Package 'ICGOR'

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Type Package

Title Fit Generalized Odds Rate Hazards Model with Interval Censored
Data

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Description
Generalized Odds Rate Hazards (GORH) model is a flexible model of fitting survival data, in-
cluding the Proportional Hazards (PH) model and the Proportional Odds (PO) Model as spe-
cial cases. This package fit the GORH model with interval censored data.

License GPL (>= 2)

Depends R (>= 2.15.0),stats,graphics,survival,ICsurv,pracma,MASS

NeedsCompilation no

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Description

Generalized Odds Rate Hazards (GORH) model is a flexible survival model which includes the Proportional Hazards (PH) model and the Proportional Odds (PO) model as special cases. When the survival data is interval censored, this package provides an efficient solution for the GORH model based on a gamma-possion data augmentation.

Details

Package:	ICGOR
Type:	Package
Version:	2.0
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License:	GPL-2

The main function is GORH, which produces the estimates for coefficients and the covariance matrix. The summary function can be used to get the test results of the coefficients. The predict function can be used to obtain the estimated survival curve for an individual with specified covariates. The plot function can be applied to generate the predicted survival curve for that individual.

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References

Zhou, J., Zhang, J. and Lu, W. (2017+). An EM Algorithm for fitting the Generalized Odds-Rate Model to Interval Censored Data. Accepted by Statistics in Medicine.

| GORH | *The Main Function to Fit the GORH Model with Interval Censored Data.* |

Description

The Generalized Odds Rate Hazards model is fitted for interval censored survival data. The EM algorithm facilitated by a gamma-poisson data augmentation is applied for estimating the coefficients in the model. The covariance matrix has closed forms based on the Louis method.

Usage

```
GORH(formula = formula(data), data = parent.frame(), r = 1, n.int = 5, order = 3,
max.iter = 1000, cov.rate = 0.001)
```

Arguments

formula	The formula for the GORH model, defined using the Surv() function.
data	The interval censored sorvival data, including the left and right end points of the time intervals and the covariates. If a subject is left(right) censored, the left(right) end point of the subject should be defined as "NA", see example.
r	The transformation parameter in the GORH model, should be greater than 0. The default is r=1 (the PO model).
n.int	Number of equally spaced interior knots of the splines. Default is 5.
order	Order of the spline basis functions. Default is 3, i.e. the cubic splines.
max.iter	The maximum number of interations for the EM algorithm. Default is 100.
cov.rate	The bound for convergence of the algorithm, which defined as the difference between the log-likelihood values of two consecutive iterations smaller than this value. Default is 0.001.

Details

The formula defined for "formula" is based on the Surv() function, where the left and right end points of the time interval are included and the type is equal to "interval2". The left(right) end points of left(right) censored individuals should be defined as "NA" in the data frame before running the function.\ The transformation parameter r is a positive number corresponding to a specific model in the GORH family of models. The special case POMC model(r=1) is set as the default. Other positive numbers can also be specified. The result for a PH model can be approximated by specifying an extremely small number for r, e.g. r=1e-6.\ The grid search method is suggested to find the best model in practice. That is, try a sequence of r values and choose the one with the greatest log-likelihood value.

Value

ParEst	A list includes the estimated coefficients (Beta,gl), the whole hessian matrix (Hessian), AIC, and the log-likelihood value(loglik).
ParVcov	The estimated covariance matrix of the coefficient Beta.

Note

The estimated hessian matrix can be very large and sometimes not invertable. In which case, we try the QR decomposition, g-inverse or even numerical methods to get the covariance matrix. Different values of hess in the ParVcov indicating the different cases. hess=0:the hessian matrix is invertable; hess=1:the QR decomposition is applied to solve the hessian matrix; hess=2:the g-inverce is applied to the hessian matrix; hess=3:the hessian matrix is obtained from numerical methods. The variance estimates may be unreliable for the cases when hess>0.

References

Zhou, J., Zhang, J. and Lu, W. (2017+). An EM Algorithm for fitting the Generalized Odds-Rate Model to Interval Censored Data. Accepted by Statistics in Medicine.

Examples

```
data(Hemophilia)
# Set Left/Right Interval End Points as NA
Hemophilia$L[Hemophilia$d1==1]<-Hemophilia$R[Hemophilia$d3==1]<-NA
# Fit PO Model (r=1)
fit<-GORH(Surv(L,R)~Low+Medium+High,data=Hemophilia,r=1)
summary(fit)

# Predict Survival Curve for a New Individual
# Specify coveriate vectors for new.x
pred1<-predict(fit,new.x=c(0,0,0))
pred2<-predict(fit,new.x=c(1,0,0))
pred3<-predict(fit,new.x=c(0,1,0))
pred4<-predict(fit,new.x=c(0,0,1))

# Plot the Survival Curves
plot(pred1,xlab="Time",ylab="Survival Probability",ylim=c(0,1))
lines(pred2$SurvTime,pred2$SurvProb,col=2)
lines(pred3$SurvTime,pred3$SurvProb,col=3)
lines(pred4$SurvTime,pred4$SurvProb,col=4)
legend(0,0.2,c("None","Low","Medium","High"),lty=1,col=1:4)
```

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plot.predict.GORH   *Plot the predicted survival curves.*

Description

Plot the predicted survival curve of the new subject.

Usage

```
## S3 method for class 'predict.GORH'
plot(x, ...)
```

Arguments

x	An object from the predict.GORH function.
...	Other plot arguments.

---

predict.GORH   *Predict survival probabilities for a new subject.*

Description

Based on the predicted model, survival probabilities are calculated for a new individual with specific covariate values. The new.x specifies the covariate vector in the GORH model for the new individual. If no values are specified, zeros will be used and the baseline survival probabilities are returned.

Usage

```
## S3 method for class 'GORH'
predict(object, ...)
```

Arguments

object	An object from the function GORH.
...	Other argumetns including new.x. See details.

Details

For a new subject, new.x gives the covariate vector in the GORH model. The argument tp gives the sequence of time points that you want to calculate the survival probabilities. If tp is not specified, then a sequence of equally spaced numbers from 0 to the largest observation time in the data are used and another argument len defines the number of equally spaced time points for calculating the survival curve, default is 100.

Value

SurvTime	Survival time points used for calculation of the survival probabilities.
SurvProb	Survival probabilities of the new individual.

---

summary.GORH   *Summary table of hypothesis tests for the coefficients in the GORH model.*

Description

Estimates, standard errors, test statistics and p values are presented for each coefficient in the GORH model.

Usage

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

Arguments

`object`	An object from the function GORH.
`...`	Other auguments to be specified.

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