

# Research Design

## 06: observational studies

Initial questions about the pre-lecture notes?

observational studies

## controlled experiments

randomizing treatment asymptotically balances  
pre-treatment differences among observations

ethics

control

expense

time

## observational studies

data readily available

selection

confounding

omitted-variable bias

balance

overlap

confounding covariates and omitted-variable bias

## confounder bias, simple example using simulated data

Treatment has no effect, potential confounding  
covariate *balanced* between treatment and control

```
set.seed(1)

N <- 1e5
sigma <- 0.5

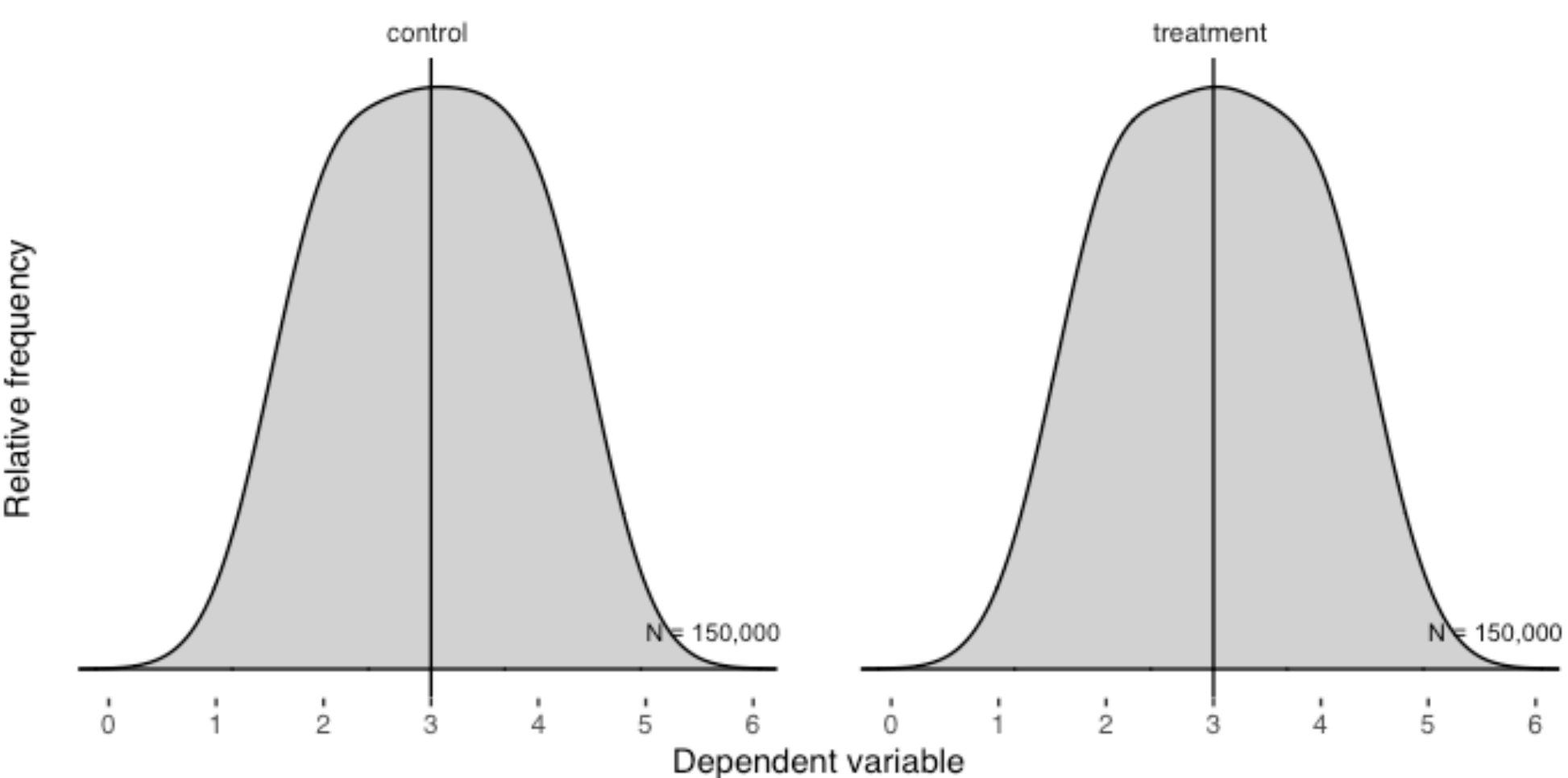
d <- data.frame(
  independent = c(rep("control", 0.5 * N), rep("treatment", 0.5 * N),
                  rep("control", 0.5 * N), rep("treatment", 0.5 * N),
                  rep("control", 0.5 * N), rep("treatment", 0.5 * N)),
  confounder = c(rep(1, N),
                 rep(2, N),
                 rep(3, N)),
  dependent = c(rnorm(N, 2, sigma),
               rnorm(N, 3, sigma),
               rnorm(N, 4, sigma))
)
```

# confounder bias, simple example using simulated data

## *omitting the confounder*

```
d_bar <- d %>% group_by(independent) %>%
  summarise(count = n(), dependent = mean(dependent))

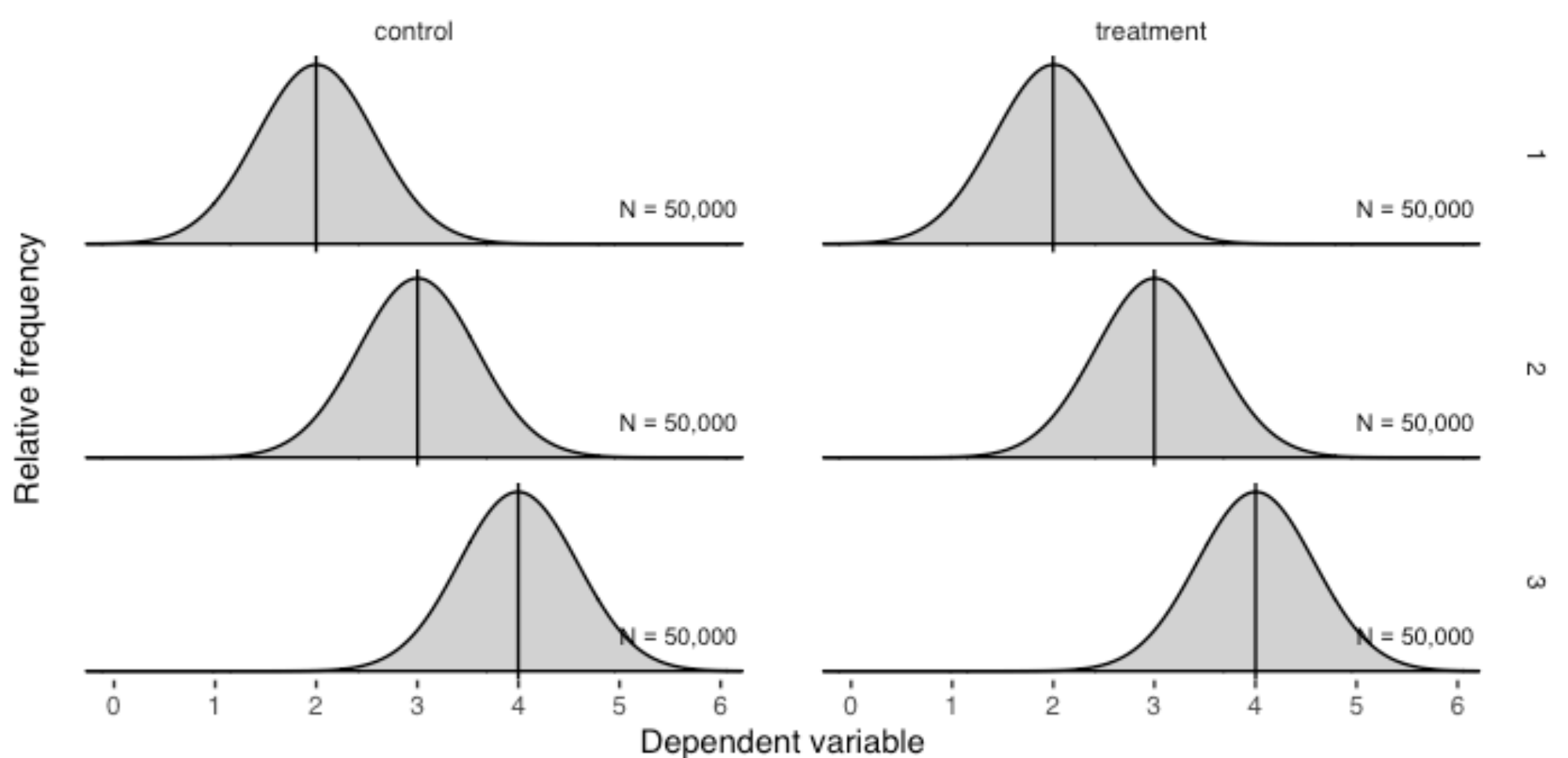
ggplot(d) +
  theme_tufte(base_family = "sans") +
  geom_density(aes(x = dependent, y = ..scaled.. * n),
    fill = "lightgray", outline.type = "both", bw = 0.25) +
  geom_vline(data = d_bar, aes(xintercept = dependent)) +
  geom_text(data = d_bar, aes(x = 5, y = N / 10,
    label = paste0("N = ", format(count, big.mark = ","))),
    size = 8/.pt, hjust = 0) +
  facet_grid( ~ independent) +
  scale_x_continuous(breaks = 0:6) +
  scale_y_continuous(breaks = NULL) +
  labs(x = "Dependent variable", y = "Relative frequency")
```



