

# IDEA study: TST and QFN cost-effectiveness comparison: HIV patients only and indeterminates included

Nathan Green

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```
# http://stackoverflow.com/questions/20060518/in-rstudio-rmarkdown-how-to-setwd
opts_chunk$set(root.dir = '/tmp')
```

```
source("../.../analysis scripts/IDEA/alt-YAML_Binomial_dectrees/indiv-dectree-sampling.R")
```

```
my.plot.bcea <- function(dat1, dat2, dat3, dat4, wtp, intllabels){
  # to test bcea plotting
  # this is better when prevalence changes in current pathway

  dat1e <- dat1$e[,1]-dat1$e[,2]
  dat2e <- dat2$e[,1]-dat2$e[,2]
  dat3e <- dat3$e[,1]-dat3$e[,2]
  dat4e <- dat4$e[,1]-dat4$e[,2]

  dat1c <- dat1$c[,2]-dat1$c[,1]
  dat2c <- dat2$c[,2]-dat2$c[,1]
  dat3c <- dat3$c[,2]-dat3$c[,1]
  dat4c <- dat4$c[,2]-dat4$c[,1]

  plot(dat1e, dat1c, ylim=c(-200,200), xlim=c(-5,5),
       xlab="Effectiveness differential", ylab="Cost differential (£)",
       col="black", pch=16)
  points(dat3e, dat3c, col="grey", pch=16)
  points(dat4e, dat4c, col="grey", pch=0)
  points(dat2e, dat2c, col="black", pch=0)

  points(median(dat1e), median(dat1c), col="red", pch=16)
  points(median(dat2e), median(dat2c), col="red", pch=16)
  points(median(dat3e), median(dat3c), col="red", pch=16)
  points(median(dat4e), median(dat4c), col="red", pch=16)

  abline(v=0, col="darkgrey")
  abline(h=0, col="darkgrey")
  abline(a=0, b = wtp)

  labtext <- paste(intllabels[1], "vs", intllabels[-1])
  legend(0,200, labtext, col=c("black", "black", "grey", "grey"), pch=c(16,0,16,0), bty = "n")#, y.inte
}
```

```
my.plot.ceac <- function(dat1, dat2, dat3, dat4, intllabels){

  dat1e.diff <- dat1$e[,1]-dat1$e[,2]
```

```

dat1c.diff <- dat1$c[,2]-dat1$c[,1]

dat2e.diff <- dat2$e[,1]-dat2$e[,2]
dat2c.diff <- dat2$c[,2]-dat2$c[,1]

dat3e.diff <- dat3$e[,1]-dat3$e[,2]
dat3c.diff <- dat3$c[,2]-dat3$c[,1]

dat4e.diff <- dat4$e[,1]-dat4$e[,2]
dat4c.diff <- dat4$c[,2]-dat4$c[,1]

j <- 1
dat1.ceac <- dat2.ceac <- dat3.ceac <- dat4.ceac <- NA
xvals <- seq(0,500000, by=10000)

for (i in xvals){
  WTP <- i/365
  dat1.ceac[j] <- sum(dat1c.diff<WTP*dat1e.diff)/length(dat1c.diff)
  dat2.ceac[j] <- sum(dat2c.diff<WTP*dat2e.diff)/length(dat2c.diff)
  dat3.ceac[j] <- sum(dat3c.diff<WTP*dat3e.diff)/length(dat3c.diff)
  dat4.ceac[j] <- sum(dat4c.diff<WTP*dat4e.diff)/length(dat4c.diff)
  j <- j+1
}

plot(xvals, dat1.ceac, type="o", ylim=c(0,1), col="black", pch=16,
      ylab="Probability of cost effectiveness", xlab="Willingness to pay (£)")
lines(x=xvals, y=dat2.ceac, type="o", col="black", pch=0)
lines(x=xvals, y=dat3.ceac, type="o", col="grey", pch=16)
lines(x=xvals, y=dat4.ceac, type="o", col="grey", pch=0)

labtext <- paste(intlabels[1], "vs", intlabels[-1])
legend(230000,1, labtext, col=c("black", "black", "grey", "grey"), pch=c(16,0,16,0), bty = "n")#, y.i
}

```

```

library(IDEAdectree)
library(BCEA)

```

```
## Warning: package 'BCEA' was built under R version 3.2.2
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.2.3
```

```

# load("C:/Users/ngreen1/Dropbox/TB/IDEA/R/packages/IDEAdectree/data/TBdata_clinical_cleaned.RData")
load("../data/TBdata_clinical_cleaned.RData")
load("../data/COSTdistns_allerror.RData")
load("../data/sensspec_env.RData")

## sensitivities and specificities from IDEA lab data
attach(sensspec.env)

dat <- list()

```

```

yearindays <- 365
WTP <- 20000/yearindays

IDEAdectree.simple.TSPOT <- function(...){IDEAdectree.simple(SPEC = TSPOT.HIV.Indet.spec.mean, SENS = TSPOT.HIV.Indet.spec.sens,
  SPECvar = TSPOT.HIV.Indet.spec.var, SENSvar = TSPOT.HIV.Indet.spec.sensvar,
  ...)}
IDEAdectree.simple.QFN <- function(...){IDEAdectree.simple(SPEC = QFN.HIV.Indet.spec.mean, SENS = QFN.HIV.Indet.spec.sens,
  SPECvar = QFN.HIV.Indet.spec.var, SENSvar = QFN.HIV.Indet.spec.sensvar,
  ...)}

## prevalence

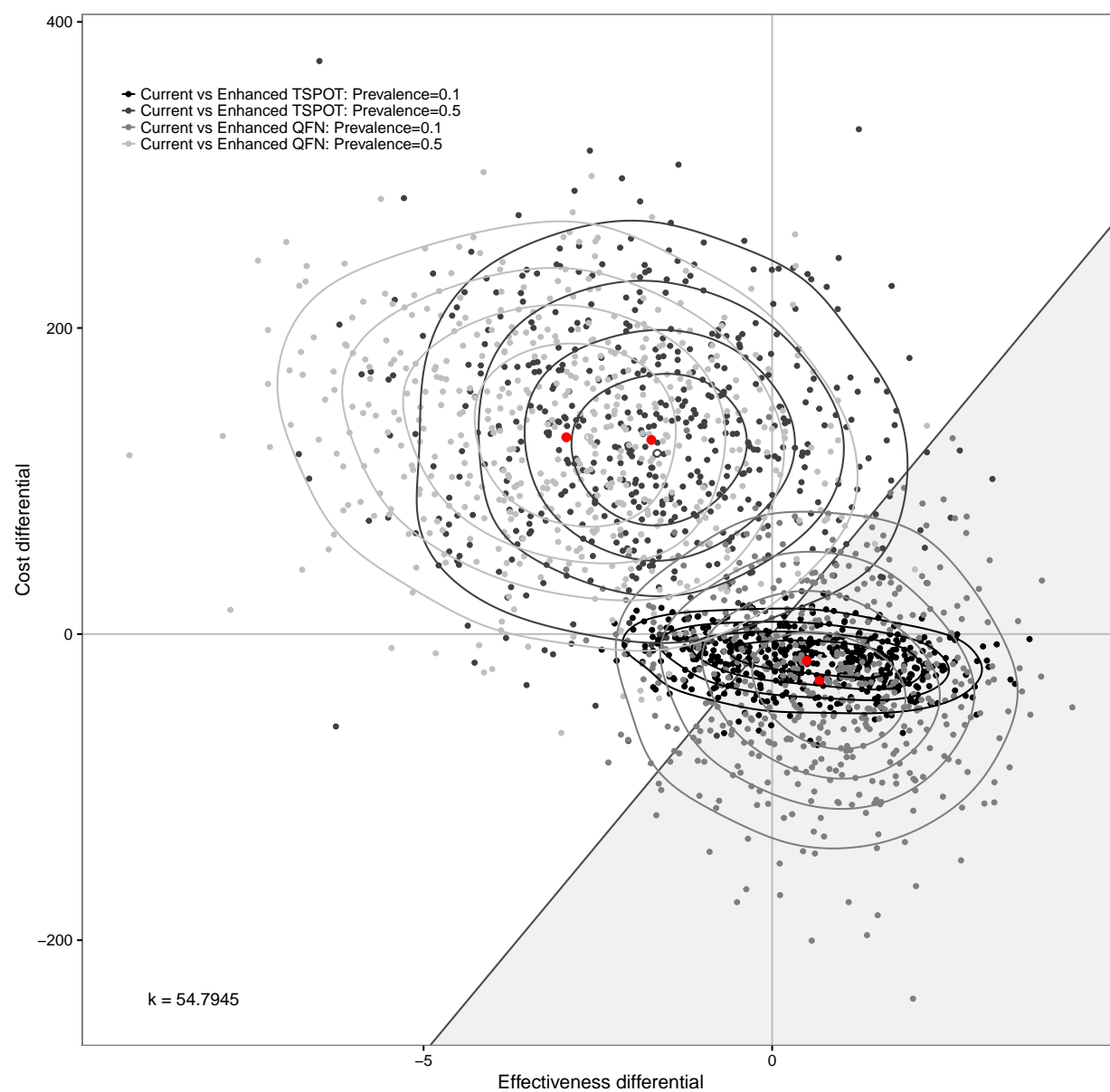
dat1 <- IDEAdectree.simple.TSPOT(data=data, prev = 0.1)
dat2 <- IDEAdectree.simple.TSPOT(data=data, prev = 0.5)
dat3 <- IDEAdectree.simple.QFN(data=data, prev = 0.1)
dat4 <- IDEAdectree.simple.QFN(data=data, prev = 0.5)
dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2], dat4$e[,2])
dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2], dat4$c[,2])

intllabels <- c("Current",
  "Enhanced TSPOT: Prevalence=0.1", "Enhanced TSPOT: Prevalence=0.5",
  "Enhanced QFN: Prevalence=0.1", "Enhanced QFN: Prevalence=0.5")

