IDEA study: TST and QFN cost-effectiveness comparison: HIV patients only and indeterminates NOT included

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29 January 2016

# 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")

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")  
load("../data/drug\_dose-cost.RData")  
  
## sensitivities and specificities from IDEA lab data  
attach(senspec.env)  
  
dat <- list()  
  
yearindays <- 365  
WTP <- c(20000, 30000)/yearindays  
  
IDEAdectree.simple.TSPOT <- function(...){IDEAdectree.simple(SPEC = TSPOT.HIV.noIndet.spec.mean, SENS = TSPOT.HIV.noIndet.sens.mean,   
 SPECvar = TSPOT.HIV.noIndet.spec.var, SENSvar = TSPOT.HIV.noIndet.sens.var,  
 ...)}  
IDEAdectree.simple.QFN <- function(...){IDEAdectree.simple(SPEC = QFN.HIV.noIndet.spec.mean, SENS = QFN.HIV.noIndet.sens.mean,   
 SPECvar = QFN.HIV.noIndet.spec.var, SENSvar = QFN.HIV.noIndet.sens.var,  
 ...)}  
  
data <- data[data$HIVpos==TRUE,] #n=151

#### Prevalence 0.1 and 0.5

## prevalence  
  
dat1 <- IDEAdectree.simple.TSPOT(data=data, name.ruleout = "TSPOT", prev = 0.1)

## Loading required package: triangle

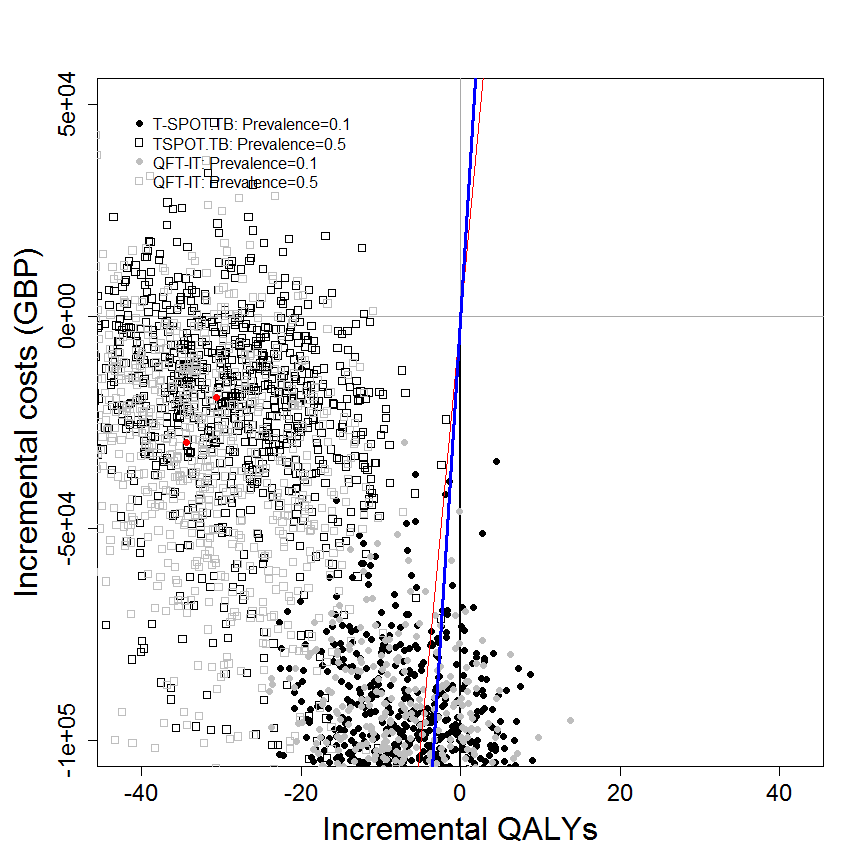
## Loading required package: assertive

dat2 <- IDEAdectree.simple.TSPOT(data=data, name.ruleout = "TSPOT", prev = 0.5)  
dat3 <- IDEAdectree.simple.QFN(data=data, name.ruleout = "QFN", prev = 0.1)  
dat4 <- IDEAdectree.simple.QFN(data=data, name.ruleout = "QFN", 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])  
  
intlabels <- c("Current",  
 "Enhanced TSPOT: Prevalence=0.1", "Enhanced TSPOT: Prevalence=0.5",  
 "Enhanced QFN: Prevalence=0.1", "Enhanced QFN: Prevalence=0.5")  
  
intlabels2 <- c("T-SPOT.TB: Prevalence=0.1", "TSPOT.TB: Prevalence=0.5",  
 "QFT-IT: Prevalence=0.1", "QFT-IT: Prevalence=0.5")  
  
