

Exercise 2: Parametric Regression

Question 1: Use marginal standardization and inverse probability weighting to estimate the average treatment effect of physician group (pg) on perceived asthma quality of care (aqoc) in the `asthma.txt` data.

We start with marginal standardization:

```
library(tidyverse)
library(here)
library(boot)
asthma <- read_delim(here("data", "asthma.txt"))

formulaVars <- "pg+age+sex+educ+insu+severity+com+pcs+mcs"
modelForm <- as.formula(paste0("aqoc ~", formulaVars))
modelForm

## aqoc ~ pg + age + sex + educ + insu + severity + com + pcs +
##      mcs

#' Regress the outcome against the confounders with interaction
ms_model <- glm(modelForm, data=asthma, family=binomial("logit"))

##' Generate predictions for everyone in the sample to obtain
##' unexposed (mu0 predictions) and exposed (mu1 predictions) risks.
mu1 <- predict(ms_model, newdata=transform(asthma, pg=1), type="response")
mu0 <- predict(ms_model, newdata=transform(asthma, pg=0), type="response")

#' Marginally adjusted odds ratio
marg_stand_OR <- (mean(mu1)/mean(1-mu1))/(mean(mu0)/mean(1-mu0))

#' Marginally adjusted risk ratio
marg_stand_RR <- mean(mu1)/mean(mu0)

#' Marginally adjusted risk difference
marg_stand_RD <- mean(mu1)-mean(mu0)
```

```
## Using the bootstrap to obtain confidence intervals for the marginally adjusted  
## risk ratio and risk difference.
```

```
bootfunc <- function(data,index){  
  boot_dat <- data[index,]  
  ms_model <- glm(modelForm,data=boot_dat,family=binomial("logit"))  
  mu1 <- predict(ms_model,newdata=transform(boot_dat,pg=1),type="response")  
  mu0 <- predict(ms_model,newdata=transform(boot_dat,pg=0),type="response")  
  
  marg_stand_OR_ <- (mean(mu1)/mean(1-mu1))/(mean(mu0)/mean(1-mu0))  
  marg_stand_RR_ <- mean(mu1)/mean(mu0)  
  marg_stand_RD_ <- mean(mu1)-mean(mu0)  
  res <- c(marg_stand_RD_,marg_stand_RR_,marg_stand_OR_)  
  return(res)  
}
```

```
## Run the boot function. Set a seed to obtain reproducibility
```

```
set.seed(123)  
boot_res <- boot(asthma,bootfunc,R=2000)  
  
boot_RD <- boot.ci(boot_res,index=1)  
boot_RR <- boot.ci(boot_res,index=2)  
boot_OR <- boot.ci(boot_res,index=3)
```

```
marg_stand_OR
```

```
## [1] 0.5405781
```

```
marg_stand_RR
```

```
## [1] 0.8288345
```

```
marg_stand_RD
```

```
## [1] -0.1295734
```

```
boot_RD
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 2000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot_res, index = 1)
##
## Intervals :
## Level      Normal      Basic
## 95%   (-0.2551, -0.0029 )   (-0.2587, -0.0056 )
##
## Level      Percentile      BCa
## 95%   (-0.2535, -0.0004 )   (-0.2509,  0.0026 )
## Calculations and Intervals on Original Scale
```

```
boot_RR
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 2000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot_res, index = 2)
##
## Intervals :
## Level      Normal      Basic
## 95%   ( 0.6729,  0.9787 )   ( 0.6583,  0.9659 )
##
## Level      Percentile      BCa
## 95%   ( 0.6918,  0.9993 )   ( 0.6958,  1.0028 )
## Calculations and Intervals on Original Scale
```

```
boot_OR
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
```

```
## Based on 2000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot_res, index = 3)
##
## Intervals :
## Level      Normal      Basic
## 95%   ( 0.1601, 0.8820 ) ( 0.0831, 0.8158 )
##
## Level      Percentile      BCa
## 95%   ( 0.2654, 0.9980 ) ( 0.2849, 1.0190 )
## Calculations and Intervals on Original Scale
```

Next we use IP weighting:

```
# create the propensity score in the dataset
asthma$propensity_score <- glm(pg ~ age+sex+educ+insu+severity+com+pcs+mcs, data = asthma, family = binomial)

# stabilized inverse probability weights
asthma$sw <- (mean(asthma$pg)/asthma$propensity_score)*asthma$pg +
  ((1-mean(asthma$pg))/(1-asthma$propensity_score))*(1-asthma$pg)

summary(asthma$sw)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.3794 0.6791 0.7627 0.9904 1.0574 9.6139
```

```
asthma %>% select(pg, aqoc, propensity_score, sw) %>% print(n = 5)
```

```
## # A tibble: 276 x 4
##       pg  aqoc propensity_score    sw
##   <dbl> <dbl>          <dbl> <dbl>
## 1     0     1          0.426 0.657
## 2     0     1          0.512 0.772
## 3     0     1          0.475 0.718
## 4     0     1          0.864 2.78
```

```
## 5      0      0      0.463 0.702
```

```
## # ... with 271 more rows
```

```
model_RD_weighted <- glm(aqoc ~ pg, data = asthma, weights=sw, family = quasibinomial("identity"))
summary(model_RD_weighted)$coefficients
```

```
##              Estimate Std. Error  t value    Pr(>|t|)
## (Intercept)  0.7876281 0.04074641 19.329998 4.161658e-53
## pg          -0.1475234 0.05468054 -2.697915 7.410489e-03
```

```
library(lmtest)
library(sandwich)
coeftest(model_RD_weighted, vcov. = vcovHC)
```

```
##
```

```
## z test of coefficients:
```

```
##
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.787628   0.047849 16.4606  < 2e-16 ***
## pg          -0.147523   0.064762 -2.2779  0.02273 *
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```