# Package ‘bcfrailph’

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**Type** Package

**Title** Semiparametric Bivariate Correlated Frailty Models Fit

**Version** 0.1.2

**Description** Fit semiparametric bivariate correlated frailty models.

**Depends** R (>= 4.0.0),survival

**Imports** stats

**License** GPL (>= 2)

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**Repository** CRAN

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## `bcfrailph` *Semi-parametric bivariate correlated frailty model.*

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### Description

Fit a semiparametric Bivariate correlated frailty model with Proportional Hazard structure.

### Usage

```
bcfrailph(
  formula,
  data,
  initfrailp = NULL,
  frailty = c("gamma", "lognormal"),
  weights = NULL,
  control = bcfrailph.control(),
  ...
)
```

### Arguments

| | |
|---|---|
| `formula` | A formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a survival object as returned by the Surv function. |
| `data` | A dataframe contain survival time, censor, covariate etc with data in columns. |
| `initfrailp` | Initial estimates for the frailty parameters. If not specified, initial frailty variance will be obtained from coxph with univariate frailty model and for correlation c(0.5) will be used. |
| `frailty` | A type of frailty distribution to be used in fit. Either gamma or lognormal. The default is gamma. |
| `weights` | vector of case weights for gamma model. the default is NULL. |
| `control` | Arguments to control bcfrailph fit. The default is `bcfrailph.control`. |
| `...` | further arguments |

### Value

An object of that contains the following components.

- `coefficients` - A vector of estimated Covariate coefficients.
- `frailparest` - A vector of estimated Frailty parameters i.e. frailty variance and correlation.
- `stderr`-A vector containing the Standard error of the Estimated parameters both covariate coefficients and frailty parameters.
- `loglilk0`- Log likelihood of without frailty model or loglik of coxph fit.
- `loglilk`-Log likelihood of Cox PH model with frailty.

- `Iloglilk`- Log likelihood of with frailty. For gamma fit it is I-likelihood or the likelihood after integrating out the frailty term.For lognormal fit it is the approximate likelihood.
- `bhaz`- an array containing unique event times and estimated baseline hazard.
- `X`-Matrix of observed covariates.
- `time`-the observed survival time.
- `censor`-censoring indicator.
- `resid`-the martingale residuals.
- `lin.prid`-the vector of linear predictors.
- `frail`-estimated Frailty values.
- `iteration`-Number of outer iterations.
- `e.time`-the vector of unique event times.
- `n.event`- the number of events at each of the unique event times.
- `convergence`-an indicator, 1 if converge and 0 otherwise.
- `history`-an array containing records of estimates and other information on each iterations.

## Note

Parameters of Bivariate correlated gamma frailty model was estimated using a modified EM approach given in Kifle et al (2022). Parameters of Bivariate correlated lognormal frailty model is based on the penalized partial likelihood approach by Rippatti and Palmgren (2000).

## References

Kifle YG, Chen DG, Haileyesus MT (2022). Multivariate Frailty Models using Survey Weights with Applications to Twins Infant Mortality in Ethiopia. Statistics and Its Interface,106(4), 1\-10.

Rippatti, S. and Palmgren, J (2000). Estimation of multivariate frailty models using penalized partial likelihood. Biometrics, 56: 1016-1022.

