EXAMPLE: ANALYSIS OF THE NHANES DATA

In this example, we will explore propensity score based analyses using the publicly available (U.S.) National Health and Nutrition Examination Survey (NHANES). For this, may use the libraries `NHANES`, `tableone`, and `Matching` in `R`. We will focus our analysis on the question of whether current smoking affects average systolic blood pressure. The variables we will need are:

- `BPSysAve` (systolic blood pressure, response),
- `SmokeNow` (smoking status: 0–No, 1–Yes),
- `Gender`,
- `Age`,
- `Race3`,
- `Education`,
- `MaritalStatus`, and
- `Poverty`

where the first two are the outcome and exposure of interest and the remaining are potential confounders. Additionally, we will restrict our attention to adults (> 17 years old) in the second wave of the survey.

```
library(NHANES);library(tableone);library(Matching) #Must be pre-loaded in R
NHANES$SmokeNow <- as.numeric(NHANES$SmokeNow)-1
small.nhanes <- na.omit(NHANES[NHANES$SurveyYr=="2011_12" & NHANES$Age > 17,c(3,4,8:11,13,25,61)])
dim(small.nhanes) ## 1377

+ [1] 1377    9

vars <- c("Gender", "Age", "Race3", "Education", "MaritalStatus", "Poverty")

fit0<-lm(BPSysAve~SmokeNow,data=small.nhanes)
round(coef(summary(fit0)),5)

+              Estimate Std. Error   t value Pr(>|t|)
+ (Intercept) 125.61381    0.63365 198.23993  0.00000
+ SmokeNow     -3.67936    0.96395  -3.81696  0.00014

fit1<-lm(BPSysAve~SmokeNow+Gender+Age+Race3+Education+MaritalStatus+HHIncome+Poverty,data=small.nhanes)
round(drop1(fit1,test='F'),5)

+ Single term deletions
+
+ Model:
+ BPSysAve ~ SmokeNow + Gender + Age + Race3 + Education + MaritalStatus +
+     HHIncome + Poverty
+               Df Sum of Sq    RSS    AIC  F value               Pr(>F)
+ <none>                     324962 7583.7
+ SmokeNow       1       336 325297 7583.1   1.3921              0.23826
+ Gender          1      3133 328095 7594.9  12.9870              0.00033 ***
+ Age             1     67002 391964 7839.8 277.7314 < 0.0000000000000002 ***
+ Race3           5      2495 327457 7584.2   2.0685              0.06680 .
+ Education       4      2982 327944 7588.2   3.0907              0.01515 *
+ MaritalStatus   5      4129 329090 7591.0   3.4228              0.00445 **
+ HHIncome       11     11696 336657 7610.3   4.4072 < 0.0000000000000002 ***
+ Poverty         1      8340 333301 7616.5  34.5697 < 0.0000000000000002 ***
+ ---
+ Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Checking Confounder balance

- In PS–based methods, the goal of the treatment model is to eliminate imbalance in the distribution of covariates between treated and untreated subjects.

  - Achieving balance on other covariates (particularly strong predictors of treatment) is unhelpful.
- The goal is *not* to build an excellent predictive model for the treatment.

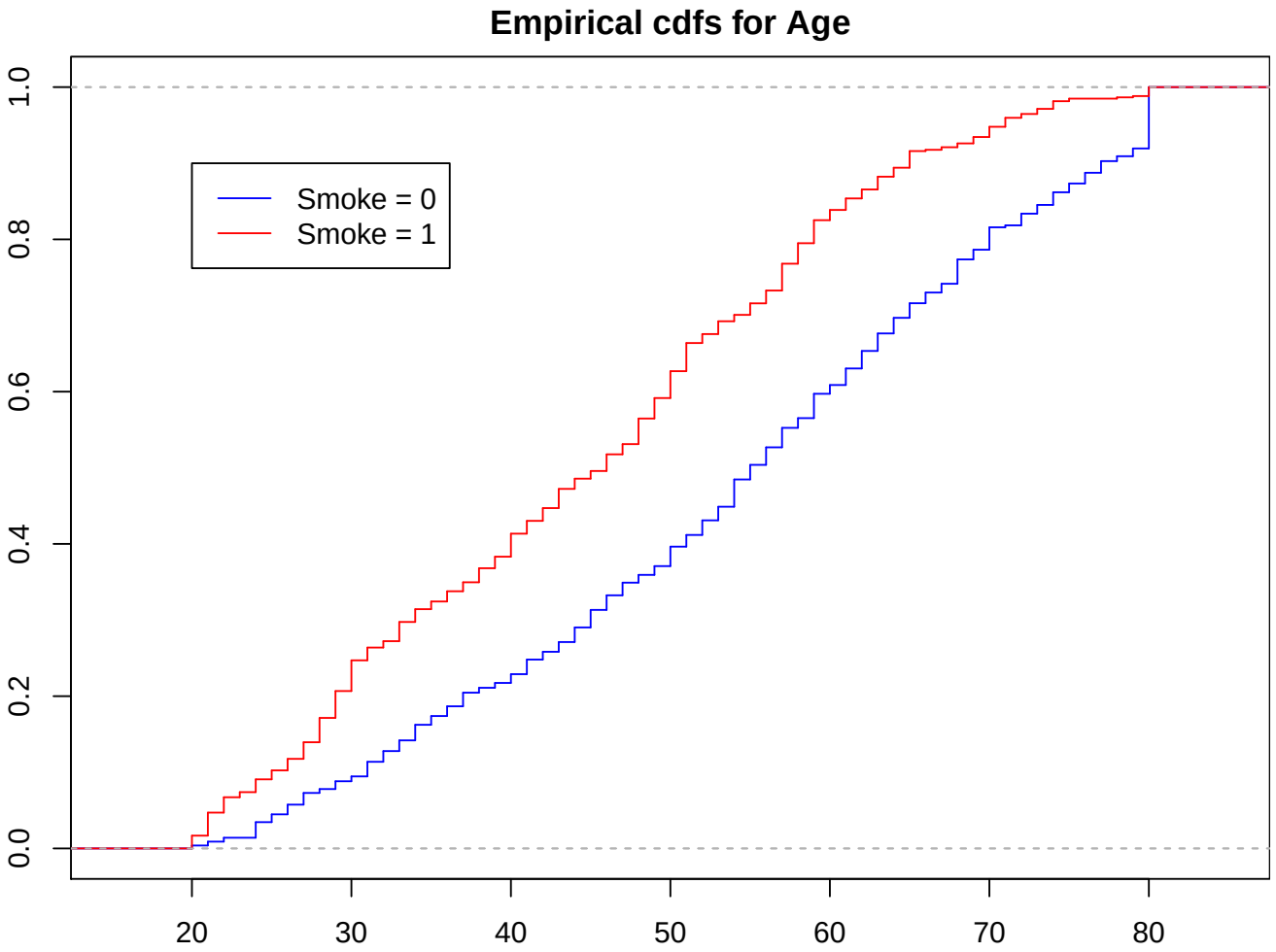
Common measures of balance include:

- Standardized mean difference (SMD) or proportion:

$$\frac{\bar{x}^{1,w} - \bar{x}^{0,w}}{\sqrt{0.5(v^{1,w} + v^{0,w})}} \qquad \text{where} \qquad \bar{x}^{z,w} = \frac{1}{n}\sum_{i=1}^{n} \frac{\mathbb{1}_z(z_i)x_i}{f^{\mathcal{O}}_{Z|X}(z_i|x_i)},$$

  i.e. the weighted sample mean of variable X among those with treatment value z, and similarly $v^{z,w}$ is the weighted variance estimate.
  - For all methods of analysis other than IPW, the weights are taken to be 1 for all subjects.
  - SMD of 0.1 or less typically considered reasonable.
- Visual examination of weighted empirical CDFs among the treated and untreated (for binary or categorical treatment).

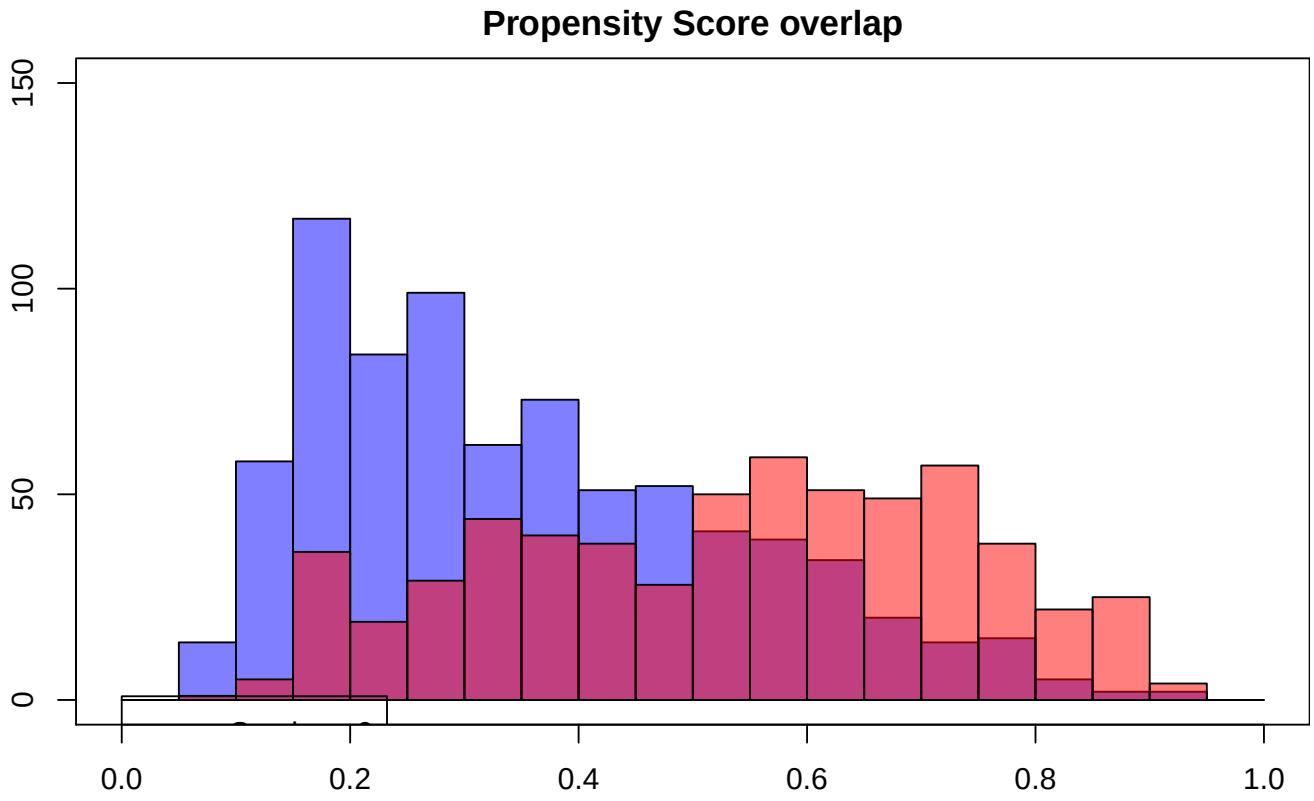
```
tabUnmatched <- CreateTableOne(vars = vars, strata = "SmokeNow", data = small.nhanes, test = FALSE)
print(tabUnmatched, smd = TRUE)