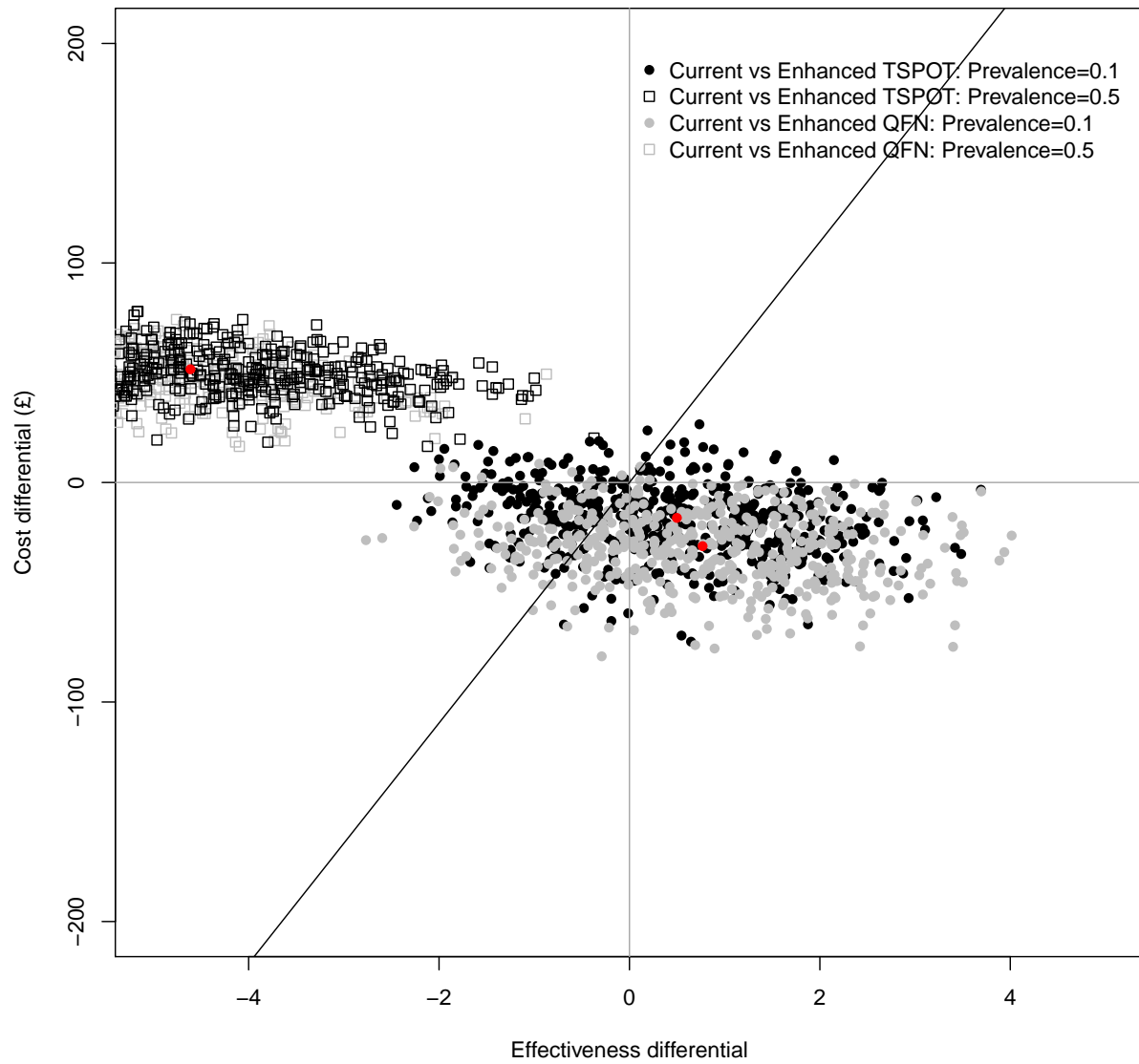
m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intllabels)
contour2(m, wtp=WTP, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))+#, xlim=c(-5,5), ylim=c(-200,200))
  ggtitle("") #+ geom_abline(intercept = 0, slope = WTP)

## Loading required namespace: MASS

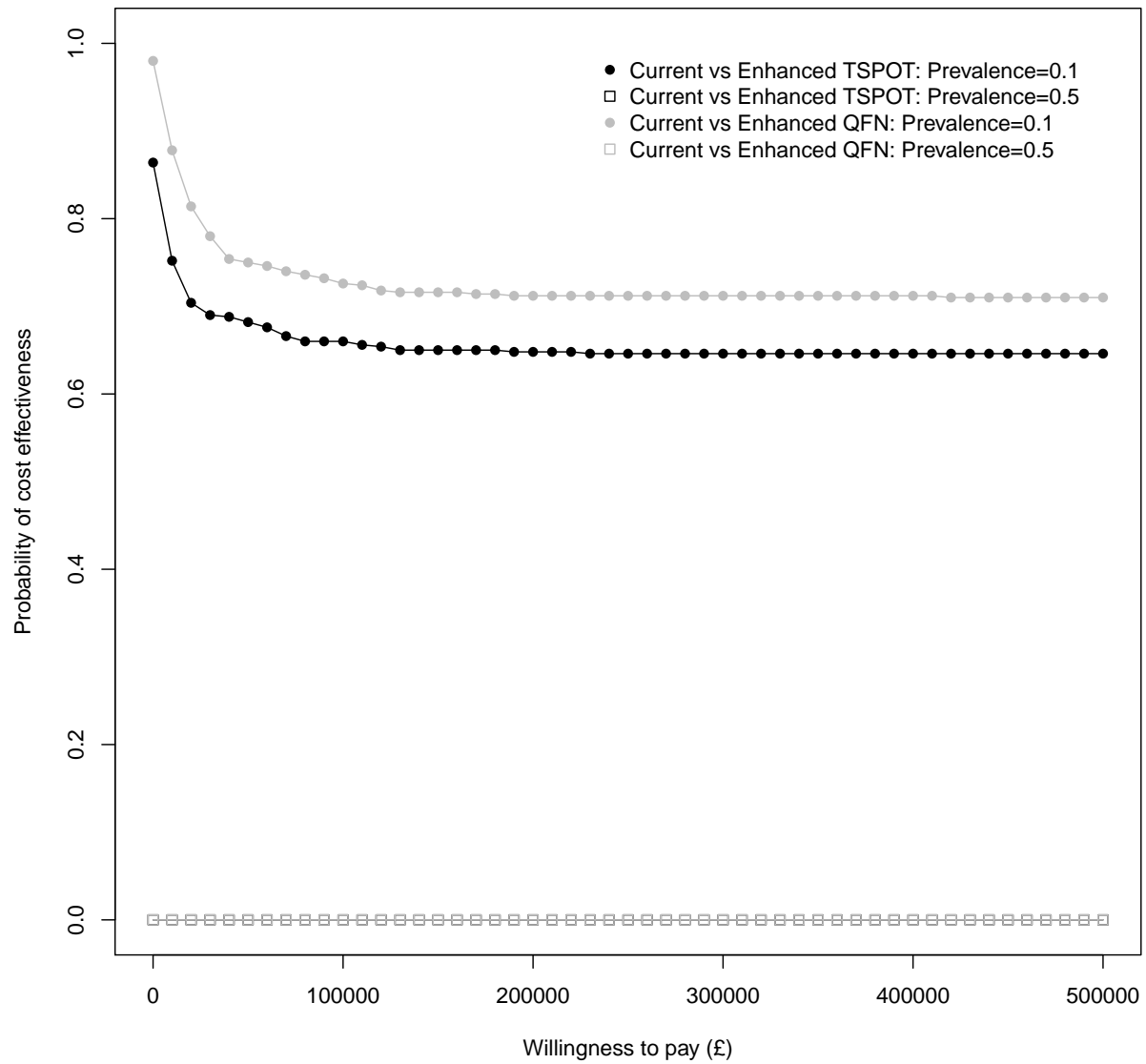
```



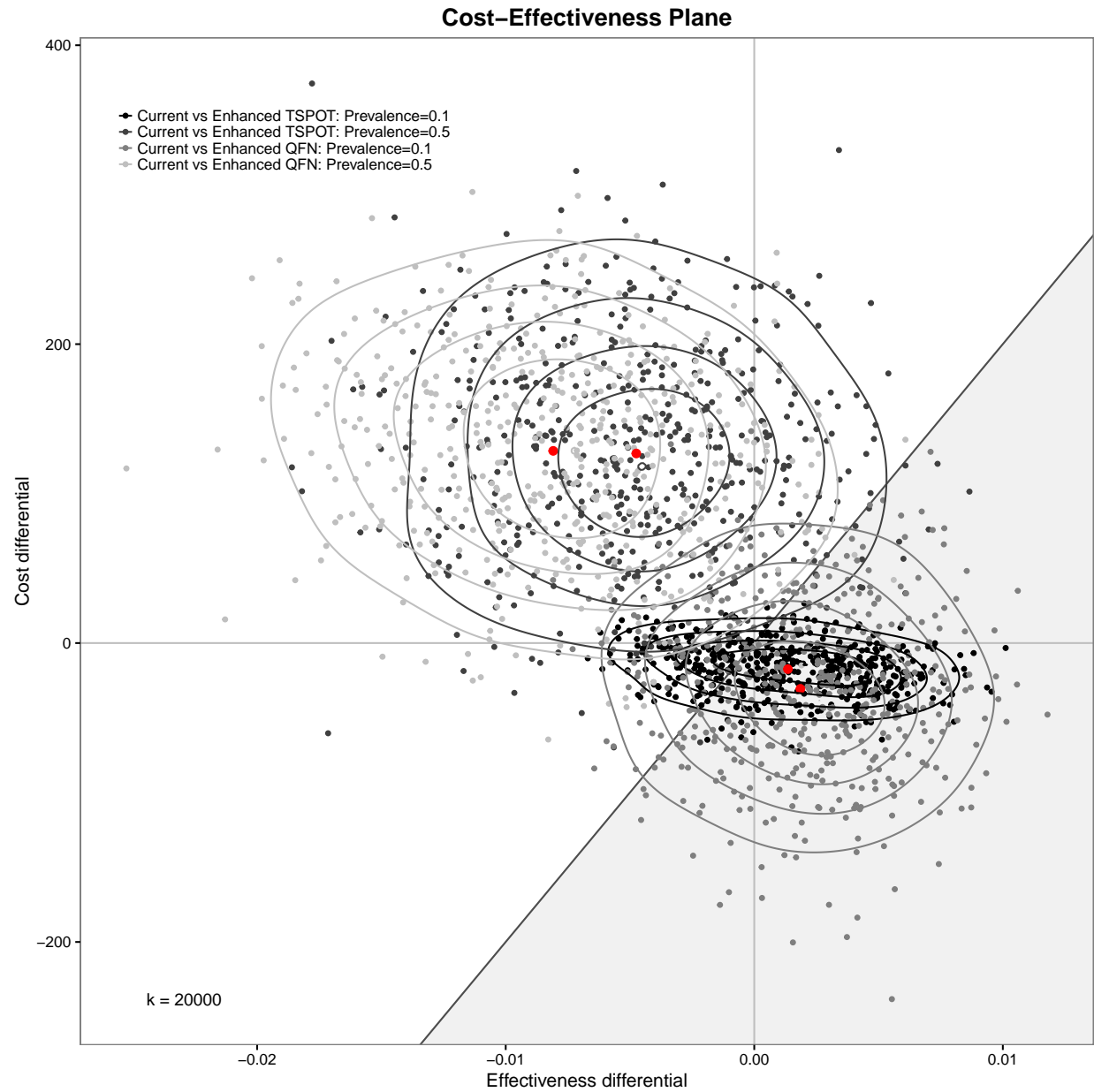
```
my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intllabels)
```



