Bayesian Analysis & Propensity Score Analysis

Computational Mathematics and Statistics

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One Minute Paper Results

What was the most important thing you learned during this class?

What important question remains unanswered for you?

Bayesian Analysis

Bayesian Analysis

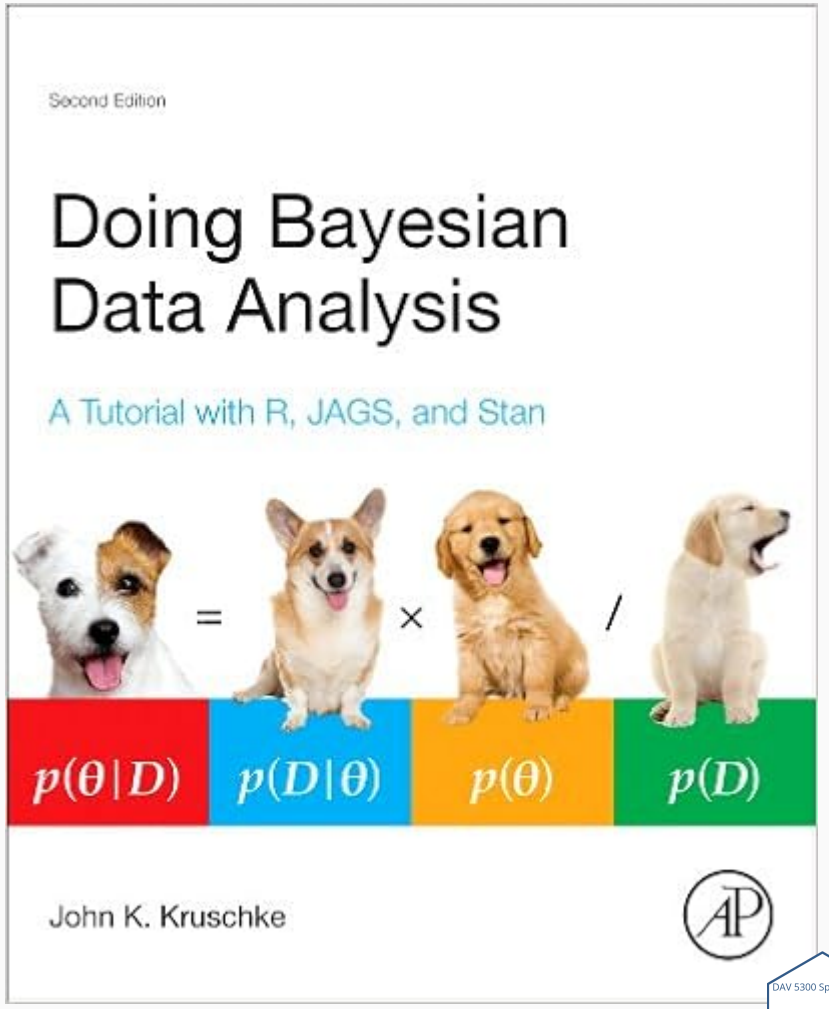
Kruschke's videos are an excelent introduction to Bayesian Analysis https://www.youtube.com/watch?v=YyohWpjl6KU!

Doing Bayesian Data Analysis, Second Edition: A Tutorial with R, JAGS, and Stan

The Theory That Would Not Die: How Bayes' Rule Cracked the Enigma Code, Hunted Down Russian Submarines, and Emerged Triumphant from Two Centuries of Controversy by Sharon Bertsch McGrayne

Video series by Rasmus Baath Part 1, Part 2, Part 3

Billiards with Fred the Frequentist and Bayer the Bayesian



Bayes Theorem

$$P(A|B) = \frac{P(B|A)P(A)}{P(B|A)P(A) + P(B|A^{'})P(A^{'})}$$

Consider the following data from a cancer test:

- 1% of women have breast cancer (and therefore 99% do not).
- 80% of mammograms detect breast cancer when it is there (and therefore 20% miss it).
- 9.6% of mammograms detect breast cancer when it's not there (and therefore 90.4% correctly return a negative result).

	Cancer (1%)	**No Cancer (99%)**
Test postive	80%	9.6%
Test negative	20%	90.4%

How accurate is the test?

Now suppose you get a positive test result. What are the chances you have cancer?
80%? 99%? 1%?

- Ok, we got a positive result. It means we're somewhere in the top row of our table. Let's not assume anything - it could be a true positive or a false positive.
- The chances of a true positive = chance you have cancer *chance test caught it* = *1%* 80% = .008
- The chances of a false positive = chance you don't have cancer *chance test caught it anyway* = *99%* 9.6% = 0.09504

	Cancer (1%)	**No Cancer (99%)**	
Test postive	True +: 1% * 80%	False +: 99% * 9.6%	**10.304%**
Test negative	False -: 1% * 20%	True -: 99% * 90.4%	**89.696%**

How accurate is the test?

$$Probability = \frac{desired \quad event}{all \quad possibilities}$$

The chance of getting a real, positive result is .008. The chance of getting any type of positive result is the chance of a true positive plus the chance of a false positive (.008 + 0.09504 = .10304).

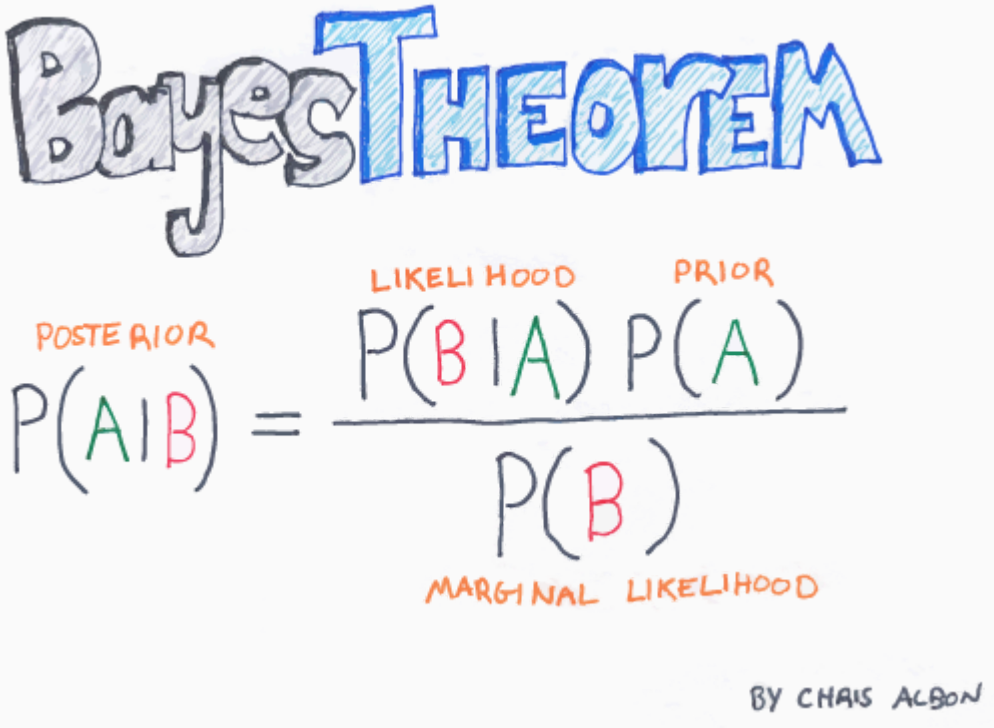
$$P(C|P) = \frac{P(P|C)P(C)}{P(P)} = \frac{.8 * .01}{.008 + 0.095} \approx .078$$

So, our chance of cancer is .008/.10304 = 0.0776, or about 7.8%.

Bayes Formula

It all comes down to the chance of a true positive result divided by the chance of any positive result. We can simplify the equation to:

$$P(A|B) = \frac{P(B|A)\,P(A)}{P(B)}$$


BayesTheorem
POSTERIOR
LIKELIHOOD
PRIOR
P(A|B) = P(B|A) P(A) / P(B)
MARGINAL LIKELIHOOD
BY CHRIS ALBON

How many fish are in the lake?

- Catch them all, count them. Not practical (or even possible)!
- We can sample some fish.

Our strategy:

1. Catch some fish.
2. Mark them.
3. Return the fish to the pond. Let them get mixed up (i.e. wait a while).
4. Catch some more fish.
5. Count how many are marked.

