Section 1: Hospital Pricing and Selection on Observables

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Econ 470 & HLTH 470

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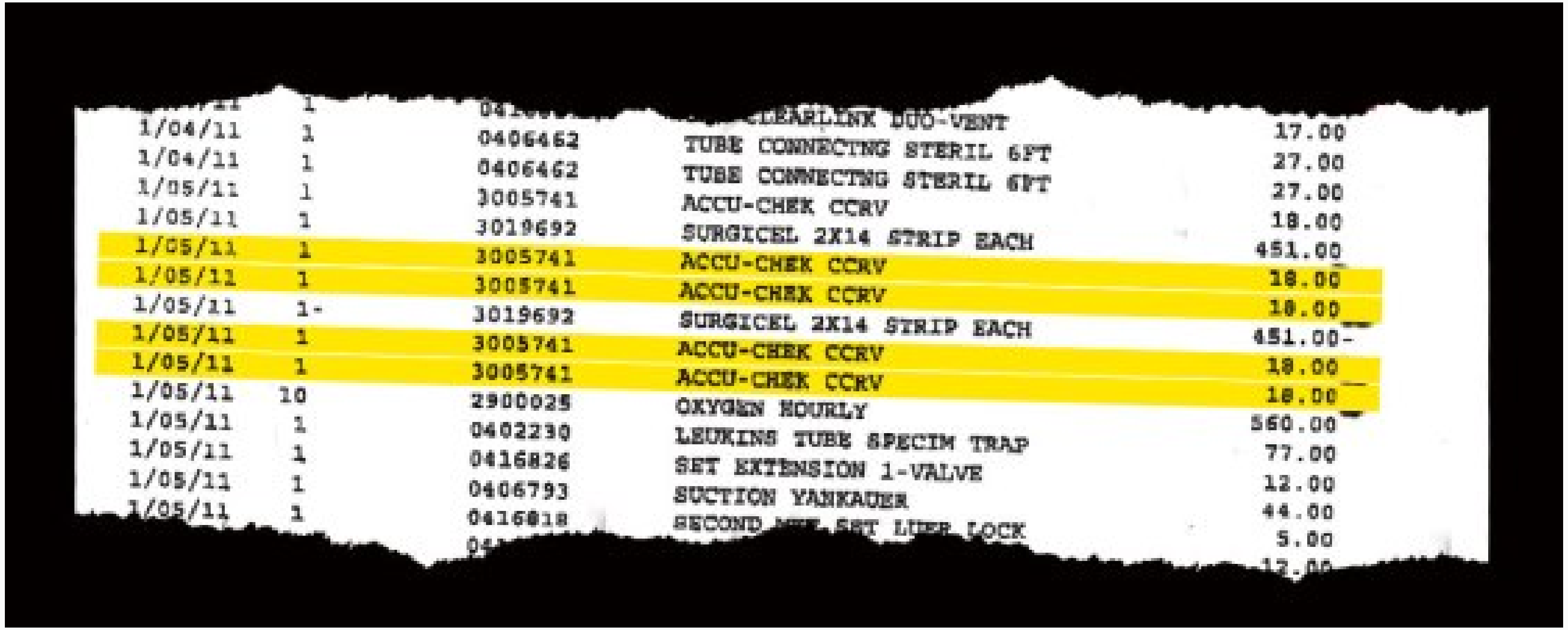
Background on Hospital Pricing

What is a hospital price?

Defining characteristic of hospital services: *it's complicated!*



1/04/11	1	0406462	TUBE CONNECTNG STERIL 6FT	27.00
1/04/11	1	0406462	TUBE CONNECTNG STERIL 6FT	27.00
1/05/11	1	3005741	ACCU-CHEK CCRV	18.00
1/05/11	1	3019692	SURGICEL 2X14 STRIP EACH	451.00
1/05/11	1	3005741	ACCU-CHEK CCRV	18.00
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1/05/11	1	3005741	ACCU-CHEK CCRV	18.00
1/05/11	1	3005741	ACCU-CHEK CCRV	18.00
1/05/11	10	2900025	OXYGEN HOURLY	560.00
1/05/11	1	0402230	LEUKINS TUBE SPECIM TRAP	77.00
1/05/11	1	0416826	SET EXTENSION 1-VALVE	12.00
1/05/11	1	0406793	SUCTION YANKAUER	44.00
1/05/11	1	0416818	SECOND [illegible] SET LUER LOCK	5.00

Brill, Steven. 2013. "Bitter Pill: Why Medical Bills are Killing Us." *Time Magazine*.

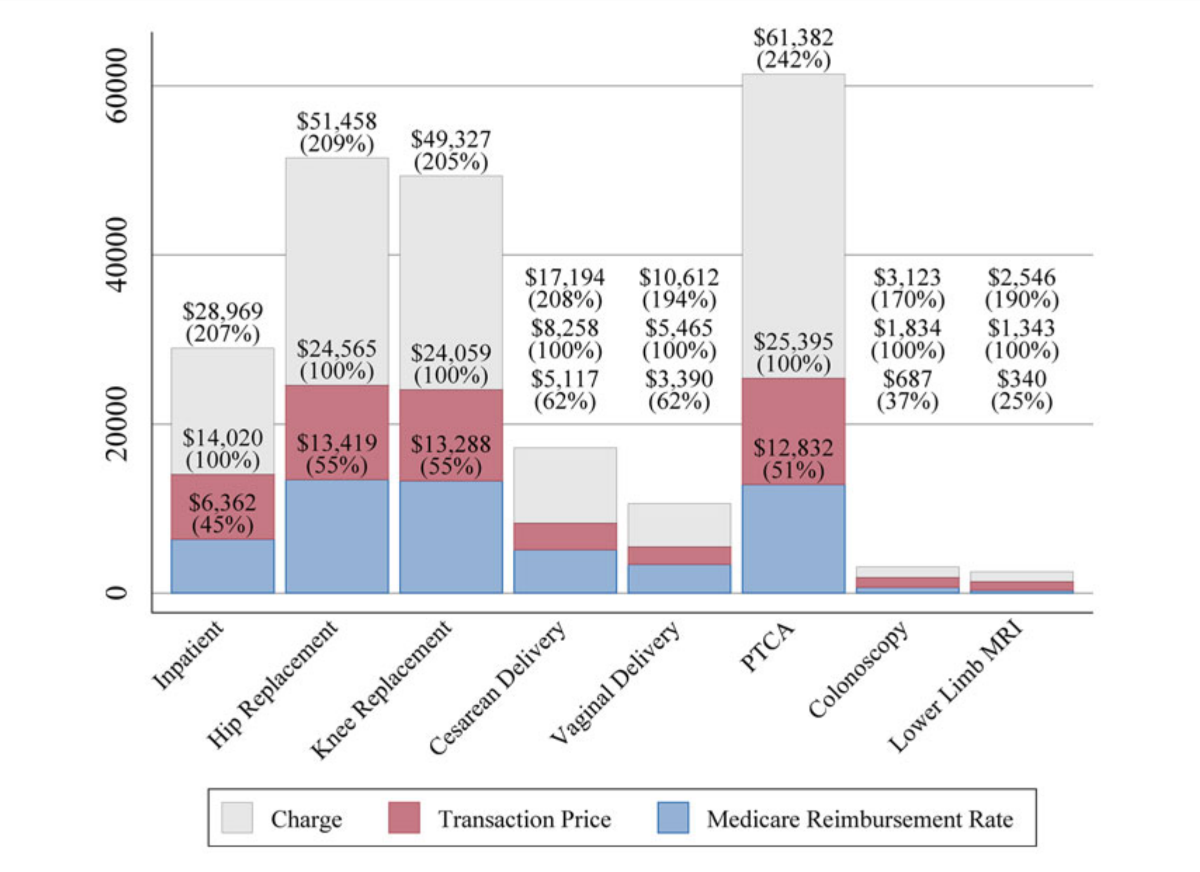
What is a hospital price?

Lots of different payers paying lots of different prices:

- Medicare fee-for-service prices
- Medicaid payments
- Private insurance negotiations (including Medicare Advantage)
- But what about the price to patients?

$$\text{Price} \neq \text{charge} \neq \text{cost} \neq \text{patient out-of-pocket spending}$$

What is a hospital price?



Source: Health Care Pricing Project

What is a hospital price?

Not clear what exactly is negotiated...

Fee-for-service

- price per procedure
- percentage of charges
- markup over Medicare rates

Capitation

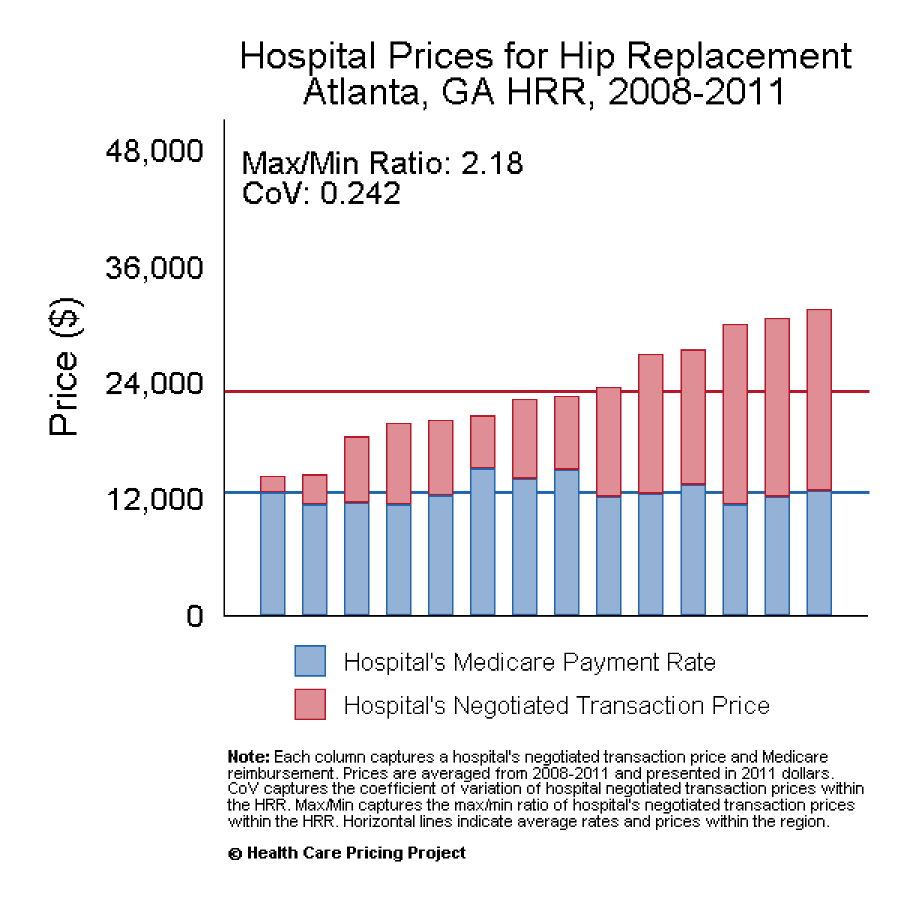
- payment per patient
- pay-for-performance
- shared savings

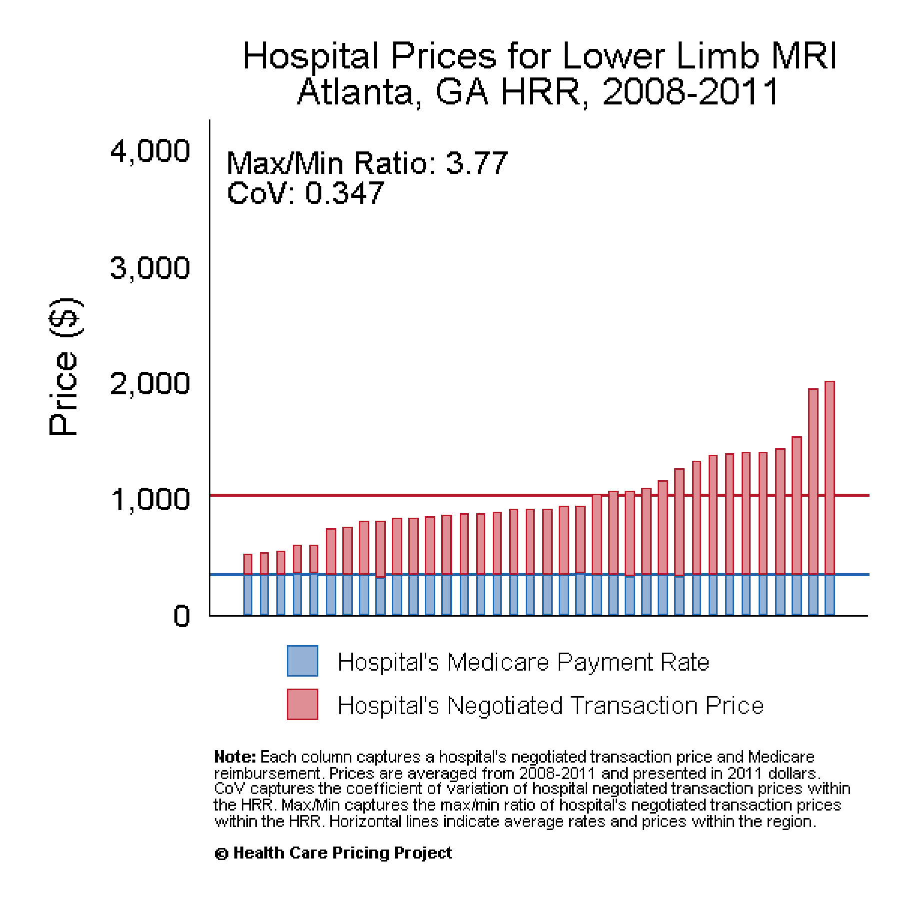
Hospital prices in real life

A few empirical facts:

1. Hospital services are expensive
2. Prices vary dramatically across different areas
3. Lack of competition is a major reason for high prices

Hospital prices in real life





Source: Health Care Pricing Project

Understanding HCRIS Data

What is HCRIS?

Healthcare Cost Report Information System ('cost reports')

- Nursing Homes (SNFs)
- Hospice
- Home Health Agencies
- Hospitals

Hospital Cost Reports

10-12 FORM CMS-2552-10 4090 (Cont.)

