

Lab 4

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Reviewing key concepts

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- Selection problem: $\mathbb{E}[Y_i(0) | D_i = 1] \neq \mathbb{E}[Y_i(0) | D_i = 0]$
- If the treated units had not received treatment, they would still have systematic differences in outcome compared to the control units

Another one of those intuitively-named concepts...

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| | Good identification | Poor identification |
|---------------------------|---------------------|---------------------|
| Substantively interesting | yep | ? |
| Substantively trivial | ? | nope |

Matching

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- Conditional ignorability: $\{Y_i(1), Y_i(0)\} \perp D_i | X_i$

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- Selection on *observables*: to condition on X , I must observe it!

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Given its limitations, is matching a causal inference method?

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- A bit of a trick question: under the right assumption,

Example from Blattman and Annan (2010)

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$$\mathbb{E}[Y_i(0)|D_i = 1] - \mathbb{E}[Y_i(0)|D_i = 0] \neq 0$$

- You should speculate (to yourself) about the nature and direction of selection bias
- What's a plausible story that could explain the inequality above?

```
child <- read.csv("child_soldiering.csv")
```

Y_i is *educ* and D_i is *abd*

Naive estimate

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```

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Produce a “naive” estimate of the average treatment effect of abduction on education

```
mean(child$educ[child$abd==1]) - mean(child$educ[child$abd==0])
```

```
## [1] -0.5954243
```

```
sqrt(var(child$educ[child$abd==1])/length(child$educ[child$abd==1]) +  
      var(child$educ[child$abd==0])/length(child$educ[child$abd==0]))
```

```
## [1] 0.222192
```

Naive ATE with regression

```
library(lmtest)
library(sandwich)
library(modelsummary)

model <- lm(educ ~ abd, data = child)
lmtest::coeftest(model, vcov = sandwich::vcovHC(model, type = "HC2"))

##
## t test of coefficients:
##
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  7.41577    0.18031 41.1271 < 2.2e-16 ***
## abd         -0.59542    0.22219 -2.6798  0.007531 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Balance test

```
library(Matching)

# Storing formula: D_i on LHS, X_i on RHS
formul <- abd ~ C.ach + C.akw + C.ata + C.kma + C.oro + C.pad + C.paj + C.pal +
  age + fthr.ed + mthr.ed + orphan96 + fthr.frm + hh.size96 + educ

# nboots is nb. of iterations fo K-S test; print.level avoids output
unmatched_bal <- Matching::MatchBalance(formul = formul,
                                         data = child,
                                         nboots = 1000,
                                         print.level = 0)

# Function above creates ugly list object
# baltest.collect manipulates it to create a matrix
baltable_unmatched <- ebal::baltest.collect(matchbal.out = unmatched_bal,
                                             var.names = colnames(child)[-1],
                                             after = FALSE)
```

Balance table

```
baltable_unmatched[, -8:-10] %>% round(3) %>% knitr::kable()
```

| | mean.Tr | mean.Co | sdiff | sdiff.pooled | var.ratio | T pval | KS pval |
|-----------|---------|---------|---------|--------------|-----------|--------|---------|
| C.ach | 0.154 | 0.115 | 10.798 | 11.440 | 1.279 | 0.126 | NA |
| C.akw | 0.158 | 0.079 | 21.678 | 24.650 | 1.829 | 0.001 | NA |
| C.ata | 0.100 | 0.197 | -32.549 | -27.668 | 0.566 | 0.000 | NA |
| C.kma | 0.152 | 0.118 | 9.259 | 9.727 | 1.231 | 0.194 | NA |
| C.oro | 0.052 | 0.136 | -37.924 | -29.119 | 0.418 | 0.000 | NA |
| C.pad | 0.121 | 0.122 | -0.199 | -0.199 | 0.994 | 0.979 | NA |
| C.paj | 0.152 | 0.104 | 13.254 | 14.269 | 1.378 | 0.055 | NA |
| C.pal | 0.113 | 0.129 | -5.208 | -5.051 | 0.888 | 0.509 | NA |
| age | 21.366 | 20.151 | 24.242 | 24.495 | 1.043 | 0.001 | 0.010 |
| fthr.ed | 5.764 | 6.068 | -8.590 | -8.465 | 0.944 | 0.266 | 0.839 |
| mthr.ed | 2.093 | 2.495 | -14.493 | -13.311 | 0.729 | 0.086 | 0.362 |
| orphan96 | 0.078 | 0.075 | 0.989 | 0.996 | 1.031 | 0.895 | NA |
| fthr.frm | 0.903 | 0.914 | -3.834 | -3.938 | 1.117 | 0.601 | NA |
| hh.size96 | 8.090 | 8.695 | -15.495 | -14.624 | 0.803 | 0.058 | 0.034 |
| educ | 6.820 | 7.416 | -21.337 | -20.508 | 0.859 | 0.008 | 0.073 |

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- Given what we know about hypothesis tests, does that setup appear reasonable?
- New-ish approach: equivalence tests

Matching procedure