For example, we initially caught 20 fish, marked them, returned them to the pond. We then caught another 20 fish and 5 of them were marked (i.e they were caught the first time).

Adopted from Rasmath Bääth useR! 2015 workshop: http://www.sumsar.net/files/academia/user_2015_tutorial_bayesian_data_analysis_short_version.pdf

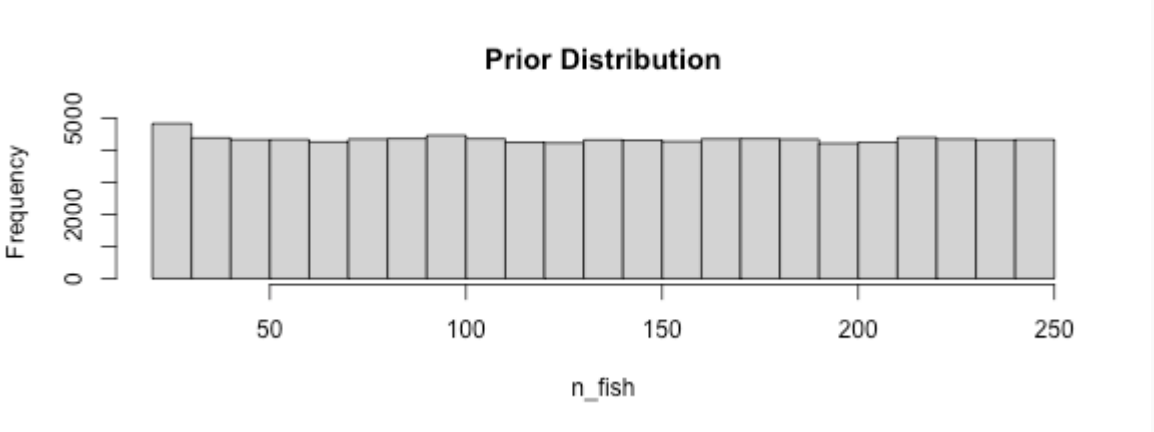
Strategy for fitting a model

Step 1: Define Prior Distribution. Draw a lot of random samples from the "prior" probability distribution on the parameters.

```
n_draw <- 100000
n_fish <- sample(20:250, n_draw, replace = TRUE)
head(n_fish, n=10)
```

```
##  [1] 211 103 179 136 185 244 186  60 220  29
```

```
hist(n_fish, main="Prior Distribution")
```



Strategy for fitting a model

Step 2: Plug in each draw into the generative model which generates "fake" data.

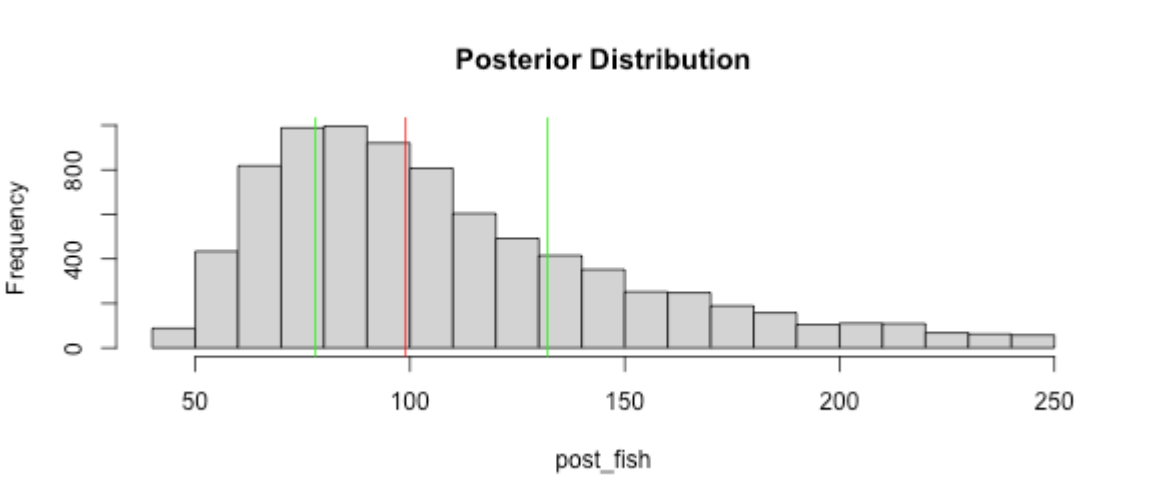
```
pick_fish <- function(n_fish) { # The generative model
    fish <- rep(0:1, c(n_fish - 20, 20))
    sum(sample(fish, 20))
}
n_marked <- rep(NA, n_draw)
for(i in 1:n_draw) {
    n_marked[i] <- pick_fish(n_fish[i])
}
head(n_marked, n=10)
```

```
##  [1]  3  3  0  3  4  1  1  7  3 14
```

Strategy for fitting a model

Step 3: Keep only those parameter values that generated the data that was actually observed (in this case, 5).

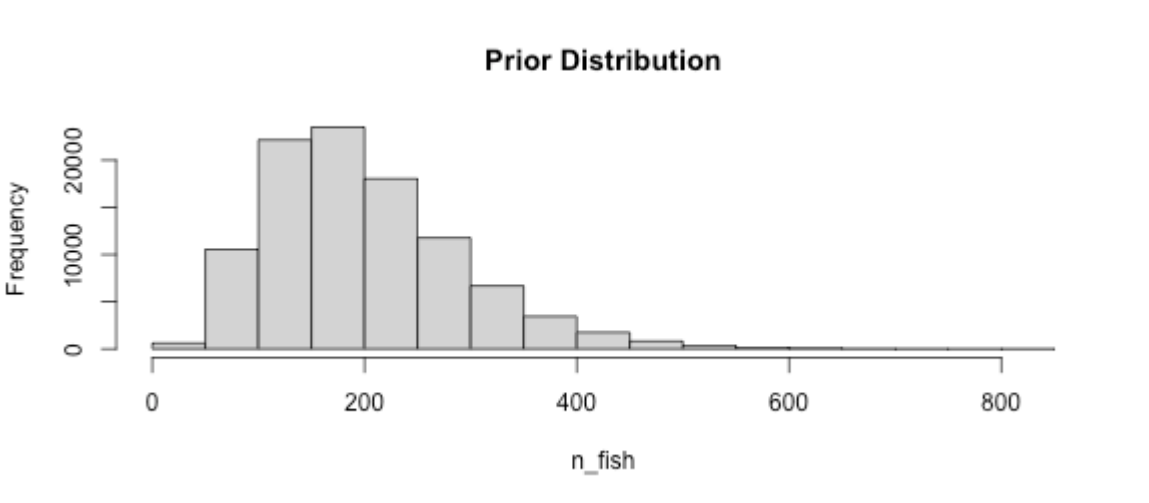
```
post_fish <- n_fish[n_marked == 5]
hist(post_fish, main='Posterior Distribution')
abline(v=median(post_fish), col='red')
abline(v=quantile(post_fish, probs=c(.25, .75)), col='green')
```



What if we have better prior information?

