Package 'MCID'

May 7, 2026

Type Package

Title Estimating the Minimal Clinically Important Difference

Version 0.1.0

Date 2021-09-07

Description Apply the marginal classification method to achieve the purpose of providing the point and interval estimates for the minimal clinically important difference based on the classical anchor-based method. For more details of the methodology, please see Zehua Zhou, Leslie J. Bisson and Jiwei Zhao (2021) <doi:10.48550/arXiv.2108.11589>.

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Encoding UTF-8

Imports stats

RoxygenNote 7.1.0

NeedsCompilation no

Author Zehua Zhou [cre, aut],
Jiwei Zhao [aut]

Maintainer Zehua Zhou <zehuazho@buffalo.edu>

Repository CRAN

Date/Publication 2021-09-10 11:20:12 UTC

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`cv.imcid` *Selection of the tuning parameters for determining the MCID at the individual level*

Description

`cv.imcid` returns the optimal tuning parameter δ and λ selected from a given grid by using k-fold cross-validation. The tuning parameters are selected for determining the MCID at the individual level

Usage

```
cv.imcid(x, y, z, lamseq, delseq, k = 5, maxit = 100, tol = 0.01)
```

Arguments

`x`	a continuous variable denoting the outcome change of interest
`y`	a binary variable denoting the patient-reported outcome derived from the anchor question
`z`	a vector or matrix denoting the patient's clinical profiles
`lamseq`	a vector containing the candidate values for the tuning parameter λ, where λ is the coefficient of the penalty term, used for avoiding the issue of model overfitting
`delseq`	a vector containing the candidate values for the tuning parameter δ, where δ is used to control the difference between the 0-1 loss and the surrogate loss. We recommend selecting the possible values from the neighborhood of the standard deviation of x
`k`	the number of groups into which the data should be split to select the tuning parameter δ by cross-validation. Defaults to 5
`maxit`	the maximum number of iterations. Defaults to 100
`tol`	the convergence tolerance. Defaults to 0.01

Value

a list including the combinations of the selected tuning parameters and the value of the corresponding target function

Examples

```
n <- 500
lambdaseq <- 10 ^ seq(-3, 3, 0.1)
deltaseq <- seq(0.1, 0.3, 0.1)
a <- 0.1
b <- 0.55
c <- -0.1
d <- 0.45
```

```
set.seed(721)
p <- 0.5
y <- 2 * rbinom(n, 1, p) - 1
z <- rnorm(n, 1, 0.1)
y_1 <- which(y == 1)
y_0 <- which(y == -1)
x <- c()
x[y_1] <- a + z[y_1] * b + rnorm(length(y_1), 0, 0.1)
x[y_0] <- c + z[y_0] * d + rnorm(length(y_0), 0, 0.1)

sel <- cv.imcid(x = x, y = y, z = z, lamseq = lambdaseq,
         delseq = deltaseq, k = 5, maxit = 100, tol = 1e-02)
sel$'Selected lambda'
sel$'Selected delta'
```

`cv.pmcid` *Selection of the tuning parameter for determining the MCID at the population level*

Description

`cv.pmcid` returns the optimal tuning parameter δ selected from a given grid by using k-fold cross-validation. The tuning parameter is selected for determining the MCID at the population level

Usage

```
cv.pmcid(x, y, delseq, k = 5, maxit = 100, tol = 0.01)
```

Arguments

`x`	a continuous variable denoting the outcome change of interest
`y`	a binary variable indicating the patient-reported outcome derived from the anchor question
`delseq`	a vector containing the candidate values for the tuning parameter δ, where δ is used to control the difference between the 0-1 loss and the surrogate loss. We recommend selecting the possible values from the neighborhood of the standard deviation of x
`k`	the number of groups into which the data should be split to select the tuning parameter δ by cross-validation. Defaults to 5
`maxit`	the maximum number of iterations. Defaults to 100
`tol`	the convergence tolerance. Defaults to 0.01

Value

a list including the selected tuning parameter and the value of the corresponding target function