# 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)  
  
  
# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

## Loading required package: MASS

## Loading required package: car

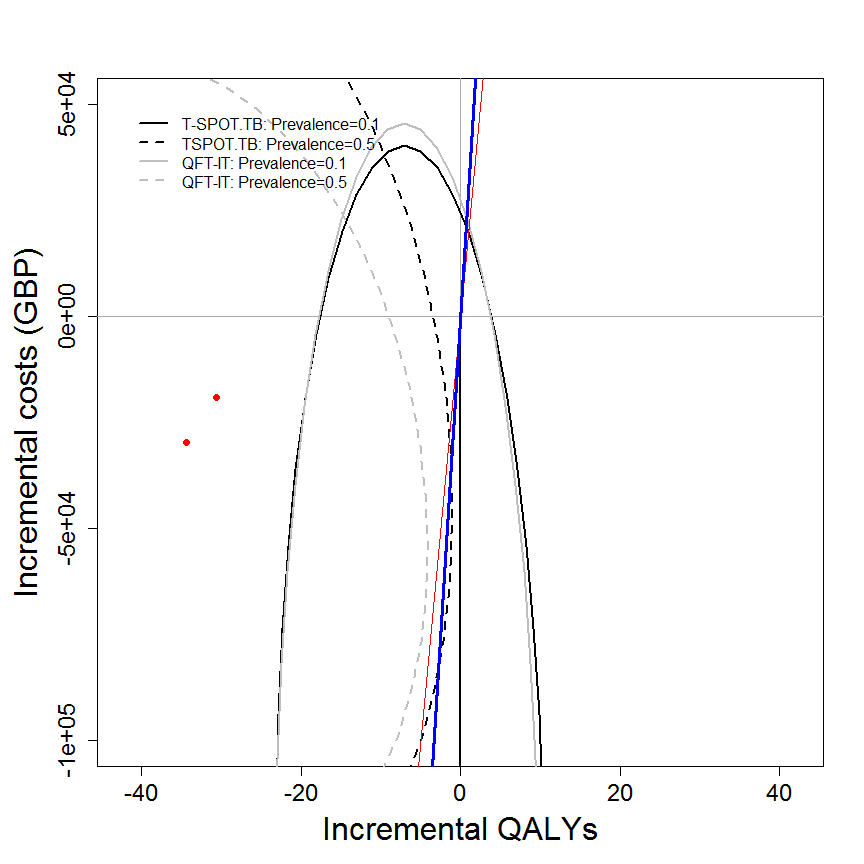
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, contour=TRUE, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

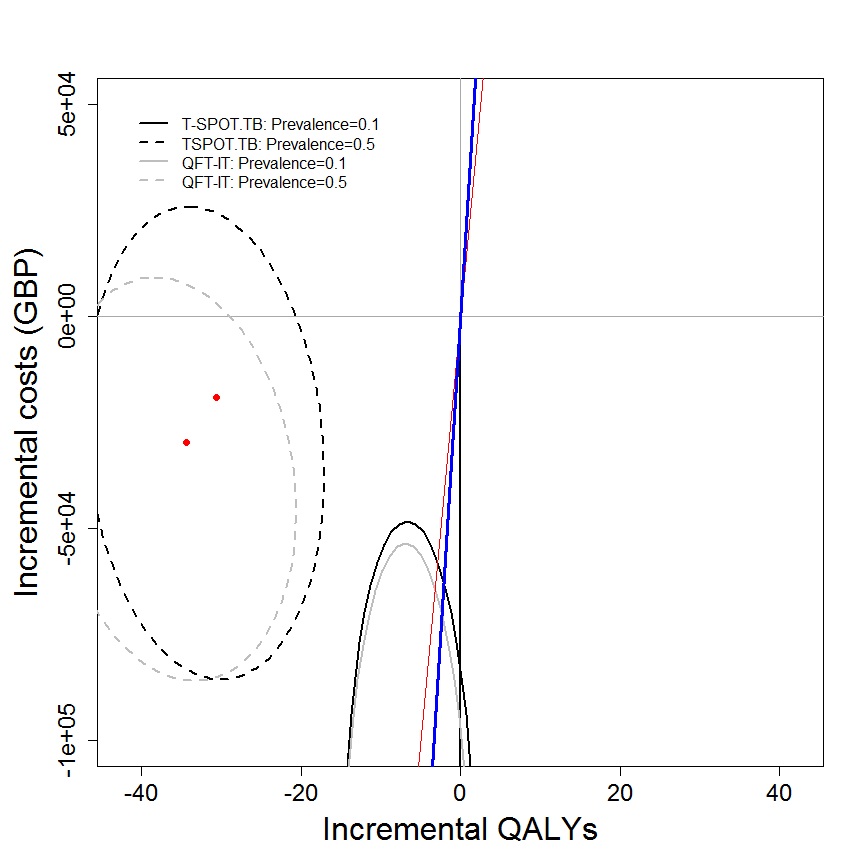
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, LEVELS=0.5, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, contour=TRUE, LEVELS=0.5, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

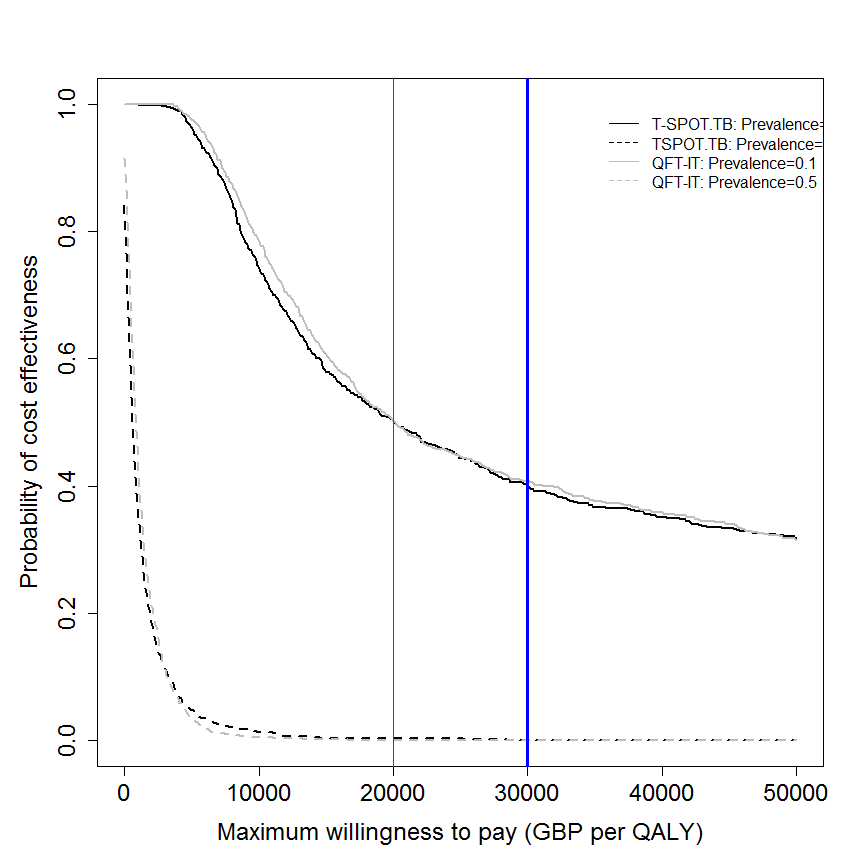
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.ceac(dat1, dat2, dat3, intlabels = c("All","HIV positive","HIV negative"), labelLong=FALSE, TITLE="(a)")  
my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels2, labelLong=FALSE, SCALEcosts=FALSE, SCALEdays=FALSE, N=769)