## See Also

`bcfrailph.control`,`simbcfrail`

## Examples

```
set.seed(4)
simdata<-simbcfrail(psize=300, cenr= c(0.3),beta=c(2),frailty=c("gamma"),
frailpar=c(0.5,0.5),bhaz=c("weibull"),
bhazpar=list(shape =c(5), scale = c(0.1)),
covartype= c("B"),covarpar=list(fargs=c(1),sargs=c(0.5)))
dataa<-simdata$data

fitbcfrgam=bcfrailph(Surv(time,censor)~ X1+frailty(PID) ,data=dataa,frailty="gamma")
fitbcfrgam


# now for lognormal
```

```
set.seed(18)
simdata<-simbcfrail(psize=100, cenr= c(0.2),beta=c(1,-0.7,0.5),frailty=c("lognormal"),
frailpar=c(0.5,-0.25),bhaz=c("exponential"),
bhazpar=list(scale = c(0.1)),covartype= c("N","N","B"),
covarpar=list(fargs=c(0,0,1),sargs=c(1,1,0.5)),comncovar=2)
dataa<-simdata$data

#fit
fitbcfrlogn=bcfrailph(Surv(time,censor)~ X1+X2+X3+frailty(PID) ,data=dataa,frailty="lognormal")
fitbcfrlogn
# the output looks like
#   Call:
#   bcfrailph(formula = Surv(time, censor) ~ X1 + X2 + X3 + frailty(PID),
#   data = dataa, frailty = "lognormal")
#
#   n=  200 and number of events= 160
#
#   Regression Coefficients:
#   Estimate   StdErr z.value   p.value
#   X1  1.09987  0.12144  9.0568 < 2.2e-16 ***
#   X2 -0.64995  0.10467 -6.2093 5.322e-10 ***
#   X3  0.34151  0.19510  1.7504   0.08005 .
#   ---
#   Frailty Distribution:Bivariate Correlated  log-normal
#   Variance of random effect = 0.459363 ( 0.1728421 )
#   Correlation Estimate of random effects = -0.4974605 ( 0.3284767 )
#   Approximated Log likelihood with frailty = -696.001
#   Log likelihood without frailty= -697.4393

## one can set the initial parameter for the frailty parameters
fitbcfrailph=bcfrailph(Surv(time,censor)~ X1+frailty(PID),data=dataa,initfrailp = c(0.1,0.5),
frailty="lognormal")
fitbcfrailph

# Not run

#if covariates are not included
fitmoe=bcfrailph(Surv(time,censor)~0,data=dataa,frailty="lognormal")
fitmoe
fitmoe=bcfrailph(Surv(time,censor)~1,data=dataa)
fitmoe

# if control is not specified correctly.
# if one needs to change only max.iter to be 100,

fitmoe=bcfrailph(Surv(time,censor)~ X1+frailty(PID),data=dataa,control=c(max.iter=100))
fitmoe

#the correct way is
fitmoe=bcfrailph(Surv(time,censor)~ X1+frailty(PID),data=dataa,
control=bcfrailph.control(max.iter=100))
fitmoe
```

```
#if initial frailty parameters are in the boundary of parameter space
fitmoe=bcfrailph(Surv(time,censor)~ X1,data=dataa,initfrailp=c(0.2,1))
fitmoe
fitmoe=bcfrailph(Surv(time,censor)~ X1,data=dataa,initfrailp=c(0,0.1))
fitmoe

#if a frailty distribution other than gamma and lognormal are specified

fitmoe=bcfrailph(Surv(time,censor)~ X1,data=dataa,,frailty="exp")
fitmoe
# End Not run
```

---

## `bcfrailph.control` *Arguments for controlling bcfrailph fits.*

### Description

This is used to set various numeric parameters controlling a bcfrailph model fits.

### Usage

```
bcfrailph.control(
  max.iter = 400,
  tol = 1e-04,
  reltol = 1e-06,
  eval.max = 500,
  iter.max = 500,
  trace = 0,
  abs.tol = 1e-20,
  rel.tol = 1e-10,
  x.tol = 1.5e-08,
  xf.tol = 2.2e-14,
  step.min = 1,
  step.max = 1,
  met = 0
)
```

### Arguments

| | |
|---|---|
| `max.iter` | Maximum number of outer iterations. The default is 400. |
| `tol` | A absolute tolerance for convergence in gamma frailty fit. The default is 1e-04. |
| `reltol` | Relative tolerance for convergence in lognormal frailty fit.The default is 1e-06. |
| `eval.max` | argument used to control nlminb fits used. |
| `iter.max` | argument used to control nlminb fits used. |

| | |
|---|---|
| `trace` | argument used to control nlminb fits used. |
| `abs.tol` | argument used to control nlminb fits used. |
| `rel.tol` | argument used to control nlminb fits used. |
| `x.tol` | argument used to control nlminb fits used. |
| `xf.tol` | argument used to control nlminb fits used. |
| `step.min` | argument used to control nlminb fits used. |
| `step.max` | argument used to control nlminb fits used. |
| `met` | procedure of optim method used. |

### Value

A list of control parameters.

