

# Package ‘genSurv’

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**Title** Generating Multi-State Survival Data

**Depends** R (>= 2.12.0)

**Suggests** survival

**Description** Generation of survival data with one (binary) time-dependent covariate. Generation of survival data arising from a progressive illness-death model.

**License** GPL-3

**URL** <https://github.com/arturstat/genSurv>

**BugReports** <https://github.com/arturstat/genSurv/issues>

**LazyLoad** yes

**NeedsCompilation** yes

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genSurv-package	<i>Generating Multi-State Survival Data</i>
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## Description

The **genSurv** software permits to generate data with one binary time-dependent covariate and data stemming from a progressive illness-death model.

## Details

Package:	genSurv
Type:	Package
Version:	1.0.6
Date:	2026-04-05
License:	GPL-3
LazyLoad:	yes

## Author(s)

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## References

- Anderson, P.K., Gill, R.D. (1982). Cox's regression model for counting processes: a large sample study. *Annals of Statistics*, **10**(4), 1100-1120. doi:[10.1214/aos/1176345976](https://doi.org/10.1214/aos/1176345976)
- Cox, D.R. (1972). Regression models and life tables. *Journal of the Royal Statistical Society: Series B*, **34**(2), 187-202. doi:[10.1111/j.25176161.1972.tb00899.x](https://doi.org/10.1111/j.25176161.1972.tb00899.x)
- Jackson, C. (2011). Multi-State Models for Panel Data: The msm Package for R. *Journal of Statistical Software*, **38**(8), 1-28. doi:[10.18637/jss.v038.i08](https://doi.org/10.18637/jss.v038.i08)
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- Johnson, N., Kotz, S. (1972). *Distribution in statistics: continuous multivariate distributions*, John Wiley and Sons.
- Lu J., Bhattacharya G. (1990). Some new constructions of bivariate weibull models. *Annals of Institute of Statistical Mathematics*, **42**(3), 543-559. doi:[10.1007/BF00049307](https://doi.org/10.1007/BF00049307)

Meira-Machado, L., Cadarso-Suárez, C., De Uña- Álvarez, J., Andersen, P.K. (2009). Multi-state models for the analysis of time to event data. *Statistical Methods in Medical Research*, **18**(2), 195-222. doi:[10.1177/0962280208092301](https://doi.org/10.1177/0962280208092301)

Meira-Machado L., Faria S. (2014). A simulation study comparing modeling approaches in an illness-death multi-state model. *Communications in Statistics - Simulation and Computation*, **43**(5), 929-946. doi:[10.1080/03610918.2012.718841](https://doi.org/10.1080/03610918.2012.718841)

Meira-Machado, L., Roca-Pardiñas, J. (2011). p3state.msm: Analyzing Survival Data from an Illness-Death Model. *Journal of Statistical Software*, **38**(3), 1-18. doi:[10.18637/jss.v038.i03](https://doi.org/10.18637/jss.v038.i03)

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Therneau, T.M., Grambsch, P.M. (2000). *Modelling survival data: Extending the Cox Model*, New York: Springer.

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as.CMM

Coerce to an object of class CMM

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## Description

Function to coerce objects of class TDCM and THMM to objects of class CMM.

## Usage

```
as.CMM(x)
is.CMM(x)
```

## Arguments

x                    Any R object.

## Value

An object with two classes one being `data.frame` and the other `CMM`.

## Author(s)

Artur Araújo, Luís Meira Machado and Susana Faria

## References

Cox, D.R. (1972). Regression models and life tables. *Journal of the Royal Statistical Society: Series B*, **34**(2), 187-202. doi:[10.1111/j.25176161.1972.tb00899.x](https://doi.org/10.1111/j.25176161.1972.tb00899.x)

Jackson, C. (2011). Multi-State Models for Panel Data: The msm Package for R. *Journal of Statistical Software*, **38**(8), 1–28. doi:[10.18637/jss.v038.i08](https://doi.org/10.18637/jss.v038.i08)

Meira-Machado, L., Cadarso-Suárez, C., De Uña- Álvarez, J., Andersen, P.K. (2009). Multi-state models for the analysis of time to event data. *Statistical Methods in Medical Research*, **18**(2), 195-222.

