Section 9: Matching

March 29, 2012

Outline

1. Motivation and Quantities of Interest
2. Matching Methods
3. Introduction to Balance Metrics
4. Matching in R

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3. Matching as preprocessing to reduce model dependence:prune data as with a non-parametric matching analysis, and then fit parametric model.

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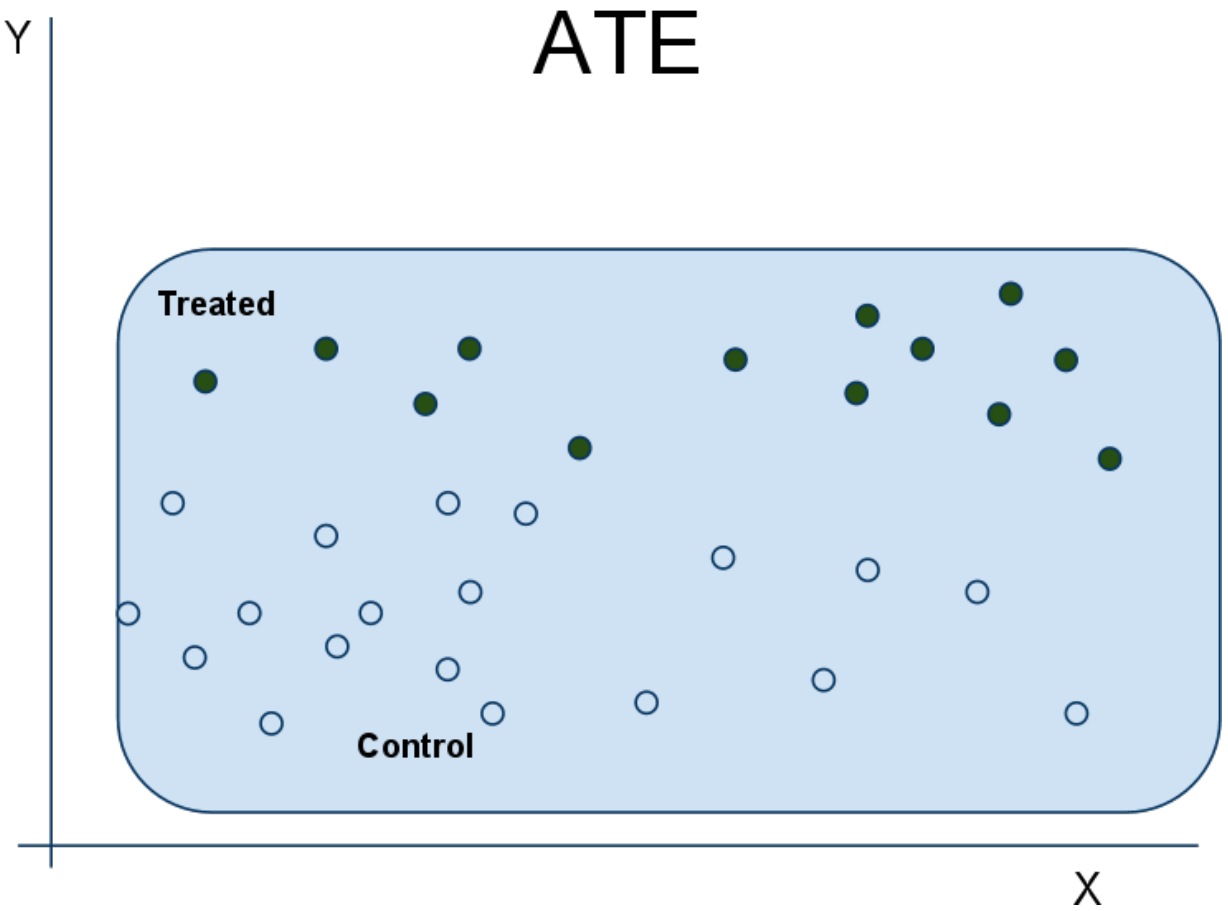

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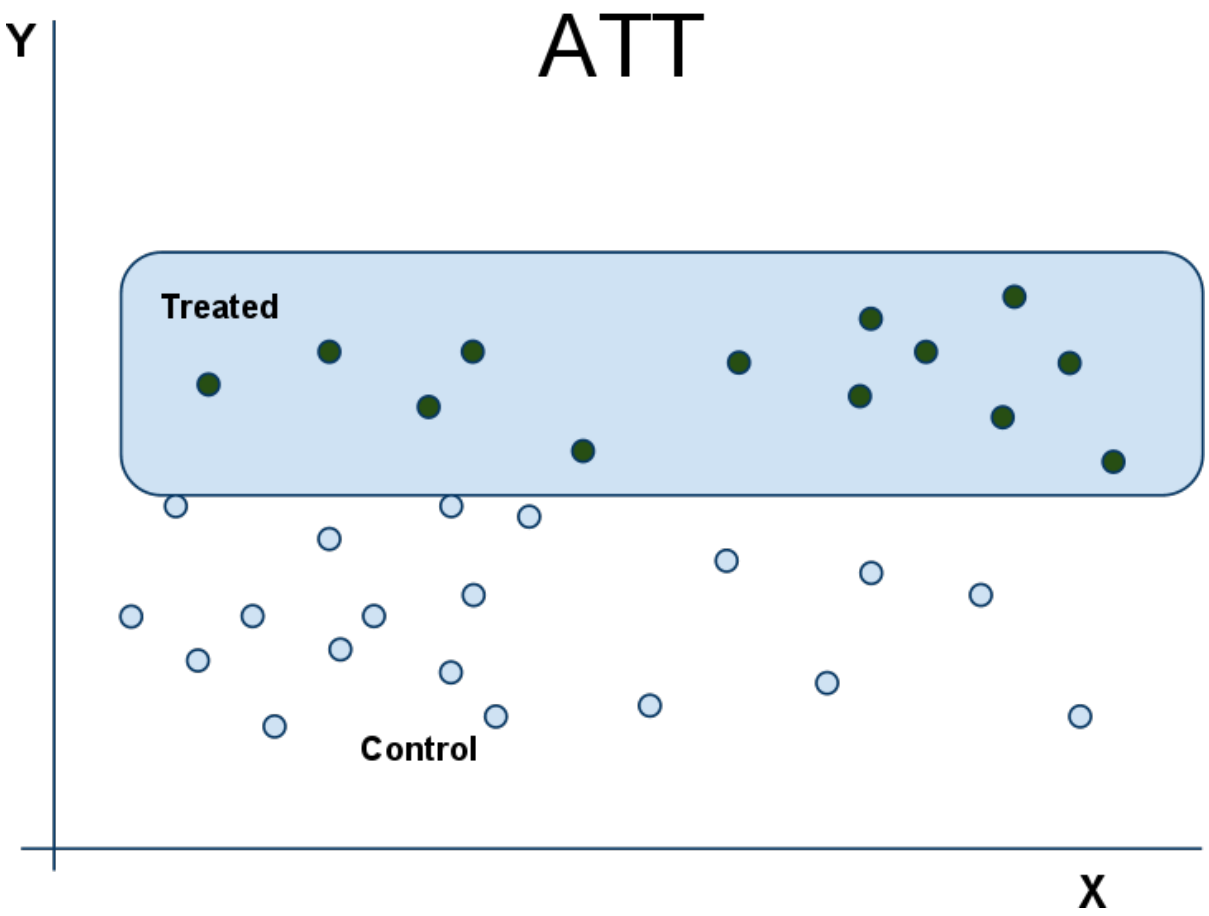

