

Package ‘ggDCA’

October 13, 2022

Title Calculate and Plot Decision Curve

Version 1.1

Description Diagnostic and prognostic models are typically evaluated with measures of accuracy that do not address clinical consequences. Decision-analytic techniques allow assessment of clinical outcomes but often require collection of additional information and may be cumbersome to apply to models that yield a continuous result.

Decision curve analysis is a suitable method for evaluating alternative diagnostic and prognostic strategies that has advantages over other commonly used measures and techniques.

This method was described by Andrew J. Vickers (2006) <[doi:10.1177/0272989X06295361](https://doi.org/10.1177/0272989X06295361)>.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Imports do, set, rms (>= 6.0.1), base.rms, survival (>= 3.1-12)

Depends R (>= 2.10), ggplot2

NeedsCompilation no

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AUDC	<i>Area under Decision Curve</i>
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Description

Area under Decision Curve

Usage

```
AUDC(x)
```

Arguments

x results of dca() function

Value

Area under decision curves for each model.

dca	<i>Calculate Decision Curve Data</i>
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Description

Calculate Decision Curve Data

Usage

```
dca(...)

## S3 method for class 'coxph'
dca(
  ...,
  model.names = do::get_names(...),
  test.harm = 0,
  new.data = NULL,
  times = "median"
)

## S3 method for class 'cph'
dca(
  ...,
  model.names = do::get_names(...),
  test.harm = 0,
  new.data = NULL,
```

```

    times = "median"
  )

  ## S3 method for class 'glm'
  dca(..., model.names = do::get_names(...), test.harm = 0, new.data = NULL)

  ## S3 method for class 'lrm'
  dca(..., model.names = do::get_names(...), test.harm = 0, new.data = NULL)

```

Arguments

...	one or more results of logistic or cox regression
model.names	names for models
test.harm	test harm, default is 0
new.data	new data for validation
times	times for cox regression, default is 'median'

Value

a dataframe contains thresholds, TPR: true positive rate, FPR: false positive rate, NB: net benefit, model: model names.

References

Vickers, A. J., & Elkin, E. B. (2006). Decision Curve Analysis: A Novel Method for Evaluating Prediction Models. *Medical Decision Making*, 26(6), 565–574. <https://doi.org/10.1177/0272989X06295361>

ggplot.rFP.p100

Plot for decision curve

Description

Plot for decision curve

Plot for decision curve

Plot Decision Curve

Usage

```

## S3 method for class 'rFP.p100'
ggplot(
  data,
  mapping,
  color = TRUE,
  linetype = TRUE,
  lwd = 1.05,
  ...,

```

```
environment = parent.frame()
)

## S3 method for class 'dca.cph'
ggplot(
  data,
  mapping,
  color = TRUE,
  linetype = TRUE,
  lwd = 1.05,
  ...,
  environment = parent.frame()
)

## S3 method for class 'dca.lrm'
ggplot(
  data,
  mapping,
  color = TRUE,
  linetype = TRUE,
  lwd = 1.05,
  ...,
  environment = parent.frame()
)
```

Arguments

data	results of dca() function
mapping	ignore
color	logical, whether models will be classified by color
linetype	logical, whether models will be classified by line type
lwd	line width
...	ignore
environment	ignore

Value

a ggplot2 picture

Examples

```
library(ggDCA)
library(rms)

##### logistic regression

model1 <- lrm(status~ANLN,LIRI)
```

```
d <- dca(model1,model.names = 'ANLN')
ggplot(d)

model2 <- lrm(status~ANLN+CENPA,LIRI)
d <- dca(model2,model.names = 'ANLN+CENPA')
ggplot(d)

model3 <- lrm(status~ANLN+CENPA+GPR182,LIRI)
d <- dca(model3,model.names = 'ANLN+CENPA+GPR182')
ggplot(d)

model4 <- lrm(status~ANLN+CENPA+GPR182+BCO2,LIRI)
d <- dca(model4,model.names = 'ANLN+CENPA+GPR182+BCO2')
ggplot(d)

d <- dca(model1,model2,model3,model4,
         model.names = c('ANLN',
                        'ANLN+CENPA',
                        'ANLN+CENPA+GPR182',
                        'ANLN+CENPA+GPR182+BCO2'))
ggplot(d,
        linetype = FALSE,
        color = c('blue','green','black','red','gray','gray'))

##### cox regression

# evaluate at median time

model1 <- coxph(Surv(time,status)~ANLN,LIRI)
d <- dca(model1,model.names = 'ANLN')
ggplot(d)

model2 <- coxph(Surv(time,status)~ANLN+CENPA,LIRI)
d <- dca(model2,model.names = 'ANLN+CENPA')
ggplot(d)

model3 <- coxph(Surv(time,status)~ANLN+CENPA+GPR182,LIRI)
d <- dca(model3,model.names = 'ANLN+CENPA+GPR182')
ggplot(d)

model4 <- coxph(Surv(time,status)~ANLN+CENPA+GPR182+BCO2,LIRI)
d <- dca(model4,model.names = 'ANLN+CENPA+GPR182+BCO2')
ggplot(d)

d <- dca(model1,model2,model3,model4,
         model.names = c('ANLN',
```

```

                                'ANLN+CENPA',
                                'ANLN+CENPA+GPR182',
                                'ANLN+CENPA+GPR182+BCO2'))
ggplot(d,
       linetype = FALSE,
       color = c('blue','green','black','red','gray','gray'))

# evaluate at different times

qt <- quantile(LIRI$time,c(0.25,0.5,0.75))
qt=round(qt,2)
model1 <- coxph(Surv(time,status)~ANLN,LIRI)
d <- dca(model1,
         model.names = 'ANLN',
         times = qt)
ggplot(d)

model2 <- coxph(Surv(time,status)~ANLN+CENPA,LIRI)
d <- dca(model2,
         model.names = 'ANLN+CENPA',
         times = qt)
ggplot(d)

model3 <- coxph(Surv(time,status)~ANLN+CENPA+GPR182,LIRI)
d <- dca(model3,
         model.names = 'ANLN+CENPA+GPR182',
         times = qt)
ggplot(d)

model4 <- coxph(Surv(time,status)~ANLN+CENPA+GPR182+BCO2,LIRI)
d <- dca(model4,
         model.names = 'ANLN+CENPA+GPR182+BCO2',
         times = qt)
ggplot(d)

d <- dca(model1,model2,model3,model4,
        model.names = c('ANLN',
                        'ANLN+CENPA',
                        'ANLN+CENPA+GPR182',
                        'ANLN+CENPA+GPR182+BCO2'),
        times = qt)
ggplot(d)

```

Description

This data is a liver cancer data from Japan Data released in ICGC database ([Link](#)). It contains time, event and four genes.

Usage

```
data(LIRI)
```

Format

An object of class `data.frame` with 232 rows and 6 columns.

Examples

```
data(LIRI)
```

range	<i>Ranges for net benefit</i>
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Description

Ranges for net benefit

Usage

```
## S3 method for class 'dca.lrm'  
range(...)
```

```
## S3 method for class 'dca.cph'  
range(...)
```

Arguments

... results of `dca()` function

Value

a dataframe contains the minimum and maximum of net benefit for each model

`rFP.p100`*Calculate reduction in false positive count*

Description

Calculate reduction in false positive count

Usage

```
rFP.p100(x)
```

Arguments

`x` result of `dca()` function

Value

a dataframe contains thresholds, `rFP.100`: reduction in false positive count per 100 patients.

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