### See Also

`bcfrailph`,`shrgamsp`

---

## `fitbccv.gammasp` *Bivariate correlated gamma frailty model fitting function.*

### Description

Semi-parametric Bivariate correlated gamma frailty model fitting function.

### Usage

```
fitbccv.gammasp(
  X,
  Y,
  initfrailp,
  weights = NULL,
  control = bcfrailph.control(),
  SE = TRUE
)
```

### Arguments

| | |
|---|---|
| `X` | Matix of predictors. This should not include an intercept. |
| `Y` | a Surv object containing 2 columns (coxph.fit). |
| `initfrailp` | Initial estimates for the frailty parameters. If not specified, initial frailty variance will be obtained from coxph with univariate gamma frailty model and for correlation c(0.5) will be used. |
| `weights` | vector of case weights. the default is NULL. |
| `control` | Arguments to control the fit. The default is `bcfrailph.control`. |
| `SE` | a logical statement whether standard errors are obtained from the mariginal log likelihood.The default is TRUE. |

## Value

An object of that contains the following components.

- `coefficients` - A vector of estimated Covariate coefficients.
- `frailparest` - A vector of estimated Frailty parameters i.e. frailty variance and correlation.
- `stderr`-A vector containing the Standard error of the Estimated parameters both covariate coefficients and frailty parameters.
- `loglilk0`- Log likelihood of without frailty model or loglik of coxph fit.
- `loglilk`-Log likelihood of Cox PH model with frailty.
- `Iloglilk`- Log likelihood of with frailty. For gamma fit it is I-likelihood or the likelihood after integrating out the frailty term.For lognormal fit it is the approximate likelihood.
- `bhaz`- an array containing unique event times and estimated baseline hazard.
- `X`-Matrix of observed covariates.
- `time`-the observed survival time.
- `censor`-censoring indicator.
- `resid`-the martingale residuals.
- `lin.prid`-the vector of linear predictors.
- `frail`-estimated Frailty values.
- `iteration`-Number of outer iterations.
- `e.time`-the vector of unique event times.
- `n.event`- the number of events at each of the unique event times.
- `convergence`-an indicator, 1 if converge and 0 otherwise.
- `history`-an array containing records of estimates and other information on each iterations.

## Note

This function is important especially for simulation studies as it reduced checking time. Parameters of Bivariate correlated gamma frailty model was estimated using a modified EM approach given in Kifle et al (2022).

## References

Kifle YG, Chen DG, Haileyesus MT (2022). Multivariate Frailty Models using Survey Weights with Applications to Twins Infant Mortality in Ethiopia. Statistics and Its Interface,106(4), 1\-10.

## See Also

`bcfrailph`

## Examples

```
set.seed(4)
simdata<-simbcfrail(psize=300, cenr= c(0.3),beta=c(2),frailty=c("gamma"),
frailpar=c(0.5,0.5),bhaz=c("weibull"),
bhazpar=list(shape =c(5), scale = c(0.1)),
covartype= c("B"),covarpar=list(fargs=c(1),sargs=c(0.5)))
Y<-simdata$Y;X<-simdata$X

bcspfit<-fitbccv.gammasp(X=X,Y=Y,initfrailp=NULL)
bcspfit$coef
bcspfit$frailpar
```

---

# `fitbccv.lognsp` *Bivariate correlated lognormal frailty model fitting function.*

## Description

Semi-parametric Bivariate correlated lognormal frailty model fitting function.