STATEMENT OF PATIENT REVENUES AND OPERATING EXPENSES	PROVIDER CCN: ______________	PERIOD: FROM ____________ TO ____________	WORKSHEET G-2, PARTS I & II

PART I - PATIENT REVENUES

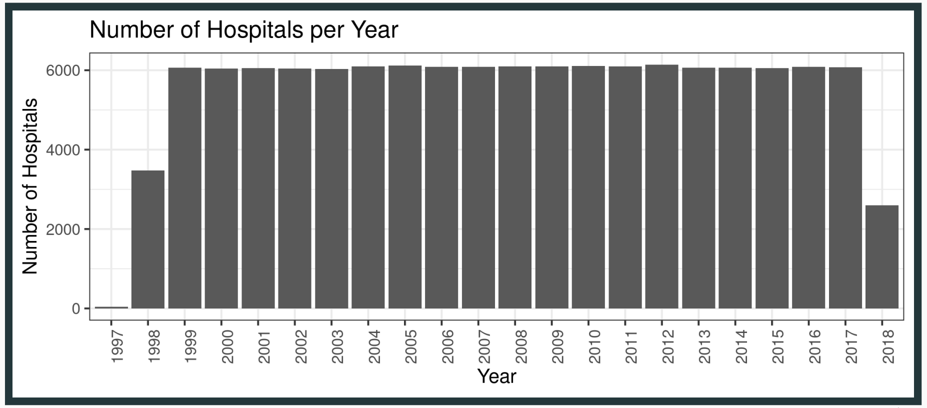
	REVENUE CENTER	INPATIENT	OUTPATIENT	TOTAL	
		1	2	3	
	GENERAL INPATIENT ROUTINE CARE SERVICES				
1	Hospital				1
2	Subprovider IPF				2
3	Subprovider IRF				3
4	Subprovider (Other)				4
5	Swing bed - SNF				5
6	Swing bed - NF				6
7	Skilled nursing facility				7
8	Nursing facility				8
9	Other long term care				9
10	Total general inpatient care services (sum of lines 1-9)				10
	INTENSIVE CARE TYPE INPATIENT HOSPITAL SERVICES				
11	Intensive care unit				11
12	Coronary care unit				12
13	Burn intensive care unit				13
14	Surgical intensive care unit				14
15	Other special care (specify)				15
16	Total intensive care type inpatient hospital services (sum of of lines 11-15)				16
17	Total inpatient routine care services (sum of lines 10 and 16)				17
18	Ancillary services				18
19	Outpatient services				19
20	Rural Health Clinic (RHC)				20
21	Federally Qualified Health Center (FQHC)				21
22	Home health agency				22

The Data

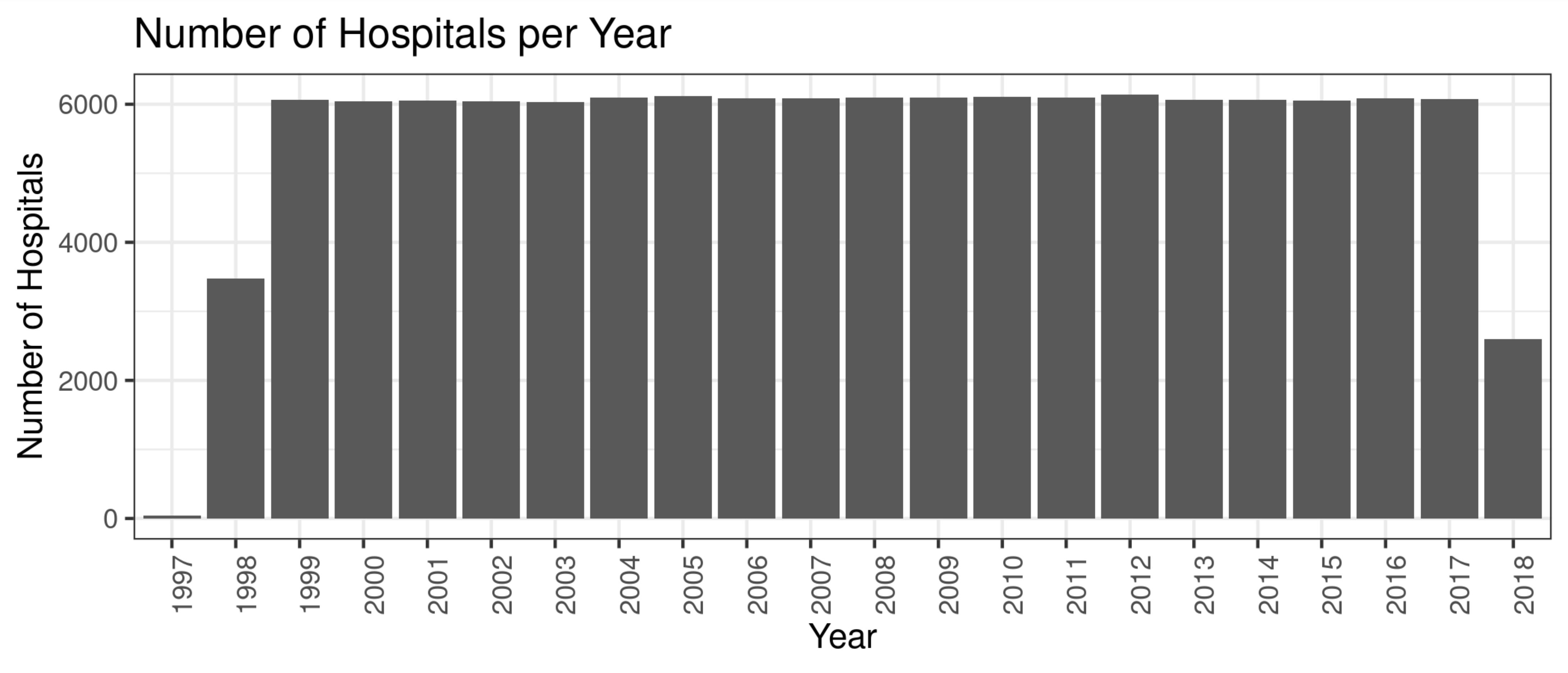
Let's work with the HCRIS GitHub repository. But forming the dataset is up to you this time.

The Data

```
hcris.data %>%
  ggplot(aes(x=as.factor(year))) +
  geom_bar() +
  labs(
    x="Year",
    y="Number of Hospitals",
    title="Number of Hospitals per Year"
  ) + theme_bw() +
  theme(axis.text.x = element_text(angle = 90, hjust=1))
```



Number of hospitals

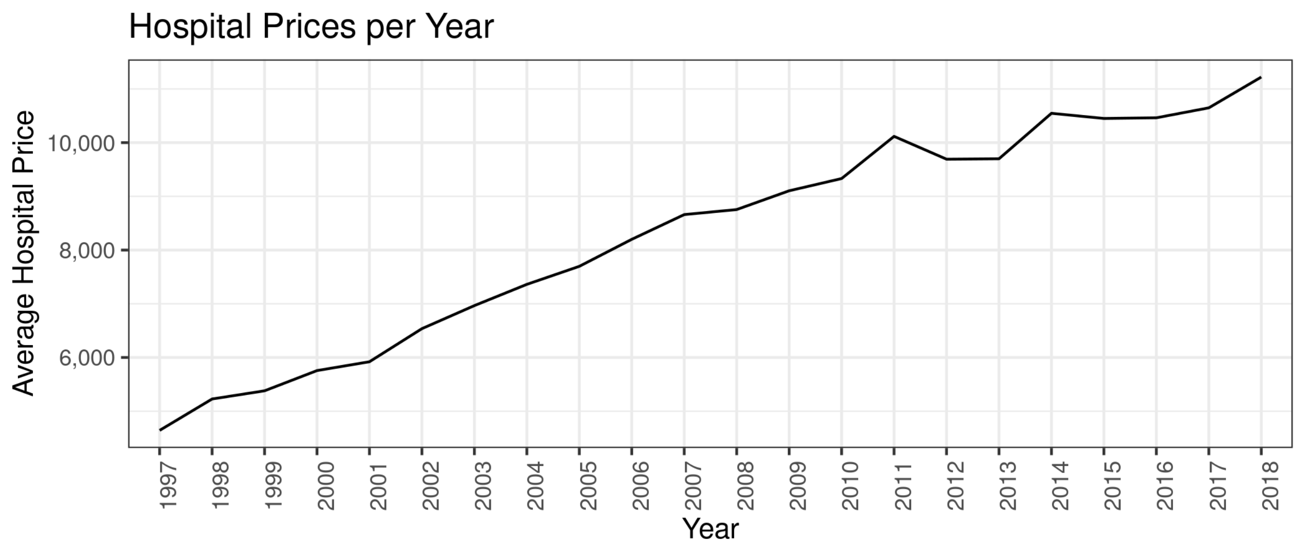


Estimating hospital prices

```
hcris.data <- hcris.data %>%
  mutate( discount_factor = 1-tot_discounts/tot_charges,
          price_num = (ip_charges + icu_charges + ancillary_charges)*discount_factor - tot_mcare_payment,
          price_denom = tot_discharges - mcare_discharges,
          price = price_num/price_denom)
```

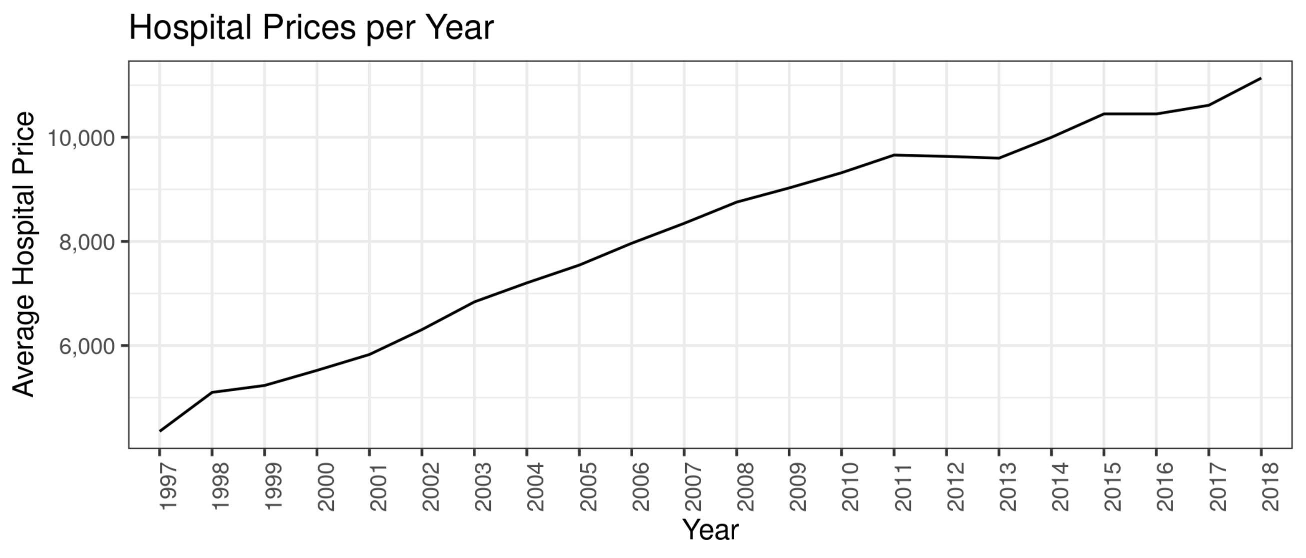
Estimating hospital prices

```
hcris.data %>% group_by(year) %>%
  filter(price_denom>10, !is.na(price_denom),
         price_num>0, !is.na(price_num)) %>%
  select(price, year) %>%
  summarize(mean_price=mean(price, na.rm=TRUE
  ggplot(aes(x=as.factor(year), y=mean_price)
  geom_line(aes(group=1)) +
  labs(
    x="Year",
    y="Average Hospital Price",
    title="Hospital Prices per Year"
  ) + scale_y_continuous(labels=comma) +
  theme_bw() + theme(axis.text.x = element_te
```



Estimating hospital prices

```
hcris.data %>% group_by(year) %>%
  filter(price_denom>100, !is.na(price_denom)
         price_num>0, !is.na(price_num),
         price<100000) %>%
  select(price, year) %>%
  summarize(mean_price=mean(price, na.rm=TRUE
  ggplot(aes(x=as.factor(year), y=mean_price)
  geom_line(aes(group=1)) +
  labs(
    x="Year",
    y="Average Hospital Price",
    title="Hospital Prices per Year"
  ) + scale_y_continuous(labels=comma) +
  theme_bw() + theme(axis.text.x = element_te
```



Potential Outcomes Framework

Causal Inference and Potential Outcomes

- **Goal:** Estimate effect of some policy or program
- Key building block for causal inference is the idea of **potential outcomes**

Some notation

Observed outcome

$$Y_i = Y_{1i} \times D_i + Y_{0i} \times (1 - D_i)$$

or

$$Y_i = \begin{cases} Y_{1i} \text{ if } D_i = 1 \\ Y_{0i} \text{ if } D_i = 0 \end{cases}$$

Assumes **SUTVA** (stable unit treatment value assumption)…no interference across units

Example of "Potential Outcomes"

Y_1 = \$75,000

Y_0 = \$60,000

Earnings due to Emory = $Y_1 - Y_0$ = \$15,000

Example of "Potential Outcomes"

Y_1 = \$75,000

Y_0 = ?

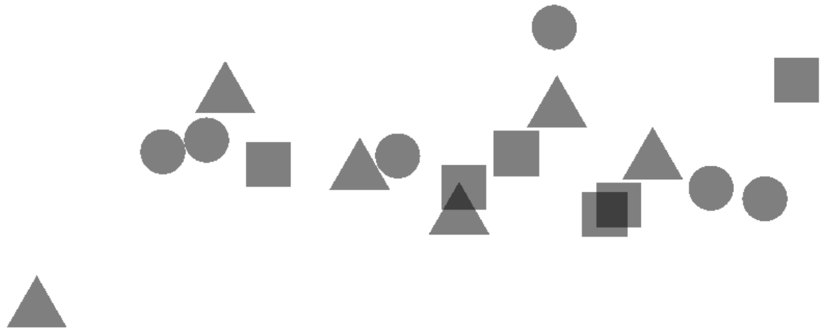
Earnings due to Emory = $Y_1 - Y_0$ = ?

Do we ever observe the potential outcomes?

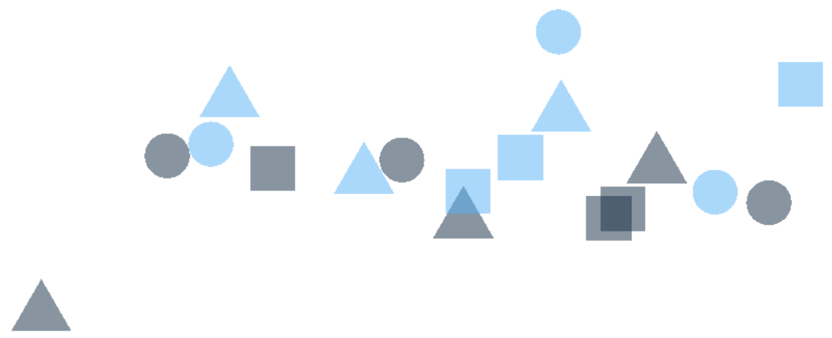
Without a time machine...hard (impossible?) to get *individual* effects.

Average Treatment Effects

Average Treatment Effect

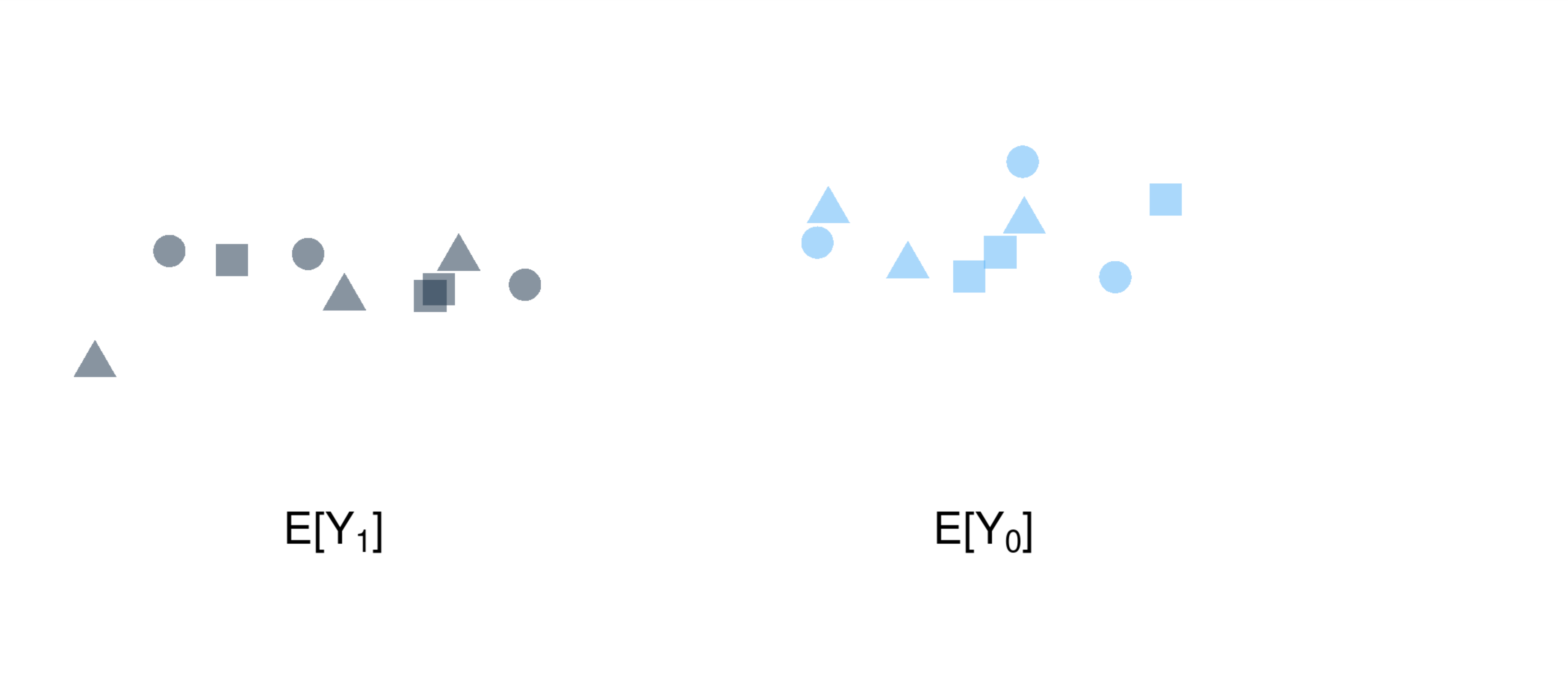


Average Treatment Effect



Average Treatment Effect

Average Treatment Effect



$$ATE = E[Y_1 - Y_0]$$

More formally

- **ATE**: $\delta_{ATE} = E[Y_1 - Y_0]$
- **ATT**: $\delta_{ATT} = E[Y_1 - Y_0|D = 1]$
- **ATU**: $\delta_{ATU} = E[Y_1 - Y_0|D = 0]$

Easy to write, hard to estimate

- In words, the potential outcome without treatment, Y_{0i}, is different between those that ultimately did and did not receive treatment.