```
my.plot.ceac(dat1, dat2, dat3, dat4, intllabels)
```

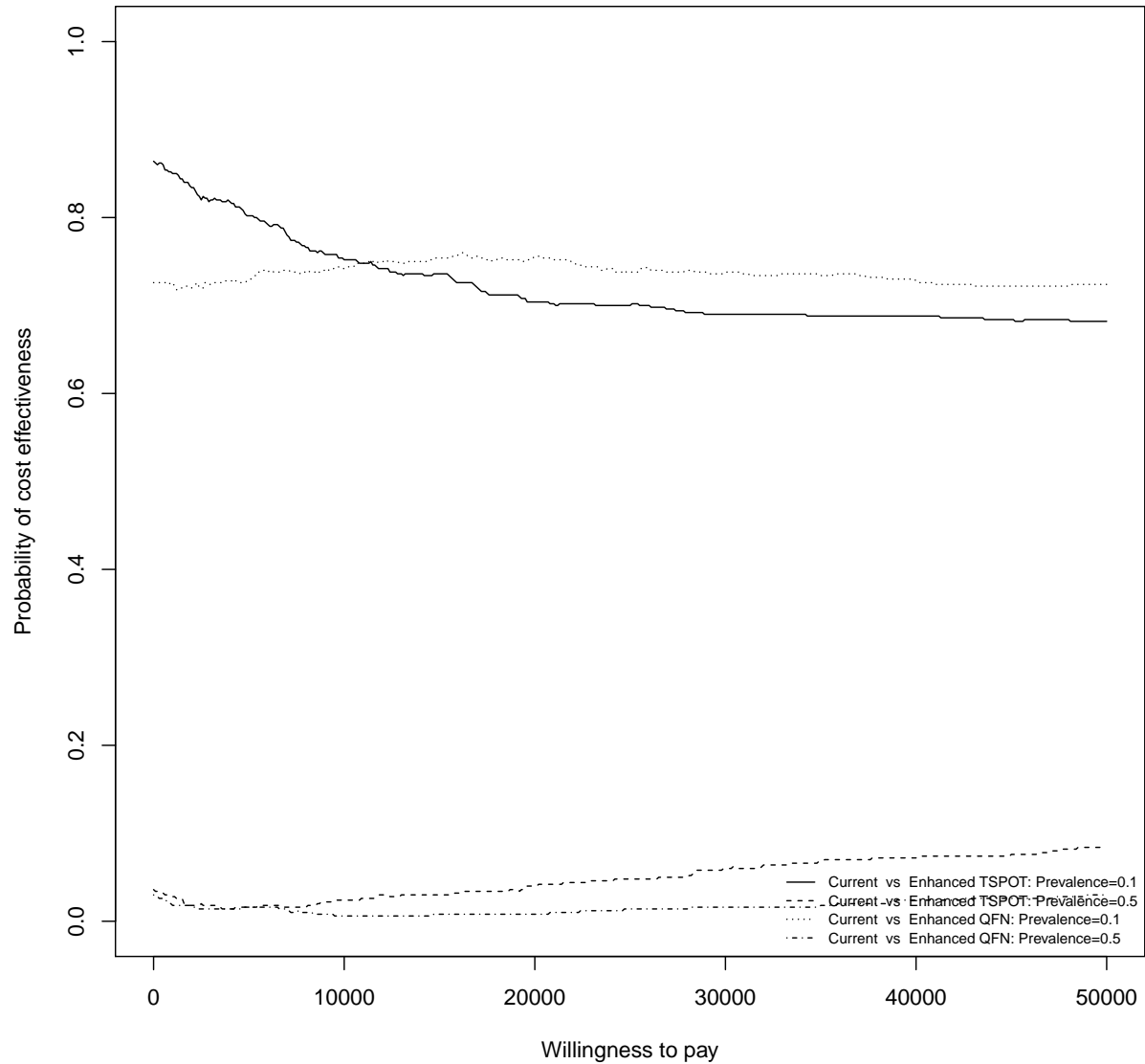


```
## in years (not days)
m <- bcea(e=dat$e/365, c=-dat$c, ref=1, interventions = intlabeleds)
contour2(m, wtp=20000, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))
```



`ceac.plot(m)`

### Cost Effectiveness Acceptability Curve



```
sink(file="../../../output_data/IDEA-BCEA-logfile.txt", append = TRUE)
summary(m)
sink()
```

```
## rule-out test cost
```

```
dat1 <- IDEAdectree.simple.TSPOT(data=data, c.ruleout = 50)
dat2 <- IDEAdectree.simple.TSPOT(data=data, c.ruleout = 200)
dat3 <- IDEAdectree.simple.QFN(data=data, c.ruleout = 50)
dat4 <- IDEAdectree.simple.QFN(data=data, c.ruleout = 200)
dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2], dat4$e[,2])
dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2], dat4$c[,2])
```

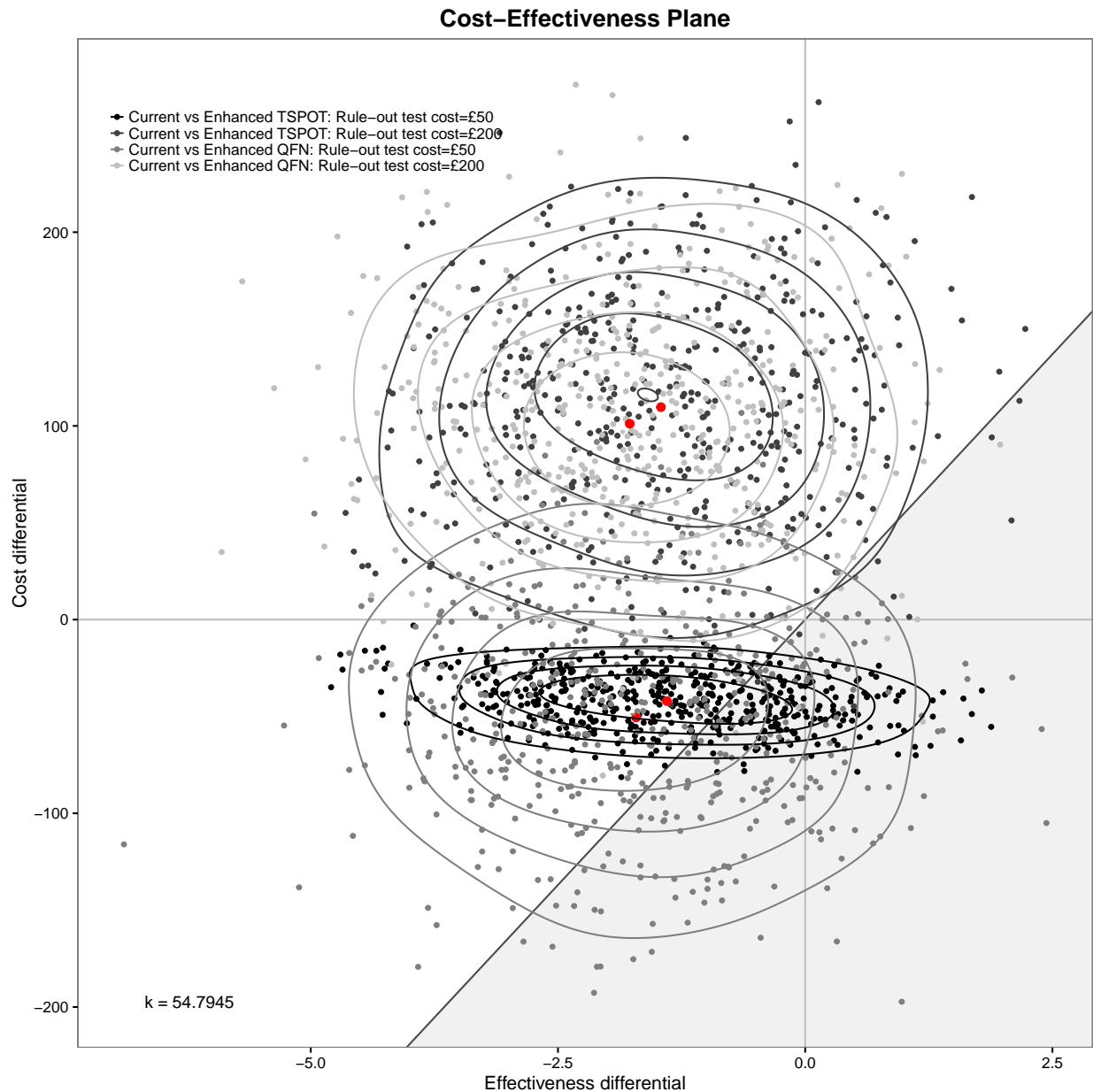


```

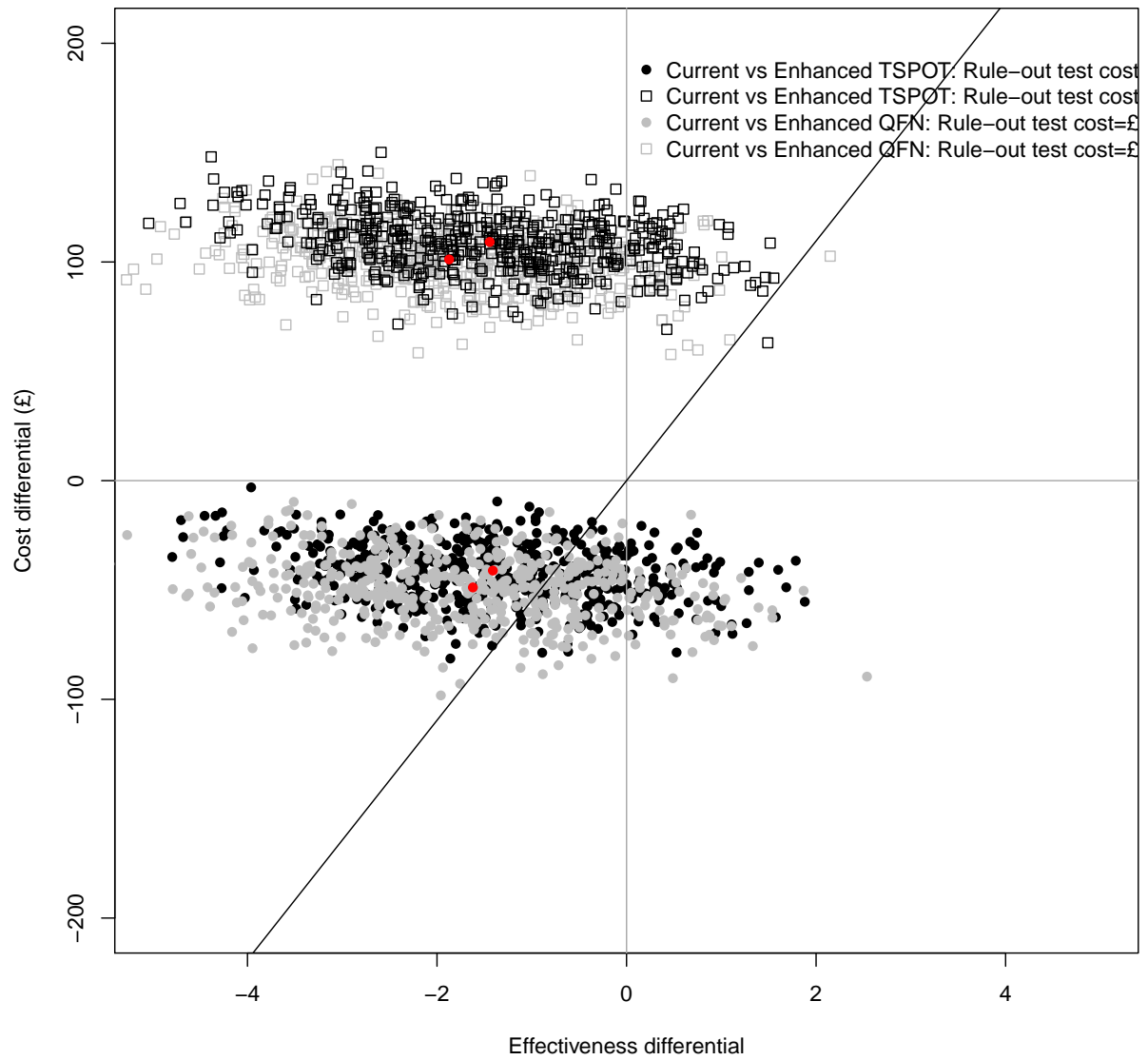
intlabeleds <- c("Current",
  "Enhanced TSPOT: Rule-out test cost=£50", "Enhanced TSPOT: Rule-out test cost=£200",
  "Enhanced QFN: Rule-out test cost=£50", "Enhanced QFN: Rule-out test cost=£200")

m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intlabeleds)
contour2(m, wtp=WTP, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))#, xlim=c(-10,10), ylim=c(-200,200)