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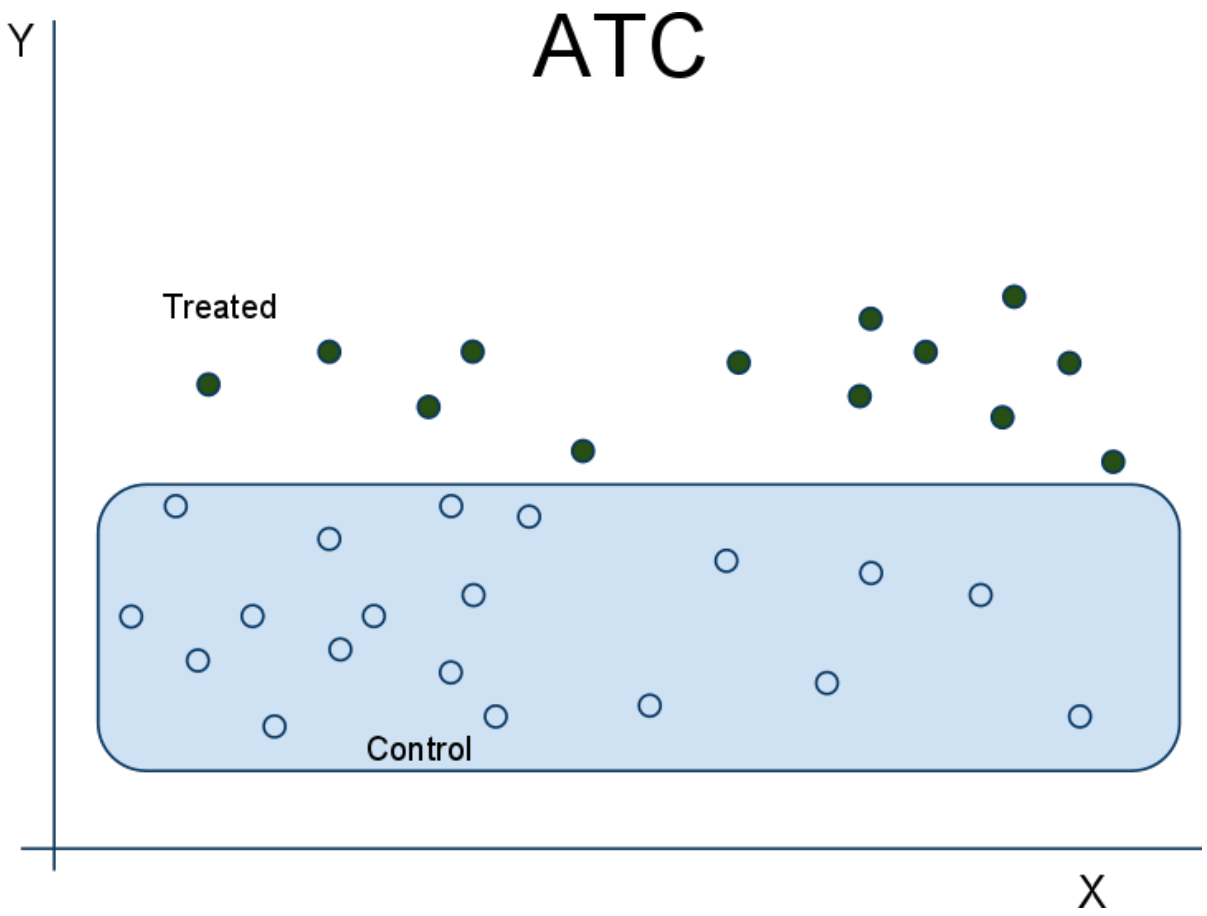

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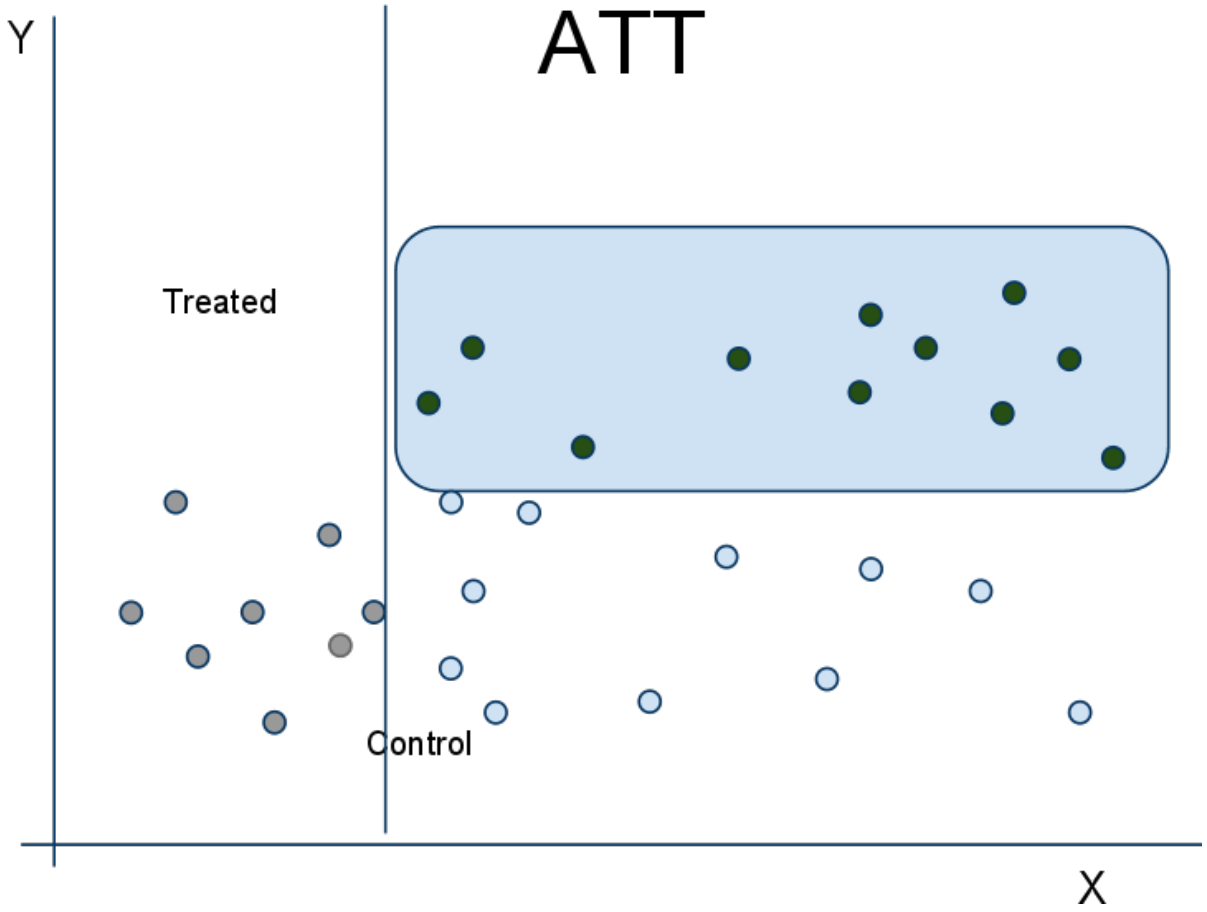

