

# Package ‘depCensoring’

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**Type** Package

**Title** Statistical Methods for Survival Data with Dependent Censoring

**Version** 0.1.4

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**Description** Several statistical methods for analyzing survival data under various forms of dependent censoring are implemented in the package. In addition to accounting for dependent censoring, it offers tools to adjust for unmeasured confounding factors. The implemented approaches allow users to estimate the dependency between survival time and dependent censoring time, based solely on observed survival data. For more details on the methods, refer to Deresa and Van Keilegom (2021) <[doi:10.1093/biomet/asaa095](https://doi.org/10.1093/biomet/asaa095)>, Czado and Van Keilegom (2023) <[doi:10.1093/biomet/asac067](https://doi.org/10.1093/biomet/asac067)>, Crommen et al. (2024) <[doi:10.1007/s11749-023-00903-9](https://doi.org/10.1007/s11749-023-00903-9)>, Deresa and Van Keilegom (2024) <[doi:10.1080/01621459.2022.2161387](https://doi.org/10.1080/01621459.2022.2161387)> and Willems et al. (2024+) <[doi:10.48550/arXiv.2403.11860](https://doi.org/10.48550/arXiv.2403.11860)>.

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<code>boot.fun</code>	<i>Nonparametric bootstrap approach for the dependent censoring model</i>
-----------------------	---

---

### Description

This function estimates the bootstrap standard errors for the finite-dimensional model parameters and for the non-parametric cumulative hazard function. Parallel computing using `foreach` has been used to speed up the estimation of standard errors.

### Usage

```
boot.fun(
  init,
  resData,
  X,
  W,
  lhat,
  cumL,
  dist,
  k,
  lb,
  ub,
  Obs.time,
  cop,
  n.boot,
  n.iter,
  ncore,
  eps
)
```

### Arguments

<code>init</code>	Initial values for the finite dimensional parameters obtained from the fit of <a href="#">fitDepCens</a>
<code>resData</code>	Data matrix with three columns; $Z$ = the observed survival time, $d1$ = the censoring indicator of $T$ and $d2$ = the censoring indicator of $C$ .
<code>X</code>	Data matrix with covariates related to $T$

W	Data matrix with covariates related to C. First column of W should be a vector of ones
lhat	Initial values for the hazard function obtained from the fit of <code>fitDepCens</code> based on the original data.
cumL	Initial values for the cumulative hazard function obtained from the fit of <code>fitDepCens</code> based on the original data.
dist	The distribution to be used for the dependent censoring time C. Only two distributions are allowed, i.e, Weibull and lognormal distributions. With the value "Weibull" as the default.
k	Dimension of X
lb	lower boundary for finite dimensional parameters
ub	Upper boundary for finite dimensional parameters
Obs.time	Observed survival time, which is the minimum of T, C and A, where A is the administrative censoring time.
cop	Which copula should be computed to account for dependency between T and C. This argument can take one of the values from <code>c("Gumbel", "Frank", "Normal")</code> .
n.boot	Number of bootstraps to use in the estimation of bootstrap standard errors.
n.iter	Number of iterations; the default is <code>n.iter = 20</code> . The larger the number of iterations, the longer the computational time.
ncore	The number of cores to use for parallel computation is configurable, with the default <code>ncore = 7</code> .
eps	Convergence error. This is set by the user in such away that the desired convergence is met; the default is <code>eps = 1e-3</code>

### Value

Bootstrap standard errors for parameter estimates and for estimated cumulative hazard function.

---

boot.funI	<i>Nonparametric bootstrap approach for the independent censoring model</i>
-----------	---

---

### Description

This function estimates the bootstrap standard errors for the finite-dimensional model parameters and for the non-parametric cumulative hazard function under the assumption of independent censoring. Parallel computing using `foreach` has been used to speed up the computation.

**Usage**

```
boot.funI(
  init,
  resData,
  X,
  W,
  lhat,
  cumL,
  dist,
  k,
  lb,
  ub,
  Obs.time,
  n.boot,
  n.iter,
  ncore,
  eps
)
```

**Arguments**

<code>init</code>	Initial values for the finite dimensional parameters obtained from the fit of <a href="#">fitIndepCens</a>
<code>resData</code>	Data matrix with three columns; $Z$ = the observed survival time, $d1$ = the censoring indicator of $T$ and $d2$ = the censoring indicator of $C$ .
<code>X</code>	Data matrix with covariates related to $T$
<code>W</code>	Data matrix with covariates related to $C$ . First column of $W$ should be a vector of ones
<code>lhat</code>	Initial values for the hazard function obtained from the fit of <a href="#">fitIndepCens</a> based on the original data
<code>cumL</code>	Initial values for the cumulative hazard function obtained from the fit of <a href="#">fitIndepCens</a> based on the original data
<code>dist</code>	The distribution to be used for the dependent censoring time $C$ . Only two distributions are allowed, i.e, Weibull and lognormal distributions. With the value "Weibull" as the default
<code>k</code>	Dimension of $X$
<code>lb</code>	lower boundary for finite dimensional parameters
<code>ub</code>	Upper boundary for finite dimensional parameters
<code>Obs.time</code>	Observed survival time, which is the minimum of $T$ , $C$ and $A$ , where $A$ is the administrative censoring time.
<code>n.boot</code>	Number of bootstraps to use in the estimation of bootstrap standard errors.
<code>n.iter</code>	Number of iterations; the default is <code>n.iter = 20</code> . The larger the number of iterations, the longer the computational time
<code>ncore</code>	The number of cores to use for parallel computation is configurable, with the default <code>ncore = 7</code> .
<code>eps</code>	Convergence error. This is set by the user in such away that the desired convergence is met; the default is <code>eps = 1e-3</code>

**Value**

Bootstrap standard errors for parameter estimates and for estimated cumulative hazard function.

---

boot.nonparTrans	<i>Nonparametric bootstrap approach for a Semiparametric transformation model under dependent censoring</i>
------------------	---

---

**Description**

This function estimates the bootstrap standard errors for the finite-dimensional model parameters and for the non-parametric transformation function. Parallel computing using foreach has been used to speed up the estimation of standard errors.

**Usage**

```
boot.nonparTrans(init, resData, X, W, n.boot, n.iter, eps)
```

**Arguments**

init	Initial values for the finite dimensional parameters obtained from the fit of <a href="#">NonParTrans</a>
resData	Data matrix with three columns; Z = the observed survival time, d1 = the censoring indicator of T and d2 = the censoring indicator of C.
X	Data matrix with covariates related to T
W	Data matrix with covariates related to C.
n.boot	Number of bootstraps to use in the estimation of bootstrap standard errors.
n.iter	Number of iterations; the default is n.iter = 15. The larger the number of iterations, the longer the computational time.
eps	Convergence error. This is set by the user in such away that the desired convergence is met; the default is eps = 1e-3

**Value**

Bootstrap standard errors for parameter estimates and for estimated cumulative hazard function.

---

Bvprob	<i>Compute bivariate survival probability</i>
--------	---

---

**Description**

This function calculates a bivariate survival probability based on multivariate normal distribution.

**Usage**

```
Bvprob(lx, ly, rho)
```

**Arguments**

lx	The first lower bound of integration
ly	The second lower bound
rho	Association parameter

---

chol2par	<i>Transform Cholesky decomposition to covariance matrix</i>
----------	--

---

**Description**

This function transforms the parameters of the Cholesky decomposition to the covariance matrix, represented as a the row-wise concatenation of the upper-triangular elements.

**Usage**

```
chol2par(par.chol1)
```

**Arguments**

par.chol1	The vector of Cholesky parameters.
-----------	------------------------------------

**Value**

Covariance matrix corresponding to the provided Cholesky decomposition.

---

<code>chol2par.elem</code>	<i>Transform Cholesky decomposition to covariance matrix parameter element.</i>
----------------------------	---

---

### Description

This function transforms the parameters of the Cholesky decomposition to a covariance matrix element. This function is used in `chol2par.R`.