An "expert" believes there are around 200 fish in the pond. Insteand of a uniform distribution, we can use a binomial distribution to define our "prior" distribution.

```
n_fish <- rnbinom(n_draw, mu = 200 - 20, size = 4) + 20
hist(n_fish, main='Prior Distribution')
```



What if we have better prior information?

```
n_marked <- rep(NA, n_draw)
for(i in 1:n_draw) {
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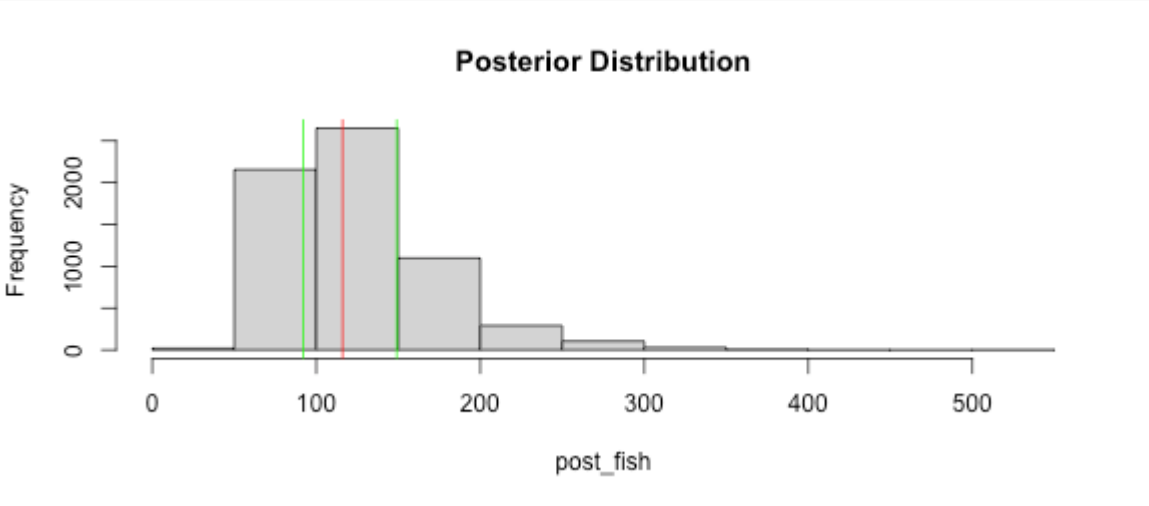


Bayes Billiards Balls

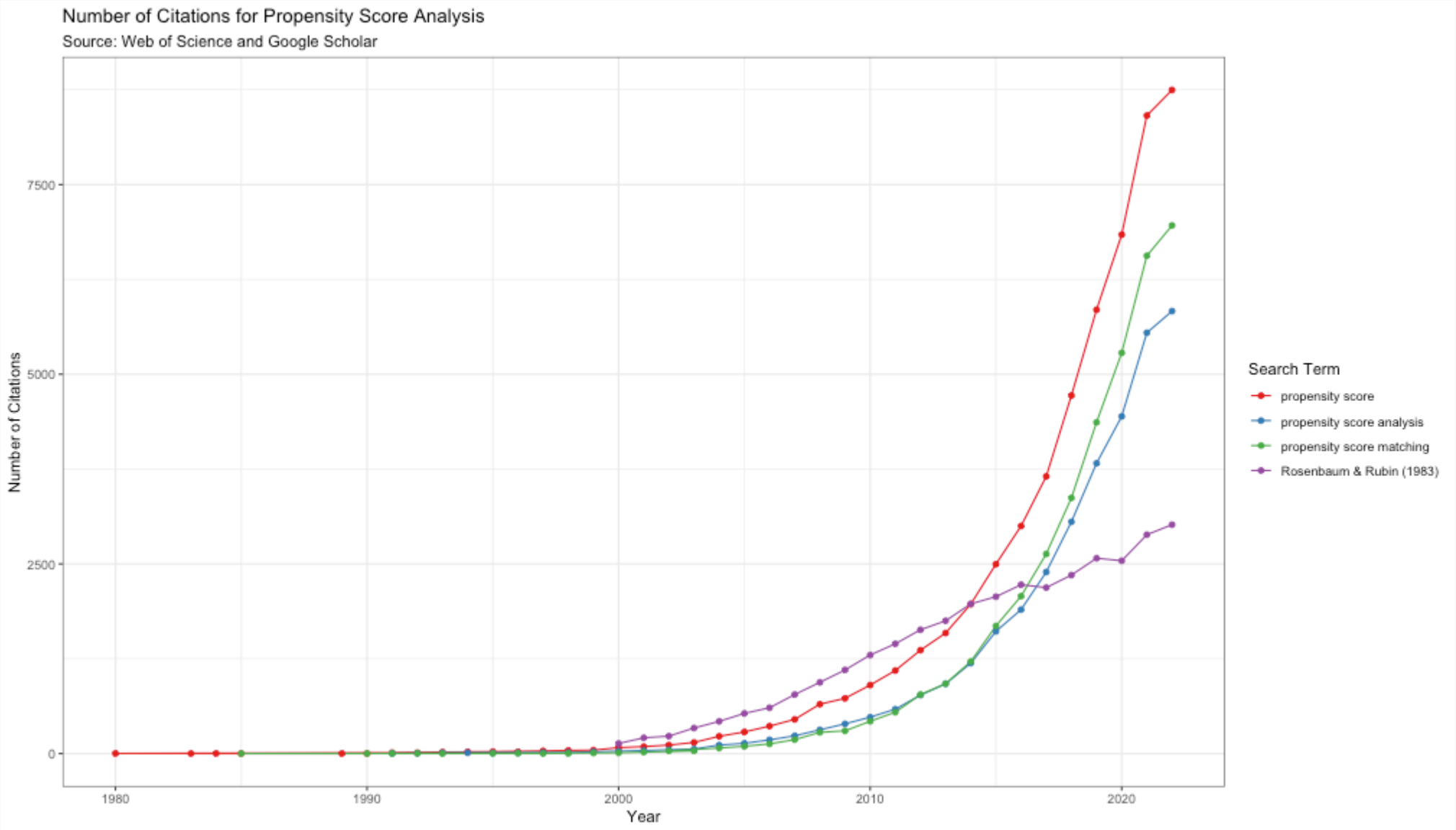
Consider a pool table of length one. An 8-ball is thrown such that the likelihood of its stopping point is uniform across the entire table (i.e. the table is perfectly level). The location of the 8-ball is recorded, but not known to the observer. Subsequent balls are thrown one at a time and all that is reported is whether the ball stopped to the left or right of the 8-ball. Given only this information, what is the position of the 8-ball? How does the estimate change as more balls are thrown and recorded?

