Package 'Copula.surv'

March 5, 2022

Type Package

Title Analysis of Bivariate Survival Data Based on Copulas

Version 1.2

Date 2022-03-05

Author Takeshi Emura

Maintainer Takeshi Emura <takeshiemura@gmail.com>

Description Simulating bivariate survival data from copula models.
Estimation of the association parameter in copula models.
Two different ways to estimate the association parameter in copula models are implemented.
A goodness-of-fit test for a given copula model is implemented.
See Emura, Lin and Wang (2010) <doi:10.1016/j.csda.2010.03.013> for details.

License GPL-2

NeedsCompilation no

Repository CRAN

Date/Publication 2022-03-05 15:20:08 UTC

R topics documented:

Copula.surv-package   *Analysis of Bivariate Survival Data*

Description

Simulating bivariate survival data from copula models. Estimation of the association parameter in copula models. Two different ways to estimate the association parameter in copula models are implemented. A goodness-of-fit test for a given copula model is implemented. See Emura, Lin and Wang (2010) <doi:10.1016/j.csda.2010.03.013> for details.

Details

Details are seen from the references.

Author(s)

Takeshi Emura Maintainer: Takeshi Emura <takeshiemura@gmail.com>

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

---

simu.BB1   *Simulating data from the BB1 copula*

Description

n pairs of (U,V) are generated from the BB1 copula. n paris of (X,Y) are generated from the corresponding bivariate survival model with the Weibull marginal distributions. The default parameters (scale1=scale2=shape1=shape2=1) give the unit exponential distributions.

Usage

```
simu.BB1(n,alpha,d=0,scale1=1,scale2=1,shape1=1,shape2=1)
```

Arguments

n	sample size
alpha	association (copula) parameter
d	BB1 copula's departure parameter from the Clayton (d=0 is the default)
scale1	scale parameter for X
scale2	scale parameter for Y
shape1	shape parameter for X
shape2	shape parameter for Y

Details

See Section 2.6 of Emura et al.(2019) for copulas and bivariate survival times.

Value

U	uniformly distributed on (0,1)
V	uniformly distributed on (0,1)
X	Weibull distributed (scale1, shape1)
Y	Weibull distributed (scale2, shape2)

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoints, Joint Frailty-Copula Models, JSS Research Series in Statistics, Springer

Examples

```
n=100
Dat=simu.BB1(n=n,alpha=1,d=2,scale1=1,scale2=2,shape1=0.5,shape2=2)
plot(Dat[,"U"],Dat[,"V"])
cor(Dat[,"U"],Dat[,"V"],method="kendall")
plot(Dat[,"X"],Dat[,"Y"])
cor(Dat[,"X"],Dat[,"Y"],method="kendall")
```

---

simu.Clayton	*Simulating data from the Clayton copula*

Description

n pairs of (U,V) are generated from the Clayton copula. n paris of (X,Y) are generated from the corresponding bivariate survival model with the Weibull marginal distributions. The default parameters (scale1=scale2=shape1=shape2=1) give the unit exponential distributions.

Usage

```
simu.Clayton(n,alpha,scale1=1,scale2=1,shape1=1,shape2=1)
```

Arguments

`n`	sample size
`alpha`	association (copula) parameter
`scale1`	scale parameter for X
`scale2`	scale parameter for Y
`shape1`	shape parameter for X
`shape2`	shape parameter for Y

Details

See Section 2.6 of Emura et al.(2019) for copulas and bivariate survival times.

Value

`U`	uniformly distributed on (0,1)
`V`	uniformly distributed on (0,1)
`X`	Weibull distributed (scale1, shape1)
`Y`	Weibull distributed (scale2, shape2)

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoints, Joint Frailty-Copula Models, JSS Research Series in Statistics, Springer

Examples

```
n=100
Dat=simu.Clayton(n=n,alpha=1,scale1=1,scale2=2,shape1=0.5,shape2=2)
plot(Dat[,"U"],Dat[,"V"])
cor(Dat[,"U"],Dat[,"V"],method="kendall")
plot(Dat[,"X"],Dat[,"Y"])
cor(Dat[,"X"],Dat[,"Y"],method="kendall")
```

---

simu.FGM   *Simulating data from the FGM copula*

Description

n pairs of (U,V) are generated from the FGM copula. n paris of (X,Y) are generated from the corresponding bivariate survival model with the Weibull marginal distributions. The default parameters (scale1=scale2=shape1=shape2=1) give the unit exponential distributions.