- e.g., treated group was going to be better on average even without treatment (higher wages, healthier, etc.)

Alleviating Selection Bias

- Easiest way to think of this is with random assignment
- In this case, treatment assignment doesn't tell us anything about Y_{0i}
- So, when D_i is randomly assigned,

$$E[Y_{0i}|D_i = 1] = E[Y_{0i}|D_i = 0],$$

such that

$$E[Y_i|D_i = 1] - E[Y_i|D_i = 0] = \delta_{ATE} = \delta_{ATT} = \delta_{ATU}$$

In practice

- Nothing more than averages

- **Estimand**:

$$\delta_{ATE} = E[Y_1 - Y_0] = E[Y|D=1] - E[Y|D=0]$$

- **Estimate**:

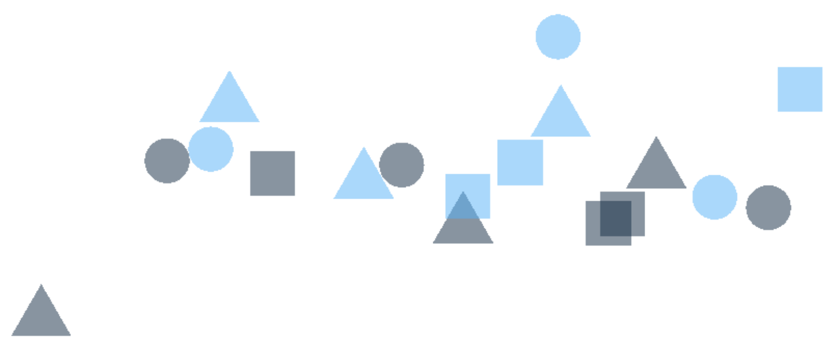
$$\hat{\delta}_{ATE} = \frac{1}{N_1}\sum_{D_i=1} Y_i - \frac{1}{N_0}\sum_{D_i=0} Y_i,$$

  where N_1 is number of treated and N_0 is number untreated (control)

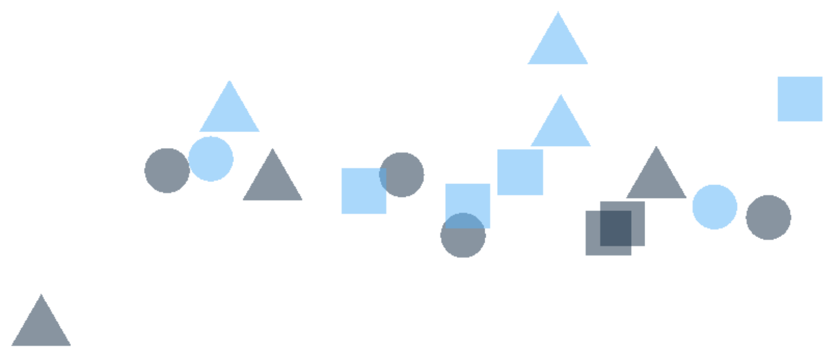
- Inference/hypothesis testing with standard two-sample t-test