## *including the confounder*

```
d_bar <- d %>% group_by(confounder, independent) %>%
  summarise(count = n(), dependent = mean(dependent))

ggplot(d) +
  theme_tufte(base_family = "sans") +
  geom_density(aes(x = dependent, y = ..scaled.. * n),
    fill = "lightgray", outline.type = "both", bw = 0.3) +
  geom_vline(data = d_bar, aes(xintercept = dependent)) +
  geom_text(data = d_bar, aes(x = 5, y = N / 10,
    label = paste0("N = ", format(count, big.mark = ","))),
    size = 8/.pt, hjust = 0) +
  facet_grid(confounder ~ independent) +
  scale_x_continuous(breaks = 0:6) +
  scale_y_continuous(breaks = NULL) +
  labs(x = "Dependent variable", y = "Relative frequency")
```



## confounder bias, simple example using simulated data

Treatment has no effect, but selecting  $z_i$  by confounding covariate may **bias the analysis**.

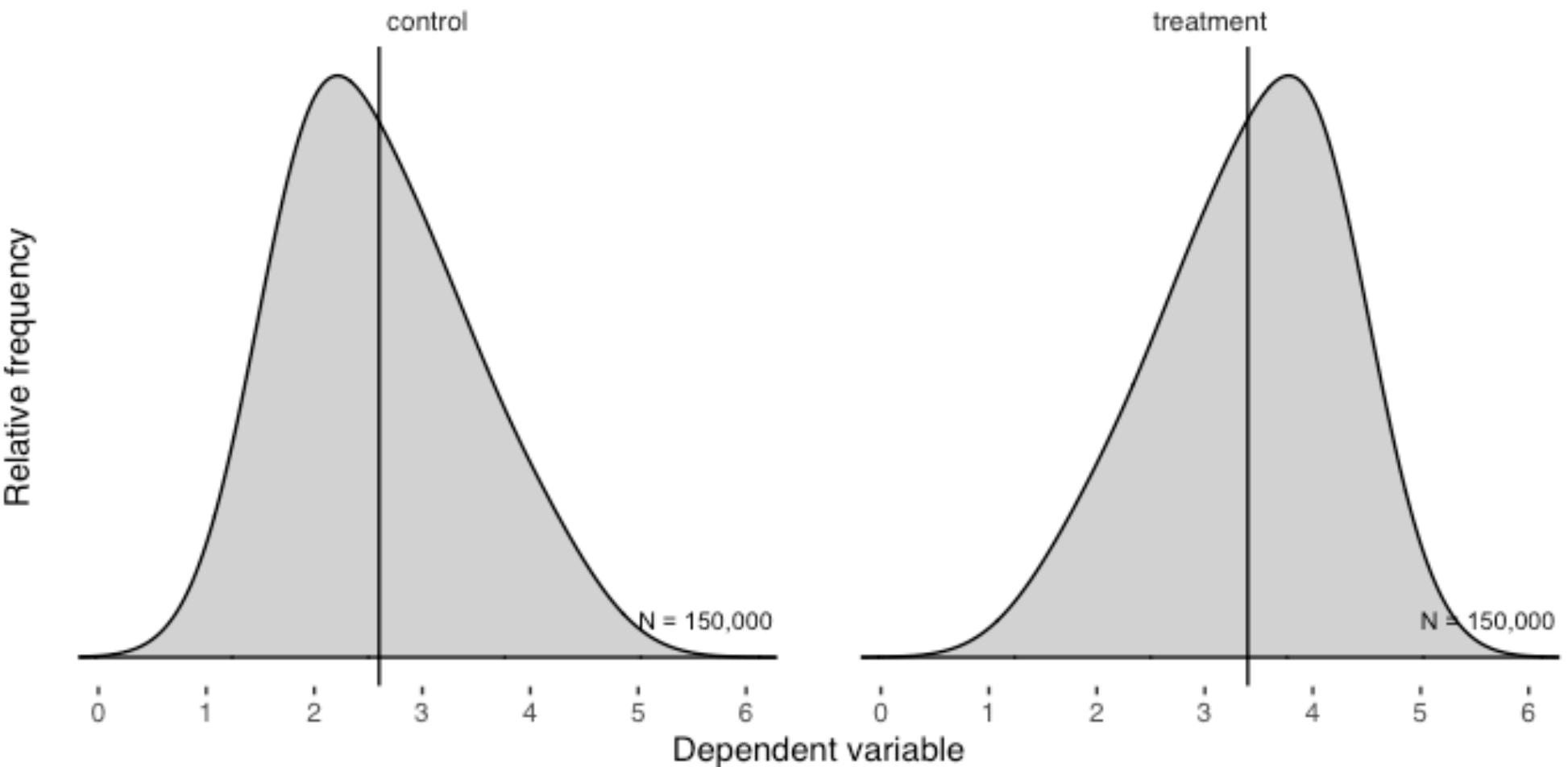
```
d <- data.frame(
  independent = c(rep("control", 0.8 * N), rep("treatment", 0.2 * N),
                  rep("control", 0.5 * N), rep("treatment", 0.5 * N),
                  rep("control", 0.2 * N), rep("treatment", 0.8 * N)),
  confounder = c(rep(1, N),
                 rep(2, N),
                 rep(3, N)),
  dependent = c(rnorm(N, 2, sigma),
               rnorm(N, 3, sigma),
               rnorm(N, 4, sigma))
)
```



