Statistical Adjustment and Assessment of Adjustment in Observational Studies

ICPSR 2018 Session 2

August 02, 2018

```
Warning: package 'dplyr' was built under R version 3.5.1
```

Today

1. Agenda: The problem of covariance adjustment to reduce "bias"/ confounding. **How can we answer the question about whether we have adjusted enough.** A simple approach: stratification on one categorical variable (and interaction effects). A more complex approach: find sets that are as similar as possible in terms of a continuous variable (bipartite matching). Balance assessment after stratification.
2. Reading for tomorrow and next week: DOS 8–9, 13 and Gelman and Hill, 2006, § 9.5, and Ho et al., 2007
3. Questions arising from the reading or assignments or life?

1. Strategies for Causal Inference
2. But first, how to assess the randomization process in an experiment.
3. Did we control for enough?

Strategies and Workflow for randomized studies

Before fielding the study

- Plan the design for interpretability and power.
- Pre-register your analysis plan and experimental design.

After outcome data have been collected

- Make the case that randomization worked.
- Increase precision with design and test statistics (and even models of effects)
- Make sure that your estimator is estimating the right thing (i.e. is not biased or at least is consistent)
- Make sure that your test has a controlled false positive rate and is as powerful as possible (i.e. the coverage rate of a confidence interval is nominal, the Type I error rate is controlled).

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Strategies for Adjustment of Observational Studies

- If you have randomized Z but not D, then IV. (Not really an observational study.)
- Find a discontinuity/A Natural Experiment (RDD: either natural experiment or continuous forcing function)
- Multiple controls (i.e. "Choice as an alternative to control" Rosenbaum, 1999)
- "Controlling For"
- Difference in Differences
- Matched Stratification (approximating a block-randomized experiment)
- Best matched subset selection (approximating a completely or simply randomized experiment)
- Weighting
- Direct theoretical modeling / Directed Acyclic Graphs (DAGS) to guide other data modeling choices.

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2. But first, how to assess the randomization process in an experiment.
3. Did we control for enough?

The Neyman-Rubin Model for (simple) experiments

This is what randomization ensures:

$$(Y_t, Y_c, X) \perp Z$$

I.e., each of X, Y_c and Y_t is balanced between treatment and control groups (in expectation; given variability from randomization).

- In controlled experiments, random assignment warrants this.
- In natural experiments, justified otherwise, this is an article of faith.
- In an experiment, the *x*es aren't necessary for inference (although they can be used, carefully, to increase precision in both the design and analysis phases of a project).
- **However, the part with the *x*es has testable consequences.**

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Covariate balance in experiments

- Arceneaux, 2005
- Kansas City, November 2003
- Completely randomized design: 14 precincts $\rightarrow$ Tx; 14 $\rightarrow$ Control.
- Substantively large baseline differences
- Differences not large compared to other possible assignments from same design; compared to other possible experiments with the same design.
- $\mathbf{Pr}(\chi^2 > x) = .91$ (Hansen and Bowers, 2008).

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How did we do this?

```
acorn <- read.csv("data/acorn03.csv", row.names=1)
xb1 <- xBalance(z ~ v_p2003 + v_m2003 + v_g2002 + v_p2002 + v_m2002 + v_s2001 +
         v_g2000 + v_p2000 + v_m2000 + v_s1999 + v_m1999 + v_g1998 +
         v_m1998 + v_s1998 + v_m1997 + v_s1997 + v_g1996 + v_p1996 +
         v_m1996 + v_s1996 + size, data=acorn,
         report = 'all')

xb1$results
```

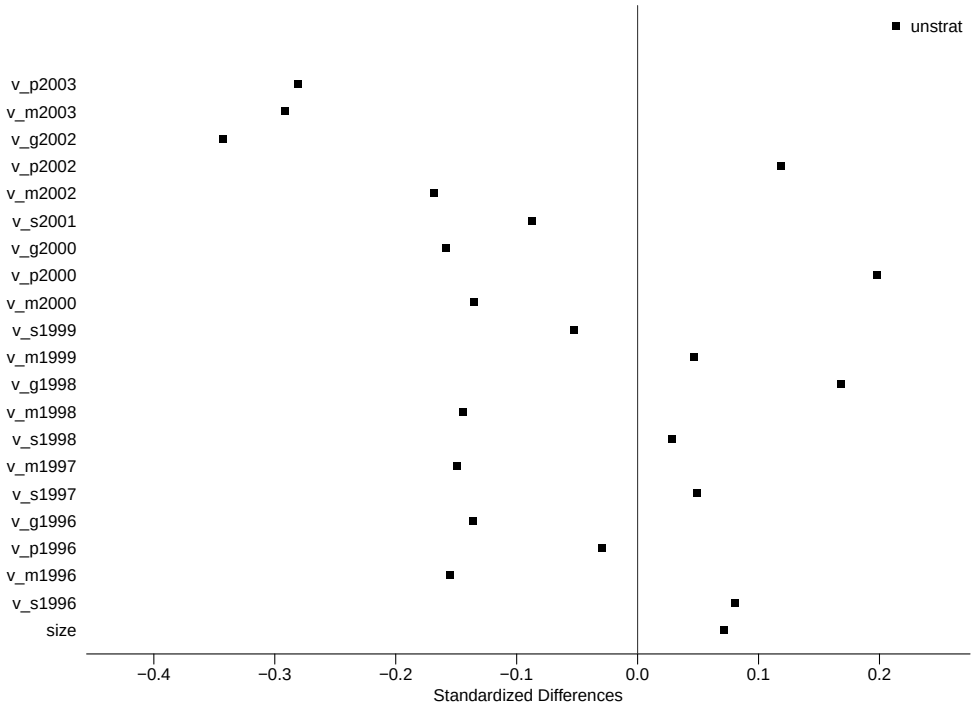
```
, , strata = unstrat

         stat
vars        Control Treatment  adj.diff adj.diff.null.sd std.diff        z      p
  v_p2003   0.12996   0.11949 -0.010469         0.013994 -0.28041 -0.74815 0.4544
  v_m2003   0.36868   0.34561 -0.023072         0.029669 -0.29171 -0.77763 0.4368
  v_g2002   0.65195   0.63083 -0.021119         0.023207 -0.34283 -0.91003 0.3628
  v_p2002   0.21589   0.22187  0.005980         0.018757  0.11848  0.31883 0.7499
  v_m2002   0.15567   0.14766 -0.008016         0.017721 -0.16841 -0.45233 0.6510
  v_s2001   0.26898   0.26327 -0.005709         0.024302 -0.08722 -0.23492 0.8143
  v_g2000   0.86812   0.85755 -0.010576         0.024878 -0.15821 -0.42512 0.6707
  v_p2000   0.20033   0.21106  0.010735         0.020187  0.19827  0.53177 0.5949
  v_m2000   0.14404   0.13849 -0.005552         0.015249 -0.13536 -0.36405 0.7158
  v_s1999   0.42957   0.42569 -0.003887         0.027343 -0.05275 -0.14216 0.8870
  v_m1999   0.31756   0.32012  0.002559         0.020532  0.04624  0.12463 0.9008
  v_g1998   0.43718   0.44900  0.011824         0.026134  0.16844  0.45243 0.6510
  v_m1998   0.18136   0.17315 -0.008210         0.021114 -0.14463 -0.38886 0.6974
  v_s1998   0.24104   0.24254  0.001496         0.019385  0.02863  0.07719 0.9385
  v_m1997   0.13388   0.12856 -0.005326         0.013300 -0.14898 -0.40047 0.6888
  v_s1997   0.15490   0.15659  0.001684         0.012635  0.04945  0.13327 0.8940
```