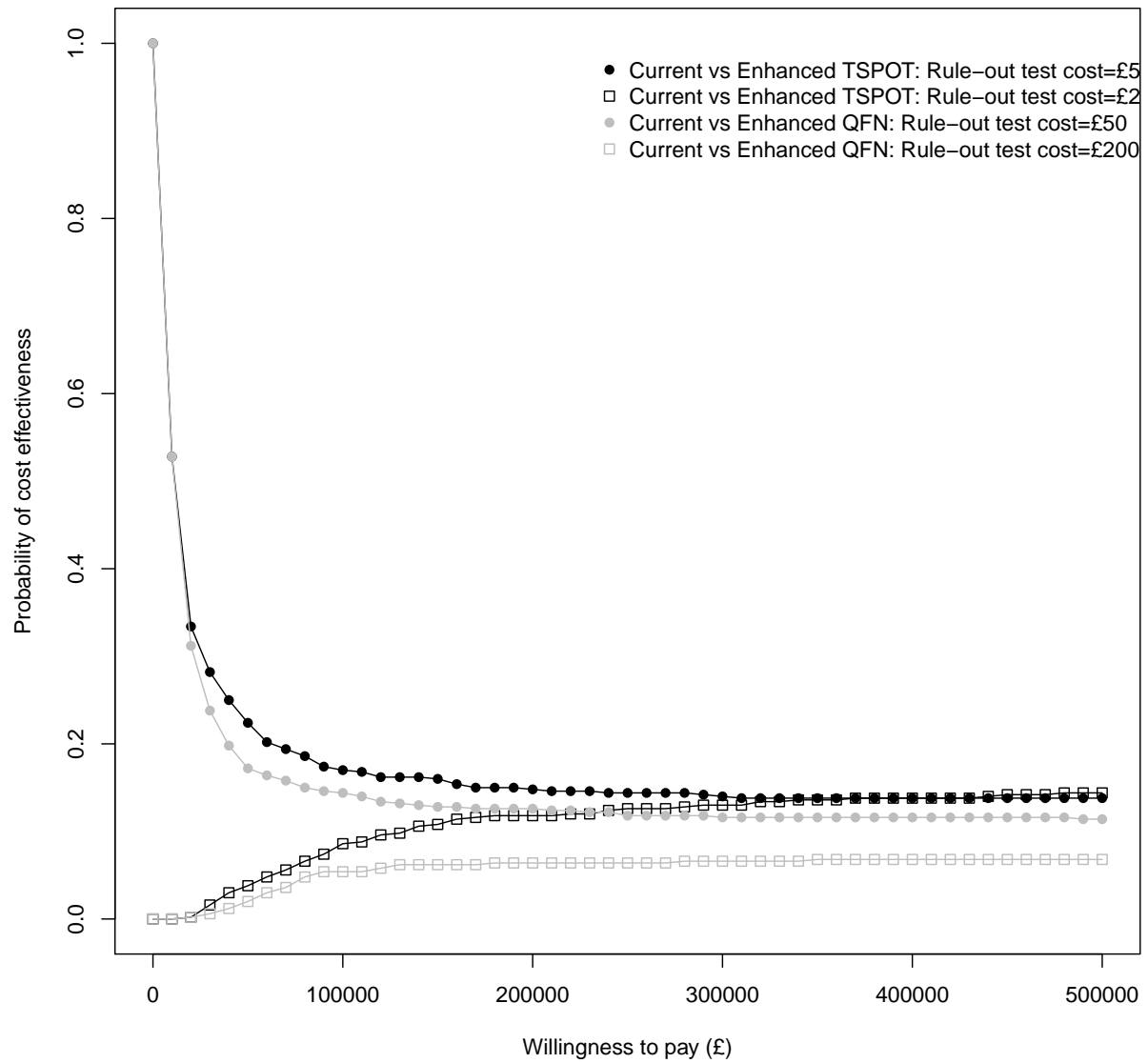
```



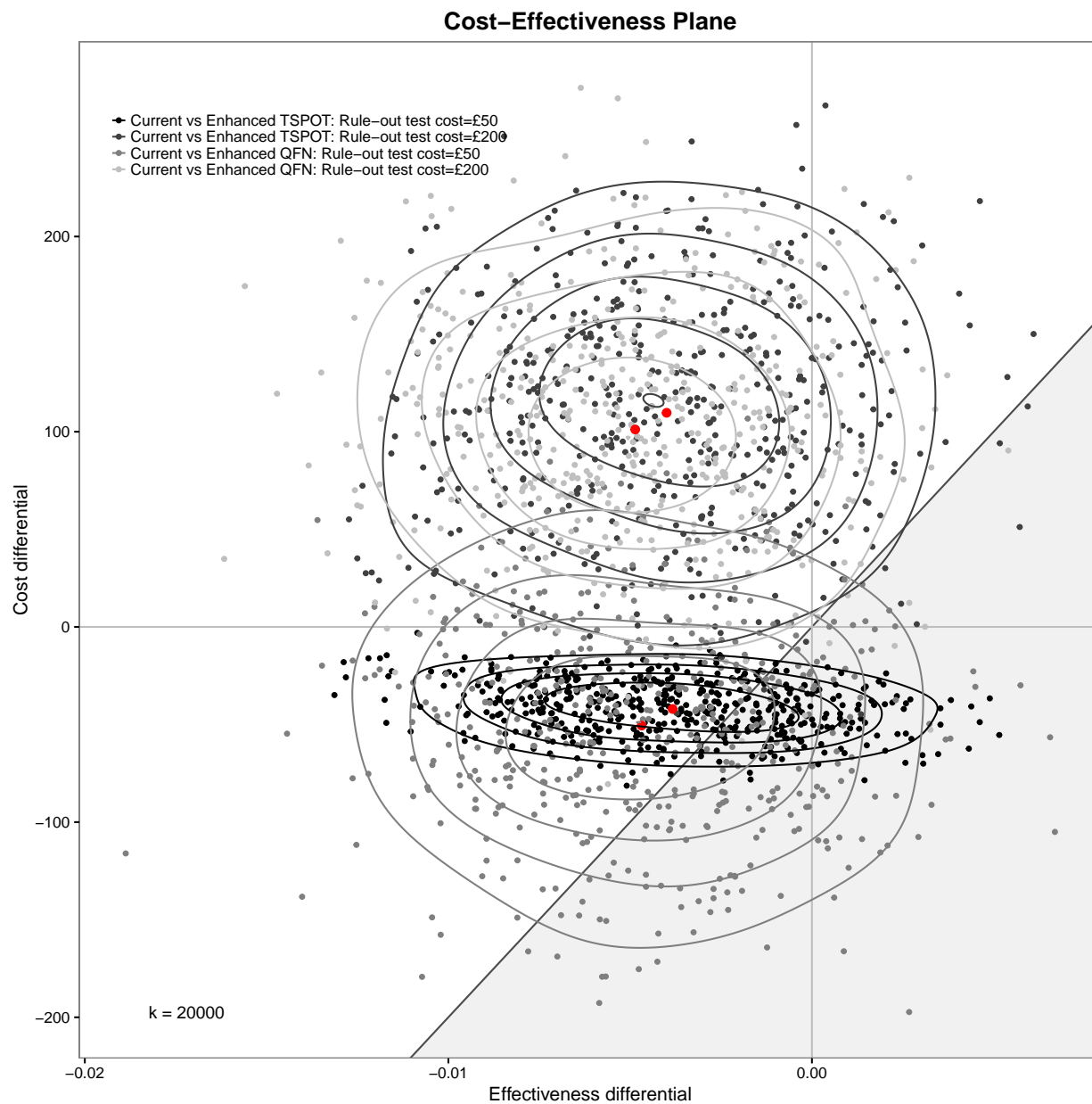
```
my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabeleds)
```



```
my.plot.ceac(dat1, dat2, dat3, dat4, intllabels)
```

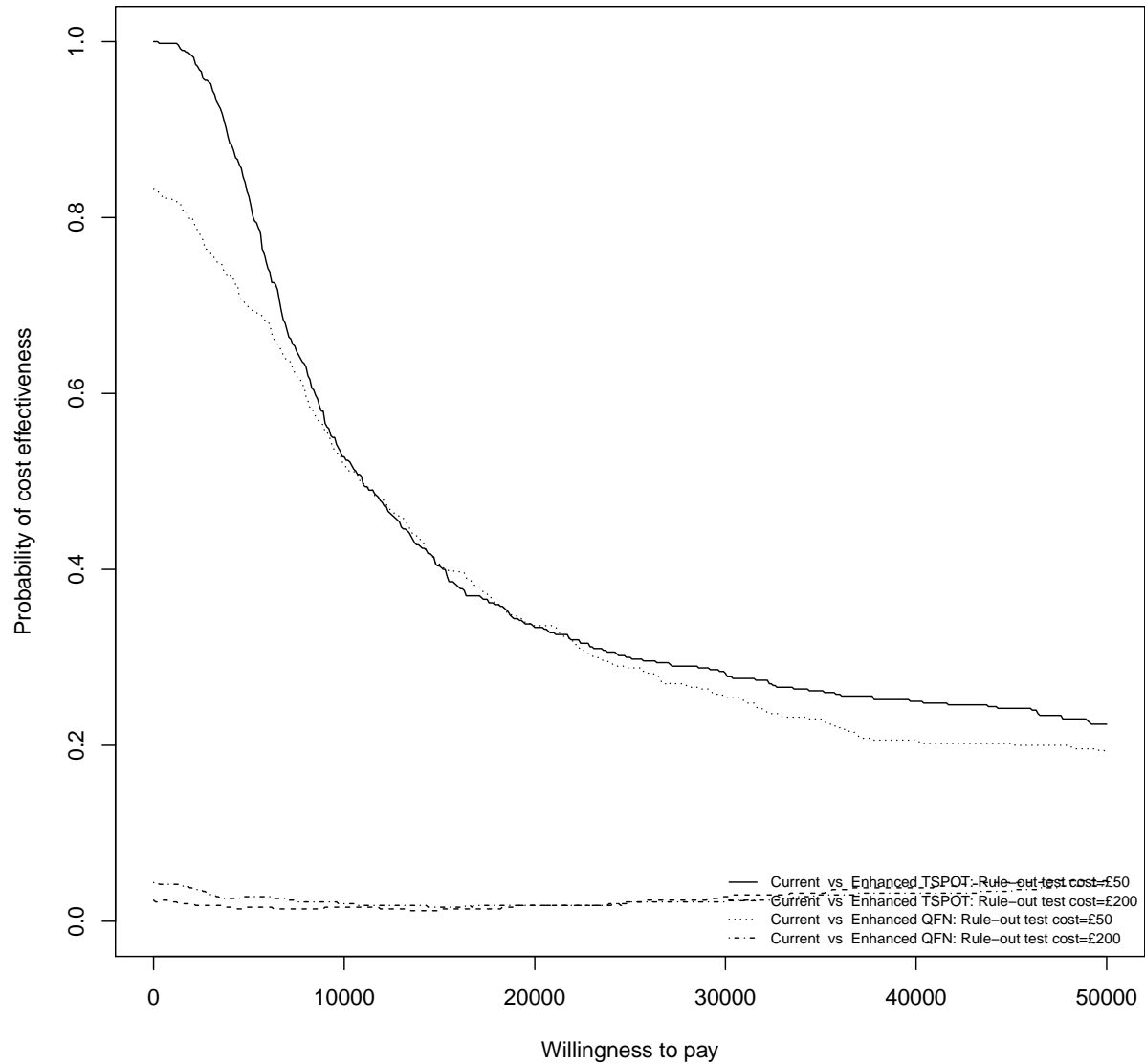


