Basecase cost-effectiveness comparison

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# source("../../../analysis scripts/IDEA/alt-YAML\_Binomial\_dectrees/indiv-dectree-sampling.R")

library(IDEAdectree)  
library(BCEA)  
library(ggplot2)  
  
# 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/senspec\_env.RData")  
  
## sensitivities and specificities from IDEA lab data  
attach(senspec.env)

## The following objects are masked from senspec.env (pos = 3):  
##   
## QFN.HIV.Indet.sens.mean, QFN.HIV.Indet.sens.var,  
## QFN.HIV.Indet.spec.mean, QFN.HIV.Indet.spec.var,  
## QFN.HIV.noIndet.sens.mean, QFN.HIV.noIndet.sens.var,  
## QFN.HIV.noIndet.spec.mean, QFN.HIV.noIndet.spec.var,  
## QFN.HIVneg.Indet.sens.mean, QFN.HIVneg.Indet.sens.var,  
## QFN.HIVneg.Indet.spec.mean, QFN.HIVneg.Indet.spec.var,  
## QFN.HIVneg.noIndet.sens.mean, QFN.HIVneg.noIndet.sens.var,  
## QFN.HIVneg.noIndet.spec.mean, QFN.HIVneg.noIndet.spec.var,  
## QFN.Indet.sens.mean, QFN.Indet.sens.var, QFN.Indet.spec.mean,  
## QFN.Indet.spec.var, QFN.noIndet.sens.mean,  
## QFN.noIndet.sens.var, QFN.noIndet.spec.mean,  
## QFN.noIndet.spec.var, TSPOT.HIV.Indet.sens.mean,  
## TSPOT.HIV.Indet.sens.var, TSPOT.HIV.Indet.spec.mean,  
## TSPOT.HIV.Indet.spec.var, TSPOT.HIV.noIndet.sens.mean,  
## TSPOT.HIV.noIndet.sens.var, TSPOT.HIV.noIndet.spec.mean,  
## TSPOT.HIV.noIndet.spec.var, TSPOT.HIVneg.Indet.sens.mean,  
## TSPOT.HIVneg.Indet.sens.var, TSPOT.HIVneg.Indet.spec.mean,  
## TSPOT.HIVneg.Indet.spec.var, TSPOT.HIVneg.noIndet.sens.mean,  
## TSPOT.HIVneg.noIndet.sens.var, TSPOT.HIVneg.noIndet.spec.mean,  
## TSPOT.HIVneg.noIndet.spec.var, TSPOT.Indet.sens.mean,  
## TSPOT.Indet.sens.var, TSPOT.Indet.spec.mean,  
## TSPOT.Indet.spec.var, TSPOT.noIndet.sens.mean,  
## TSPOT.noIndet.sens.var, TSPOT.noIndet.spec.mean,  
## TSPOT.noIndet.spec.var