# confounder bias, simple example using simulated data

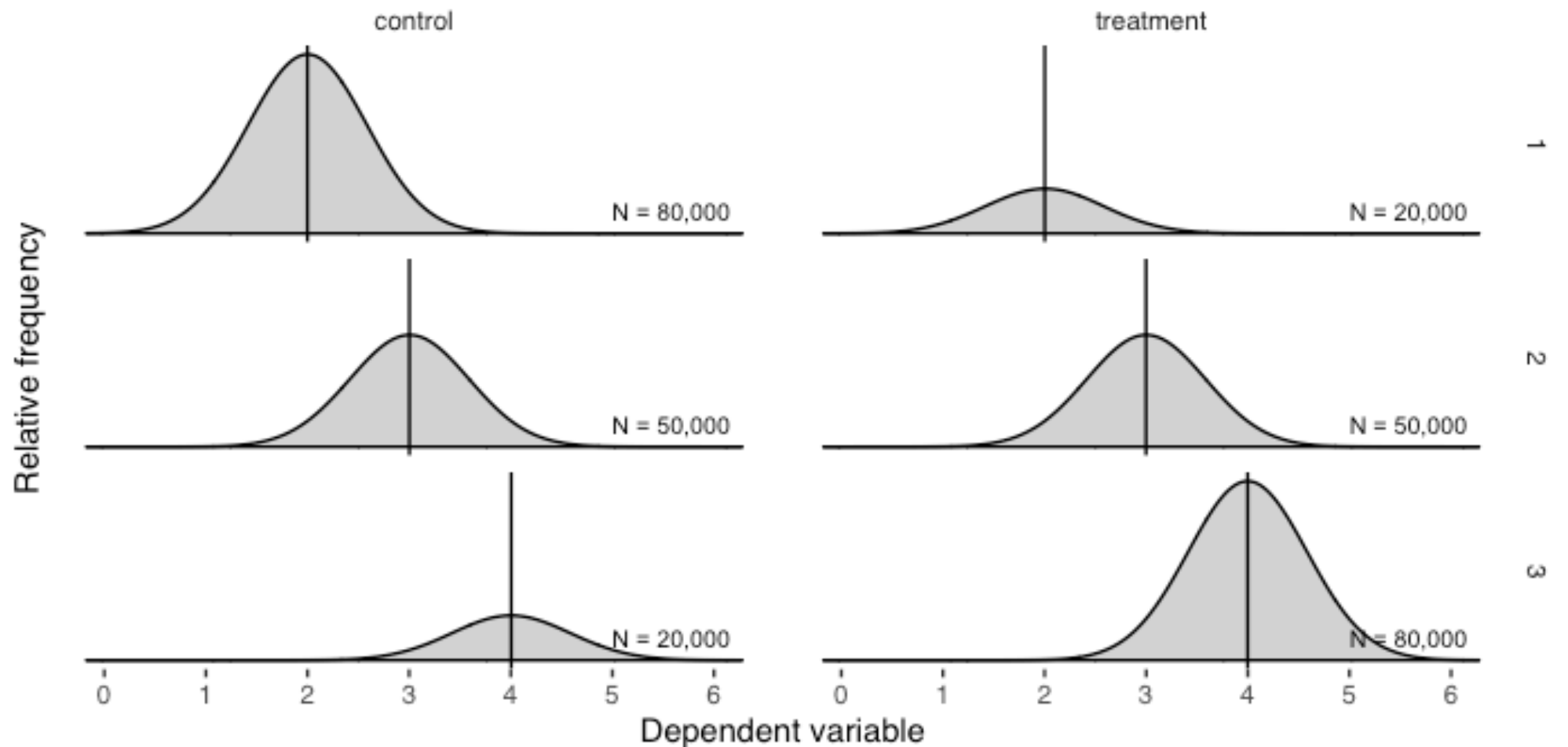
## *omitting the confounder*

```
d_bar <- d %>% group_by(independent) %>%  
  summarise(count = n(), dependent = mean(dependent))  
  
ggplot(d) +  
  theme_tufte(base_family = "sans") +  
  geom_density(aes(x = dependent, y = ..scaled.. * n),  
    fill = "lightgray", outline.type = "both", bw = 0.25) +  
  geom_vline(data = d_bar, aes(xintercept = dependent)) +  
  geom_text(data = d_bar, aes(x = 5, y = N / 10,  
    label = paste0("N = ", format(count, big.mark = ", "))),  
    size = 8/.pt, hjust = 0) +  
  facet_grid( ~ independent) +  
  scale_x_continuous(breaks = 0:6) +  
  scale_y_continuous(breaks = NULL) +  
  labs(x = "Dependent variable", y = "Relative frequency")
```



## *including the confounder*

```
d_bar <- d %>% group_by(confounder, independent) %>%  
  summarise(count = n(), dependent = mean(dependent))  
  
ggplot(d) +  
  theme_tufte(base_family = "sans") +  
  geom_density(aes(x = dependent, y = ..scaled.. * n),  
    fill = "lightgray", outline.type = "both", bw = 0.3) +  
  geom_vline(data = d_bar, aes(xintercept = dependent)) +  
  geom_text(data = d_bar, aes(x = 5, y = N / 10,  
    label = paste0("N = ", format(count, big.mark = ", "))),  
    size = 8/.pt, hjust = 0) +  
  facet_grid(confounder ~ independent) +  
  scale_x_continuous(breaks = 0:6) +  
  scale_y_continuous(breaks = NULL) +  
  labs(x = "Dependent variable", y = "Relative frequency")
```



## confounder bias, simple example using simulated data

Treatment has an effect, but selecting  $z_i$  by confounding covariate may **mask the effect**.

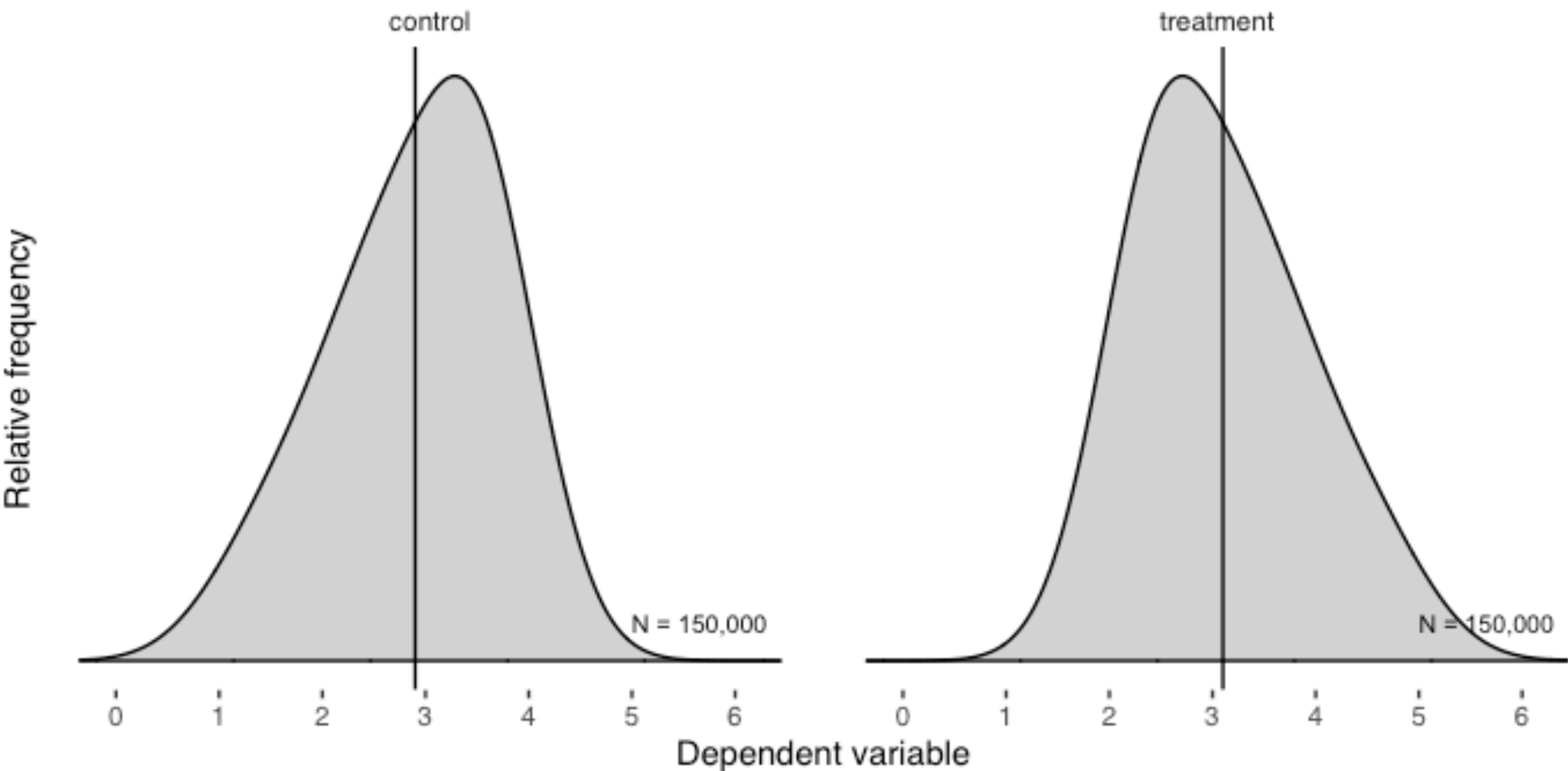
```
d <- data.frame(
  independent = c(rep("control", 0.2 * N), rep("treatment", 0.8 * N),
                  rep("control", 0.5 * N), rep("treatment", 0.5 * N),
                  rep("control", 0.8 * N), rep("treatment", 0.2 * N)),
  confounder = c(rep(1, N),
                 rep(2, N),
                 rep(3, N)),
  dependent = c(rnorm(0.2 * N, 1.5, sigma), rnorm(0.8 * N, 2.5, sigma),
               rnorm(0.5 * N, 2.5, sigma), rnorm(0.5 * N, 3.5, sigma),
               rnorm(0.8 * N, 3.5, sigma), rnorm(0.2 * N, 4.5, sigma))
)
```