### Usage

```
chol2par.elem(a, b, par.chol1)
```

### Arguments

<code>a</code>	The row index of the covariance matrix element to be computed.
<code>b</code>	The column index of the covariance matrix element to be computed.
<code>par.chol1</code>	The vector of Cholesky parameters.

### Value

Specified element of the covariance matrix resulting from the provided Cholesky decomposition.

---

<code>CompC</code>	<i>Compute phi function</i>
--------------------	-----------------------------

---

### Description

This function estimates phi function at fixed time point `t`

### Usage

```
CompC(theta, t, X, W, ld, cop, dist)
```

### Arguments

<code>theta</code>	Estimated parameter values/initial values for finite dimensional parameters
<code>t</code>	A fixed time point
<code>X</code>	Data matrix with covariates related to T
<code>W</code>	Data matrix with covariates related to C. First column of W should be ones
<code>ld</code>	Output of <code>Solve1</code> function at a fixed time <code>t</code>
<code>cop</code>	Which copula should be computed to account for dependency between T and C. This argument can take one of the values from <code>c("Gumbel", "Frank", "Normal")</code> . The default copula model is "Frank".



dist	The distribution to be used for the dependent censoring C. Only two distributions are allowed, i.e, Weibull and lognormal distributions. With the value "Weibull" as the default.
------	---

---

cr.lik	<i>Competing risk likelihood function.</i>
--------	--

---

### Description

This function implements the second step likelihood function of the competing risk model defined in Willems et al. (2024+).

### Usage

```
cr.lik(
  n,
  s,
  Y,
  admin,
  cens.indcs,
  M,
  Sigma,
  beta.mat,
  sigma.vct,
  rho.mat,
  theta.vct
)
```

### Arguments

n	The sample size.
s	The number of competing risks.
Y	The observed times.
admin	Boolean value indicating whether or not administrative censoring should be taken into account.
cens.indcs	matrix of censoring indicators (each row corresponds to a single observation).
M	Design matrix, consisting of [intercept, exo.cov, Z, cf]. Note that cf represents the multiple ways of 'handling' the endogenous covariate Z, see also the documentation of 'estimate.cmprsk.R'. When there is no confounding, M will be [intercept, exo.cov].
Sigma	The covariance matrix.
beta.mat	Matrix containing all of the covariate effects.
sigma.vct	Vector of standard deviations. Should be equal to $\sqrt{\text{diag}(\text{Sigma})}$ .
rho.mat	The correlation matrix.
theta.vct	Vector containing the parameters of the Yeo-Johnsontrans- formations.

**Value**

Evaluation of the log-likelihood function

**References**

Willems et al. (2024+). Flexible control function approach under competing risks (in preparation).

---

dat.sim.reg.comp.risks

*Data generation function for competing risks data*

---

**Description**

This function generates competing risk data that can be used in simulation studies.

**Usage**

```
dat.sim.reg.comp.risks(
  n,
  par,
  iseed,
  s,
  conf,
  Zbin,
  Wbin,
  type.cov,
  A.upper = 15
)
```

**Arguments**

n	The sample size of the generated data set.
par	List of parameter vectors for each component of the transformation model.
iseed	Random seed.
s	The number of competing risks. Note that the given parameter vector could specify the parameters for the model with more than $s$ competing risks, but in this case only the first $s$ sets of parameters will be considered.
conf	Boolean value indicating whether the data set should contain confounding.
Zbin	Indicator whether the confounded variable is binary $Z_{bin} = 1$ or not $Z_{bin} = 0$ . If $conf = FALSE$ , this variable is ignored.
Wbin	Indicator whether the instrument is binary ( $Z_{bin} = 1$ ) or not $Z_{bin} = 0$ .
type.cov	Vector of characters "c" and "b", indicating which exogenous covariates should be continuous "c" or binary "b".
A.upper	The upper bound on the support of the administrative censoring distribution. This can be used to control for the amount of administrative censoring in the data. Default is $A.upper = 15$ . $A.upper = NULL$ will return a data set without administrative censoring.

**Value**

A generated data set

---

dchol2par	<i>Derivative of transform Cholesky decomposition to covariance matrix.</i>
-----------	---

---

**Description**

This function defines the derivative of the transformation function that maps Cholesky parameters to the full covariance matrix.

**Usage**

```
dchol2par(par . chol1)
```

**Arguments**

par . chol1	The vector of Cholesky parameters.
-------------	------------------------------------

**Value**

Derivative of the function that transforms the cholesky parameters to the full covariance matrix.

---

dchol2par . elem	<i>Derivative of transform Cholesky decomposition to covariance matrix element.</i>
------------------	---

---

**Description**

This function defines the derivative of the transformation function that maps Cholesky parameters to a covariance matrix element. This function is used in dchol2par.R.

**Usage**

```
dchol2par . elem(k, q, a, b, par . chol1)
```

**Arguments**

k	The row index of the parameter with respect to which to take the derivative.
q	the column index of the parameter with respect to which to take the derivative.
a	The row index of the covariance matrix element to be computed.
b	The column index of the covariance matrix element to be computed.
par . chol1	The vector of Cholesky parameters.

**Value**

Derivative of the function that transforms the cholesky parameters to the specified element of the covariance matrix, evaluated at the specified arguments.

---

Distance	<i>Distance between vectors</i>
----------	---------------------------------

---

**Description**

This function computes distance between two vectors based on L2-norm

This function computes distance between two vectors based on L2-norm

**Usage**

Distance(b, a)

Distance(b, a)

**Arguments**

b                      Second vector

a                      First vector

---

DYJtrans	<i>Derivative of the Yeo-Johnson transformation function</i>
----------	--

---

**Description**

Evaluates the derivative of the Yeo-Johnson transformation at the provided argument.

**Usage**

DYJtrans(y, theta)

**Arguments**

y                      The argument to be supplied to the derivative of the Yeo-Johnson transformation.

theta                  The parameter of the Yeo-Johnson transformation. This should be a number in the range [0,2].

**Value**

The transformed value of y.

---

estimate.cf	<i>Estimate the control function</i>
-------------	--------------------------------------

---

### Description

This function estimates the control function for the endogenous variable based on the provided covariates. This function is called inside estimate.cmprsk.R.

### Usage

```
estimate.cf(XandW, Z, Zbin, gammaest = NULL)
```

### Arguments

XandW	Design matrix of exogenous covariates.
Z	Endogenous covariate.
Zbin	Boolean value indicating whether endogenous covariate is binary.
gammaest	Vector of pre-estimated parameter vector. If NULL, this function will first estimate gammaest. Default value is gammaest = NULL.

### Value

List containing the vector of values for the control function and the regression parameters of the first step.

---

estimate.cmprsk	<i>Estimate the competing risks model of Rutten, Willems et al. (20XX).</i>
-----------------	---

---

### Description

This function estimates the parameters in the competing risks model described in Willems et al. (2024+). Note that this model extends the model of Crommen, Beyhum and Van Keilegom (2024) and as such, this function also implements their methodology.