```
DATA606::shiny_demo('BayesBilliards', package='DATA606')
```

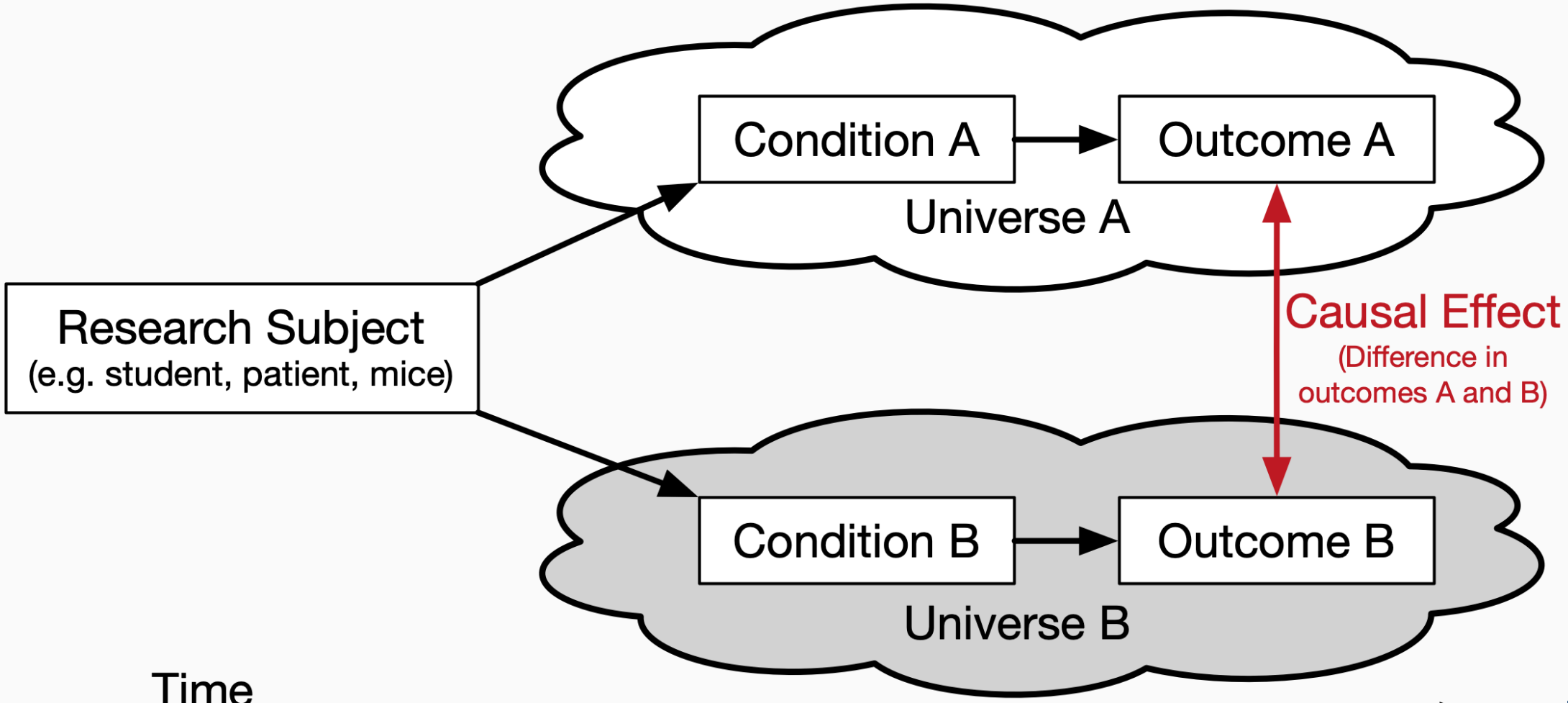
See also: http://www.bryer.org/post/2016-02-21-bayes_billiards_shiny/

Propensity Score Analysis

Popularity of Propensity Score Analysis



Counterfactuals



The only difference between universes A and B is conditions A and B and, potentially, outcomes A and B.

The Randomized Experiment

Considered to be the *gold standard* for estimating causal effects.

- Effects can be estimated using simple means between groups, or blocks in randomized block design.
- Randomization presumes unbiasedness and balance between groups.

However, randomization is often not feasible for many reasons, especially in educational contexts.

The **strong ignorability assumption** states that:

$$(Y_i(1), Y_i(0)) \perp\!\!\!\perp T_i | X_i = x$$

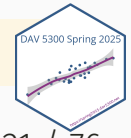
for all X_i.

RCT Example

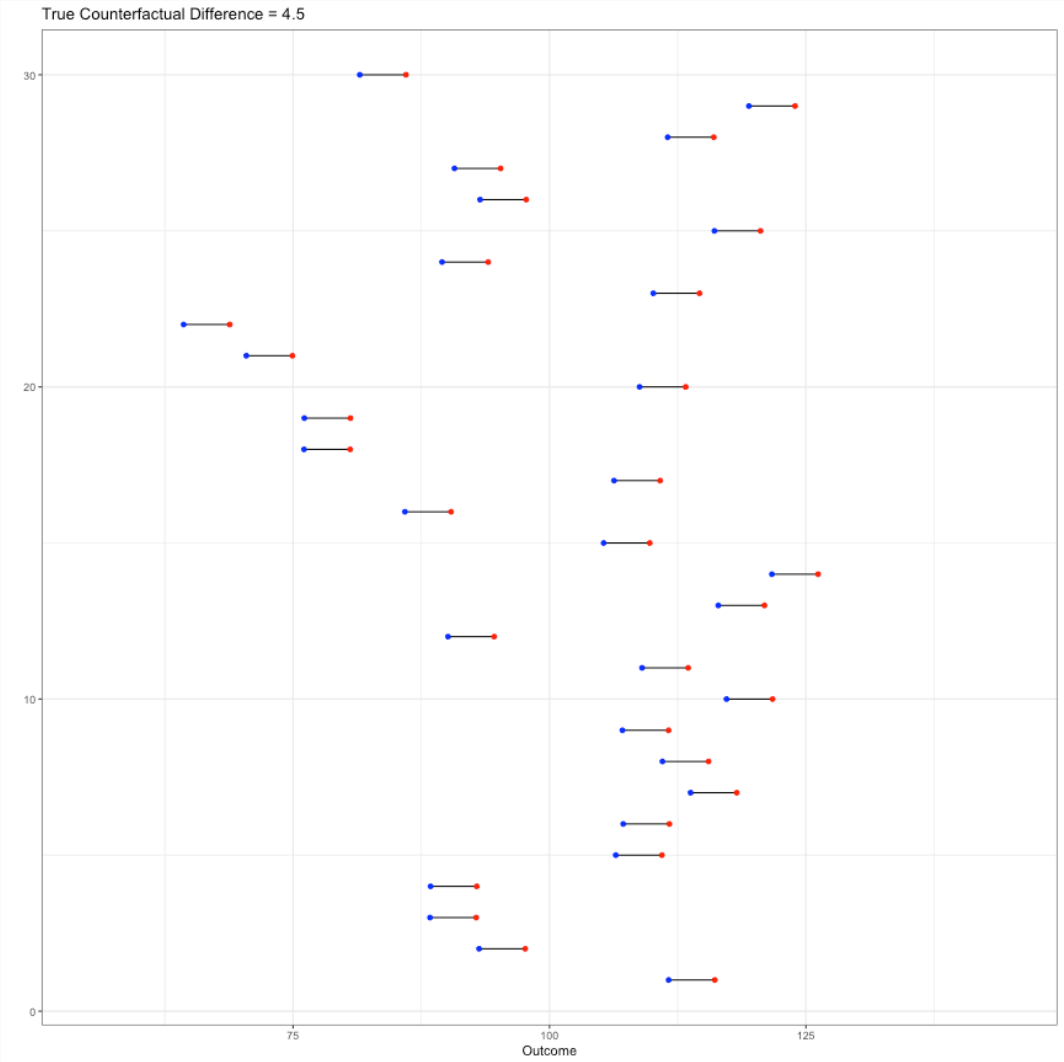
```
set.seed(2112)
pop.mean <- 100
pop.sd <- 15
pop.es <- .3
n <- 30
thedata <- data.frame(
    id = 1:30,
    center = rnorm(n, mean = pop.mean, sd = pop.sd),
    stringsAsFactors = FALSE
)
val <- pop.sd * pop.es / 2
thedata$placebo <- thedata$center - val
thedata$treatment <- thedata$center + val
thedata$diff <- thedata$treatment - thedata$placebo
thedata$RCT_Assignment <- sample(c('placebo', 'treatment'), n, replace = TRUE)
thedata$RCT_Value <- as.numeric(apply(thedata, 1,
                    FUN = function(x) { return(x[x['RCT_Assignment']]) }))
head(thedata, n = 3)
```