# confounder bias, simple example using simulated data

## *omitting the confounder*

```
d_bar <- d %>% group_by(independent) %>%
  summarise(count = n(), dependent = mean(dependent))

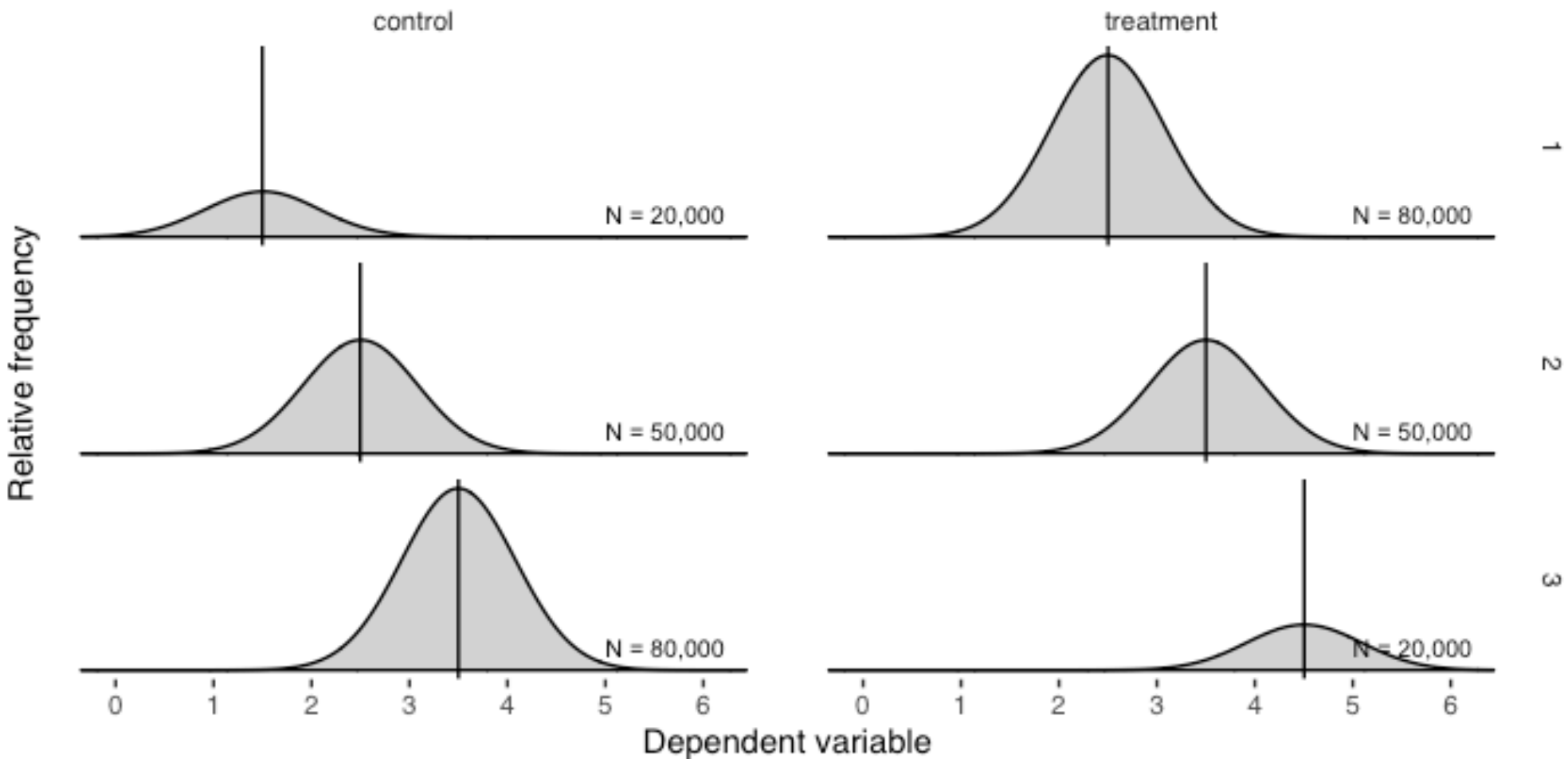
ggplot(d) +
  theme_tufte(base_family = "sans") +
  geom_density(aes(x = dependent, y = ..scaled.. * n),
    fill = "lightgray", outline.type = "both", bw = 0.25) +
  geom_vline(data = d_bar, aes(xintercept = dependent)) +
  geom_text(data = d_bar, aes(x = 5, y = N / 10,
    label = paste0("N = ", format(count, big.mark = ","))),
    size = 8/.pt, hjust = 0) +
  facet_grid( ~ independent) +
  scale_x_continuous(breaks = 0:6) +
  scale_y_continuous(breaks = NULL) +
  labs(x = "Dependent variable", y = "Relative frequency")
```



## *including the confounder*

```
d_bar <- d %>% group_by(confounder, independent) %>%
  summarise(count = n(), dependent = mean(dependent))

ggplot(d) +
  theme_tufte(base_family = "sans") +
  geom_density(aes(x = dependent, y = ..scaled.. * n),
    fill = "lightgray", outline.type = "both", bw = 0.3) +
  geom_vline(data = d_bar, aes(xintercept = dependent)) +
  geom_text(data = d_bar, aes(x = 5, y = N / 10,
    label = paste0("N = ", format(count, big.mark = ","))),
    size = 8/.pt, hjust = 0) +
  facet_grid(confounder ~ independent) +
  scale_x_continuous(breaks = 0:6) +
  scale_y_continuous(breaks = NULL) +
  labs(x = "Dependent variable", y = "Relative frequency")
```



regression adjustments, stratification, matching,  
and weighting, and combinations of these

## adjustments with multivariate models

# multivariate models, relationship of classical statistics to regression models

Let's simulate some example data,

```
set.seed(1)
n_0 <- 20
y_0 <- rnorm(n_0, 2.0, 5.0)

n_1 <- 30
y_1 <- rnorm(n_1, 8.0, 5.0)
```

We get these statistics by *regressing on a constant*:

$$y \sim \beta_0 \cdot 1 + \epsilon$$

$$\epsilon \sim \text{Normal}(0, \sigma)$$

and calculate sample means  $\bar{y}$  and standard deviation  $s$ :

```
mean(y_0)
sd(y_0) / sqrt(n_0)

mean(y_1)
sd(y_1) / sqrt(n_1)
```

```
sim_0 <- data.frame(y_0)
glm_0 <- glm(y_0 ~ 1, data = sim_0)

sim_1 <- data.frame(y_1)
glm_1 <- glm(y_1 ~ 1, data = sim_1)
```

# multivariate models, relationship of classical statistics to regression models

Let's simulate some example data,

```
set.seed(1)
n_0 <- 20
y_0 <- rnorm(n_0, 2.0, 5.0)

n_1 <- 30
y_1 <- rnorm(n_1, 8.0, 5.0)
```

recall calculating  $\bar{x}_1 - \bar{x}_0$  and standard deviation  $s$ :

```
diff <- mean(y_1) - mean(y_0)

s_0 <- sd(y_0) / sqrt(n_0)
s_1 <- sd(y_1) / sqrt(n_1)

s <- sqrt(s_0 ^ 2 + s_1 ^ 2)
```

or get the difference by *regressing on an indicator*:

$$y \sim \beta_0 \cdot 1 + \beta_1 \cdot x_1 + \epsilon$$

$$x_{1,i} = \begin{cases} 0, & z_i = 0 \\ 1, & z_i = 1 \end{cases}$$

$$\epsilon \sim \text{Normal}(0, \sigma)$$

```
y <- c(y_0, y_1)
x <- c(rep(0, n_0), rep(1, n_1))
sim <- data.frame(x, y)

glm_delta <- glm(y ~ x, data = sim)
```

Note: the sample standard deviation  $s$  differs slightly because the regression model estimates a single residual standard deviation parameter, as compared to the difference calculation which uses separate values of  $s_0$  and  $s_1$ .

multivariate models, adjusting for multiple covariates

If we assume *additivity*, we can adjust for **multiple covariates** using regression, *e.g.*:

$$y \sim \beta_0 + \beta_1 x_1 + \dots + \beta_n x_n + \epsilon$$



# propensity scores and matching

propensity scores and matching, restructure observational data to resemble a randomized experiment