+                      Stratified by SmokeNow
+                       0             1             SMD
+   n                     782           595
+   Gender = male (%)     432 (55.2)    369 (62.0)   0.138
+   Age (mean (SD))     54.33 (16.52) 44.96 (15.11)  0.592
+   Race3 (%)                                        0.315
+      Asian               25 ( 3.2)     15 ( 2.5)
+      Black               43 ( 5.5)     64 (10.8)
+      Hispanic            26 ( 3.3)     38 ( 6.4)
+      Mexican             45 ( 5.8)     35 ( 5.9)
+      White              630 (80.6)    416 (69.9)
+      Other               13 ( 1.7)     27 ( 4.5)
+   Education (%)                                    0.512
+      8th Grade           59 ( 7.5)     33 ( 5.5)
+      9 - 11th Grade      71 ( 9.1)    120 (20.2)
+      High School        152 (19.4)    151 (25.4)
+      Some College       256 (32.7)    210 (35.3)
+      College Grad       244 (31.2)     81 (13.6)
+   MaritalStatus (%)                                0.488
+      Divorced            85 (10.9)     77 (12.9)
+      LivePartner         61 ( 7.8)     96 (16.1)
+      Married            453 (57.9)    240 (40.3)
+      NeverMarried       108 (13.8)    142 (23.9)
+      Separated            6 ( 0.8)     14 ( 2.4)
+      Widowed             69 ( 8.8)     26 ( 4.4)
+   Poverty (mean (SD))  3.11 (1.65)   2.38 (1.58)   0.453