Selection on Observables

Average Treatment Effect

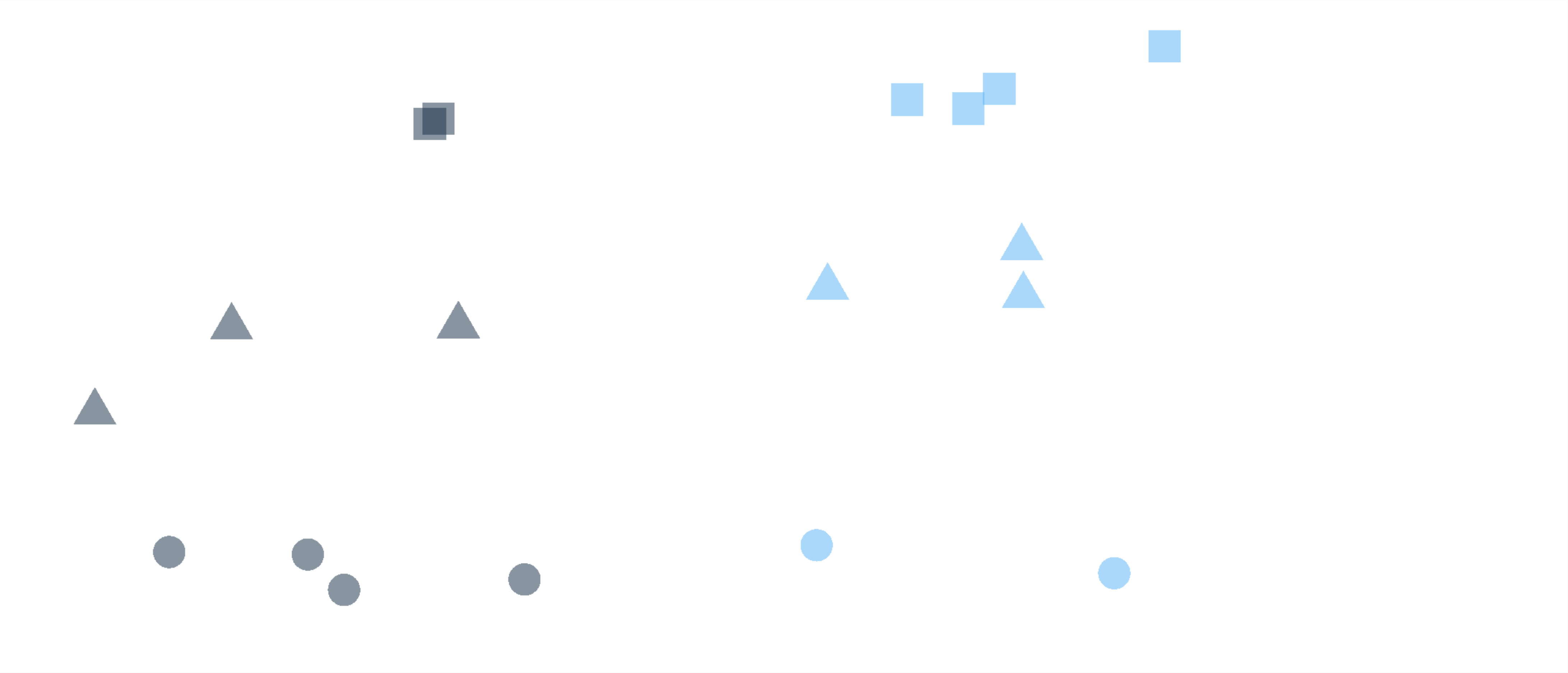


…with Selection

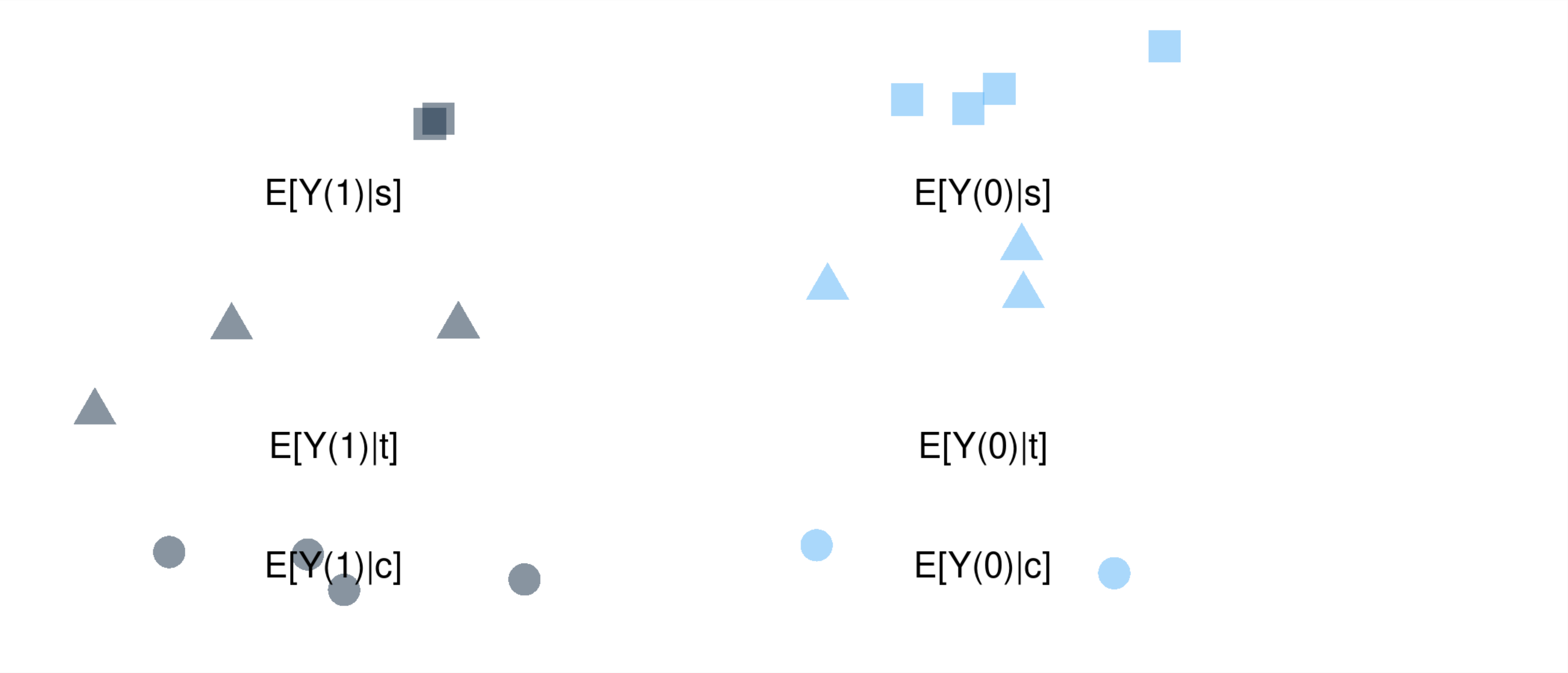


...with Selection

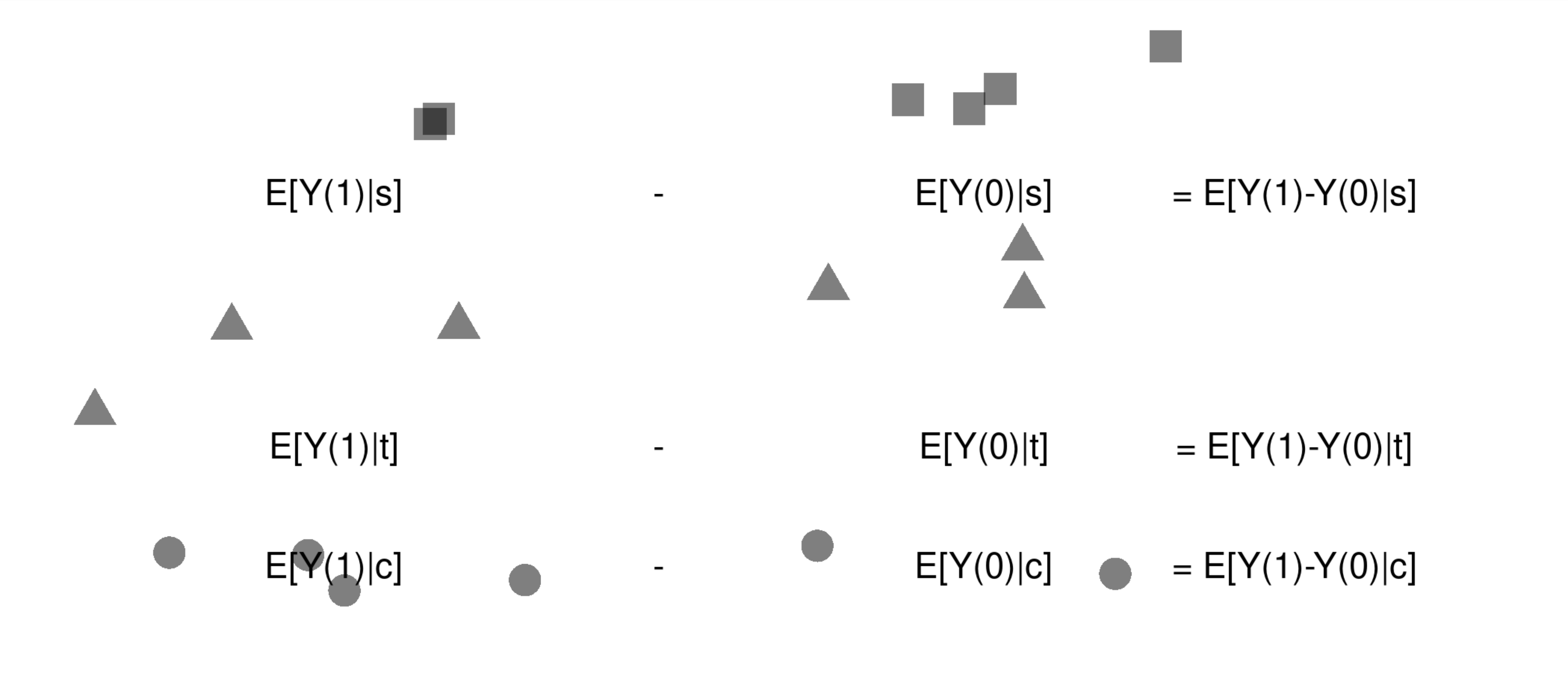
...with Selection



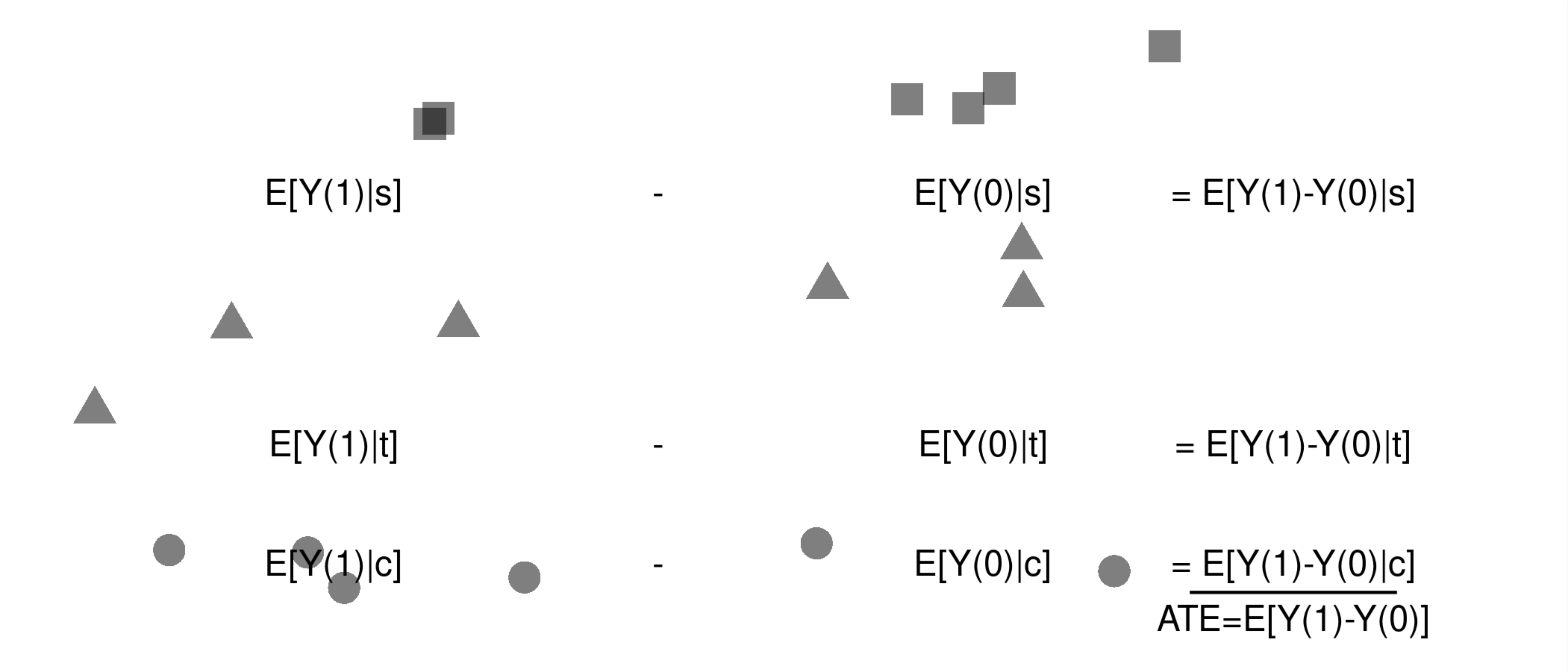
...with Selection



Assumption 1: Selection on Observables



Assumption 1: Selection on Observables



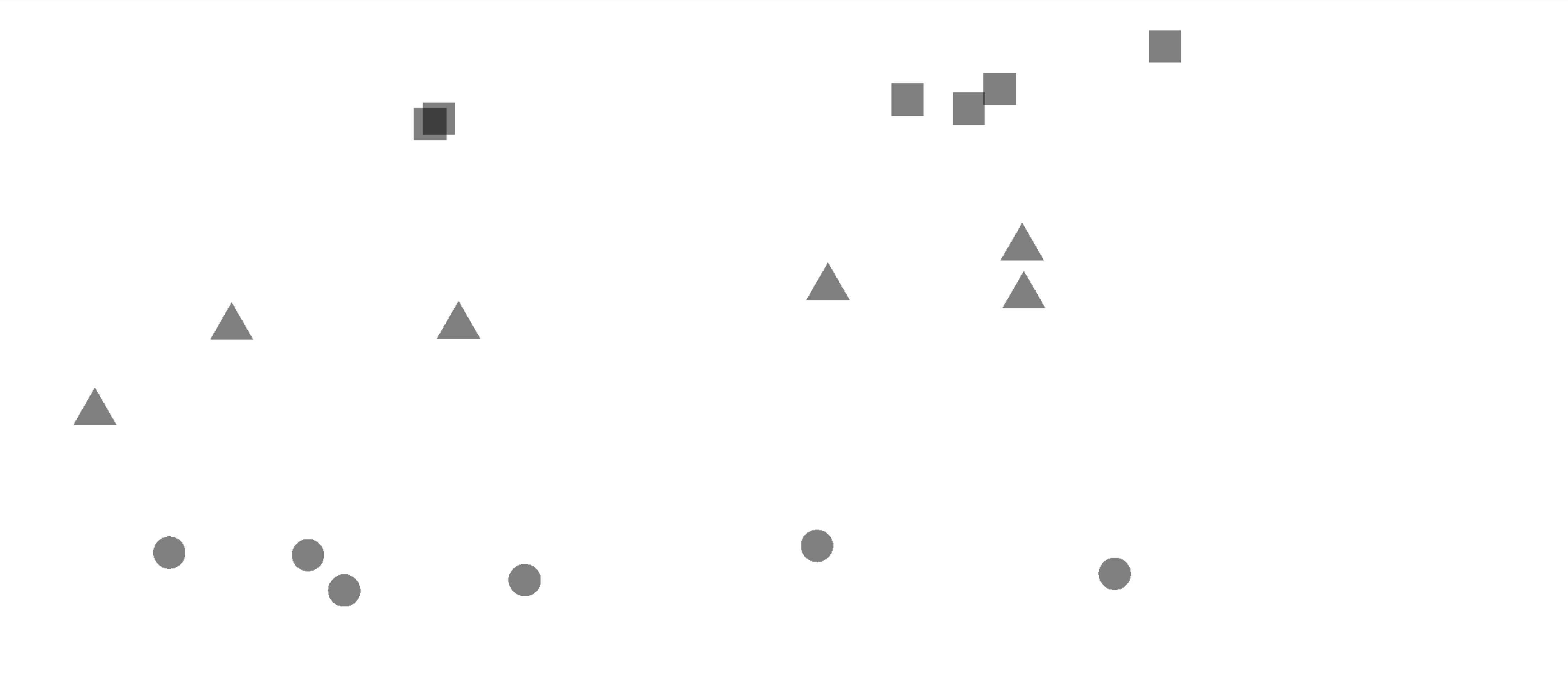
Assumption 1: Selection on Observables

More formally:

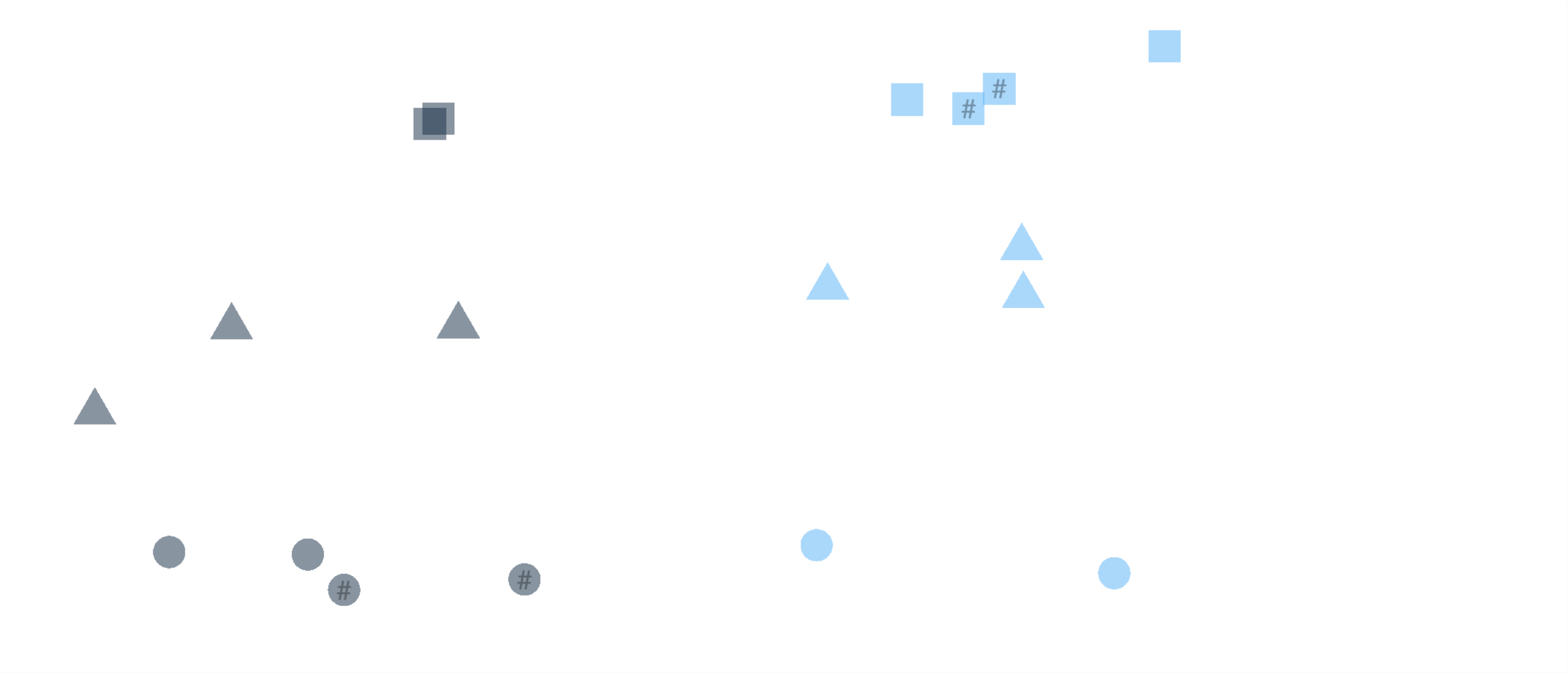
- $E[Y(1)|W, shape] = E[Y(1)|shape]$
- $Y(1), Y(0) \perp\!\!\!\perp W|shape$

In words...nothing unobserved that determines treatment selection and affects your outcome of interest.

Violation of Selection on Observables



Violation of Selection on Observables

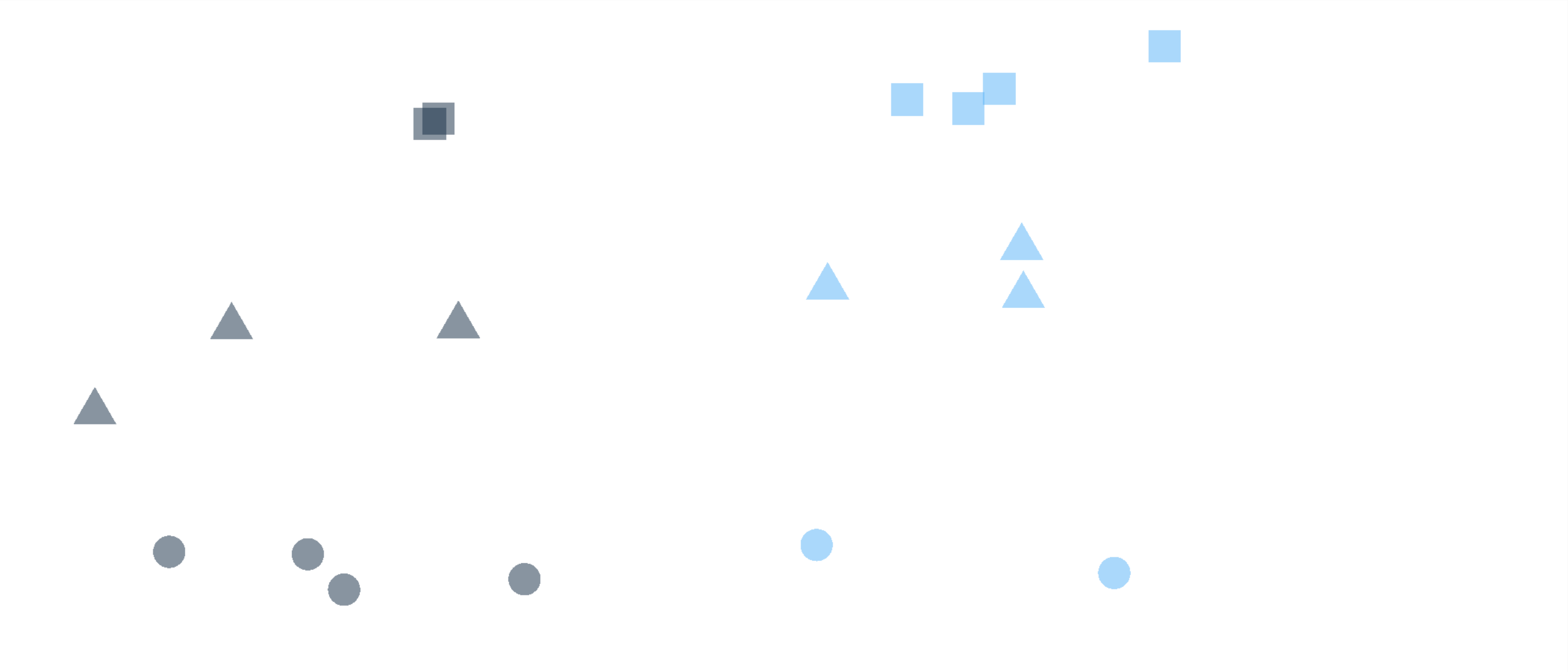


Assumption 2: Common Support

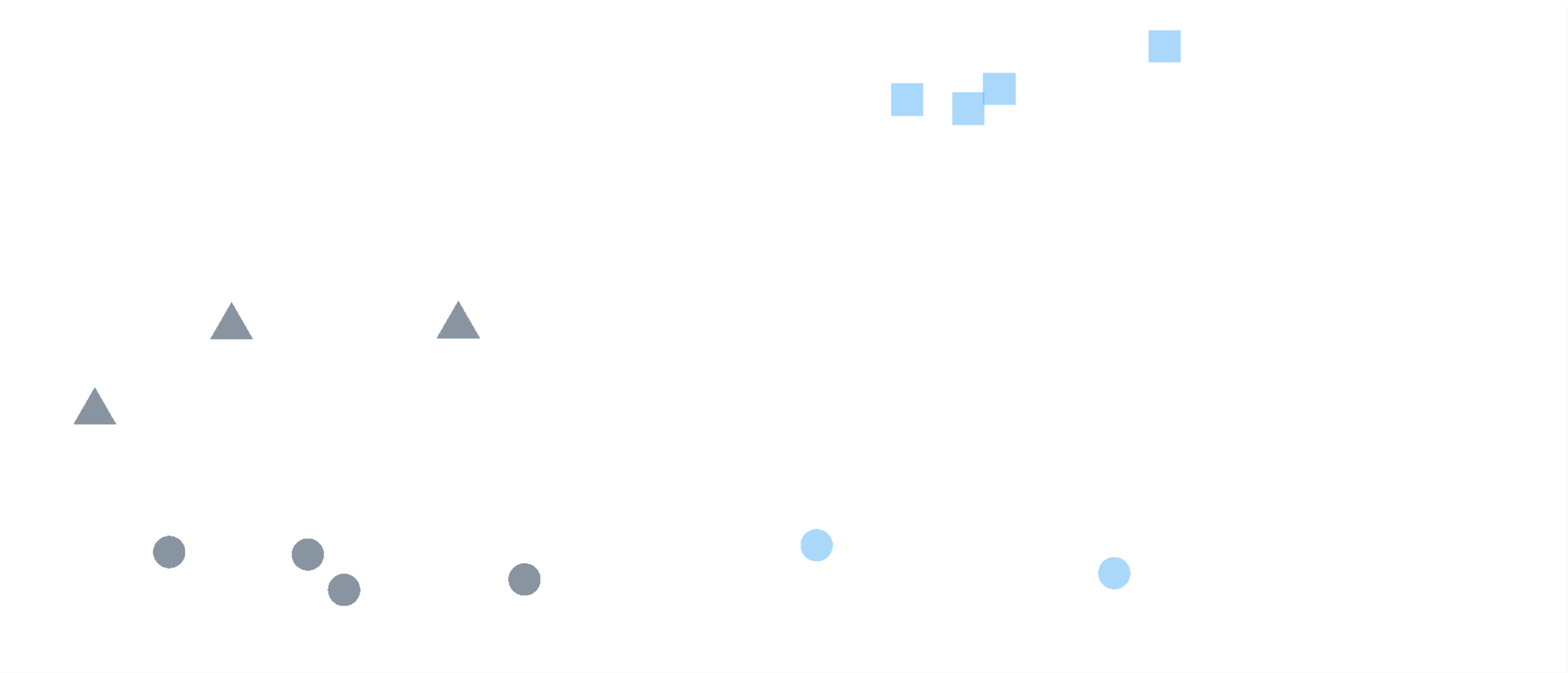
Someone of each type must be in both the treated and untreated groups

$$0 < \Pr(W = 1|X) < 1$$

Assumption 2: Common Support



Violation of Common Support



Causal Inference with Observational Data

Fundamental Problem of Causal Inference

Potential outcomes:

- $Y_i(1)$ for $W_i = 1$
- $Y_i(0)$ for $W_i = 0$

Average treatment effect is $E[Y_i(1) - Y_i(0)]$, but:

- $E[Y_i | W_i = 1] \neq E[Y_i(1)]$
- $E[Y_i | W_i = 0] \neq E[Y_i(0)]$

Fundamental Problem of Causal Inference

- We don't observe the counterfactual outcome...what would have happened if a treated unit was actually untreated.

- *ALL* attempts at causal inference represent some attempt at estimating the counterfactual outcome. We need an estimate for $E[Y_i(0)]$ among those that were treated, and vice versa for $E[Y_i(1)]$.

