Package ‘invGauss’

February 20, 2015

Type Package
Title Threshold regression that fits the (randomized drift) inverse Gaussian distribution to survival data.
Version 1.1
Date 2014-03-29
Author Hakon K. Gjessing
Maintainer Hakon K. Gjessing <hakon.gjessing@fhi.no>
Depends survival
Imports optimx
Description invGauss fits the (randomized drift) inverse Gaussian distribution to survival data. The model is described in Aalen OO, Borgan O, Gjessing HK. Survival and Event History Analysis. A Process Point of View. Springer, 2008. It is based on describing time to event as the barrier hitting time of a Wiener process, where drift towards the barrier has been randomized with a Gaussian distribution. The model allows covariates to influence starting values of the Wiener process and/or average drift towards a barrier, with a user-defined choice of link functions.
License GPL (>= 2)
URL http://www.uib.no/smis/gjessing/projects/invgauss/
NeedsCompilation no
Repository CRAN
Date/Publication 2014-03-28 14:06:47

R topics documented:

d.orophar.rec ......................................................... 2
invGauss ............................................................. 3
summary.invGauss .................................................. 5

Index 8
Carcinoma of the oropharynx

Description

An example from clinical medicine given by Kalbfleisch and Prentice (2002), a clinical trial on 195 patients with carcinoma of the oropharynx carried out by the Radiation Therapy Oncology Group in the United States. The patients were randomized into two treatment groups ("standard" and "test" treatment), and survival times were measured in days (rather, years in this recoded data set) from diagnosis.

Usage

d.oropa.rec

Format

A number of covariates were recorded for each patient at the entry to the study:

sex  (1 = male, 2 = female)
treatment group  (1 = standard, 2 = test)
grade  (1 = well differentiated, 2 = moderately differentiated, 3 = poorly differentiated)
age in years at diagnosis
condition  (1 = no disability, 2 = restricted work, 3 = requires assistance with self-care, 4 = confined to bed)
T-stage  (an index of size and infiltration of tumor ranging from 1 to 4, with 1 indicating a small tumor and 4 a massive invasive tumor)
N-stage  (an index of lymph node metastasis ranging from 0 to 3, with 0 indicating no evidence of metastases and 3 indicating multiple positive nodes or fixed positive nodes)

References

invGauss

Threshold regression that fits the (randomized drift) inverse Gaussian distribution to survival data.

Description

invGauss fits the (randomized drift) inverse Gaussian distribution to survival data. The model is described in Aalen OO, Borgan O, Gjessing HK. Survival and Event History Analysis. A Process Point of View. Springer, 2008. It is based on describing time to event as the barrier hitting time of a Wiener process, where drift towards the barrier has been randomized with a Gaussian distribution. The model allows covariates to influence starting values of the Wiener process and/or average drift towards a barrier, with a user-defined choice of link functions.

Usage

invGauss(formula.mu, formula.c = ~1, link.mu = identity, link.c = exp, data, mu = TRUE, tau = TRUE, verbose = FALSE, protect = FALSE, opti.method = "BFGS", use.gradient = TRUE, link.mu.deriv = function(x) 1, link.c.deriv = exp)

Arguments

formula.mu Standard survival formula, like formula.mu = Surv(time, status) ~ covar1 + covar2.
formula.c Formula without the left hand side, like formula.c = ~ covar1 + covar2.
link.mu Link function used with formula.mu. Default is identity. Note that it should be the function itself, not the name of the function.
link.c Link function used with formula.c. Default is exp. Note that it should be the function itself, not the name of the function.
data Data frame to be used.
mu If you need to supply your own initial value for mu. If mu is numeric, invGauss will use it as the initial value, otherwise (if mu = TRUE) it will provide a rough estimate for an initial value.
tau Like mu above.
verbose If TRUE, invGauss prints some information along the way.
protect Somewhat experimental. If TRUE, possible negative values in the likelihood are eliminated to avoid crashes. Probably most useful when link is identity.
opti.method invGauss uses the optimx package to provide a selection of optimization tools. Default is "BFGS", which calls the optim function with method = "BFGS". The standard optim default of "Nelder-Mead" seems at times unreliable when used in invGauss. See the optimx package documentation for other options.
use.gradient By default, invGauss uses analytical gradients in the optimization.
link.mu.deriv If the user modifies link.mu and use.gradient = TRUE, the derivative of the link function must also be supplied. See Details.
link.c.deriv If the user modifies link.c and use.gradient = TRUE, the derivative of the link function must also be supplied. See Details.
invGauss uses by default analytical gradients in the optimization, although this does not appear to make much difference. When `use.gradient = TRUE` if the user changes one of the link functions, the corresponding derivative must also be supplied. For instance, if `link.mu` is set to `exp`, so should `link.mu.deriv`. Similarly, if, for instance, `link.c` is changed to `identity`, then `link.c.deriv` should be function(x) 1.