Usage

```
simu.FGM(n,alpha,scale1=1,scale2=1,shape1=1,shape2=1)
```

Arguments

n	sample size
alpha	association (copula) parameter; -1<=alpha<=1
scale1	scale parameter for X
scale2	scale parameter for Y
shape1	shape parameter for X
shape2	shape parameter for Y

Details

See Section 2.6 of Emura et al.(2019) for copulas and bivariate survival times.

Value

U	uniformly distributed on (0,1)
V	uniformly distributed on (0,1)
X	Weibull distributed (scale1, shape1)
Y	Weibull distributed (scale2, shape2)

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoints, Joint Frailty-Copula Models, JSS Research Series in Statistics, Springer

Examples

```
n=100
Dat=simu.FGM(n=n,alpha=1,scale1=1,scale2=2,shape1=0.5,shape2=2)
plot(Dat[,"U"],Dat[,"V"])
cor(Dat[,"U"],Dat[,"V"],method="kendall")
plot(Dat[,"X"],Dat[,"Y"])
cor(Dat[,"X"],Dat[,"Y"],method="kendall")
```

---

simu.Frank	*Simulating data from the Frank copula*

Description

n pairs of (U,V) are generated from the Frank copula. n paris of (X,Y) are generated from the corresponding bivariate survival model with the Weibull marginal distributions. The default parameters (scale1=scale2=shape1=shape2=1) give the unit exponential distributions.

Usage

```
simu.Frank(n,alpha,scale1=1,scale2=1,shape1=1,shape2=1)
```

Arguments

n	sample size
alpha	association (copula) parameter
scale1	scale parameter for X
scale2	scale parameter for Y
shape1	shape parameter for X
shape2	shape parameter for Y

Details

See Section 2.6 of Emura et al.(2019) for copulas and bivariate survival times.

Value

U	uniformly distributed on (0,1)
V	uniformly distributed on (0,1)
X	Weibull distributed (scale1, shape1)
Y	Weibull distributed (scale2, shape2)

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoints, Joint Frailty-Copula Models, JSS Research Series in Statistics, Springer

Examples

```
n=100
Dat=simu.Frank(n=n,alpha=10,scale1=1,scale2=2,shape1=0.5,shape2=2)
plot(Dat[,"U"],Dat[,"V"])
cor(Dat[,"U"],Dat[,"V"],method="kendall")
plot(Dat[,"X"],Dat[,"Y"])
cor(Dat[,"X"],Dat[,"Y"],method="kendall")
```

---

simu.Gumbel	*Simulating data from the Gumbel copula*

Description

n pairs of (U,V) are generated from the Gumbel copula. n paris of (X,Y) are generated from the corresponding bivariate survival model with the Weibull marginal distributions. The default parameters (scale1=scale2=shape1=shape2=1) give the unit exponential distributions.

Usage

```
simu.Gumbel(n,alpha,scale1=1,scale2=1,shape1=1,shape2=1)
```

Arguments

n	sample size
alpha	association (copula) parameter
scale1	scale parameter for X
scale2	scale parameter for Y
shape1	shape parameter for X
shape2	shape parameter for Y

Details

See Section 2.6 of Emura et al.(2019) for copulas and bivariate survival times.

Value

U	uniformly distributed on (0,1)
V	uniformly distributed on (0,1)
X	Weibull distributed (scale1, shape1)
Y	Weibull distributed (scale2, shape2)

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoints, Joint Frailty-Copula Models, JSS Research Series in Statistics, Springer

Examples

```
n=100
Dat=simu.Gumbel(n=n,alpha=1,scale1=1,scale2=2,shape1=0.5,shape2=2)
plot(Dat[,"U"],Dat[,"V"])
cor(Dat[,"U"],Dat[,"V"],method="kendall")
plot(Dat[,"X"],Dat[,"Y"])
cor(Dat[,"X"],Dat[,"Y"],method="kendall")
```

Test.Clayton   *A goodness-of-fit test for the Clayton copula*

Description

Perform a goodness-of-fit test for the Clayton copula based on Emura, Lin and Wang (2010). The test is asymptotically equivalent to the test of Shih (1998).