Meira-Machado L., Faria S. (2014). A simulation study comparing modeling approaches in an illness-death multi-state model. *Communications in Statistics - Simulation and Computation*, **43**(5), 929-946. doi:10.1080/03610918.2012.718841

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Meira-Machado, L., Sestelo M. (2019). Estimation in the progressive illness-death model: a nonexhaustive review. *Biometrical Journal*, **61**(2), 245–263. doi:10.1002/bimj.201700200

Therneau, T.M., Grambsch, P.M. (2000). *Modelling survival data: Extending the Cox Model*, New York: Springer.

### See Also

[as.TDCM](#), [as.THMM](#), [genCMM](#), [genTDCM](#), [genTHMM](#).

### Examples

```
# generate TDCM data
tdcmdata <- genTDCM(n=100, dist="exponential", corr=0, dist.par=c(1,1),
model.cens="uniform", cens.par=1, beta=c(-3,2), lambda=10)

# coerce TDCM data to CMM data
cmmdata0 <- as.CMM(tcmdata)
head(cmmdata0, n=20L)

# generate THMM data
thmmdata <- genTHMM( n=100, model.cens="uniform", cens.par=80, beta= c(0.09,0.08,-0.09),
covar=80, rate= c(0.05,0.04,0.05) )

# coerce THMM data to CMM data
cmmdata1 <- as.CMM(thmmdata)
head(cmmdata1, n=20L)
```

---

as.TDCM

*Coerce to an object of class TDCM*

---

### Description

Function to coerce objects of class CMM and THMM to objects of class TDCM.

### Usage

```
as.TDCM(x)
is.TDCM(x)
```

### Arguments

x Any R object.

**Value**

An object with two classes one being `data.frame` and the other `TDCM`.

**Author(s)**

Artur Araújo, Luís Meira Machado and Susana Faria

**References**

- Cox, D.R. (1972). Regression models and life tables. *Journal of the Royal Statistical Society: Series B*, **34**(2), 187-202. doi:[10.1111/j.25176161.1972.tb00899.x](https://doi.org/10.1111/j.25176161.1972.tb00899.x)
- Jackson, C. (2011). Multi-State Models for Panel Data: The `msm` Package for R. *Journal of Statistical Software*, **38**(8), 1–28. doi:[10.18637/jss.v038.i08](https://doi.org/10.18637/jss.v038.i08)
- Meira-Machado, L., Cadarso-Suárez, C., De Uña-Álvarez, J., Andersen, P.K. (2009). Multi-state models for the analysis of time to event data. *Statistical Methods in Medical Research*, **18**(2), 195-222. doi:[10.1177/0962280208092301](https://doi.org/10.1177/0962280208092301)
- Meira-Machado L., Faria S. (2014). A simulation study comparing modeling approaches in an illness-death multi-state model. *Communications in Statistics - Simulation and Computation*, **43**(5), 929-946. doi:[10.1080/03610918.2012.718841](https://doi.org/10.1080/03610918.2012.718841)
- Meira-Machado, L., Roca-Pardiñas, J. (2011). `p3state.msm`: Analyzing Survival Data from an Illness-Death Model. *Journal of Statistical Software*, **38**(3), 1-18. doi:[10.18637/jss.v038.i03](https://doi.org/10.18637/jss.v038.i03)
- Meira-Machado, L., Sestelo M. (2019). Estimation in the progressive illness-death model: a nonexhaustive review. *Biometrical Journal*, **61**(2), 245–263. doi:[10.1002/bimj.201700200](https://doi.org/10.1002/bimj.201700200)
- Therneau, T.M., Grambsch, P.M. (2000). *Modelling survival data: Extending the Cox Model*, New York: Springer.