How did we do this?

```
xb1$overall
```

```
        chisquare df p.value
unstrat     12.93 21   0.911
```

```
plot(xb1)
```



DeMystifying xBalance

```
d.stat<-function(zz, mm, ss){
  ## this is the d statistic (harmonic mean weighted diff of means statistic)
  ## from Hansen and Bowers 2008
  h.fn<-function(n, m){(m*(n-m))/n}
  myssn<-apply(mm, 2, function(x){sum((zz-unsplit(tapply(zz, ss, mean), ss))*x)})
  hs<-tapply(zz, ss, function(z){h.fn(m=sum(z), n=length(z))})
  mywtsum<-sum(hs)
  myadjdiff<-myssn/mywtsum
  return(myadjdiff)
}
```

Calculate the reference distribution of the d-stat and the d^2 stat

Does d^2 follow a χ^2 distribution in this case?

For all vectors $z \in \Omega$ get adj.diffs. This is the distribution of the d statistic

```
acorncovs<-c("v_p2003","v_m2003","v_g2002","v_p2002","v_m2002","v_s2001","v_g2000","v_p2000","v_
d.dist<-replicate(10000, d.stat(sample(acorn$z), acorn[,acorncovs], ss=rep(1,nrow(acorn))))
```

Get the randomization-based *p*-values:

```
xb1ds <- xb1$results[,"adj.diff",]
xb1ps <- xb1$results[,"p",]
obs.d<-d.stat(acorn$z, acorn[, acorncovs], rep(1,nrow(acorn)))
dps <- matrix(NA,nrow=length(obs.d),ncol=1)
for(i in 1:length(obs.d)){
  dps[i,] <- 2*min( mean(d.dist[i,] >= obs.d[i]),mean(d.dist[i,] <= obs.d[i]))
}
## You can compare this to the results from xBalance
round(cbind(randinfps=dps[,1],xbps=xb1ps,obsdstats=obs.d,xbdstats=xb1ds),3)
```

```
         randinfps  xbps obsdstats xbdstats
v_p2003      0.454 0.454    -0.010   -0.010
v_m2003      0.450 0.437    -0.023   -0.023
v_g2002      0.384 0.363    -0.021   -0.021
v_p2002      0.775 0.750     0.006    0.006
v_m2002      0.656 0.651    -0.008   -0.008
v_s2001      0.801 0.814    -0.006   -0.006
v_g2000      0.726 0.671    -0.011   -0.011
v_p2000      0.612 0.595     0.011    0.011
```

Calculate the reference distribution of the d-stat and the d^2 stat

The d^2 statistic is a linear function of the d-statistics that accounts for the covariance between those statistics (across the possible assignments under the null hypothesis of no effects).

```
d2.stat <- function(dstats,ddist=NULL,theinvcov=NULL){
  ## d is the vector of d statistics
  ## ddist is the matrix of the null reference distributions of the d statistics
  if(is.null(theinvcov) & !is.null(ddist)){
    as.numeric( t(dstats) %*% solve(cov(t(ddist))) %*% dstats)
  } else {
    as.numeric( t(dstats) %*% theinvcov %*% dstats)
  }
}
```

Calculate the reference distribution of the d-stat and the d^2 stat

The distribution of the d^2 statistic arises from the distribution of the d statistics — for each draw from the set of treatment assignments we can collapse the d-statistics into one d^2. And so we can calculate the p-value for the d^2.

```
## Here we have the inverse of the covariance/variance matrix of the d statistics
invCovDDist <- solve(cov(t(d.dist)))
obs.d2<- d2.stat(obs.d,d.dist,invCovDDist)

d2.dist<-apply(d.dist, 2, function(thed){
                  d2.stat(thed,theinvcov=invCovDDist)
          })
## The chi-squared reference distribution only uses a one-sided p-value going in the positive di
d2p<-mean(d2.dist>=obs.d2)
cbind(obs.d2,d2p)
```

```
     obs.d2    d2p
[1,]  12.78 0.9934
```

```
xb1$overall
```

