DecisionCurve: example for the manuscript

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Install the package

You may navigate to the source package and use

```
install.packages("../DecisionCurve_0.2.tar.gz", repos = NULL, type = "source")
```

Getting started

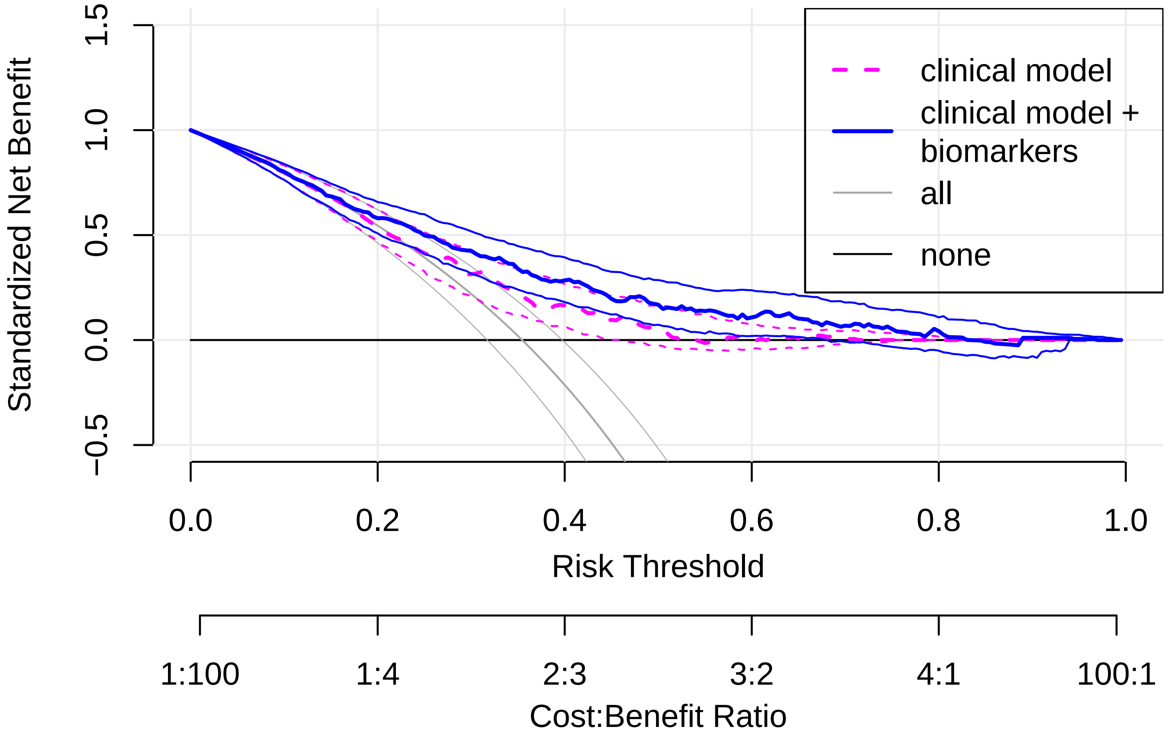
```
library(DecisionCurve)
```

```
## Loading required package: testthat
## Loading required package: reshape
## Loading required package: pander
## Loading required package: MASS
```

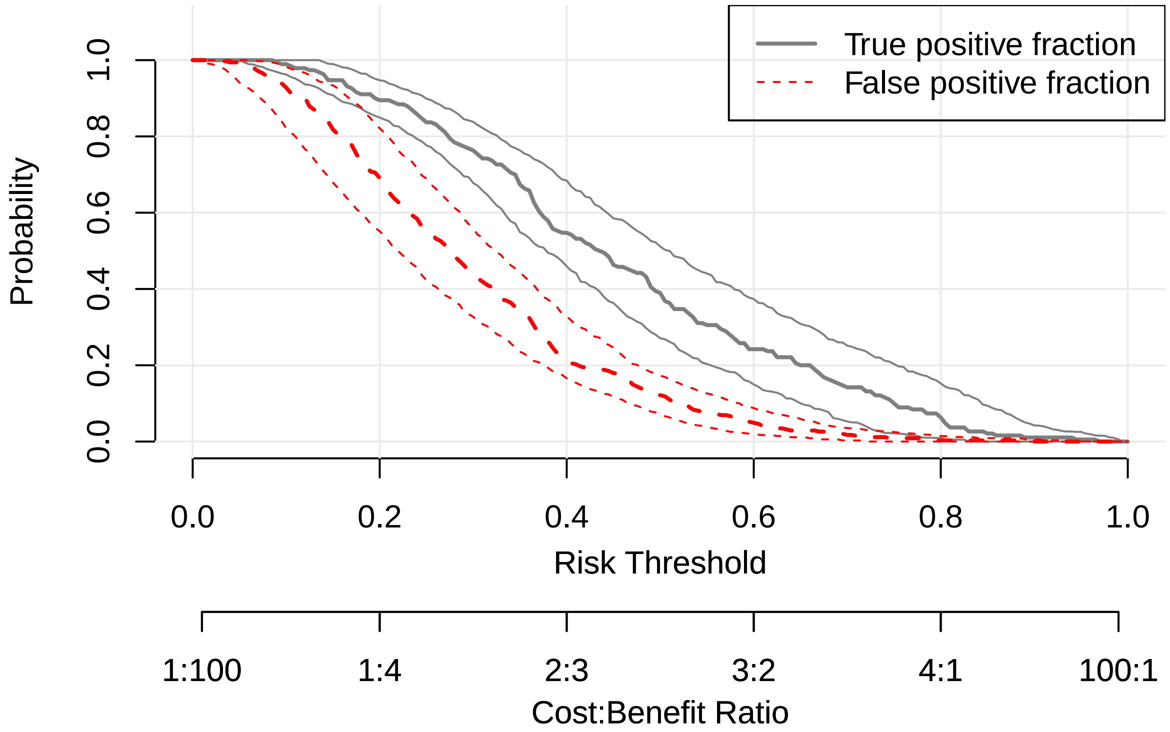
```
dcaData <- read.csv(file = "../../../Desktop/GenProbe_PCA3_Dataset_2007.09.19.csv")

#head(dcaData)
#table(dcaData$Cancer)
#hist(dcaData$Age.At.Urine.Collect)
#table(dcaData$Hx.of.Bx)
#table(dcaData$Susp.DRE)
#hist(log(dcaData$Serum.PSA))
#hist(log(dcaData$PCA3.Score))


#remove missing data
cc <- complete.cases(dcaData[,c("Age.At.Urine.Collect", "Hx.of.Bx", "Susp.DRE", "Cancer", "Serum.PSA",
dcaData <- dcaData[cc,]

set.seed(123)
#first use DecisionCurve with the default settings (set bootstraps = 25 here to reduce computation time
baseline.model <- decision_curve(Cancer ~ Age.At.Urine.Collect + Hx.of.Bx + Susp.DRE, #fitting a logist
                                thresholds = seq(0, 1, by = .005),
                                data = dcaData,
                                bootstraps = 500)



set.seed(123)
full.model <- decision_curve(Cancer ~ Age.At.Urine.Collect + Hx.of.Bx + Susp.DRE + log(Serum.PSA) + log
                                thresholds = seq(0, 1, by = .005),
                                data = dcaData,
                                bootstraps = 500)
```

```r
#plot the curves together
plot_decision_curve( list(baseline.model, full.model),
                     ylim = c(-.5, 1.5),
                     col = c("magenta", "blue"),
                     lty = c(2, 1),
                     curve.names = c("clinical model", "clinical model + \nbiomarkers"))
```