**See Also**

[as.CMM](#), [as.THMM](#), [genCMM](#), [genTDCM](#), [genTHMM](#).

**Examples**

```
# generate CMM data
cmmdata <- genCMM( n=1000, model.cens="uniform", cens.par=2.5, beta=c(2,1,-1),
covar=10, rate=c(1,5,1,5,1,5) )

# coerce CMM data to TDCM data
tdcmdata0 <- as.TDCM(cmmdata)
head(tcmdata0, n=20L)

# generate THMM data
thmmdata <- genTHMM( n=100, model.cens="uniform", cens.par=80, beta= c(0.09,0.08,-0.09),
covar=80, rate= c(0.05,0.04,0.05) )

# coerce THMM data to TDCM data
tdcmdata1 <- as.TDCM(thmmdata)
head(tcmdata1, n=20L)
```

---

`as.THMM`*Coerce to an object of class THMM*

---

## Description

Function to coerce objects of class CMM and TDCM to objects of class THMM.

## Usage

```
as.THMM(x)
is.THMM(x)
```

## Arguments

`x` Any R object.

## Value

An object with two classes one being `data.frame` and the other THMM.

## Author(s)

Artur Araújo, Luís Meira Machado and Susana Faria

## References

- Cox, D.R. (1972). Regression models and life tables. *Journal of the Royal Statistical Society: Series B*, **34**(2), 187-202. doi:[10.1111/j.25176161.1972.tb00899.x](https://doi.org/10.1111/j.25176161.1972.tb00899.x)
- Jackson, C. (2011). Multi-State Models for Panel Data: The msm Package for R. *Journal of Statistical Software*, **38**(8), 1–28. doi:[10.18637/jss.v038.i08](https://doi.org/10.18637/jss.v038.i08)
- Meira-Machado, L., Cadarso-Suárez, C., De Uña-Álvarez, J., Andersen, P.K. (2009). Multi-state models for the analysis of time to event data. *Statistical Methods in Medical Research*, **18**(2), 195-222. doi:[10.1177/0962280208092301](https://doi.org/10.1177/0962280208092301)
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- Meira-Machado, L., Sestelo M. (2019). Estimation in the progressive illness-death model: a nonexhaustive review. *Biometrical Journal*, **61**(2), 245–263. doi:[10.1002/bimj.201700200](https://doi.org/10.1002/bimj.201700200)
- Therneau, T.M., Grambsch, P.M. (2000). *Modelling survival data: Extending the Cox Model*, New York: Springer.

## See Also

`as.CMM`, `as.TDCM`, `genCMM`, `genTDCM`, `genTHMM`.

**Examples**

```
# generate CMM data
cmmdata <- genCMM( n=1000, model.cens="uniform", cens.par=2.5, beta=c(2,1,-1),
covar=10, rate=c(1,5,1,5,1,5) )

# coerce CMM data to THMM data
thmmdata0 <- as.THMM(cmmdata)
head(thmmdata0, n=20L)

# generate TDCM data
tdcmdata <- genTDCM(n=100, dist="exponential", corr=0, dist.par=c(1,1),
model.cens="uniform", cens.par=1, beta=c(-3,2), lambda=10)

# coerce TDCM data to THMM data
thmmdata1 <- as.THMM(tdcmdata)
head(thmmdata1, n=20L)
```

genCMM

*Generation of Cox Markov data from an illness-death model***Description**

Generation of Cox Markov data from an illness-death model.

**Usage**

```
genCMM(n, model.cens, cens.par, beta, covar, rate)
```

**Arguments**

n	Sample size.
model.cens	Model for censorship. Possible values are "uniform" and "exponential".
cens.par	Parameter for the censorship distribution. Must be greater than 0.
beta	Vector of three regression parameters for the three transitions: (beta_12,beta_13,beta_23).
covar	Parameter for generating the time-fixed covariate. An uniform distribution is used.
rate	Vector of dimension six: (shape1, scale1, shape2, scale2, shape3, scale3). A Weibull baseline hazard function is assumed (with two parameters) for each transition (see details below).