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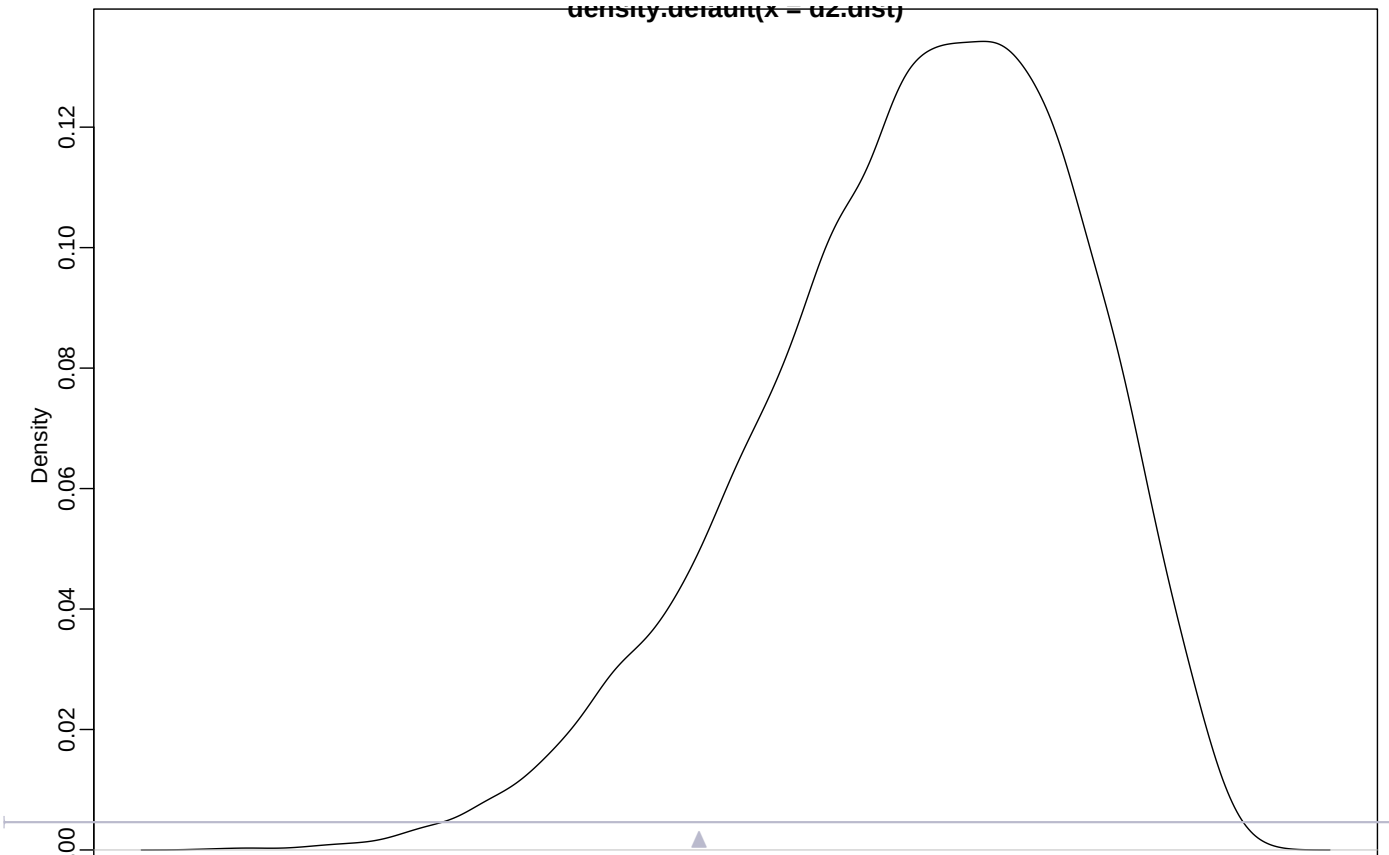
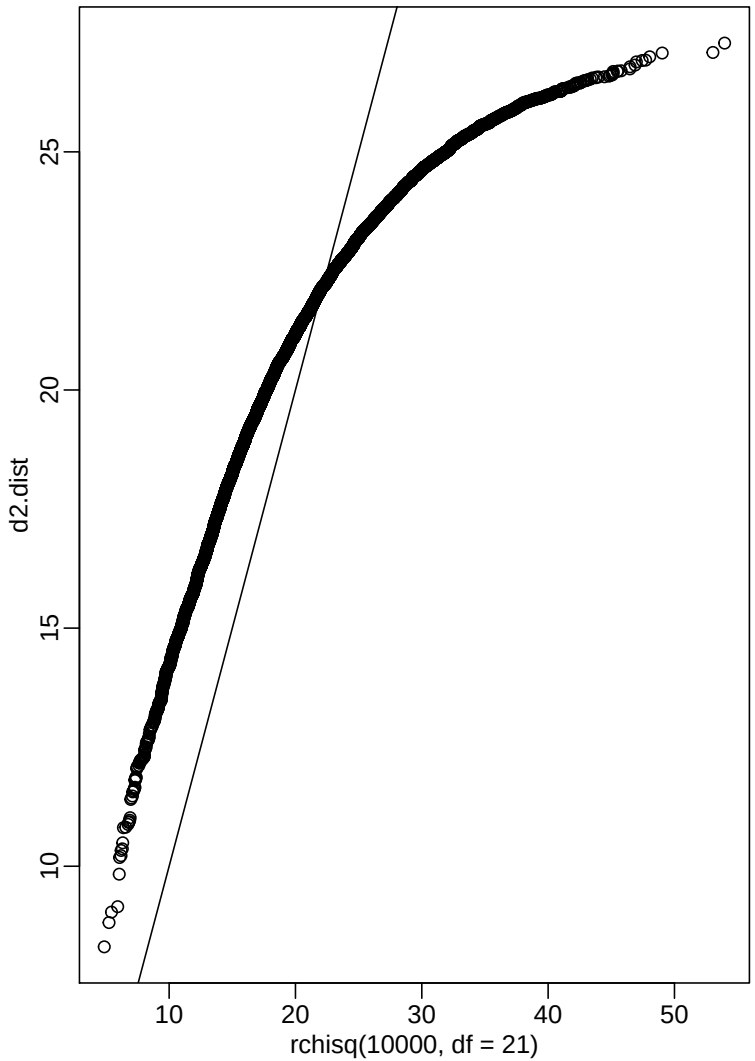
The distribution of the d^2 statistic arises from the distribution of the d statistics — for each draw from the set of treatment assignments we can collapse the d-statistics into one d^2. And so we can calculate the p-value for the d^2.