```
##   id    center   placebo treatment diff RCT_Assignment RCT_Value
## 1  1 113.86506 111.61506 116.11506  4.5      treatment 116.11506
## 2  2  95.38746  93.13746  97.63746  4.5      treatment  97.63746
## 3  3  90.60380  88.35380  92.85380  4.5      treatment  92.85380
```

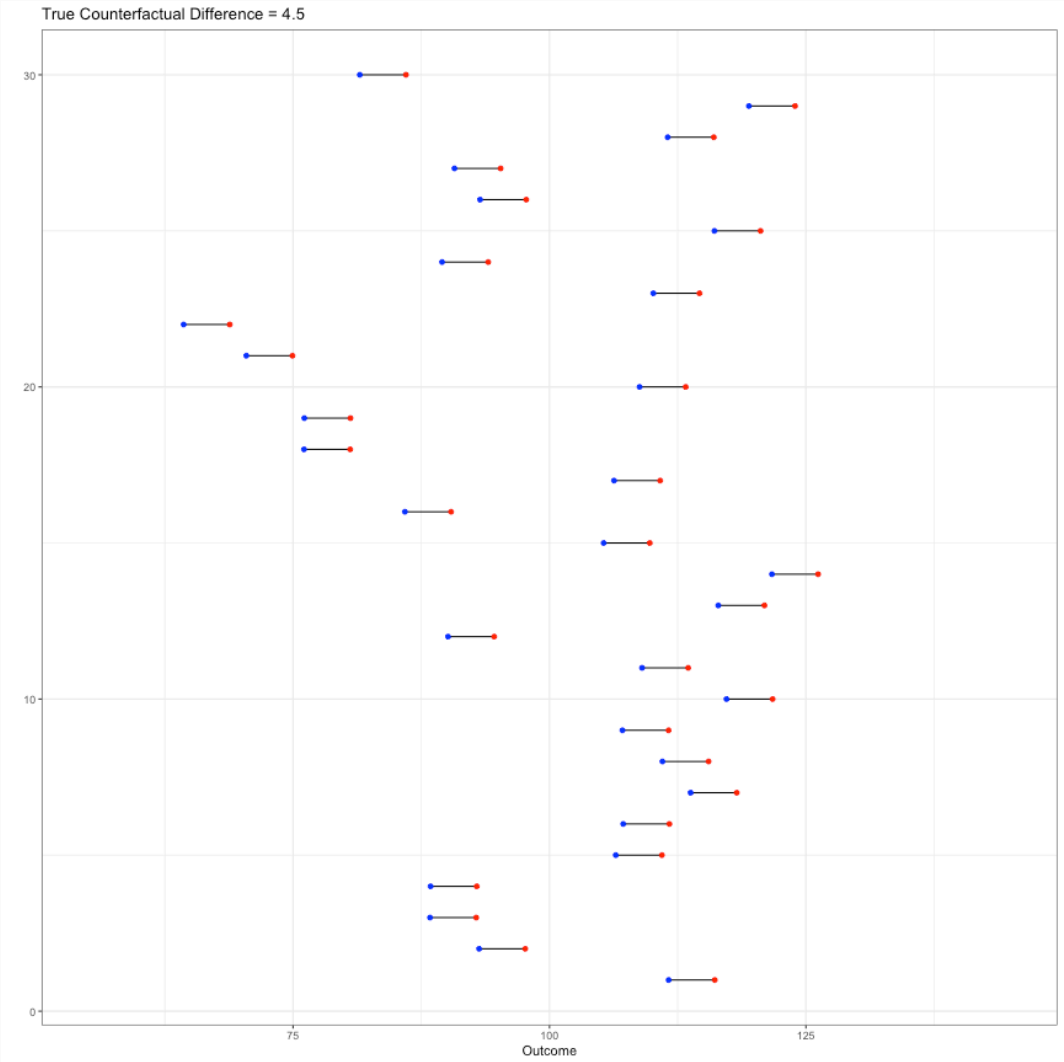
```
tab.out <- describeBy(thedata$RCT_Value, group = thedata$RCT_Assignment, mat = TRUE, skew = FALSE)
```

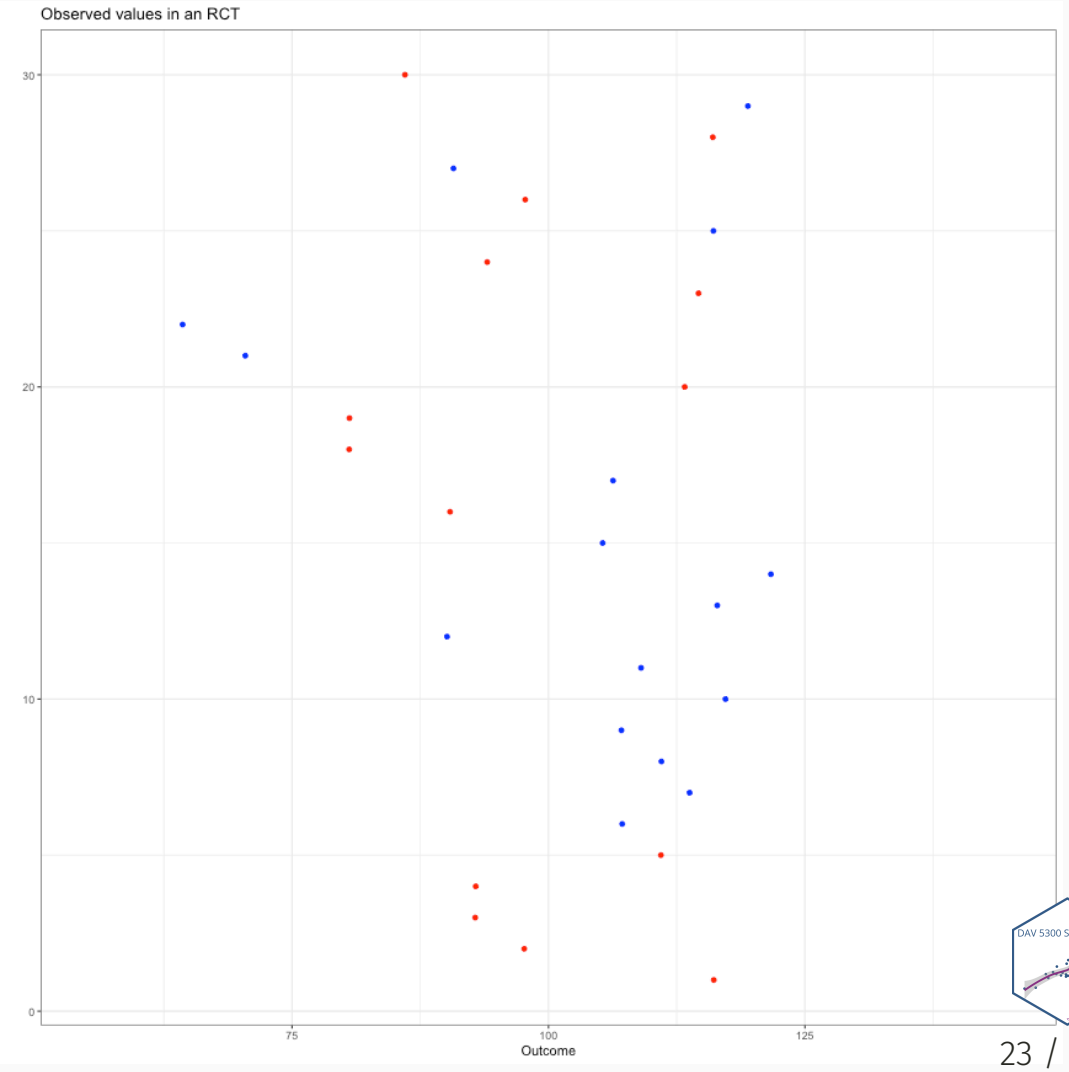


True Counterfactual

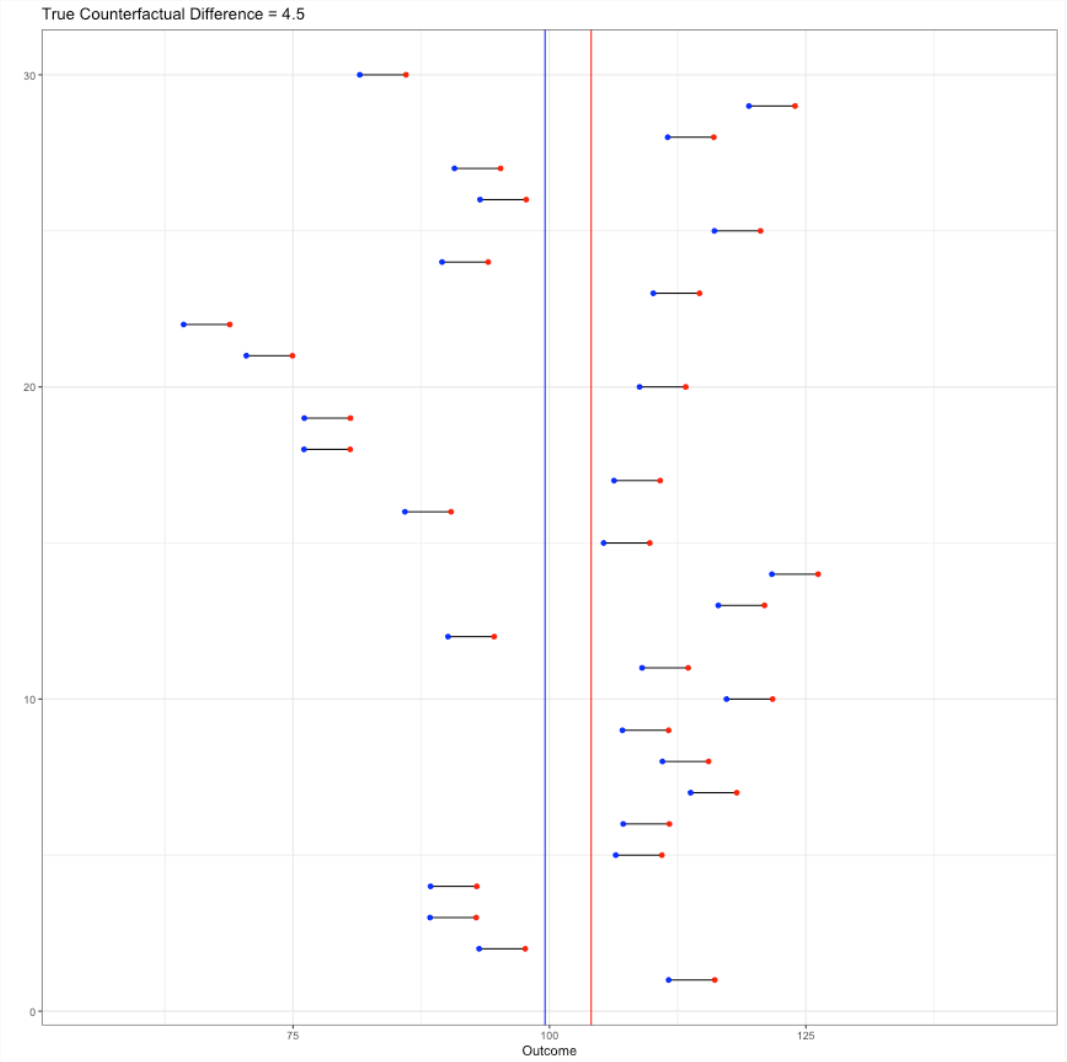


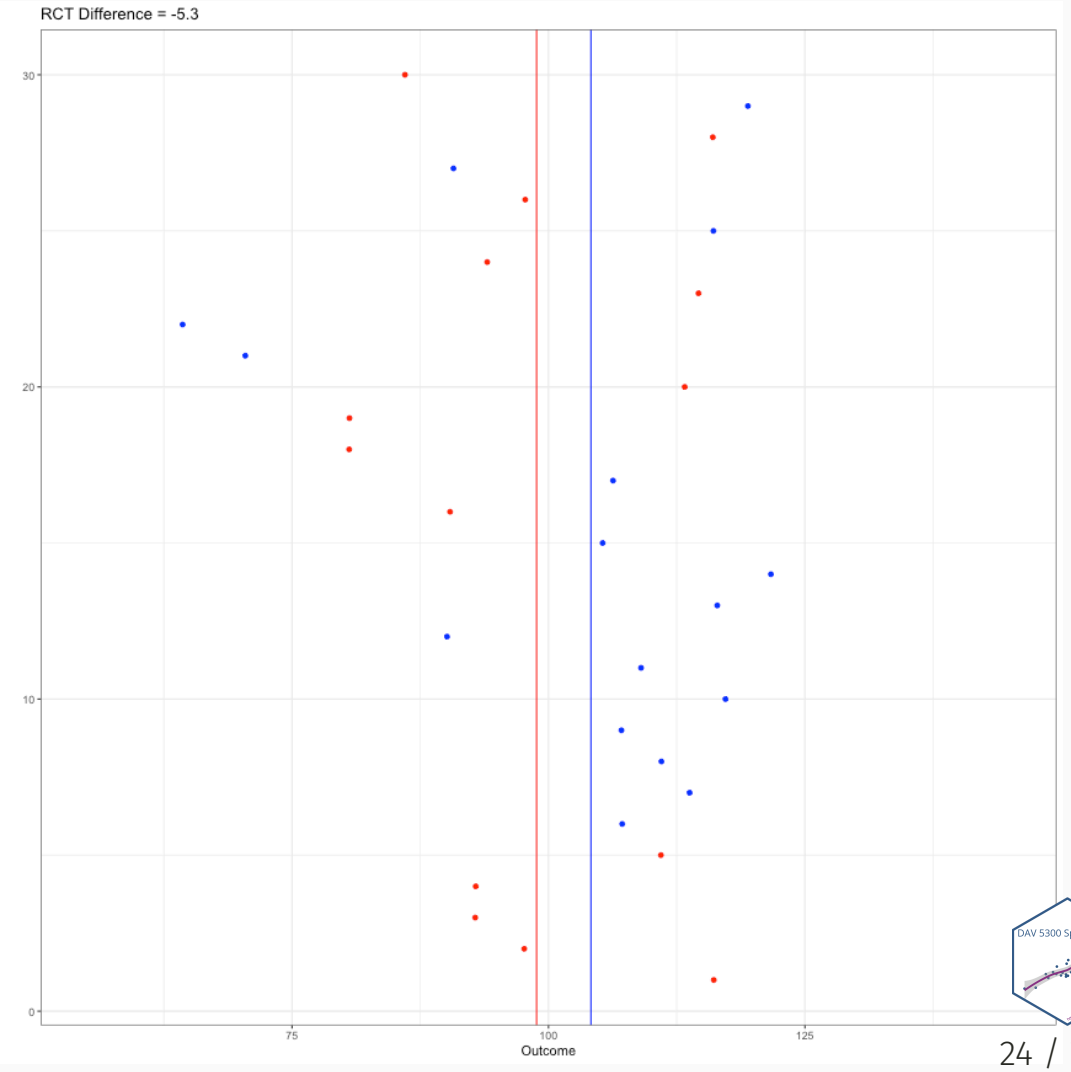
True Counterfactual (left) vs. One RCT (right)



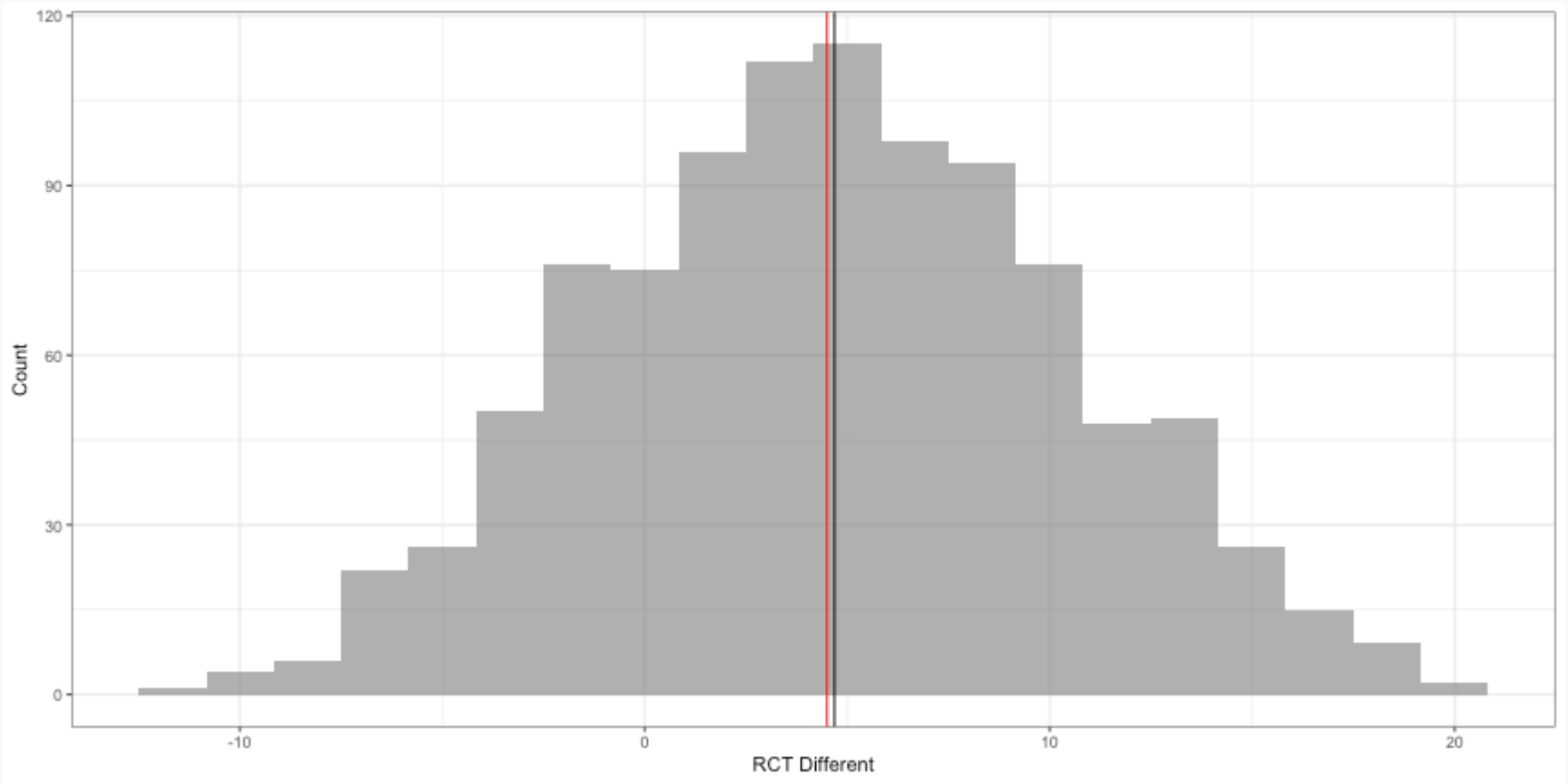


True Counterfactual (left) vs. One RCT (right)





Distribution of Differences from 1,000 RCTs



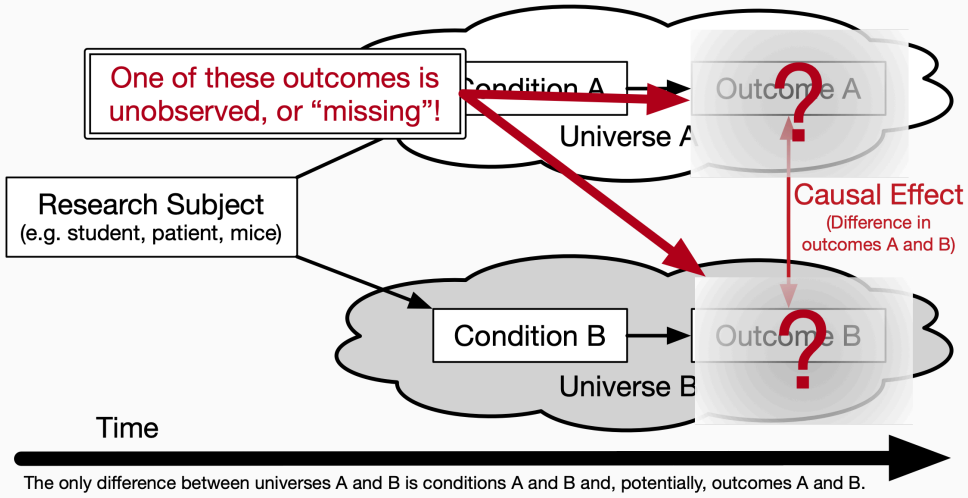
Rubin's Causal Model

- The causal effect of a treatment is the difference in an individual's outcome under the situation they were given the treatment and not (referred to as a counterfactual).

$$\delta_i = Y_{i1} - Y_{i0}$$

- However, it is impossible to directly observe δ_i (referred to as *The Fundamental Problem of Causal Inference*, Holland 1986).

- Rubin frames this problem as a "missing data problem" (see Rubin, 1974, 1977, 1978, 1980, and Holland, 1986).



Propensity Score Analysis

The propensity score is the "conditional probability of assignment to a particular treatment given a vector of observed covariates" (Rosenbaum & Rubin, 1983, p. 41). The probability of being in the treatment:

$$\pi(X_i) \equiv Pr(T_i = 1|X_i)$$

The balancing property under exogeneity:

$$T_i \perp\!\!\!\perp X_i \mid \pi(X_i)$$

We can then restate the **ignorability assumption** with the propensity score:

$$(Y_i(1), Y_i(0)) \perp\!\!\!\perp T_i \mid \pi(X_i)$$

Treatment Effects

The average treatment effect (ATE) is defined as:

$$E(r_1) - E(r_0)$$

where $E(.)$ is the expectation in the population. For a set of covariates, X, and outcomes Y where 0 denotes control and 1 treatment, we define ATE as:

$$ATE = E(Y_1 - Y_0|X) = E(Y_1|X) - E(Y_0|X)$$

As we will see later there are alternative treatment effects (estimands) we can estimate instead of ATE.

What Rosenbaum and Rubin (1983) proved in their seminal paper is that the propensity score is a univariate representation of the multivariate matrix. As we will see later, two observations with very similar propensity scores will look similar across all the observed covariates.

Propensity Score Analysis in Three Phases

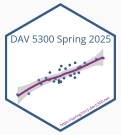
Simulated Example

We will simulate a dataset with three covariates, `x1` and `x2` which are continuous and `x3` which is categorical. The assumed treatment effect is 1.5.