**Details**

The Weibull distribution with shape parameter  $\lambda$  and scale parameter  $\theta$  has hazard function given by:

$$\alpha(t) = \lambda\theta t^{\theta-1}$$

**Value**

An object with two classes, `data.frame` and `CMM`. The data structure used for generating survival data from the Cox Markov Model (CMM) is similar as for the time-dependent Cox model (TDCM). In this case the data structure has one more variable representing the transition (variable `trans`). `trans=1` denotes the transition from State 1 to State 3 (without observing the intermediate event; State 2); `trans=2` denotes the transition from State 1 to State 2; and `trans=3` denotes the transition from State 2 to State 3 (absorbing).

**Author(s)**

Artur Araújo, Luís Meira Machado and Susana Faria

**References**

Meira-Machado, L., Cadarso-Suárez, C., De Uña-Álvarez, J., Andersen, P.K. (2009). Multi-state models for the analysis of time to event data. *Statistical Methods in Medical Research*, **18**(2), 195-222. doi:[10.1177/0962280208092301](https://doi.org/10.1177/0962280208092301)

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Meira-Machado, L., Roca-Pardiñas, J. (2011). p3state.msm: Analyzing Survival Data from an Illness-Death Model. *Journal of Statistical Software*, **38**(3), 1-18. doi:[10.18637/jss.v038.i03](https://doi.org/10.18637/jss.v038.i03)

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Therneau, T.M., Grambsch, P.M. (2000). *Modelling survival data: Extending the Cox Model*, New York: Springer.

**See Also**

[genCPHM](#), [genTDCM](#), [genTHMM](#).

**Examples**

```
cmmdata <- genCMM( n=1000, model.cens="uniform", cens.par=2.5, beta=c(2,1,-1),
covar=10, rate=c(1,5,1,5,1,5) )
head(cmmdata, n=20L)
library(survival)
fit_13<-coxph(Surv(start,stop,event)~covariate, data=cmmdata, subset=c(trans==1))
fit_13
fit_12<-coxph(Surv(start,stop,event)~covariate, data=cmmdata, subset=c(trans==2))
fit_12
fit_23<-coxph(Surv(start,stop,event)~covariate, data=cmmdata, subset=c(trans==3))
fit_23
```

---

`genCPHM`*Generation of survival data from a Cox Proportional Hazard Model*

---

**Description**

Generation of survival data from a Cox Proportional Hazard Model.

**Usage**

```
genCPHM(n, model.cens, cens.par, beta, covar)
```

**Arguments**

<code>n</code>	Sample size.
<code>model.cens</code>	Model for censorship. Possible values are "uniform" and "exponential".
<code>cens.par</code>	Parameter for the censorship distribution. Must be greater than 0.
<code>beta</code>	Regression parameter for the time-fixed covariate.
<code>covar</code>	Parameter for generating the time-fixed covariate. An uniform distribution is used.

**Value**

An object with two classes, `data.frame` and `CPHM`.

**Author(s)**

Artur Araújo, Luís Meira Machado and Susana Faria

**References**

- Cox, D.R. (1972). Regression models and life tables. *Journal of the Royal Statistical Society: Series B*, **34**(2), 187-202. doi:[10.1111/j.25176161.1972.tb00899.x](https://doi.org/10.1111/j.25176161.1972.tb00899.x)
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- Meira-Machado, L., Sestelo M. (2019). Estimation in the progressive illness-death model: a nonexhaustive review. *Biometrical Journal*, **61**(2), 245–263. doi:[10.1002/bimj.201700200](https://doi.org/10.1002/bimj.201700200)

**See Also**

[genCMM](#), [genTDCM](#), [genTHMM](#).