### Usage

```
estimate.cmprsk(
  data,
  admin,
  conf,
  eoi.indicator.names = NULL,
  Zbin = NULL,
  inst = "cf",
  realV = NULL,
  eps = 0.001
)
```

**Arguments**

<code>data</code>	<p>A data frame, adhering to the following formatting rules:</p> <ul style="list-style-type: none"> <li>• The first column, named "y", contains the observed times.</li> <li>• The next columns, named "delta1", delta2, etc. contain the indicators for each of the competing risks.</li> <li>• The next column, named da, contains the censoring indicator (independent censoring).</li> <li>• The next column should be a column of all ones (representing the intercept), names <math>x_0</math>.</li> <li>• The subsequent columns should contain the values of the covariates, named <math>x_1</math>, <math>x_2</math>, etc.</li> <li>• When applicable, the next column should contain the values of the endogenous variable. This column should be named z.</li> <li>• When z is provided and an instrument for z is available, the next column, named w, should contain the values for the instrument.</li> </ul>
<code>admin</code>	Boolean value indicating whether the data contains administrative censoring.
<code>conf</code>	Boolean value indicating whether the data contains confounding and hence indicating the presence of z and, possibly, w.
<code>eoi.indicator.names</code>	Vector of names of the censoring indicator columns pertaining to events of interest. Events of interest will be modeled allowing dependence between them, whereas all censoring events (corresponding to indicator columns not listed in <code>eoi.indicator.names</code> ) will be treated as independent of every other event. If <code>eoi.indicator.names == NULL</code> , all events will be modeled dependently.
<code>Zbin</code>	Indicator value indicating whether ( <code>Zbin = TRUE</code> ) or not ( <code>Zbin = FALSE</code> ) the endogenous covariate is binary. Default is <code>Zbin = NULL</code> , corresponding to the case when <code>conf == FALSE</code> .
<code>inst</code>	Variable encoding which approach should be used for dealing with the confounding. <code>inst = "cf"</code> indicates that the control function approach should be used. <code>inst = "W"</code> indicates that the instrumental variable should be used 'as is'. <code>inst = "None"</code> indicates that Z will be treated as an exogenous covariate. Finally, when <code>inst = "oracle"</code> , this function will access the argument <code>realV</code> and use it as the values for the control function. Default is <code>inst = "cf"</code> .
<code>realV</code>	Vector of numerics with length equal to the number of rows in <code>data</code> . Used to provide the true values of the instrumental function to the estimation procedure.
<code>eps</code>	Value that will be added to the diagonal of the covariance matrix during estimation in order to ensure strictly positive variances.

**Value**

A list of parameter estimates in the second stage of the estimation algorithm (hence omitting the estimates for the control function), as well as an estimate of their variance and confidence intervals.

## References

- Willems et al. (2024+). Flexible control function approach under competing risks (in preparation).
- Crommen, G., Beyhum, J., and Van Keilegom, I. (2024). An instrumental variable approach under dependent censoring. *Test*, 33(2), 473-495.

## Examples

```
n <- 200

# Set parameters
gamma <- c(1, 2, 1.5, -1)
theta <- c(0.5, 1.5)
eta1 <- c(1, -1, 2, -1.5, 0.5)
eta2 <- c(0.5, 1, 1, 3, 0)

# Generate exogenous covariates
x0 <- rep(1, n)
x1 <- rnorm(n)
x2 <- rbinom(n, 1, 0.5)

# Generate confounder and instrument
w <- rnorm(n)
V <- rnorm(n, 0, 2)
z <- cbind(x0, x1, x2, w) %*% gamma + V
realV <- z - (cbind(x0, x1, x2, w) %*% gamma)

# Generate event times
err <- MASS::mvrnorm(n, mu = c(0, 0), Sigma =
matrix(c(3, 1, 1, 2), nrow = 2, byrow = TRUE))
bn <- cbind(x0, x1, x2, z, realV) %*% cbind(eta1, eta2) + err
Lambda_T1 <- bn[,1]; Lambda_T2 <- bn[,2]
x.ind = (Lambda_T1>0)
y.ind <- (Lambda_T2>0)
T1 <- rep(0,length(Lambda_T1))
T2 <- rep(0,length(Lambda_T2))
T1[x.ind] = ((theta[1]*Lambda_T1[x.ind]+1)^(1/theta[1])-1)
T1[!x.ind] = 1-(1-(2-theta[1])*Lambda_T1[!x.ind])^(1/(2-theta[1]))
T2[y.ind] = ((theta[2]*Lambda_T2[y.ind]+1)^(1/theta[2])-1)
T2[!y.ind] = 1-(1-(2-theta[2])*Lambda_T2[!y.ind])^(1/(2-theta[2]))
# Generate administrative censoring time
C <- runif(n, 0, 40)

# Create observed data set
y <- pmin(T1, T2, C)
delta1 <- as.numeric(T1 == y)
delta2 <- as.numeric(T2 == y)
da <- as.numeric(C == y)
data <- data.frame(cbind(y, delta1, delta2, da, x0, x1, x2, z, w))
colnames(data) <- c("y", "delta1", "delta2", "da", "x0", "x1", "x2", "z", "w")

# Estimate the model
```

```

admin <- TRUE           # There is administrative censoring in the data.
conf <- TRUE           # There is confounding in the data (z)
eoi.indicator.names <- NULL # We will not impose that T1 and T2 are independent
Zbin <- FALSE         # The confounding variable z is not binary
inst <- "cf"          # Use the control function approach
# Since we don't use the oracle estimator, this argument is ignored anyway
realV <- NULL
estimate.cmprsk(data, admin, conf, eoi.indicator.names, Zbin, inst, realV)

```

---

fitDepCens

*Fit Dependent Censoring Models*


---

## Description

This function allows to estimate the dependency parameter along all other model parameters. First, estimates the cumulative hazard function, and then at the second stage it estimates other model parameters assuming that the cumulative hazard function is known. The details for implementing the dependent censoring methodology can be found in Deresa and Van Keilegom (2024).

## Usage

```

fitDepCens(
  resData,
  X,
  W,
  cop = c("Frank", "Gumbel", "Normal"),
  dist = c("Weibull", "lognormal"),
  start = NULL,
  n.iter = 50,
  bootstrap = TRUE,
  n.boot = 150,
  ncore = 7,
  eps = 1e-04
)

```

## Arguments

resData	Data matrix with three columns; $Z$ = the observed survival time, $d1$ = the censoring indicator of $T$ and $d2$ = the censoring indicator of $C$ .
X	Data matrix with covariates related to $T$ .
W	Data matrix with covariates related to $C$ . First column of $W$ should be a vector of ones.
cop	Which copula should be computed to account for dependency between $T$ and $C$ . This argument can take one of the values from <code>c("Gumbel", "Frank", "Normal")</code> .



<code>dist</code>	The distribution to be used for the censoring time $C$ . Only two distributions are allowed, i.e., Weibull and lognormal distributions. With the value "Weibull" as the default.
<code>start</code>	Initial values for the finite dimensional parameters. If <code>start</code> is NULL, the initial values will be obtained by fitting a Cox model for survival time $T$ and a Weibull model for dependent censoring $C$ .
<code>n.iter</code>	Number of iterations; the default is <code>n.iter = 50</code> . The larger the number of iterations, the longer the computational time.
<code>bootstrap</code>	A boolean indicating whether to compute bootstrap standard errors for making inferences.
<code>n.boot</code>	Number of bootstrap samples to use in the estimation of bootstrap standard errors if <code>bootstrap = TRUE</code> . The default is <code>n.boot = 150</code> . But, higher values of <code>n.boot</code> are recommended for obtaining good estimates of bootstrap standard errors.
<code>ncore</code>	The number of cores to use for parallel computation in bootstrapping, with the default <code>ncore = 7</code> .
<code>eps</code>	Convergence error. This is set by the user in such way that the desired convergence is met; the default is <code>eps = 1e-4</code> .

### Value

This function returns a fit of dependent censoring model; parameter estimates, estimate of the cumulative hazard function, bootstrap standard errors for finite-dimensional parameters, the nonparametric cumulative hazard function, etc.

### References

Deresa and Van Keilegom (2024). Copula based Cox proportional hazards models for dependent censoring, *Journal of the American Statistical Association*, 119:1044-1054.