**Value**

An object of class `invGauss` is returned. This is a list, where the most important elements are:

- **coefficients**: Estimated coefficients
- **cov.unscaled**: The variance-covariance matrix of the estimated coefficients
- **loglik**: The maximized log-likelihood
- **AIC**: AIC value

The `summary` function provides more details about the result, in particular coefficient values with standard errors, Z statistic, and Wald tests.

(There is also an undocumented `invGauss::predict.invGauss` function, but use it at your own risk...)

**Warning**

For some datasets, `invGauss` may have a hard time converging. This may be due to either inappropriate parameter starting values or a hazard shape that is incompatible with the hitting time distribution. Running a simpler model or setting the starting values manually may help. Sometimes, the exact choice of zero on the time scale may be important since some of the model hazards increase steeply immediately after zero. Adding or subtracting a small value from all event/censoring times may help. The new default optimization method "BFGS" seems to do a better job than "Nelder-Mead".

**Note**

Further information is found on the web page.

**Author(s)**

Hakon K. Gjessing  
Professor of Biostatistics  
Division of Epidemiology  
Norwegian Institute of Public Health  
<hakon.gjessing@fhi.no>  
[http://www.uib.no/smis/gjessing](http://www.uib.no/smis/gjessing)
References
Web Site: http://www.uib.no/smis/gjessing/projects/invgauss/

See Also
summary.invGauss

Examples

# Simple run:
data(d.orophare.rec)
res <- invGauss(formula = surv(time, status) ~ 1, data = d.orophare.rec)
summary(res)

# Use covariates for c, with exponential link function
data(d.orophare.rec)
res <- invGauss(formula = surv(time, status) ~ 1, formula.c = ~ cond + nstage + tstage, data = d.orophare.rec) # MODEL 5 (TABLE 10.2, page 412) IN SPRINGER BOOK
summary(res)

summary.invGauss  Summarize the estimation result from invGauss

Description
To be used on a result from invGauss. The summary function provides estimates, standard errors etc.

Usage
## S3 method for class 'invGauss'
summary(object, covariance = FALSE, ...)

Arguments

  object          Result from running invGauss.
  covariance     Logical, indicates whether the asymptotic variance-covariance matrix for the parameter estimates should be returned.
                  ...
  ...            Other arguments (ignored).
Details


Value

Returns a list with the most important results from invGauss, including coefficients with standard errors and Wald tests:

- **coefficients**: Estimated coefficients, with standard errors and Wald tests
- **cov.unscaled**: The variance-covariance matrix of the estimated coefficients
- **loglik**: The maximized log-likelihood
- **AIC**: AIC value

Note

Further information is found on the web page

Author(s)

Hakon K. Gjessing
Professor of Biostatistics
Division of Epidemiology
Norwegian Institute of Public Health
<hakon.gjessing@fhi.no>
http://www.uib.no/smis/gjessing

References

Web Site: http://www.uib.no/smis/gjessing/projects/invgauss/

See Also

invGauss

Examples

```r
# Simple run:
data(d.orophia.rec)
res <- invGauss(formula=Surv(time, status) ~ 1, data = d.orophia.rec)
summary(res)
```
# Use covariates for c, with exponential link function

```r
data(d.orofha.rec)
res <- invGauss(formula.mu = Surv(time, status) ~ 1, formula.c = ~ cond + nstage + tstage,
data = d.orofha.rec) # MODEL 5 (TABLE 10.2) IN SPRINGER BOOK
summary(res)
```
Index

*Topic datasets
  d.oropharec, 2

d.oropharec, 2

invGauss, 3, 6

summary.invGauss, 5, 5