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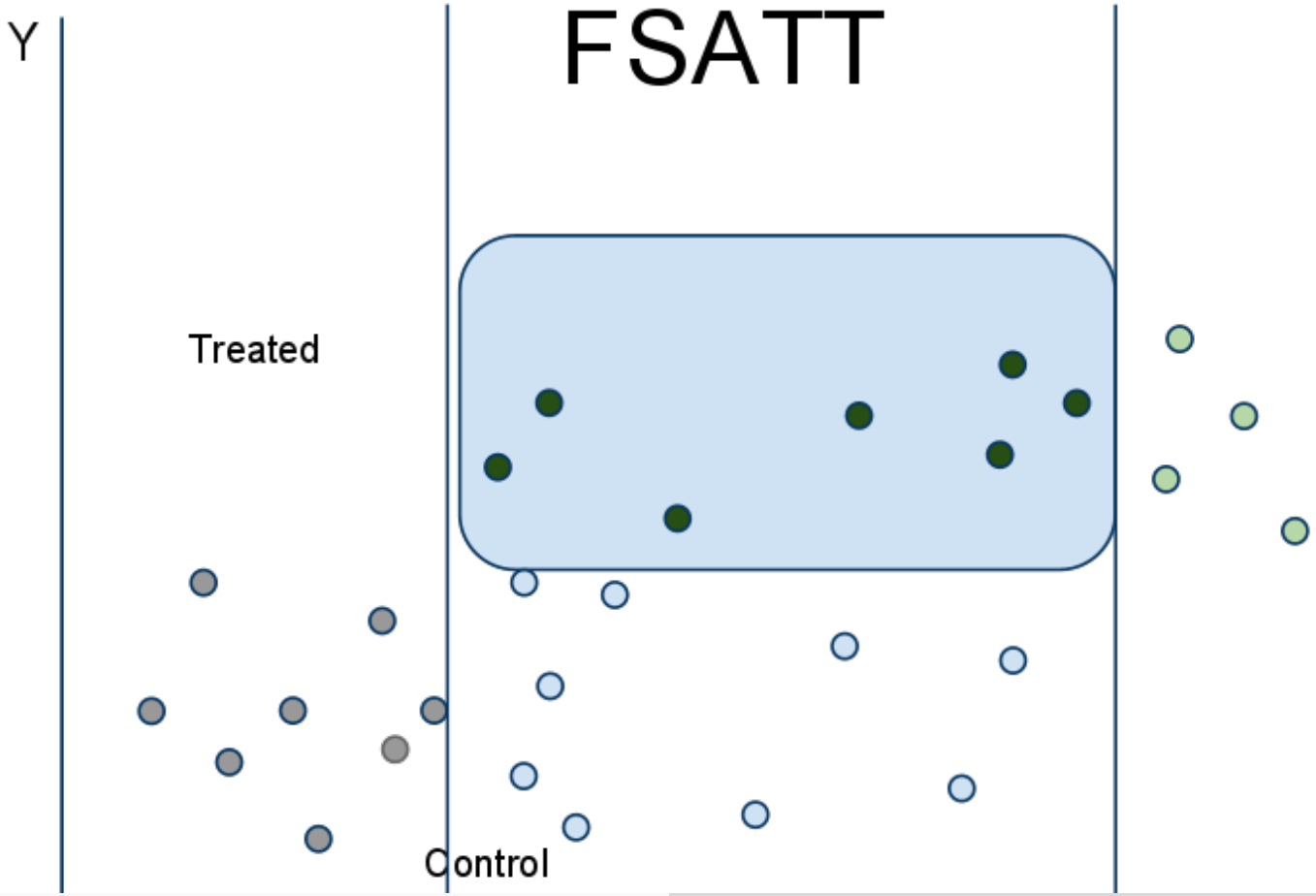

Ignorability: One More Time

That first step (e.g. $E[Y^1] = E[Y|T = 1]$) is only valid under the ignorability assumption: $(Y^0, Y^1) \perp T$. In particular, note that this implies:

- Assumption 1: $E[Y^1|T = 1] = E[Y^1|T = 0]$
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In this case, it appears that those who will be negatively affected by treatment are opting for control.

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The same average outcomes are used to construct these (four different $E[Y|T = t, X = x]$'s) but they are *weighted* differently.

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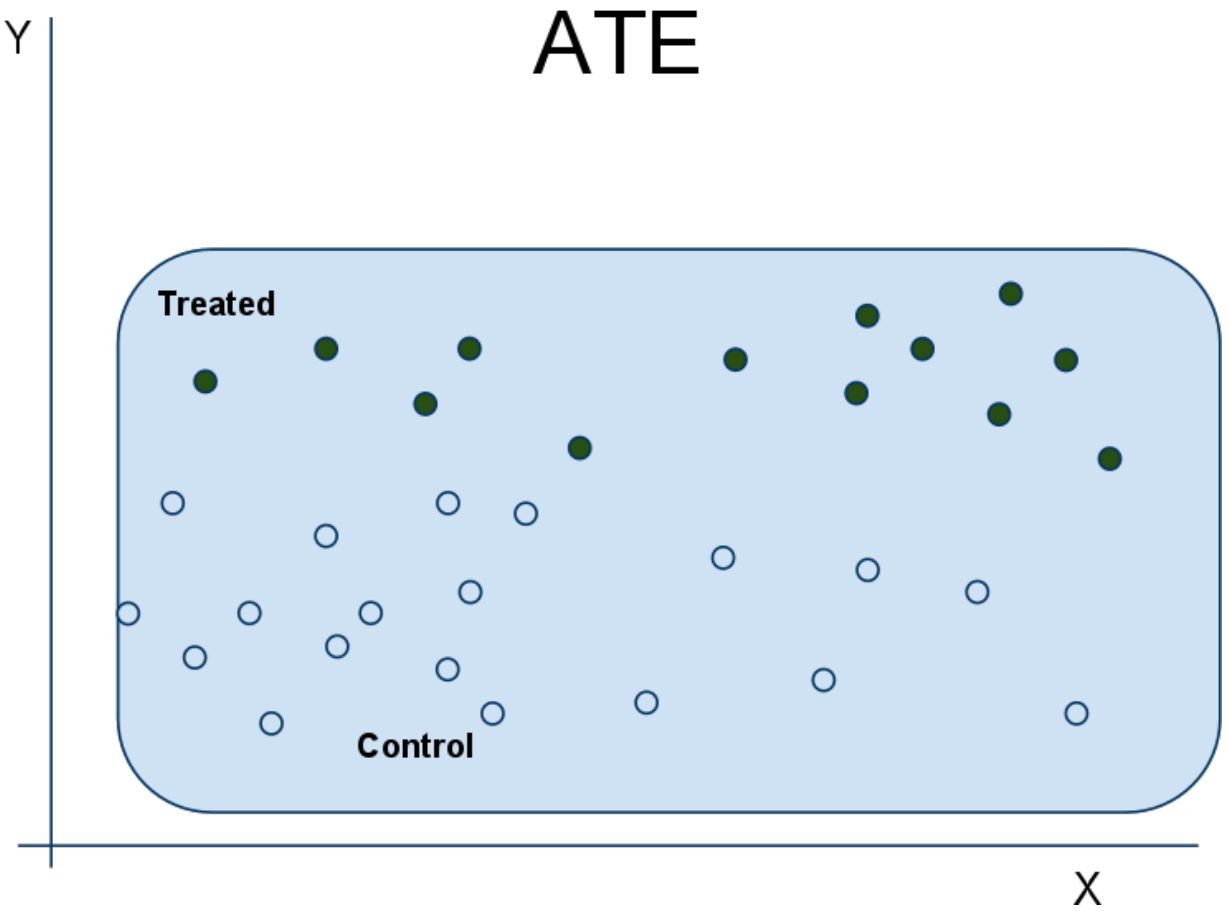