## Usage

```
fitbccv.lognsp(X, Y, initfrailp, control = bcfrailph.control())
```

## Arguments

| | |
|---|---|
| `X` | Matix of predictors. This should not include an intercept. |
| `Y` | a Surv object containing 2 columns (coxph.fit). |
| `initfrailp` | Initial estimates for the frailty parameters. If not specified, initial frailty variance will be obtained from coxph with univariate lognormal frailty model and for correlation c(0.5) will be used. |
| `control` | Arguments to control the fit. The default is `bcfrailph.control`. |

## Value

An object of that contains the following components.

- `coefficients` - A vector of estimated Covariate coefficients.
- `frailparest` - A vector of estimated Frailty parameters i.e. frailty variance and correlation.
- `stderr`-A vector containing the Standard error of the Estimated parameters both covariate coefficients and frailty parameters.
- `loglilk0`- Log likelihood of without frailty model or loglik of coxph fit.
- `loglilk`-Log likelihood of Cox PH model with frailty.
- `Iloglilk`- Log likelihood of with frailty. For gamma fit it is I-likelihood or the likelihood after integrating out the frailty term.For lognormal fit it is the approximate likelihood.

- `bhaz`- an array containing unique event times and estimated baseline hazard.
- `X`-Matrix of observed covariates.
- `time`-the observed survival time.
- `censor`-censoring indicator.
- `resid`-the martingale residuals.
- `lin.prid`-the vector of linear predictors.
- `frail`-estimated Frailty values.
- `iteration`-Number of outer iterations.
- `e.time`-the vector of unique event times.
- `n.event`- the number of events at each of the unique event times.
- `convergence`-an indicator, 1 if converge and 0 otherwise.
- `history`-an array containing records of estimates and other information on each iterations.

## Note

This function is important especially for simulation studies as it reduced checking time. Parameters of Bivariate correlated lognormal frailty model is based on the penalized partial likelihood approach by Rippatti and Palmgren (2000).

## References

Rippatti, S. and Palmgren, J (2000). Estimation of multivariate frailty models using penalized partial likelihood. Biometrics, 56: 1016-1022.

## See Also

`bcfrailph`

## Examples

```
set.seed(18)
simdata<-simbcfrail(psize=100, cenr= c(0.2),beta=c(1,-0.7,0.5),frailty=c("lognormal"),
frailpar=c(0.5,-0.25),bhaz=c("exponential"),
bhazpar=list(scale = c(0.1)),covartype= c("N","N","B"),
covarpar=list(fargs=c(0,0,1),sargs=c(1,1,0.5)),comncovar=2)
Y<-simdata$Y;X<-simdata$X

bcspfit<-fitbccv.lognsp(X=X,Y=Y,initfrailp=NULL)
bcspfit$coef
bcspfit$frailpar
```

## `plot.bcfrailph` *Plot bcfrailph*

### Description

Generics to print the S3 class bcfrailph.

### Usage

```
## S3 method for class 'bcfrailph'
plot(
  x,
  lty = 1,
  col = 1,
  type = "l",
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  main = NULL,
  conf.int = FALSE,
  ...
)
```

### Arguments

| | |
|---|---|
| `x` | A class `bcfrailph` object. |
| `lty` | Line type line type 1 is a solid line (the default). |
| `col` | Colors to be used for points. |
| `type` | The type of plot produced. type="l" Plot lines (the default) and type="p" Plot individual points. |
| `xlim` | range of variable on the x axis. |
| `ylim` | range of variable on the y axis. |
| `xlab` | Axis label for the x axis. |
| `main` | main is a string for figure title, placed at the top of the plot in a large font. |
| `conf.int` | whether confidence interval is included in the plot the deafault is FALSE. |
| `...` | ignored |

### Details

Calls `plot.bcfrailph()`.

### Value

An plot of `plot.bcfrailph` object.

## Note

The plot of cumulative baseline hazard function.