```
vars <- c("age", "fthr.ed", "mthr.ed", "orphan96", "fthr.frm", "hh.size96")
match_out <- Matching::Match(Y = child$educ,
                             Tr = child$abd,
                             X = child[,vars],
                             M = 1,
                             Weight = 2,
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- Here *Weight* = 2 means the Mahalanobis distance
- *exact* to force exact matching and prune treated units without a perfect buddy

ATT estimate

```
summary(match_out)
```

```
##  
## Estimate... -0.50152  
## AI SE..... 0.26428  
## T-stat..... -1.8976  
## p.val..... 0.057744  
##  
## Original number of observations..... 741  
## Original number of treated obs..... 462  
## Matched number of observations..... 462  
## Matched number of observations (unweighted). 521  
##  
## Number of obs dropped by 'exact' or 'caliper' 0
```

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X <- match_out$mdata[[3]]
```

```
# The first treated observation (i=1) and its buddy (i=2)  
rbind(X[1,], X[1+nrow(X)/2,]) %>% knitr::kable("latex")
```

| age | fthr.ed | mthr.ed | orphan96 | fthr.frm | hh.size96 |
|-----|---------|---------|----------|----------|-----------|
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What do you think of this match? Good counterfactual? Seems like it...but the unobservables! Think about $\{Y_i(1), Y_i(0) \perp D_i | X_i\}$

Retrieving the Mahalanobis distance

```
X_control <- child[child$abd==0,vars]
X_treat <- child[child$abd==1,vars]

library(StatMatch)
X_control$dist_i1 <-
  mahalanobis.dist(data.x = X_treat[1,vars],
                   data.y = X_control[,vars]) %>% as.vector()

knitr::kable(plyr::rbind.fill(X_treat[1,], X_control[1:7,]))
```

| age | fthr.ed | mthr.ed | orphan96 | fthr.frm | hh.size96 | dist_i1 |
|-----|---------|---------|----------|----------|-----------|----------|
| 21 | 7 | 4 | 0 | 1 | 9 | NA |
| 29 | 7 | 0 | 0 | 1 | 11 | 2.066150 |
| 14 | 0 | 0 | 0 | 1 | 17 | 3.303101 |
| 19 | 4 | 4 | 0 | 1 | 6 | 1.106657 |
| 16 | 0 | 0 | 0 | 1 | 8 | 2.270651 |
| 16 | 0 | 0 | 0 | 1 | 5 | 2.351817 |
| 15 | 0 | 0 | 0 | 1 | 4 | 2.513462 |
| 29 | 7 | 0 | 0 | 1 | 8 | 2.030444 |

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To prune or not to prune?

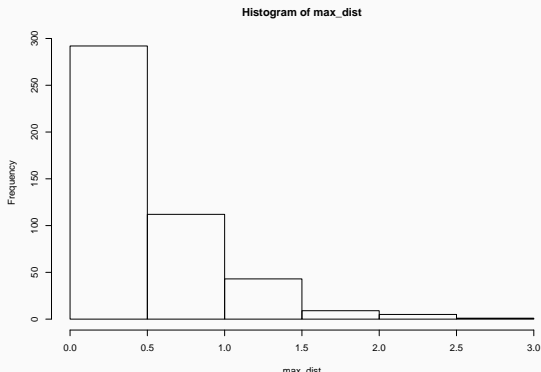
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- King, Lucas, and Nielsen 2017: balance-sample size frontier

Let's find the treated unit with the most dissimilar buddy...

To prune or not to prune?