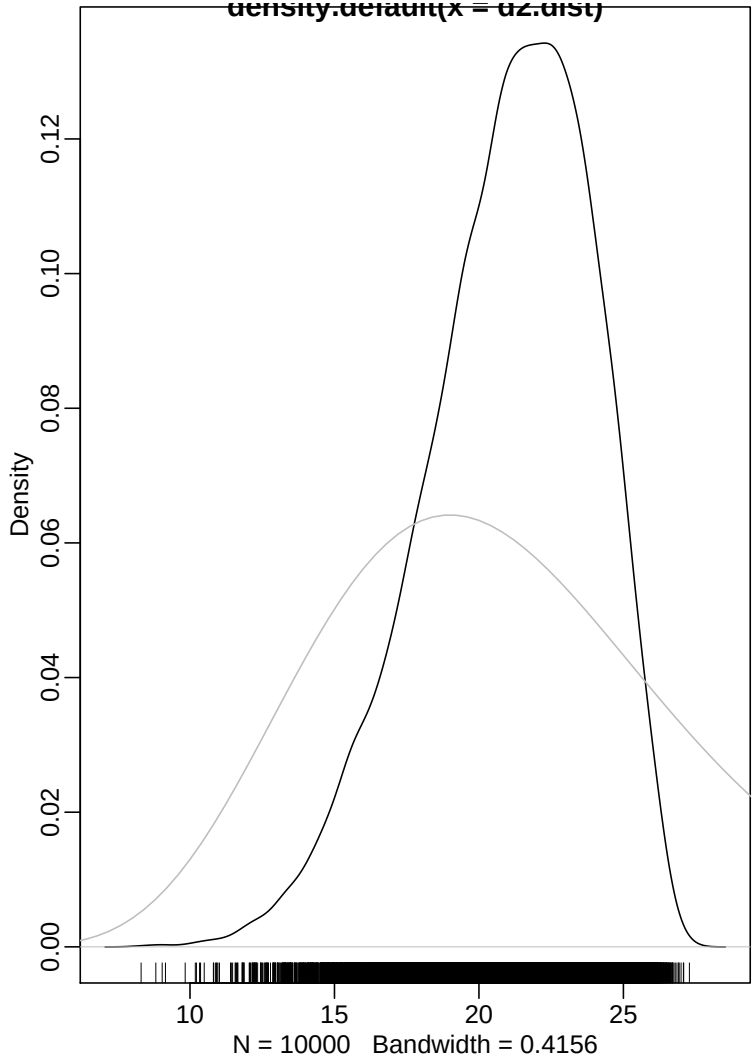
```
plot(density(d2.dist))
rug(d2.dist)
```



Why differences between xBalance and d2?

I suspect that $N = 28$ is too small. `xBalance` uses an asymptotic approximation to the randomization distribution.





Does xBalance have a controlled false positive rate here?

```
xbfn <- function(){
    acorn$newz <- sample(acorn$z)
    xb1 <- xBalance(newz ~ v_p2003 + v_m2003 + v_g2002 + v_p2002 + v_m2002 + v_s2001 +
            v_g2000 + v_p2000 + v_m2000 + v_s1999 + v_m1999 + v_g1998 +
            v_m1998 + v_s1998 + v_m1997 + v_s1997 + v_g1996 + v_p1996 +
            v_m1996 + v_s1996 + size, data=acorn,
        report = 'chisquare.test')
    return(xb1$overall[["p.value"]])
}

res <- replicate(1000,xbfn())
```

```
summary(res)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  0.192   0.331   0.432   0.459   0.558   0.976
```

```
mean(res <= .05)
```

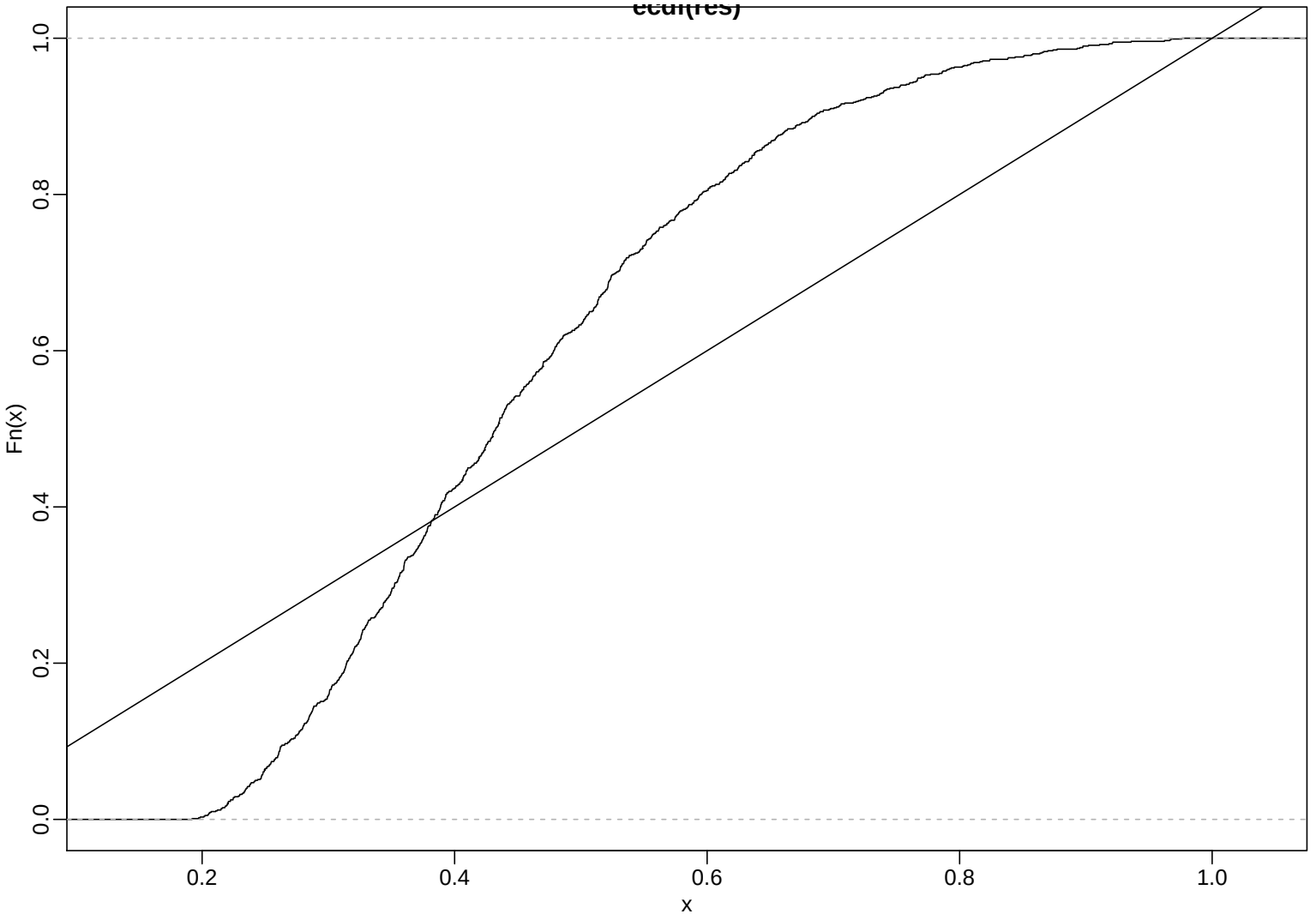
```
[1] 0
```

```
mean(res <= .2)
```

```
[1] 0.003
```