## See Also

`bcfrailph`

## Examples

```
set.seed(24)
simdata<-simbcfrail(psize=100, cenr= c(0),beta=c(-1),frailty=c("gamma"),
frailpar=c(0.4,0.5),bhaz=c("weibull"),
bhazpar=list(shape =c(0.9), scale = c(2)),
covartype= c("B"),covarpar=list(fargs=c(1),sargs=c(0.5)))
dataa<-simdata$data ## the generated data set.

#fit
bcfit=bcfrailph(Surv(time, censor) ~ X1+frailty(PID),data=dataa)
plot(bcfit)
```

---

# `print.bcfrailph` *Print bcfrailph*

## Description

Generics to print the S3 class bcfrailph.

## Usage

```
## S3 method for class 'bcfrailph'
print(x, ...)
```

## Arguments

| | |
|---|---|
| `x` | A class `bcfrailph` object. |
| `...` | ignored |

## Details

Calls `print.bcfrailph()`.

## Value

An object of `print.bcfrailph`, with some more human-readable results from `bcfrailph` object.

## Note

The summary function is currently identical to the print function.

## See Also

bcfrailph

## Examples

```
set.seed(4)
simdata<-simbcfrail(psize=300, cenr= c(0.3),beta=c(2),frailty=c("gamma"),
frailpar=c(0.5,0.5),bhaz=c("weibull"),
bhazpar=list(shape =c(5), scale = c(0.1)),
covartype= c("B"),covarpar=list(fargs=c(1),sargs=c(0.5)))
dataa<-simdata$data

fitbcfrailph=bcfrailph(Surv(time,censor)~ X1+frailty(PID) ,data=dataa,frail_distrn=c("gamma"))
fitbcfrailph
```

---

# `print.shrgamsp` *Print shrgamsp*

## Description

Generics to print the S3 class shrgamsp.

## Usage

```
## S3 method for class 'shrgamsp'
print(x, ...)
```

## Arguments

| | |
|---|---|
| `x` | A class `shrgamsp` object. |
| `...` | ignored |

## Details

Calls `print.shrgamsp()`.

## Value

An object of `print.shrgamsp`, with some more human-readable results from `shrgamsp` object.

## Note

The summary function is currently identical to the print function.

## See Also

bcfrailph

---

## `shrgamsp` *Cox PH model with univariate and bivariate shared gamma frailty model.*

---

### Description

Fit Cox PH model with univariate and bivariate shared gamma frailty model.

### Usage

```
shrgamsp(
  formula,
  data,
  weights = NULL,
  initfrailp = NULL,
  control = bcfrailph.control(),
  ...
)
```

### Arguments

| | |
|---|---|
| `formula` | A formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function. |
| `data` | A dataframe contain survival time, censor, covariate etc with data in columns. |
| `weights` | vector of case weights for gamma model. the default is NULL. |
| `initfrailp` | Initial estimates for the frailty parameters. The default is c(0.5). |
| `control` | Arguments to control the fit. The default is `bcfrailph.control`. |
| `...` | further arguments |

### Value

An object of shrgamsp contains the following components.

- `coefficients` - A vector of estimated Covariate coefficients.
- `frailparest` - A vector of estimated Frailty parameters i.e. frailty variance and correlation.
- `vcov`- Variance Covariance matrix of the Estimated Covariate coefficients obtained from the observed information matrix.
- `stderr`-A vector containing the Standard error of the Estimated parameters both covariate coefficients and frailty parameter.
- `loglik0`- Log likelihood of without frailty model.
- `loglik`-Log likelihood of Cox PH model with frailty.
- `Iloglilk`- Log likelihood of with frailty model after integrating out the frailty term.
- `bhaz`- an array containing unique event times and estimated baseline hazard.

- `X`-Matrix of observed covariates.
- `time`-the observed survival time.
- `censor`-censoring indicator.
- `resid`-the martingale residuals.
- `lin.prid`-the vector of linear predictors.
- `frail`-estimated Frailty values.
- `iteration`-Number of outer iterations.
- `e.time`-the vector of unique event times.
- `n.event`- the number of events at each of the unique event times.
- `convergence`-an indicator of convergence . see `nlminb`.