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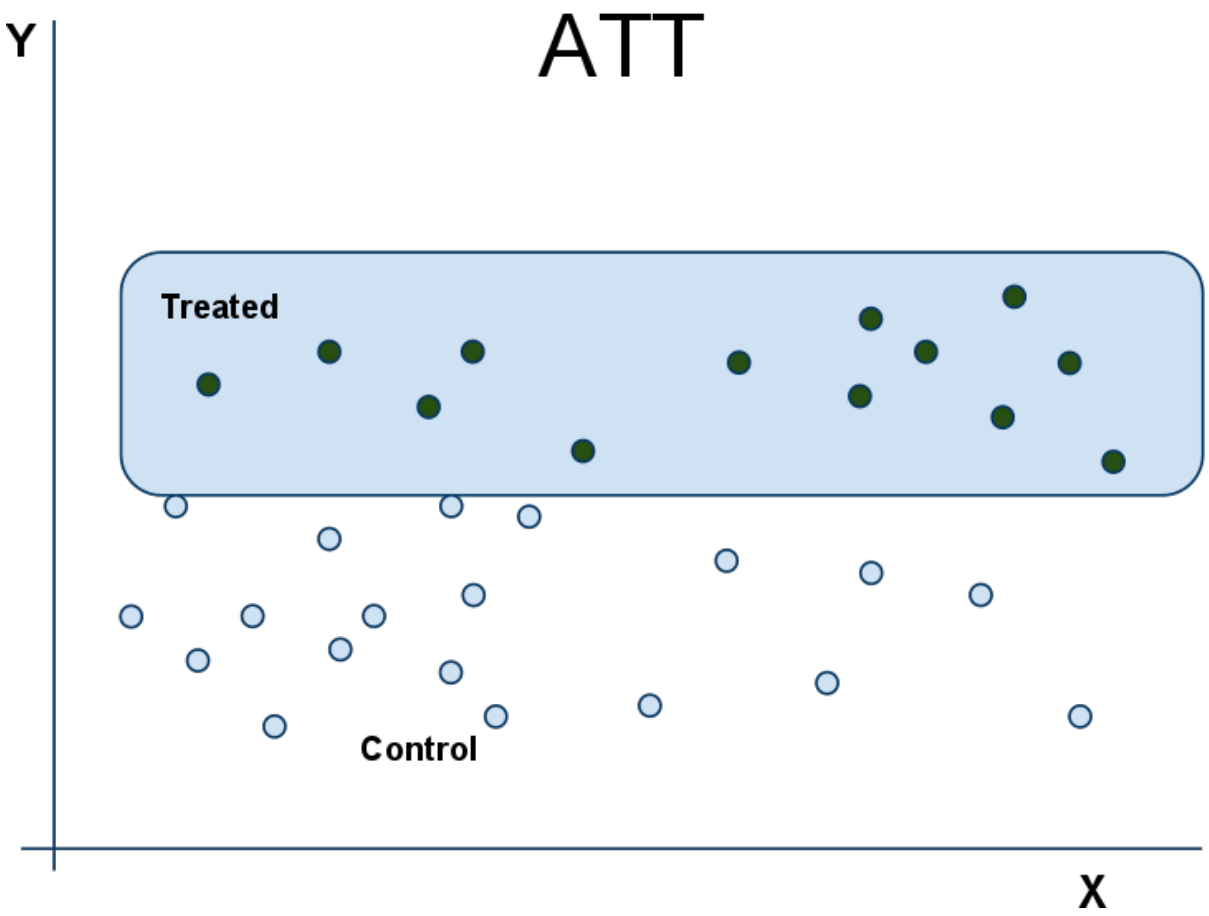

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- 3. Assess our matching procedure (balance checking).

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- 5. Sensitivity testing for either the confoundedness assumption or the parametric model.

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From "Matching Methods for Causal Inference: A Review and a Look Forward" Stuart 2009.

Distance $\Rightarrow$ Matches

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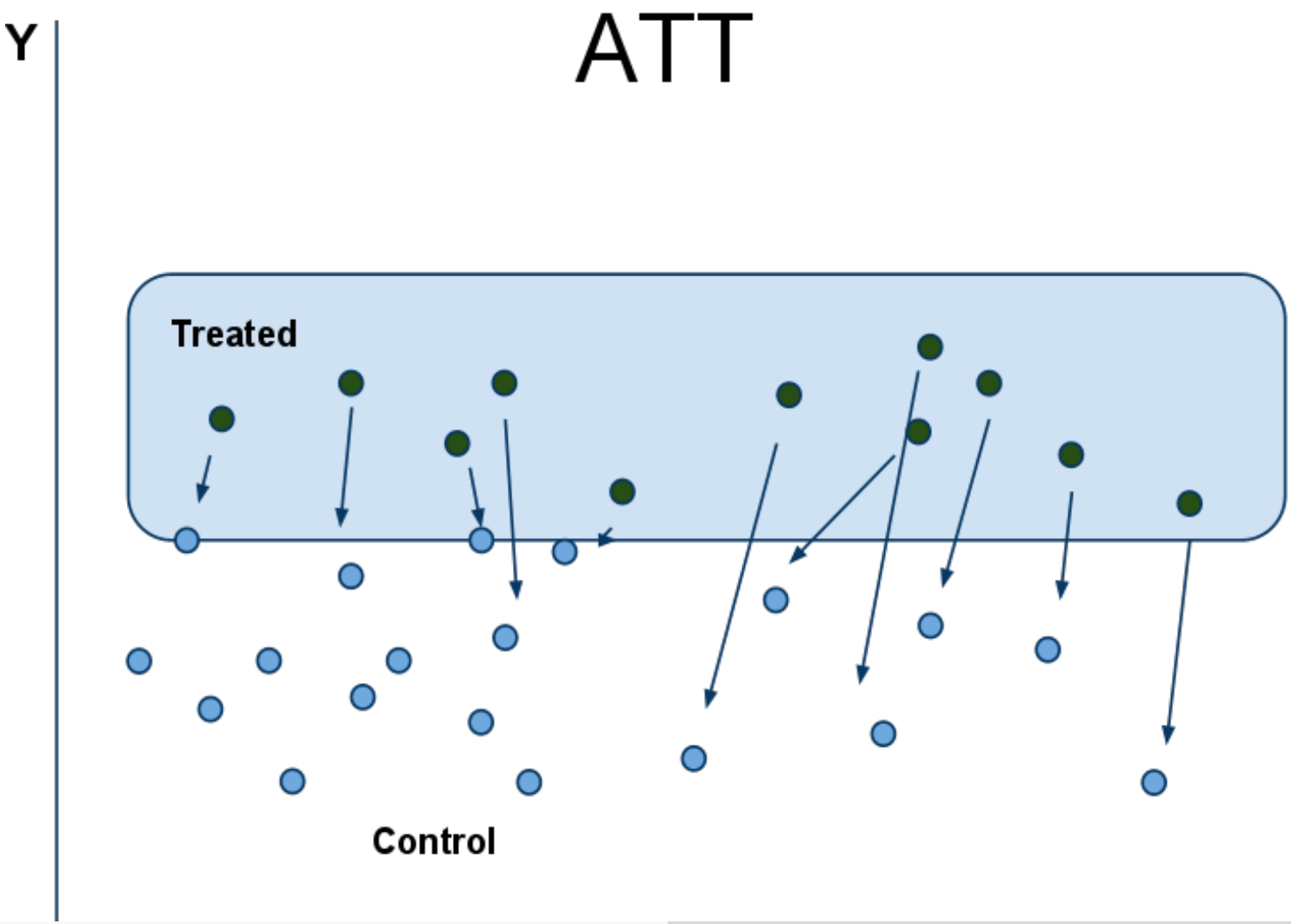
General points: These methods give weights of zero or 1 to observations, depending on whether they are matched.

Visualizing Nearest Neighbor and Optimal Matches



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  - To get the ATE, weight by $w_i = \frac{T_i}{\hat{e}_i} + \frac{(1-T_i)}{(1-\hat{e}_i)}$
  - to get the ATT, weight by $w_i = T_i + (1 - T_i)\frac{\hat{e}_i}{1-\hat{e}_i}$

