

Package ‘frailtyHL’

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Type Package

Title Frailty Models via H-likelihood

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Description The frailtyHL package implements the h-likelihood estimation procedures for frailty models. The package fits Cox's proportional hazards models with random effects (or frailties). For the frailty distribution lognormal and gamma are allowed. The h-likelihood uses the Laplace approximation when the numerical integration is intractable, giving a statistically efficient estimation in frailty models.

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frailtyHL-package *H-likelihood Approach for Frailty Models*

Description

The frailtyHL package fits frailty models which are Cox's proportional hazards models incorporating random effects. The function implements the h-likelihood estimation procedures. For the frailty distribution lognormal and gamma are allowed. The h-likelihood uses the Laplace approximation when the numerical integration is intractable, giving a statistically efficient estimation in frailty models. (Ha, Lee and Song, 2001; Ha and Lee, 2003, 2005; Lee, Nelder and Pawitan, 2006).

Details

Package:	frailtyHL
Type:	Package
Version:	1.1
Date:	2012-05-04
License:	Unlimited
LazyLoad:	yes

This is version 1.1 of the frailtyHL package.

Author(s)

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References

Ha, I. D. and Lee, Y. (2003). Estimating frailty models via Poisson Hierarchical generalized linear models. *Journal of Computational and Graphical Statistics*, 12, 663–681.

Ha, I. D. and Lee, Y. (2005). Comparison of hierarchical likelihood versus orthodox best linear unbiased predictor approaches for frailty models. *Biometrika*, 92, 717–723.

Ha, I. D., Lee, Y. and Song, J. K. (2001). Hierarchical likelihood approach for frailty models. *Biometrika*, 88, 233–243.

Lee, Y., Nelder, J. A. and Pawitan, Y. (2006). Generalised linear models with random effects: unified analysis via h-likelihood. Chapman & Hall: London.

See Also

<[frailtyHL](#)>

Examples

```
data(kidney)
kidney_g12<-frailtyHL(Surv(time,status)~sex+age+(1|id),kidney,
RandDist="Gamma",mord=1,dord=2)
```

cgd

*Chronic Granulomatous Disease (CGD) Infection Data***Description**

The CGD data set in Fleming and Harrington (1991) is from a placebo-controlled randomized trial of gamma interferon in chronic granulomatous disease. In total, 128 patients from 13 hospitals were followed for about 1 year. The number of patients per hospital ranged from 4 to 26. Each patient may experience more than one infection. The survival times (times-to-event) are the times between recurrent CGD infections on each patient (i.e. gap times). Censoring occurred at the last observation for all patients, except one, who experienced a serious infection on the date he left the study.

Usage

```
data(cgd)
```

Format

CGD data set contains 15 columns and 203 rows. A brief description of the data column is given below.

`id` Patient number for 128 patients.

`center` Enrolling center number for 13 hospitals.

`random` Date of randomization.

`treat` Gamma-interferon treatment(rIFN-g) or placebo(Placebo).

`sex` Sex of each patient(male, female).

`age` Age of each patient at study entry, in years.

`height` Height of each patient at study entry, in cm.

`weight` Weight of each patient at study entry, in kg.

`inherit` Pattern of inheritance (autosomal recessive, X-linked).

`steroids` Using corticosteroids at times of study entry(1=Yes, 0=No).

`proylac` Using prophylactic antibiotics at time of study entry(1=Yes, 0=No).

`hos.cat` A categorization of the hospital region into 4 groups.

`tstart` Start of each time interval.

`enum` Sequence number. For each patient, the infection records are in sequence number order.

`tstop` End of each time interval.

`status` Censoring indicator (1=uncensored, 0=censored).

References

- Fleming, T. R. and Harrington, D. R. (1991). Counting processes and survival analysis. Wiley: New York.
- Therneasu, T. (2012). survival: survival analysis, including penalised likelihood. <http://CRAN.R-project.org/package=survival>. R package version 2.36-14.