Step 1: Defining the confounders and estimand

Step 2: Estimating the propensity score

Step 3: Matching to restructure the data

Step 4: Diagnostics for balance and overlap

*Repeat steps 2–4 until adequate balance is achieved*

Step 5: Estimating a treatment effect using the restructured data

— Gelman et al. 2020

propensity scores and matching, example — step 1: defining the confounders and estimand



**Observations:** About 2 million residential properties in Mid-Atlantic region sold between 2005 and 2018.

**Estimand:** effect of expected coastal flooding on sale price of single-family residential properties

**Potential confounders?**



# propensity scores and matching, example — step 1: defining the confounders and estimand



**Observations:** About 2 million residential properties in Mid-Atlantic region sold between 2005 and 2018.

**Estimand:** effect of expected coastal flooding on sale price of single-family residential properties

**Confounders:** location, neighborhood or region, area of property, area of building, month and year of sale, ...



propensity scores and matching, example — step 1: defining the confounders and estimand



Data summary			
Name	Number of rows	Number of columns	Piped data
Column type frequency:	factor	numeric	8 16
Group variables	None		

Variable type: factor

skim_variable	missing	complete	n_unique
fsid	0	35228	35228
saleyear	0	35228	13
instrumentdate	0	35228	3425
blocks	0	35228	7426
blkgrs	0	35228	787
tracts	0	35228	339
contys	0	35228	22
states	0	35228	3

Variable type: numeric

skim_variable	missing	complete	mean	sd	p0	p25	p50	p75	p100
transferamount	0	35228	347225.18	309423.10	4450.00	157500.00	275000.00	440000.00	950000.00
Pr_Sq_Ft	0	35228	182.58	105.58	10.03	111.54	166.67	238.33	544.68
x	0	35228	-75.95	0.59	-77.25	-76.48	-76.17	-75.28	-74.77
y	0	35228	38.81	0.46	37.96	38.48	38.78	39.13	40.25
coastdistft	0	35228	1350.51	3559.09	0.00	43.00	398.00	980.00	55951.00
yearbuilt	0	35228	1969.56	37.25	1700.00	1950.00	1977.00	2000.00	2018.00
fld_fsid	0	35228	0.12	0.26	0.00	0.00	0.00	0.08	1.00
fld_blocks	0	35228	0.13	0.22	0.00	0.00	0.03	0.16	1.00
fld_blkgrs	0	35228	0.13	0.17	0.00	0.02	0.07	0.17	0.93
fld_tracts	0	35228	0.11	0.15	0.00	0.01	0.05	0.14	0.90
fld_contys	0	35228	0.06	0.11	0.00	0.01	0.02	0.05	0.57
fld_states	0	35228	0.03	0.01	0.00	0.02	0.03	0.03	0.04
rdem_fsid	0	35228	0.12	0.23	0.00	0.00	0.01	0.11	1.00
log_areabuilding	0	35228	7.42	0.46	4.72	7.10	7.40	7.72	10.17
log_arealotacres	0	35228	-1.10	1.14	-4.78	-1.76	-1.22	-0.56	9.59
log_coastdistft	0	35228	5.01	2.93	0.00	3.78	5.99	6.89	10.93



# propensity scores and matching, example — steps 2 & 3: estimating propensity score, matching to restructure data

## Steps 2 and 3

Matching method: non-parametric **propensity scores** (Diamond, 2013) given co-variates including building area, property area, geographic location, distance from coast, government boundaries, year built, sale month and year... from *treatment* (expected flooding) and *control* (expected no flooding) groups used to **match treatment to control**.

```
library(Matching)

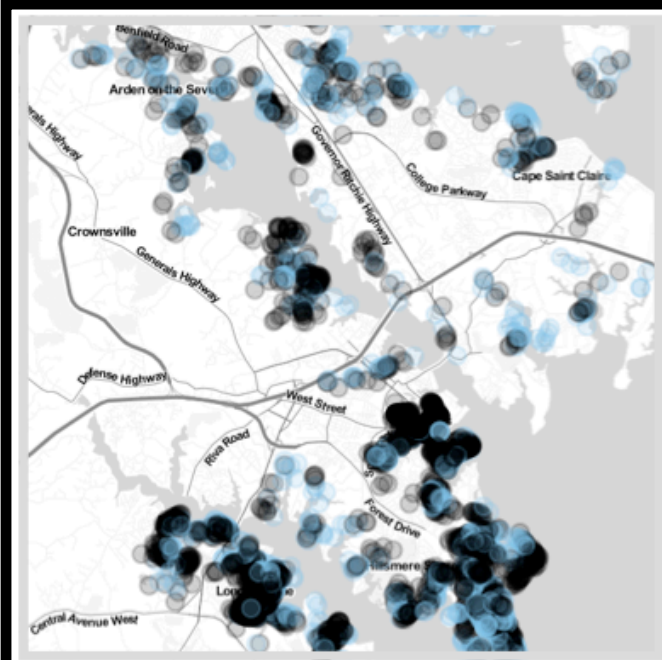
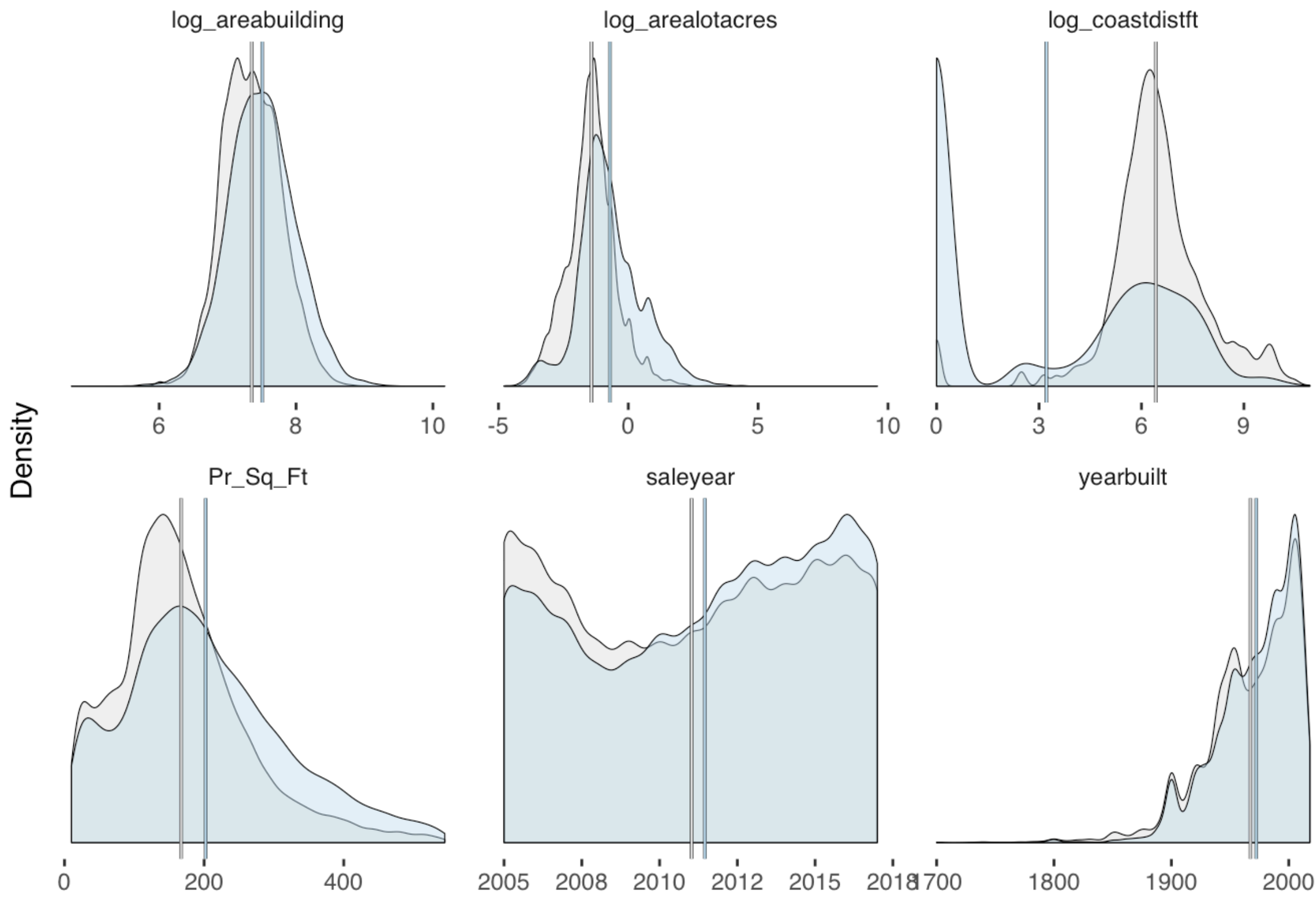
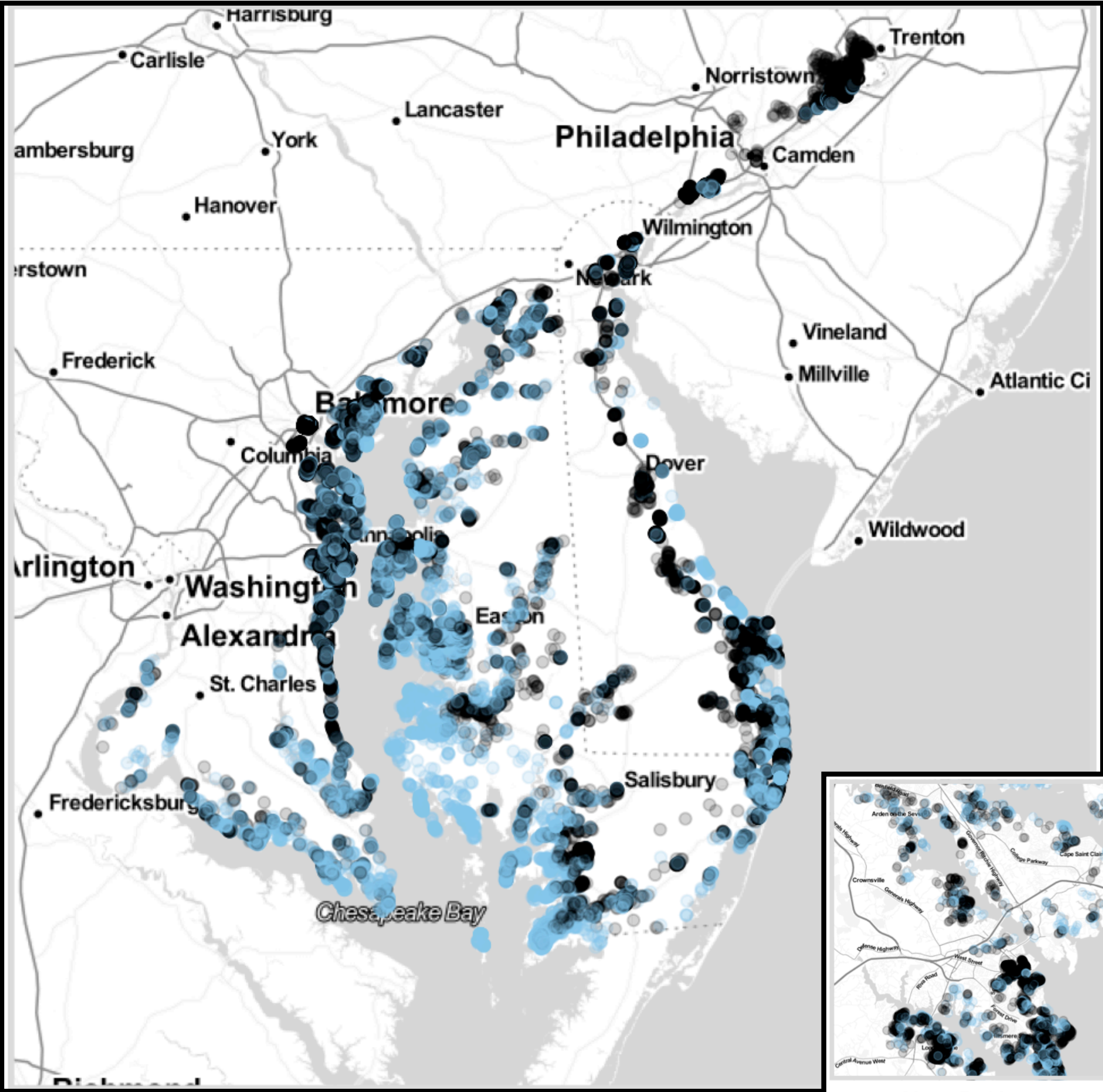
prop_scores <- with(d, GenMatch(Tr = __, X = __, ...))
matches <- Match(Y = __, Tr = __, X = __, Weight.matrix = prop_scores, ...)

treated <- d[matches$index.treated, ]
control <- d[matches$index.control, ]
```