## The following objects are masked from senspec.env (pos = 4):  
##   
## QFN.HIV.Indet.sens.mean, QFN.HIV.Indet.sens.var,  
## QFN.HIV.Indet.spec.mean, QFN.HIV.Indet.spec.var,  
## QFN.HIV.noIndet.sens.mean, QFN.HIV.noIndet.sens.var,  
## QFN.HIV.noIndet.spec.mean, QFN.HIV.noIndet.spec.var,  
## QFN.HIVneg.Indet.sens.mean, QFN.HIVneg.Indet.sens.var,  
## QFN.HIVneg.Indet.spec.mean, QFN.HIVneg.Indet.spec.var,  
## QFN.HIVneg.noIndet.sens.mean, QFN.HIVneg.noIndet.sens.var,  
## QFN.HIVneg.noIndet.spec.mean, QFN.HIVneg.noIndet.spec.var,  
## QFN.Indet.sens.mean, QFN.Indet.sens.var, QFN.Indet.spec.mean,  
## QFN.Indet.spec.var, QFN.noIndet.sens.mean,  
## QFN.noIndet.sens.var, QFN.noIndet.spec.mean,  
## QFN.noIndet.spec.var, TSPOT.HIV.Indet.sens.mean,  
## TSPOT.HIV.Indet.sens.var, TSPOT.HIV.Indet.spec.mean,  
## TSPOT.HIV.Indet.spec.var, TSPOT.HIV.noIndet.sens.mean,  
## TSPOT.HIV.noIndet.sens.var, TSPOT.HIV.noIndet.spec.mean,  
## TSPOT.HIV.noIndet.spec.var, TSPOT.HIVneg.Indet.sens.mean,  
## TSPOT.HIVneg.Indet.sens.var, TSPOT.HIVneg.Indet.spec.mean,  
## TSPOT.HIVneg.Indet.spec.var, TSPOT.HIVneg.noIndet.sens.mean,  
## TSPOT.HIVneg.noIndet.sens.var, TSPOT.HIVneg.noIndet.spec.mean,  
## TSPOT.HIVneg.noIndet.spec.var, TSPOT.Indet.sens.mean,  
## TSPOT.Indet.sens.var, TSPOT.Indet.spec.mean,  
## TSPOT.Indet.spec.var, TSPOT.noIndet.sens.mean,  
## TSPOT.noIndet.sens.var, TSPOT.noIndet.spec.mean,  
## TSPOT.noIndet.spec.var

## The following objects are masked from senspec.env (pos = 5):  
##   
## QFN.HIV.Indet.sens.mean, QFN.HIV.Indet.sens.var,  
## QFN.HIV.Indet.spec.mean, QFN.HIV.Indet.spec.var,  
## QFN.HIV.noIndet.sens.mean, QFN.HIV.noIndet.sens.var,  
## QFN.HIV.noIndet.spec.mean, QFN.HIV.noIndet.spec.var,  
## QFN.HIVneg.Indet.sens.mean, QFN.HIVneg.Indet.sens.var,  
## QFN.HIVneg.Indet.spec.mean, QFN.HIVneg.Indet.spec.var,  
## QFN.HIVneg.noIndet.sens.mean, QFN.HIVneg.noIndet.sens.var,  
## QFN.HIVneg.noIndet.spec.mean, QFN.HIVneg.noIndet.spec.var,  
## QFN.Indet.sens.mean, QFN.Indet.sens.var, QFN.Indet.spec.mean,  
## QFN.Indet.spec.var, QFN.noIndet.sens.mean,  
## QFN.noIndet.sens.var, QFN.noIndet.spec.mean,  
## QFN.noIndet.spec.var, TSPOT.HIV.Indet.sens.mean,  
## TSPOT.HIV.Indet.sens.var, TSPOT.HIV.Indet.spec.mean,  
## TSPOT.HIV.Indet.spec.var, TSPOT.HIV.noIndet.sens.mean,  
## TSPOT.HIV.noIndet.sens.var, TSPOT.HIV.noIndet.spec.mean,  
## TSPOT.HIV.noIndet.spec.var, TSPOT.HIVneg.Indet.sens.mean,  
## TSPOT.HIVneg.Indet.sens.var, TSPOT.HIVneg.Indet.spec.mean,  
## TSPOT.HIVneg.Indet.spec.var, TSPOT.HIVneg.noIndet.sens.mean,  
## TSPOT.HIVneg.noIndet.sens.var, TSPOT.HIVneg.noIndet.spec.mean,  
## TSPOT.HIVneg.noIndet.spec.var, TSPOT.Indet.sens.mean,  
## TSPOT.Indet.sens.var, TSPOT.Indet.spec.mean,  
## TSPOT.Indet.spec.var, TSPOT.noIndet.sens.mean,  
## TSPOT.noIndet.sens.var, TSPOT.noIndet.spec.mean,  
## TSPOT.noIndet.spec.var