Does xBalance have a controlled false positive rate here?

```
plot(ecdf(res))
abline(0,1)
```



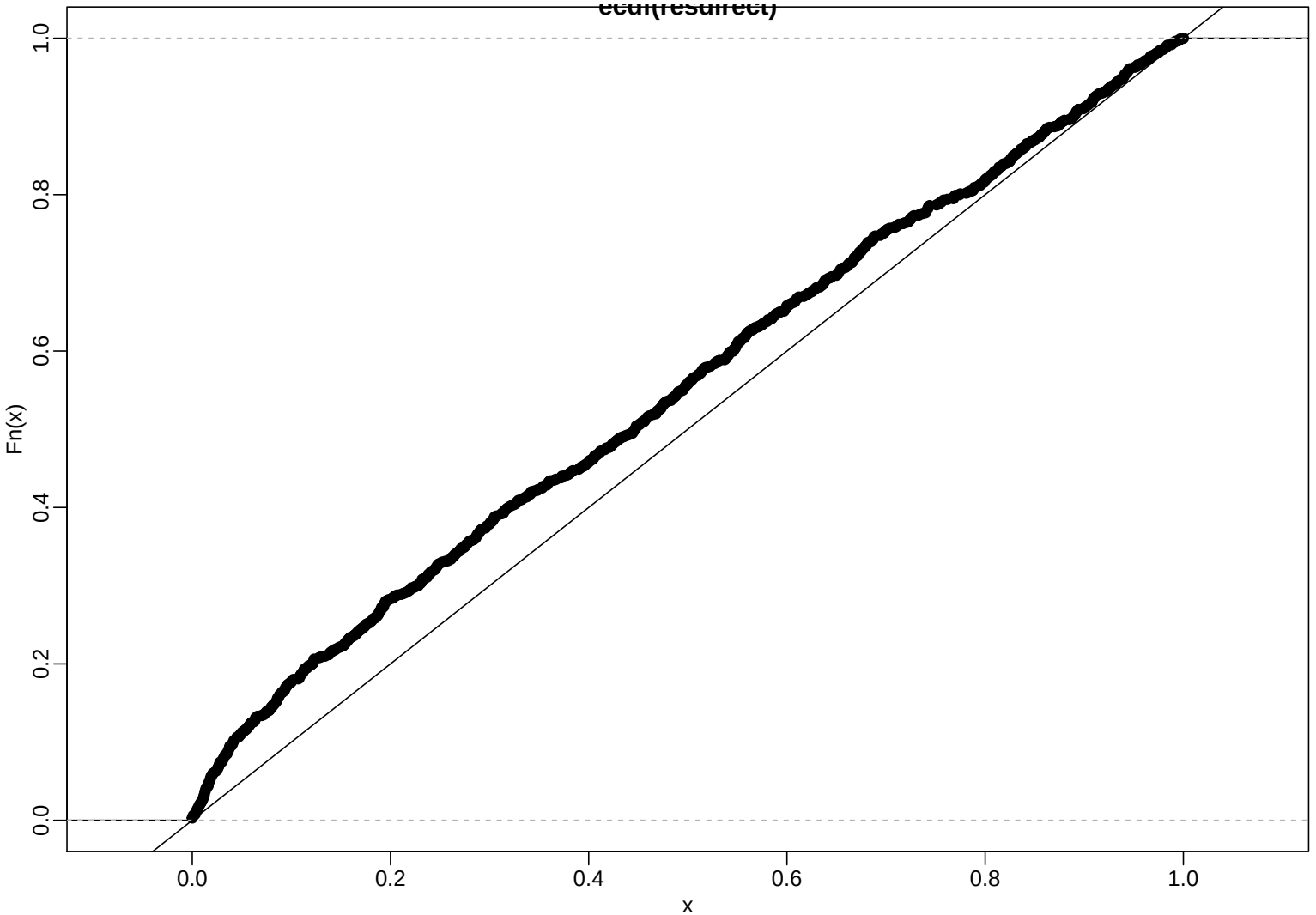
Does the simulation based approach have a controlled false positive rate here?

```
d2pfn <- function(z,X){
    newz <- sample(z)

    d.dist<-replicate(1000, d.stat(sample(newz), X, ss=rep(1,nrow(X))))

    obs.d<-d.stat(newz, X, rep(1,nrow(X)))

    dps <- matrix(NA,nrow=length(obs.d),ncol=1)
    for(i in 1:length(obs.d)){
        dps[i,] <- 2*min( mean(d.dist[i,] >= obs.d[i]),mean(d.dist[i,] <= obs.d[i]))
    }

    invCovDDist <- solve(cov(t(d.dist)))
    obs.d2<- d2.stat(obs.d,d.dist,invCovDDist)

    d2.dist<-apply(d.dist, 2, function(thed){
                   d2.stat(thed,theinvcov=invCovDDist)
        })

    d2p<-mean(d2.dist>=obs.d2)

    return(d2p)
}
```

```
resdirect <- replicate(1000,d2pfn(z=acorn$z,X=acorn[,acorncovs]))
```

Does xBalance have a controlled false positive rate here?

```
plot(ecdf(resdirect))
abline(0,1)
```



1. Strategies for Causal Inference
2. But first, how to assess the randomization process in an experiment.
3. Did we control for enough?