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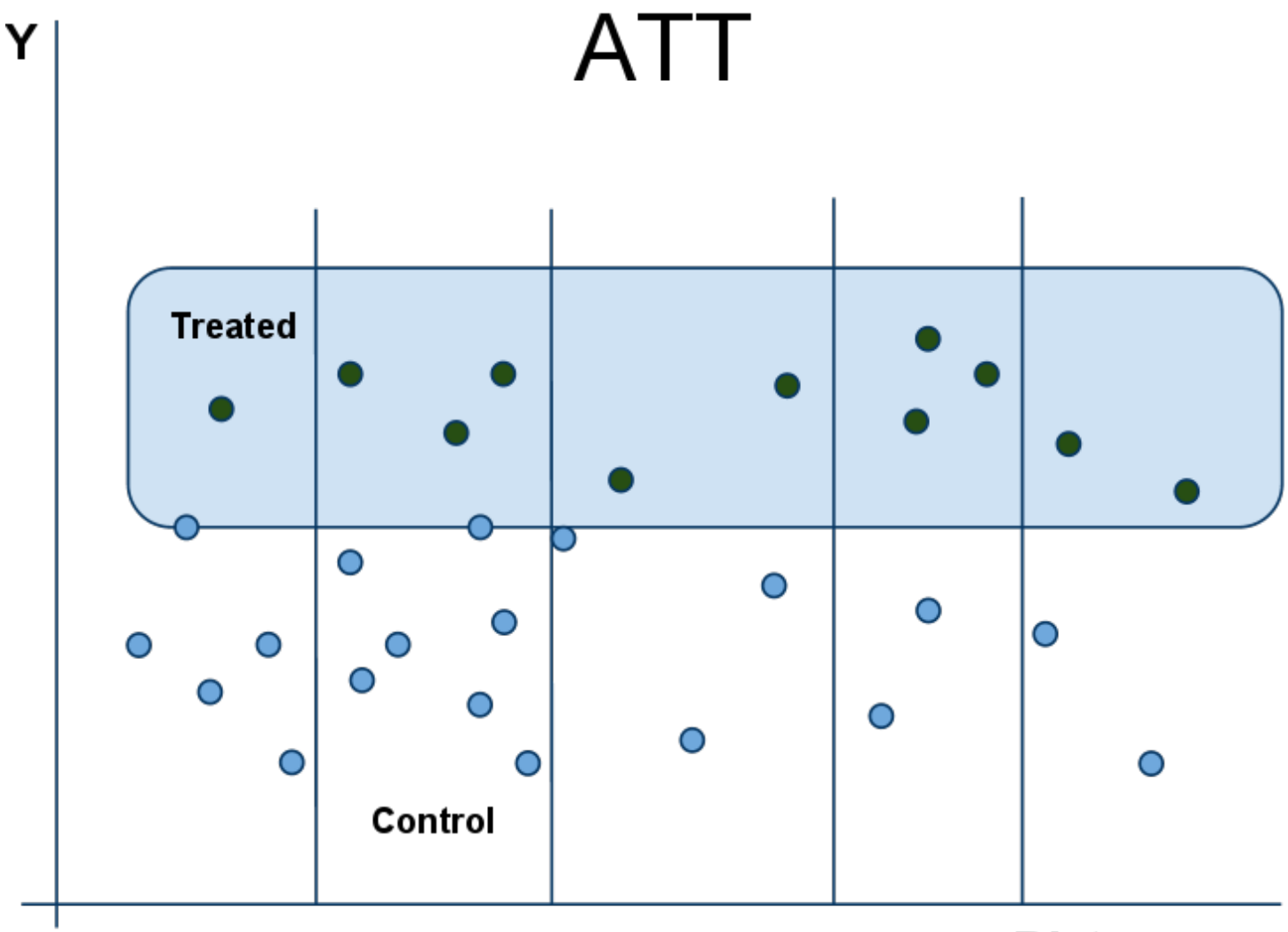

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- Similar to sub-classification, but the classification is not based on a distance metric, it's based on substantive knowledge of the covariates.
- This allows us to get the benefits of exact matching without the problems of high dimensionality.
- CEM also weights to get the ATT and the ATE depending on how many observations are in the coarsened categories.

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General point: Pros and Cons of K to K matching are very similar to the bias-varaince tradeoff we talked about for matching in class.

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  - More complicated because matched controls are not independent.
  - Should be aware of how many times you are using one control.

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2. Matching Methods
3. Introduction to Balance Metrics
4. Matching in R

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If they are very close, then we have matched well. Illustrative example: exact matching leads to identical multivariate distributions $f(X|T = 1) = f(X|T = 0)$.

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4. L1.

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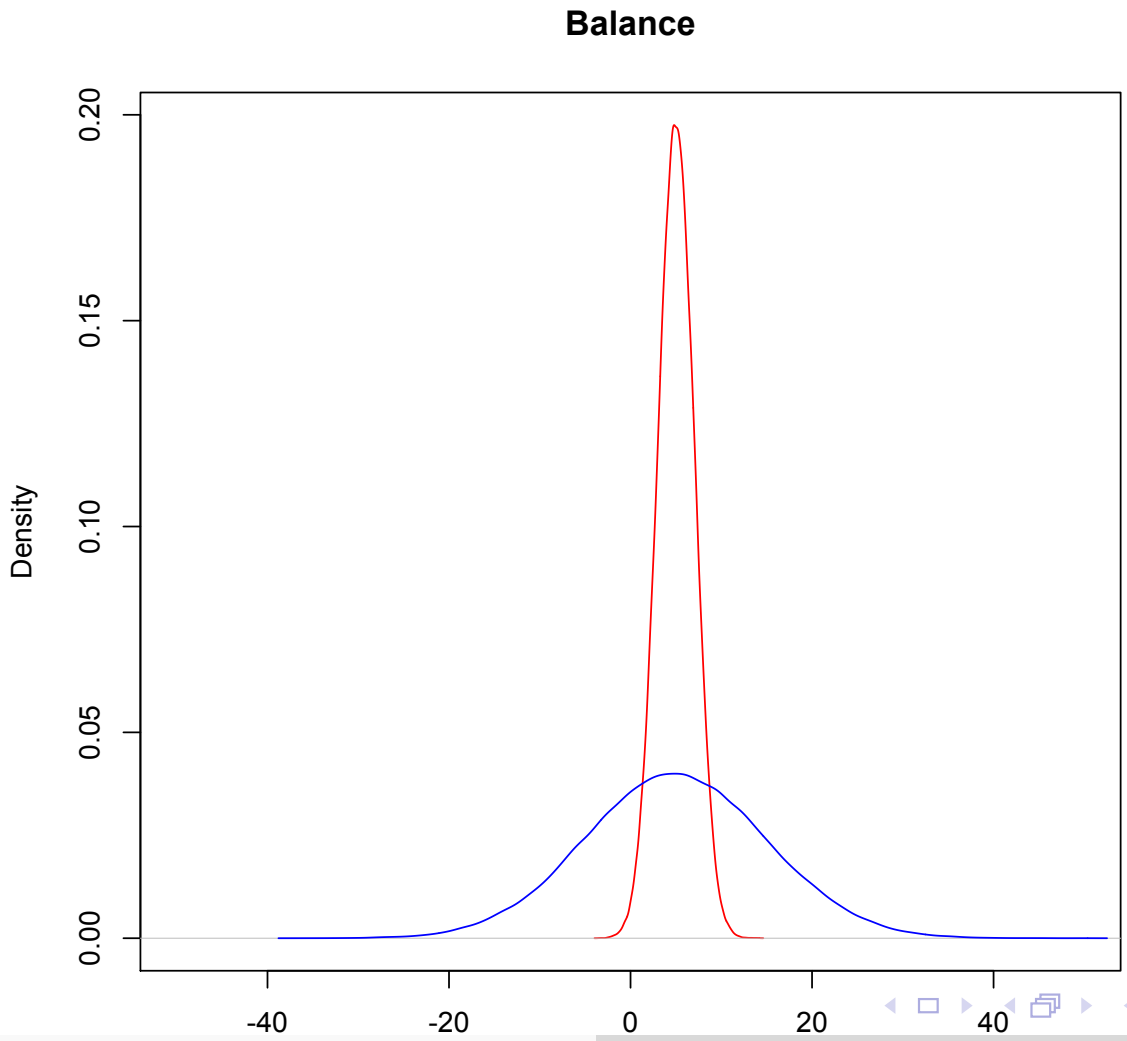