## The following objects are masked from senspec.env (pos = 6):  
##   
## QFN.HIV.Indet.sens.mean, QFN.HIV.Indet.sens.var,  
## QFN.HIV.Indet.spec.mean, QFN.HIV.Indet.spec.var,  
## QFN.HIV.noIndet.sens.mean, QFN.HIV.noIndet.sens.var,  
## QFN.HIV.noIndet.spec.mean, QFN.HIV.noIndet.spec.var,  
## QFN.HIVneg.Indet.sens.mean, QFN.HIVneg.Indet.sens.var,  
## QFN.HIVneg.Indet.spec.mean, QFN.HIVneg.Indet.spec.var,  
## QFN.HIVneg.noIndet.sens.mean, QFN.HIVneg.noIndet.sens.var,  
## QFN.HIVneg.noIndet.spec.mean, QFN.HIVneg.noIndet.spec.var,  
## QFN.Indet.sens.mean, QFN.Indet.sens.var, QFN.Indet.spec.mean,  
## QFN.Indet.spec.var, QFN.noIndet.sens.mean,  
## QFN.noIndet.sens.var, QFN.noIndet.spec.mean,  
## QFN.noIndet.spec.var, TSPOT.HIV.Indet.sens.mean,  
## TSPOT.HIV.Indet.sens.var, TSPOT.HIV.Indet.spec.mean,  
## TSPOT.HIV.Indet.spec.var, TSPOT.HIV.noIndet.sens.mean,  
## TSPOT.HIV.noIndet.sens.var, TSPOT.HIV.noIndet.spec.mean,  
## TSPOT.HIV.noIndet.spec.var, TSPOT.HIVneg.Indet.sens.mean,  
## TSPOT.HIVneg.Indet.sens.var, TSPOT.HIVneg.Indet.spec.mean,  
## TSPOT.HIVneg.Indet.spec.var, TSPOT.HIVneg.noIndet.sens.mean,  
## TSPOT.HIVneg.noIndet.sens.var, TSPOT.HIVneg.noIndet.spec.mean,  
## TSPOT.HIVneg.noIndet.spec.var, TSPOT.Indet.sens.mean,  
## TSPOT.Indet.sens.var, TSPOT.Indet.spec.mean,  
## TSPOT.Indet.spec.var, TSPOT.noIndet.sens.mean,  
## TSPOT.noIndet.sens.var, TSPOT.noIndet.spec.mean,  
## TSPOT.noIndet.spec.var

## The following objects are masked from senspec.env (pos = 7):  
##   
## QFN.HIV.Indet.sens.mean, QFN.HIV.Indet.sens.var,  
## QFN.HIV.Indet.spec.mean, QFN.HIV.Indet.spec.var,  
## QFN.HIV.noIndet.sens.mean, QFN.HIV.noIndet.sens.var,  
## QFN.HIV.noIndet.spec.mean, QFN.HIV.noIndet.spec.var,  
## QFN.HIVneg.Indet.sens.mean, QFN.HIVneg.Indet.sens.var,  
## QFN.HIVneg.Indet.spec.mean, QFN.HIVneg.Indet.spec.var,  
## QFN.HIVneg.noIndet.sens.mean, QFN.HIVneg.noIndet.sens.var,  
## QFN.HIVneg.noIndet.spec.mean, QFN.HIVneg.noIndet.spec.var,  
## QFN.Indet.sens.mean, QFN.Indet.sens.var, QFN.Indet.spec.mean,  
## QFN.Indet.spec.var, QFN.noIndet.sens.mean,  
## QFN.noIndet.sens.var, QFN.noIndet.spec.mean,  
## QFN.noIndet.spec.var, TSPOT.HIV.Indet.sens.mean,  
## TSPOT.HIV.Indet.sens.var, TSPOT.HIV.Indet.spec.mean,  
## TSPOT.HIV.Indet.spec.var, TSPOT.HIV.noIndet.sens.mean,  
## TSPOT.HIV.noIndet.sens.var, TSPOT.HIV.noIndet.spec.mean,  
## TSPOT.HIV.noIndet.spec.var, TSPOT.HIVneg.Indet.sens.mean,  
## TSPOT.HIVneg.Indet.sens.var, TSPOT.HIVneg.Indet.spec.mean,  
## TSPOT.HIVneg.Indet.spec.var, TSPOT.HIVneg.noIndet.sens.mean,  
## TSPOT.HIVneg.noIndet.sens.var, TSPOT.HIVneg.noIndet.spec.mean,  
## TSPOT.HIVneg.noIndet.spec.var, TSPOT.Indet.sens.mean,  
## TSPOT.Indet.sens.var, TSPOT.Indet.spec.mean,  
## TSPOT.Indet.spec.var, TSPOT.noIndet.sens.mean,  
## TSPOT.noIndet.sens.var, TSPOT.noIndet.spec.mean,  
## TSPOT.noIndet.spec.var

