```
R version 3.2.1 (2015-06-18) -- "World-Famous Astronaut"
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Platform: x86_64-apple-darwin13.4.0 (64-bit)

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  Natural language support but running in an English locale

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[R.app GUI 1.66 (6956) x86_64-apple-darwin13.4.0]

>
> rm(list=ls(all=TRUE))
>
> set.seed(123)
>
> library(MASS)
> library(matrixStats)
matrixStats v0.14.2 (2015-06-23) successfully loaded. See ?matrixStats for help.
>
> setwd("~/Dropbox/beliefs_incomplete data/Paper/PSRM/final/replication_archive/Leadership/")
>
>
> ### Load the data
> data <- read.table("HMS_Data.raw.txt", header=T)
>
>
> ### Run original model
>
> obs_Q3 <- ifelse(is.na(data$CQ3a_Clinic_or_Hospitals)==F & is.na(data$FQ3a_Clinic)==F, 1, 0)
> q3_data <- subset(data, obs_Q3 == 1)
>
> m <- glm(CQ3a_Clinic_or_Hospitals ~ FQ3a_Clinic, family=binomial(link="logit"), data=q3_data)
> summary(m)

Call:
glm(formula = CQ3a_Clinic_or_Hospitals ~ FQ3a_Clinic, family = binomial(link = "logit"),
    data = q3_data)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.4473  -1.4473   0.9297   0.9297   1.9348

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.7047     0.7687  -2.218  0.02658 *
FQ3a_Clinic   2.3199     0.8173   2.839  0.00453 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 96.124  on 69  degrees of freedom
Residual deviance: 85.033  on 68  degrees of freedom
AIC: 89.033

Number of Fisher Scoring iterations: 4

>
> yes <- 1/(1+exp(-(c(1,1) %*% coef(m))))
> no <- 1/(1+exp(-(c(1,0) %*% coef(m))))
> atepoint <- yes-no
> atepoint
          [,1]
[1,] 0.4952767
>
> draw <- mvrnorm(1000, coef(m), vcov(m))
> yesvec <- 1/(1+exp(-(draw %*% c(1,1))))
> novec <- 1/(1+exp(-(draw %*% c(1,0))))
> atepointvec <- yesvec-novec
> quantile(atepointvec, c(0.025, 0.975))
     2.5%     97.5%
0.1942842 0.6527476
>
>
>
> ### Run the sensitivity analysis: Scenario (a)
>
> etavec = seq(0, 0.99, length.out=100)
>
> results <-  NULL
> for(i in 1:length(etavec)){
+     res <- NULL
+     count <- 1
+     while(count <= 500){
+         # create data given eta
+         q3_data$newtreat <- NA
+         q3_data$newtreat[q3_data$FQ3a_Clinic==0 & q3_data$CQ3a_Clinic_or_Hospitals==0] <- rbinom(length(q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==0 & q3_data
$CQ3a_Clinic_or_Hospitals==0]), 1, etavec[i])
+         q3_data$newtreat[q3_data$FQ3a_Clinic==1 & q3_data$CQ3a_Clinic_or_Hospitals==1] <- rbinom(length(q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==1 & q3_data
$CQ3a_Clinic_or_Hospitals==1]), 1, 1-etavec[i])
+         q3_data$newtreat[q3_data$FQ3a_Clinic==0 & q3_data$CQ3a_Clinic_or_Hospitals==1] <- q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==0 & q3_data$CQ3a_Clinic_or_Hospitals==1]
+         q3_data$newtreat[q3_data$FQ3a_Clinic==1 & q3_data$CQ3a_Clinic_or_Hospitals==0] <- q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==1 & q3_data$CQ3a_Clinic_or_Hospitals==0]
+         if(0 %in% c(table(q3_data$newtreat, q3_data$CQ3a_Clinic_or_Hospitals))) next
+
+         # run model and get ATE
+         m <- glm(CQ3a_Clinic_or_Hospitals ~ newtreat, family=binomial(link="logit"), data=q3_data)
+         summary(m)
+
+         yes <- 1/(1+exp(-(c(1,1) %*% coef(m))))
+         no <- 1/(1+exp(-(c(1,0) %*% coef(m))))
+         atepoint <- yes-no
+
+         draw <- mvrnorm(1000, coef(m), vcov(m))
+         yesvec <- 1/(1+exp(-(draw %*% c(1,1))))
+         novec <- 1/(1+exp(-(draw %*% c(1,0))))
+         atepointvec <- yesvec-novec
+
+         #res <- rbind(res, c(atepoint, sd(atepointvec)))
```

```
+         res <- rbind(res, c(atepoint, quantile(atepointvec, 0.025), quantile(atepointvec, 0.975)))
+         count <- count+1