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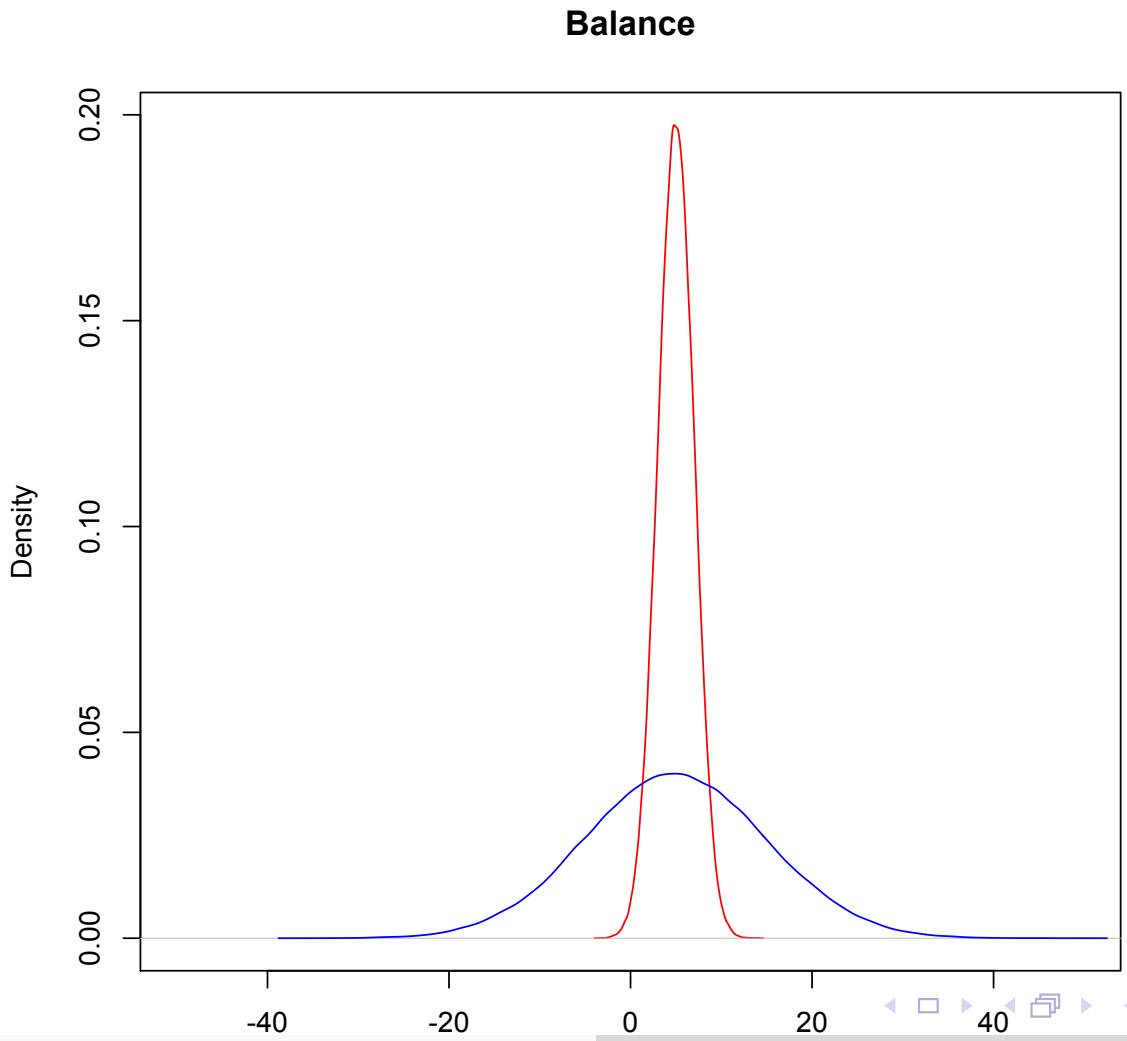

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We then have a set of frequencies $f_1, ..., f_k$ where f_i is the proportion of treated observations which fall in bin i; likewise $g_1, ..., g_k$ are the proportions of control observations falling in bin i. Then

$$L_1(f, g) = \frac{1}{2} \sum_{i=1,...,k} |f_i - g_i|.$$

If balance is perfect this equals 0; if completely imperfect, 1.

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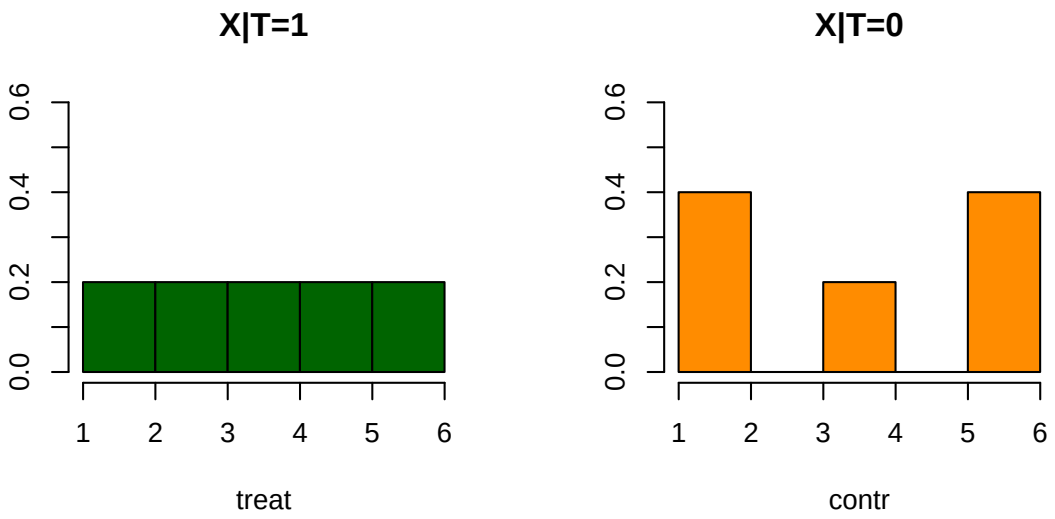

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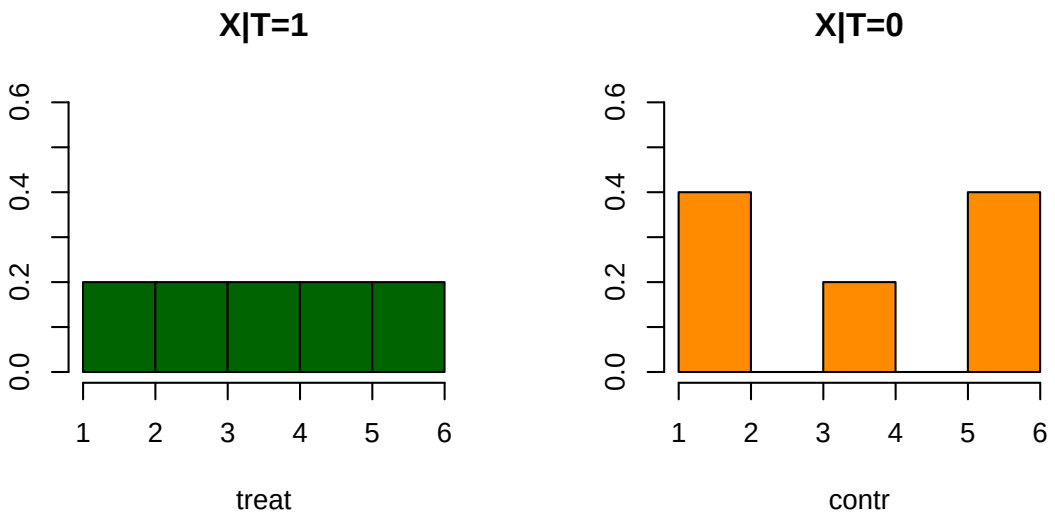

$$L_1(f, g) = \frac{1}{2}(.2 + .2 + 0 + .2 + .2) = .4.$$

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- `re74`, `re75`
- `u74`, `u75` both indicators of unemployment

Get the Data Setup

```
install.packages("MatchIt")
install.packages("cem")
library(MatchIt)
library(cem)
library(Zelig)

## LOAD DATA: Lalonde (1986) dataset; from cem package
data(LL)
```

