicator variable.
episode	Character string with the name of the output variable of the grouped time (a factor variable).

## Details

If cuts is missing, nothing is done. Internally, this function first calls `survival::survSplit` and then `stats::aggregate`.

## Value

A data frame with exposure time and number of events aggregated by time intervals and covariates. If all covariates are factors, this usually results in a huge reduction of the size of the data frame, but otherwise the size of the output may be larger than the size of the input data frame.

**Note**

Episodes, or parts of episodes, outside  $\min(\text{cuts})$ ,  $\max(\text{cuts})$  are cut off. With continuous covariates, consider rounding them so that the number of distinct observed values is not too large.

**Author(s)**

Göran Broström

---

tpchreg	<i>Proportional hazards regression with piecewise constant hazards and tabular data.</i>
---------	--

---

**Description**

Proportional hazards regression with piecewise constant hazards and tabular data.

**Usage**

```
tpchreg(formula, data, time, weights, last, subset, na.action,
        contrasts = NULL, start.coef = NULL,
        control = list(epsilon = 1.e-8, maxit = 200, trace = FALSE))
```

**Arguments**

formula	a formula with 'oe(count, exposure) ~ x1 + ...'
data	a data frame with occurrence/exposure data plus covariates.
time	the time variable, a factor character vector indicating time intervals, or numeric, indicating the start of intervals.
weights	Case weights.
last	If time is numeric, the closing of the last interval.
subset	subset of data, not implemented yet.
na.action	Not implemented yet.
contrasts	Not implemented yet.
start.coef	For the moment equal to zero, not used.
control	list of control parameters for the optimization.

**Note**

The interpretation of cuts is different from that in [hpch](#). This is intentional.

**See Also**

[oe](#).

## Examples

```
sw <- swepop
sw$deaths <- swedeaths$deaths
fit <- tpchreg(oe(deaths, pop) ~ strata(sex) + I(year - 2000),
time = age, last = 101, data = sw[sw$year >= 2000, ])
summary(fit)
```

---

weibreg

*Weibull Regression*


---

## Description

Proportional hazards model with baseline hazard(s) from the Weibull family of distributions. Allows for stratification with different scale and shape in each stratum, and left truncated and right censored data.

## Usage

```
weibreg(
  formula = formula(data),
  data = parent.frame(),
  na.action = getOption("na.action"),
  init,
  shape = 0,
  control = list(eps = 1e-04, maxiter = 10, trace = FALSE),
  singular.ok = TRUE,
  model = FALSE,
  x = FALSE,
  y = TRUE,
  center = 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.
data	a data.frame in which to interpret the variables named in the formula.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
init	vector of initial values of the iteration. Default initial value is zero for all variables.
shape	If positive, the shape parameter is fixed at that value (in each stratum). If zero or negative, the shape parameter is estimated. If more than one stratum is present in data, each stratum gets its own estimate.

control	a list with components <code>eps</code> (convergence criterion), <code>maxiter</code> (maximum number of iterations), and <code>silent</code> (logical, controlling amount of output). You can change any component without mention the other(s).
singular.ok	Not used.
model	Not used.
x	Return the design matrix in the model object?
y	Return the response in the model object?
center	Deprecated, and not used. Will be removed in the future.

### Details

The parameterization is the same as in [coxreg](#) and [coxph](#), but different from the one used by [survreg](#). The model is

$$h(t; a, b, \beta, z) = (a/b)(t/b)^{a-1} \exp(z\beta)$$

This is in correspondence with [Weibull](#). To compare regression coefficients with those from `survreg` you need to divide by estimated shape ( $\hat{a}$ ) and change sign. The p-values and test statistics are however the same, with one exception; the score test is done at maximized scale and shape in `weibreg`.

This model is a Weibull distribution with shape parameter  $a$  and scale parameter  $b \exp(-z\beta/a)$

### Value

A list of class `c("weibreg", "coxreg")` with components

coefficients	Fitted parameter estimates.
var	Covariance matrix of the estimates.
loglik	Vector of length two; first component is the value at the initial parameter values, the second componet is the maximized value.
score	The score test statistic (at the initial value).
linear.predictors	The estimated linear predictors.
means	Means of the columns of the design matrix.
w.means	Weighted (against exposure time) means of covariates; weighted relative frequencies of levels of factors.
n	Number of spells in indata (possibly after removal of cases with NA's).
events	Number of events in data.
terms	Used by extractor functions.
assign	Used by extractor functions.
wald.test	The Wald test statistic (at the initial value).
y	The Surv vector.
isF	Logical vector indicating the covariates that are factors.
covars	The covariates.



ttr	Total Time at Risk.
levels	List of levels of factors.
formula	The calling formula.
call	The call.
method	The method.
convergence	Did the optimization converge?
fail	Did the optimization fail? (Is NULL if not).
pfixed	TRUE if shape was fixed in the estimation.

### Warning

The print method `print.weibreg` doesn't work if threeway or higher order interactions are present.

Note further that covariates are internally centered, if `center = TRUE`, by this function, and this is not corrected for in the output. This affects the estimate of  $\log(scale)$ , but nothing else. If you don't like this, set `center = FALSE`.

### Note

This function is not maintained, and may behave in unpredictable ways. Use `phreg` with `dist = "weibull"` (the default) instead! Will soon be declared deprecated.

### Author(s)

Göran Broström

### See Also

`phreg`, `coxreg`, `print.weibreg`

### Examples