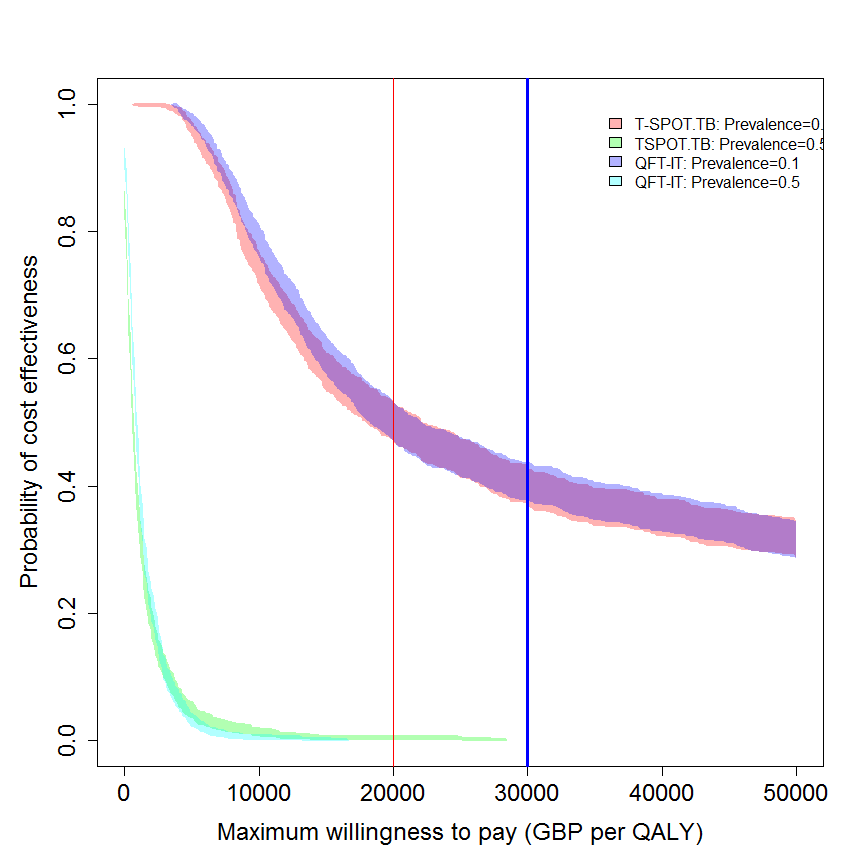
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels2, labelLong=FALSE, SCALEcosts=FALSE, SCALEdays=FALSE, N=769, CI=TRUE)

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



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

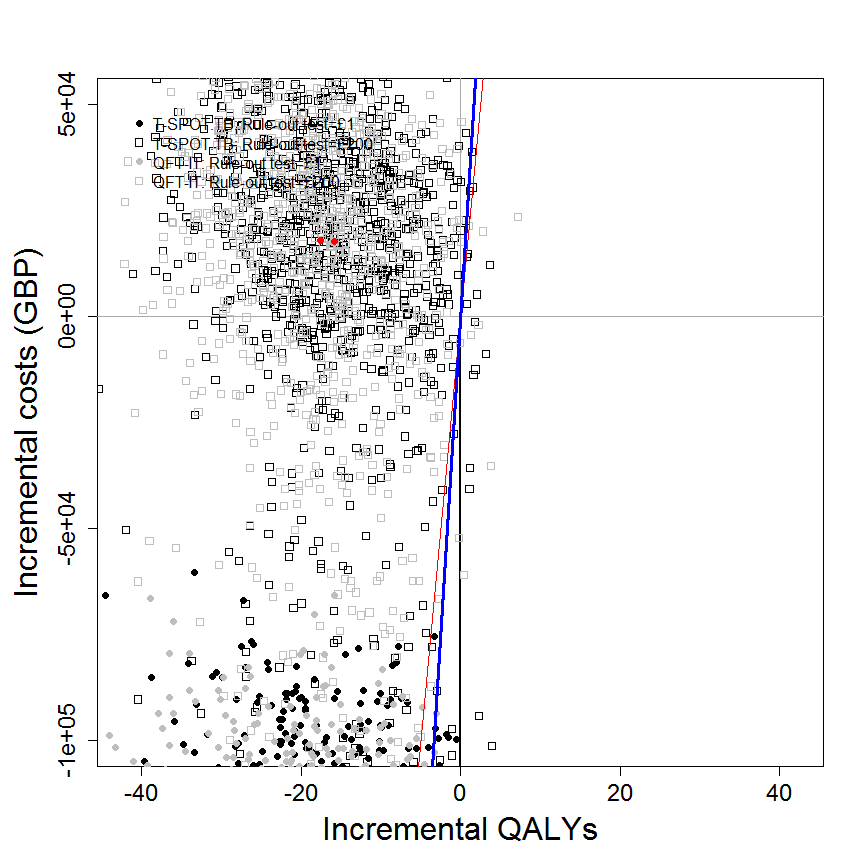
# par(mfrow=c(2,2))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, LEVELS=0.5, YLIM=c(-200,200))  
# my.plot.ceac(dat1, dat2, dat3, dat4, intlabels)  
  