### Examples

```
# Toy data example to illustrate implementation
n = 300
beta = c(0.5)
lambd = 0.35
eta = c(0.9,0.4)
X = cbind(rbinom(n,1,0.5))
W = cbind(rep(1,n),rbinom(n,1,0.5))
# generate dependency structure from Frank
frank.cop <- copula::frankCopula(param = 5,dim = 2)
U = copula::rCopula(n,frank.cop)
T1 = (-log(1-U[,1]))/(lambd*exp(X*beta))           # Survival time
T2 = (-log(1-U[,2]))^(1.1)*exp(W%*%eta)           # Censoring time
A = runif(n,0,15)                                  # administrative censoring time
Z = pmin(T1,T2,A)
d1 = as.numeric(Z==T1)
d2 = as.numeric(Z==T2)
resData = data.frame("Z" = Z, "d1" = d1, "d2" = d2) # should be data frame
```

```

colnames(W) <- c("ones", "cov1")
colnames(X) <- "cov.surv"

# Fit dependent censoring model

fit <- fitDepCens(resData = resData, X = X, W = W, bootstrap = FALSE)

# parameter estimates

fit$parameterEstimates

# summary fit results
summary(fit)

# plot cumulative hazard vs time

plot(fit$observedTime, fit$cumhazardFunction, type = "l", xlab = "Time",
      ylab = "Estimated cumulative hazard function")

```

---

fitIndepCens

*Fit Independent Censoring Models*


---

## Description

This function allows to estimate all model parameters under the assumption of independent censoring. First, estimates the cumulative hazard function, and then at the second stage it estimates other model parameters assuming that the cumulative hazard is known.

## Usage

```

fitIndepCens(
  resData,
  X,
  W,
  dist = c("Weibull", "lognormal"),
  start = NULL,
  n.iter = 50,
  bootstrap = TRUE,
  n.boot = 150,
  ncore = 7,
  eps = 1e-04
)

```

## Arguments

`resData` Data matrix with three columns;  $Z$  = the observed survival time,  $d1$  = the censoring indicator of  $T$  and  $d2$  = the censoring indicator of  $C$ .

X	Data matrix with covariates related to T.
W	Data matrix with covariates related to C. First column of W should be ones.
dist	The distribution to be used for the censoring time C. Only two distributions are allowed, i.e, Weibull and lognormal distributions. With the value "Weibull" as the default.
start	Initial values for the finite dimensional parameters. If start is NULL, the initial values will be obtained by fitting a Cox model for survival time T and a Weibull model for censoring time C.
n.iter	Number of iterations; the default is n.iter = 50. The larger the number of iterations, the longer the computational time.
bootstrap	A boolean indicating whether to compute bootstrap standard errors for making inferences.
n.boot	Number of bootstrap samples to use in the estimation of bootstrap standard errors if bootstrap = TRUE. The default is n.boot = 150. But, higher values of n.boot are recommended for obtaining good estimates of bootstrap standard errors.
ncore	The number of cores to use for parallel computation is configurable, with the default ncore = 7.
eps	Convergence error. This is set by the user in such away that the desired convergence is met; the default is eps = 1e-4.

### Value

This function returns a fit of independent censoring model; parameter estimates, estimate of the cumulative hazard function, bootstrap standard errors for finite-dimensional parameters, the non-parametric cumulative hazard function, etc.

### Examples

```
# Toy data example to illustrate implementation
n = 300
beta = c(0.5)
lambda = 0.35
eta = c(0.9,0.4)
X = cbind(rbinom(n,1,0.5))
W = cbind(rep(1,n),rbinom(n,1,0.5))
# generate dependency structure from Frank
frank.cop <- copula::frankCopula(param = 5,dim = 2)
U = copula::rCopula(n,frank.cop)
T1 = (-log(1-U[,1]))/(lambda*exp(X*beta))           # Survival time'
T2 = (-log(1-U[,2]))^(1.1)*exp(W%*%eta)           # Censoring time
A = runif(n,0,15)                                   # administrative censoring time
Z = pmin(T1,T2,A)
d1 = as.numeric(Z==T1)
d2 = as.numeric(Z==T2)
resData = data.frame("Z" = Z,"d1" = d1, "d2" = d2)  # should be data frame
```

```
colnames(W) <- c("ones", "cov1")
colnames(X) <- "cov.surv"

# Fit independent censoring model

fitI <- fitIndepCens(resData = resData, X = X, W = W, bootstrap = FALSE)

# parameter estimates

fitI$parameterEstimates

# summary fit results
summary(fitI)

# plot cumulative hazard vs time

plot(fitI$observedTime, fitI$cumhazardFunction, type = "l", xlab = "Time",
     ylab = "Estimated cumulative hazard function")
```

---

IYJtrans

*Inverse Yeo-Johnson transformation function*

---

### **Description**

Computes the inverse Yeo-Johnson transformation of the provided argument.

### **Usage**

```
IYJtrans(y, theta)
```

### **Arguments**

y	The argument to be supplied to the inverse Yeo-Johnson transformation.
theta	The parameter of the inverted Yeo-Johnson transformation. This should be a number in the range [0,2].

### **Value**

The transformed value of y.

---

LikCopInd	<i>Loglikelihood function under independent censoring</i>
-----------	---

---

**Description**

Loglikelihood function under independent censoring

**Usage**

```
LikCopInd(theta, resData, X, W, lhat, cumL, dist)
```

**Arguments**

theta	Estimated parameter values/initial values for finite dimensional parameters
resData	Data matrix with three columns; $Z$ = the observed survival time, $d1$ = the censoring indicator of $T$ and $d2$ = the censoring indicator of $C$ .
X	Data matrix with covariates related to $T$
W	Data matrix with covariates related to $C$ . First column of $W$ should be ones
lhat	The estimated hazard function obtained from the output of <a href="#">SolveLI</a> .
cumL	The estimated cumulative hazard function from the output of <a href="#">SolveLI</a> .
dist	The distribution to be used for the dependent censoring $C$ . Only two distributions are allowed, i.e, Weibull and lognormal distributions. With the value "Weibull" as the default. @importFrom stats nlnmb pnorm qnorm sd

**Value**

Maximized log-likelihood value

---

LikF.cmprsk	<i>Second step log-likelihood function.</i>
-------------	---

---

**Description**

This function defines the log-likelihood used to estimate the second step in the competing risks extension of the model described in Willems et al. (2024+).

**Usage**

```
LikF.cmprsk(par, data, admin, conf, cf)
```

**Arguments**

par	Vector of all second step model parameters, consisting of the regression parameters, variance-covariance matrix elements and transformation parameters.
data	Data frame resulting from the 'uniformize.data.R' function.
admin	Boolean value indicating whether the data contains administrative censoring.
conf	Boolean value indicating whether the data contains confounding and hence indicating the presence of Z and W.
cf	"Control function" to be used. This can either be the (i) estimated control function, (ii) the true control function, (iii) the instrumental variable, or (iv) nothing (cf = NULL). Option (ii) is used when comparing the two-step estimator to the oracle estimator, and option (iii) is used to compare the two-step estimator with the naive estimator.

**Value**

Log-likelihood evaluation of the second step.

**References**

Willems et al. (2024+). Flexible control function approach under competing risks (in preparation).

---

likF.cmprsk.Cholesky *Wrapper implementing likelihood function using Cholesky factorization.*

---

**Description**

This function parametrizes the covariance matrix using its Cholesky decomposition, so that optimization of the likelihood can be done based on this parametrization, and positive-definiteness of the covariance matrix is guaranteed at each step of the optimization algorithm.

**Usage**

```
likF.cmprsk.Cholesky(par.chol, data, admin, conf, cf, eps = 0.001)
```

**Arguments**

par.chol	Vector of all second step model parameters, consisting of the regression parameters, Cholesky decomposition of the variance-covariance matrix elements and transformation parameters.
data	Data frame resulting from the 'uniformize.data.R' function.
admin	Boolean value indicating whether the data contains administrative censoring.
conf	Boolean value indicating whether the data contains confounding and hence indicating the presence of Z and W.

cf	"Control function" to be used. This can either be the (i) estimated control function, (ii) the true control function, (iii) the instrumental variable, or (iv) nothing (cf = NULL). Option (ii) is used when comparing the two-step estimator to the oracle estimator, and option (iii) is used to compare the two-step estimator with the naive estimator.
eps	Minimum value for the diagonal elements in the covariance matrix. Default is eps = 0.001.

**Value**

Log-likelihood evaluation of the second step.

---

 LikGamma1

---

*First step log-likelihood function for Z continuous*


---

**Description**

This function defines the maximum likelihood used to estimate the control function in the case of a continuous endogenous variable.