```
## in years (not days)
m <- bcea(e=dat$e/365, c=-dat$c, ref=1, interventions = intlabeleds)
contour2(m, wtp=20000, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))
```



`ceac.plot(m)`

### Cost Effectiveness Acceptability Curve



```
sink(file="../../../output_data/IDEA-BCEA-logfile.txt", append = TRUE)
summary(m)
sink()
```

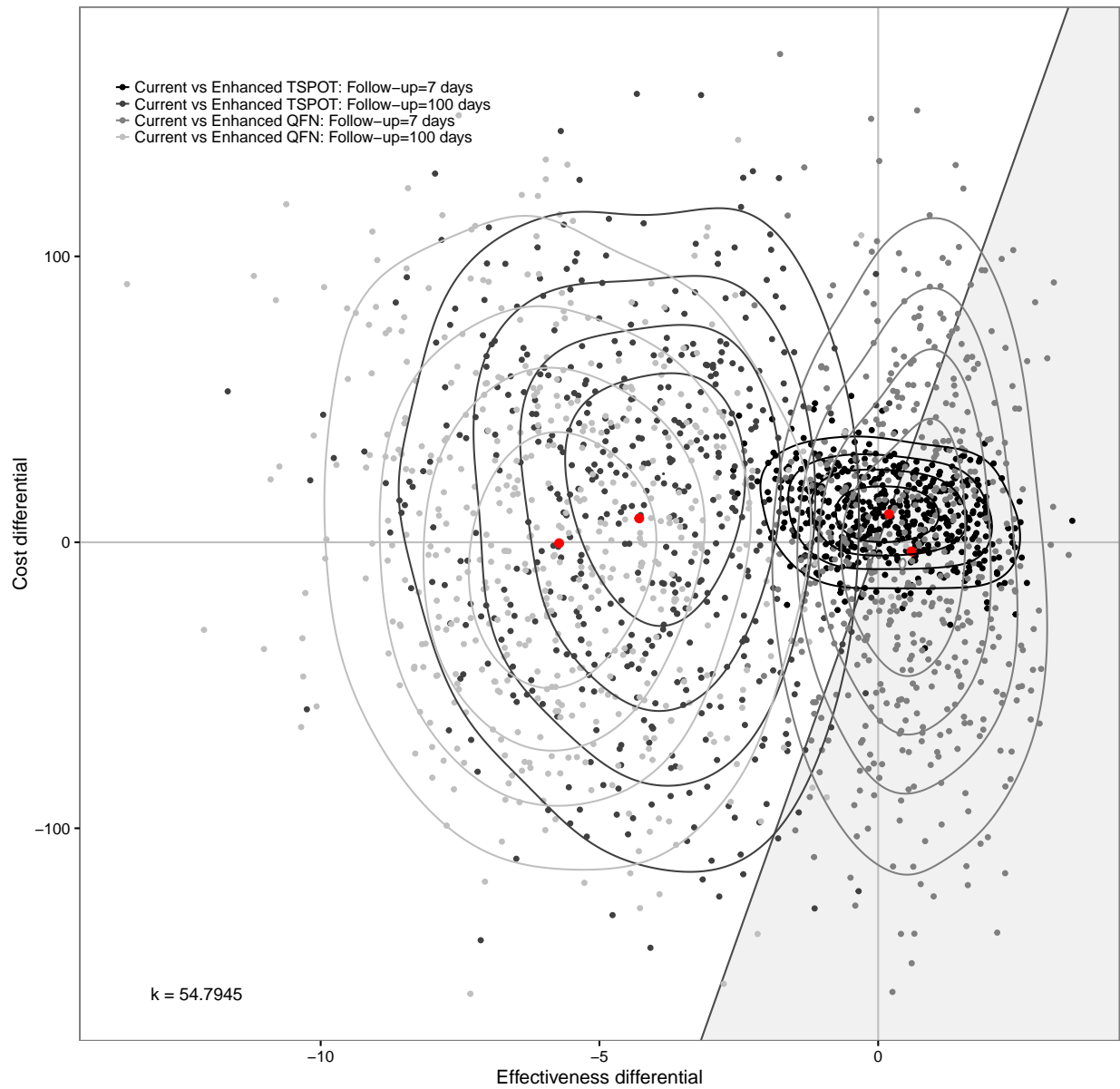
```
## False negative follow-up time
```

```
dat1 <- IDEAdectree.simple.TSPOT(data=data, FNtime = 7)
dat2 <- IDEAdectree.simple.TSPOT(data=data, FNtime = 100)
dat3 <- IDEAdectree.simple.QFN(data=data, FNtime = 7)
dat4 <- IDEAdectree.simple.QFN(data=data, FNtime = 100)
dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2], dat4$e[,2])
dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2], dat4$c[,2])
```

```

intlabeleds <- c("Current","Enhanced TSPOT: Follow-up=7 days","Enhanced TSPOT: Follow-up=100 days",
                "Enhanced QFN: Follow-up=7 days","Enhanced QFN: Follow-up=100 days")
m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intlabeleds)
contour2(m, wtp=WTP, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))+#, xlim=c(-10,10), ylim=c(-200,200)
ggtitle("")

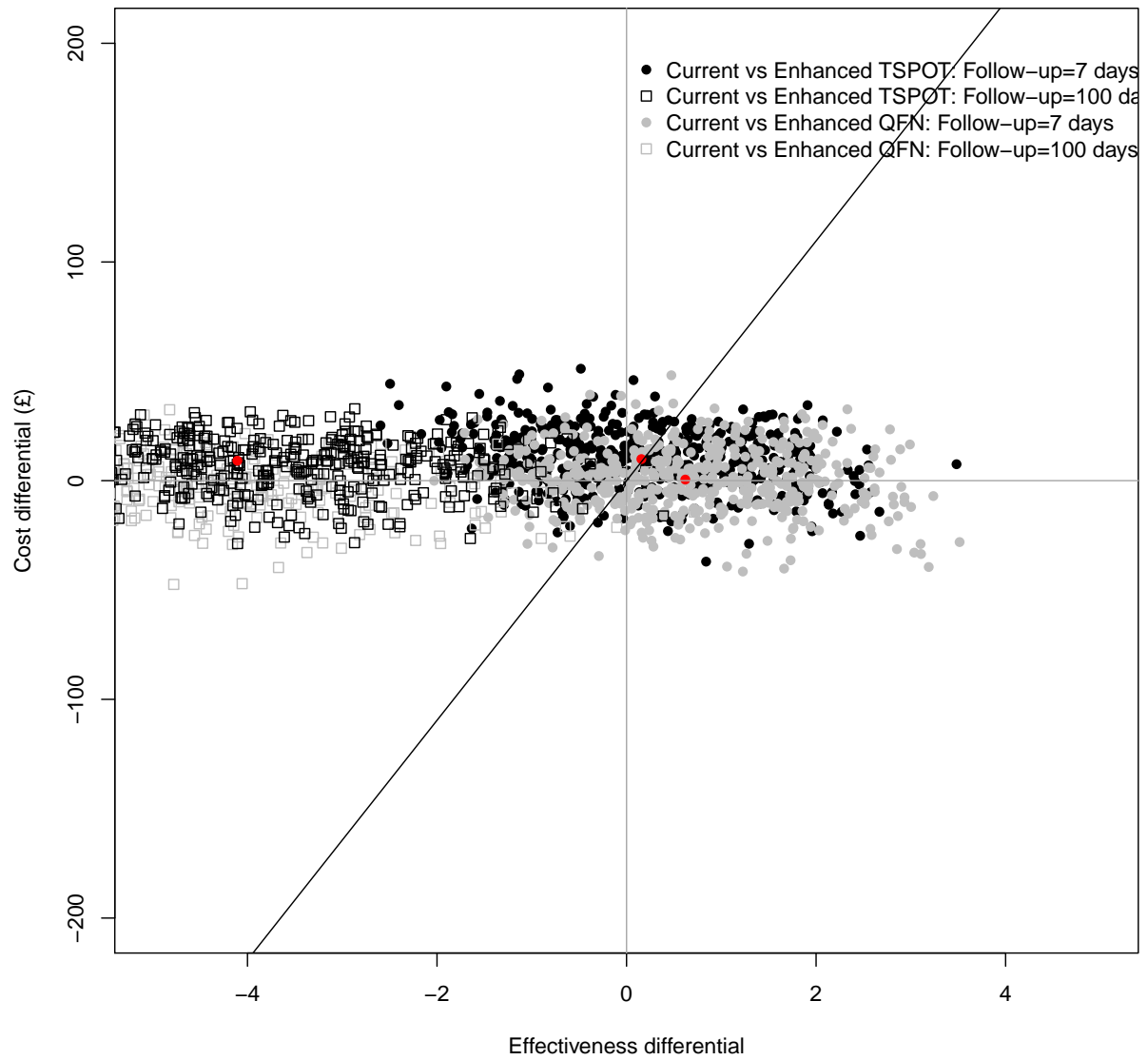
```



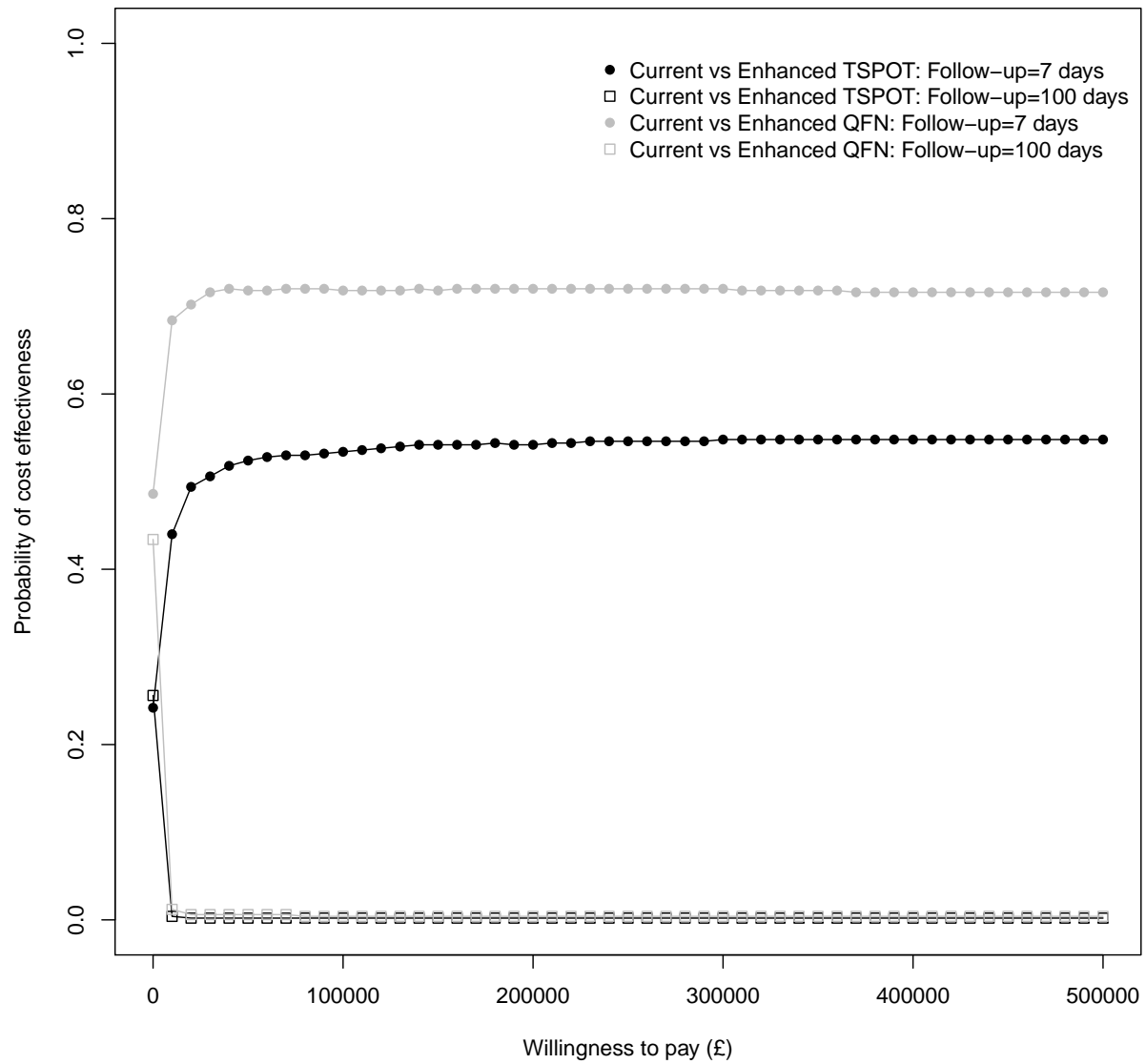
```