```
dist <- list()
for(i in 1:nrow(X_treat)){
  dist[[i]] <- mahalanobis.dist(data.x = X_treat[i,vars],
                                data.y = X_control[,vars]) %>% as.vector()
}
max_dist <- sapply(dist, min)
hist(max_dist)
```



To prune or not to prune

```
X_buddies <- X[(nrow(X)/2+1):(nrow(X)),]  
treat_max <- X_treat[which.max(max_dist),]  
control_max <- matrix(X_buddies[which.max(max_dist),], nrow=1) %>%  
  as.data.frame() %>%  
  setNames(vars)  
  
knitr::kable(rbind(treat_max, control_max))
```

| | age | fthr.ed | mthr.ed | orphan96 | fthr.frm | hh.size96 |
|-----|-----|---------|---------|----------|----------|-----------|
| 609 | 21 | 12 | 4 | 1 | 0 | 6 |
| 1 | 16 | 7 | 0 | 0 | 1 | 13 |

Balance after matching

```
matched_bal <- Matching::MatchBalance(formul = formul,  
                                     data = child,  
                                     match.out = match_out,  
                                     ks = TRUE,  
                                     nboots = 1000,  
                                     print.level = 0)  
  
baltable_matched <- ebal::baltest.collect(matchbal.out = matched_bal,  
                                          var.names = colnames(child)[-1],  
                                          after = TRUE) %>% as.data.frame()  
  
baltable_matched[, -8:-10] %>% round(3) %>% knitr::kable()
```

Balance after matching

| | mean.Tr | mean.Co | sdiff | sdiff.pooled | var.ratio | T pval | KS |
|-----------|---------|---------|---------|--------------|-----------|--------|-------|
| C.ach | 0.154 | 0.100 | 14.888 | 14.888 | 1.446 | 0.015 | |
| C.akw | 0.158 | 0.098 | 16.301 | 16.301 | 1.498 | 0.005 | |
| C.ata | 0.100 | 0.222 | -40.727 | -40.727 | 0.520 | 0.000 | |
| C.kma | 0.152 | 0.116 | 10.010 | 10.010 | 1.258 | 0.106 | |
| C.oro | 0.052 | 0.137 | -38.452 | -38.452 | 0.416 | 0.000 | |
| C.pad | 0.121 | 0.089 | 9.937 | 9.937 | 1.317 | 0.120 | |
| C.paj | 0.152 | 0.116 | 9.910 | 9.910 | 1.254 | 0.102 | |
| C.pal | 0.113 | 0.122 | -3.079 | -3.079 | 0.931 | 0.654 | |
| age | 21.366 | 21.133 | 4.640 | 4.640 | 1.068 | 0.009 | 0.000 |
| fthr.ed | 5.764 | 5.682 | 2.324 | 2.324 | 1.086 | 0.170 | 0.000 |
| mthr.ed | 2.093 | 2.069 | 0.859 | 0.859 | 0.999 | 0.489 | 0.000 |
| orphan96 | 0.078 | 0.078 | 0.000 | 0.000 | 1.000 | 1.000 | |
| fthr.frm | 0.903 | 0.903 | 0.000 | 0.000 | 1.000 | 1.000 | 21 |
| lth.in.96 | 0.000 | 0.000 | 0.000 | 0.000 | 1.000 | 0.100 | |

Propensity score

$$\pi(X_i) = Pr(D_i = 1|X_i)$$

Generate PS for each unit and match on PS