Causal inference with observational data

Solution for now: find covariates X_i such that the following assumptions are plausible:

1. Selection on observables:

$$Y_i(1), Y_i(0) \perp\!\!\!\perp W_i | X_i$$

2. Common support:

$$0 < \Pr(W_i = 1 | X_i) < 1$$

Causal inference with observational data

With selection on observables and common support:

1. Matching estimators:

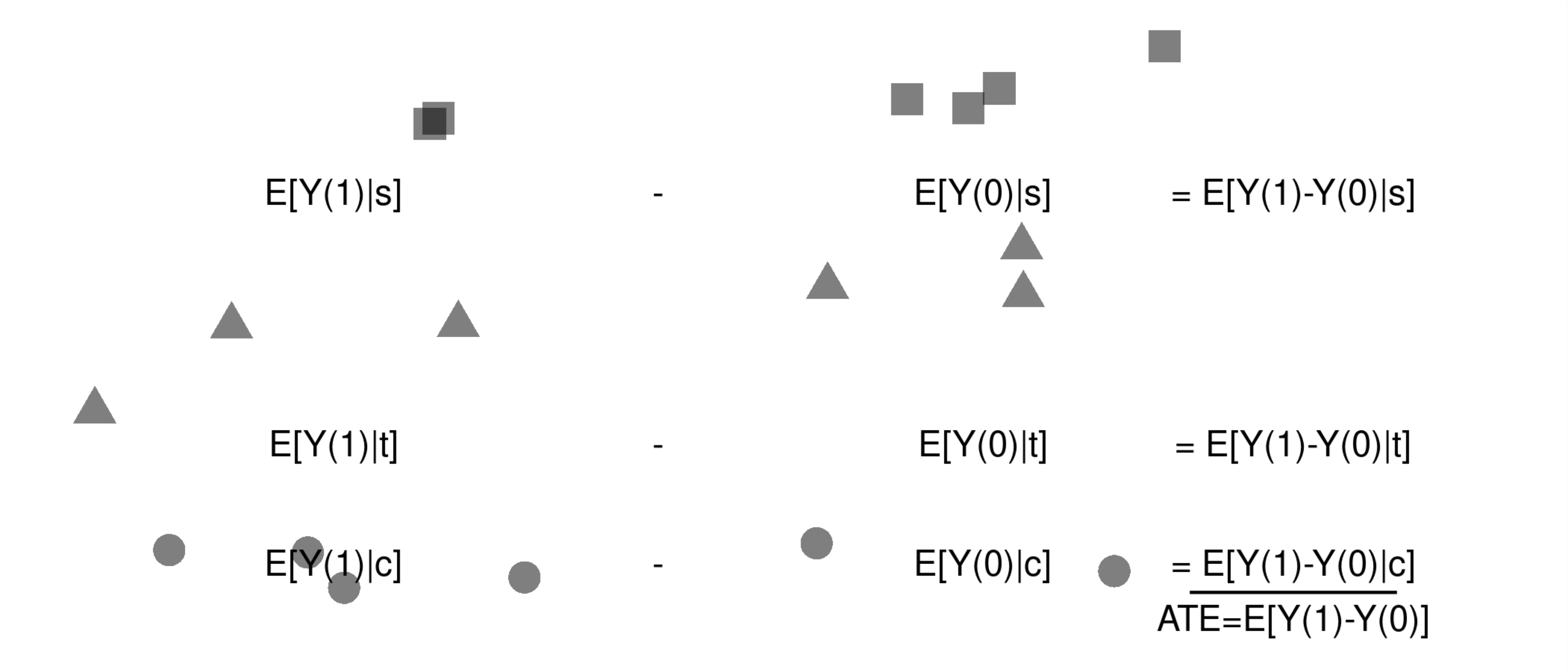
$$E[Y_i(1) - Y_i(0)] = E[E[Y_i|W_i = 1, X_i] - E[Y_i|W_i = 0, X_i]]$$

2. Regression estimators:

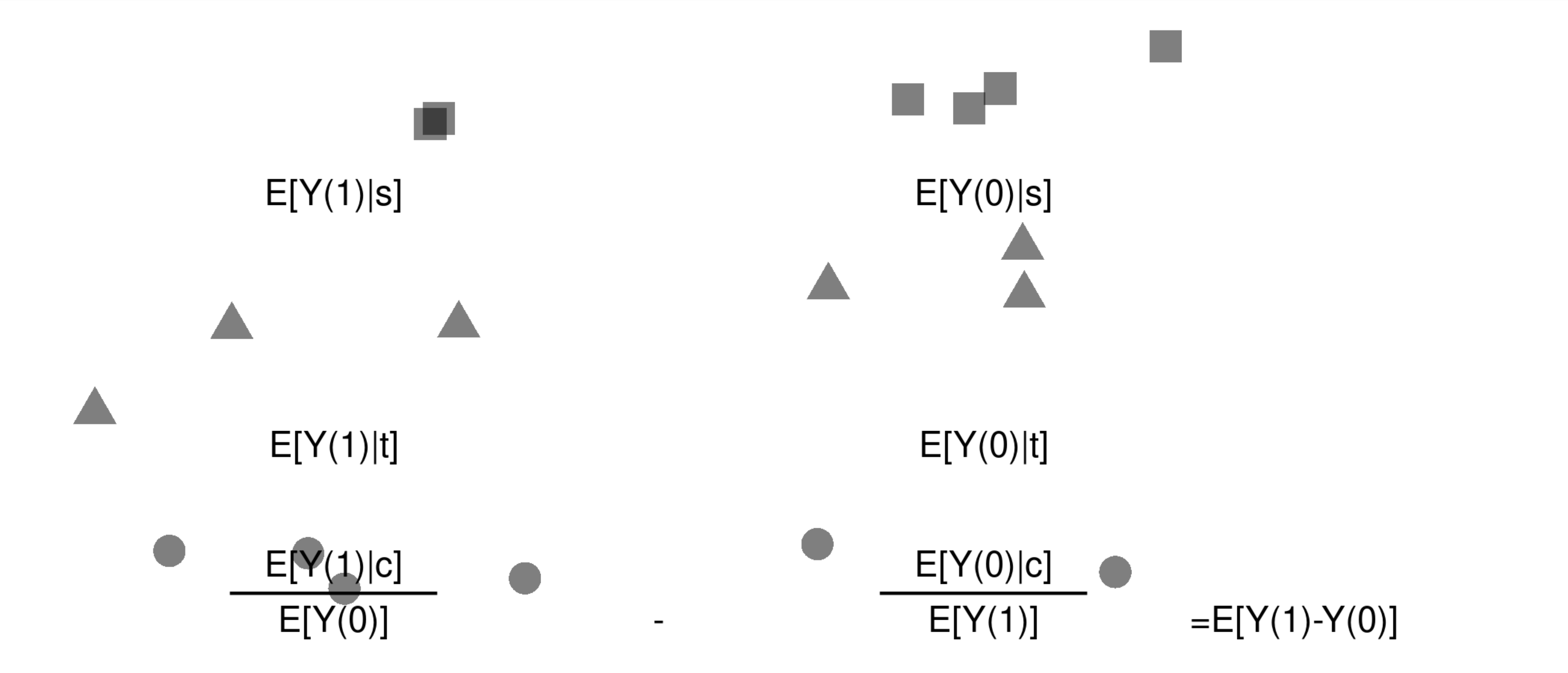
$$E[Y_i(1) - Y_i(0)] = E[E[Y_i|W_i = 1, X_i]] - E[E[Y_i|W_i = 0, X_i]]$$

What's the difference?

Matching


E[Y(1)|s] - E[Y(0)|s] = E[Y(1)-Y(0)|s]
E[Y(1)|t] - E[Y(0)|t] = E[Y(1)-Y(0)|t]
E[Y(1)|c] - E[Y(0)|c] = E[Y(1)-Y(0)|c]
ATE=E[Y(1)-Y(0)]

Regression



Estimation options

- Matching
- Weighting
- Regression
- Doubly-robust weighting + regression (won't cover)

Matching: The process

1. For each observation i, find the m "nearest" neighbors, $J_m(i)$.

2. Impute $\hat{Y}_i(0)$ and $\hat{Y}_i(1)$ for each observation:

$$\hat{Y}_i(0) = \begin{cases} Y_i & \text{if} \quad W_i = 0 \\ \frac{1}{m} \sum_{j \in J_m(i)} Y_j & \text{if} \quad W_i = 1 \end{cases}$$

$$\hat{Y}_i(1) = \begin{cases} Y_i & \text{if} \quad W_i = 1 \\ \frac{1}{m} \sum_{j \in J_m(i)} Y_j & \text{if} \quad W_i = 0 \end{cases}$$

3. Form "matched" ATE:
$\hat{\delta}^{\text{match}} = \frac{1}{N} \sum_{i=1}^{N} \left(\hat{Y}_i(1) - \hat{Y}_i(0) \right)$

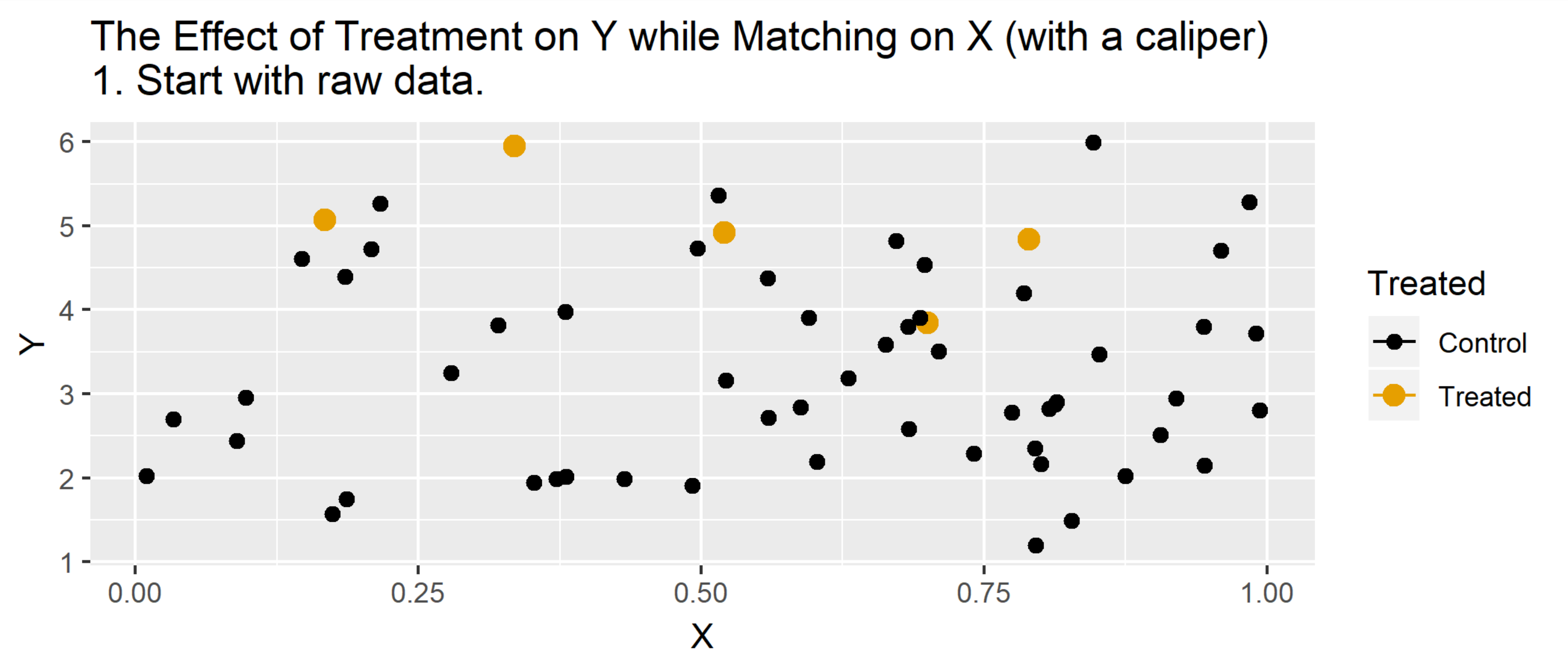
Matching: Defining "nearest"

1. Euclidean distance:
   $\sum_{k=1}^{K}(X_{ik} - X_{jk})^2$

2. Scaled Euclidean distance:
   $\sum_{k=1}^{K} \frac{1}{\sigma_{X_k}^2}(X_{ik} - X_{jk})^2$

3. Mahalanobis distance:
   $(X_i - X_j)'\Sigma_X^{-1}(X_i - X_j)$

Animation for matching



Weighting

1. Estimate propensity score `ps ← glm(W~X, family=binomial, data)`, denoted $\hat{\pi}(X_i)$
2. Weight by inverse of propensity score

$$\hat{\mu}_1 = \frac{\sum_{i=1}^N \frac{Y_i W_i}{\hat{\pi}(X_i)}}{\sum_{i=1}^N \frac{W_i}{\hat{\pi}(X_i)}} \text{ and } \hat{\mu}_0 = \frac{\sum_{i=1}^N \frac{Y_i(1-W_i)}{1-\hat{\pi}(X_i)}}{\sum_{i=1}^N \frac{1-W_i}{1-\hat{\pi}(X_i)}}$$

3. Form "inverse-propensity weighted" ATE:

$$\hat{\delta}^{IPW} = \hat{\mu}_1 - \hat{\mu}_0$$

Regression

1. Regress Y_i on X_i among $W_i = 1$ to form $\hat{\mu}_1(X_i)$
2. Regress Y_i on X_i among $W_i = 0$ to form $\hat{\mu}_0(X_i)$
3. Form difference in predictions:

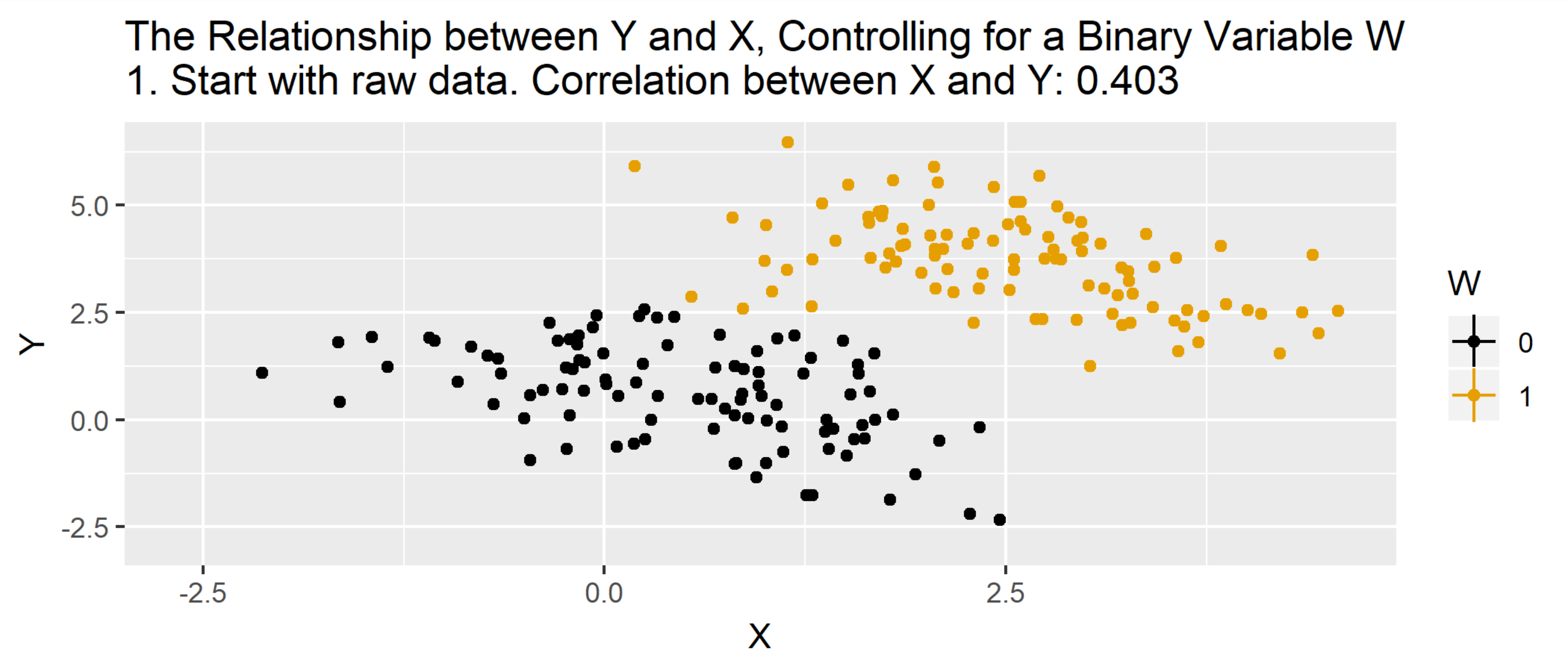
$$\hat{\delta}^{reg} = \frac{1}{N} \sum_{i=1}^{N} (\hat{\mu}_1(X_i) - \hat{\mu}_0(X_i))$$

Regression

Or estimate in one step,

$$Y_i = \delta W_i + \beta X_i + W_i \times \left(X_i - \bar{X}\right)\gamma + \varepsilon_i$$