Smoke<-small.nhanes$SmokeNow
age0 <- small.nhanes$Age[Smoke==0]
age1 <- small.nhanes$Age[Smoke==1]
ecdf0 <- ecdf(age0)
ecdf1 <- ecdf(age1)
par(mar=c(2,2,2,0))
plot(ecdf0, verticals=TRUE, do.points=FALSE,main='Empirical cdfs for Age',col='blue')
plot(ecdf1, verticals=TRUE, do.points=FALSE, add=TRUE, col='red')
legend(20,0.9,c('Smoke = 0', 'Smoke = 1'),col=c('blue','red'),lty=1)
```



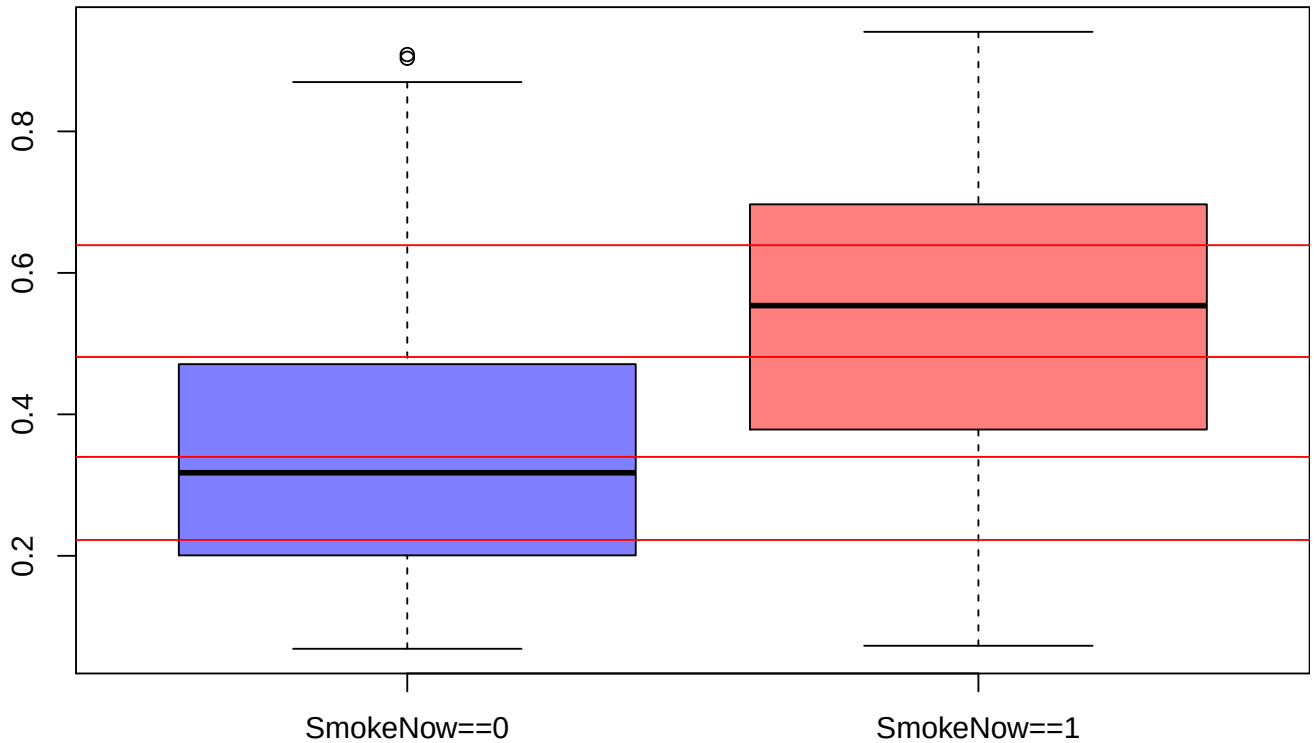
There is clear age imbalance between the two smoking groups. This implies that if Age is also a possible predictor of the outcome, then it is a possible confounder.

Building the propensity score: We attempt to build and assess a propensity score model using the available covariates:

```
ps.mod <- glm(SmokeNow~Gender+Age+Race3+Education+MaritalStatus+HHIncome+Poverty,
              data=small.nhanes,family="binomial")
ps.lr <- predict(ps.mod,type="response")
summary(ps.lr)

+    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
+ 0.06858 0.25228 0.40382 0.43210 0.59621 0.94074

ps0<-ps.lr[Smoke==0]
ps1<-ps.lr[Smoke==1]
quints <- c(0,quantile(ps.lr,seq(.2,1,.2)))
rbind(table(cut(ps.lr[Smoke==0],quints)),
      table(cut(ps.lr[Smoke==1],quints)))

+      (0,0.222] (0.222,0.34] (0.34,0.481] (0.481,0.639] (0.639,0.941]
+ [1,]       231          194          167           121            69
+ [2,]        47           82          105           157           204

