

Package ‘OTRselect’

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Type Package

Title Variable Selection for Optimal Treatment Decision

Version 1.3

Date 2025-05-03

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Description A penalized regression framework that can simultaneously estimate the optimal treatment strategy and identify important variables.
Appropriate for either censored or uncensored continuous response.

License GPL-2

Depends stats, lars, survival, methods

NeedsCompilation no

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OTRselect-package *Variable Selection for Optimal Treatment Decision*

Description

A penalized regression framework that can simultaneously estimate the optimal treatment strategy and identify important variables. Appropriate for either censored or uncensored continuous response.

Details

The DESCRIPTION file:

```
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Title:            Variable Selection for Optimal Treatment Decision
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Authors@R:        c(person(given = "Wenbin", family = "Lu", role = "aut"), person(given = c("Hao", "Helen"), family = "Z
Description:      A penalized regression framework that can simultaneously estimate the optimal treatment strategy and i
License:          GPL-2
Depends:          stats, lars, survival, methods
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```

Index of help topics:

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OTRselect-package  Variable Selection for Optimal Treatment
                   Decision
Qhat               Mean Response or Restricted Mean Response Given
                   a Treatment Regime
censored           Variable Selection for Optimal Treatment
                   Decision with Censored Survival Times
uncensored         Variable Selection for Optimal Treatment
                   Decision with Uncensored Continuous Response
```

Function `censored` performs variable selection for censored continuous response. Function `uncensored` performs variable selection for uncensored continuous response. Function `Qhat` estimates the restricted mean response given a treatment regime for censored data or the mean response given a treatment regime for uncensored data.

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References

- Lu, W., Zhang, H. H., and Zeng, D. (2013). Variable selection for optimal treatment decision. *Statistical Methods in Medical Research*, 22, 493–504. PMID: PMC3303960.
- Geng, Y., Lu, W., and Zhang, H. H. (2015). On optimal treatment regimes selection for mean survival time. *Statistics in Medicine*, 34, 1169–1184. PMID: PMC4355217.

censored	<i>Variable Selection for Optimal Treatment Decision with Censored Survival Times</i>
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Description

A penalized regression framework that can simultaneously estimate the optimal treatment strategy and identify important variables when the response is continuous and censored. This method uses an inverse probability weighted least squares estimation with adaptive LASSO penalty for variable selection.

Usage

```
censored(x, y, a, delta, propen, phi, logY = TRUE,
         intercept = TRUE)
```

Arguments

x	Matrix or data.frame of model covariates.
y	Vector of response. Note that this data is used to estimate the Kaplan-Meier Curve and should not be log(T).
a	Vector of treatment received. Treatments must be coded as integers or numerics that can be recast as integers without loss of information.
delta	Event indicator vector. The indicator must be coded as 0/1 where 0=no event and 1=event.
propen	Vector or matrix of propensity scores for each treatment. If a vector, the propensity is assumed to be the same for all samples. Column or element order must correspond to the sort order of the treatment variable, i.e., 0,1,2,3,... If the number of columns/elements in propen is one fewer than the total number of treatment options, it is assumed that the base or lowest valued treatment has not been provided.
phi	A character {'c' or 'l'} indicating if the constant ('c') or linear ('l') baseline mean function is to be used.
logY	TRUE/FALSE indicating if log(y) is to be used for regression.
intercept	TRUE/FALSE indicating if an intercept is to be included in phi model.

Value

A list object containing

beta A vector of the estimated regression coefficients after variable selection.
 optTx The estimated optimal treatment for each sample.

Author(s)

Wenbin Lu, Hao Helen Zhang, Yuan Geng, and Shannon T. Holloway

References

Geng, Y., Lu, W., and Zhang, H. H. (2015). On optimal treatment regimes selection for mean survival time. *Statistics in Medicine*, 34, 1169–1184. PMID: PMC4355217.

