

决策曲线分析法

Decision Curve Analysis

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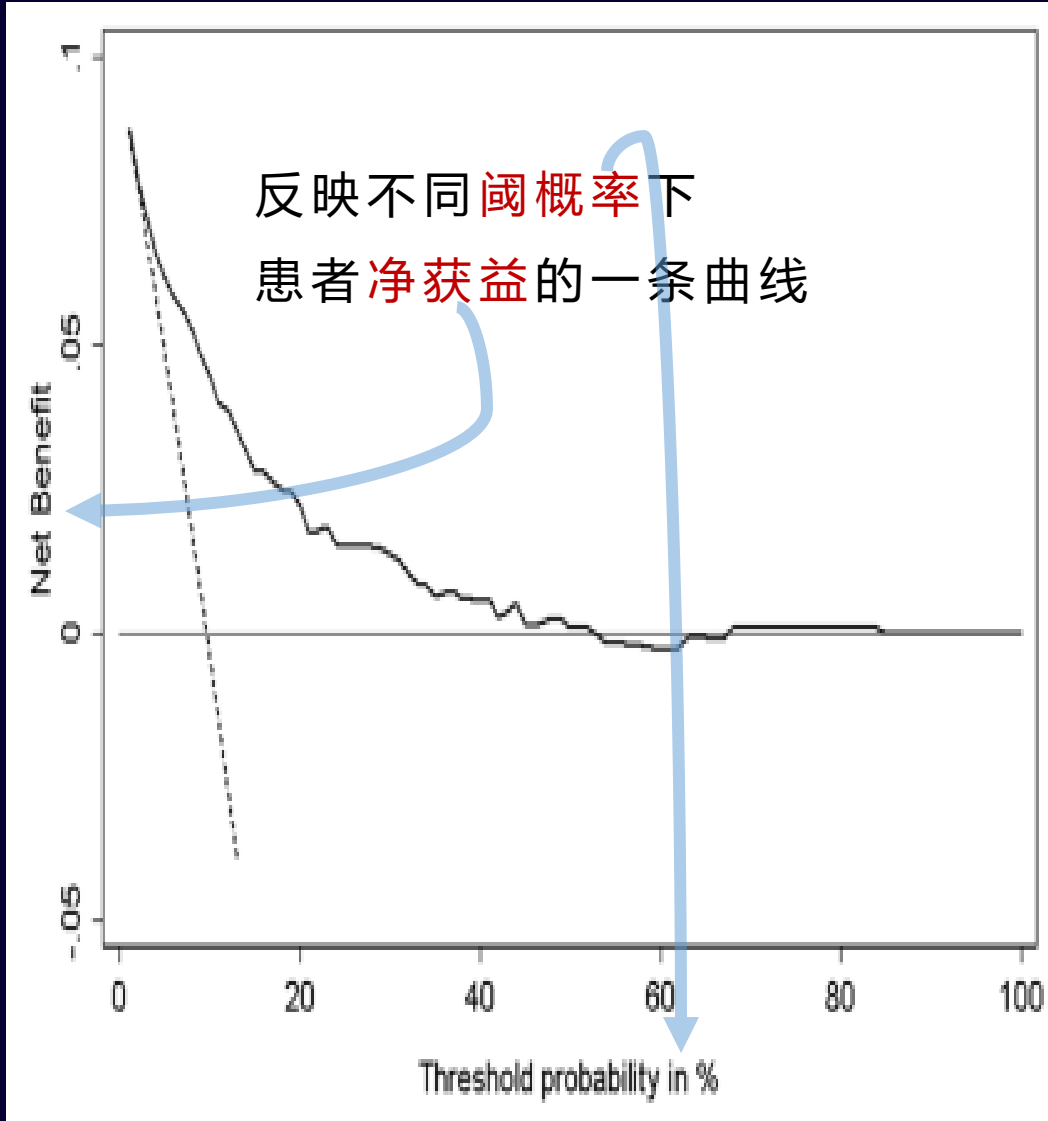
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决策曲线分析是什么

What is DCA (Decision Curve Analysis)



2006年，纽约纪念斯隆凯特琳癌症研究所的Andrew Vickers博士和Elena Elkin博士研究出的一种新的评价诊断/预测模型优劣的方法。

A Novel Method for Evaluating Prediction Models

与ROC的区别：

ROC反映的是敏感性和特异性，DCA关注的是患者的净获益，同时考虑了因诊断结果而带来的获益和损失，能告诉我们哪种方法更值得使用

The ROC metric focuses solely on the predictive accuracy of a model. DCA methods incorporate consequences and can tell us which of several alternative models should be used.