## 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)

sink(file="../../../output\_data/IDEA-BCEA-logfile.txt", append = TRUE)  
summary(m)  
sink()

#### Rule-out test cost 1 and 200 GBP

## rule-out test cost  
  
dat1 <- IDEAdectree.simple.TSPOT(data=data, c.ruleout = 1)  
dat2 <- IDEAdectree.simple.TSPOT(data=data, c.ruleout = 200)  
dat3 <- IDEAdectree.simple.QFN(data=data, c.ruleout = 1)  
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])  
  
intlabels <- c("Current",  
 "Enhanced TSPOT: Rule-out test=£1", "Enhanced TSPOT: Rule-out test=£200",  
 "Enhanced QFN: Rule-out test=£1", "Enhanced QFN: Rule-out test=£200")  
  
intlabels2 <- c("T-SPOT.TB: Rule-out test=£1", "T-SPOT.TB: Rule-out test=£200",  
 "QFT-IT: Rule-out test=£1", "QFT-IT: Rule-out test=£200")  
  
# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

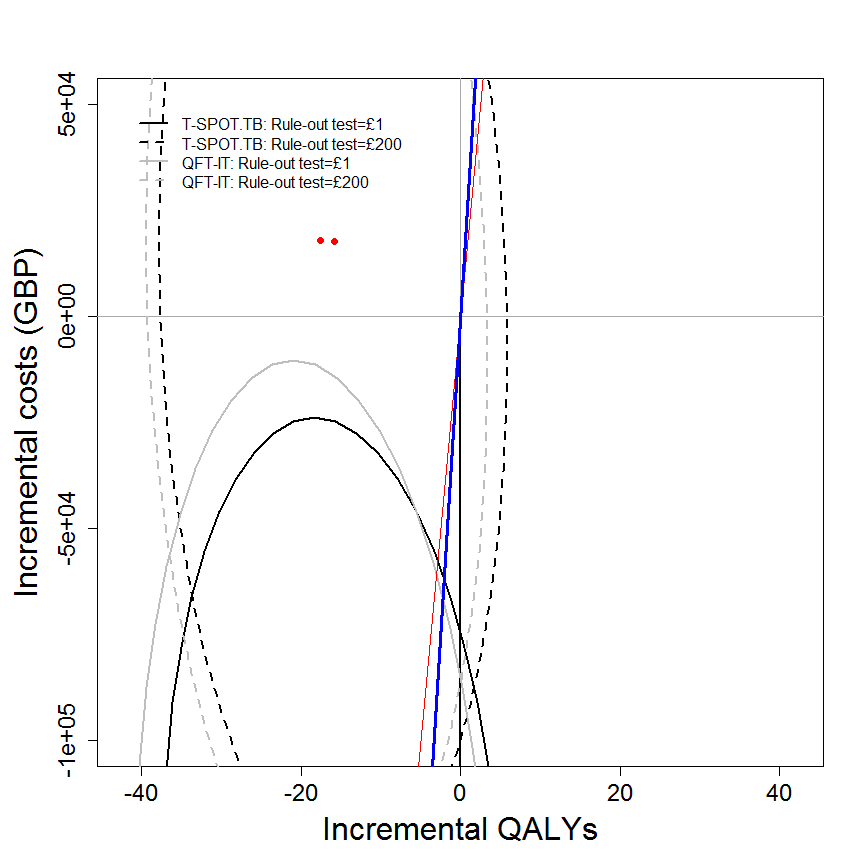
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, contour=TRUE, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

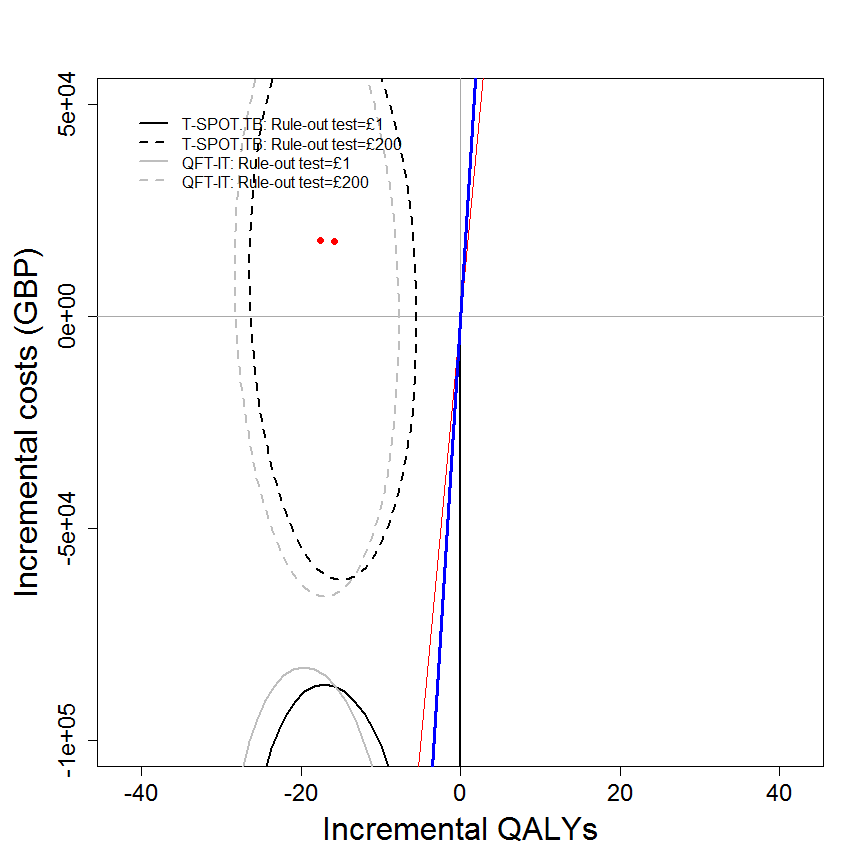
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, LEVELS=0.5, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, contour=TRUE, LEVELS=0.5, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