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabeleds)

```

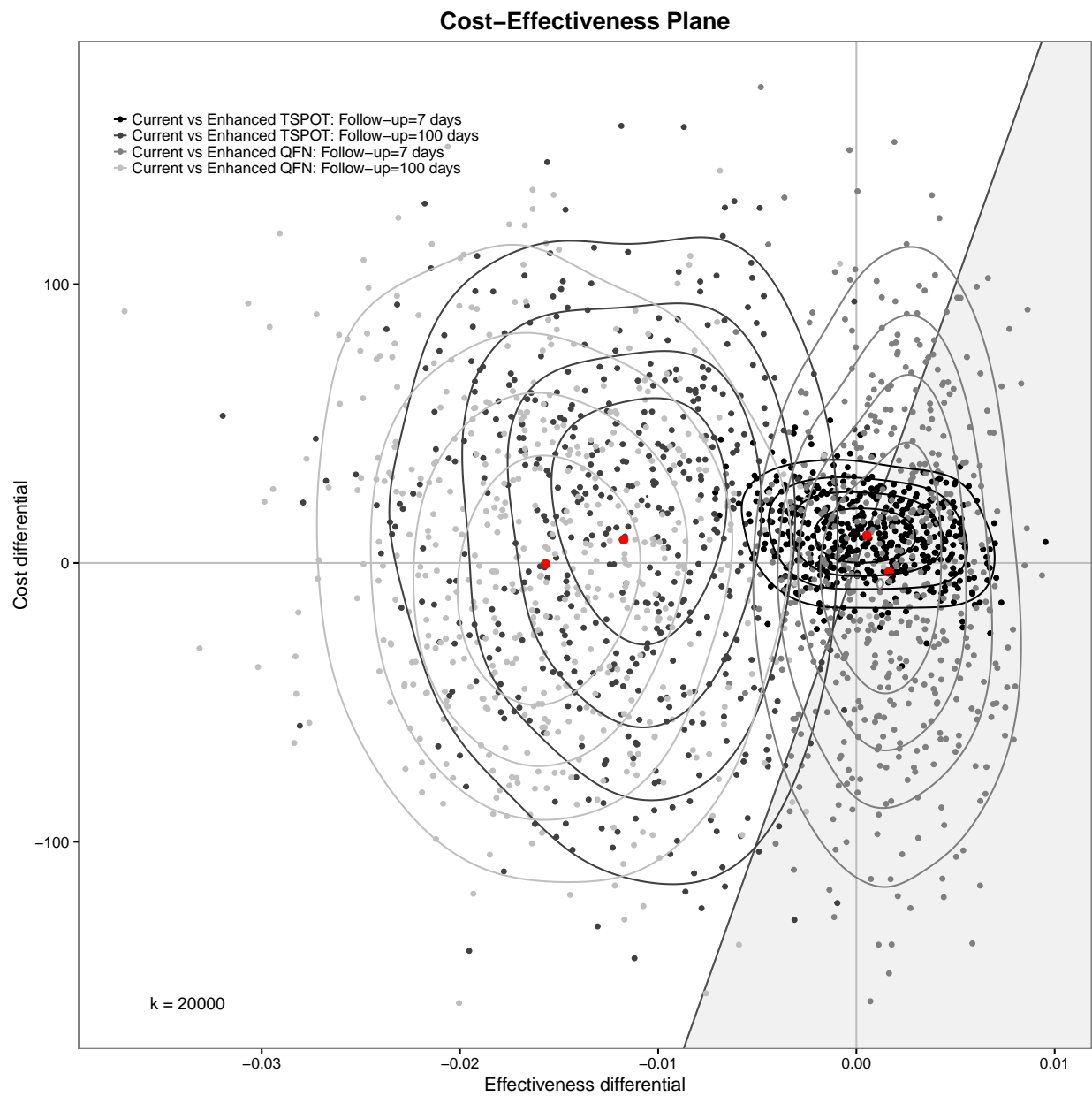


```
my.plot.ceac(dat1, dat2, dat3, dat4, intllabels)
```



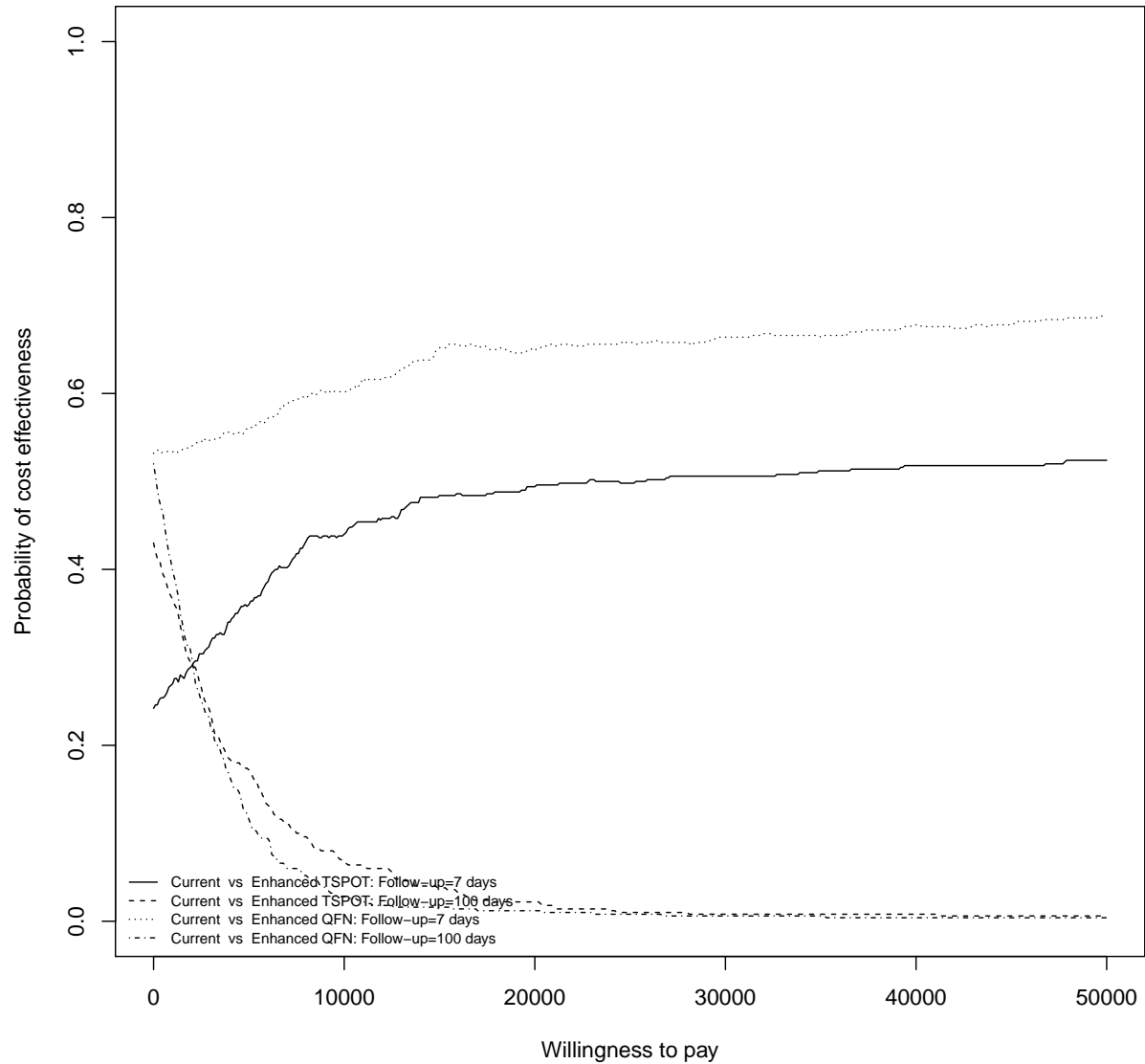
```
## in years (not days)
m <- bcea(e=dat$e/365, c=-dat$c, ref=1, interventions = intlabeleds)
contour2(m, wtp=20000, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))
```