Examples

```
sigma <- diag(10)
ct <- 0.5^{1L:9L}
rst <- unlist(sapply(1L:9L,function(x){ct[1L:{10L-x}]}))
sigma[lower.tri(sigma)] <- rst
sigma[upper.tri(sigma)] <- t(sigma)[upper.tri(sigma)]

M <- t(chol(sigma))
Z <- matrix(rnorm(1000),10,100)
X <- t(M*%Z)

A <- rbinom(100,1,0.5)

Y <- rweibull(100,shape=0.5,scale=1)
C <- rweibull(100,shape=0.5,scale=1.5)

delta <- as.integer(C <= Y)

Y[delta > 0.5] <- C[delta>0.5]

dat <- data.frame(X,A,exp(Y),delta)
colnames(dat) <- c(paste("X",1:10,sep=""), "a", "y", "del")

censored(x = X,
         y = Y,
         a = A,
         delta = delta,
         propen = 0.5,
         phi = "c",
         logY = TRUE,
         intercept = TRUE)
```

Qhat	<i>Mean Response or Restricted Mean Response Given a Treatment Regime</i>
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Description

Estimates the mean response given a treatment regime if data is uncensored. If data is censored, estimates the restricted mean response given a treatment regime.

Usage

```
Qhat(y, a, g, wgt = NULL)
```

Arguments

y	vector of responses. Note if <code>logY = TRUE</code> in <code>censored</code> , this value should also be the logarithm.
a	vector of treatments received.
g	vector of the given treatment regime.
wgt	weights to be used if response is censored.

Value

Returns the estimated mean response or restricted mean response.

Author(s)

Wenbin Lu, Hao Helen Zhang, Donglin Zeng, Yuan Geng, and Shannon T. Holloway

References

Lu, W., Zhang, H. H., and Zeng, D. (2013). Variable selection for optimal treatment decision. *Statistical Methods in Medical Research*, 22, 493–504. PMID: PMC3303960.

Geng, Y., Lu, W., and Zhang, H. H. (2015). On optimal treatment regimes selection for mean survival time. *Statistics in Medicine*, 34, 1169–1184. PMID: PMC4355217.

Examples

```
y <- rnorm(100)
a <- rbinom(100, 1, 0.5)
g <- integer(100)

Qhat(y = y, a = a, g = g)
```

uncensored *Variable Selection for Optimal Treatment Decision with Uncensored Continuous Response*

Description

A penalized regression framework that can simultaneously estimate the optimal treatment strategy and identify important variables when the response is continuous and not censored. This method uses an inverse probability weighted least squares estimation with adaptive LASSO penalty for variable selection.

Usage

```
uncensored(x, y, a, propen, phi, intercept = TRUE)
```

Arguments

x	Matrix or data.frame of model covariates.
y	Vector of response. Note that this data is used to estimate the Kaplan-Meier Curve and should not be log(T).
a	Vector of treatment received. Treatments must be coded as integers or numerics that can be recast as integers without loss of information.
propen	Vector or matrix of propensity scores for each treatment. If a vector, the propensity is assumed to be the same for all samples. Column or element order must correspond to the sort order of the treatment variable, i.e., 0,1,2,3,... If the number of columns/elements in propen is one fewer than the total number of treatment options, it is assumed that the base or lowest valued treatment has not been provided.
phi	A character {'c' or 'l'} indicating if the constant ('c') or linear ('l') baseline mean function is to be used.
intercept	TRUE/FALSE indicating if an intercept is to be included in phi model.

Value

A list object containing

beta	A vector of the estimated regression coefficients after variable selection.
optTx	The estimated optimal treatment for each sample.

Author(s)

Wenbin Lu, Hao Helen Zhang, Donglin Zeng, and Shannon T. Holloway

References

Lu, W., Zhang, H. H., and Zeng, D. (2013). Variable selection for optimal treatment decision. *Statistical Methods in Medical Research*, 22, 493–504. PMID: PMC3303960.

Examples

```
sigma <- diag(10)
ct <- 0.5^{1L:9L}
rst <- unlist(sapply(1L:9L,function(x){ct[1L:{10L-x}]}))
sigma[lower.tri(sigma)] <- rst
sigma[upper.tri(sigma)] <- t(sigma)[upper.tri(sigma)]

M <- t(chol(sigma))
Z <- matrix(rnorm(1000),10,100)
X <- t(M %*% Z)

gamma1 <- c(1, -1, rep(0,8))
beta <- c(1,1,rep(0,7), -0.9, 0.8)

A <- rbinom(100,1,0.5)

Y <- 1.0 + X %*% gamma1 +
  A*{cbind(1.0,X)%*%beta} + rnorm(100,0,.25)

dat <- data.frame(X,A,Y)

uncensored(x=X,
           y = Y,
           a = A,
           propen = 0.5,
           phi = "c",
           intercept = TRUE)
```

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