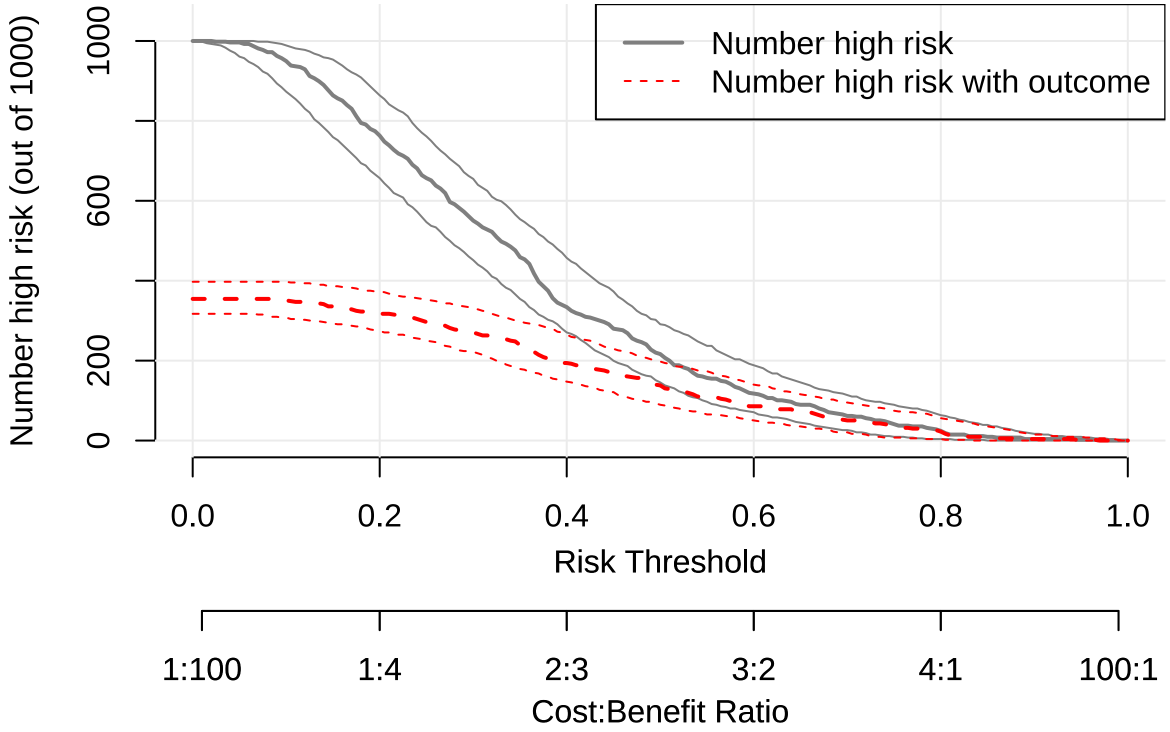
```
## Note: When multiple decision curves are plotted, decision curves for 'all' are calculated using the 
```



```r
plot_roc_components(full.model, curve.names = "baseline model",
                    xlim = c(0, 1), col = c("grey50", "red"),
                    ylim = c(0, 1.1))
```



```
plot_clinical_impact(full.model, curve.names = "baseline model",col = c("grey50", "red"), population.si
```


Number high risk
Number high risk with outcome
Number high risk (out of 1000)
Risk Threshold
1:100
1:4
2:3
3:2
4:1
100:1
Cost:Benefit Ratio