Animation for regression



Simulated data

Now let's do some matching, re-weighting, and regression with simulated data:

```
n ← 5000
select.dat ← tibble(
  x = runif(n, 0, 1),
  z = rnorm(n, 0, 1),
  w = (x>0.65),
  y = -2.5 + 4*w + 1.5*x + rnorm(n,0,1),
  w_alt = ( x + z > 0.35),
  y_alt = -2.5 + 4*w_alt + 1.5*x + 2.25*z + rnorm(n,0,1)
)
```

Simulation: nearest neighbor matching

```
nn.est1 <- Matching::Match(Y=select.dat$y,
                           Tr=select.dat$w,
                           X=select.dat$x,
                           M=1,
                           Weight=1,
                           estimand="ATE")
summary(nn.est1)
```

```
##
## Estimate...  4.0175
## AI SE......  0.52954
## T-stat.....  7.5869
## p.val......  3.2863e-14
##
## Original number of observations..............  5000
## Original number of treated obs...............  1732
## Matched number of observations...............  5000
## Matched number of observations  (unweighted).  5016
```

Simulation: nearest neighbor matching

```r
nn.est2 <- Matching::Match(Y=select.dat$y,
                           Tr=select.dat$w,
                           X=select.dat$x,
                           M=1,
                           Weight=2,
                           estimand="ATE")
summary(nn.est2)
```

```
##
## Estimate...  4.0175
## AI SE......  0.52954
## T-stat.....  7.5869
## p.val......  3.2863e-14
##
## Original number of observations..............  5000
## Original number of treated obs...............  1732
## Matched number of observations...............  5000
## Matched number of observations  (unweighted).  5016
```

Simulation: regression

```r
reg1.dat <- select.dat %>% filter(w==1)
reg1 <- lm(y ~ x, data=reg1.dat)

reg0.dat <- select.dat %>% filter(w==0)
reg0 <- lm(y ~ x, data=reg0.dat)
pred1 <- predict(reg1,new=select.dat)
pred0 <- predict(reg0,new=select.dat)
mean(pred1-pred0)
```

```
## [1] 4.076999
```

Violation of selection on observables

NN Matching

```
nn.est3 <- Matching::Match(Y=select.dat$y_alt,
                           Tr=select.dat$w_alt,
                           X=select.dat$x,
                           M=1,
                           Weight=2,
                           estimand="ATE")
summary(nn.est3)
```

```
##
## Estimate...  7.6642
## AI SE......  0.052903
## T-stat.....  144.87
## p.val......  < 2.22e-16
##
## Original number of observations..............  5000
## Original number of treated obs...............  2748
## Matched number of observations...............  5000
## Matched number of observations  (unweighted).  23014
```

Regression

```
reg1.dat <- select.dat %>% filter(w_alt==1)
reg1 <- lm(y_alt ~ x, data=reg1.dat)

reg0.dat <- select.dat %>% filter(w_alt==0)
reg0 <- lm(y_alt ~ x, data=reg0.dat)
pred1_alt <- predict(reg1,new=select.dat)
pred0_alt <- predict(reg0,new=select.dat)
mean(pred1_alt-pred0_alt)
```

```
## [1] 7.646532
```

Pricing and Hospital Profit Status

Penalized hospitals

```
final.hcris <- hcris.data %>% ungroup() %>%
  filter(price_denom>100, !is.na(price_denom),
         price_num>0, !is.na(price_num),
         price<100000,
         beds>30, year==2012) %>%
  mutate( hvbp_payment = ifelse(is.na(hvbp_payment),0,hvbp_payment),
          hrrp_payment = ifelse(is.na(hrrp_payment),0,abs(hrrp_payment)),
    penalty = (hvbp_payment-hrrp_payment<0))
```

Summary stats

Always important to look at your data before doing any formal analysis. Ask yourself a few questions:

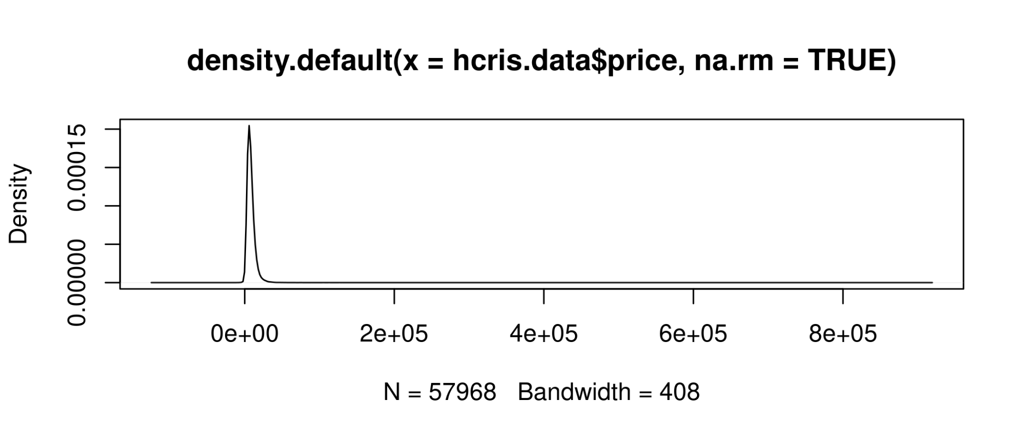
1. Are the magnitudes reasonable?
2. Are there lots of missing values?
3. Are there clear examples of misreporting?

Summary stats

```
summary(hcris.data$price)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
## -123697    4783    7113     Inf   10230     Inf   63662 
```

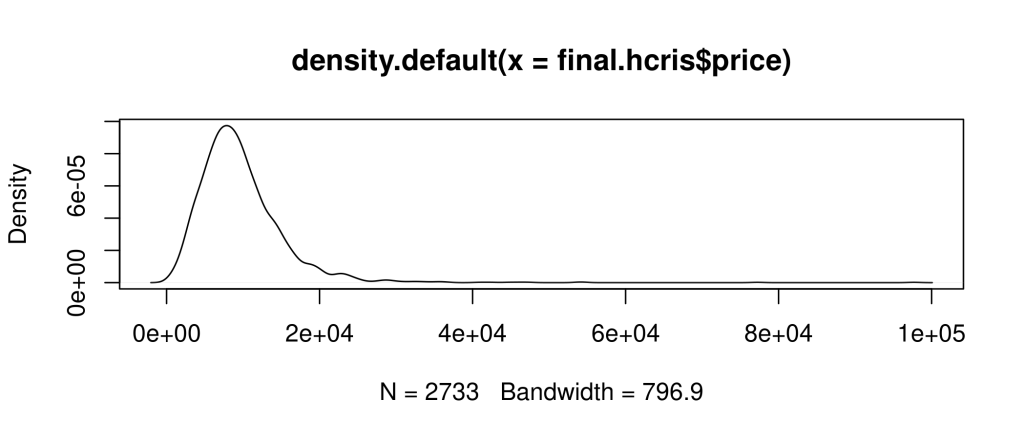
```
plot(density(hcris.data$price, na.rm=TRUE))
```




```
summary(final.hcris$price)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   340.8  6129.9  8705.4  9646.9 11905.4 97688.8 
```

```
plot(density(final.hcris$price))
```



Dealing with problems

We've adopted a very brute force way to deal with outlier prices. Other approaches include:

1. Investigate very closely the hospitals with extreme values
2. Winsorize at certain thresholds (replace extreme values with pre-determined thresholds)
3. Impute prices for extreme hospitals

Differences among penalized hospitals

- Mean price among penalized hospitals: 9,896.31
- Mean price among non-penalized hospitals: 9,560.41
- Mean difference: 335.9

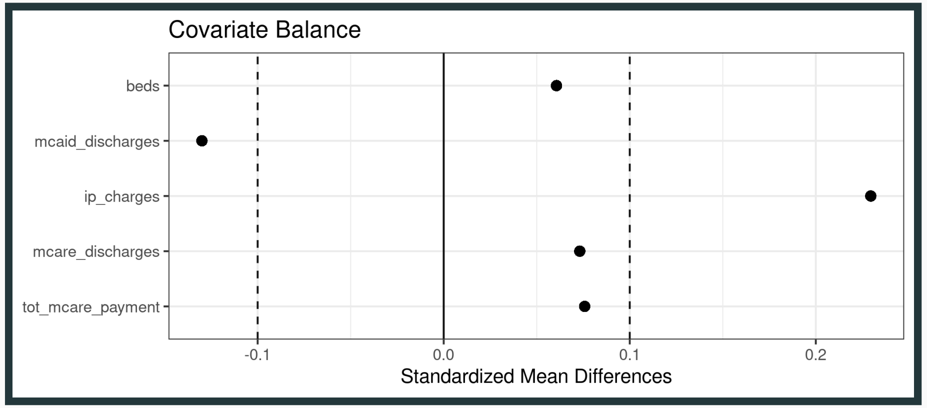
Comparison of hospitals

Are penalized hospitals sufficiently similar to non-penalized hospitals?

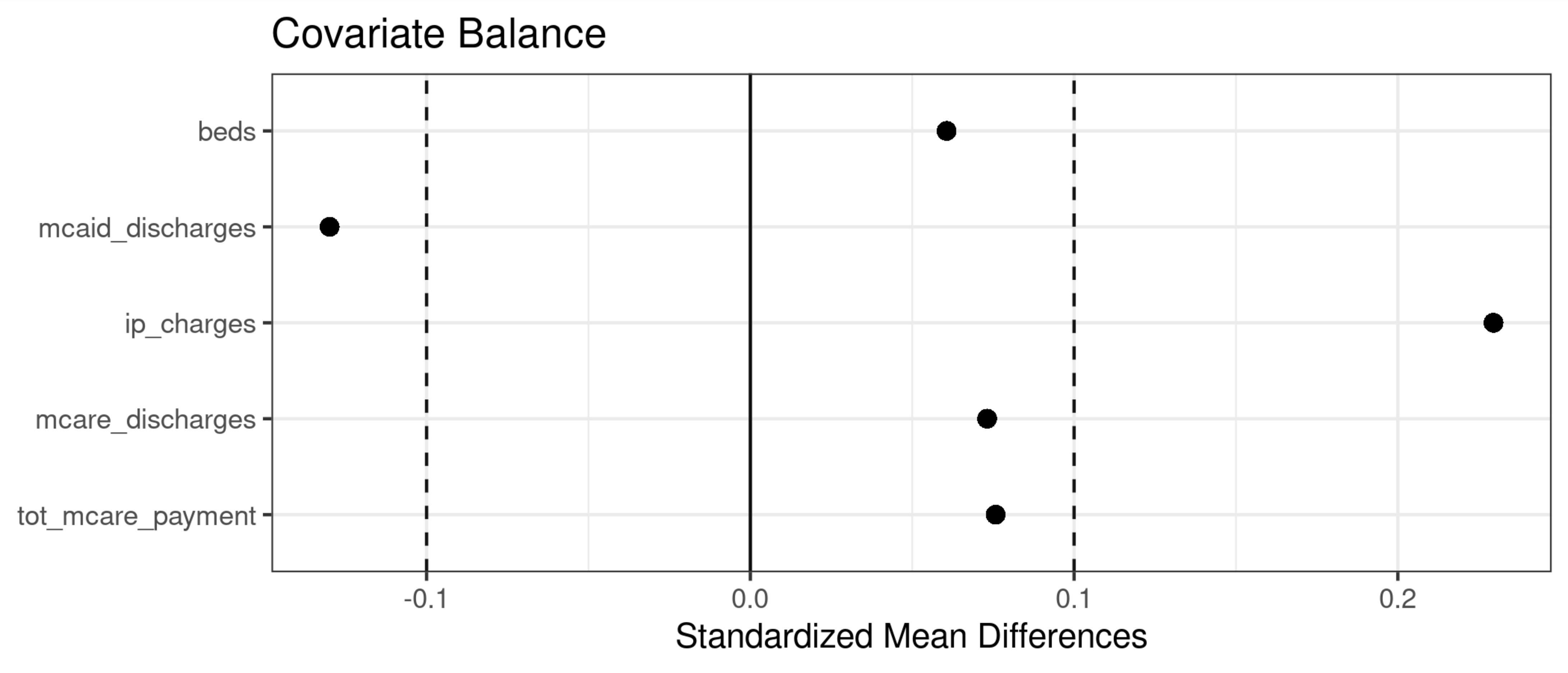
Let's look at covariate balance using a love plot, part of the `library(cobalt)` package.

Love plots without adjustment

```
love.plot(bal.tab(lp.covs,treat=lp.vars$penalty), colors="black", shapes="circle", threshold=0.1) +
  theme_bw() + theme(legend.position="none")
```



Love plots without adjustment



Using matching to improve balance

Some things to think about:

- exact versus nearest neighbor
- with or without ties (and how to break ties)
- measure of distance

1. Exact Matching

```
m.exact <- Matching::Match(Y=lp.vars$price,
                           Tr=lp.vars$penalty,
                           X=lp.covs,
                           M=1,
                           exact=TRUE)
print(m.exact)
```

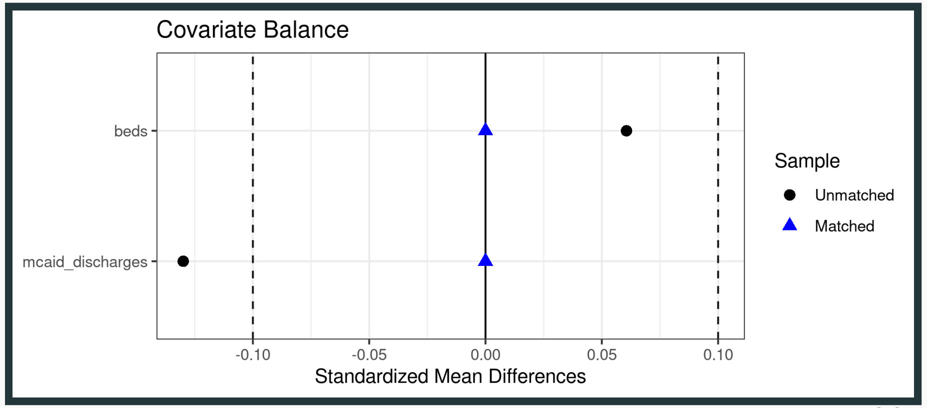
```
## [1] NA
## attr(,"class")
## [1] "Match"
```

1. Exact Matching (on a subset)

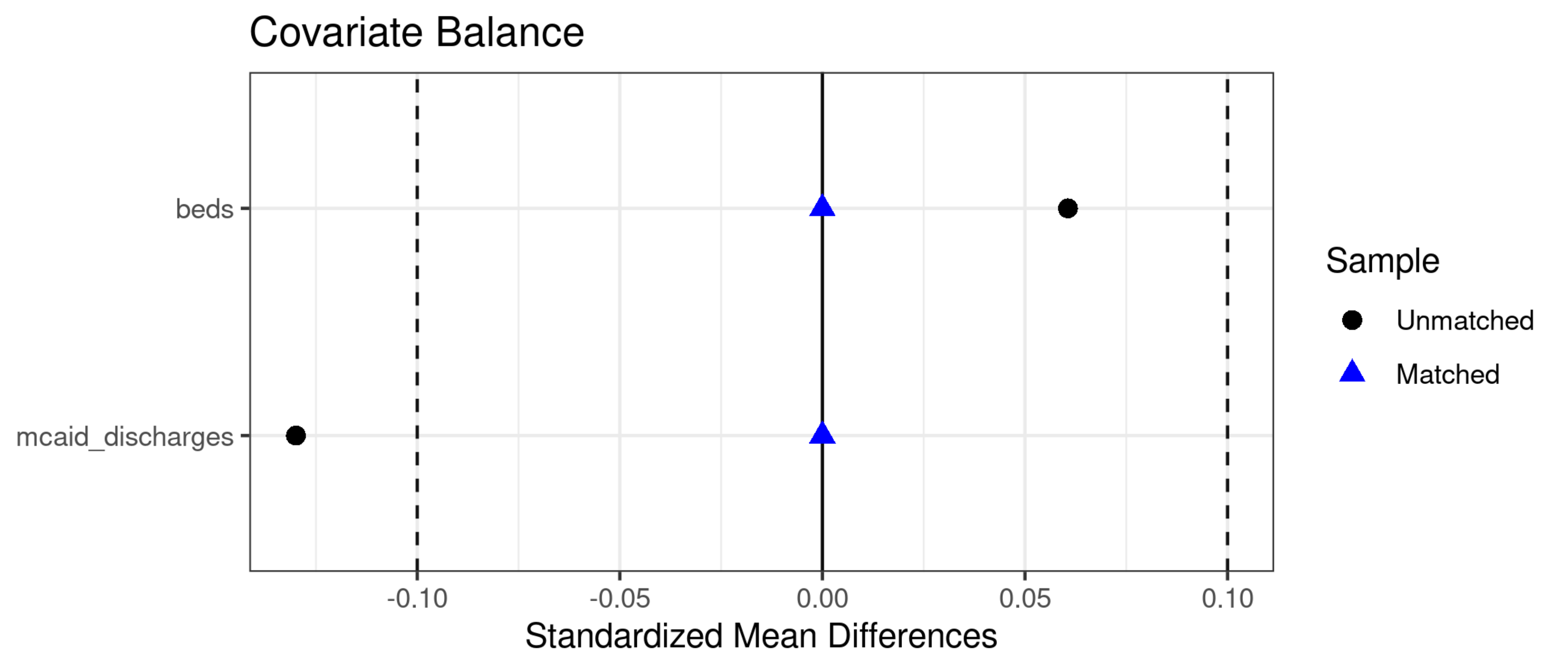
```
lp.covs2 <- lp.covs %>% select(beds, mcaid_discharges)
m.exact <- Matching::Match(Y=lp.vars$price,
                           Tr=lp.vars$penalty,
                           X=lp.covs2,
                           M=1,
                           exact=TRUE,
                           estimand="ATE")
```