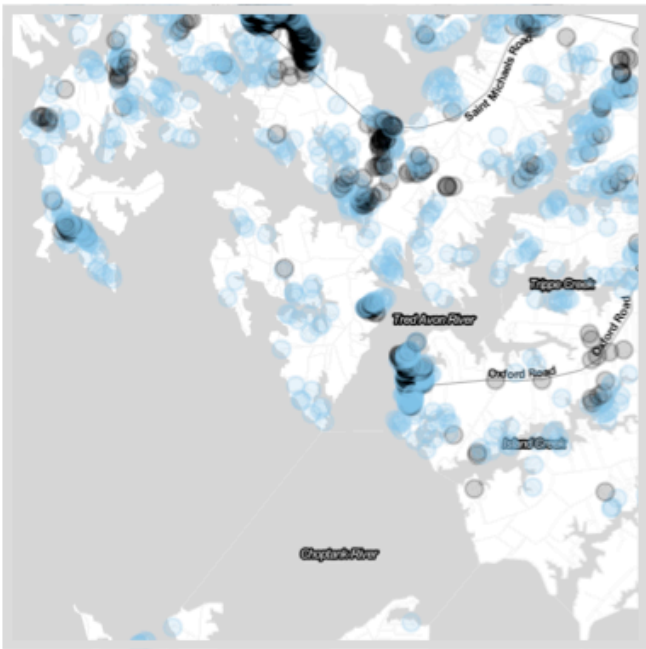




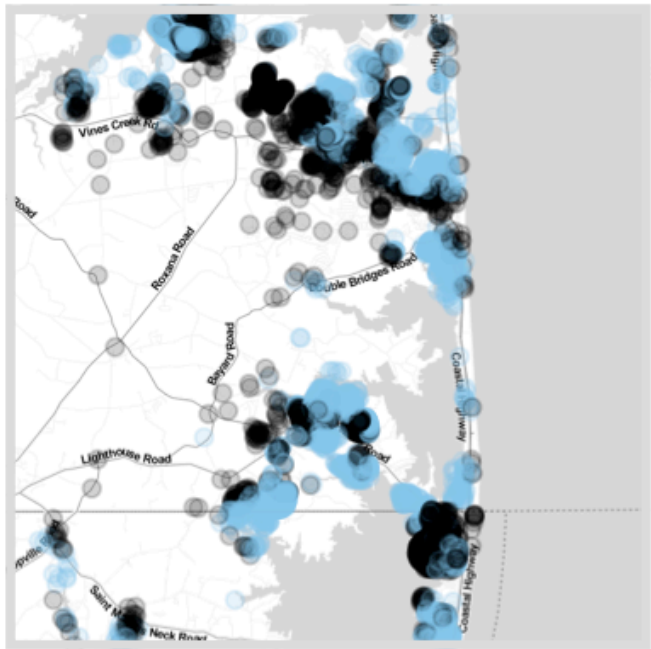
propensity scores and matching, example — step 4: diagnostics for balance and overlap