**Examples**

```
cphmdata <- genCPHM(n=1000, model.cens="exponential", cens.par=2, beta= 2, covar=1)
head(cphmdata, n=20L)
library(survival)
fit<-coxph(Surv(time,status)~covariate,data=cphmdata)
summary(fit)
```

genTDCM

*Generating data from a Cox model with time-dependent covariates***Description**

Generating data from a Cox model with time-dependent covariates.

**Usage**

```
genTDCM(n, dist, corr, dist.par, model.cens, cens.par, beta, lambda)
```

**Arguments**

n	Sample size.
dist	Bivariate distribution assumed for generating the two covariates (time-fixed and time-dependent). Possible bivariate distributions are "exponential" and "weibull" (see details below).
corr	Correlation parameter. Possible values for the bivariate exponential distribution are between -1 and 1 (0 for independency). Any value between 0 (not included) and 1 (1 for independency) is accepted for the bivariate weibull distribution.
dist.par	Vector of parameters for the allowed distributions. Two (scale) parameters for the bivariate exponential distribution and four (2 shape parameters and 2 scale parameters) for the bivariate weibull distribution: (shape1, scale1, shape2, scale2). See details below.
model.cens	Model for censorship. Possible values are "uniform" and "exponential".
cens.par	Parameter for the censorship distribution. Must be greater than 0.
beta	Vector of two regression parameters for the two covariates.
lambda	Parameter for an exponential distribution. An exponential distribution is assumed for the baseline hazard function.

**Details**

The bivariate exponential distribution, also known as Farlie-Gumbel-Morgenstern distribution is given by

$$F(x, y) = F_1(x)F_2(y)[1 + \alpha(1 - F_1(x))(1 - F_2(y))]$$

for  $x \geq 0$  and  $y \geq 0$ . Where the marginal distribution functions  $F_1$  and  $F_2$  are exponential with scale parameters  $\theta_1$  and  $\theta_2$  and correlation parameter  $\alpha$ ,  $-1 \leq \alpha \leq 1$ .

The bivariate Weibull distribution with two-parameter marginal distributions. It's survival function is given by

$$S(x, y) = P(X > x, Y > y) = e^{-\left[\left(\frac{x}{\theta_1}\right)^{\frac{\beta_1}{\delta}} + \left(\frac{y}{\theta_2}\right)^{\frac{\beta_2}{\delta}}\right]^{\delta}}$$

Where  $0 < \delta \leq 1$  and each marginal distribution has shape parameter  $\beta_i$  and a scale parameter  $\theta_i$ ,  $i = 1, 2$ .

## Value

An object with two classes, `data.frame` and `TDCM`. To accommodate time-dependent effects, we used a counting process data-structure, introduced by Andersen and Gill (1982). In this data-structure, apart the time-fixed covariates (named `covariate`), an individual's survival data is expressed by three variables: `start`, `stop` and `event`. Individuals without change in the time-dependent covariate (named `tdcov`) are represented by only one line of data, whereas patients with a change in the time-dependent covariate must be represented by two lines. For these patients, the first line represents the time period until the change in the time-dependent covariate; the second line represents the time period that passes from that change to the end of the follow-up. For each line of data, variables `start` and `stop` mark the time interval (`start`, `stop`) for the data, while `event` is an indicator variable taking on value 1 if there was a death at time `stop`, and 0 otherwise. More details about this data-structure can be found in papers by (Meira-Machado et al., 2009).