## Note

This is just a `coxph` model with gamma frailty and the differences between `coxph` with gamma frailty fit and `shrgamsp` fit is on the standard errors of the covariates cofficients. Here, the standard errors of the estimated covariate coefficients and the frailty variance parameter are obtained using the standard errors estimation approach given in Klein and Moeschberger (2003).

## References

Duchateau, L., Janssen, P. (2008) The Frailty Model. Springer, New York.

Klein, J. P., and Moeschberger, M. L. (2003), Survival analysis: techniques for censored and truncated data, New York: Springer.

## See Also

`bcfrailph`

## Examples

```
set.seed(2)
n1=500;IID=array(1:n1)
X1<-runif(n1,  min=0, max=1)
z=rgamma(n1,shape=2,scale=0.5)
u1<-runif(n1,  min=0, max=1)
time<- 1/0.1*log(1-0.1*log(u1)/(0.0001*exp(3*X1)*z))
censor=rep(1,n1)
dataa <- data.frame(time=time, X1=X1,censor=censor,IID=IID)

fitcoxfr=shrgamsp(Surv(time,censor)~ X1+frailty(IID) ,data=dataa)
fitcoxfr
```

---

`simbcfrail` *Simulate data from bivariate correlated frailty models.*

---

## Description

Simulate data from bivariate correlated gamma or lognormal frailty models with or without covariates.

## Usage

```
simbcfrail(
  psize,
  cenr = c(0),
  beta = c(0.5),
  frailty,
  frailpar = c(0.5, 0.25),
  bhaz = c("weibull"),
  bhazpar = list(shape = c(0.5), scale = c(0.01)),
  covartype = c("B"),
  covarpar = list(fargs = c(1), sargs = c(0.5)),
  inpcovar = NULL,
  inpcen = NULL,
  comncovar = NULL
)
```

## Arguments

| | |
|---|---|
| `psize` | pair size. |
| `cenr` | censored rate. The default is zero.. |
| `beta` | Covariate coefficient. |
| `frailty` | A type of frailty distribution to be used. Either gamma or lognormal. |
| `frailpar` | vector of frailty parameters, variance and correlation respectively. The default is c(0.5,0.25) meaning variance 0.5 and correlation 0.25. |
| `bhaz` | A type of baseline hazard distribution to be used. it can be weibull, gompertz or exponential. |
| `bhazpar` | is a `list` containing `scale` and`shape` of the specified baseline hazard distribution. |
| `covartype` | specified the distribution from which covariate(s) are goining to be sampled. covartype can be c("B","N","U")denoting binomial, normal or uniform, respectively. For example, `covartype=c("B","B")` to generate two covariates both from a binomial distribution. |
| `covarpar` | is a `list` containing parmeters of the specified covariate distribution with first and second arguments denoted by `fargs` and `sargs`, respectively. For example, if `covartype=c("B","U")` and `covarpar=list(fargs=c(1,0.3),sargs=c(0.5,1.3)),` |

| | |
|---|---|
| | generates two independent covariates from a binomial distribution (with parameters size=1 and probs=0.5) and from uniform distributions (with parameters min=0.3 and max=1.3). |
| `inpcovar` | is a `list` i.e,list(covar1=x1,covar2=x2) to input covariates with both x1 and x2 is in matrix form. |
| `inpcen` | is a `list` containing `cent1` and `cent2` denoting censoring time for the first and the second subjects in pairs respectively. |
| `comncovar` | if common covariates are needed. |

## Value

An object of class `simbcfrail` that contain the following:

- `data` A data frame i.e, the simulated data set. IID is individual Id, PID is pair ID, time is the simulated survival time, censor is censoring indicator and X1 denote the simulated covariate.
- `X` Covariates in Matrix form.
- `Y` A matrix contains generated survival time and censoring.
- `numberofpair` The specified number of pairs.
- `censoredrate` The specified censored rate.
- `fraildist` The specified frailty distribution.
- `frailpar` The specified frailty parameters.