Look at the Data Before Matching

```
mean(LL$re78[LL$treated == 1]) - mean(LL$re78[LL$treated == 0])
[1] 886.3038
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   + re74 + re75 + hispanic + u74 + u75, data = LL))
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   + re74 + re75 + hispanic + u74 + u75, data = LL))
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```
Call:
lm(formula = re78 ~ treated + age + education + black + married +
    nodegree + re74 + re75 + hispanic + u74 + u75, data = LL)

Residuals:
   Min     1Q Median     3Q    Max
-10395  -4431  -1455   3189  53911

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.186e+03  2.638e+03   1.208   0.2276
treated      8.237e+02  4.685e+02   1.758   0.0791 .
age          1.024e+01  3.707e+01   0.276   0.7824
education    2.006e+02  1.805e+02   1.111   0.2669
black       -1.419e+03  8.019e+02  -1.770   0.0772 .
married      4.854e+01  6.522e+02   0.074   0.9407
nodegree    -2.996e+02  7.480e+02  -0.401   0.6889
re74         1.274e-01  7.526e-02   1.693   0.0909 .
```

Checking Imbalance in R

```
pre.imbalance <- imbalance(group=LL$treated,
  data=LL, drop=c("treated","re78"))
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pre.imbalance

Multivariate Imbalance Measure: L1=0.735
Percentage of local common support: LCS=12.4%

Univariate Imbalance Measures:

           statistic   type min 25%   50%   75%     max
age        1.792e-01 (diff)  0   1   0.00  -1.0    -6.0
education  1.922e-01 (diff)  1   0   1.00   1.0     2.0
married    1.070e-02 (diff)  0   0   0.00   0.0     0.0
...
re74      -1.015e+02 (diff)  0   0  69.73 584.9 -2139.0
re75       3.942e+01 (diff)  0   0 294.18 660.7   490.4
```

Exact Matching

```
exact.match <- matchit(formula= treated ~ age + education
    + black + married + nodegree + re74 + re75 + hispanic +
    u74 + u75, data = LL, method = "exact")
```

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Call:
matchit(formula = treated ~ age + education + black + married +
    nodegree + re74 + re75 + hispanic + u74 + u75, data = LL,
    method = "exact")

Exact Subclasses: 36

Sample sizes:
          Control Treated
All           425     297
Matched        74      55
```

Exact Matching

```
exact.data <- match.data(exact.match)
```

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```

```
head(exact.data)
          u74 u75   weights subclass
     16110   1   1 1.0000000        1
     16141   1   1 1.0000000        2
 ... 16148   1   1 1.0000000        3
     16156   1   1 0.6727273        3
     16164   1   1 1.0000000        4
     16182   1   1 4.0363636       14
```

What is the Treatment Effect?

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summary(exact.model)
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summary(exact.model)


rmula = re78 ~ treated, data = exact.data, weights = exact.data$

Residuals:
   Min      1Q Median      3Q     Max
 -6482  -4584  -2123    2784   28842

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   3951.7      670.1   5.897 3.14e-08 ***
treated       1306.1     1026.2   1.273    0.205
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

Residual standard error: 5764 on 127 degrees of freedom
```

Treatment Effect Again

```
y.treat <-
weighted.mean(exact.data$re78[exact.data$treated == 1],
  exact.data$weights[exact.data$treated == 1])
```

Treatment Effect Again

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weighted.mean(exact.data$re78[exact.data$treated == 1],
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y.cont <-
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  exact.data$weights[exact.data$treated == 0])
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Treatment Effect Again

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weighted.mean(exact.data$re78[exact.data$treated == 1],
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y.cont <-
weighted.mean(exact.data$re78[exact.data$treated == 0],
  exact.data$weights[exact.data$treated == 0])


y.treat-y.cont
[1] 1306.075

lm(re78 ~ treated+ age + education + black
+ married + nodegree + re74 + re75
   + hispanic + u74 + u75, data = exact.data,
   weights=exact.data$weights)
```

Nearest Neighbor Matching

```
nearest.match <- matchit(formula = treated ~ age + education
  + black + married + nodegree + re74 + re75 + hispanic +
  u74 + u75, data = LL, method = "nearest", distance = "logit")
```

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```
pre.balance <- summary(nearest.match)$sum.all
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```

```
pre.balance <- summary(nearest.match)$sum.all
```

```
post.balance <- summary(nearest.match)$sum.matched
```

Nearest Neighbor Matching

```
plot(x = (pre.balance[,1] - pre.balance[,2])/pre.balance[,3],
     y = 1:nrow(pre.balance), pch = 19, col = "burlywood2",
     xlab = "Standardized Imbalance", axes = FALSE,
     xlim = c(-.25,.25), ylab = "")
```

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plot(x = (pre.balance[,1] - pre.balance[,2])/pre.balance[,3],
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points(x = (post.balance[,1] - post.balance[,2])/post.balance[,3
     y = 1:nrow(post.balance), pch = 19, col = "cadetblue2")
abline(v = 0, lty = "dashed")
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axis(1)
axis(2, at = 11:1, labels = rownames(pre.balance),
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axis(1)
axis(2, at = 11:1, labels = rownames(pre.balance),
    las = 1, cex.axis = .8)


legend("topright", legend = c("Pre-match","Post-match"),
   pch = c(19,19),
   col = c("burlywood2","cadetblue2"), cex = .8)
```
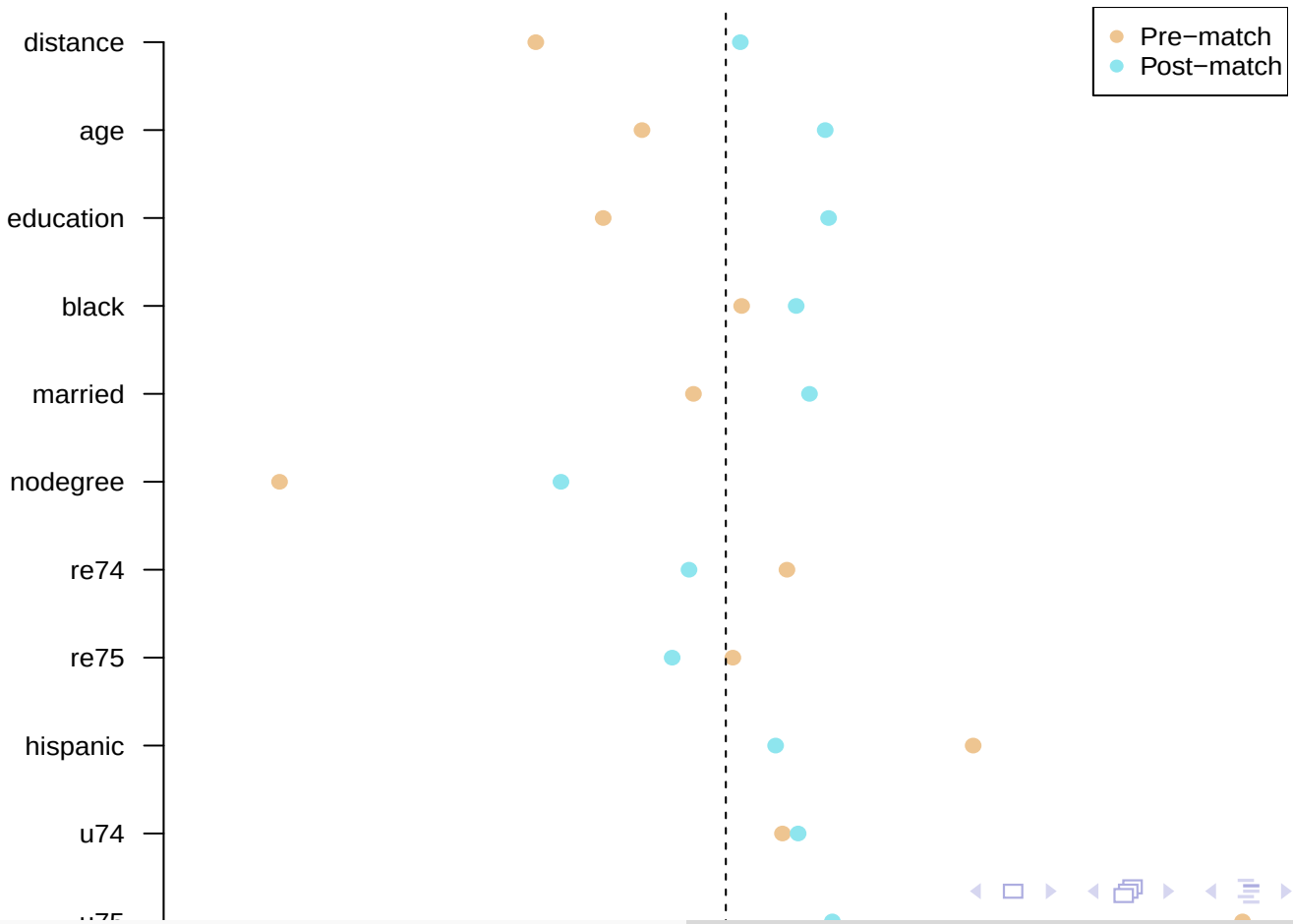