```
ceac.plot(m, pos=c(0,0))
```

### Cost Effectiveness Acceptability Curve



```
sink(file="../../../output_data/IDEA-BCEA-logfile.txt", append = TRUE)
summary(m)
sink()
```

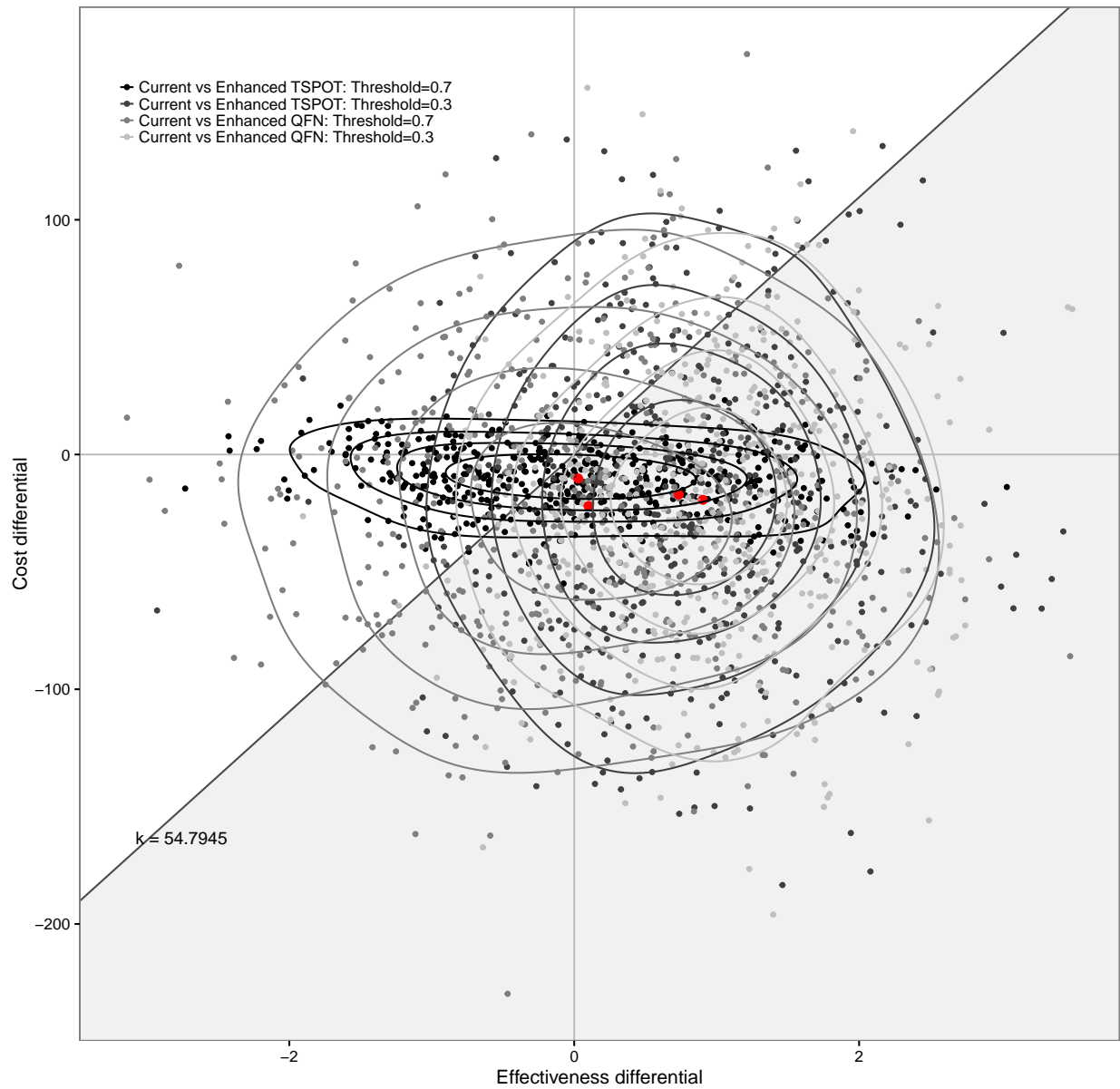
```
## clinical judgement cut-off values
```

```
dat1 <- IDEAdectree.simple.TSPOT(data=data, cutoff = 0.7)
dat2 <- IDEAdectree.simple.TSPOT(data=data, cutoff = 0.3)
dat3 <- IDEAdectree.simple.QFN(data=data, cutoff = 0.7)
dat4 <- IDEAdectree.simple.QFN(data=data, cutoff = 0.3)
dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2], dat4$e[,2])
dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2], dat4$c[,2])
```

```

intlabeleds <- c("Current","Enhanced TSPOT: Threshold=0.7","Enhanced TSPOT: Threshold=0.3",
                "Enhanced QFN: Threshold=0.7","Enhanced QFN: Threshold=0.3")
m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intlabeleds)
contour2(m, wtp=WTP, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))+#, xlim=c(-10,10), ylim=c(-200,200)
ggtitle("")

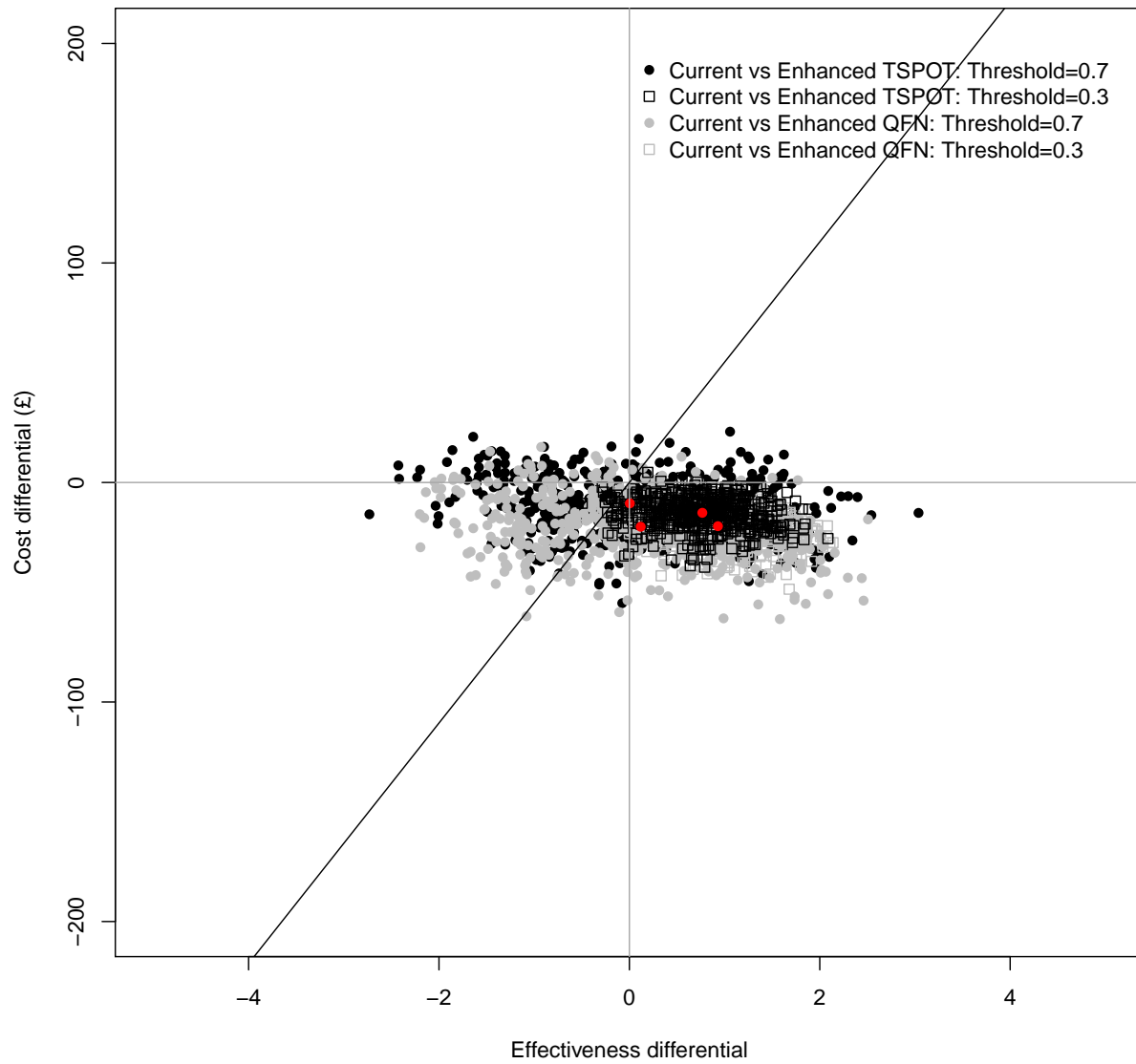
```



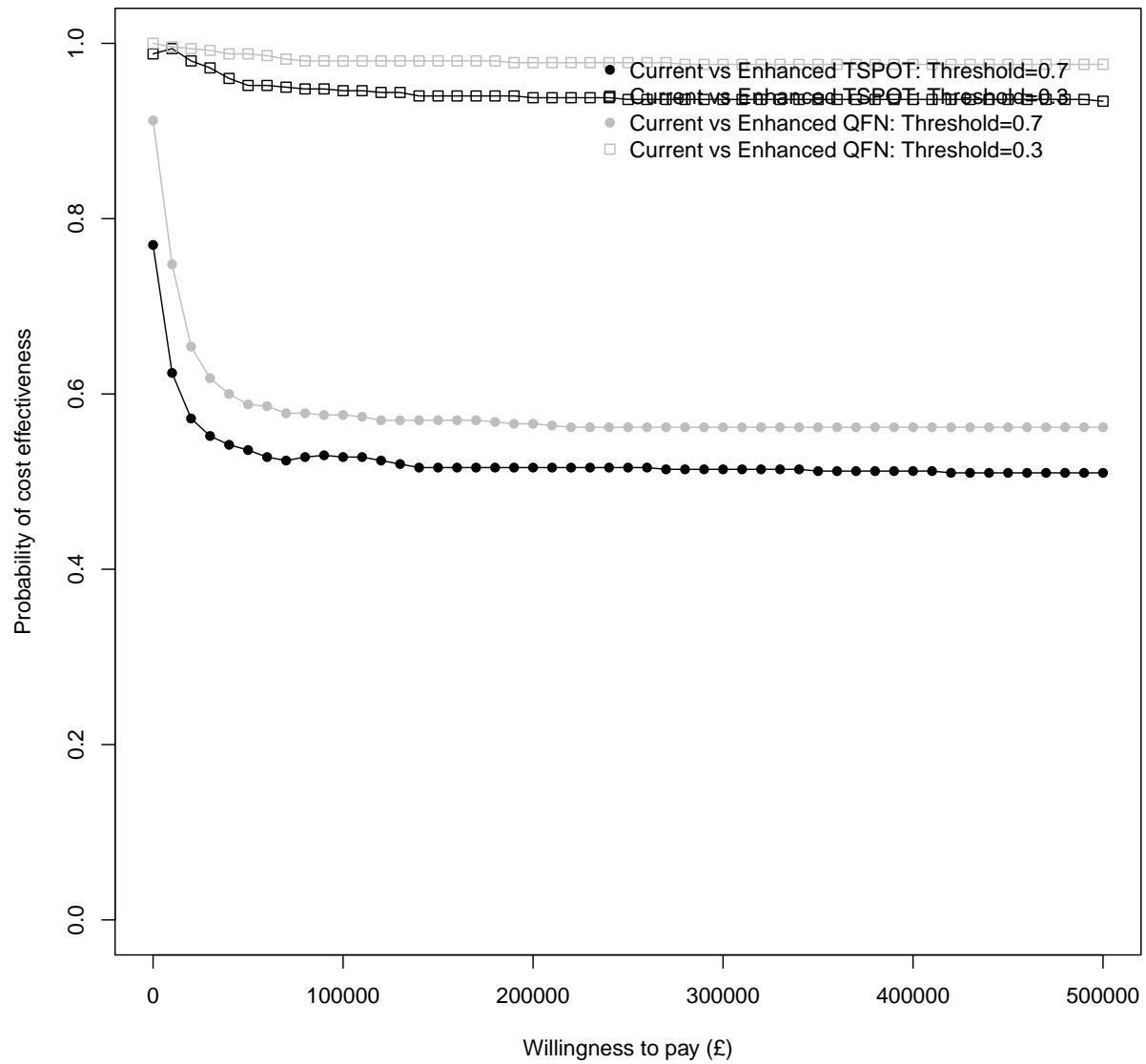
```