## Author(s)

Artur Araújo, Luís Meira Machado and Susana Faria

## References

- Anderson, P.K., Gill, R.D. (1982). Cox's regression model for counting processes: a large sample study. *Annals of Statistics*, **10**(4), 1100-1120. doi:10.1214/aos/1176345976
- Cox, D.R. (1972). Regression models and life tables. *Journal of the Royal Statistical Society: Series B*, **34**(2), 187-202. doi:10.1111/j.25176161.1972.tb00899.x
- Johnson, M. E. (1987). *Multivariate Statistical Simulation*, John Wiley and Sons.
- Johnson, N., Kotz, S. (1972). *Distribution in statistics: continuous multivariate distributions*, John Wiley and Sons.
- Lu J., Bhattacharya G. (1990). Some new constructions of bivariate weibull models. *Annals of Institute of Statistical Mathematics*, **42**(3), 543-559. doi:10.1007/BF00049307
- Meira-Machado, L., Cadarso-Suárez, C., De Uña-Álvarez, J., Andersen, P.K. (2009). Multi-state models for the analysis of time to event data. *Statistical Methods in Medical Research*, **18**(2), 195-222. doi:10.1177/0962280208092301
- Meira-Machado L., Faria S. (2014). A simulation study comparing modeling approaches in an illness-death multi-state model. *Communications in Statistics - Simulation and Computation*, **43**(5), 929-946. doi:10.1080/03610918.2012.718841
- Meira-Machado, L., Sestelo M. (2019). Estimation in the progressive illness-death model: a nonexhaustive review. *Biometrical Journal*, **61**(2), 245-263. doi:10.1002/bimj.201700200
- Therneau, T.M., Grambsch, P.M. (2000). *Modelling survival data: Extending the Cox Model*, New York: Springer.

**See Also**

[genCMM](#), [genCPHM](#), [genTHMM](#).

**Examples**

```
tdcmdata <- genTDCM(n=1000, dist="weibull", corr=0.8, dist.par=c(2,3,2,3),
model.cens="uniform", cens.par=2.5, beta=c(-3.3,4), lambda=1)
head(tdcmdata, n=20L)
library(survival)
fit1<-coxph(Surv(start,stop,event)~tdcov+covariate,data=tdcmdata)
summary(fit1)

tdcmdata2 <- genTDCM(n=1000, dist="exponential", corr=0, dist.par=c(1,1),
model.cens="uniform", cens.par=1, beta=c(-3,2), lambda=0.5)
head(tdcmdata2, n=20L)
fit2<-coxph(Surv(start,stop,event)~tdcov+covariate,data=tdcmdata2)
summary(fit2)
```

---

genTHMM

*Generation of survival data from a time-homogeneous Markov model*

---

**Description**

Generation of survival data from a time-homogeneous Markov model.

**Usage**

```
genTHMM(n, model.cens, cens.par, beta, covar, rate)
```

**Arguments**

n	Sample size.
model.cens	Model for censorship. Possible values are "uniform" and "exponential".
cens.par	Parameter for the censorship distribution. Must be greater than 0.
beta	Vector of three regression parameters for the three transitions: (beta_12,beta_13,beta_23).
covar	Parameter for generating the time-fixed covariate. An uniform distribution is used.
rate	Vector of dimension three. We assume an exponential baseline hazard function with constant hazard rate for each transition.

**Value**

An object with two classes, `data.frame` and `THMM`. For generating survival data from the THMM model, the counting process data structure must contain the following variables: `id`, `time`, `state`, `covariate`. Each patient is identified by `id`. The variable `time` represents time for each interval of follow-up while variable `state` denotes the state of the individual. Variable `covariate` is the (time-fixed) covariate to be studied in the regression model. Individuals without change in the time dependent covariate are represented by two lines of data, whereas patients with a change in the time-dependent covariate must be represented by three lines.

**Author(s)**

Artur Araújo, Luís Meira Machado and Susana Faria

**References**

- Jackson, C. (2011). Multi-State Models for Panel Data: The msm Package for R. *Journal of Statistical Software*, **38**(8), 1–28. doi:10.18637/jss.v038.i08
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**See Also**

[genCMM](#), [genTDCM](#), [genCPHM](#).

**Examples**

```
thmdata <- genTHMM( n=100, model.cens="uniform", cens.par=80, beta= c(0.09,0.08,-0.09),  
covar=80, rate= c(0.05,0.04,0.05) )  
head(thmdata, n=20L)
```

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