**Usage**

LikGamma1(gamma, Z, M)

**Arguments**

gamma	Vector of coefficients in the linear model used to estimate the control function.
Z	Endogenous covariate.
M	Design matrix, containing an intercept, the exogenous covariates and the instrumental variable.

**Value**

Returns the log-likelihood function corresponding to the data, evaluated at the point gamma.

---

 LikGamma2

*First step log-likelihood function for Z binary.*


---

**Description**

This function defines the maximum likelihood used to estimate the control function in the case of a binary endogenous variable.

**Usage**

```
LikGamma2(gamma, Z, M)
```

**Arguments**

gamma	Vector of coefficients in the logistic model used to estimate the control function.
Z	Endogenous covariate.
M	Design matrix, containing an intercept, the exogenous covariates and the instrumental variable.

**Value**

Returns the log-likelihood function corresponding to the data, evaluated at the point gamma.

---

 LikI.bis

*Second likelihood function needed to fit the independence model in the second step of the estimation procedure.*


---

**Description**

This function defines the log-likelihood used in estimating the second step in the competing risks extension of the model described in Willems et al. (2024+). The results of this function will serve as starting values for subsequent optimizations (LikI.comprsk.R and LikF.cmprsk.R)

**Usage**

```
LikI.bis(par, data, admin, conf, cf)
```

**Arguments**

par	Vector of all second step model parameters, consisting of the regression parameters, variance-covariance matrix elements and transformation parameters.
data	Data frame resulting from the 'uniformize.data.R' function.
admin	Boolean value indicating whether the data contains administrative censoring.



conf	Boolean value indicating whether the data contains confounding and hence indicating the presence of Z and W
cf	"Control function" to be used. This can either be the (i) estimated control function, (ii) the true control function, (iii) the instrumental variable, or (iv) nothing (cf = NULL). Option (ii) is used when comparing the two-step estimator to the oracle estimator, and option (iii) is used to compare the two-step estimator with the naive estimator.

**Value**

Starting values for subsequent optimization function used in the second step of the estimation procedure.

**References**

Willems et al. (2024+). Flexible control function approach under competing risks (in preparation).

---

LikI.cmprsk	<i>Second step log-likelihood function under independence assumption.</i>
-------------	---

---

**Description**

This function defines the log-likelihood used to estimate the second step in the competing risks extension assuming independence of some of the competing risks in the model described in Willems et al. (2024+).

**Usage**

```
LikI.cmprsk(par, data, eoi.indicator.names, admin, conf, cf)
```

**Arguments**

par	Vector of all second step model parameters, consisting of the regression parameters, variance-covariance matrix elements and transformation parameters.
data	Data frame resulting from the 'uniformize.data.R' function.
eoi.indicator.names	Vector of names of the censoring indicator columns pertaining to events of interest. Events of interest will be modeled allowing dependence between them, whereas all censoring events (corresponding to indicator columns not listed in eoi.indicator.names) will be treated as independent of every other event.
admin	Boolean value indicating whether the data contains administrative censoring.
conf	Boolean value indicating whether the data contains confounding and hence indicating the presence of Z and W
cf	"Control function" to be used. This can either be the (i) estimated control function, (ii) the true control function, (iii) the instrumental variable, or (iv) nothing (cf = NULL). Option (ii) is used when comparing the two-step estimator to the oracle estimator, and option (iii) is used to compare the two-step estimator with the naive estimator.

**Value**

Log-likelihood evaluation for the second step in the estimation procedure.

**References**

Willems et al. (2024+). Flexible control function approach under competing risks (in preparation).

---

LikI.cmprsk.Cholesky *Wrapper implementing likelihood function assuming independence between competing risks and censoring using Cholesky factorization.*

---

**Description**

This function does the same as LikI.cmprsk (in fact, it even calls said function), but it parametrizes the covariance matrix using its Cholesky decomposition in order to guarantee positive definiteness. This function is never used, might not work and could be deleted.

**Usage**

```
LikI.cmprsk.Cholesky(
  par.chol,
  data,
  eoi.indicator.names,
  admin,
  conf,
  cf,
  eps = 0.001
)
```

**Arguments**

<code>par.chol</code>	Vector of all second step model parameters, consisting of the regression parameters, Cholesky decomposition of the variance-covariance matrix elements and transformation parameters.
<code>data</code>	Data frame resulting from the 'uniformize.data.R' function.
<code>eoi.indicator.names</code>	Vector of names of the censoring indicator columns pertaining to events of interest. Events of interest will be modeled allowing dependence between them, whereas all censoring events (corresponding to indicator columns not listed in <code>eoi.indicator.names</code> ) will be treated as independent of every other event.
<code>admin</code>	Boolean value indicating whether the data contains administrative censoring.
<code>conf</code>	Boolean value indicating whether the data contains confounding and hence indicating the presence of Z and W.

cf	"Control function" to be used. This can either be the (i) estimated control function, (ii) the true control function, (iii) the instrumental variable, or (iv) nothing (cf = NULL). Option (ii) is used when comparing the two-step estimator to the oracle estimator, and option (iii) is used to compare the two-step estimator with the naive estimator.
eps	Minimum value for the diagonal elements in the covariance matrix. Default is eps = 0.001.

**Value**

Log-likelihood evaluation for the second step in the estimation procedure.

---

likIFG.cmprsk.Cholesky

*Full likelihood (including estimation of control function).*

---

**Description**

This function defines the 'full' likelihood of the model. Specifically, it includes the estimation of the control function in the computation of the likelihood. This function is used in the estimation of the variance of the estimates (variance.cmprsk.R).

**Usage**

```
likIFG.cmprsk.Cholesky(
  parhatG,
  data,
  eoi.indicator.names,
  admin,
  conf,
  Zbin,
  inst
)
```

**Arguments**

parhatG	The full parameter vector.
data	Data frame.
eoi.indicator.names	Vector of names of the censoring indicator columns pertaining to events of interest. Events of interest will be modeled allowing dependence between them, whereas all censoring events (corresponding to indicator columns not listed in eoi.indicator.names) will be treated as independent of every other event. If eoi.indicator.names == NULL, all events will be modelled dependently.
admin	Boolean value indicating whether the data contains administrative censoring.

conf	Boolean value indicating whether the data contains confounding and hence indicating the presence of Z and W.
Zbin	Boolean value indicating whether the confounding variable is binary.
inst	Type of instrumental function to be used.

**Value**

Full model log-likelihood evaluation.

---

`loglike.clayton.unconstrained`  
*Log-likelihood function for the Clayton copula.*

---

**Description**

This likelihood function is maximized to estimate the model parameters under the Clayton copula.

**Usage**

```
loglike.clayton.unconstrained(para, Y, Delta, Dist.T, Dist.C)
```

**Arguments**

para	Estimated parameter values/initial values.
Y	Follow-up time.
Delta	Censoring indicator.
Dist.T	The distribution to be used for the survival time T. This argument can take one of the values from <code>c("lnorm", "weibull")</code> and has to be the same as Dist.C.
Dist.C	The distribution to be used for the censoring time C. This argument can take one of the values from <code>c("lnorm", "weibull")</code> and has to be the same as Dist.T.

**Value**

Maximized log-likelihood value.

---

`loglike.frank.unconstrained`*Log-likelihood function for the Frank copula.*

---

**Description**

This likelihood function is maximized to estimate the model parameters under the Frank copula.

**Usage**

```
loglike.frank.unconstrained(para, Y, Delta, Dist.T, Dist.C)
```

**Arguments**

<code>para</code>	Estimated parameter values/initial values.
<code>Y</code>	Follow-up time.
<code>Delta</code>	Censoring indicator.
<code>Dist.T</code>	The distribution to be used for the survival time T. This argument can take one of the values from <code>c("lnorm", "weibull", "llogis")</code> .
<code>Dist.C</code>	The distribution to be used for the censoring time C. This argument can take one of the values from <code>c("lnorm", "weibull", "llogis")</code> .

**Value**

Maximized log-likelihood value.

---

`loglike.gaussian.unconstrained`*Log-likelihood function for the Gaussian copula.*

---

**Description**

This likelihood function is maximized to estimate the model parameters under the Gaussian copula.