## The following objects are masked from senspec.env (pos = 8):  
##   
## QFN.HIV.Indet.sens.mean, QFN.HIV.Indet.sens.var,  
## QFN.HIV.Indet.spec.mean, QFN.HIV.Indet.spec.var,  
## QFN.HIV.noIndet.sens.mean, QFN.HIV.noIndet.sens.var,  
## QFN.HIV.noIndet.spec.mean, QFN.HIV.noIndet.spec.var,  
## QFN.HIVneg.Indet.sens.mean, QFN.HIVneg.Indet.sens.var,  
## QFN.HIVneg.Indet.spec.mean, QFN.HIVneg.Indet.spec.var,  
## QFN.HIVneg.noIndet.sens.mean, QFN.HIVneg.noIndet.sens.var,  
## QFN.HIVneg.noIndet.spec.mean, QFN.HIVneg.noIndet.spec.var,  
## QFN.Indet.sens.mean, QFN.Indet.sens.var, QFN.Indet.spec.mean,  
## QFN.Indet.spec.var, QFN.noIndet.sens.mean,  
## QFN.noIndet.sens.var, QFN.noIndet.spec.mean,  
## QFN.noIndet.spec.var, TSPOT.HIV.Indet.sens.mean,  
## TSPOT.HIV.Indet.sens.var, TSPOT.HIV.Indet.spec.mean,  
## TSPOT.HIV.Indet.spec.var, TSPOT.HIV.noIndet.sens.mean,  
## TSPOT.HIV.noIndet.sens.var, TSPOT.HIV.noIndet.spec.mean,  
## TSPOT.HIV.noIndet.spec.var, TSPOT.HIVneg.Indet.sens.mean,  
## TSPOT.HIVneg.Indet.sens.var, TSPOT.HIVneg.Indet.spec.mean,  
## TSPOT.HIVneg.Indet.spec.var, TSPOT.HIVneg.noIndet.sens.mean,  
## TSPOT.HIVneg.noIndet.sens.var, TSPOT.HIVneg.noIndet.spec.mean,  
## TSPOT.HIVneg.noIndet.spec.var, TSPOT.Indet.sens.mean,  
## TSPOT.Indet.sens.var, TSPOT.Indet.spec.mean,  
## TSPOT.Indet.spec.var, TSPOT.noIndet.sens.mean,  
## TSPOT.noIndet.sens.var, TSPOT.noIndet.spec.mean,  
## TSPOT.noIndet.spec.var