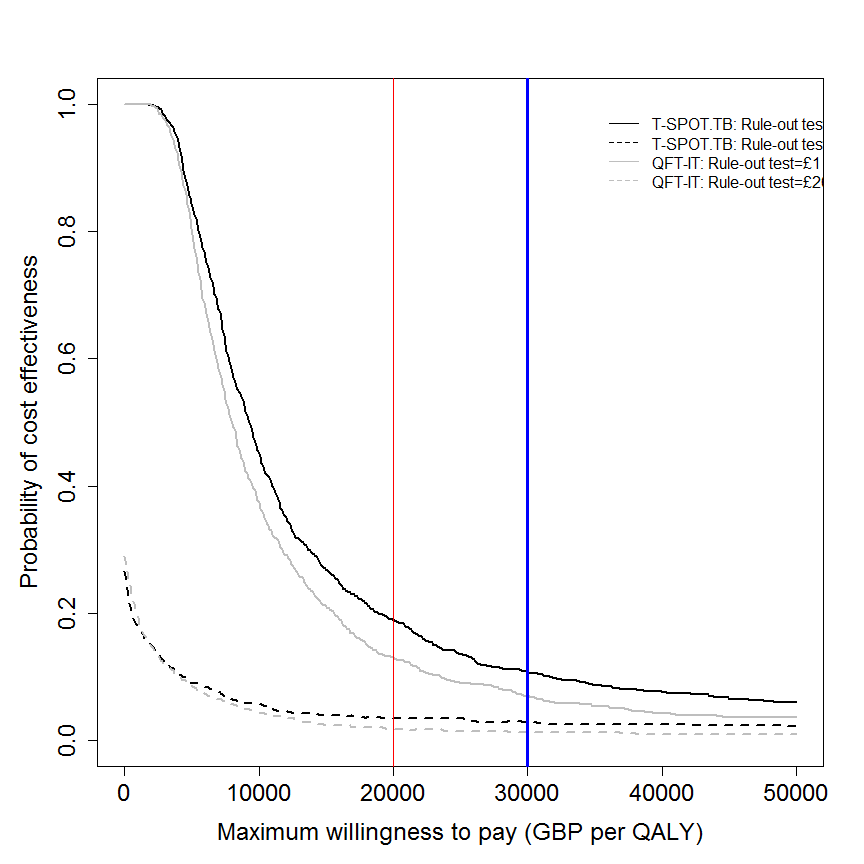
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.ceac(dat1, dat2, dat3, intlabels = c("All","HIV positive","HIV negative"), labelLong=FALSE, TITLE="(a)")  
my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels2, labelLong=FALSE, SCALEcosts=FALSE, SCALEdays=FALSE, N=769)

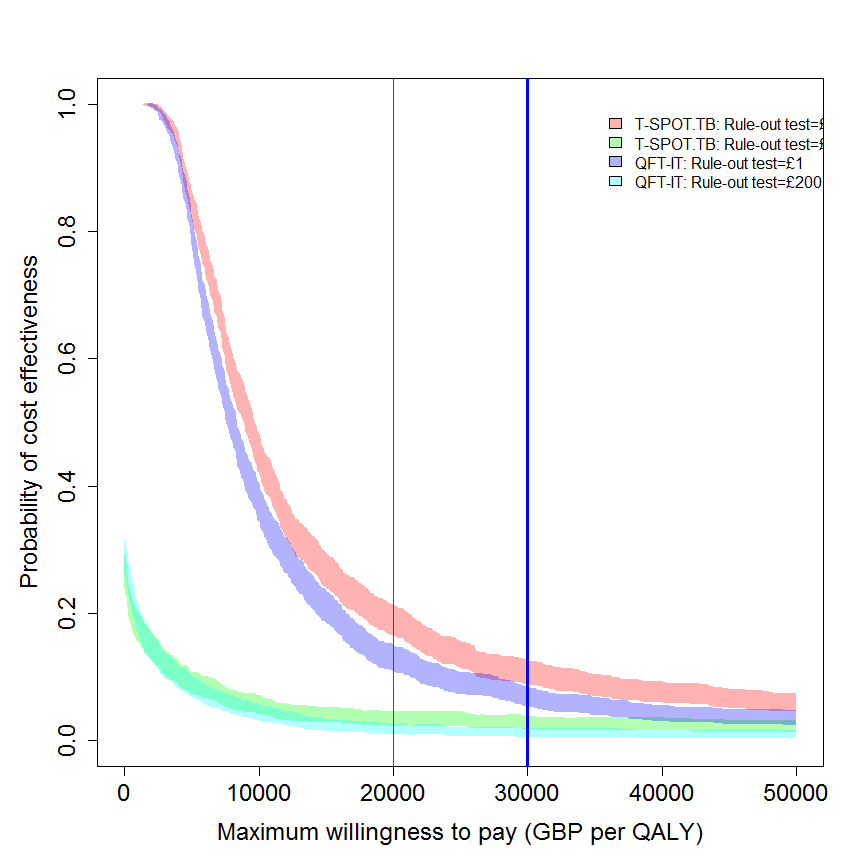
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels2, labelLong=FALSE, SCALEcosts=FALSE, SCALEdays=FALSE, N=769, CI=TRUE)

