

# Package ‘GORCure’

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**Type** Package

**Title** Fit Generalized Odds Rate Mixture Cure Model with Interval  
Censored Data

**Version** 2.0

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**Description** Generalized Odds Rate Mixture Cure (GORMC) model is a flexible model of fitting survival data with a cure fraction, including the Proportional Hazards Mixture Cure (PHMC) model and the Proportional Odds Mixture Cure Model as special cases. This package fit the GORMC model with interval censored data.

**License** GPL (>= 2)

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

**NeedsCompilation** no

**Repository** CRAN

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GORCure-package	<i>Fit Generalized Odds Rate Mixture Cure Model with Interval Censored Data</i>
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### Description

Generalized Odds Rate Mixture Cure (GORMC) model is a flexible cure model which includes the Proportional Hazards Mixture Cure (PHMC) model and the Proportional Odds Mixture Cure (POMC) model as special cases. When the survival data is interval censored, this package provides an efficient solution for the GORMC model based on a gamma-poisson data augmentation.

### Details

Package:	GORCure
Type:	Package
Version:	2.0
Date:	2017-01-12
License:	GPL-2

The main function is GORMC, 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 cure rate and survival curve for an individual with specified covariates for the cure rate and survival parts separately. 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+). Computationally Efficient Estimation for the Generalized Odds Rate Mixture Cure Model with Interval Censored Data.

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GORMC	<i>Fitting the GORMC model with interval censored data.</i>
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### Description

The Generalized Odds Rate Mixture Cure 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 both the cure rate part and the survival part. The covariance matrix has closed forms based on the Louis method.

**Usage**

```
GORMC(survfun = formula(data), curefun = formula(data), data = parent.frame(),
      r = 0, n.int = 5, order = 3, max.iter = 1000, cov.rate = 0.001)
```

**Arguments**

survfun	A formula for the survival part in the GORMC model, defined using the Surv function and type="interval2".
curefun	The formula of predictors of the cure rate part in the GORMC model.
data	The interval censored survival data, including the left and right end points of the time intervals and the covariates for the cure rate part and the survival part. 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 GORMC model, should be greater than or equal to 0. r=0 refers to the PHMC model and r=1 refers to the POMC model. The default is 0.
n.int	Number of 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 iterations for the EM algorithm. Default is 1000.
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 "survfun" 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 nonnegative number corresponding to a specific model in the GORMC family of models. Special cases include the PHMC model(r=0) and the POMC model(r=1). Other positive numbers can also be specified. 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 (Eta,Beta,g1), the whole hessian matrix (Hessian), AIC, and the log-likelihood value(loglik).
ParVcov	The estimated covariance matrix of the coefficients Eta and 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+). Computationally Efficient Estimation for the Generalized Odds Rate Mixture Cure Model with Interval Censored Data.

## Examples

```

data(Hemophilia)
head(Hemophilia)
# Set Left/Right Interval End Points as NA
Hemophilia$L[Hemophilia$d1==1]<-Hemophilia$R[Hemophilia$d3==1]<-NA

# Fit PHMC Model (r=0)
fit<-GORMC(survfun=Surv(L,R)~Low+Medium+High,curefun=~Low+Medium+High,
data=Hemophilia,r=0)
summary(fit)

# Fit POMC Model (r=1)
# fit<-GORMC(survfun=Surv(L,R)~Low+Medium+High,curefun=~Low+Medium+High,
# data=Hemophilia,r=1)
# summary(fit)

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

# Obtain Cure Rates
pred1$CureRate
pred2$CureRate
pred3$CureRate
pred4$CureRate

# Plot the Survival Curves
plot(pred1,xlab="Time",ylab="Survival Probability",ylim=c(0,1))
lines(pred2$Survival,col=2)
lines(pred3$Survival,col=3)
lines(pred4$Survival,col=4)
legend(0,0.3,c("None","Low","Medium","High"),lty=1,col=1:4)

# Not run: Grid Search r
# rr<-seq(0,2,0.2)
# logl<-numeric()
# for(i in 1:length(rr)){
# fit<-GORMC(survfun=Surv(L,R)~Low+Medium+High,curefun=~Low+Medium+High,
# data=Hemophilia,r=rr[i])
# logl[i]<-fit$ParEst$loglik
# }
# plot(rr,logl,type="l",xlab="r",ylab="Log-likelihood")

```

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

---

### Description

Plot the predicted survival curve of the new subject.

### Usage

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

### Arguments

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

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predict.GORMC              *Predict cure rate and overall survival curve for a new subject.*

---

### Description

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

### Usage

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

### Arguments

object                  An object from the function GORMC.  
 ...                    Other argumetns including new.x and new.z. See details.

### Details

For a new subject, new.x and new.z correspond to the covariate vector in the survival part and the cure rate part. The first input of new.z is always 1 corresponding to the intercept. tp is an argument specifying the time points at which survival probabilities will be predicted. If no value specified for tp, a sequence of equally spaced time points from 0 to the largest observation time will be used and the total length of the sequence is defined by an argument len. The default value of len is 100.

**Value**

CureRate	Estimated cure rate of the new subject.
Survival	A data frame including the time points and survival probabilities.

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summary.GORMC	<i>Summary table of hypothesis tests for the coefficients in the GORMC model.</i>
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**Description**

Estimates, standard errors, test statistics and p values are presented for each coefficient in the GORMC model. The "INC" indicate the covariate is in the cure rate (incidence) part, "LAT" indicate the covariate is in the survival (latency) part.

**Usage**

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

**Arguments**

object	An object from the function GORMC.
...	Other arguments to be specified.

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