Usage

```
Test.Clayton(x.obs,y.obs,dx,dy,lower=0.001,upper=50,U.plot=TRUE)
```

Arguments

x.obs	censored times for X
y.obs	censored times for Y
dx	censoring indicators for X
dy	censoring indicators for Y
lower	lower bound for the association parameter
upper	upper bound for the association parameter
U.plot	if TRUE, draw the plot of U_1(theta)

Details

See the references.

Value

theta1	association parameter by the pseudo-likelihood estimator
theta2	association parameter by the unweighted estimator
Stat	log(theta1)-log(theta2)
Z	Z-value of the goodness-of-fit for the Clayton copula
P	P-value of the goodness-of-fit for the Clayton copula

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Shih JH (1998) A goodness-of-fit test for association in a bivariate survival model. Biometrika 85: 189-200

Examples

```
n=20
theta_true=2 ## association parameter ##
r1_true=2 ## hazard for X
r2_true=2 ## hazard for Y

set.seed(1)
V1=runif(n)
V2=runif(n)
X=-1/r1_true*log(1-V1)
W=(1-V1)^(-theta_true)
Y=1/theta_true/r2_true*log(  1-W+W*(1-V2)^(-theta_true/(theta_true+1))  )
C=runif(n,min=0,max=5)

x.obs=pmin(X,C)
y.obs=pmin(Y,C)
dx=X<=C
dy=Y<=C

Test.Clayton(x.obs,y.obs,dx,dy)
```

Test.Gumbel	*A goodness-of-fit test for the Gumbel copula*

Description

Perform a goodness-of-fit test for the Gumbel copula based on Emura, Lin and Wang (2010).

Usage

```
Test.Gumbel(x.obs,y.obs,dx,dy,lower=0.01,upper=50,U.plot=TRUE)
```

Arguments

x.obs	censored times for X
y.obs	censored times for Y
dx	censoring indicators for X
dy	censoring indicators for Y
lower	lower bound for the association parameter
upper	upper bound for the association parameter
U.plot	if TRUE, draw the plot of U_1(theta) and U_2(theta)

Details

See the references.

Value

theta1	association parameter by the pseudo-likelihood estimator
theta2	association parameter by the unweighted estimator
Stat	log(theta1)-log(theta2)
Z	Z-value of the goodness-of-fit for the Clayton copula
P	P-value of the goodness-of-fit for the Clayton copula

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Examples

```
x.obs=c(1,2,3,4,5,6,7,8,9,10,11,12,13,14,15)
y.obs=c(2,1,4,5,6,8,3,7,10,9,11,12,13,14,15)
dx=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1)
dy=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1)
Test.Gumbel(x.obs,y.obs,dx,dy)
```

| U1.Clayton | *Estimation of an association parameter via the pseudo-likelihood* |

Description

Estimate the association parameter of the Clayton copula using bivariate survival data. The estimator was derived by Clayton (1978) and reformulated by Emura, Lin and Wang (2010).

Usage

```
U1.Clayton(x.obs,y.obs,dx,dy,lower=0.001,upper=50,U.plot=TRUE)
```

Arguments

x.obs	censored times for X
y.obs	censored times for Y
dx	censoring indicators for X
dy	censoring indicators for Y
lower	lower bound for the association parameter
upper	upper bound for the association parameter
U.plot	if TRUE, draw the plot of U_1(theta)

Details

Details are seen from the references.

Value

theta	association parameter
tau	Kendall's tau (=theta/(theta+2))

Author(s)

Takeshi Emura

References

Clayton DG (1978). A model for association in bivariate life tables and its application to epidemiological studies of familial tendency in chronic disease incidence. Biometrika 65: 141-51.