par(mar=c(2,2,2,0))
hist(ps0, col=rgb(0,0,1,0.5), breaks=seq(0,1,by=0.05), ylim=c(0,150),
       main="Propensity Score overlap", xlab="PS")
hist(ps1, col=rgb(1,0,0,0.5), breaks=seq(0,1,by=0.05), add=T);box()
legend(0,0.9,c('Smoke = 0', 'Smoke = 1'),col=c(rgb(0,0,1,0.5),rgb(1,0,0,0.5)),lty=1)
```

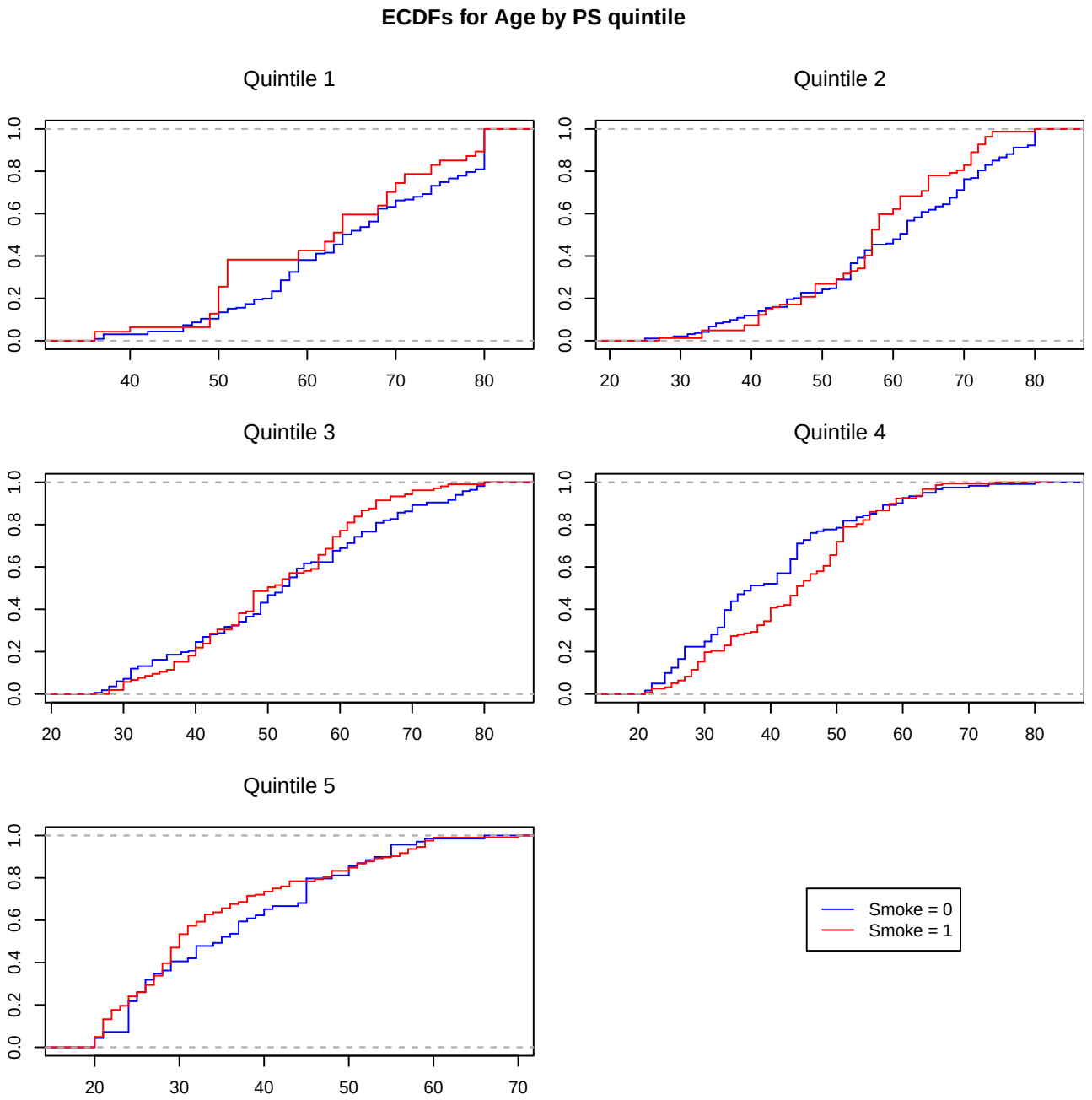



```
boxplot(ps0,ps1,ylab="PS",xlab="Treatment Group",names=c('SmokeNow==0','SmokeNow==1'),
            col=c(rgb(0,0,1,0.5),rgb(1,0,0,0.5)));abline(h=quints[2:5],col="red")
```



We can therefore proceed to check for balance knowing we have sufficient numbers of smokers and non-smokers in each quintile to ensure the stratum-specific estimates are not too unstable.

```r
Pcat<-as.numeric(cut(ps.lr,quints,include.lowest=T))
par(mar=c(2,3,4,0),mfrow=c(3,2),oma=c(0,0,2,0))
for(k in 1:5){
    age0 <- small.nhanes$Age[Smoke==0 & Pcat==k]
    age1 <- small.nhanes$Age[Smoke==1 & Pcat==k]
    ecdf0 <- ecdf(age0)
    ecdf1 <- ecdf(age1)
    plot(ecdf0, verticals=TRUE, do.points=FALSE,
        main=substitute(paste('Quintile ',k),list(k=k)),col='blue')
    plot(ecdf1, verticals=TRUE, do.points=FALSE, add=TRUE, col='red')
}
plot(age0,type='n',ylim=range(0,1),axes=FALSE)
title("ECDFs for Age by PS quintile",outer = TRUE)
legend(30,0.75,c('Smoke = 0', 'Smoke = 1'),col=c('blue','red'),lty=1)
```



Balance does not appear to have been achieved: we have SMDs > 0.1 for at least three quintiles for all variables,

and the empirical CDFs of age do not overlap in several quintiles.

```
W<-(Smoke==0)/(1-ps.lr)+(Smoke==1)/ps.lr
smd.mat<-ExtractSmd(tabUnmatched)
for(k in 1:5){
    nhanesQ<-small.nhanes[Pcat == k,]
    tabQs <- CreateTableOne(vars = vars, strata = "SmokeNow", data = nhanesQ, test = FALSE)
    smd.mat<-cbind(smd.mat,ExtractSmd(tabQs))
}
colnames(smd.mat)<-c('Original','Q1','Q2','Q3','Q4','Q5')
round(smd.mat,4)

+               Original     Q1     Q2     Q3     Q4     Q5
+ Gender          0.1379 0.1017 0.1043 0.0286 0.2003 0.0308
+ Age             0.5918 0.2574 0.1715 0.0993 0.3106 0.1642
+ Race3           0.3148 0.3169 0.1117 0.3444 0.4147 0.2869
+ Education       0.5119 0.5378 0.4167 0.2800 0.2378 0.3018
+ MaritalStatus   0.4877 0.4320 0.2386 0.2725 0.2332 0.2608
+ Poverty         0.4530 0.0865 0.1256 0.1136 0.0041 0.1455
```

We may try to find evidence in smaller PS strata, such as those formed by deciles of the propensity score.

```
dec <- c(0,quantile(ps.lr,seq(0.1,1,.1)))
Pcat10 <- cut(ps.lr,dec,labels=1:10)
SMD.10.table <- ExtractSmd(tabUnmatched)
for(k in 1:10) {
   tabPSdec <- CreateTableOne(vars = vars, strata = "SmokeNow",
             data = small.nhanes[Pcat10==k,], test = FALSE)
   SMD.10.table <- cbind(SMD.10.table,ExtractSmd(tabPSdec))
}
colnames(SMD.10.table)<-c('Original','Q1','Q2','Q3','Q4','Q5','Q6','Q7','Q8','Q9','Q10')
round(SMD.10.table,4)

