

Package: CUtools (via r-universe)

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Type Package

Title Clinical Utility Tools to Analyze a Predictive Model

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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

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

Description

The clinical utility plot shows two magnitudes, the number of events missclassified 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

<code>Prob</code>	A vector with the event probability values provided by the biomarker
<code>yt</code>	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 missclassified 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
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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)
#Estimate 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 missclassified 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 missclassified events

Efficacy	Efficacy of the biomarker Prob at a specific z rate of missclassified events
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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	<i>Efficacy curve for a predictive model/biomarker</i>
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Description

The curve plot the efficacy of a predictive model for different missclassification 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 missclassified 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	<i>Test to compare efficacy of two models for a percentage of misclassified events</i>
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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)
```

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