## See Also

`bcfrailph`,`simstdybcf`

## Examples

```
set.seed(4)
simdata<-simbcfrail(psize=300, cenr= c(0.3),beta=c(2),frailty=c("gamma"),
frailpar=c(0.5,0.5),bhaz=c("weibull"),
bhazpar=list(shape =c(5), scale = c(0.1)),
covartype= c("B"),covarpar=list(fargs=c(1),sargs=c(0.5)))
dataa<-simdata$data
head(dataa)


# If data generation is from bivariate correlated lognormal frailty model,
set.seed(18)
simdata<-simbcfrail(psize=100, cenr= c(0.2),beta=c(1,-0.7,0.5),frailty=c("lognormal"),
frailpar=c(0.5,-0.25),bhaz=c("exponential"),
bhazpar=list(scale = c(0.1)),covartype= c("N","N","B"),
covarpar=list(fargs=c(0,0,1),sargs=c(1,1,0.5)),comncovar=2)
dataa<-simdata$data
head(dataa)

# If common covariate is desired, out of 3, covariate 2 is common for the pair.
set.seed(18)
```

```
simdata<-simbcfrail(psize=100, cenr= c(0.2),beta=c(1,-0.7,0.5),frailty=c("lognormal"),
frailpar=c(0.5,-0.25),bhaz=c("exponential"),
bhazpar=list(scale = c(0.1)),covartype= c("N","N","B"),
covarpar=list(fargs=c(0,0,1),sargs=c(1,1,0.5)),comncovar=2)
dataa<-simdata$data
head(dataa)

# If generate from biv-correlated gamma model, weibull baseline without covariate,
set.seed(4)
simdata<-simbcfrail(psize=300, cenr= c(0.3),beta=NULL,frailty=c("gamma"),
frailpar=c(0.5,0.5),bhaz=c("weibull"),bhazpar=list(shape =c(5), scale = c(0.1)))
dataa<-simdata$data
head(dataa)
```

---

## `simstdybcf` *Simulation study for bivariate correlated frailty models.*

### Description

Simulation study for bivariate correlated gamma and lognormal frailty models with and without covariates.

### Usage

```
simstdybcf(
  Rep,
  mfit = NULL,
  psize,
  cenr = c(0),
  beta = c(0.5),
  frailty,
  frailpar = c(0.5, 0.25),
  bhaz = c("weibull"),
  bhazpar = list(shape = c(0.5), scale = c(0.01)),
  covartype = c("B"),
  covarpar = list(fargs = c(1), sargs = c(0.5)),
  inpcovar = NULL,
  inpcen = NULL,
  comncovar = NULL
)
```

### Arguments

| | |
|---|---|
| `Rep` | number of replications. |

| | |
|---|---|
| `mfit` | A type of frailty model to be fit in addition to `bcfrailph`. mfit can be c("cox","shrg") where `cox` is for univariate or bivariate shared lognormal and gamma model fit using `coxph` and `shrg` is for univariate or bivariate shared gamma model fit using `shrgamsp`. |
| `psize` | pair size. |
| `cenr` | censored rate. The default is zero.. |
| `beta` | Covariate coefficient. |
| `frailty` | A type of frailty distribution to be used. Either gamma or lognormal. |
| `frailpar` | vector of frailty parameters, variance and correlation respectively. The default is c(0.5,0.25) meaning variance 0.5 and correlation 0.25. |
| `bhaz` | A type of baseline hazard distribution to be used. it can be weibull, gompertz or exponential. |
| `bhazpar` | is a `list` containing `scale` and`shape` of the specified baseline hazard distribution. |
| `covartype` | specified the distribution from which covariate(s) are goining to be sampled. covartype can be c("B","N","U")denoting binomial, normal or uniform, respectively. For example, `covartype=c("B","B")` to generate two covariates both from a binomial distribution. |
| `covarpar` | is a `list` containing parmeters of the specified covariate distribution with first and second arguments denoted by `fargs` and `sargs`, respectively. For example, if `covartype=c("B","U")` and `covarpar=list(fargs=c(1,0.3),sargs=c(0.5,1.3))`, generates two independent covariates from a binomial distribution (with parameters size=1 and probs=0.5) and from uniform distributions (with parameters min=0.3 and max=1.3). |
| `inpcovar` | is a `list` i.e,list(covar1=x1,covar2=x2) to input covariates with both x1 and x2 is in matrix form. |
| `inpcen` | is a `list` containing `cent1` and `cent2` denoting censoring time for the first and the second subjects in pairs respectively. |
| `comncovar` | if common covariates are needed. |