决策曲线分析中的基本概念

Some concepts in DCA

- 阈概率：

当某诊断方法判断患者患病的概率大于某个值就认为患者要接受干预，这个值就是阈概率。

Threshold Probability (Pt) :

When a diagnostic method judges that the probability of a patient being ill is greater than a certain value, it is considered that the patient needs to receive intervention, and this value is the threshold probability.

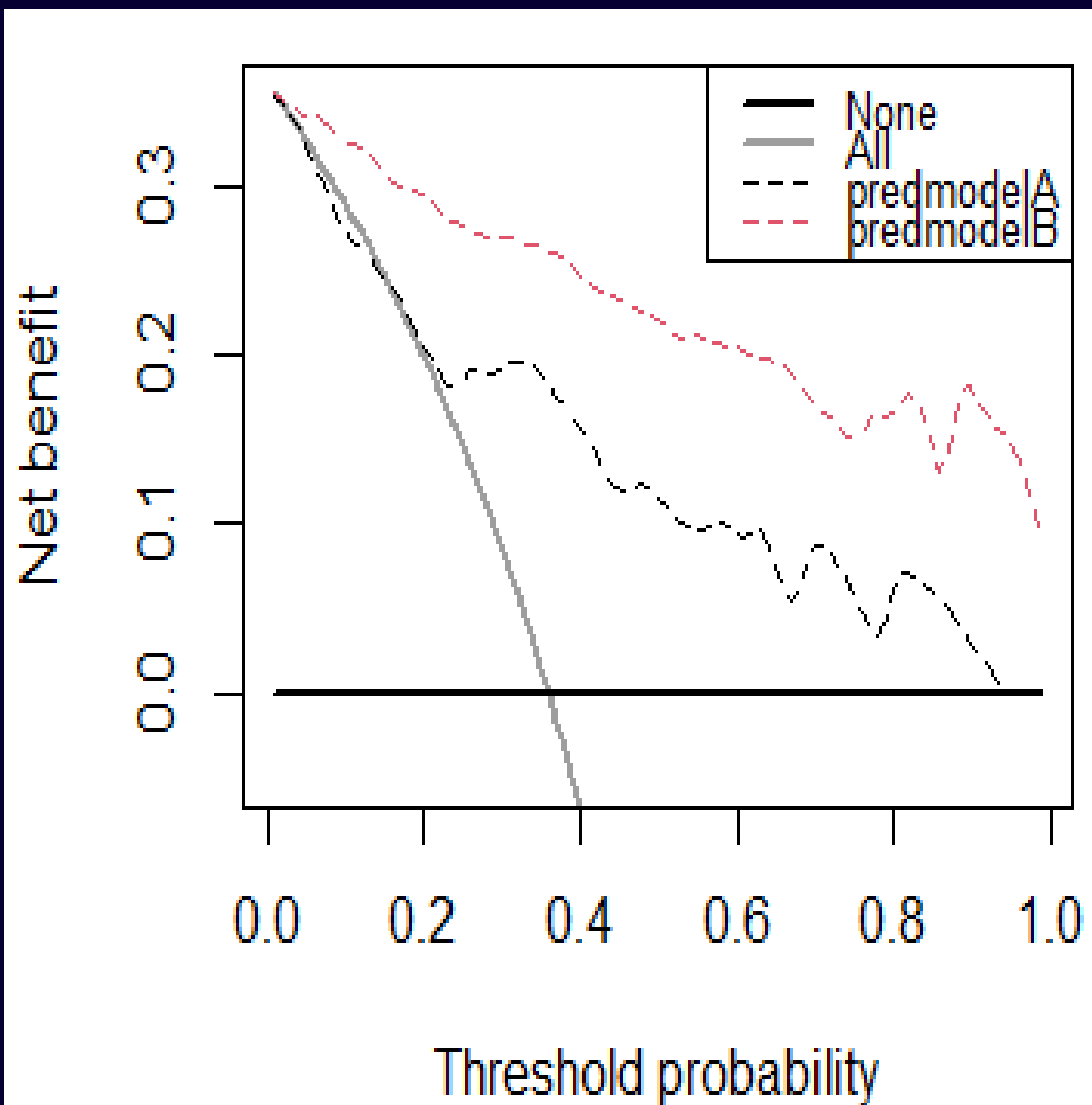
- 净获益：

获益（真阳性）-损失（假阳性）

Net Benefit (NB) :

Gain (true positive)-loss (false positive)

决策曲线分析的原理 Principle of DCA



Pt	truth		NB=A-B	
	+	-		
0.4	Diagnosis +	45 (A)	5 (B)	40
	Diagnosis -	10 (C)	40 (D)	
0.5	Diagnosis +	40 (A)	10 (B)	30
	Diagnosis -	15 (C)	45 (D)	
0.6	Diagnosis +	35 (A)	12 (B)	23
	Diagnosis -	20 (C)	43 (D)	
...	

* 实际分析中，NB是用现患率校正之后的

如何绘制决策曲线

How to draw a DCA curve

应用R语言的dca函数，代码如下：

```
source("dca.R")
library(rms)
library(foreign)
mydata<-read.table("dcaTest.csv",header=T,sep = ",")
attach(mydata)
modelA <- glm(Y~ x1+x2 +x3, data = mydata, family = binomial(link="logit"),x=TRUE)
modelB <- glm(Y~ x1+x2, data = mydata, family = binomial(link="logit"),x=TRUE)