Introducing the Medellin Data

```
load(url("http://jakebowers.org/Data/meddat.rda"))
```

The data Cerdá collected tell us about the roughly 45 neighborhoods in the study, 22 of which had access to the Metrocable line and 23 did not.
We don't have a formal codebook. Here are some guesses about the meanings of some of the variables. There are more variables in the data file than those listed here.

```
## The Intervention
nhTrt         Intervention neighborhood (0=no Metrocable station, 1=Metrocable station)

## Some Covariates (there are others, see the paper itself)
nh03          Neighborhood id
nhGroup       Treatment (T) or Control (C)
nhTrt         Treatment (1) or Control (0)
nhHom         Mean homicide rate per 100,000 population in 2003
nhDistCenter Distance to city center (km)
nhLogHom      Log Homicide (i.e. log(nhHom))

## Outcomes (BE03,CE03,PV03,QP03,TP03 are baseline versions)
BE      Neighborhood amenities Score 2008
CE      Collective Efficacy Score 2008
PV      Perceived Violence Score 2008
QP      Trust in local agencies Score 2008
TP      Reliance on police Score 2008
hom     Homicide rate per 100,000 population Score 2008-2003 (in log odds)
```

What is the effect of the Metrocable on Homicides?

One approach: Estimate the average treatment effect of Metrocable on Homicides after the stations were built.

```
## code here
themeans<-group_by(meddat,nhTrt) %>% summarise(ybar=mean(HomRate08))
diff(themeans$ybar)
```

```
[1] -0.2899
```

```
lmOne <- lm(HomRate08~nhTrt,meddat)
coef(lmOne)["nhTrt"]
```

```
  nhTrt
-0.2899
```

```
library(estimatr)
difference_in_means(HomRate08~nhTrt,meddat)
```

```
Design:  Standard
      Estimate Std. Error t value Pr(>|t|) CI Lower CI Upper    DF
nhTrt  -0.2899     0.1508  -1.922  0.06137  -0.5942  0.01445 41.87
```

In principle, how might we use the testing approach to take a first stab at this question?

```
## code here
```

What are alternative explanations for this effect?

We claim that the policy intervention had some effect. What are alternative explanations?

Do we have any concerns about confounding?

Sometimes people ask about "bias from observed confounding" or "bias from selection on observables".

How would we interpret the following results? (Recall how we justified the use of `xBalance` in terms of randomization above.)

```
xbMed1 <- xBalance(nhTrt~nhAboveHS,data=meddat,report="all")
xbMed1$overall
```

```
        chisquare df p.value
unstrat     4.598  1 0.03201
```

```
xbMed1$results
```

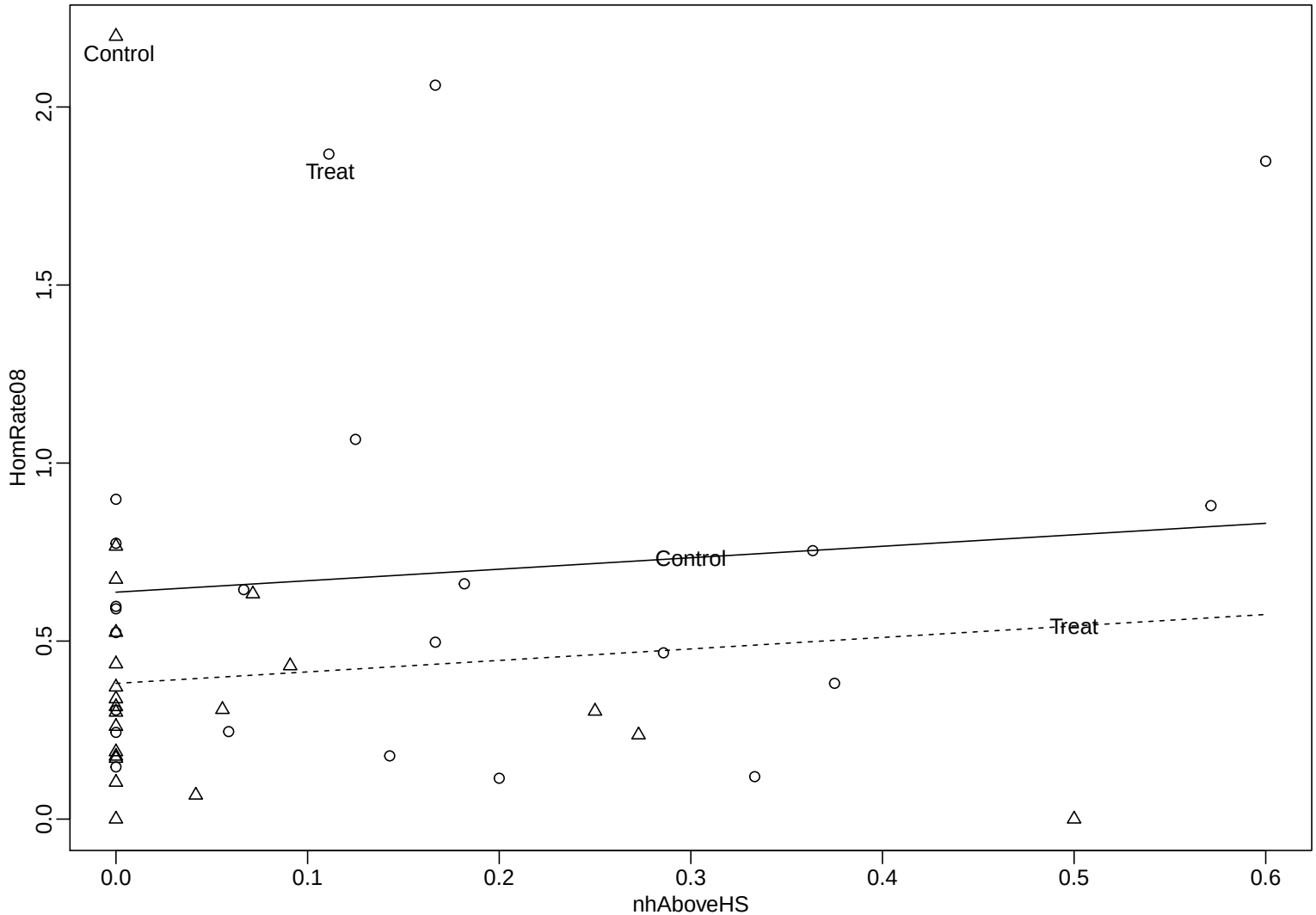
```
, , strata = unstrat

           stat
vars        Control Treatment adj.diff adj.diff.null.sd std.diff      z       p
  nhAboveHS   0.163   0.05829  -0.1047          0.04883   -0.668 -2.144 0.03201

attr(,"originals")
[1] "nhAboveHS"
```