Near Baltimore



Near Easton

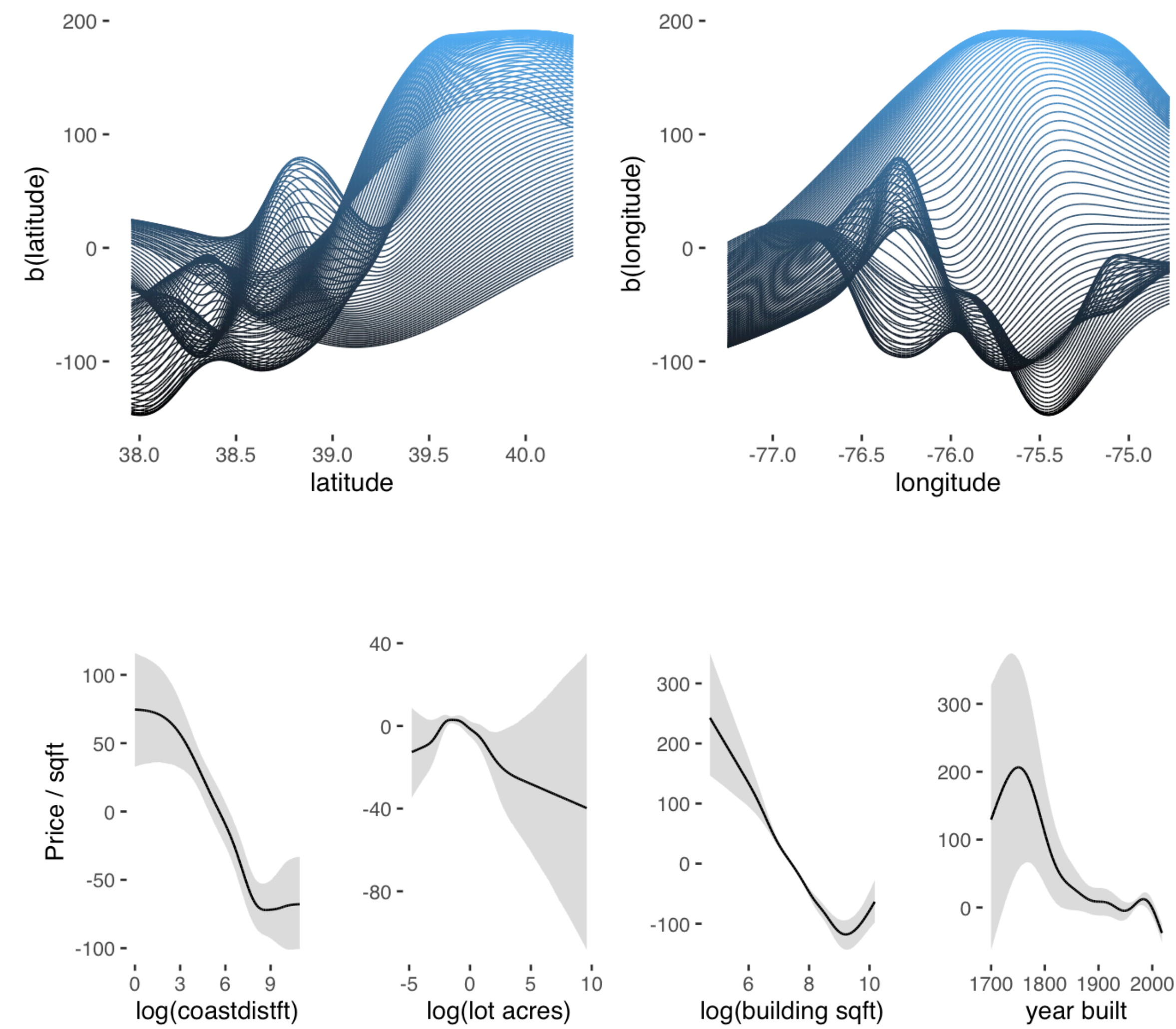
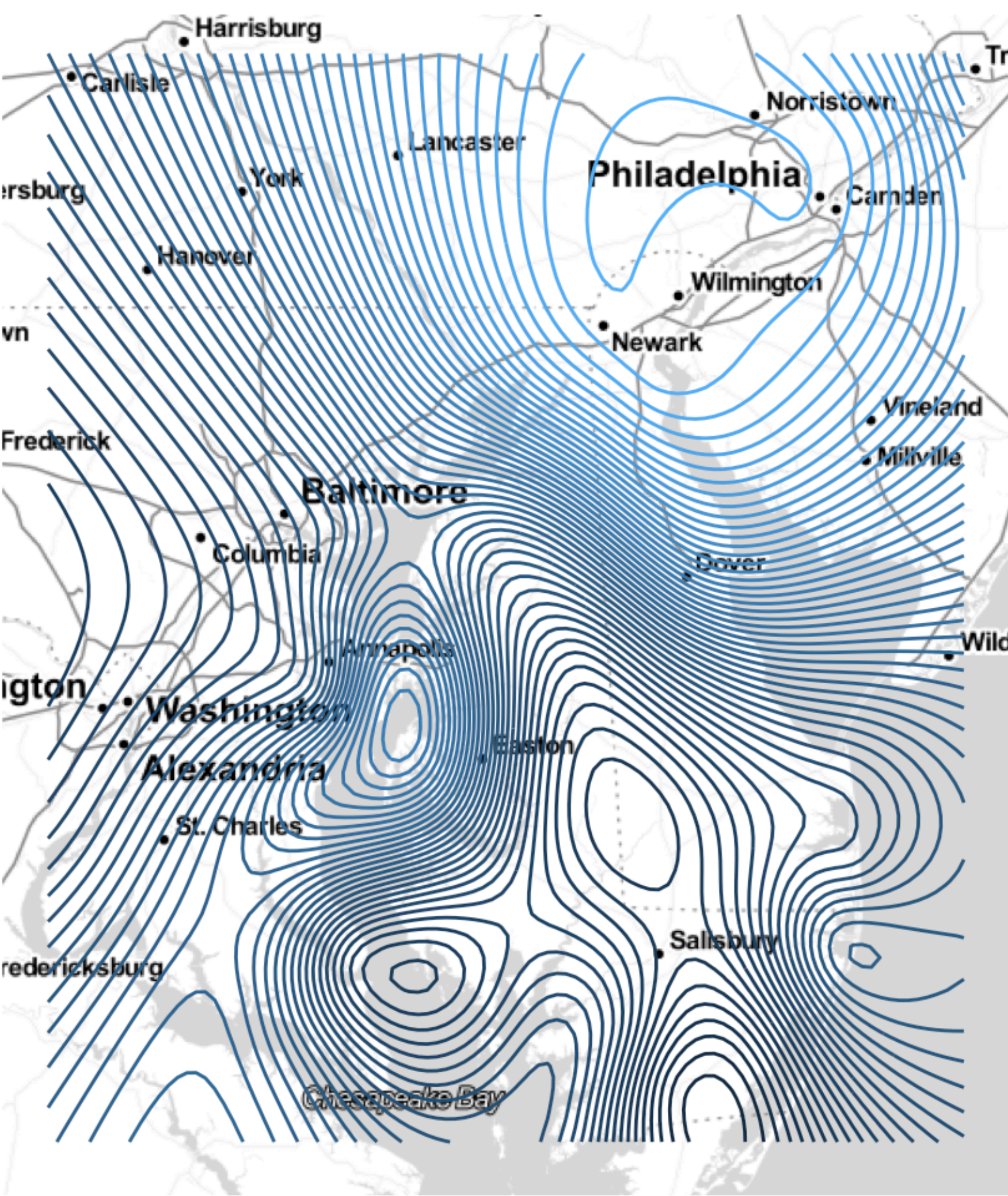


Near Fenwick Island



propensity scores and matching, example — step 5: estimate treatment effects, after adjustments for covariates