Examples

```
data(cgd)
```

frailtyHL

Fitting Frailty Models using H-likelihood Approach

Description

frailtyHL is used to fit frailty models using h-likelihood estimation procedures. For the frailty distribution lognormal and gamma are allowed. In particular, nested (multilevel) frailty models allow survival studies for hierarchically clustered data by including two iid normal random effects. The h-likelihood uses the Laplace approximation when the numerical integration is intractable, giving a statistically efficient estimation in frailty models. (Ha, Lee and Song, 2001; Ha and Lee, 2003, 2005; Lee, Nelder and Pawitan, 2006).

Usage

```
frailtyHL(formula,data,weights,subset,na.action,
RandDist="Normal",mord=0,dord=1,Maxiter=200,
convergence=10^-6, varfixed=FALSE, varinit=c(0.1))
```

Arguments

formula	A formula object, with the response on the left of a ~ operator, and the terms for the fixed and random effects on the right. e.g. formula=Surv(time,status)~x+(1 id), time : survival time, status : censoring indicator having 1 (0) for uncensored (censored) observation, x : fixed covariate, id : random effect.
data	Dataframe for formulaMain.
weights	Vector of case weights.
subset	Expression indicating which subset of the rows of data should be used in the fit. All observations are included by default.
na.action	A missing-data filter function.
RandDist	Distribution for random effect ("Normal" or "Gamma").
mord	The order of Laplace approximation to fit the mean parameters (0 or 1); default=0.
dord	The order of Laplace approximation to fit the dispersion components (1 or 2); default=1.
Maxiter	The maximum number of iterations; default=200.

convergence	Specify the convergence criterion, the default is 1e-6.
varfixed	Logical value: if TRUE (FALSE), the value of one or more of the variance terms for the frailties is fixed (estimated).
varinit	Starting values for frailties, the default is 0.1.

Details

frailtyHL package produces estimates of fixed effects and frailty parameters as well as their standard errors. Also, frailtyHL makes it possible to fit models where the frailty distribution is normal and gamma and estimate variance components when frailty structure is allowed to be shared or nested.

References

- Ha, I. D. and Lee, Y. (2003). Estimating frailty models via Poisson Hierarchical generalized linear models. *Journal of Computational and Graphical Statistics*, 12, 663–681.
- Ha, I. D. and Lee, Y. (2005). Comparison of hierarchical likelihood versus orthodox best linear unbiased predictor approaches for frailty models. *Biometrika*, 92, 717–723.
- Ha, I. D., Lee, Y. and Song, J. K. (2001). Hierarchical likelihood approach for frailty models. *Biometrika*, 88, 233–243.
- Lee, Y., Nelder, J. A. and Pawitan, Y. (2006). *Generalised linear models with random effects: unified analysis via h-likelihood*. Chapman & Hall: London.

See Also

[<summary.frailtyHL>](#)

Examples

```
#### Analysis of kidney data
data(kidney)
#### Normal frailty model using order = 0, 1 for the mean and dispersion
kidney_ln01<-frailtyHL(Surv(time,status)~sex+age+(1|id),kidney,
RandDist="Normal",mord=0,dord=1)
#### Normal frailty model using order = 1, 1 for the mean and dispersion
kidney_ln11<-frailtyHL(Surv(time,status)~sex+age+(1|id),kidney,
RandDist="Normal",mord=1,dord=1)
#### Gamma frailty model using order = 0, 2 for the mean and dispersion
kidney_g02<-frailtyHL(Surv(time,status)~sex+age+(1|id),kidney,
RandDist="Gamma",mord=0,dord=2)
#### Gamma frailty model using order = 1, 2 for the mean and dispersion
kidney_g12<-frailtyHL(Surv(time,status)~sex+age+(1|id),kidney,
RandDist="Gamma",mord=1,dord=2)

#### Analysis of rats data
data(rats)
#### Cox model
rat_cox<-frailtyHL(Surv(time,status)~rx+(1|litter),rats,
varfixed=TRUE,varinit=c(0))
#### Normal frailty model using order = 1, 1 for the mean and dispersion
rat_ln11<-frailtyHL(Surv(time,status)~rx+(1|litter),rats,
```

```

RandDist="Normal",mord=1,dord=1,varinit=c(0.9))
#### Gamma frailty model using order = 1, 2 for the mean and dispersion
rat_g12<-frailtyHL(Surv(time,status)~rx+(1|litter),rats,
RandDist="Gamma",mord=1,dord=2,convergence=10^-4,varinit=c(0.9))

#### Analysis of CGD data
data(cgd)
#### Multilevel normal frailty model using order = 1, 1 for the mean and dispersion
cgd_ln11<-frailtyHL(Surv(tstop-tstart,status)~treat+(1|center)+(1|id),cgd,
RandDist="Normal",mord=1,dord=1,convergence=10^-4,varinit=c(0.03,1.0))