How would you adjust for Proportion Above HS Degree?

Part of the Metrocable effect is not about Metrocable per se, but rather about the education of people in the neighborhood. How should we remove `nhAboveHS` from our estimate or test? What strategies can you think of?

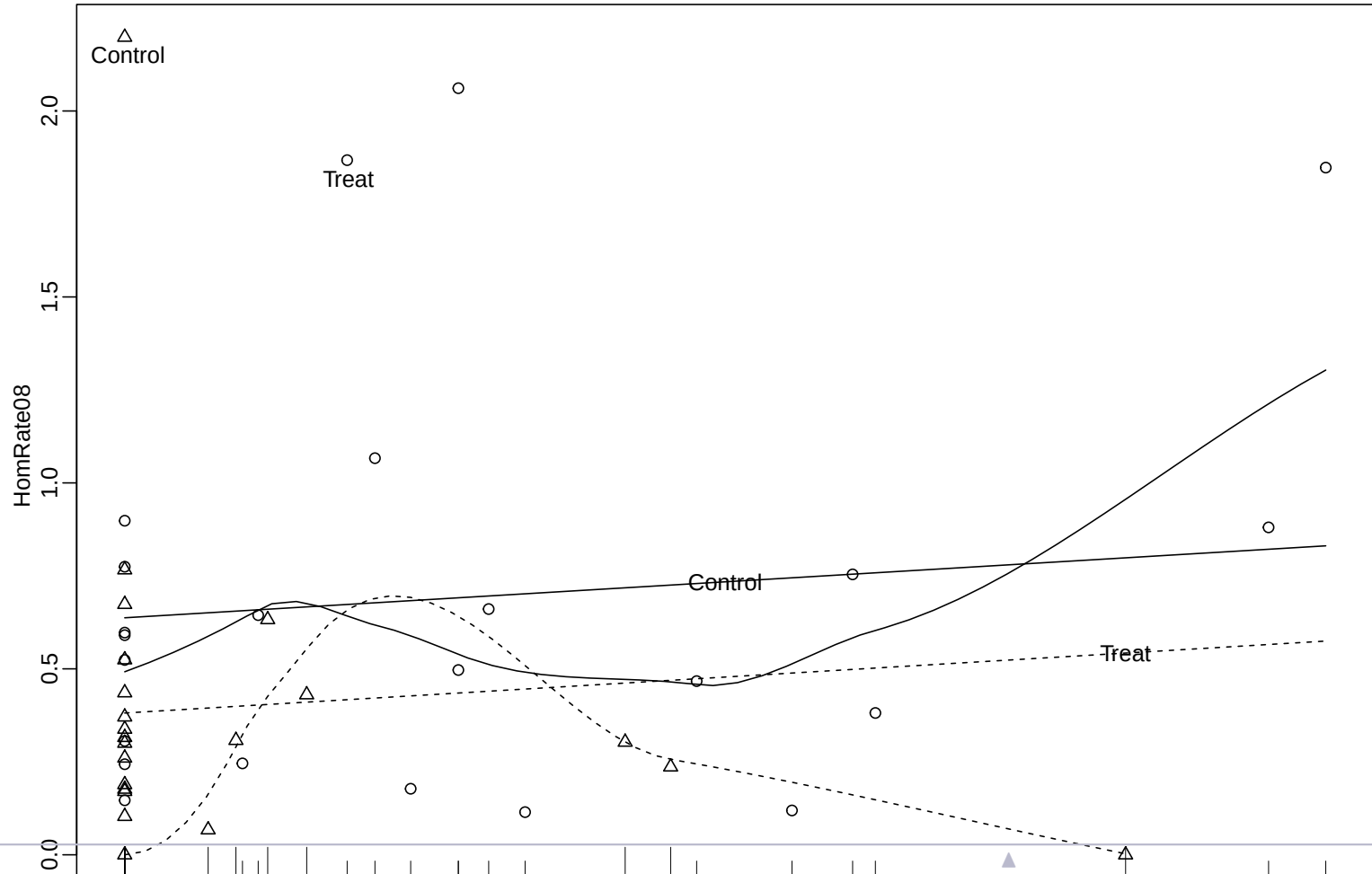
One approach to this problem: model-based adjustment

Let's try to just adjust for this covariate in a very common manner:



Did we adjust enough? Assessing extrapolation/interpolation problems.

Maybe adding some more information to the plot can help us decide whether, and to what extend, we effectively "controlled for" the proportion of the neighborhood with more than High School education.



Back to the randomized experiment to help make a case for appropriate adjustment

It seems like arguments about plots may be difficult to resolve. How about going back to xBalance? The idea of a standard against which we can compare a given design. How might we do this in this case?

