Package ‘CUtools’

July 21, 2025

Type Package

Title Clinical Utility Tools to Analyze a Predictive Model

Version 0.1.0

Description Package to analyze the clinical utility of a biomarker. It provides the clinical utility curve, clinical utility table, efficacy of a biomarker, clinical efficacy curve and tests to compare efficacy between markers.

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.1

NeedsCompilation no

Author Maria Escorihuela [aut],
Luis Mariano Esteban [aut, cre],
Gerardo Sanz [aut],
Angel Borque [aut]

Maintainer Luis Mariano Esteban <`lmeste@unizar.es`>

Repository CRAN

Date/Publication 2025-02-07 18:40:02 UTC

Contents

`CUC_plot` *Plot the clinical utility of a biomarker*

Description

The clinical utility plot shows two magnitudes, the number of events missclassfied below a cut off point and the saved treatments. In the X axis we can see the different cut off points and in the Y axis the magnitudes above defined.

Usage

```
CUC_plot(Prob,yt)
```

Arguments

`Prob`	A vector with the event probability values provided by the biomarker
`yt`	A vector with the actual event values

Details

Prob must be a numeric vector with values between 0 and 1 and yt a numeric vector with dichotomic values 0/1

Value

The function returns the clinical utility curve

Author(s)

Maria Escorihuela, Luis Mariano Esteban, Gerardo Sanz, Angel Borque

Examples

```
###We generate a marker to serve as an example and plot the CUC curve
Prob<-c(rnorm(1000,0.4,0.1),rnorm(1000,0.6,0.05))
yt<-rep(c(0,1),c(1000,1000))
CUC_plot(Prob,yt)
```

`CUC_table` *Clinical utility tools to analyze a predictive model*

Description

Efficacy of a biomarker defined by the treatment saved below a cut-off point minus the missclasified events.

Usage

```
CUC_table(Th,Prob,yt)
```

Arguments

`Th`	The vector of cutoff points used to estimate efficacy at those points.
`Prob`	A vector with the event probability values provided by the biomarker.
`yt`	A vector with the actual event values

Details

Prob must be a numeric vector with values between 0 and 1, yt a numeric vector with dichotomic values 0/1 and z a numeric value between 0 and 100

Value

The returned object contains the following components:

`CUC_table`	A data frame with three columns, the threshold points, the rate of missing events and the rate of avoided treatments

Author(s)

Maria Escorihuela, Luis Mariano Esteban, Gerardo Sanz, Angel Borque

Examples

```
###We generate a marker to serve as an example

Prob<-c(rnorm(1000,0.4,0.1),rnorm(1000,0.5,0.05))
yt<-rep(c(0,1),c(1000,1000))
#We choose a grid of threshold points.
Th<-seq(1,100)
#Estimte the Clinical utility table
CUC_table(Th, Prob, yt)
```

`Efficacy` *Estimate the efficacy of a biomarker*

Description

The efficacy of a biomarker is defined by the treatment saved below a cut-off point minus the missclasified events.

Usage

```
Efficacy(Prob,yt,z)
```

Arguments

`Prob`	A vector with the event probability values provided by the biomarker
`yt`	A vector with the actual event values
`z`	The misclassification rate at which the effectiveness of the marker will be estimated.

Details

Prob must be a numeric vector with values between 0 and 1, yt a numeric vector with dichotomic values 0/1 and z a numeric value between 0 and 100

Value

The returned object contains the Efficacy of the biomarker Prob at a specific z rate of missclasified events

`Efficacy`	Efficacy of the biomarker Prob at a specific z rate of missclasified events

Author(s)

Maria Escorihuela, Luis Mariano Esteban, Gerardo Sanz, Angel Borque

Examples

```
###We generate a marker to serve as an example

Prob<-c(rnorm(10000,0.4,0.1),rnorm(10000,0.5,0.05))
yt<-rep(c(0,1),c(10000,10000))
#We choose a rate of 10% for misclassified events.
Efficacy(Prob=Prob,yt=yt,z=10)
```

`Efficacy_curve` *Efficacy curve for a predictive model/biomarker*

Description

The curve plot the efficacy of a predictive model for different missclassfication event rates

Usage

```
Efficacy_curve(Prob,yt)
```

Arguments

`Prob`	A vector with the event probability values provided by the biomarker
`yt`	A vector with the actual event values

Details

Prob must be a numeric vector with values between 0 and 1, yt a numeric vector with dichotomic values 0/1 and z a numeric value between 0 and 100

Value

The returned fit object of Efficacy_curve contains the plot of the Efficacy curve.

`EfficacyCurve`	Plot of the Efficacy of the biomarker Prob at different rates of missclasified events

Author(s)

Maria Escorihuela, Luis Mariano Esteban, Gerardo Sanz, Angel Borque

Examples

```
###We generate a marker to serve as an example and plot the curve

Prob<-c(rnorm(1000,0.4,0.1),rnorm(1000,0.5,0.05))
yt<-rep(c(0,1),c(1000,1000))

Efficacy_curve(Prob=Prob,yt=yt)
```

`Efficacy_test` *Test to compare efficacy of two models for a percentage of misclassified events*

Description

Test to compare the efficacy of two markers for paired or unpaired cases

Usage

```
Efficacy_test( paired, Prob1,Prob2,yt1,yt2,z)
```

Arguments

`paired`	if sample is paired 1 else 0
`Prob1`	A vector with the event probability values provided by the biomarker 1
`yt1`	A vector with the actual event values for the biomarker 1
`Prob2`	A vector with the event probability values provided by the biomarker 2
`yt2`	A vector with the actual event values for the biomarker 2
`z`	The misclassification rate at which the effectiveness of the marker will be estimated.

Details

Prob1 and Prob2 must be numeric vectors with values between 0 and 1, yt1 and yt2 numeric vectors with dichotomic values 0/1 and z a numeric value between 0 and 100. in a case of a paired comparison, yt1 and yt2 must be the same vector.

Value

The returned results of a test.

`Efficacy_test`	It gives the result of the comparison test between markers in terms of efficacy

Author(s)

Maria Escorihuela, Luis Mariano Esteban, Gerardo Sanz, Angel Borque

Examples

```
###We generate a marker to serve as an example
Prob1<-c(rnorm(10000,0.4,0.1),rnorm(10000,0.5,0.05))
Prob2<-c(rnorm(10000,0.4,0.1),rnorm(10000,0.5,0.05))
yt1<-rep(c(0,1),c(10000,10000))
yt2<-rep(c(0,1),c(10000,10000))
#We choose a rate of 10% for misclassified events.
```

```
##For a paired test

Efficacy_test(paired=1,Prob1,Prob2,yt1,yt2,z=10)

##For a unpaired test

Efficacy_test(paired=0,Prob1,Prob2,yt1,yt2,z=10)
```

Index