```

kidney

Kidney Infection Data

Description

The data presented by McGilchrist and Aisbett (1991) consist of times to the first and second recurrences of infection in 38 kidney patients using a portable dialysis machine. Infections can occur at the location of insertion of the catheter. The catheter is later removed if infection occurs and can be removed for other reasons, in which case the observation is censored.

Usage

```
data(kidney)
```

Format

Kidney data set contains 8 columns and 76 rows. A brief description of the data column is given below.

id Patient number for 38 patients.
time Time to infection since insertion of the catheter
status Censoring indicator(1=uncensored, 0=censored).
age Age of each patient, in years.
sex Sex of each patient(1=male, 2=female).
disease Disease type(GN, AN, PKD, Other).
frail Frailty estimate from original paper.

References

McGilchrist, C. A. and Aisbett, C. W. (1991). Regression with frailty in survival analysis. *Biometrics*, 47, 461–466.

Therneau, T. (2012). survival: survival analysis, including penalised likelihood. <http://CRAN.R-project.org/package=survival>. R package version 2.36-14.

Examples

```
data(kidney)
```

rats	<i>Rats data</i>
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Description

Rats data set presented by Mantel et al. (1977) is based on a tumorigenesis study of 50 litters of female rats. For each litter, one rat was selected to receive the drug and the other two rats were placebo-treated controls. The survival time is the time to the development of tumor, measured in weeks. Death before occurrence of tumor yields a right-censored observation; 40 rats developed a tumor, leading to censoring of about 73 percent.

Usage

```
data(rats)
```

Format

Rats data set contains 4 columns and 150 rows. A brief description of the data column is given below.

`litter` Litter number for 50 female rats.

`rx` Treatment(1=drug, 0=placebo)

`time` Time to the development of tumor in weeks.

`status` Censoring indicator(1=uncensored, 0=censored).

References

Mantel, N., Bohidar N. R. and Ciminera, J. L. (1977). Mantel-Haenszel analyses of litter-matched time-to-response data, with modifications for recovery of interlitter information. *Cancer Research*, 37, 3863–3868.

Therneau, T. (2012). *survival: survival analysis, including penalised likelihood*. <http://CRAN.R-project.org/package=survival>. R package version 2.36-14.

Examples

```
data(rats)
```

summary.frailtyHL *Summary Method for frailtyHL Object*

Description

It provides standard summary statistics for the fitted frailtyHL objects.

Usage

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

Arguments

object	A frailtyHL object.
...	other arguments

Details

When applied to a frailtyHL object summary statistics are produced if the underlying model estimation converged. Otherwise, produces an error message.

Value

It returns a list of summary.frailtyHL object containing the following statistics and tables.

Model	A selected model of log-normal or gamma frailty models.
formula	The formula used in the underlying frailtyHL .
Method	The order of Laplace approximation mord and dord used in the underlying frailtyHL .
FixCoef	A two-dimensional matrix of fixed effects parameter estimates, repective standard errors and t-values.
RandCoef	A two-dimensional matrix of random effects estimates and repective standard errors.
likelihood	Vectors of $-2 * \text{likleihood}$.
iter	Number of iterations used in frailtyHL estimation.
convergence	A text, "converged" if the estimation converged and "did not converge" oterwise.
aic	Three AIC criteria(cAIC, mAIC, rAIC) based on conditional likelihood, marginal likelihood and restricted likelihood

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