**Usage**

```
loglike.gaussian.unconstrained(para, Y, Delta, Dist.T, Dist.C)
```

**Arguments**

para	Estimated parameter values/initial values.
Y	Follow-up time.
Delta	Censoring indicator.
Dist.T	The distribution to be used for the survival time T. This argument can only the value "lnorm".
Dist.C	The distribution to be used for the censoring time C. This argument can only the value "lnorm".

**Value**

Maximized log-likelihood value.

---

`loglike.gumbel.unconstrained`

*Log-likelihood function for the Gumbel copula.*

---

**Description**

This likelihood function is maximized to estimate the model parameters under the Gumbel copula.

**Usage**

```
loglike.gumbel.unconstrained(para, Y, Delta, Dist.T, Dist.C)
```

**Arguments**

para	Estimated parameter values/initial values.
Y	Follow-up time.
Delta	Censoring indicator.
Dist.T	The distribution to be used for the survival time T. This argument can take one of the values from <code>c("lnorm", "weibull")</code> and has to be the same as Dist.C.
Dist.C	The distribution to be used for the censoring time C. This argument can take one of the values from <code>c("lnorm", "weibull")</code> and has to be the same as Dist.T.

**Value**

Maximized log-likelihood value.

---

`loglike.indep.unconstrained`*Log-likelihood function for the independence copula.*

---

**Description**

This likelihood function is maximized to estimate the model parameters under the independence copula.

**Usage**

```
loglike.indep.unconstrained(para, Y, Delta, Dist.T, Dist.C)
```

**Arguments**

<code>para</code>	Estimated parameter values/initial values.
<code>Y</code>	Follow-up time.
<code>Delta</code>	Censoring indicator.
<code>Dist.T</code>	The distribution to be used for the survival time T. This argument can take one of the values from <code>c("lnorm", "weibull", "llogis")</code> .
<code>Dist.C</code>	The distribution to be used for the censoring time C. This argument can take one of the values from <code>c("lnorm", "weibull", "llogis")</code> .

**Value**

Maximized log-likelihood value.

---

`log_transform`*Logarithmic transformation function.*

---

**Description**

Computes the logarithm of a number.

**Usage**

```
log_transform(y)
```

**Arguments**

<code>y</code>	Numerical value of which the logarithm is computed.
----------------	---

**Value**

This function returns the logarithm of the provided argument `y` if it is greater than zero. If `y` is smaller than zero, it will return 0.

---

 Longfun

*Long format*


---

**Description**

Change hazard and cumulative hazard to long format

**Usage**

Longfun(Z, T1, lhat, Lhat)

**Arguments**

Z	Observed survival time, which is the minimum of T, C and A, where A is the administrative censoring time.
T1	Distinct observed survival time
lhat	Hazard function estimate
Lhat	Cumulative hazard function estimate

---

 LongNPT

*Change H to long format*


---

**Description**

Change a nonparametric transformation function to long format

**Usage**

LongNPT(Z, T1, H)

**Arguments**

Z	Observed survival time, which is the minimum of T, C and A, where A is the administrative censoring time.
T1	Distinct observed survival time
H	Nonparametric transformation function estimate



---

NonParTrans

*Fit a semiparametric transformation model for dependent censoring*


---

### Description

This function allows to estimate the dependency parameter along all other model parameters. First, estimates a non-parametric transformation function, and then at the second stage it estimates other model parameters assuming that the non-parametric function is known. The details for implementing the dependent censoring methodology can be found in Deresa and Van Keilegom (2021).

### Usage

```
NonParTrans(
  resData,
  X,
  W,
  start = NULL,
  n.iter = 15,
  bootstrap = FALSE,
  n.boot = 50,
  eps = 0.001
)
```

### Arguments

<code>resData</code>	Data matrix with three columns; $Z$ = the observed survival time, $d1$ = the censoring indicator of $T$ and $d2$ = the censoring indicator of $C$ .
<code>X</code>	Data matrix with covariates related to $T$
<code>W</code>	Data matrix with covariates related to $C$
<code>start</code>	Initial values for the finite dimensional parameters. If <code>start</code> is <code>NULL</code> , the initial values will be obtained by fitting an Accelerated failure time models.
<code>n.iter</code>	Number of iterations; the default is <code>n.iter = 20</code> . The larger the number of iterations, the longer the computational time.
<code>bootstrap</code>	A boolean indicating whether to compute bootstrap standard errors for making inferences.
<code>n.boot</code>	Number of bootstrap samples to use in the estimation of bootstrap standard errors if <code>bootstrap = TRUE</code> . The default is <code>n.boot = 50</code> . But, higher values of <code>n.boot</code> are recommended for obtaining good estimates of bootstrap standard errors.
<code>eps</code>	Convergence error. This is set by the user in such way that the desired convergence is met; the default is <code>eps = 1e-3</code> .

### Value

This function returns a fit of a semiparametric transformation model; parameter estimates, estimate of the non-parametric transformation function, bootstrap standard errors for finite-dimensional parameters, the nonparametric cumulative hazard function, etc.

## References

Deresa, N. and Van Keilegom, I. (2021). On semiparametric modelling, estimation and inference for survival data subject to dependent censoring, *Biometrika*, 108, 965–979.

## Examples

```
# Toy data example to illustrate implementation
n = 300
beta = c(0.5, 1); eta = c(1,1.5); rho = 0.70
sigma = matrix(c(1,rho,rho,1),ncol=2)
err = MASS::mvrnorm(n, mu = c(0,0) , Sigma=sigma)
err1 = err[,1]; err2 = err[,2]
x1 = rbinom(n,1,0.5); x2 = runif(n,-1,1)
X = matrix(c(x1,x2),ncol=2,nrow=n); W = X # data matrix
T1 = X%%beta+err1
C = W%%eta+err2
T1 = exp(T1); C = exp(C)
A = runif(n,0,8); Y = pmin(T1,C,A)
d1 = as.numeric(Y==T1)
d2 = as.numeric(Y==C)
resData = data.frame("Z" = Y,"d1" = d1, "d2" = d2) # should be data frame
colnames(X) = c("X1", "X2")
colnames(W) = c("W1", "W2")

# Bootstrap is false by default
output = NonParTrans(resData = resData, X = X, W = W, n.iter = 2)
output$parameterEstimates
```

---

optimlikelihood

*Fit the dependent censoring models.*

---

## Description

Estimates the model parameters by maximizing the log-likelihood.

## Usage

```
optimlikelihood(Y, Delta, Copula, Dist.T, Dist.C, start)
```

## Arguments

Y	Follow-up time.
Delta	Censoring indicator.
Copula	The copula family. This argument can take values from c("frank", "gumbel", "clayton", "gaussian",
Dist.T	The distribution to be used for the survival time T. This argument can take one of the values from c("lnorm", "weibull", "llogis").

Dist.C	The distribution to be used for the censoring time C. This argument can take one of the values from <code>c("lnorm", "weibull", "llogis")</code> .
start	Starting values

**Value**

A list containing the minimized negative log-likelihood using the independence copula model, the estimated parameter values for the model with the independence copula, the minimized negative log-likelihood using the specified copula model and the estimated parameter values for the model with the specified copula.

---

ParamCop	<i>Estimation of a parametric dependent censoring model without co-variates.</i>
----------	--

---

**Description**

Note that it is not assumed that the association parameter of the copula function is known, unlike most other papers in the literature. The details for implementing the methodology can be found in Czado and Van Keilegom (2023).

**Usage**

```
ParamCop(Y, Delta, Copula, Dist.T, Dist.C, start = c(1, 1, 1, 1))
```

**Arguments**

Y	Follow-up time.
Delta	Censoring indicator.
Copula	The copula family. This argument can take values from <code>c("frank", "gumbel", "clayton", "gaussian", "lnorm", "weibull", "llogis")</code> .
Dist.T	The distribution to be used for the survival time T. This argument can take one of the values from <code>c("lnorm", "weibull", "llogis")</code> .
Dist.C	The distribution to be used for the censoring time C. This argument can take one of the values from <code>c("lnorm", "weibull", "llogis")</code> .
start	Starting values

**Value**

A table containing the minimized negative log-likelihood using the independence copula model, the estimated parameter values for the model with the independence copula, the minimized negative log-likelihood using the specified copula model and the estimated parameter values for the model with the specified copula.