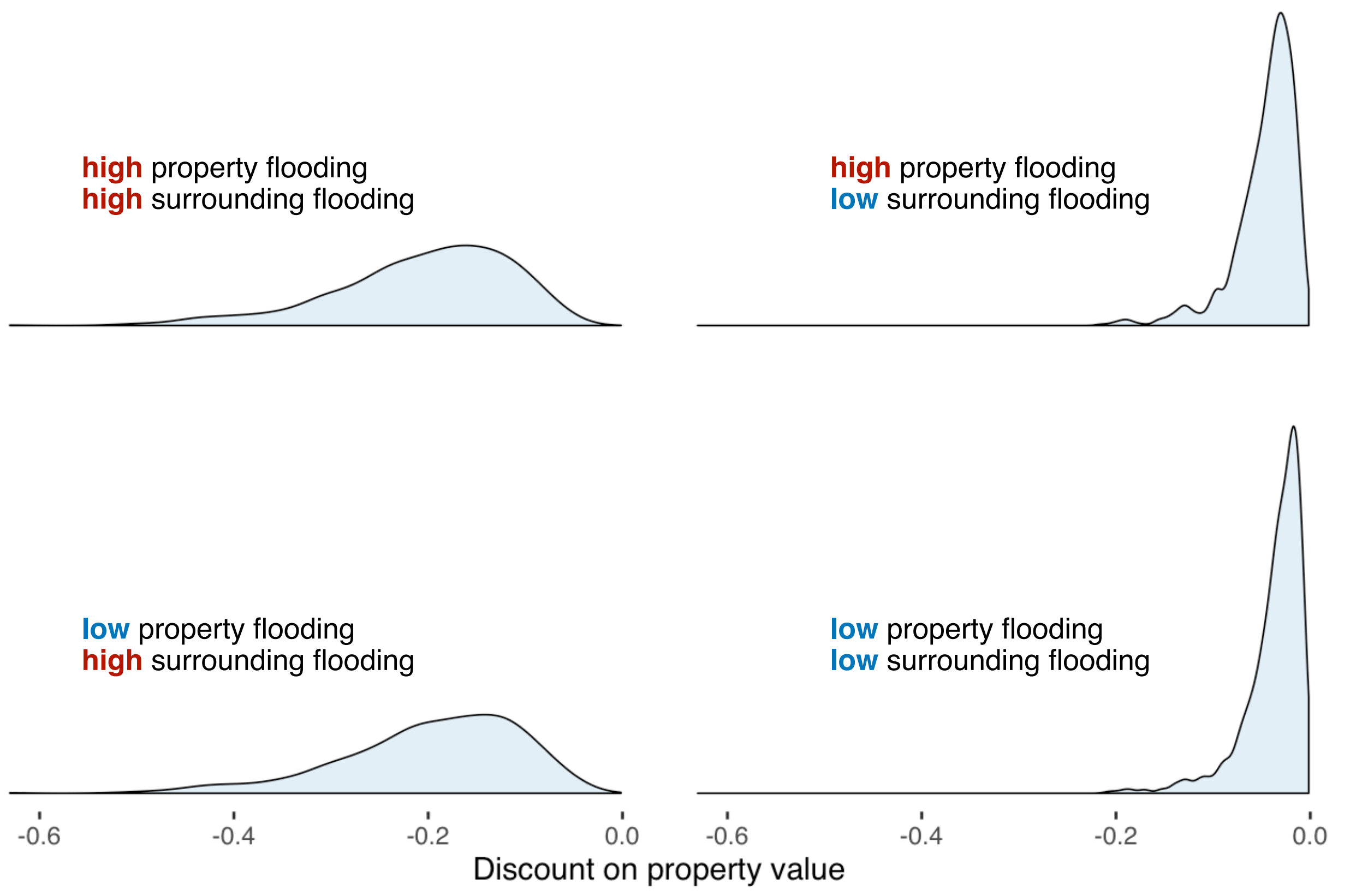
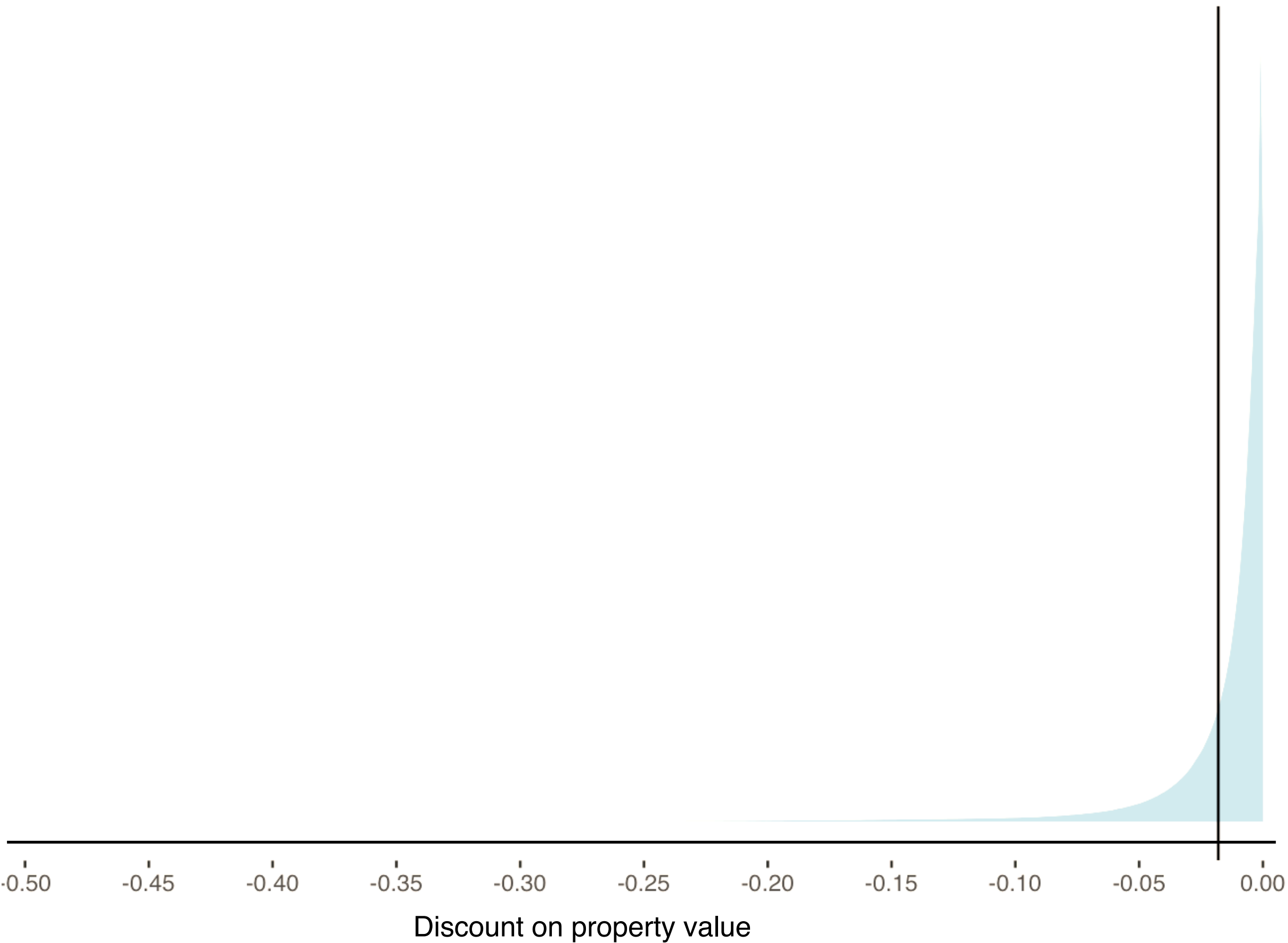
(Custom Bayesian) model still included adjustments because matching won't create perfect balance and overlap ...





Year-over-year fractional discount of price per square foot of property associated with expected flooding.

Counterfactuals: expected flooding in are surrounding property areas may matter more than property flooding.



group project work

# References

**Diamond**, Alexis, and Jasjeet S. Sekhon. *Genetic Matching for Estimating Causal Effects: A General Multivariate Matching Method for Achieving Balance in Observational Studies*. *Review of Economics and Statistics* 95, no. 3 (July 2013): 932–45.

**Gelman**, Andrew, Jennifer Hill, and Aki Ventari. “Observational Studies with All Confounders Assumed to Be Measured, Chp. 20.” In *Regression and Other Stories*. S.l.: Cambridge University Press, 2020.

**Ho**, Daniel E, Kosuke Imai, Gary King, and Elizabeth A Stuart. *Matching as Nonparametric Preprocessing for Reducing Model Dependence in Parametric Causal Inference*. *Political Analysis* 15, no. 3 (2007): 199–236.

**Rosenbaum**, Paul. *Design of Observational Studies*. Springer Nature, 2021.

———. *Observation and Experiment: An Introduction to Causal Inference*. Harvard University Press, 2017.

———. *Observational Studies*. Second. Springer, 2002.

**Sekhon**, Jasjeet S. *Multivariate and Propensity Score Matching Software with Automated Balance Optimization: The Matching Package for R*. *Journal of Statistical Software* 42, no. 7 (2011).

**Teele**, Dawn Langan. *Field Experiments and Their Critics: Essays on the Uses and Abuses of Experimentation in the Social Sciences*. New Haven: Yale University Press, 2014.