## The following objects are masked from senspec.env (pos = 9):  
##   
## QFN.HIV.Indet.sens.mean, QFN.HIV.Indet.sens.var,  
## QFN.HIV.Indet.spec.mean, QFN.HIV.Indet.spec.var,  
## QFN.HIV.noIndet.sens.mean, QFN.HIV.noIndet.sens.var,  
## QFN.HIV.noIndet.spec.mean, QFN.HIV.noIndet.spec.var,  
## QFN.HIVneg.Indet.sens.mean, QFN.HIVneg.Indet.sens.var,  
## QFN.HIVneg.Indet.spec.mean, QFN.HIVneg.Indet.spec.var,  
## QFN.HIVneg.noIndet.sens.mean, QFN.HIVneg.noIndet.sens.var,  
## QFN.HIVneg.noIndet.spec.mean, QFN.HIVneg.noIndet.spec.var,  
## QFN.Indet.sens.mean, QFN.Indet.sens.var, QFN.Indet.spec.mean,  
## QFN.Indet.spec.var, QFN.noIndet.sens.mean,  
## QFN.noIndet.sens.var, QFN.noIndet.spec.mean,  
## QFN.noIndet.spec.var, TSPOT.HIV.Indet.sens.mean,  
## TSPOT.HIV.Indet.sens.var, TSPOT.HIV.Indet.spec.mean,  
## TSPOT.HIV.Indet.spec.var, TSPOT.HIV.noIndet.sens.mean,  
## TSPOT.HIV.noIndet.sens.var, TSPOT.HIV.noIndet.spec.mean,  
## TSPOT.HIV.noIndet.spec.var, TSPOT.HIVneg.Indet.sens.mean,  
## TSPOT.HIVneg.Indet.sens.var, TSPOT.HIVneg.Indet.spec.mean,  
## TSPOT.HIVneg.Indet.spec.var, TSPOT.HIVneg.noIndet.sens.mean,  
## TSPOT.HIVneg.noIndet.sens.var, TSPOT.HIVneg.noIndet.spec.mean,  
## TSPOT.HIVneg.noIndet.spec.var, TSPOT.Indet.sens.mean,  
## TSPOT.Indet.sens.var, TSPOT.Indet.spec.mean,  
## TSPOT.Indet.spec.var, TSPOT.noIndet.sens.mean,  
## TSPOT.noIndet.sens.var, TSPOT.noIndet.spec.mean,  
## TSPOT.noIndet.spec.var

dat <- list()  
  
yearindays <- 365  
WTP <- c(20000, 30000)/yearindays

dat1 <- IDEAdectree.simple(data=data, name.ruleout = "TSPOT",  
 SPEC = TSPOT.noIndet.spec.mean, SENS = TSPOT.noIndet.sens.mean,   
 SPECvar = TSPOT.noIndet.spec.var, SENSvar = TSPOT.noIndet.sens.var)  
dat2 <- IDEAdectree.simple(data=data, name.ruleout = "TSPOT",  
 SPEC = TSPOT.HIV.noIndet.spec.mean, SENS = TSPOT.HIV.noIndet.sens.mean,   
 SPECvar = TSPOT.HIV.noIndet.spec.var, SENSvar = TSPOT.HIV.noIndet.sens.var)  
dat3 <- IDEAdectree.simple(data=data, name.ruleout = "TSPOT",  
 SPEC = TSPOT.HIVneg.noIndet.spec.mean, SENS = TSPOT.HIVneg.noIndet.sens.mean,   
 SPECvar = TSPOT.HIVneg.noIndet.spec.var, SENSvar = TSPOT.HIVneg.noIndet.sens.var)  
  
dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2])  
dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2])  
  
intlabels <- c("Current",  
 "Enhanced TSPOT: All, no Indets", "Enhanced TSPOT: All, with Indets",  
 "Enhanced TSPOT: HIV, no Indets", "Enhanced TSPOT: HIV, with Indets")  
  
m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intlabels)  
  
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)

## Warning in x \* wtp: longer object length is not a multiple of shorter  
## object length

## Warning in y[3] <- x1 \* wtp: number of items to replace is not a multiple  
## of replacement length

plot of chunk TSPOT\_noIndeterminates

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels = intlabels, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_noIndeterminates

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_noIndeterminates

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, LEVELS=0.5, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_noIndeterminates

my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels)