mydata$predmodelA<- predict(newdata=mydata,modelA,"response")
mydata$predmodelB<- predict(newdata=mydata,modelB,"response")
dca(data=mydata, outcome="EAD",
    predictors=c("predmodelA", "predmodelB"),
    smooth="TRUE",
    probability=c("TRUE", "TRUE"))
```

DCA的应用示例

For example

用DCA曲线评价两种预测EAD的模型效率

Evaluate the predictive power of two models to predict EAD by DCA.

```
1 source("D:/R_demo/DCA/dca.R")
2 #library(nricens)
3 library(rms)
4 library(foreign)
5 mydata<-read.table("D:/R_demo/DCA/dcaTest.csv",header=T,sep = ",")
6 attach(mydata)
7 modelA <- glm(EAD~ LPC_1+age +gender+BMI, data = mydata, family = b
8 modelB <- glm(EAD~ LPC_2+AST_1+age +gender+BMI, data = mydata, fami
9 modelC <- glm(EAD~ LPC_2, data = mydata, family = binomial(link="lo
10 mydata$predmodelA<- predict(newdata=mydata,modelA,"response")
11 mydata$predmodelB<- predict(newdata=mydata,modelB,"response")
12 mydata$predmodelC<- predict(newdata=mydata,modelC,"response")
13 #dca(data=mydata, outcome="EAD", predictors=c("predmodelA", "predmo
14 dca(data=mydata, outcome="EAD", predictors=c("predmodelA", "predmod
15 |
16 ▾ #####
17 <
```