+               Original     Q1     Q2     Q3     Q4     Q5     Q6     Q7
+ Gender          0.1379 0.0733 0.2857 0.2263 0.1167 0.2086 0.2267 0.2029
+ Age             0.5918 0.4091 0.1160 0.1359 0.1182 0.1356 0.0119 0.0223
+ Race3           0.3148 0.4563 0.5138 0.3124 0.1007 0.4134 0.4281 0.6159
+ Education       0.5119 0.4904 0.6253 0.7638 0.4040 0.5052 0.3837 0.3111
+ MaritalStatus   0.4877 0.6894 0.4963 0.7846 0.4276 0.4922 0.1702 0.2716
+ Poverty         0.4530 0.0340 0.0791 0.1044 0.1343 0.0866 0.1344 0.0347
+                   Q8     Q9    Q10
+ Gender         0.2496 0.0551 0.0850
+ Age            0.6445 0.1597 0.1157
+ Race3          0.3408 0.3786 0.6859
+ Education      0.6091 0.3403 0.5431
+ MaritalStatus 0.4277 0.3800 0.3180
+ Poverty        0.0248 0.0735 0.3522
```

This does not assist with providing evidence of balance.

Matching: We now attempt matching using the propensity score. The function `MatchBalance` from the `Matching` library provides many more details than `CreateTableOne`, including:

- mean, median, and maximum difference in empirical CDF plots,
- mean, median, and maximum difference in empirical QQ plots,
- Kolmogorov-Smirnov statistics,
- ratio of variances,
- p-value for t-test.
- Note that SMDs reported are multiplied by 100.

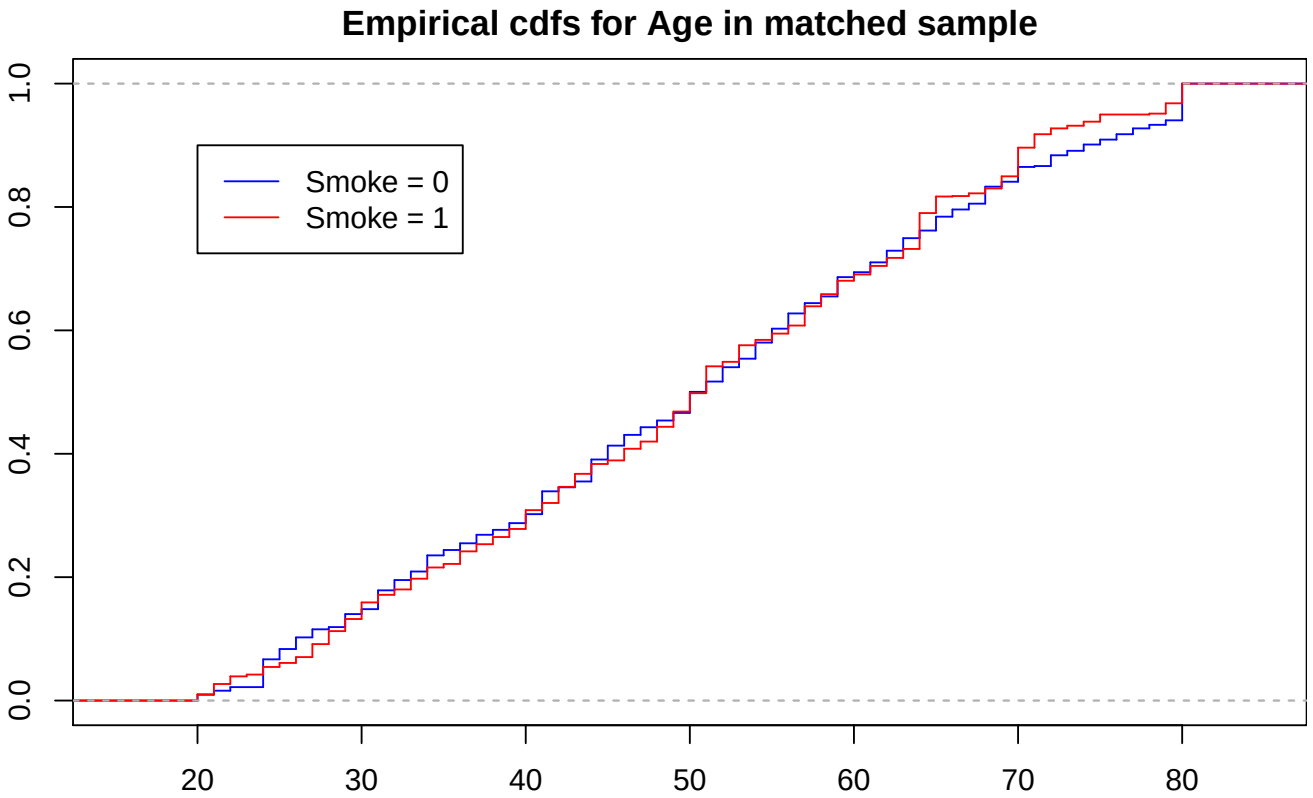
```
small.nhanes$ps.lr<-ps.lr
ps.lr.match <- Match(Tr=small.nhanes$SmokeNow,X=small.nhanes$ps.lr,estimand="ATE",ties=FALSE)
matched.samp <- small.nhanes[c(ps.lr.match$index.control,ps.lr.match$index.treated),]
table(table(c(ps.lr.match$index.control, ps.lr.match$index.treated)))

+
+   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  23  29
+ 841 264 119  51  41  20   9   2   3   3   6   2   4   5   3   1   1   1
+  38
+   1

tabMatched <- CreateTableOne(vars = vars, strata = "SmokeNow",data = matched.samp, test = FALSE)
MatchBalance(SmokeNow~Gender+Age+Education+MaritalStatus+Poverty,data=small.nhanes,match.out=ps.lr.match)

+
+ ***** (V1) Gendermale *****
+                        Before Matching     After Matching
+ mean treatment........    0.62017        0.54394
+ mean control.........    0.55243        0.55483
+ std mean diff.........     13.945        -2.1863
+
+ mean raw eQQ diff.....   0.068908       0.010893
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.033869      0.0054466
+ med  eCDF diff........   0.033869      0.0054466
+ max  eCDF diff........   0.067738       0.010893
+
+ var ratio (Tr/Co).....     0.9531         1.0044
+ T-test p-value........   0.011311        0.55172
+
+
+ ***** (V2) Age *****
+                        Before Matching     After Matching
+ mean treatment........     44.958         50.238
+ mean control.........     54.327         50.418
+ std mean diff.........    -62.015        -1.1114
+
+ mean raw eQQ diff.....     9.3294         1.0174
+ med  raw eQQ diff.....         10              1
+ max  raw eQQ diff.....         14              5
+
+ mean eCDF diff........     0.1536       0.016679
+ med  eCDF diff........    0.15554       0.015251
+ max  eCDF diff........     0.2521       0.051561
+
+ var ratio (Tr/Co).....    0.83608        0.91224
+ T-test p-value........ < 0.00000000000000222         0.7115
+ KS Bootstrap p-value.. < 0.00000000000000222          0.036
+ KS Naive p-value...... < 0.00000000000000222        0.05142
+ KS Statistic.........     0.2521       0.051561
+
+
+ ***** (V3) Education9 - 11th Grade *****
+                        Before Matching     After Matching
+ mean treatment........    0.20168        0.14306
+ mean control.........   0.090793        0.14234
+ std mean diff.........     27.612        0.20733
+
+ mean raw eQQ diff.....    0.11092     0.00072622
+ med  raw eQQ diff.....          0              0
```