```
n <- 500
treatment_effect <- 1.5
X <- mvtnorm::rmvnorm(
    n,
    mean = c(0.5, 1, 0),
    sigma = matrix(c(2, 1, 1,
                     1, 1, 1,
                     1, 1, 1),
                     ncol = 3) )
dat <- tibble(
    x1 = X[, 1],
    x2 = X[, 2],
    x3 = X[, 3] > 0,
    treatment = as.numeric(- 0.5 +
                               0.25 * x1 +
                               0.75 * x2 +
                               0.05 * x3 +
                               rnorm(n, 0, 1) > 0),
    outcome = treatment_effect * treatment +
        rnorm(n, 0, 1)
)
```

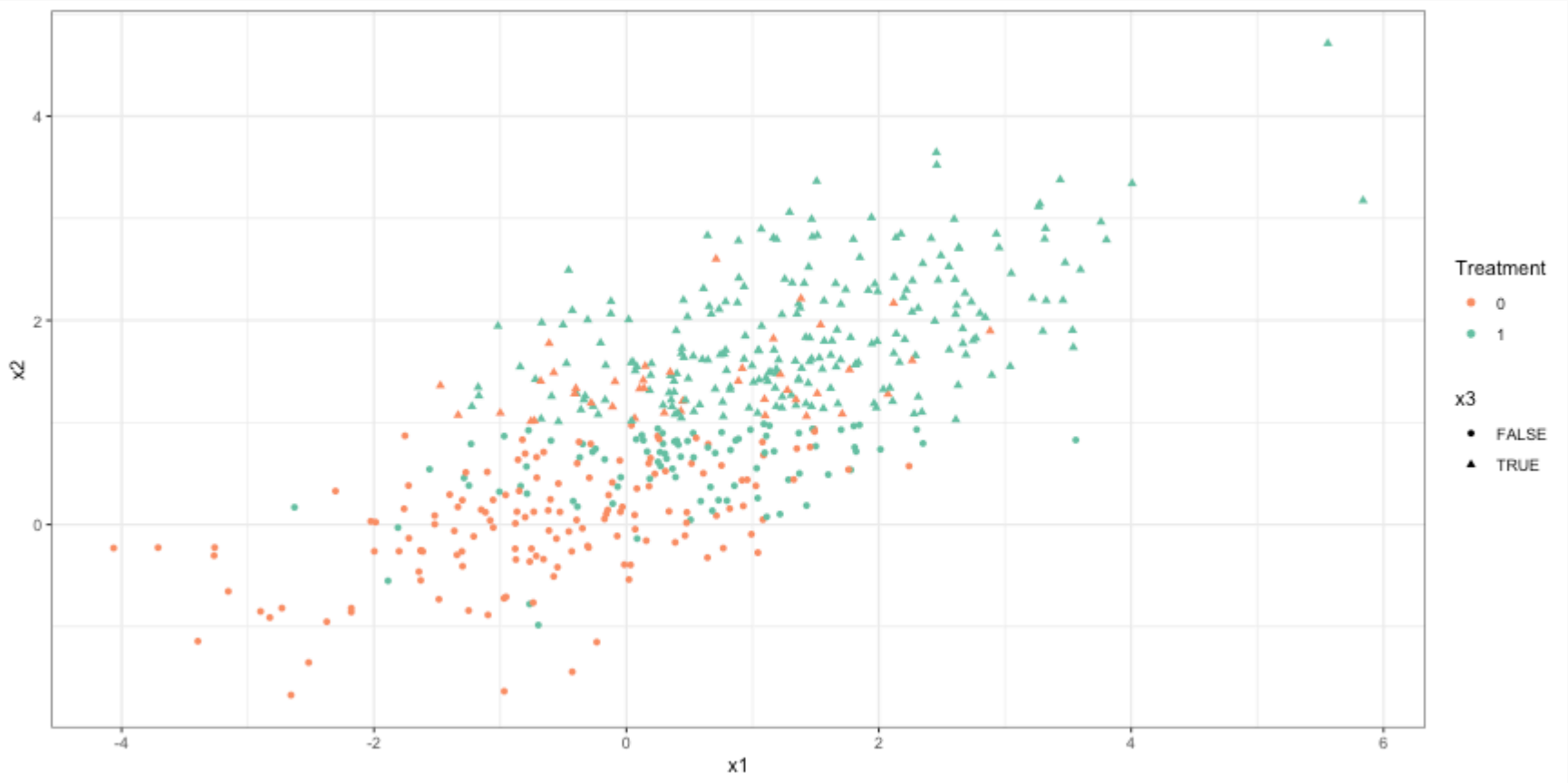
```
head(dat, n = 6)
```