Attempt 1: Stratification ... but two estimates rather than one adjusted estimate

```
lm1a <- lm(HomRate08~nhTrt,data=meddat,subset=nhAboveHS>=.1)
lm1b <- lm(HomRate08~nhTrt,data=meddat,subset=nhAboveHS<=.1)
```

Attempt 2: Stratified adjustment

```
lm1c <- lm(HomRate08~nhTrt+I(nhAboveHS>=.1),data=meddat)
coef(lm1c)["nhTrt"]
```

```
 nhTrt
-0.224
```

And balance assessment after stratification:

```
xbHS1 <- xBalance(nhTrt~nhAboveHS,strata=list(hs=~I(nhAboveHS>=.1)),data=meddat,report="all")
xbHS1$overall
```

```
   chisquare df p.value
hs    0.3912  1  0.5317
```

```
xbHS1$results
```

The Curse of Dimensionality and linear adjustment for one more variable.

What about more than one variable? Have we controlled for both population density and educational attainment enough? How would we know?

```
lm2x <- lm(HomRate08 ~ nhTrt + nhPopD + nhAboveHS, data=meddat)
coef(lm2x)["nhTrt"]
```

```
   nhTrt
-0.1224
```

Maybe another plot?

```
meddat$nhTrtF <- factor(meddat$nhTrt)
library(car)
scatter3d(HomRate08~nhAboveHS+nhPopD,
      groups=meddat$nhTrtF,
      data=meddat,surface=TRUE,
    fit=c("linear")) #additive"))
```

Can we improve stratified adjustment?

Rather than two strata, why not three?

```
lm1cut3 <- lm(HomRate08~nhTrt+cut(nhAboveHS,3),data=meddat)
coef(lm1cut3)["nhTrt"]
```

```
  nhTrt
-0.3161
```

But why those cuts? And why not 4? Why not...?

One idea: collect observations into strata such that the sum of the differences in means of nhAboveHS within strata is smallest? This is the idea behind `optmatch` and other matching approaches.

The optmatch workflow: The distance matrix

Introduction to optmatch workflow. To minimize differences requires a matrix of those differences (in general terms, a matrix of distances between the treated and control units)

```
tmp <- meddat$nhAboveHS
names(tmp) <- rownames(meddat)
absdist <- match_on(tmp, z = meddat$nhTrt,data=meddat)
absdist[1:3,1:3]
```

```
         control
treatment     23      24     25
        1 0.1429 0.00000 0.1667
        2 0.1429 0.00000 0.1667
        3 0.0873 0.05556 0.1111
```

```
abs(meddat$nhAboveHS[meddat$nhTrt==1][1] - meddat$nhAboveHS[meddat$nhTrt==0][1] )
```

```
[1] 0.1429
```

Do the match

```
fm1 <- fullmatch(absdist,data=meddat)
summary(fm1, min.controls=0, max.controls=Inf )
```

```
Structure of matched sets:
7:1 2:1 1:1 1:2 1:4 1:5
  1   2   7   2   1   1
Effective Sample Size:  17.4
(equivalent number of matched pairs).
```

```
table(meddat$nhTrt,fm1)
```

```
   fm1
    1.1 1.10 1.15 1.16 1.17 1.19 1.2 1.20 1.3 1.4 1.5 1.6 1.7 1.9
  0   1    1    5    1    1    4   1    1   1   1   1   2   2   1
  1   2    1    1    2    7    1   1    1   1   1   1   1   1   1
```

Evaluate the matched design: Within set differences

Look within sets:

```
meddat$fm1 <- fm1
rawmndiffs <- with(meddat, mean(nhAboveHS[nhTrt==1]) - mean(nhAboveHS[nhTrt==0]))
setdiffs <- meddat %>% group_by(fm1) %>% summarize(mneddiffs =
                           mean(nhAboveHS[nhTrt==1]) -
                           mean(nhAboveHS[nhTrt==0]),
                         mnAboveHS = mean(nhAboveHS),
                         minAboveHS = min(nhAboveHS),
                         maxAboveHS = max(nhAboveHS))

setdiffs
```

```
# A tibble: 14 x 5
   fm1   mneddiffs mnAboveHS minAboveHS maxAboveHS
   <fct>     <dbl>     <dbl>      <dbl>      <dbl>
 1 1.1     0          0          0          0
 2 1.10    0          0          0          0
 3 1.15   -0.0516     0.134      0.0909     0.167
 4 1.16   -0.0102     0.0520     0.0417     0.0588
 5 1.17    0          0          0          0
 6 1.19   -0.0667     0.326      0.273      0.375
 7 1.2     0          0          0          0
 8 1.20    0.00476    0.0690     0.0667     0.0714
 9 1.3     0          0          0          0
10 1.4     0          0          0          0
11 1.5     0          0          0          0
12 1.6     0.0591     0.211      0.182      0.25
13 1.7    -0.0857     0.557      0.5        0.6
14 1.8     0          0          0          0
```

Evaluate the matched design: Compare to a randomized experiment.

```
xbHS2 <- xBalance(nhTrt~nhAboveHS,
                  strata=list(nostrat=NULL,
                              hsmatch=~fm1),
                  data=meddat,report="all")
xbHS2$results
```

```
, , strata = nostrat

           stat
vars        Control Treatment adj.diff adj.diff.null.sd std.diff      z       p
  nhAboveHS   0.163   0.05829  -0.1047          0.04883   -0.668 -2.144 0.03201

, , strata = hsmatch

           stat
vars        Control Treatment adj.diff adj.diff.null.sd std.diff      z       p
  nhAboveHS   0.113   0.09937 -0.01366         0.008237 -0.08714 -1.658 0.09728

attr(,"originals")
[1] "nhAboveHS"
```

```
xbHS2$overall
```

```
        chisquare df p.value
nostrat     4.598  1 0.03201
hsmatch     2.750  1 0.09728
```

Summary of the Day

- We can assess the randomization of a randomized experiment easily using covariates (X): compare the observed treatment-vs-control differences in X with those consistent with no differences that would emerge from repeating the design.
- How to justify an adjustment strategy for an observational study? The linear model adjustment strategy is difficult to justify. A stratification based strategy is easier to justify, inspect, learn from. (We can compare our stratification to a block randomized experiment, to a known design, a known standard.)
- How to choose a stratification? We can do it by hand. Or we can delegate to a computer (i.e. `optmatch`) — we can think of it as an optimization problem and ask the computer to optimize.

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