```
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.055444     0.00036311
+ med  eCDF diff........   0.055444     0.00036311
+ max  eCDF diff........    0.11089     0.00072622
+
+ var ratio (Tr/Co).....     1.9512         1.0043
+ T-test p-value........ 0.000000014534        0.95522
+
+
+ ***** (V4) EducationHigh School *****
+                         Before Matching     After Matching
+ mean treatment........    0.25378        0.22658
+ mean control..........    0.19437        0.21714
+ std mean diff.........      13.64         2.2544
+
+ mean raw eQQ diff.....   0.060504      0.0094408
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.029704      0.0047204
+ med  eCDF diff........   0.029704      0.0047204
+ max  eCDF diff........   0.059408      0.0094408
+
+ var ratio (Tr/Co).....     1.2098         1.0309
+ T-test p-value........   0.009248        0.54751
+
+
+ ***** (V5) EducationSome College *****
+                         Before Matching     After Matching
+ mean treatment........    0.35294        0.33551
+ mean control..........    0.32737        0.33115
+ std mean diff.........     5.3473        0.92249
+
+ mean raw eQQ diff.....   0.026891      0.0043573
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.012788      0.0021786
+ med  eCDF diff........   0.012788      0.0021786
+ max  eCDF diff........   0.025575      0.0043573
+
+ var ratio (Tr/Co).....     1.0375         1.0066
+ T-test p-value........    0.32201        0.81341
+
+
+ ***** (V6) EducationCollege Grad *****
+                         Before Matching     After Matching
+ mean treatment........    0.13613        0.20334
+ mean control..........    0.31202        0.24473
+ std mean diff.........    -51.246        -10.281
+
+ mean raw eQQ diff.....    0.17479       0.041394
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.087943       0.020697
+ med  eCDF diff........   0.087943       0.020697
+ max  eCDF diff........    0.17589       0.041394
+
+ var ratio (Tr/Co).....    0.54806         0.8764
```

```
+ T-test p-value........ 0.0000000000000013323      0.0030419
+
+
+ ***** (V7) MaritalStatusLivePartner *****
+                        Before Matching     After Matching
+ mean treatment........    0.16134        0.10094
+ mean control..........   0.078005        0.10022
+ std mean diff.........     22.637        0.24098
+
+ mean raw eQQ diff.....   0.084034     0.00072622
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........    0.04167     0.00036311
+ med  eCDF diff........    0.04167     0.00036311
+ max  eCDF diff........   0.083339     0.00072622
+
+ var ratio (Tr/Co).....     1.8822         1.0064
+ T-test p-value........ 0.0000035776        0.94886
+
+
+ ***** (V8) MaritalStatusMarried *****
+                        Before Matching     After Matching
+ mean treatment........    0.40336        0.50327
+ mean control..........    0.57928        0.51561
+ std mean diff.........    -35.831        -2.4683
+
+ mean raw eQQ diff.....    0.17479       0.012346
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.087961      0.0061728
+ med  eCDF diff........   0.087961      0.0061728
+ max  eCDF diff........    0.17592       0.012346
+
+ var ratio (Tr/Co).....    0.98787         1.0009
+ T-test p-value........ 0.000000000073435        0.48218
+
+
+ ***** (V9) MaritalStatusNeverMarried *****
+                        Before Matching     After Matching
+ mean treatment........    0.23866         0.1663
+ mean control..........    0.13811        0.15904
+ std mean diff.........     23.569         1.9496
+
+ mean raw eQQ diff.....    0.10084      0.0072622
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.050274      0.0036311
+ med  eCDF diff........   0.050274      0.0036311
+ max  eCDF diff........    0.10055      0.0072622
+
+ var ratio (Tr/Co).....     1.5271         1.0366
+ T-test p-value........ 0.0000029703        0.59922
+
+
+ ***** (V10) MaritalStatusSeparated *****
+                        Before Matching     After Matching
+ mean treatment........   0.023529       0.013798
+ mean control..........  0.0076726       0.023239
```

```
+ std mean diff.........     10.452        -8.0902
+
+ mean raw eQQ diff.....   0.016807      0.0094408
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........  0.0079284      0.0047204
+ med  eCDF diff........  0.0079284      0.0047204
+ max  eCDF diff........   0.015857      0.0094408
+
+ var ratio (Tr/Co).....     3.0189        0.59949
+ T-test p-value........   0.022929       0.068587
+
+
+ ***** (V11) MaritalStatusWidowed *****
+                         Before Matching     After Matching
+ mean treatment........   0.043697       0.093682
+ mean control..........   0.088235       0.069717
+ std mean diff.........    -21.769         8.2216
+
+ mean raw eQQ diff.....   0.043697       0.023965
+ med  raw eQQ diff.....          0              0
+ max  raw eQQ diff.....          1              1
+
+ mean eCDF diff........   0.022269       0.011983
+ med  eCDF diff........   0.022269       0.011983
+ max  eCDF diff........   0.044538       0.023965
+
+ var ratio (Tr/Co).....    0.51964         1.3091
+ T-test p-value........ 0.00073816       0.018023
+
+
+ ***** (V12) Poverty *****
+                         Before Matching     After Matching
+ mean treatment........     2.3776         2.6524
+ mean control..........     3.1091         2.7301
+ std mean diff.........    -46.293        -4.7739
+
+ mean raw eQQ diff.....      0.728        0.10669
+ med  raw eQQ diff.....        0.7            0.1
+ max  raw eQQ diff.....       1.65           0.39
+
+ mean eCDF diff........    0.13667       0.022172
+ med  eCDF diff........    0.15502       0.023239
+ max  eCDF diff........    0.20409       0.056645
+
+ var ratio (Tr/Co).....    0.91853         1.0015
+ T-test p-value........ 0.00000000000000022204         0.1612
+ KS Bootstrap p-value.. < 0.000000000000000222          0.022
+ KS Naive p-value...... 0.0000000000011907       0.024109
+ KS Statistic..........    0.20409       0.056645
+
+
+ Before Matching Minimum p.value: < 0.000000000000000222
+ Variable Name(s): Age Poverty  Number(s): 2 12
+
+ After Matching Minimum p.value: 0.0030419
+ Variable Name(s): EducationCollege Grad  Number(s): 6
```