```
## # A tibble: 6 × 5
##       x1    x2 x3    treatment outcome
##    <dbl> <dbl> <lgl>     <dbl>   <dbl>
## 1  1.35  0.744 FALSE         0  1.46
## 2  0.149 1.55  TRUE          0 -0.924
## 3  2.47  2.39  TRUE          1 -0.0527
## 4  2.29  1.66  TRUE          1  1.05
## 5  2.93  2.85  TRUE          1  0.721
## 6 -0.867 0.125 FALSE         0  0.723
```

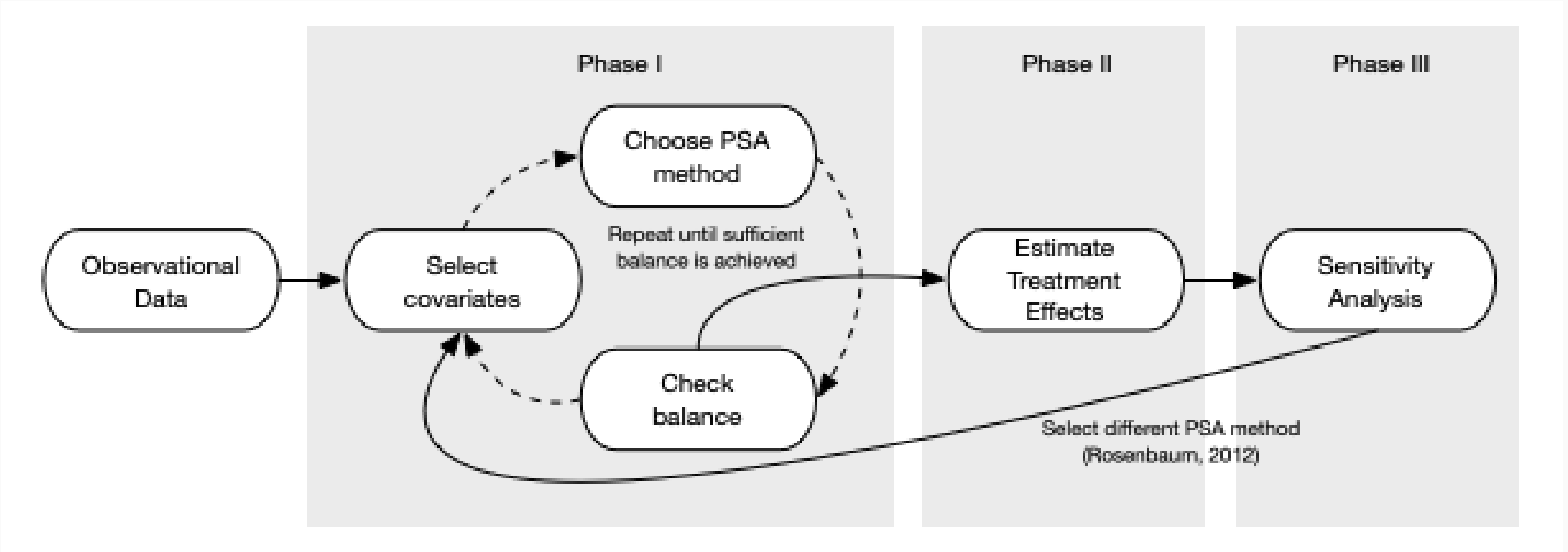


Scatterplot

