

# Package ‘CUtools’

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**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

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

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

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

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**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)
```

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

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**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)
```

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Efficacy

*Estimate the efficacy of a biomarker*

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### 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)
```

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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)
```

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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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