Examples

```
n <- 500
deltaseq <- seq(0.1, 1, 0.1)
a <- 0.2
b <- -0.1
p <- 0.5

set.seed(115)
y <- 2 * rbinom(n, 1, p) - 1
y_1 <- which(y == 1)
y_0 <- which(y == -1)
x <- c()
x[y_1] <- rnorm(length(y_1), a, 0.1)
x[y_0] <- rnorm(length(y_0), b, 0.1)

sel <- cv.pmcid(x = x, y = y, delseq = deltaseq, k = 5,
         maxit = 100, tol = 1e-02)
sel$'Selected delta'
sel$'Function value'
```

`imcid` *Point and interval estimation for the MCID at the individual level*

Description

We formulate the individualized MCID as a linear function of the patients' clinical profiles. `imcid` returns the point estimate for the linear coefficients of the MCID at the individual level

Usage

```
imcid(x, y, z, n, lambda, delta, maxit = 100, tol = 0.01, alpha = 0.05)
```

Arguments

`x`	a continuous variable denoting the outcome change of interest
`y`	a binary variable indicating the patient-reported outcome derived from the anchor question
`z`	a vector or matrix denoting the patient's clinical profiles
`n`	the sample size
`lambda`	the selected tuning parameter λ, can be returned by `cv.imcid`
`delta`	the selected tuning parameter δ, can be returned by `cv.imcid`
`maxit`	the maximum number of iterations. Defaults to 100
`tol`	the convergence tolerance. Defaults to 0.01
`alpha`	nominal level of the confidence interval. Defaults to 0.05

Value

a list including the point estimates for the linear coefficients of the individualized MCID and their standard errors, and the corresponding confidence intervals based on the asymptotic normality

Examples

```
n <- 500
lambdaseq <- 10 ^ seq(-3, 3, 0.1)
deltaseq <- seq(0.1, 0.3, 0.1)
a <- 0.1
b <- 0.55
c <- -0.1
d <- 0.45
### True linear coefficients of the individualized MCID: ###
### beta0=0, beta1=0.5 ###

set.seed(115)
p <- 0.5
y <- 2 * rbinom(n, 1, p) - 1
z <- rnorm(n, 1, 0.1)
y_1 <- which(y == 1)
y_0 <- which(y == -1)
x <- c()
x[y_1] <- a + z[y_1] * b + rnorm(length(y_1), 0, 0.1)
x[y_0] <- c + z[y_0] * d + rnorm(length(y_0), 0, 0.1)
sel <- cv.imcid(x = x, y = y, z = z, lamseq = lambdaseq,
         delseq = deltaseq, k = 5, maxit = 100, tol = 1e-02)
lamsel <- sel$'Selected lambda'
delsel <- sel$'Selected delta'
result <- imcid(x = x, y = y, z = z, n = n, lambda = lamsel,
         delta = delsel, maxit = 100, tol = 1e-02, alpha = 0.05)
result$'Point estimates'
result$'Standard errors'
result$'Confidence intervals'
```

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pmcid *Point and interval estimation for the MCID at the population level*

Description

pmcid returns the point estimate for the MCID at the population level

Usage

```
pmcid(x, y, n, delta, maxit = 100, tol = 0.01, alpha = 0.05)
```

Arguments

x	a continuous variable denoting the outcome change of interest
y	a binary variable indicating the patient-reported outcome derived from the anchor question
n	the sample size
delta	the selected tuning parameter δ, can be returned by `cv.pmcid`
maxit	the maximum number of iterations. Defaults to 100
tol	the convergence tolerance. Defaults to 0.01
alpha	nominal level of the confidence interval. Defaults to 0.05

Value

a list including the point estimate of the population MCID and its standard error, and the confidence interval based on the asymptotic normality

Examples

```
n <- 500
deltaseq <- seq(0.1, 1, 0.1)
a <- 0.2
b <- -0.1
p <- 0.5
### True MCID is 0.5 ###

set.seed(115)
y <- 2 * rbinom(n, 1, p) - 1
y_1 <- which(y == 1)
y_0 <- which(y == -1)
x <- c()
x[y_1] <- rnorm(length(y_1), a, 0.1)
x[y_0] <- rnorm(length(y_0), b, 0.1)

sel <- cv.pmcid(x = x, y = y, delseq = deltaseq, k = 5,
         maxit = 100, tol = 1e-02)
delsel <- sel$'Selected delta'

result <- pmcid(x = x, y = y, n = n, delta = delsel,
            maxit = 100, tol = 1e-02, alpha = 0.05)
result$'Point estimate'
result$'Standard error'
result$'Confidence interval'
```

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