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Examples

```
n=200
theta_true=2 ## association parameter ##
r1_true=1 ## hazard for X
r2_true=1 ## hazard for Y

set.seed(1)
V1=runif(n)
V2=runif(n)
X=-1/r1_true*log(1-V1)
W=(1-V1)^(-theta_true)
Y=1/theta_true/r2_true*log(  1-W+W*(1-V2)^(-theta_true/(theta_true+1))  )
C=runif(n,min=0,max=5)

x.obs=pmin(X,C)
y.obs=pmin(Y,C)
dx=X<=C
dy=Y<=C

U1.Clayton(x.obs,y.obs,dx,dy)
```

U1.Gumbel   *Estimation of an association parameter via the unweighted estimator*

Description

Estimate the association parameter of the Gumbel copula using bivariate survival data. The estimator was derived by Emura, Lin and Wang (2010).

Usage

```
U1.Gumbel(x.obs,y.obs,dx,dy,lower=0.01,upper=50,U.plot=TRUE)
```

Arguments

x.obs	censored times for X
y.obs	censored times for Y
dx	censoring indicators for X
dy	censoring indicators for Y
lower	lower bound for the association parameter
upper	upper bound for the association parameter
U.plot	if TRUE, draw the plot of U_1(theta)

Details

Details are seen from the references.

Value

theta	association parameter
tau	Kendall's tau (=theta/(theta+2))

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Examples

```
x.obs=c(1,2,3,4,5,6,7,8,9,10,11,12,13,14,15)
y.obs=c(2,1,4,5,6,8,3,7,10,9,11,12,13,14,15)
dx=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1)
dy=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1)
U1.Gumbel(x.obs,y.obs,dx,dy)
```

U2.Clayton	*Estimation of an association parameter via the unweighted estimator*

Description

Estimate the association parameter of the Clayton copula using bivariate survival data. The estimator was defined as the unweighted estimator in Emura, Lin and Wang (2010).

Usage

```
U2.Clayton(x.obs,y.obs,dx,dy)
```

Arguments

x.obs	censored times for X
y.obs	censored times for Y
dx	censoring indicators for X
dy	censoring indicators for Y

Details

Details are seen from the references.

Value

theta	association parameter
tau	Kendall's tau (=theta/(theta+2))

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Examples

```
n=200
theta_true=2 ## association parameter ##
r1_true=1 ## hazard for X
r2_true=1 ## hazard for Y

set.seed(1)
V1=runif(n)
V2=runif(n)
X=-1/r1_true*log(1-V1)
W=(1-V1)^(-theta_true)
Y=1/theta_true/r2_true*log(  1-W+W*(1-V2)^(-theta_true/(theta_true+1))  )
C=runif(n,min=0,max=5)

x.obs=pmin(X,C)
y.obs=pmin(Y,C)
dx=X<=C
dy=Y<=C

U2.Clayton(x.obs,y.obs,dx,dy)
```

U2.Gumbel   *Estimation of an association parameter via the pseudo-likelihood*

Description

Estimate the association parameter of the Gumbel copula using bivariate survival data. The estimator was derived by Emura, Lin and Wang (2010).

Usage

```
U2.Gumbel(x.obs,y.obs,dx,dy,lower=0.01,upper=50,U.plot=TRUE)
```

Arguments

x.obs	censored times for X
y.obs	censored times for Y
dx	censoring indicators for X

dy	censoring indicators for Y
lower	lower bound for the association parameter
upper	upper bound for the association parameter
U.plot	if TRUE, draw the plot of U_1(theta)

Details

Details are seen from the references.

Value

theta	association parameter
tau	Kendall's tau (=theta/(theta+1))

Author(s)

Takeshi Emura

References

Emura T, Lin CW, Wang W (2010) A goodness-of-fit test for Archimedean copula models in the presence of right censoring, Compt Stat Data Anal 54: 3033-43

Examples

```
x.obs=c(1,2,3,4,5)
y.obs=c(2,1,4,5,6)
dx=c(1,1,1,1,1)
dy=c(1,1,1,1,1)
U2.Gumbel(x.obs,y.obs,dx,dy)
```

Index