1. Exact Matching (on a subset)

```
love.plot(bal.tab(m.exact, covs = lp.covs2, treat = lp.vars$penalty),
          threshold=0.1,
          grid=FALSE, sample.names=c("Unmatched", "Matched"),
          position="top", shapes=c("circle","triangle"),
          colors=c("black","blue")) +
  theme_bw()
```



1. Exact Matching (on a subset)

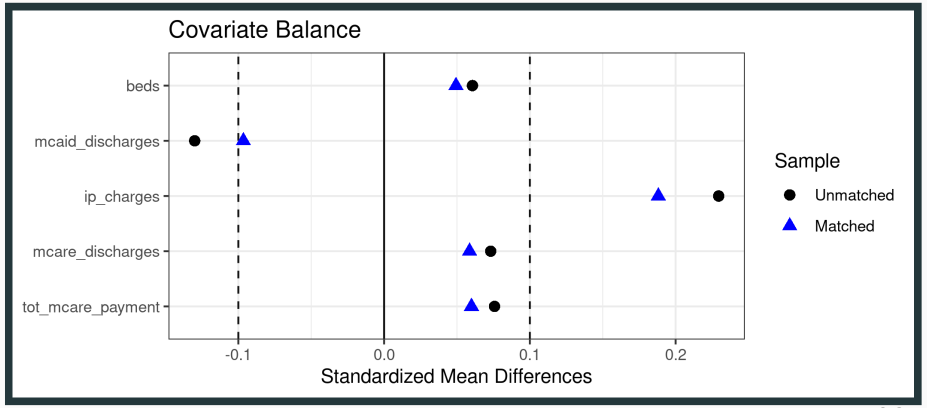


2. Nearest neighbor matching (inverse variance)

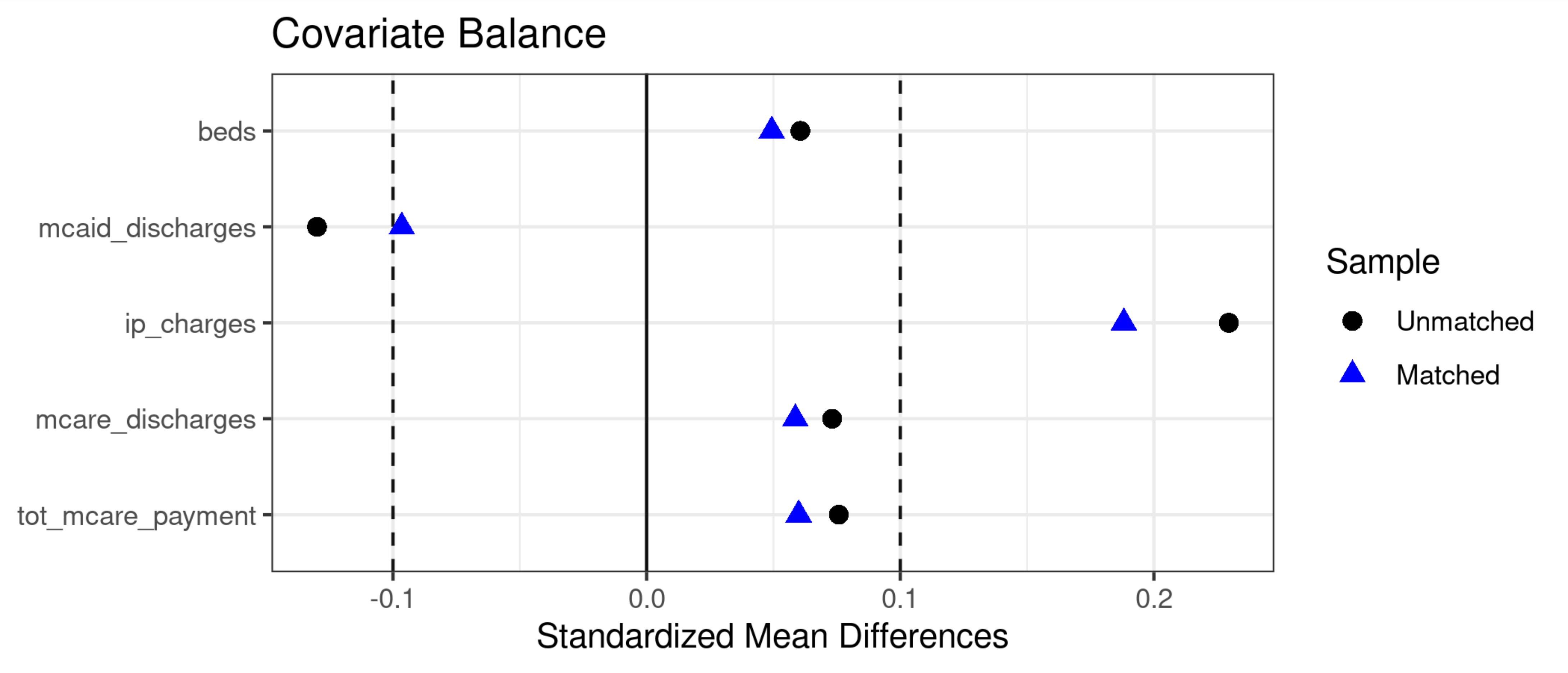
```
m.nn.var <- Matching::Match(Y=lp.vars$price,
                            Tr=lp.vars$penalty,
                            X=lp.covs,
                            M=4,
                            Weight=1,
                            estimand="ATE")

v.name=data.frame(new=c("Beds","Medicaid Discharges", "Inaptient Charges",
                   "Medicare Discharges", "Medicare Payments"))
```

2. Nearest neighbor matching (inverse variance)

```
love.plot(bal.tab(m.nn.var, covs = lp.covs, treat = lp.vars$penalty),
          threshold=0.1,
          var.names=v.name,
          grid=FALSE, sample.names=c("Unmatched", "Matched"),
          position="top", shapes=c("circle","triangle"),
          colors=c("black","blue")) +
  theme_bw()
```



2. Nearest neighbor matching (inverse variance)

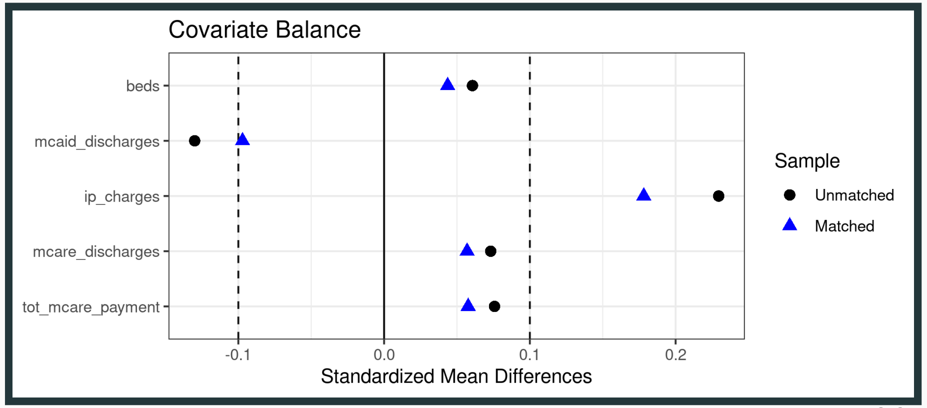


2. Nearest neighbor matching (inverse variance)

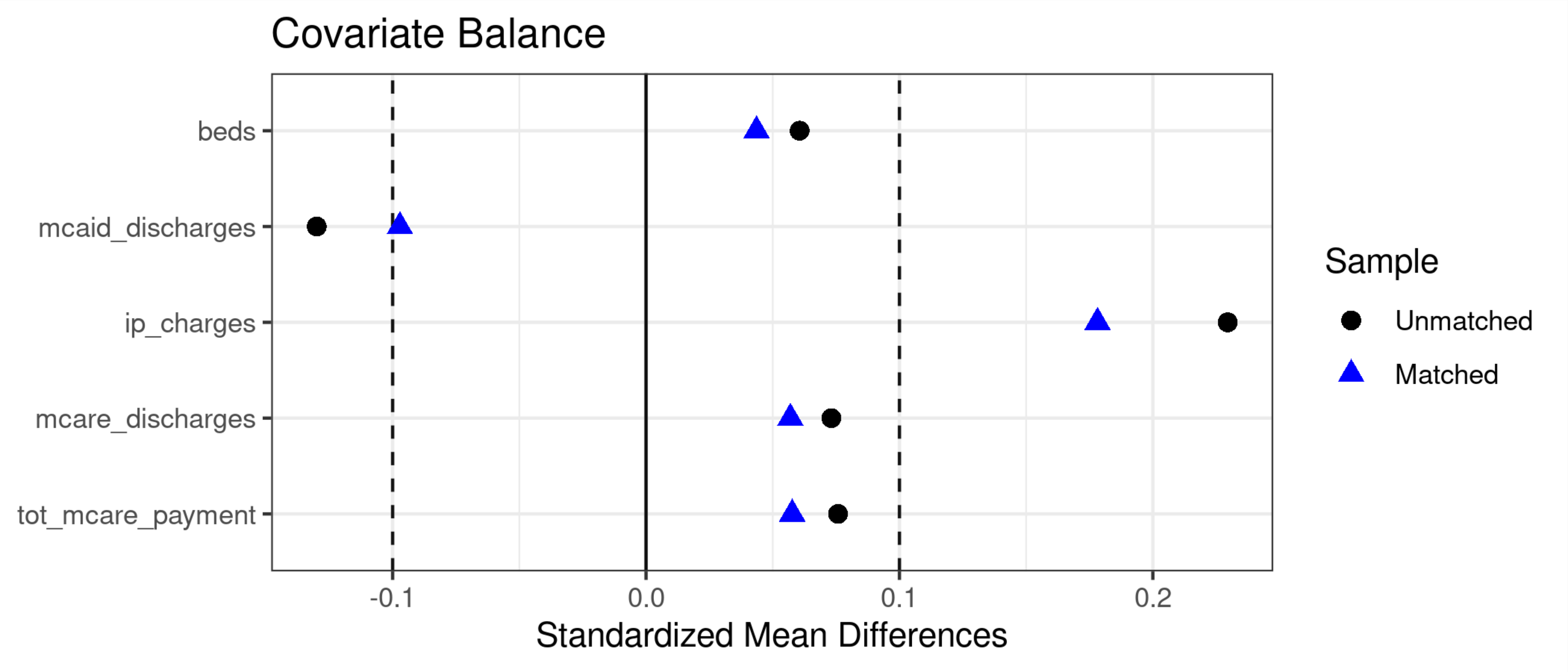
```
m.nn.var2 ← Matching::Match(Y=lp.vars$price,
                            Tr=lp.vars$penalty,
                            X=lp.covs,
                            M=1,
                            Weight=1,
                            estimand="ATE")
```

2. Nearest neighbor matching (inverse variance)

```
love.plot(bal.tab(m.nn.var2, covs = lp.covs, treat = lp.vars$penalty),
          threshold=0.1,
          var.names=v.name,
          grid=FALSE, sample.names=c("Unmatched", "Matched"),
          position="top", shapes=c("circle","triangle"),
          colors=c("black","blue")) +
  theme_bw()
```



2. Nearest neighbor matching (inverse variance)

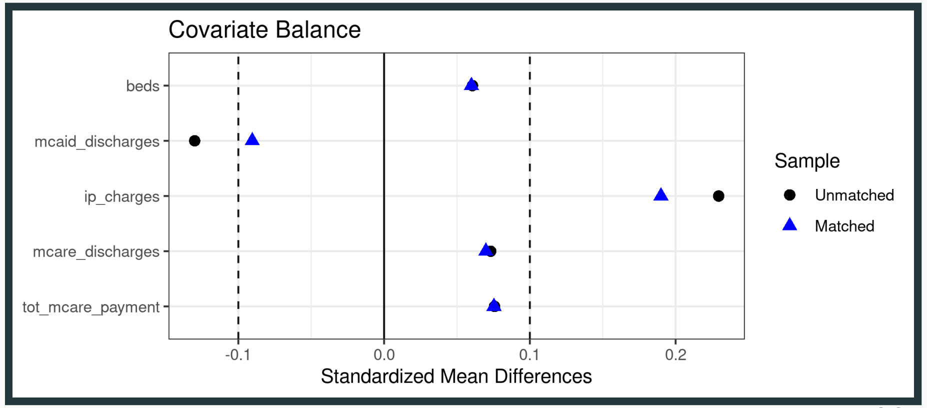


2. Nearest neighbor matching (Mahalanobis)

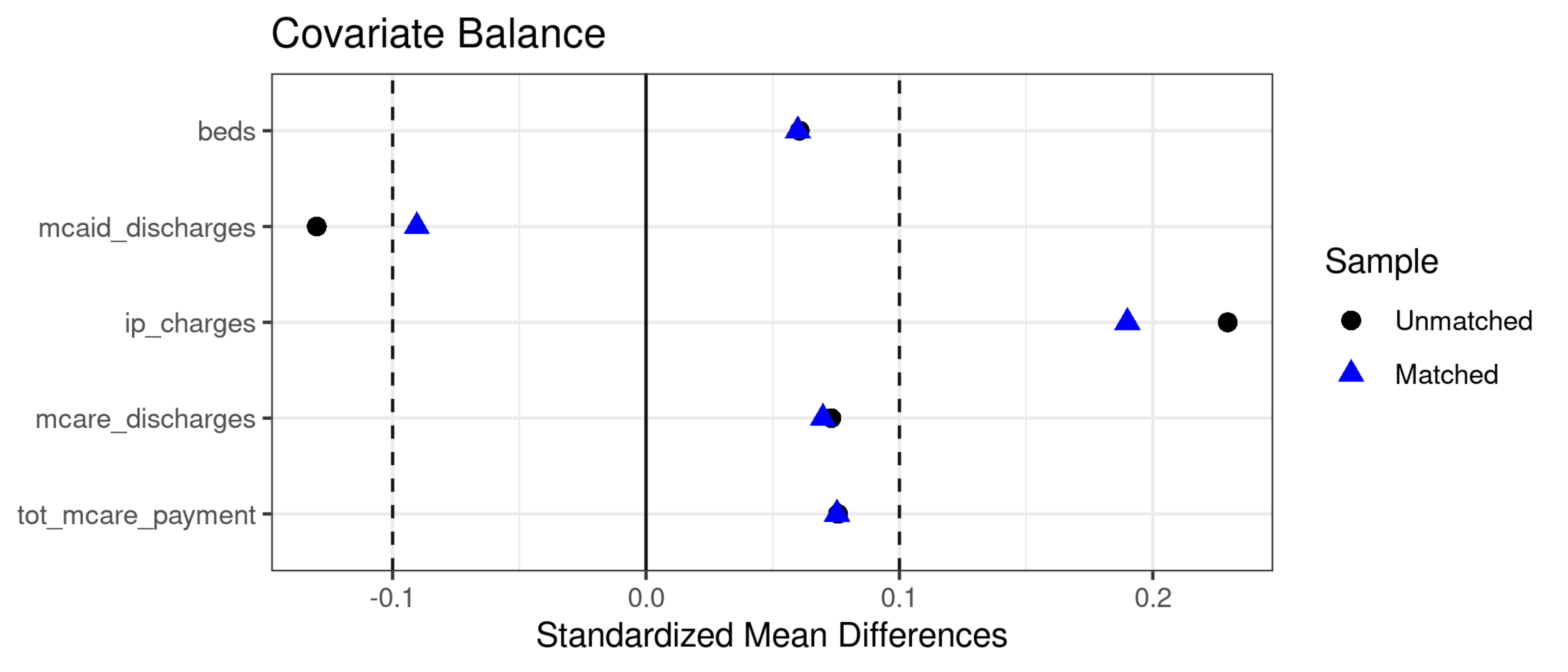
```r
m.nn.md <- Matching::Match(Y=lp.vars$price,
                           Tr=lp.vars$penalty,
                           X=lp.covs,
                           M=1,
                           Weight=2,
                           estimand="ATE")
```

