

# Package: isoSurv (via r-universe)

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**Type** Package

**Title** Isotonic Regression on Survival Analysis

**Version** 0.3.0

**Date** 2023-9-1

**Description** Nonparametric estimation on survival analysis under order-restrictions.

**Depends** R (>= 3.6.0), Iso, survival, stats, graphics

**License** GPL (>= 2)

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**NeedsCompilation** no

**Author** Yunro Chung [aut, cre]  
(<https://orcid.org/0000-0001-9125-9277>)

**Maintainer** Yunro Chung <yunro.chung@asu.edu>

**Repository** <https://ze23i651096531.r-universe.dev>

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**RemoteUrl** <https://github.com/cran/isoSurv>

**RemoteRef** HEAD

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isoSurv-package

*Isotonic Regression on Survival Analysis*

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### Description

Nonparametric estimation on survival analysis under order restrictions

### Details

Package: isoph  
Type: Package  
Version: 0.3.0  
Date: 2023-9-1  
License: GPL (>= 2)

### Author(s)

Yunro Chung [aut,cre] Maintainer: Yunro Chung <yunro.chung@asu.edu>

### References

Yunro Chung, Anastasia Ivanova, Michael G. Hudgens, Jason P. Fine (2018), Partial likelihood estimation of isotonic proportional hazards models, *Biometrika*, 105(1), 133-148. doi:10.1093/biomet/asx064

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disoph

*Fit Double Isotonic Proportional Hazards Model*

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### Description

Nonparametric estimation of monotone baseline hazard and monotone covariate effect functions in the proportional hazards model.

### Usage

```
disoph(formula, bshape, data, maxiter, eps)
```

**Arguments**

formula	formula object: $\text{response} \sim \text{iso}(z, \text{shape} = \text{"increasing"}) + x_1 + x_2 + \dots + x_p$ . The response must be right-censored survival outcome using the <code>Surv</code> function in the survival package. The <code>iso</code> function attributes the covariate $z$ ' name, shape and anchor point.
bshape	direction of the baseline hazard function ( $bshape = \text{"increasing"}$ or $\text{"decreasing"}$ ).
data	data.frame includes variables named in the formula argument.
maxiter	maximum number of iteration (default is $10^4$ ).
eps	stopping convergence criteria (default is $10^{-3}$ ).

**Details**

The `disoph` function computes  $(\lambda_0, \psi, \beta)$  in the isotonic proportional hazards model, defined as

$$\lambda(t|z, x) = \lambda_0(t) \exp(\psi(z) + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p),$$

based on the full likelihood, where  $\lambda_0$  is a monotone increasing (or decreasing) baseline hazard function,  $\psi$  is a monotone increasing (or decreasing) covariate effect function,  $z$  is a univariate variable,  $(x_1, x_2, \dots, x_p)$  is a set of covariates, and  $\beta = (\beta_1, \beta_2, \dots, \beta_p)$  is a set of corresponding regression parameters. It allows to estimate  $(\lambda_0, \beta)$  only if `iso(z, shape = "increasing")` is removed in the formula object. Likewise, It allows to estimate  $(\lambda_0, \psi)$  only if  $x$  is removed in the formula object. Using the nonparametric maximum likelihood approaches, estimated  $\lambda_0$  and  $\psi$  are right continuous increasing (or left continuous decreasing) step functions. Compared to the standard partial likelihood approach, the full likelihood approach in the `disoph` function additionally use shape-information on  $\lambda_0$ , resulting in more efficient estimators especially for a finite sample size.

For the anchor constraint, one point has to be fixed with  $\psi(K) = 0$  to solve the identifiability problem, e.g.  $\lambda_0(t) \exp(\psi(z)) = (\lambda_0(t) \exp(-c)) (\exp(\psi(z) + c))$  for any constant  $c$ .  $K$  is called an anchor point. By default, we set  $K$  as a median of values of  $z$ 's. The choice of anchor points are not important because, for example, different anchor points results in the same hazard ratios.

**Value**

A list of class `disoph`:

<code>iso.bh</code>	data.frame with $t$ and estimated $\lambda_0(t)$ .
<code>iso.cov</code>	data.frame with $z$ and estimated $\psi(z)$ .
<code>beta</code>	estimated $\beta_1, \beta_2, \dots, \beta_p$ .
<code>conv</code>	algorithm convergence status.
<code>iter</code>	total number of iterations.
<code>Zk</code>	anchor satisfying estimated $\psi(Zk) = 0$ .
<code>shape.bh</code>	order restriction on $\lambda_0$ .
<code>shape.cov</code>	order restriction on $\psi$ .

**Author(s)**

Yunro Chung [auth, cre]

## References

Yunro Chung, Double Isotonic Proportional Hazards Models with Applications to Dose-Finding Studies. In preparation.