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_noIndeterminates

## 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))

plot of chunk TSPOT\_noIndeterminates

ceac.plot(m)

plot of chunk TSPOT\_noIndeterminates

dat1 <- IDEAdectree.simple(data=data, name.ruleout = "TSPOT",  
 SPEC = TSPOT.Indet.spec.mean, SENS = TSPOT.Indet.sens.mean,   
 SPECvar = TSPOT.Indet.spec.var, SENSvar = TSPOT.Indet.sens.var)  
dat2 <- IDEAdectree.simple(data=data, name.ruleout = "TSPOT",  
 SPEC = TSPOT.HIV.Indet.spec.mean, SENS = TSPOT.HIV.Indet.sens.mean,   
 SPECvar = TSPOT.HIV.Indet.spec.var, SENSvar = TSPOT.HIV.Indet.sens.var)  
dat3 <- IDEAdectree.simple(data=data, name.ruleout = "TSPOT",  
 SPEC = TSPOT.HIVneg.Indet.spec.mean, SENS = TSPOT.HIVneg.Indet.sens.mean,   
 SPECvar = TSPOT.HIVneg.Indet.spec.var, SENSvar = TSPOT.HIVneg.Indet.sens.var)  
  
dat$e <- cbind(dat1$e, dat2$e[,2], dat3$e[,2])  
dat$c <- cbind(dat1$c, dat2$c[,2], dat3$c[,2])  
  
intlabels <- c("Current",  
 "Enhanced TSPOT: All, no Indets", "Enhanced TSPOT: All, with Indets",  
 "Enhanced TSPOT: HIV, no Indets", "Enhanced TSPOT: HIV, with Indets")  
  
m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intlabels)  
  
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)

## Warning in x \* wtp: longer object length is not a multiple of shorter  
## object length

## Warning in y[3] <- x1 \* wtp: number of items to replace is not a multiple  
## of replacement length

plot of chunk TSPOT\_withIndeterminates

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels = intlabels, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_withIndeterminates

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_withIndeterminates

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, LEVELS=0.5, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_withIndeterminates

my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels)

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk TSPOT\_withIndeterminates

## 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))

plot of chunk TSPOT\_withIndeterminates

ceac.plot(m)

plot of chunk TSPOT\_withIndeterminates

dat1 <- IDEAdectree.simple(data=data, name.ruleout = "QFN",  
 SPEC = QFN.noIndet.spec.mean, SENS = QFN.noIndet.sens.mean,   
 SPECvar = QFN.noIndet.spec.var, SENSvar = QFN.noIndet.sens.var)  
dat2 <- IDEAdectree.simple(data=data, name.ruleout = "QFN",  
 SPEC = QFN.Indet.spec.mean, SENS = QFN.Indet.sens.mean,   
 SPECvar = QFN.Indet.spec.var, SENSvar = QFN.Indet.sens.var)  
dat3 <- IDEAdectree.simple(data=data, name.ruleout = "QFN",  
 SPEC = QFN.HIV.noIndet.spec.mean, SENS = QFN.HIV.noIndet.sens.mean,   
 SPECvar = QFN.HIV.noIndet.spec.var, SENSvar = QFN.HIV.noIndet.sens.var)  
dat4 <- IDEAdectree.simple(data=data, name.ruleout = "QFN",  
 SPEC = QFN.HIV.Indet.spec.mean, SENS = QFN.HIV.Indet.sens.mean,   
 SPECvar = QFN.HIV.Indet.spec.var, SENSvar = QFN.HIV.Indet.sens.var)  
  
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])  
  
intlabels <- c("Current",  
 "Enhanced QFN: All, no Indets", "Enhanced QFN: All, with Indets",  
 "Enhanced QFN: HIV, no Indets", "Enhanced QFN: HIV, with Indets")  
  
m <- bcea(e=dat$e, c=-dat$c, ref=1, interventions = intlabels)  
  
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)

## Warning in x \* wtp: longer object length is not a multiple of shorter  
## object length

## Warning in y[3] <- x1 \* wtp: number of items to replace is not a multiple  
## of replacement length

plot of chunk QFN

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk QFN

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk QFN

my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, LEVELS=0.5, wtpNEG = "Y")

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk QFN

my.plot.ceac(dat1, dat2, dat3, dat4, intlabels)

## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used

plot of chunk QFN

## 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))

plot of chunk QFN

ceac.plot(m)

plot of chunk QFN

detach(senspec.env)