2. Nearest neighbor matching (Mahalanobis)

```
love.plot(bal.tab(m.nn.md, covs = lp.covs, treat = lp.vars$penalty),
          threshold=0.1,
          var.names=v.name,
          grid=FALSE, sample.names=c("Unmatched", "Matched"),
          position="top", shapes=c("circle","triangle"),
          colors=c("black","blue")) +
  theme_bw()
```



2. Nearest neighbor matching (Mahalanobis)

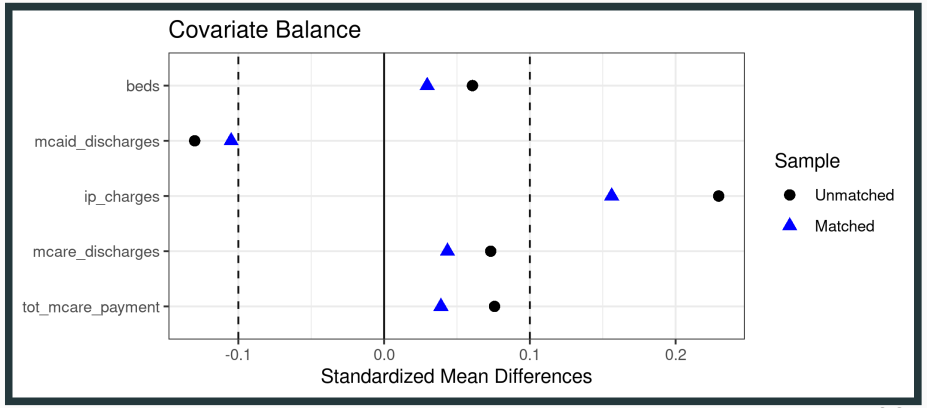


2. Nearest neighbor matching (propensity score)

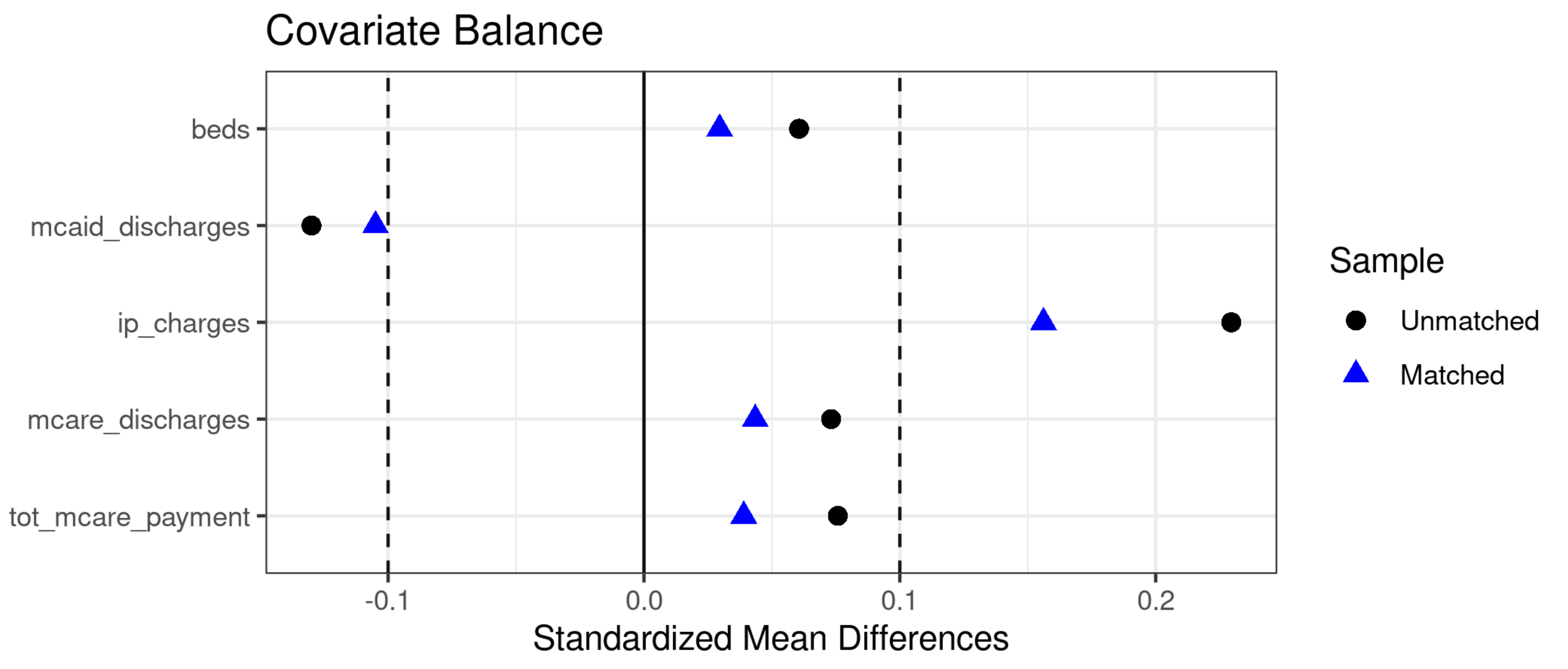
```
logit.model <- glm(penalty ~ beds + mcaid_discharges + ip_charges + mcare_discharges +
            tot_mcare_payment, family=binomial, data=lp.vars)
ps <- fitted(logit.model)
m.nn.ps <- Matching::Match(Y=lp.vars$price,
                           Tr=lp.vars$penalty,
                           X=ps,
                           M=1,
                           estimand="ATE")
```

2. Nearest neighbor matching (propensity score)

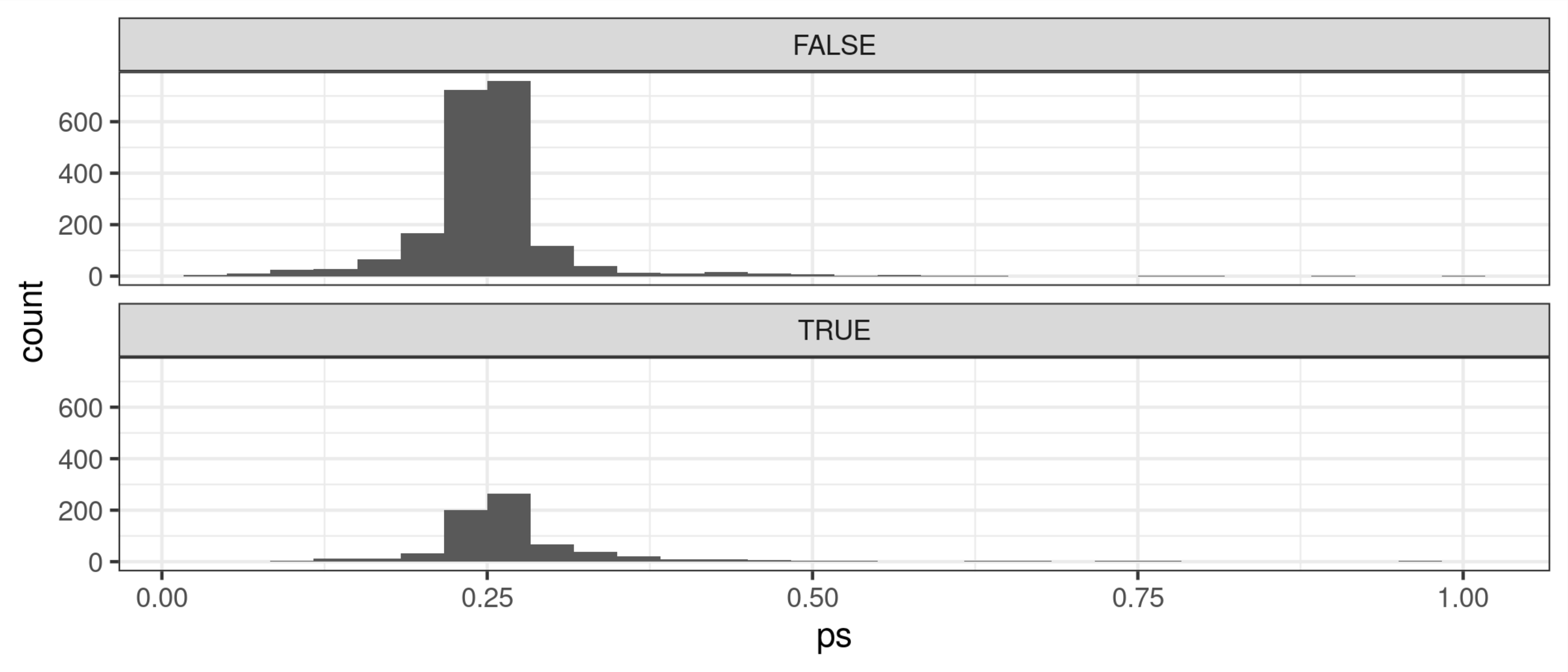
```
love.plot(bal.tab(m.nn.ps, covs = lp.covs, treat = lp.vars$penalty),
          threshold=0.1,
          var.names=v.name,
          grid=FALSE, sample.names=c("Unmatched", "Matched"),
          position="top", shapes=c("circle","triangle"),
          colors=c("black","blue")) +
  theme_bw()
```



2. Nearest neighbor matching (propensity score)



3. Weighting



FALSE
TRUE
count
600
400
200
0
600
400
200
0
0.00
0.25
0.50
0.75
1.00
ps

Results: Exact matching

```
##
## Estimate...  1777.6
## AI SE......  34.725
## T-stat.....  51.191
## p.val......  < 2.22e-16
##
## Original number of observations..............  2707
## Original number of treated obs...............  698
## Matched number of observations...............  12
## Matched number of observations  (unweighted).  12
##
## Number of obs dropped by 'exact' or 'caliper'  2695
```

Results: Nearest neighbor

- Inverse variance

```
##
## Estimate...  -526.95
## AI SE......  223.06
## T-stat.....  -2.3623
## p.val......  0.01816
##
## Original number of observations..............  2707
## Original number of treated obs...............  698
## Matched number of observations...............  2707
## Matched number of observations  (unweighted).  2711
```

Results: Nearest neighbor

- Mahalanobis

```
##
## Estimate...  -492.82
## AI SE......  223.55
## T-stat.....  -2.2046
## p.val......  0.027485
##
## Original number of observations..............  2707
## Original number of treated obs...............  698
## Matched number of observations...............  2707
## Matched number of observations  (unweighted).  2708
```

Results: Nearest neighbor

- Propensity score

```
##
## Estimate...  -201.03
## AI SE......  275.76
## T-stat.....  -0.72898
## p.val......  0.46601
##
## Original number of observations..............  2707
## Original number of treated obs...............  698
## Matched number of observations...............  2707
## Matched number of observations  (unweighted).  14795
```

Results: IPW weighting

```r
lp.vars <- lp.vars %>%
  mutate(ipw = case_when(
    penalty==1 ~ 1/ps,
    penalty==0 ~ 1/(1-ps),
    TRUE ~ NA_real_
  ))
mean.t1 <- lp.vars %>% filter(penalty==1) %>%
  select(price, ipw) %>% summarize(mean_p=weighted.mean(price,w=ipw))
mean.t0 <- lp.vars %>% filter(penalty==0) %>%
  select(price, ipw) %>% summarize(mean_p=weighted.mean(price,w=ipw))
mean.t1$mean_p - mean.t0$mean_p
```

```
## [1] -196.8922
```

Results: IPW weighting with regression

```
ipw.reg <- lm(price ~ penalty, data=lp.vars, weights=ipw)
summary(ipw.reg)
```

```
##
## Call:
## lm(formula = price ~ penalty, data = lp.vars, weights = ipw)
##
## Weighted Residuals:
##    Min     1Q Median     3Q    Max
## -18691  -4802  -1422   2651  94137
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   9876.4      147.8  66.808   <2e-16 ***
## penaltyTRUE   -196.9      211.2  -0.932    0.351
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7829 on 2705 degrees of freedom
## Multiple R-squared:  0.0003211,    Adjusted R-squared:  -4.85e-05
## F-statistic: 0.8688 on 1 and 2705 DF,  p-value: 0.3514
```

Results: Regression

```
reg1.dat <- lp.vars %>% filter(penalty==1, complete.cases(.))
reg1 <- lm(price ~ beds+ mcaid_discharges + ip_charges + mcare_discharges +
            tot_mcare_payment, data=reg1.dat)

reg0.dat <- lp.vars %>% filter(penalty==0, complete.cases(.))
reg0 <- lm(price ~ beds + mcaid_discharges + ip_charges + mcare_discharges +
            tot_mcare_payment, data=reg0.dat)
pred1 <- predict(reg1,new=lp.vars)
pred0 <- predict(reg0,new=lp.vars)
mean(pred1-pred0)
```

```
## [1] -5.845761
```

Results: Regression in one step

```
reg.dat <- lp.vars %>% ungroup() %>% filter(complete.cases(.)) %>%
  mutate(beds_diff = penalty*(beds - mean(beds)),
         mcaid_diff = penalty*(mcaid_discharges - mean(mcaid_discharges)),
         ip_diff = penalty*(ip_charges - mean(ip_charges)),
         mcare_diff = penalty*(mcare_discharges - mean(mcare_discharges)),
         mpay_diff = penalty*(tot_mcare_payment - mean(tot_mcare_payment)))
reg <- lm(price ~ penalty + beds + mcaid_discharges + ip_charges + mcare_discharges + tot_mcare_payment +
            beds_diff + mcaid_diff + ip_diff + mcare_diff + mpay_diff,
          data=reg.dat)
```

Results: Regression in one step

```
##
## Call:
## lm(formula = price ~ penalty + beds + mcaid_discharges + ip_charges +
##     mcare_discharges + tot_mcare_payment + beds_diff + mcaid_diff +
##     ip_diff + mcare_diff + mpay_diff, data = reg.dat)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -38175  -2900   -597   2105  67409
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        8.466e+03  1.711e+02  49.482  < 2e-16 ***
## penaltyTRUE       -5.846e+00  2.124e+02  -0.028  0.97804
## beds               1.107e+00  1.421e+00   0.779  0.43618
## mcaid_discharges  -4.714e-01  7.296e-02  -6.462 1.23e-10 ***
## ip_charges         6.426e-06  1.285e-06   5.002 6.04e-07 ***
## mcare_discharges  -8.122e-01  9.257e-02  -8.774  < 2e-16 ***
## tot_mcare_payment  9.502e-05  6.858e-06  13.857  < 2e-16 ***
## beds_diff          2.517e+00  2.986e+00   0.843  0.39931
## mcaid_diff         1.058e-01  1.570e-01   0.674  0.50050
## ip_diff           -4.534e-06  2.027e-06  -2.237  0.02539 *
## mcare_diff         4.806e-01  1.809e-01   2.657  0.00793 **
## mpay_diff         -5.452e-05  1.321e-05  -4.128 3.78e-05 ***
## ---
```

Summary of ATEs

1. Exact matching: 1777.63
2. NN matching, inverse variance: -526.95
3. NN matching, mahalanobis: -492.82
4. NN matching, pscore: -201.03
5. Inverse pscore weighting: -196.89
6. IPW regression: -196.89
7. Regression: -5.85
8. Regression 1-step: -5.85

So what have we learned?

Key assumptions for causal inference

1. Selection on observables
2. Common support

These become more nuanced but the intuition is the same in almost all questions of causal inference.

Causal effect assuming selection on observables

If we assume selection on observables holds, then we only need to condition on the relevant covariates to identify a causal effect. But we still need to ensure common support...

1. Matching
2. Reweighting
3. Regression