```r
age0 <- matched.samp$Age[matched.samp$SmokeNow==0]
age1 <- matched.samp$Age[matched.samp$SmokeNow==1]
ecdf0 <- ecdf(age0)
ecdf1 <- ecdf(age1)
par(mar=c(2,2,2,0))
plot(ecdf0, verticals=TRUE, do.points=FALSE,main='Empirical cdfs for Age in matched sample',col='blue')
plot(ecdf1, verticals=TRUE, do.points=FALSE, add=TRUE, col='red')
legend(20,0.9,c('Smoke = 0', 'Smoke = 1'),col=c('blue','red'),lty=1)
```



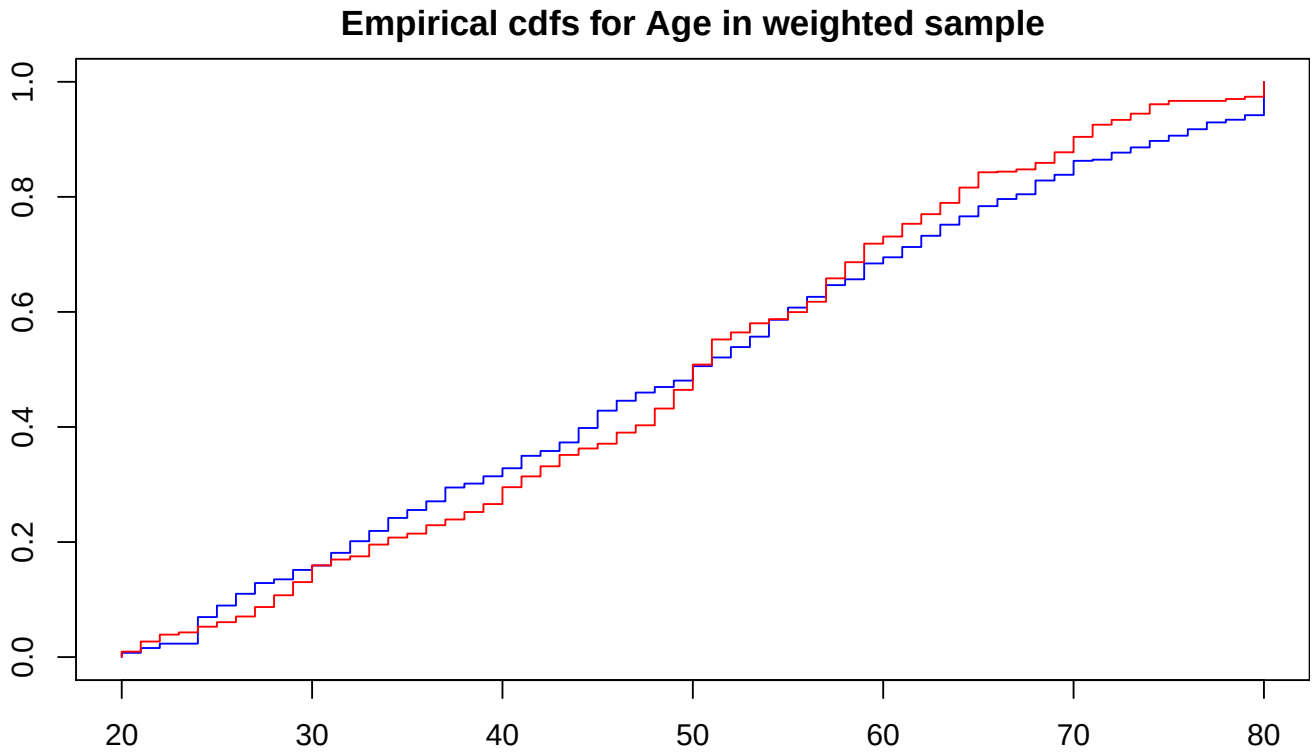
Inverse Weighting: We can construct an inverse weighted (IPW) sample and examine it using the `survey` and `Hmisc` packages.

```r
library(survey);library(Hmisc);library(htmlwidgets) #Must be pre-loaded in R
ps.lr.weight <- small.nhanes$SmokeNow/ps.lr + (1-small.nhanes$SmokeNow)/(1-ps.lr)
nhanes.IPW.lr <- svydesign(ids=~0, data=small.nhanes, weights=ps.lr.weight)
tabIPW <- svyCreateTableOne(vars = vars, strata = "SmokeNow",data = nhanes.IPW.lr, test = FALSE)
print(tabIPW, smd = TRUE)
```

```
+                      Stratified by SmokeNow
+                       0               1               SMD
+   n                    1379.0          1379.7
+   Gender = male (%)     797.4 (57.8)    781.8 (56.7)   0.023
+   Age (mean (SD))       50.06 (17.16)   49.83 (15.42)  0.014
+   Race3 (%)                                            0.052
+      Asian               40.4 ( 2.9)     37.9 ( 2.7)
+      Black              119.0 ( 8.6)    103.3 ( 7.5)
+      Hispanic            75.5 ( 5.5)     70.6 ( 5.1)
+      Mexican             81.2 ( 5.9)     87.9 ( 6.4)
+      White             1019.8 (74.0)   1038.8 (75.3)
+      Other               43.0 ( 3.1)     41.2 ( 3.0)
+   Education (%)                                        0.029
+      8th Grade           89.4 ( 6.5)     96.2 ( 7.0)
+      9 - 11th Grade     184.6 (13.4)    185.8 (13.5)
```

```
+      High School        293.9 (21.3)    285.5 (20.7)
+      Some College       482.7 (35.0)    474.2 (34.4)
+      College Grad       328.4 (23.8)    338.1 (24.5)
+   MaritalStatus (%)                                   0.023
+      Divorced           161.0 (11.7)    165.1 (12.0)
+      LivePartner        154.6 (11.2)    150.8 (10.9)
+      Married            695.0 (50.4)    690.1 (50.0)
+      NeverMarried       249.9 (18.1)    254.0 (18.4)
+      Separated           23.1 ( 1.7)     20.5 ( 1.5)
+      Widowed             95.4 ( 6.9)     99.2 ( 7.2)
+   Poverty (mean (SD))    2.80 (1.67)     2.80 (1.63)  <0.001
```

```
temp0 <- Ecdf(small.nhanes$Age[Smoke==0],weights=ps.lr.weight[Smoke==0],pl=FALSE)
temp1 <- Ecdf(small.nhanes$Age[Smoke==1],weights=ps.lr.weight[Smoke==1],pl=FALSE)
par(mar=c(2,2,2,0))
plot(temp0$x,temp0$y,ylab="ECDF(Age)",xlab="Age",
       main='Empirical cdfs for Age in weighted sample',col='blue',type="s",lwd=1)
lines(temp1$x,temp1$y,col="red",lwd=1,type='s')
```




```
smd.mat<-cbind(smd.mat,ExtractSmd(tabMatched))
smd.mat<-cbind(smd.mat,ExtractSmd(tabIPW))
colnames(smd.mat)<-c('Original','Q1','Q2','Q3','Q4','Q5',"Match",'IPW')
round(smd.mat,4)
```