```
dat <- data.frame(time = c(4, 3, 1, 1, 2, 2, 3),
                  status = c(1, 1, 1, 0, 1, 1, 0),
                  x = c(0, 2, 1, 1, 1, 0, 0),
                  sex = c(0, 0, 0, 0, 1, 1, 1))
weibreg( Surv(time, status) ~ x + strata(sex), data = dat) #stratified model
```

weibreg.fit

*Weibull regression***Description**

This function is called by [weibreg](#), but it can also be directly called by a user.

**Usage**

```
weibreg.fit(X, Y, strata, offset, init, shape, control, center = TRUE)
```

**Arguments**

X	The design (covariate) matrix.
Y	A survival object, the response.
strata	A stratum variable.
offset	Offset.
init	Initial regression parameter values.
shape	If positive, a fixed value of the shape parameter in the Weibull distribution. Otherwise, the shape is estimated.
control	Controls convergence and output.
center	Should covariates be centered?

**Details**

See [weibreg](#) for more detail.

**Value**

coefficients	Estimated regression coefficients plus estimated scale and shape coefficients, sorted by strata, if present.
var	
loglik	Vector of length 2. The first component is the maximized loglikelihood with only scale and shape in the model, the second the final maximum.
score	Score test statistic at initial values
linear.predictors	Linear predictors for each interval.
means	Means of the covariates
conver	TRUE if convergence
fail	TRUE if failure
iter	Number of Newton-Raphson iterates.
n.strata	The number of strata in the data.

**Author(s)**

Göran Broström

**See Also**[weibreg](#)

---

Weibull*The (Cumulative) Hazard Function of a Weibull Distribution*

---

**Description**

`hweibull` calculates the hazard function of a Weibull distribution, and `Hweibull` calculates the corresponding cumulative hazard function.

**Usage**

```
hweibull(x, shape, scale = 1, log = FALSE)
```

**Arguments**

<code>x</code>	Vector of quantiles.
<code>shape</code>	The shape parameter.
<code>scale</code>	The scale parameter, defaults to 1.
<code>log</code>	logical; if TRUE, the log of the hazard function is given.

**Details**

See [dweibull](#).

**Value**

The (cumulative) hazard function, evaluated at `x`.

**Author(s)**

Göran Broström

**See Also**[pweibull](#)**Examples**

```
hweibull(3, 2, 1)
dweibull(3, 2, 1) / pweibull(3, 2, 1, lower.tail = FALSE)
Hweibull(3, 2, 1)
-pweibull(3, 2, 1, log.p = TRUE, lower.tail = FALSE)
```

wfunk

*Loglikelihood function of a Weibull regression***Description**

Calculates minus the log likelihood function and its first and second order derivatives for data from a Weibull regression model. Is called by [weibreg](#).

**Usage**

```
wfunk(
  beta = NULL,
  lambda,
  p,
  X = NULL,
  Y,
  offset = rep(0, length(Y)),
  ord = 2,
  pfixed = FALSE
)
```

**Arguments**

beta	Regression parameters
lambda	The scale paramater
p	The shape parameter
X	The design (covariate) matrix.
Y	The response, a survival object.
offset	Offset.
ord	ord = 0 means only loglikelihood, 1 means score vector as well, 2 loglikelihood, score and hessian.
pfixed	Logical, if TRUE the shape parameter is regarded as a known constant in the calculations, meaning that it is not cosidered in the partial derivatives.

**Details**

Note that the function returns log likelihood, score vector and minus hessian, i.e. the observed information. The model is

$$h(t; p, \lambda, \beta, z) = p/\lambda(t/\lambda)^{(p-1)} \exp(-(t/\lambda)^p) \exp(z\beta)$$

This is in correspondence with [dweibull](#).

**Value**

A list with components

f	The log likelihood. Present if <code>ord &gt;= 0</code>
fp	The score vector. Present if <code>ord &gt;= 1</code>
fpp	The negative of the hessian. Present if <code>ord &gt;= 2</code>

**Author(s)**

Göran Broström

**See Also**

[weibreg](#)

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