## Value

An object of class `simstdybcf` that contain the following:

- `Result` a summary result containing true parameter, mean of estimates, mean of the standard errors of the estimates, standard deviation of estimates, and 95% CI coverage probability.
- `estimates` a matrix containing estimates of parameters at each replications.
- `estimateSE` a matrix containing standard error of estimates at each replications.
- `coverage` a matrix containing an indicator whether the true parameter lies within a 95% CI at each replications or not.
- `TMAT` a matrix containing the generated artificial unique event times at each replications for gamma model.
- `h0MAT` a matrix containing the estimated baseline hazards at each replications for gamma model.
- `h0SEMAT` a matrix containing SE of the estimated baseline hazards at each replications for gamma model.

### See Also

simbcfrail

### Examples

```
set.seed(2)
sim<-simstdybcf(Rep=5,psize=100, cenr= c(0.2),beta=c(1,-0.7,0.5),
frailty=c("lognormal"),frailpar=c(0.5,-0.25),bhaz=c("exponential"),
bhazpar=list(scale = c(0.1)),covartype= c("N","N","B"),
covarpar=list(fargs=c(0,0,1),sargs=c(1,1,0.5)),comncovar=2)
Res<-sim$Result
Res


# In addition to bcfrailph fit, if coxph with univariate lognormal frailty model is desired to run,

sim<-simstdybcf(Rep=5,mfit="cox",psize=100, cenr= c(0.2),beta=c(1,-0.7,0.5),
frailty=c("lognormal"),frailpar=c(0.5,-0.25),bhaz=c("exponential"),
bhazpar=list(scale = c(0.1)),covartype= c("N","N","B"),
covarpar=list(fargs=c(0,0,1),sargs=c(1,1,0.5)),comncovar=2)
Res<-sim$Result # bcfrailph fit result
Res
Resc<-sim$Resultc # coxph with univariate lognormal frailty model fit result
Resc
```

---

## `summary.bcfrailph` *Print bcfrailph*

### Description

Generics to print the S3 class bcfrailph.

### Usage

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

### Arguments

| | |
|---|---|
| `object` | A class `bcfrailph` object. |
| `...` | ignored |

### Details

Calls `print.bcfrailph()`.

## Value

An object of `summary.bcfrailph`, with some more human-readable results from `bcfrailph` object.

## Note

The summary function is currently identical to the print function.

## See Also

`bcfrailph`

## Examples

```
set.seed(4)
simdata<-simbcfrail(psize=300, cenr= c(0.3),beta=c(2),frailty=c("gamma"),
frailpar=c(0.5,0.5),bhaz=c("weibull"),
bhazpar=list(shape =c(5), scale = c(0.1)),
covartype= c("B"),covarpar=list(fargs=c(1),sargs=c(0.5)))
dataa<-simdata$data

fitbcfrailph=bcfrailph(Surv(time,censor)~ X1+frailty(PID) ,data=dataa,frail_distrn=c("gamma"))
fitbcfrailph
summary(fitbcfrailph)
```

---

# `summary.shrgamsp` *Print shrgamsp*

## Description

Generics to print the S3 class shrgamsp.

## Usage

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

## Arguments

| | |
|---|---|
| `object` | A class shrgamsp object. |
| `...` | ignored |

## Details

Calls `print.shrgamsp()`.

## Value

An object of `summary.shrgamsp`, with some more human-readable results from `shrgamsp` object.

## Note

The summary function is currently identical to the print function.

## See Also

`bcfrailph`

# Index