Nearest Neighbor Matching



Nearest Neighbor Matching

```
nearest.data <- match.data(nearest.match)
```

Nearest Neighbor Matching

```
nearest.data <- match.data(nearest.match)


head(nearest.data)
ack married nodegree      re74       re75
15993       1  33        12     0       1        0     0.000     0.0000
15994       1  20        12     0       1        0  8644.156  8644.1562
15995       0  39        12     1       1        0 19785.320  6608.1372
15996       1  49         8     0       1        1  9714.597  7285.9478
15997       0  26         8     0       1        1 37211.758 36941.2656
16000       0  27        12     1       1        0     0.000   752.3901
            re78 hispanic u74 u75  distance weights
15993 12418.0703        0   1   1 0.5237630       1
15994 11656.5059        0   0   0 0.5519635       1
15995   499.2572        0   0   0 0.4759660       1
15996 16717.1211        0   0   0 0.4460371       1
15997 30247.5000        0   0   0 0.3516366       1
16000     0.0000        0   1   0 0.5904726       1

## non-parametric estimate of the ATT
mean(nearest.data$re78[nearest.data$treated == 1]) - mean(nearest.data$re78[nearest.data$treated == 0])
[1] 1042.897

## A model-based estimate of the ATT

nearest.model <- lm(re78 ~ treated + age + education + black
  + married + nodegree + re74 + re75 + hispanic + u74 + u75,
  data = nearest.data)
```

CEM: Automatic Coarsening

```
auto.match <- matchit(formula = treated ~ age + education
  + black + married + nodegree + re74 + re75 + hispanic +
  u74 + u75, data = LL, method = "cem")
```

CEM: Automatic Coarsening

```
auto.match <- matchit(formula = treated ~ age + education
  + black + married + nodegree + re74 + re75 + hispanic +
  u74 + u75, data = LL, method = "cem")
```

```
auto.match
Call:
matchit(formula = treated ~ age + education + black + married +
    nodegree + re74 + re75 + hispanic + u74 + u75, data = LL,
    method = "cem")

Sample sizes:
             Control Treated
All              425     297
Matched        222     163
Unmatched      203     134
Discarded        0       0
```

CEM: User Coarsening

```
re74cut <- hist(LL$re74, plot=FALSE)$breaks
```

CEM: User Coarsening

```
re74cut <- hist(LL$re74, plot=FALSE)$breaks

re75cut <- seq(0, max(LL$re75)+1000, by=1000)
```

CEM: User Coarsening

```
re74cut <- hist(LL$re74, plot=FALSE)$breaks

re75cut <- seq(0, max(LL$re75)+1000, by=1000)

agecut <- c(20.5, 25.5, 30.5,35.5,40.5)
```

CEM: User Coarsening

```
re74cut <- hist(LL$re74, plot=FALSE)$breaks

re75cut <- seq(0, max(LL$re75)+1000, by=1000)

agecut <- c(20.5, 25.5, 30.5,35.5,40.5)

my.cutpoints <- list(re75=re75cut, re74=re74cut, age=agecut)
```

CEM: User Coarsening

```
re74cut <- hist(LL$re74, plot=FALSE)$breaks

re75cut <- seq(0, max(LL$re75)+1000, by=1000)

agecut <- c(20.5, 25.5, 30.5,35.5,40.5)

my.cutpoints <- list(re75=re75cut, re74=re74cut, age=agecut)

user.match <-  matchit(formula = treated ~ age + education
  + black + married + nodegree + re74 + re75 + hispanic +
  u74 + u75, data = LL, method = "cem", cutpoints
  = my.cutpoints)
```

CEM: User Coarsening

```
user.data <- match.data(user.match)
auto.data <- match.data(auto.match)
```

CEM: User Coarsening

```
user.data <- match.data(user.match)
auto.data <- match.data(auto.match)

user.imb <- imbalance(group=user.data$treated, data=user.data,
drop=c("treated","re78","distance","weights","subclass"))
```

CEM: User Coarsening

```
user.data <- match.data(user.match)
auto.data <- match.data(auto.match)

user.imb <- imbalance(group=user.data$treated, data=user.data,
drop=c("treated","re78","distance","weights","subclass"))

auto.imb <- imbalance(group=auto.data$treated, data=auto.data,
drop=c("treated","re78","distance","weights","subclass"))
```

CEM: User Coarsening

```
user.data <- match.data(user.match)
auto.data <- match.data(auto.match)

user.imb <- imbalance(group=user.data$treated, data=user.data,
drop=c("treated","re78","distance","weights","subclass"))

auto.imb <- imbalance(group=auto.data$treated, data=auto.data,
drop=c("treated","re78","distance","weights","subclass"))

user.imb$L1

Multivariate Imbalance Measure: L1=0.437
Percentage of local common support: LCS=43.1%
```

CEM: User Coarsening

```
user.data <- match.data(user.match)
auto.data <- match.data(auto.match)

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drop=c("treated","re78","distance","weights","subclass"))

auto.imb <- imbalance(group=auto.data$treated, data=auto.data,
drop=c("treated","re78","distance","weights","subclass"))

user.imb$L1

Multivariate Imbalance Measure: L1=0.437
Percentage of local common support: LCS=43.1%
```

CEM: Compare the Two

```
summary(user.match)$nn
           Control Treated
All            425     297
Matched        182     136
Unmatched      243     161
Discarded        0       0
```

CEM: Compare the Two

```
summary(user.match)$nn
           Control Treated
All            425     297
Matched        182     136
Unmatched      243     161
Discarded        0       0
```

```
summary(auto.match)$nn
           Control Treated
All            425     297
Matched        222     163
Unmatched      203     134
Discarded        0       0
```

CEM: Causal Effects

```
cem.match <- cem(treatment = "treated", data = LL,
    drop = "re78")
```

CEM: Causal Effects

```
cem.match <- cem(treatment = "treated", data = LL,
    drop = "re78")
```

```
cem.match.att <- att(obj=cem.match, formula=re78 ~ treated,
    data = LL, model="linear")
```

CEM: Causal Effects

```
cem.match <- cem(treatment = "treated", data = LL,
    drop = "re78")
```

```
cem.match.att <- att(obj=cem.match, formula=re78 ~ treated,
    data = LL, model="linear")
```

```
cem.match.att # default is linear model
 G0   G1
All        425 297
Matched    222 163
Unmatched 203 134

Linear regression model on CEM matched data:
```

CEM: Causal Effects with a Model

```
cem.match.att2 <- att(obj=user.match, formula=re78 ~ treated +
age+education+black+married+nodegree+re74+re75
+hispanic+u74+u75,
data = LL, model="linear")
```

CEM: Causal Effects with a Model

```
cem.match.att2 <- att(obj=user.match, formula=re78 ~ treated +
age+education+black+married+nodegree+re74+re75
+hispanic+u74+u75,
data = LL, model="linear")
```

```
cem.match.att2
 G0   G1
All        425 297
Matched    222 163
Unmatched 203 134

Linear regression model on CEM matched data:

SATT point estimate: 550.962564 (p.value=0.368242)
95% conf. interval: [-647.777701, 1749.702830]
```