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabeleds)

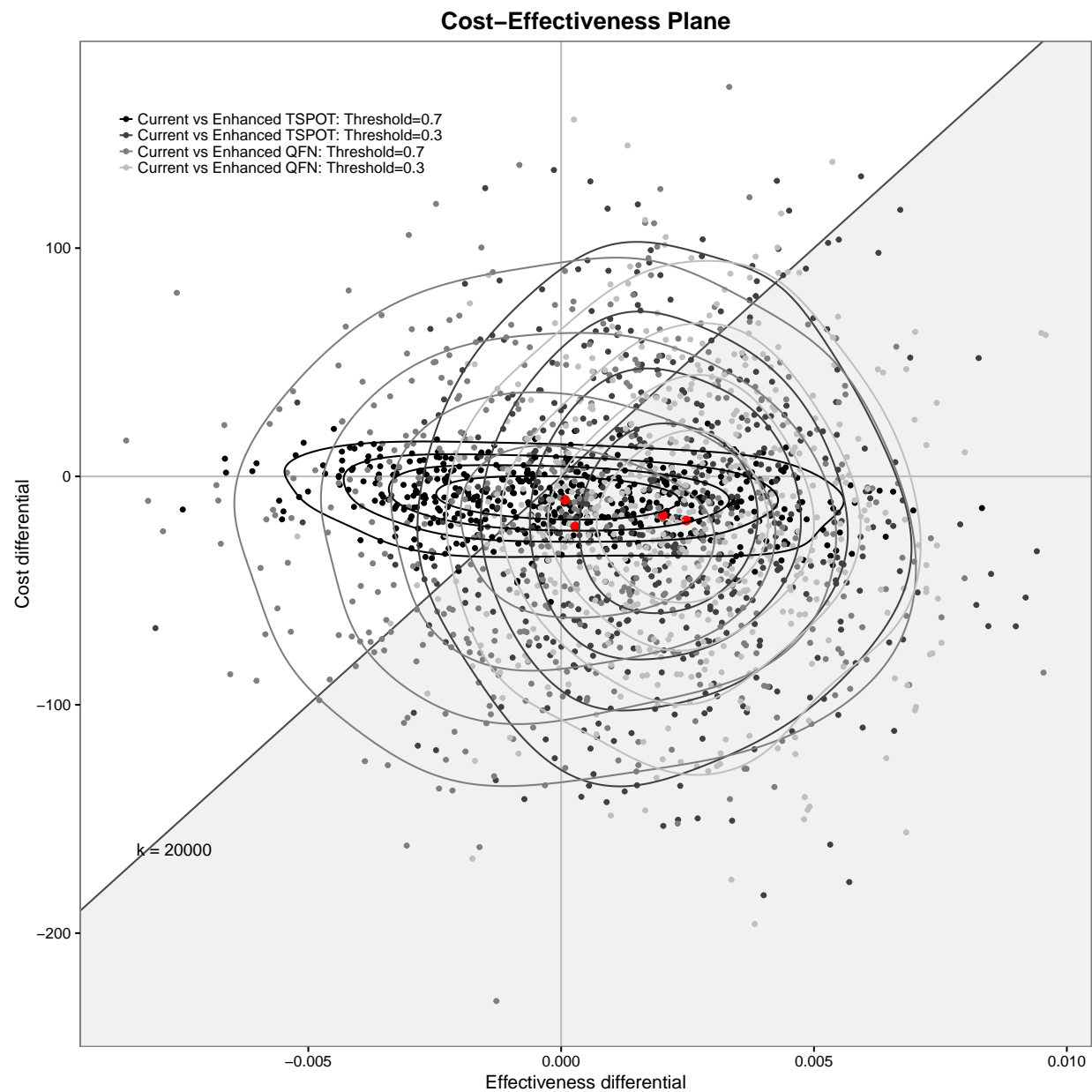
```



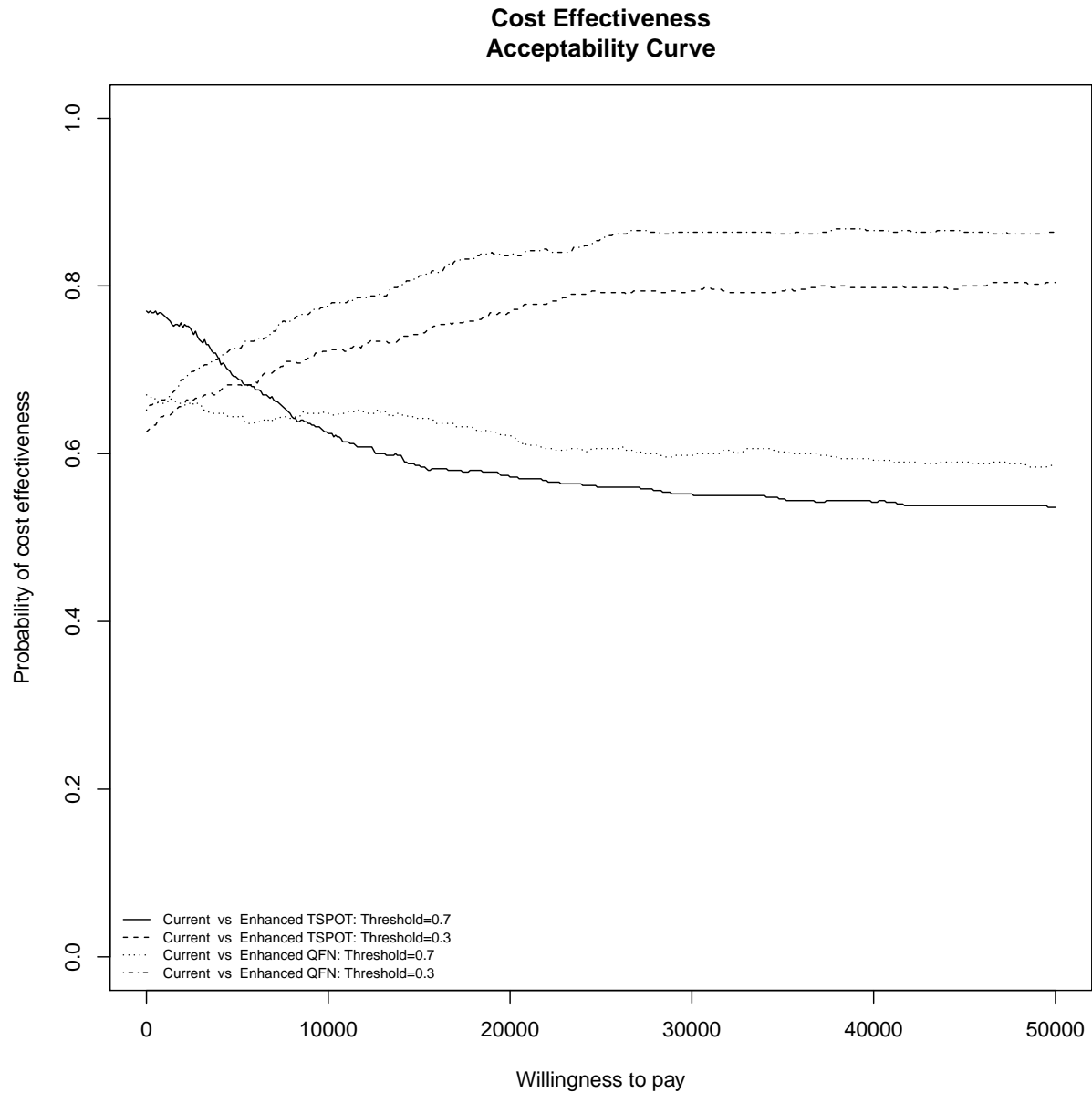
```
my.plot.ceac(dat1, dat2, dat3, dat4, intllabels)
```



```
## in years (not days)
m <- bcea(e=dat$e/365, c=-dat$c, ref=1, interventions = intlabels)
contour2(m, wtp=20000, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9))
```



```
ceac.plot(m, pos=c(0,0))
```



```
sink(file="../../../output_data/IDEA-BCEA-logfile.txt", append = TRUE)
summary(m)
sink()
```

```
## Ethnic group
#
# dat1 <- IDEAdectree.simple.1cutoff(data=data[data$Ethnclass=="Indian Sub-continent",])
# dat2 <- IDEAdectree.simple.1cutoff(data=data[data$Ethnclass=="Black",])
# dat3 <- IDEAdectree.simple.1cutoff(data=data[data$Ethnclass=="White",])
# dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2])
# dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2])
#
# intlabeled <- c("Current", "Enhanced: Indian Sub-continent", "Enhanced: Black", "Enhanced: White")
```

```
# m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intllabels)
# contour2(m, wtp=WTP, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9), xlim=c(-5,20), ylim=c(-400,100))
#
# sink(file="../../output_data/IDEA-BCEA-logfile.txt", append = TRUE)
# summary(m)
# sink()
```

```
## cob incidence
```

```
#
# dat1 <- IDEAdectree.simple.1cutoff(data=data[data$WHOCut%in%c("[40,100)", "[100,150)", "[150,200)", "[200,400)", "[400,1e+04)"),
# dat2 <- IDEAdectree.simple.1cutoff(data=data[data$WHOCut%in%c("[100,150)", "[150,200)", "[200,400)", "[400,1e+04)"),
# dat2 <- IDEAdectree.simple.1cutoff(data=data[data$WHOCut%in%c("[150,200)", "[200,400)", "[400,1e+04)"),
# dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2])
# dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2])
#
# intllabels <- c("Current","Enhanced: >40/100000","Enhanced: >100/100000","Enhanced: >150/100000")
# m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intllabels)
# contour2(m, wtp=WTP, graph = "ggplot2", ICER.size=2, pos=c(0.1,0.9), xlim=c(-5,20), ylim=c(-400,100))
#
# sink(file="../../output_data/IDEA-BCEA-logfile.txt", append = TRUE)
# summary(m)
# sink()
```

```
detach(senspec.env)
```