## Examples

```
#test1
test1=data.frame(
  time= c(2, 5, 1, 7, 9, 5, 3, 6, 8, 9, 7, 4, 5, 2, 8),
  status=c(0, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1),
  z=     c(2, 1, 1, 3, 5, 6, 7, 9, 3, 0, 2, 7, 3, 9, 4)
)
disoph.fit1=disoph(Surv(time, status)~iso(z,shape="inc"),bshape="inc",data=test1)
print(disoph.fit1)
plot(disoph.fit1)

#test2
test2=data.frame(
  time= c(2, 5, 1, 7, 9, 5, 3, 6, 8, 9, 7, 4, 5, 2, 8),
  status=c(0, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1),
  z=     c(2, 1, 1, 3, 5, 6, 7, 9, 3, 0, 2, 7, 3, 9, 4),
  trt=   c(1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0),
  x=     c(1, 2, 3, 4, 5, 6, 7, 8, 9, 1, 2, 3, 4, 5, 6)
)
disoph.fit2=disoph(Surv(time, status)~iso(z,shape="inc")+trt+x,bshape="inc",data=test2)
print(disoph.fit2)
plot(disoph.fit2)
```

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iso

*Attributions of isotonic covariate effect*

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## Description

attributes the covariate with respect to the name, direction, anchor point, and class.

## Usage

```
iso(z, shape)
```

## Arguments

**z** a univariate covariate.  
**shape** a direction of  $z$  (*shape*="increasing" or "decreasing").

## Details

Internal function. The iso function attributes the covariate  $z$  for its name, shape, anchor point and class, where the anchor point is set to a median of  $z$ 's, and class is set to "iso covariate"

**Value**

The value  $z$  with attribution of its name, shape and median anchor point.

**Author(s)**

Yunro Chung [cre]

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 isoph

---

*Fit Isotonic Proportional Hazards Model*


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**Description**

Nonparametric estimation of a monotone covariate effect under the proportional hazards model.

**Usage**

```
isoph(formula, data, maxiter, eps)
```

**Arguments**

formula	a formula object: $\text{response} \sim \text{iso}(z, \text{shape} = \text{"increasing"}) + x_1 + x_2 + \dots + x_p$ . The response must be right-censored survival outcome using the Surv function in the survival package. The iso function attributes the covariate $z$ ' name, shape and anchor point.
data	data.frame includes variables named in the formula argument.
maxiter	maximum number of iteration (default is $10^4$ ).
eps	stopping convergence criteria (default is $10^{-3}$ ).

**Details**

The isoph function estimates  $(\psi, \beta)$  in the isotonic proportional hazards model, defined as

$$\lambda(t|z, x) = \lambda_0(t) \exp(\psi(z) + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p),$$

based on the partial likelihood with unspecified baseline hazard function  $\lambda_0$ , where  $\psi$  is a monotone increasing (or decreasing) covariate effect function,  $z$  is a univariate variable,  $x = (x_1, x_2, \dots, x_p)$  is a set of covariates, and  $\beta = (\beta_1, \beta_2, \dots, \beta_p)$  is a set of corresponding regression parameters. It allows to estimate  $\psi$  only if  $x$  is removed in the formula object. Using the nonparametric maximum likelihood approaches, estimated  $\psi$  is a right continuous increasing (or left continuous decreasing) step function.

For the anchor constraint, one point has to be fixed with  $\psi(K) = 0$  to solve the identifiability problem, e.g.  $\lambda_0(t) \exp(\psi(z)) = (\lambda_0(t) \exp(-c)) (\exp(\psi(z) + c))$  for any constant  $c$ .  $K$  is called an anchor point. By default, we set  $K$  as a median of values of  $z$ 's. The choice of anchor points are not important because, for example, different anchor points results in the same hazard ratios.

**Value**

A list of class isoph:

iso.cov	data.frame with $z$ and estimated $\psi$ .
beta	estimated $\beta_1, \beta_2, \dots, \beta_p$ .
conv	algorithm convergence status.
iter	total number of iterations.
Zk	anchor point satisfying $\psi(Zk)=0$ .
shape	Order-restriction imposed on $\psi$ .

**Author(s)**

Yunro Chung [aut, cre]

**References**

Yunro Chung, Anastasia Ivanova, Michael G. Hudgens, Jason P. Fine, Partial likelihood estimation of isotonic proportional hazards models, *Biometrika*. 2018, 105 (1), 133-148. doi:10.1093/biomet/asx064

**Examples**

```
# test1
test1=data.frame(
  time= c(2, 5, 1, 7, 9, 5, 3, 6, 8, 9, 7, 4, 5, 2, 8),
  status=c(0, 1, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1),
  z=    c(2, 1, 1, 3, 5, 6, 7, 9, 3, 0, 2, 7, 3, 9, 4)
)
isoph.fit1=isoph(Surv(time, status)~iso(z,shape="inc"),data=test1)
print(isoph.fit1)
plot(isoph.fit1)

# test2
test2=data.frame(
  time= c(2, 5, 1, 7, 9, 5, 3, 6, 8, 9, 7, 4, 5, 2, 8),
  status=c(0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1),
  z=    c(2, 1, 1, 3, 5, 6, 7, 9, 3, 0, 2, 7, 3, 9, 4),
  trt=  c(1, 1, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0)
)
isoph.fit2=isoph(Surv(time, status)~iso(z,shape="inc")+trt, data=test2)
print(isoph.fit2)
plot(isoph.fit2)
```

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