Package ‘MCID’

October 12, 2022

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

License GPL (>= 2)

Encoding UTF-8

Imports stats

RoxygenNote 7.1.0

NeedsCompilation no

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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 $\delta$ and $\lambda$ 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 $\lambda$, where $\lambda$ 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 $\delta$, where $\delta$ 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 $\delta$ 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

```r
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
```
```r
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.pmcid(x = x, y = y, delseq = lambdaseq,
            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 \( \delta \) 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**

```r
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 \( \delta \), where \( \delta \) 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 \( \delta \) 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

```r
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

```r
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 \( \lambda \), can be returned by `cv.imcid`
- **delta**: the selected tuning parameter \( \delta \), can be returned by `cv.imcid`
- **maxit**: the maximum number of iterations. Defaults to 100
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<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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<tbody>
<tr>
<td>tol</td>
<td>the convergence tolerance. Defaults to 0.01</td>
</tr>
<tr>
<td>alpha</td>
<td>nominal level of the confidence interval. Defaults to 0.05</td>
</tr>
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</table>

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

```r
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)
result <- imcid(x = x, y = y, z = z, lambda = lamsel,
                 delta = delsel, maxit = 100, tol = 1e-02)
result$'Point estimates'
result$'Standard errors'
result$'Confidence intervals'
```

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