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



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

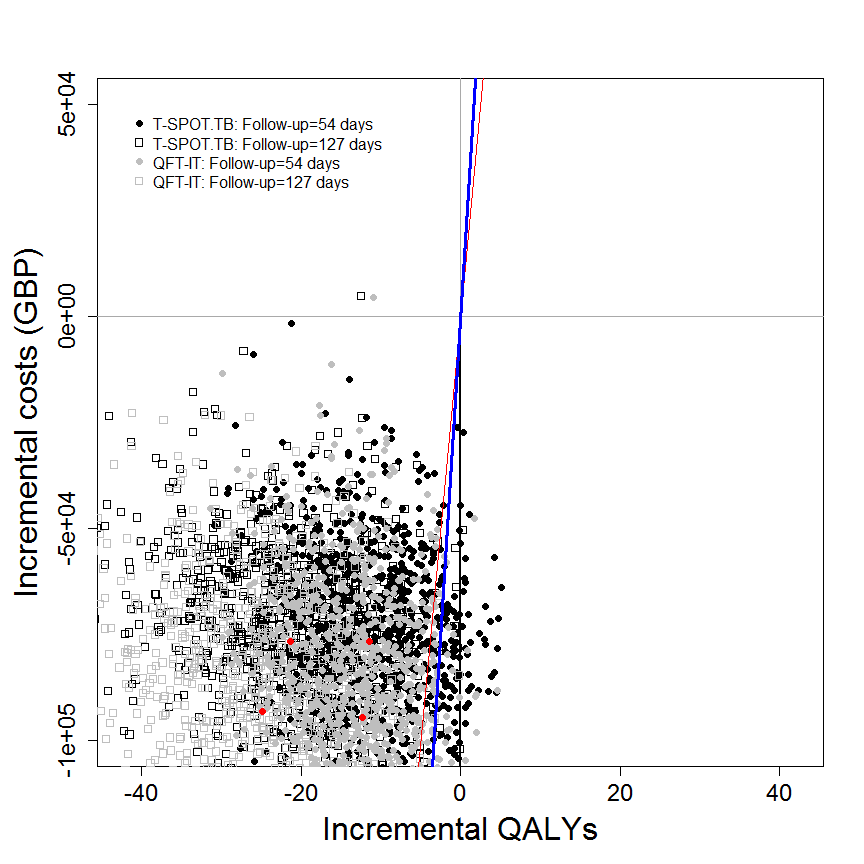
# par(mfrow=c(2,2))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, LEVELS=0.5, YLIM=c(-200,200))  
# my.plot.ceac(dat1, dat2, dat3, dat4, intlabels)  
  
## 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)

sink(file="../../../output\_data/IDEA-BCEA-logfile.txt", append = TRUE)  
summary(m)  
sink()

#### Follow-up visit 54 and 127 days

## False negative follow-up time  
  
dat1 <- IDEAdectree.simple.TSPOT(data=data, name.ruleout = "TSPOT", FNtime = 54, FNdist=FALSE)  
dat2 <- IDEAdectree.simple.TSPOT(data=data, name.ruleout = "TSPOT", FNtime = 127, FNdist=FALSE)  
dat3 <- IDEAdectree.simple.QFN(data=data, name.ruleout = "QFN", FNtime = 54, FNdist=FALSE)  
dat4 <- IDEAdectree.simple.QFN(data=data, name.ruleout = "QFN", FNtime = 127, FNdist=FALSE)  
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 TSPOT: Follow-up=7 days","Enhanced TSPOT: Follow-up=100 days",  
 "Enhanced QFN: Follow-up=7 days","Enhanced QFN: Follow-up=100 days")  
  
intlabels2 <- c("T-SPOT.TB: Follow-up=54 days","T-SPOT.TB: Follow-up=127 days",  
 "QFT-IT: Follow-up=54 days","QFT-IT: Follow-up=127 days")  
  
# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

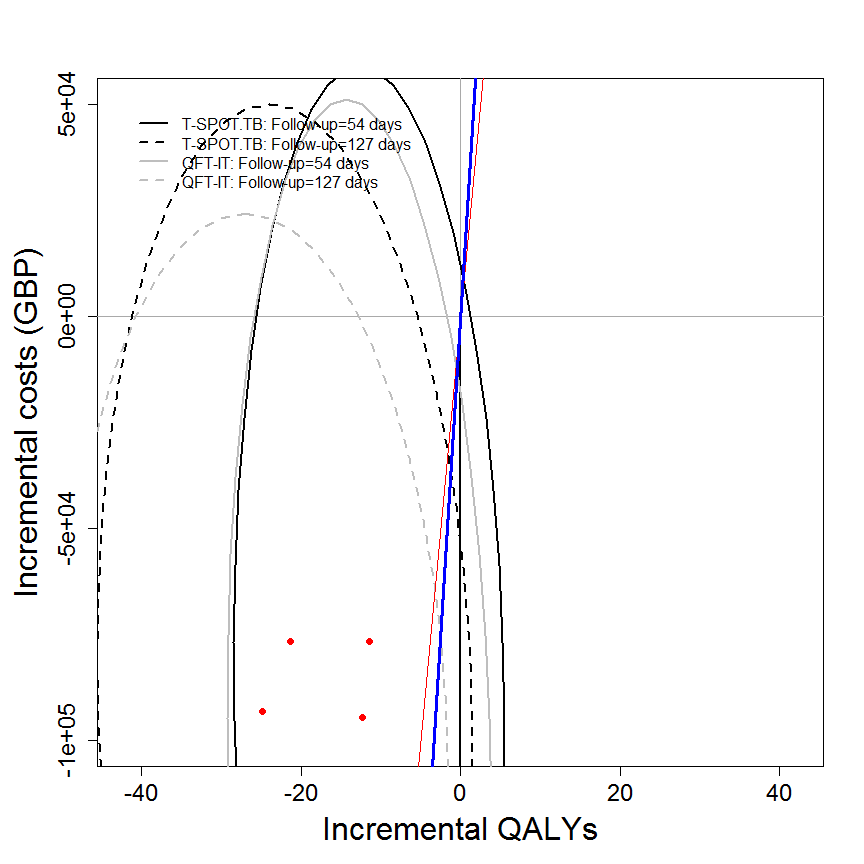
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, contour=TRUE, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