+     }
+     results <- rbind(results, c(etavec[i], colMedians(res)))
+ }
>
> colnames(results) <- c("eta", "pointest", "lowerci95", "upperci95")
> results <- as.data.frame(results)
>
>
> # Figure 5(a)
> quartz(type="pdf", width=5, height=5, file="output/leadership_q3_sc1.pdf")
> par(mar = c(4,4,0.3,0.3), mgp=c(2.5,1,0), family="CMU Serif")
> plot(1:length(results$pointest), results$pointest, type="n", ylim=c(-1, 1), xlab = expression(eta), ylab="Average Treatment Effect", xaxt="n")
> polygon(c(1:length(results$pointest), rev(1:length(results$pointest))), c(results$lowerci95,rev(results$upperci95)), col="grey", border=NA)
> points(1:length(results$pointest), results$pointest, type="l", lwd=3)
> axis(1, at=seq(1, 100, length.out=6), labels = seq(0, 1, length.out=6), las=2)
> abline(h=0, col = "black", lwd=2)
> lines(c(1,1), c(results$lowerci95[1], results$upperci95[1]), lwd=3)
> points(1, results$pointest[1], pch=16)
> dev.off()
null device
          1
>
>
>
>
>
> ### Run the sensitivity analysis: Scenario (b)
>
> etavec = seq(0, 0.99, length.out=100)
>
> results <-  NULL
> for(i in 1:length(etavec)){
+     res <- NULL
+     count <- 1
+     while(count <= 500){
+         # create data given eta
+         q3_data$newtreat <- NA
+         q3_data$newtreat[q3_data$FQ3a_Clinic==0 & q3_data$CQ3a_Clinic_or_Hospitals==1] <- rbinom(length(q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==0 & q3_data
$CQ3a_Clinic_or_Hospitals==1]), 1, etavec[i])
+         q3_data$newtreat[q3_data$FQ3a_Clinic==1 & q3_data$CQ3a_Clinic_or_Hospitals==0] <- rbinom(length(q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==1 & q3_data
$CQ3a_Clinic_or_Hospitals==0]), 1, 1-etavec[i])
+         q3_data$newtreat[q3_data$FQ3a_Clinic==1 & q3_data$CQ3a_Clinic_or_Hospitals==1] <- q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==1 & q3_data$CQ3a_Clinic_or_Hospitals==1]
+         q3_data$newtreat[q3_data$FQ3a_Clinic==0 & q3_data$CQ3a_Clinic_or_Hospitals==0] <- q3_data$FQ3a_Clinic[q3_data$FQ3a_Clinic==0 & q3_data$CQ3a_Clinic_or_Hospitals==0]
+         if(0 %in% c(table(q3_data$newtreat, q3_data$CQ3a_Clinic_or_Hospitals))) next
+
+         # run model and get ATE
+         m <- glm(CQ3a_Clinic_or_Hospitals ~ newtreat, family=binomial(link="logit"), data=q3_data)
+         summary(m)
+
+         yes <- 1/(1+exp(-(c(1,1) %*% coef(m))))
+         no <- 1/(1+exp(-(c(1,0) %*% coef(m))))
+         atepoint <- yes-no
+
+         draw <- mvrnorm(1000, coef(m), vcov(m))
+         yesvec <- 1/(1+exp(-(draw %*% c(1,1))))
+         novec <- 1/(1+exp(-(draw %*% c(1,0))))
+         atepointvec <- yesvec-novec
+
+         #res <- rbind(res, c(atepoint, sd(atepointvec)))
+         res <- rbind(res, c(atepoint, quantile(atepointvec, 0.025), quantile(atepointvec, 0.975)))
+         count <- count+1
+     }
+     results <- rbind(results, c(etavec[i], colMedians(res)))
+ }
>
> colnames(results) <- c("eta", "pointest", "lowerci95", "upperci95")
> results <- as.data.frame(results)
>
>
> # Figure 5(b)
> quartz(type="pdf", width=5, height=5, file="output/leadership_q3_sc2.pdf")
> par(mar = c(4,4,0.3,0.3), mgp=c(2.5,1,0), family="CMU Serif")
> plot(1:length(results$pointest), results$pointest, type="n", ylim=c(-1, 1), xlab = expression(eta), ylab="Average Treatment Effect", xaxt="n")
> polygon(c(1:length(results$pointest), rev(1:length(results$pointest))), c(results$lowerci95,rev(results$upperci95)), col="grey", border=NA)
> points(1:length(results$pointest), results$pointest, type="l", lwd=3)
> axis(1, at=seq(1, 100, length.out=6), labels = seq(0, 1, length.out=6), las=2)
> abline(h=0, col = "black", lwd=2)
> lines(c(1,1), c(results$lowerci95[1], results$upperci95[1]), lwd=3)
> points(1, results$pointest[1], pch=16)
> dev.off()
null device
          1
>
```