```
+               Original     Q1     Q2     Q3     Q4     Q5  Match    IPW
+ Gender          0.1379 0.1017 0.1043 0.0286 0.2003 0.0308 0.0219 0.0235
+ Age             0.5918 0.2574 0.1715 0.0993 0.3106 0.1642 0.0109 0.0139
+ Race3           0.3148 0.3169 0.1117 0.3444 0.4147 0.2869 0.1172 0.0516
+ Education       0.5119 0.5378 0.4167 0.2800 0.2378 0.3018 0.1320 0.0292
+ MaritalStatus   0.4877 0.4320 0.2386 0.2725 0.2332 0.2608 0.1155 0.0235
+ Poverty         0.4530 0.0865 0.1256 0.1136 0.0041 0.1455 0.0478 0.0001
```

Here the matched and inverse weighted samples exhibit good balance.

Summary:

- Creating or restoring confounder balance is essential to estimating a causal effect.
- It can be hard to assess overlap or achieve balance in high dimensions.
- The propensity score, a scalar summary of confounding variables, simplifies this task.
- However:
  - fitting a model for treatment does not guarantee balance,
  - fitting a model that predicts treatment with a high degree of precision can be unhelpful.

Estimating the ATE: We proceed now to estimating the average treatment effect (ATE), using:

- outcome regression,
- PS stratification,
- PS matching,
- PS regression,
- IPW.

We will use the PS estimated via logistic regression, as this provided the best balance.

- **Linear regression:**

```
coef(lm(BPSysAve~SmokeNow,data=small.nhanes))[2]
+  SmokeNow
+ -3.679357
coef(lm(BPSysAve~SmokeNow+Gender+Age+Race3+Education+MaritalStatus+HHIncome+Poverty,data=small.nhanes)
+  SmokeNow
+ -1.097768
```

  The naive conditional effect estimate is more than 3 times greater than its confounder-adjusted counterpart.

- **Outcome regression no interaction:**

```
nhanes.allsmoke <- small.nhanes
nhanes.allsmoke$SmokeNow <- 1
nhanes.nosmoke <- small.nhanes
nhanes.nosmoke$SmokeNow <- 0
mod1.lm <- lm(BPSysAve~SmokeNow+Gender+Age+Race3+Education+MaritalStatus+HHIncome+Poverty,
      data=small.nhanes)
APO.lm.1 <- mean(predict(mod1.lm,nhanes.allsmoke))
APO.lm.0 <- mean(predict(mod1.lm,nhanes.nosmoke))
APO.lm.1 - APO.lm.0
+ [1] -1.097768
```

  Conditional and marginal effect are the same in a linear model with no interaction.

- **Outcome regression with interactions:**

```
mod1.lmX <- lm(BPSysAve~SmokeNow+Gender+Age+Race3+Education+
     MaritalStatus+HHIncome+Poverty+SmokeNow:HHIncome+SmokeNow:Gender+SmokeNow:Age,data=small.nhanes)
APO.lmX.1 <- mean(predict(mod1.lmX,nhanes.allsmoke))
APO.lmX.0 <- mean(predict(mod1.lmX,nhanes.nosmoke))
APO.lmX.1 - APO.lmX.0
+ [1] -1.402538
```

- **PS stratification**

```
Y<-small.nhanes$BPSysAve
ps.lr.quints <- cut(ps.lr,quints,labels=1:5)
p.strat <- table(ps.lr.quints)/length(ps.lr.quints)
ATE.strat <- rep(NA,5)
for(j in 1:5) {
    ATE.strat[j] <- mean(Y[Smoke == 1 & ps.lr.quints==j])-mean(Y[Smoke == 0 & ps.lr.quints==j])
}
ATE.strat
```

```
+ [1] -8.1736207 -2.2701785 -0.2062732 -1.1820287  2.8633845
sum(ATE.strat*p.strat)
+ [1] -1.816879
```

- **PS matching**

```
ps.lr.match <- Match(Tr=small.nhanes$SmokeNow,
      X=small.nhanes$ps.lr,estimand="ATE",ties=FALSE)
matched.samp <- small.nhanes[c(ps.lr.match$index.control,ps.lr.match$index.treated),]

dim(matched.samp)
+ [1] 2754   10
mean(matched.samp$BPSysAve[matched.samp$SmokeNow == 1]) -
    mean(matched.samp$BPSysAve[matched.samp$SmokeNow == 0])
+ [1] -0.7850399
```

- **PS regression**

```
library(splines)
mod1.PSlm1 <- lm(BPSysAve~SmokeNow+ps.lr,data=small.nhanes)
APO.PSlm1.1 <- mean(predict(mod1.PSlm1,nhanes.allsmoke))
APO.PSlm1.0 <- mean(predict(mod1.PSlm1,nhanes.nosmoke))
APO.PSlm1.1 - APO.PSlm1.0
+ [1] -1.10791
mod1.PSlm2 <- lm(BPSysAve~SmokeNow+ps.lr+I(ps.lr^2),
     data=small.nhanes)
APO.PSlm2.1 <- mean(predict(mod1.PSlm2,nhanes.allsmoke))
APO.PSlm2.0 <- mean(predict(mod1.PSlm2,nhanes.nosmoke))
APO.PSlm2.1 - APO.PSlm2.0
+ [1] -1.110337
mod1.PSlm3 <- lm(BPSysAve~SmokeNow+bs(ps.lr,df=4),
     data=small.nhanes)
APO.PSlm3.1 <- mean(predict(mod1.PSlm3,nhanes.allsmoke))
APO.PSlm3.0 <- mean(predict(mod1.PSlm3,nhanes.nosmoke))
APO.PSlm3.1 - APO.PSlm3.0
+ [1] -1.133493
```

- **IPW**

```
ps.lr.weight <- Smoke/ps.lr + (1-Smoke)/(1-ps.lr)
mean(Smoke*Y*ps.lr.weight) -mean((1-Smoke)*Y*ps.lr.weight)
+ [1] -1.928655
coef(lm(Y ~ Smoke, weights = ps.lr.weight))[2]
+     Smoke
+ -1.991233
```

Additional considerations:

- All of the PS approaches considered rely on substitution estimators.
  - In PS regression, we plug in an estimated PS as a covariate.
  - In IPW, we plug in estimated weights.
- We need to account for this when estimating standard errors and/or confidence intervals.
- Analytically derived asymptotic variances can be used, but are not provided in many standard software packages.
- The easiest approach is to bootstrap.
- Note, however, that the bootstrap is *not* valid for matching.