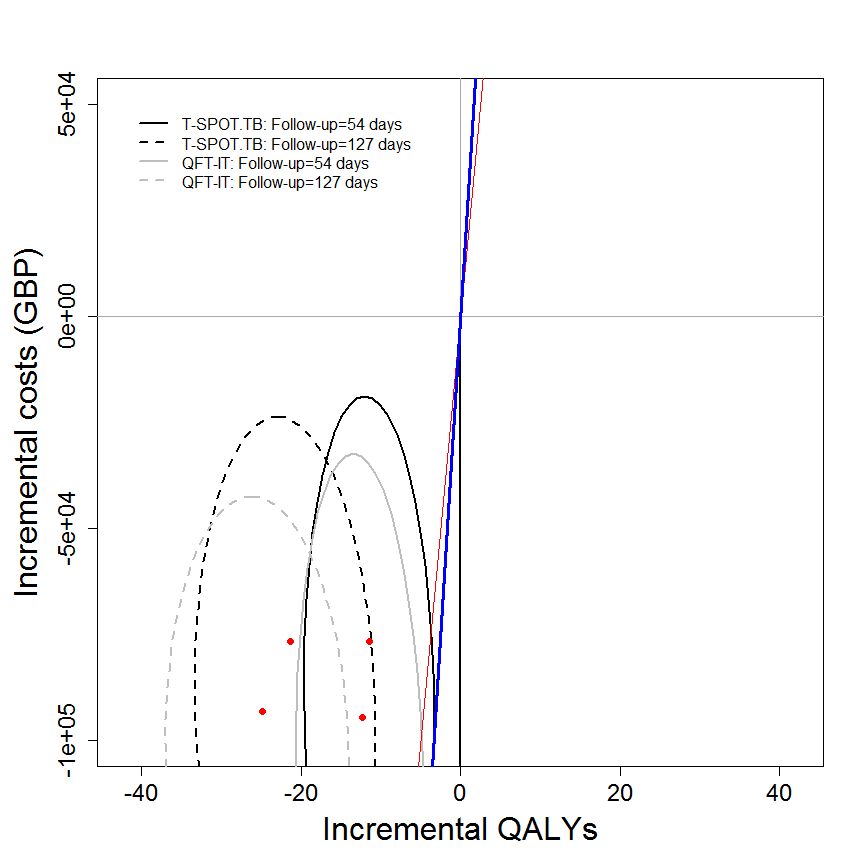
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, LEVELS=0.5, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, dat4, wtp=WTP\*yearindays, intlabels = intlabels2, contour=TRUE, LEVELS=0.5, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, N=769)

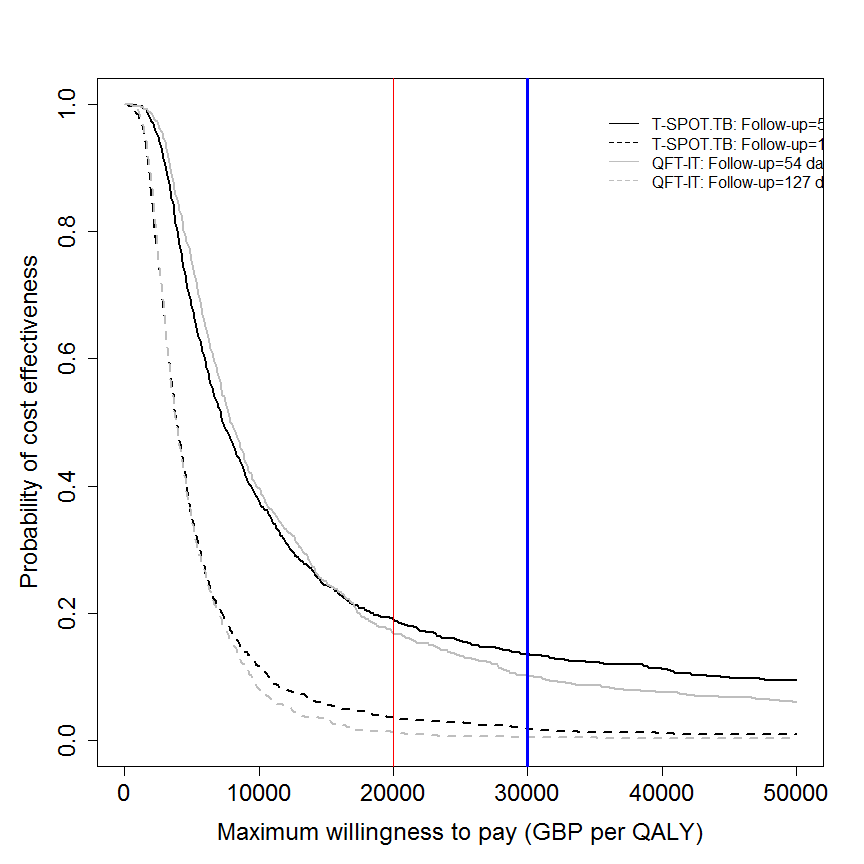
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# my.plot.ceac(dat1, dat2, dat3, intlabels = c("All","HIV positive","HIV negative"), labelLong=FALSE, TITLE="(a)")  
my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels2, labelLong=FALSE, SCALEcosts=FALSE, SCALEdays=FALSE, N=769)