15:1 (Top Level) R Script

Console Terminal x

D:/R_demo/DCA/ ↗

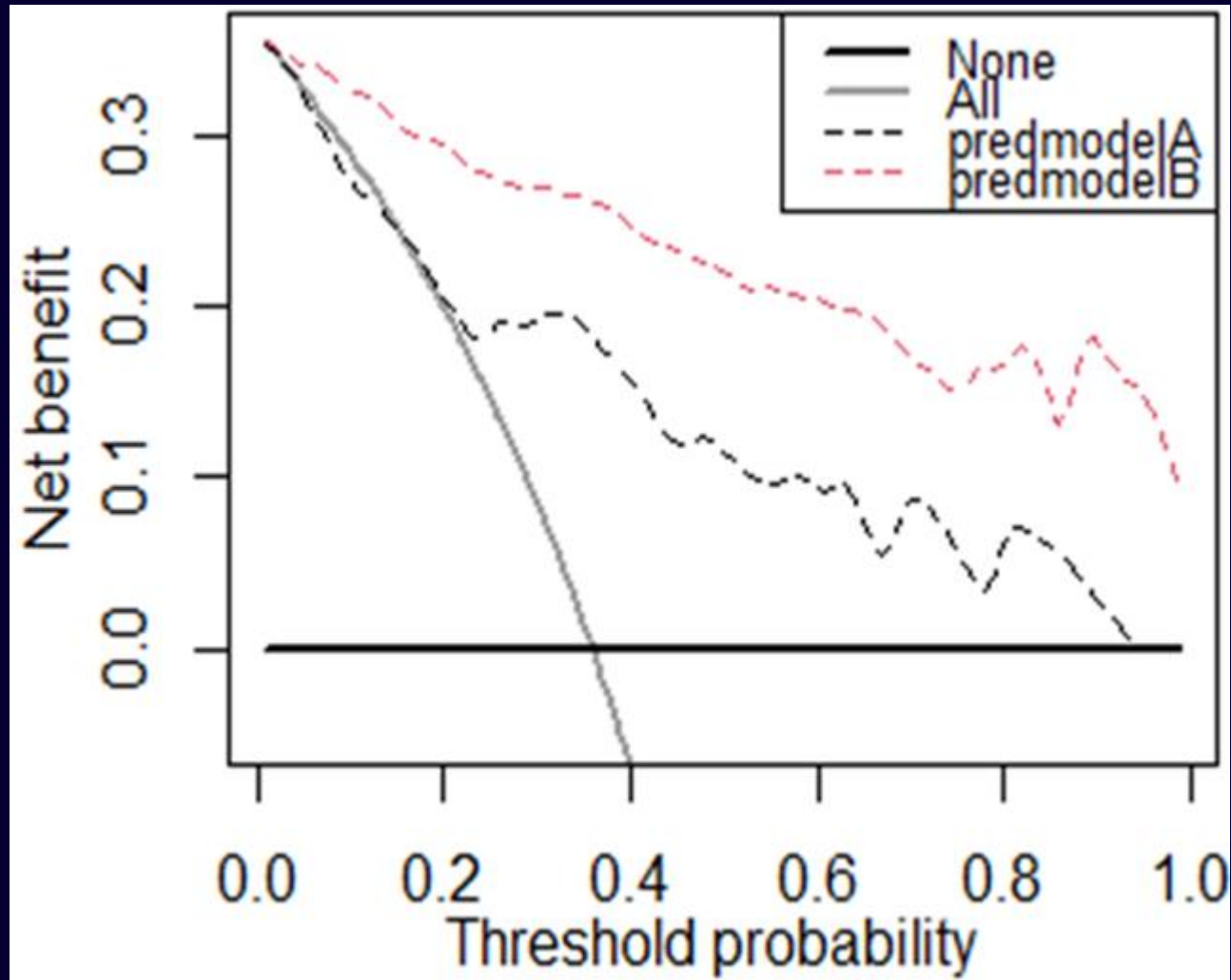
96	0.96	62.5000000	63.08333	62.49012369	63.075212
97	0.97	62.8865979	63.25773	62.87602798	63.281548
98	0.98	63.2653061	63.48980	63.26063795	63.495583
99	0.99	63.6363636	63.72727	63.64252923	63.718646

>

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怎么看决策曲线

How to interpret a DCA curve



曲线下面积越大,

诊断/预测模型越优

(曲线越远离“无效L”, 越好)

The larger the area under the curve, the better the diagnosis/prediction model.

(The farther the curve is from “Worthless ‘L’”, the better)

决策曲线是以患者群体总的净获益
为关注点的评价方法

净获益 = 获益 - 损失

欢迎联系，共享代码