**References**

Czado and Van Keilegom (2023). Dependent censoring based on parametric copulas. *Biometrika*, 110(3), 721-738.

**Examples**

```
tau = 0.75
Copula = "frank"
Dist.T = "weibull"
Dist.C = "lnorm"
par.T = c(2,1)
par.C = c(1,2)
n=1000

simdata<-TCsim(tau,Copula,Dist.T,Dist.C,par.T,par.C,n)

Y = simdata[[1]]
Delta = simdata[[2]]

ParamCop(Y,Delta,Copula,Dist.T,Dist.C)
```

---

power_transform	<i>Power transformation function.</i>
-----------------	---------------------------------------

---

**Description**

Computes a given power of a number.

**Usage**

```
power_transform(y, pw)
```

**Arguments**

y	The number which one wants to raise to a certain power pw.
pw	The power to which to raise y.

**Value**

This function returns the result of raising y to the power pw when  $y > 0$ . Otherwise, it will return 1.

---

PseudoL	<i>Likelihood function under dependent censoring</i>
---------	--

---

**Description**

The PseudoL function is maximized in order to estimate the finite dimensional model parameters, including the dependency parameter. This function assumes that the cumulative hazard function is known.

**Usage**

```
PseudoL(theta, resData, X, W, lhat, cumL, cop, dist)
```

**Arguments**

theta	Estimated parameter values/initial values for finite dimensional parameters
resData	Data matrix with three columns; Z = the observed survival time, d1 = the censoring indicator of T and d2 = the censoring indicator of C.
X	Data matrix with covariates related to T
W	Data matrix with covariates related to C. First column of W should be ones
lhat	The estimated hazard function obtained from the output of <a href="#">SolveL</a> .
cumL	The estimated cumulative hazard function from the output of <a href="#">SolveL</a> .
cop	Which copula should be computed to account for dependency between T and C. This argument can take one of the values from c("Gumbel", "Frank", "Normal"). The default copula model is "Frank".
dist	The distribution to be used for the dependent censoring C. Only two distributions are allowed, i.e. Weibull and lognormal distributions. With the value "Weibull" as the default.

**Value**

maximized log-likelihood value

---

ScoreEqn	<i>Score equations of finite parameters</i>
----------	---

---

**Description**

This function computes the score vectors and the Jacobean matrix for finite model parameters.

**Usage**

```
ScoreEqn(theta, resData, X, W, H)
```

**Arguments**

theta	Vector of parameters in the semiparametric transformation model.
resData	Data matrix with three columns; $Z$ = the observed survival time, $d1$ = the censoring indicator of T and $d2$ = the censoring indicator of C.
X	Data matrix with covariates related to T.
W	Data matrix with covariates related to C.
H	The estimated non-parametric transformation function for a given value of theta

---

SearchIndicate	<i>Search function</i>
----------------	------------------------

---

**Description**

Function to indicate position of  $t$  in observed survival time

**Usage**

```
SearchIndicate(t, T1)
```

**Arguments**

t	fixed time t
T1	distinct observed survival time

---

SolveH	<i>Estimate a nonparametric transformation function</i>
--------	---

---

**Description**

This function estimates the nonparametric transformation function  $H$  when the survival time and censoring time are dependent given covariates. The estimating equation of  $H$  was derived based on the martingale ideas. More details about the derivation of a nonparametric estimator of  $H$  and its estimation algorithm can be found in Deresa and Van Keilegom (2021).

**Usage**

```
SolveH(theta, resData, X, W)
```

**Arguments**

theta	Vector of parameters in the semiparametric transformation model.
resData	Data matrix with three columns; $Z$ = the observed survival time, $d1$ = the censoring indicator of T and $d2$ = the censoring indicator of C.
X	Data matrix with covariates related to T.
W	Data matrix with covariates related to C.

**Value**

Returns the estimated transformation function H for a fixed value of parameters theta.

**References**

Deresa, N. and Van Keilegom, I. (2021). On semiparametric modelling, estimation and inference for survival data subject to dependent censoring, *Biometrika*, 108, 965–979.

---

SolveHt1	<i>Estimating equation for Ht1</i>
----------	------------------------------------

---

**Description**

This function obtains an estimating equation of H at the first observed survival time t1.

**Usage**

```
SolveHt1(Ht1, Z, nu, t, X, W, theta)
```

**Arguments**

Ht1	The solver solves for an optimal value of Ht1 by equating the estimating equation to zero.
Z	The observed survival time, which is the minimum of T, C and A.
nu	The censoring indicator for T or C
t	A fixed time point
X	Data matrix with covariates related to T.
W	Data matrix with covariates related to C.
theta	Vector of parameters

---

SolveL	<i>Cumulative hazard function of survival time under dependent censoring</i>
--------	--

---

**Description**

This function estimates the cumulative hazard function of survival time (T) under dependent censoring (C). The estimation makes use of the estimating equations derived based on martingale ideas.

**Usage**

```
SolveL(
  theta,
  resData,
  X,
  W,
  cop = c("Frank", "Gumbel", "Normal"),
  dist = c("Weibull", "lognormal")
)
```

**Arguments**

theta	Estimated parameter values/initial values for finite dimensional parameters
resData	Data matrix with three columns; Z = the observed survival time, d1 = the censoring indicator of T and d2 = the censoring indicator of C.
X	Data matrix with covariates related to T
W	Data matrix with covariates related to C. First column of W should be ones
cop	Which copula should be computed to account for dependency between T and C. This argument can take one of the values from c("Gumbel", "Frank", "Normal"). The default copula model is "Frank".
dist	The distribution to be used for the dependent censoring C. Only two distributions are allowed, i.e, Weibull and lognormal distributions. With the value "Weibull" as the default.

**Value**

This function returns an estimated hazard function, cumulative hazard function and distinct observed survival times;

**Examples**

```
n = 200
beta = c(0.5)
lambd = 0.35
eta = c(0.9,0.4)
X = cbind(rbinom(n,1,0.5))
W = cbind(rep(1,n),rbinom(n,1,0.5))
frank.cop <- copula::frankCopula(param = 5,dim = 2)
U = copula::rCopula(n,frank.cop)
T1 = (-log(1-U[,1]))/(lambd*exp(X*beta))      # Survival time'
T2 = (-log(1-U[,2]))^(1.1)*exp(W%*%eta)      # Censoring time
A = runif(n,0,15)                            # administrative censoring time
Z = pmin(T1,T2,A)
d1 = as.numeric(Z==T1)
d2 = as.numeric(Z==T2)
resData = data.frame("Z" = Z, "d1" = d1, "d2" = d2)
theta = c(0.3,1,0.3,1,2)

# Estimate cumulative hazard function
```



```

cumFit <- SolveL(theta, resData,X,W)
cumhaz = cumFit$cumhaz
time = cumFit$times

# plot hazard vs time

plot(time, cumhaz, type = "l",xlab = "Time",
ylab = "Estimated cumulative hazard function")

```

---

SolveLI	<i>Cumulative hazard function of survival time under independent censoring</i>
---------	--

---

### Description

This function estimates the cumulative hazard function of survival time (T) under the assumption of independent censoring. The estimating equation is derived based on martingale ideas.