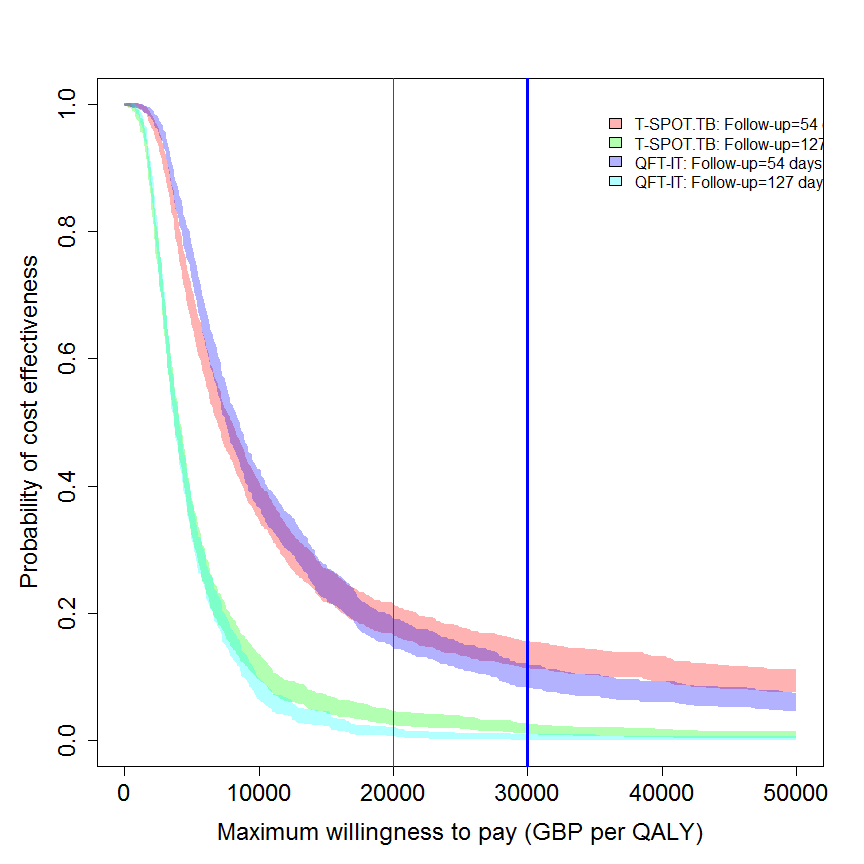
## Warning in if (is.na(dat4)) {: the condition has length > 1 and only the  
## first element will be used



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

my.plot.ceac(dat1, dat2, dat3, dat4, intlabels = intlabels2, labelLong=FALSE, SCALEcosts=FALSE, SCALEdays=FALSE, N=769, CI=TRUE)

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



## [[1]]  
## NULL  
##   
## [[2]]  
## NULL

# par(mfrow=c(2,2))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, LEVELS=0.5, YLIM=c(-200,200))  
# my.plot.ceac(dat1, dat2, dat3, dat4, intlabels)  
  
## 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()

## clinical judgement cut-off values  
  
dat1 <- IDEAdectree.simple.TSPOT(data=data, name.ruleout = "TSPOT", cutoff = 0.7)  
dat2 <- IDEAdectree.simple.TSPOT(data=data, name.ruleout = "TSPOT", cutoff = 0.3)  
dat3 <- IDEAdectree.simple.QFN(data=data, name.ruleout = "QFN", cutoff = 0.7)  
dat4 <- IDEAdectree.simple.QFN(data=data, name.ruleout = "QFN", 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])  
  
intlabels <- c("Current","Enhanced TSPOT: Threshold=0.7","Enhanced TSPOT: Threshold=0.3",  
 "Enhanced QFN: Threshold=0.7","Enhanced QFN: Threshold=0.3")  
  
# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, wtp=WTP\*yearindays, intlabels = c("All","HIV positive","HIV negative"), wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, TITLE="(a)", N=769)  
  
# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, wtp=WTP\*yearindays, intlabels = c("All","HIV positive","HIV negative"), contour=TRUE, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, TITLE="(a)", N=769)  
  
# my.plot.bcea(dat1, dat2, dat3, wtp=WTP, intlabels = intlabels, contour=TRUE, LEVELS=0.5, wtpNEG = "Y")  
my.plot.bcea(dat1, dat2, dat3, wtp=WTP\*yearindays, intlabels = c("All","HIV positive","HIV negative"), contour=TRUE, LEVELS=0.5, wtpNEG = "Y", SCALEcosts=FALSE, SCALEdays=FALSE, labelLong=FALSE, TITLE="(a)", N=769)  
  
# my.plot.ceac(dat1, dat2, dat3, intlabels = c("All","HIV positive","HIV negative"), labelLong=FALSE, TITLE="(a)")  
my.plot.ceac(dat1, dat2, dat3, intlabels = c("All","HIV positive","HIV negative"), labelLong=FALSE, TITLE="(a)", SCALEcosts=FALSE, SCALEdays=FALSE, N=769)  
my.plot.ceac(dat1, dat2, dat3, intlabels = c("All","HIV positive","HIV negative"), labelLong=FALSE, TITLE="(a)", SCALEcosts=FALSE, SCALEdays=FALSE, N=769, CI=TRUE)  
  
# par(mfrow=c(2,2))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, YLIM=c(-200,200))  
# my.plot.bcea(dat1, dat2, dat3, dat4, WTP, intlabels, contour=TRUE, LEVELS=0.5, YLIM=c(-200,200))  
# my.plot.ceac(dat1, dat2, dat3, dat4, intlabels)  
  
## 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",])  
# dat2 <- 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$c[,2])  
#   
# intlabels <- c("Current","Enhanced: Indian Sub-continent","Enhanced: Black","Enhanced: White")  
# m <- bcea(e=dat$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(-5,20), ylim=c(-400,100)) + ggtitle("")  
#   
# 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$c[,2])  
#   
# intlabels <- c("Current","Enhanced: >40/100000","Enhanced: >100/100000","Enhanced: >150/100000")  
# m <- bcea(e=dat$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(-5,20), ylim=c(-400,100)) + ggtitle("")  
#   
# sink(file="../../../output\_data/IDEA-BCEA-logfile.txt", append = TRUE)  
# summary(m)  
# sink()

detach(senspec.env)