### Usage

```
SolveLI(theta, resData, X)
```

### Arguments

theta	Estimated parameter values/initial values for finite dimensional parameters
resData	Data matrix with three columns; Z = the observed survival time, d1 = the censoring indicator of T and d2 = the censoring indicator of C.
X	Data matrix with covariates related to T

### Value

This function returns an estimated hazard function, cumulative hazard function and distinct observed survival times;

### Examples

```

n = 200
beta = c(0.5)
lambd = 0.35
eta = c(0.9,0.4)
X = cbind(rbinom(n,1,0.5))
W = cbind(rep(1,n),rbinom(n,1,0.5))
frank.cop <- copula::frankCopula(param = 5,dim = 2)
U = copula::rCopula(n,frank.cop)
T1 = (-log(1-U[,1]))/(lambd*exp(X*beta))           # Survival time'
T2 = (-log(1-U[,2]))^(1.1)*exp(W%*%eta)           # Censoring time

```

```

A = runif(n,0,15) # administrative censoring time
Z = pmin(T1,T2,A)
d1 = as.numeric(Z==T1)
d2 = as.numeric(Z==T2)
resData = data.frame("Z" = Z, "d1" = d1, "d2" = d2)
theta = c(0.3,1,0.3,1)

# Estimate cumulative hazard function

cumFit_ind <- SolveLI(theta, resData,X)

cumhaz = cumFit_ind$cumhaz
time = cumFit_ind$times

# plot hazard vs time

plot(time, cumhaz, type = "l",xlab = "Time",
ylab = "Estimated cumulative hazard function")

```

---

SolveScore

*Estimate finite parameters based on score equations*


---

## Description

This function estimates the model parameters

## Usage

```
SolveScore(theta, resData, X, W, H, eps = 0.001)
```

## Arguments

theta	Vector of parameters in the semiparametric transformation model.
resData	Data matrix with three columns; Z = the observed survival time, d1 = the censoring indicator of T and d2 = the censoring indicator of C.
X	Data matrix with covariates related to T.
W	Data matrix with covariates related to C.
H	The estimated non-parametric transformation function for a given value of theta.
eps	Convergence error.

---

summary.depFit      *Summary of depCensoringFit object*

---

**Description**

Summary of depCensoringFit object

**Usage**

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

**Arguments**

object      Output of [fitDepCens](#) function  
...      Further arguments

**Value**

Summary of dependent censoring model fit in the form of table

---

summary.indepFit      *Summary of indepCensoringFit object*

---

**Description**

Summary of indepCensoringFit object

**Usage**

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

**Arguments**

object      Output of [fitIndepCens](#) function  
...      Further arguments

**Value**

Summary of independent censoring model fit in the form of table

TCsim

*Function to simulate (Y,Delta) from the copula based model for (T,C).***Description**

Generates the follow-up time and censoring indicator according to the specified model.

**Usage**

```
TCsim(
  tau = 0,
  Copula = "frank",
  Dist.T = "lnorm",
  Dist.C = "lnorm",
  par.T = c(0, 1),
  par.C = c(0, 1),
  n = 10000
)
```

**Arguments**

tau	Value of Kendall's tau for (T,C). The default value is 0.
Copula	The copula family. This argument can take values from c("frank", "gumbel", "clayton", "gaussian", "t", "copula"). The default copula model is "frank".
Dist.T	Distribution of the survival time T. This argument can take one of the values from c("lnorm", "weibull", "llogis"). The default distribution is "lnorm".
Dist.C	Distribution of the censoring time C. This argument can take one of the values from c("lnorm", "weibull", "llogis"). The default distribution is "lnorm".
par.T	Parameter values for the distribution of T.
par.C	Parameter values for the distribution of C.
n	Sample size.

**Value**

A list containing the generated follow-up times and censoring indicators.

**Examples**

```
tau = 0.5
Copula = "gaussian"
Dist.T = "lnorm"
Dist.C = "lnorm"
par.T = c(1,1)
par.C = c(2,2)
n=1000
```

```

simdata <- TCsim(tau,Copula,Dist.T,Dist.C,par.T,par.C,n)
Y = simdata[[1]]
Delta = simdata[[2]]
hist(Y)
mean(Delta)

```

---

uniformize.data	<i>Standardize data format</i>
-----------------	--------------------------------

---

### Description

Checks the required preconditions of the data and possibly restructures the data.

### Usage

```

uniformize.data(
  data,
  admin = FALSE,
  conf = FALSE,
  comp.risks = FALSE,
  Zbin = NULL,
  Wbin = NULL
)

```

### Arguments

data	A data frame that should contain columns named Y and delta (unless comp.risks = TRUE, see later).
admin	Boolean value indicating whether the provided data frame contains administrative (i.e. independent) censoring on top of the dependent censoring (in the column named delta). The default is admin = FALSE.
conf	Boolean value indicating whether the provided data frame contains a confounded variable and a corresponding instrument. If conf = TRUE, the provided data frame should contain columns named Z and W, corresponding to the confounded variable and instrument, respectively. Moreover, Zbin and Wbin should be specified. The default value is conf = FALSE.
comp.risks	Boolean value indicating whether the provided data frame contains competing risks. If comp.risks = TRUE, the given data frame should contain the columns delta1, delta2, etc., corresponding to the indicators I(Y = T1), I(Y = T2), etc. respectively. The default is comp.risks = FALSE.
Zbin	Boolean or integer value (0, 1) indicating whether the confounded variable is binary. Zbin = TRUE or Zbin = 1 means that Z is binary. Zbin = FALSE or Zbin = 0 means that Z is continuous.
Wbin	Boolean or integer value (0, 1) indicating whether the instrument is binary. Wbin = TRUE or Wbin = 1 means that W is binary. Wbin = FALSE or Wbin = 0 means that W is continuous.

**Value**

Returns the uniformized data set.

---

variance.cmprsk	<i>Compute the variance of the estimates.</i>
-----------------	---

---

**Description**

This function computes the variance of the estimates computed by the 'estimate.cmprsk.R' function.

**Usage**

```
variance.cmprsk(
  parhatc,
  gammaest,
  data,
  admin,
  conf,
  inst,
  cf,
  eoi.indicator.names,
  Zbin,
  use.chol,
  n.trans,
  totparl
)
```

**Arguments**

parhatc	Vector of estimated parameters, computed in the first part of estimate.cmprsk.R.
gammaest	Vector of estimated parameters in the regression model for the control function.
data	A data frame.
admin	Boolean value indicating whether the data contains administrative censoring.
conf	Boolean value indicating whether the data contains confounding and hence indicating the presence of z and, possibly, w.
inst	Variable encoding which approach should be used for dealing with the confounding. inst = "cf" indicates that the control function approach should be used. inst = "W" indicates that the instrumental variable should be used 'as is'. inst = "None" indicates that Z will be treated as an exogenous covariate. Finally, when inst = "oracle", this function will access the argument realV and use it as the values for the control function. Default is inst = "cf".
cf	The control function used to estimate the second step.

<code>eoi.indicator.names</code>	Vector of names of the censoring indicator columns pertaining to events of interest. Events of interest will be modeled allowing dependence between them, whereas all censoring events (corresponding to indicator columns not listed in <code>eoi.indicator.names</code> ) will be treated as independent of every other event. If <code>eoi.indicator.names == NULL</code> , all events will be modeled dependently.
<code>Zbin</code>	Indicator value indicating whether ( <code>Zbin = TRUE</code> ) or not ( <code>Zbin = FALSE</code> ) the endogenous covariate is binary. Default is <code>Zbin = NULL</code> , corresponding to the case when <code>conf == FALSE</code> .
<code>use.chol</code>	Boolean value indicating whether the cholesky decomposition was used in estimating the covariance matrix.
<code>n.trans</code>	Number of competing risks in the model (and hence, number of transformation models).
<code>totpar1</code>	Total number of covariate effects (including intercepts) in all of the transformation models combined.

**Value**

Variance estimates of the provided vector of estimated parameters.

---

YJtrans	<i>Yeo-Johnson transformation function</i>
---------	--

---

**Description**

Computes the Yeo-Johnson transformation of the provided argument.

**Usage**

```
YJtrans(y, theta)
```

**Arguments**

<code>y</code>	The argument to be supplied to the Yeo-Johnson transformation.
<code>theta</code>	The parameter of the Yeo-Johnson transformation. This should be a number in the range $[0,2]$ .

**Value**

The transformed value of `y`.

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