```
ggplot(dat, aes(x = x1, y = x2, shape = x3, color = factor(treatment))) +
    geom_point() + scale_color_manual('Treatment', values = cols)
```



Steps for Implementing Propensity Score Analysis



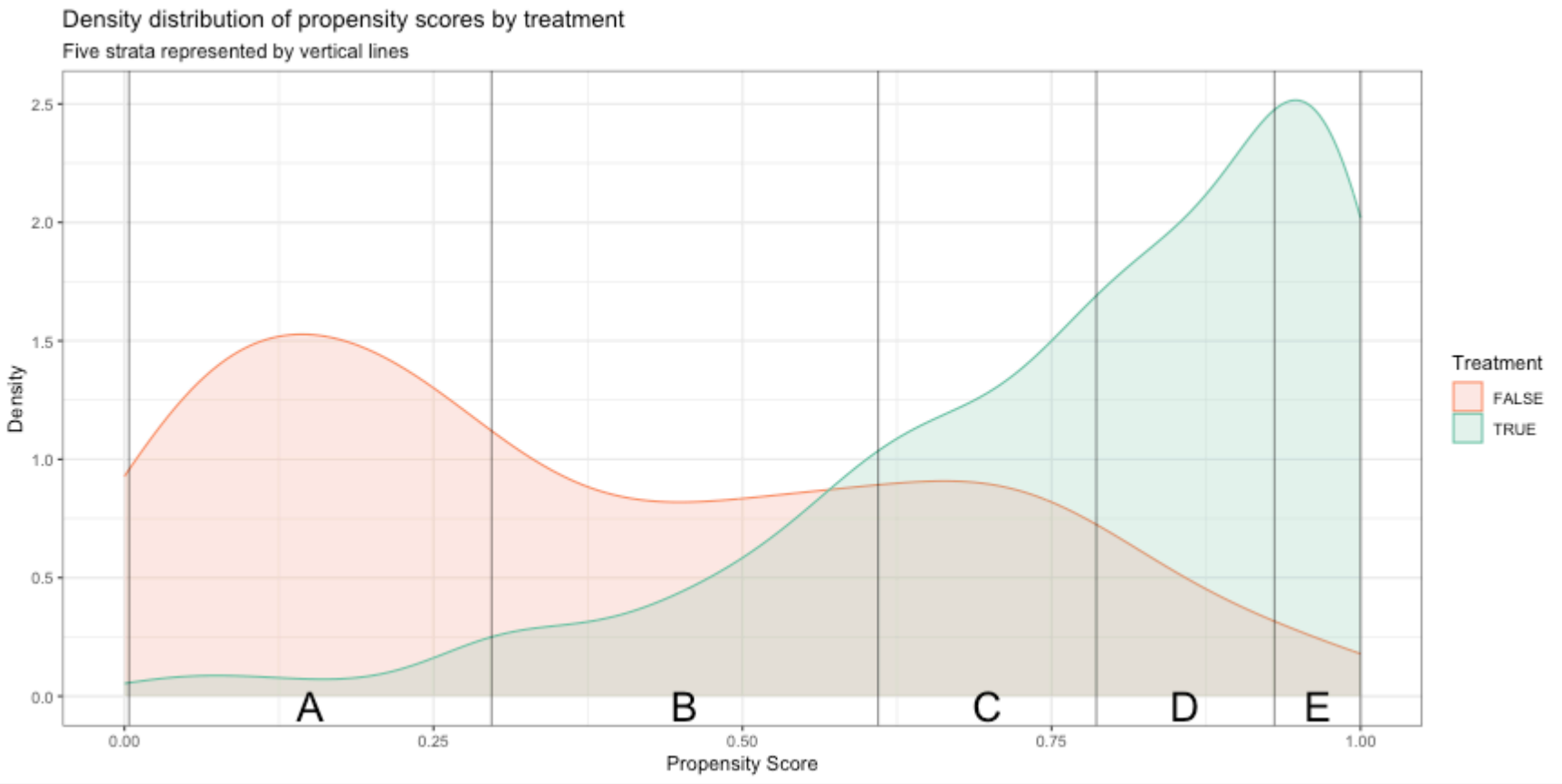
Propensity score methods

There are three major approaches for conducting PSA:

- **Stratification** Treatment and comparison units are divided into strata (or subclasses) so that treated and comparison units are similar within each strata. Cochran (1968) observed that creating five subclassifications (stratum) removes at least 90% of the bias in the estimated treatment effect.
- **Matching** - Each treatment unit is paired with a comparison unit based upon the pre-treatment covariates.
- **Weighting** Each observation is weighted by the inverse of the probability of being in that group.

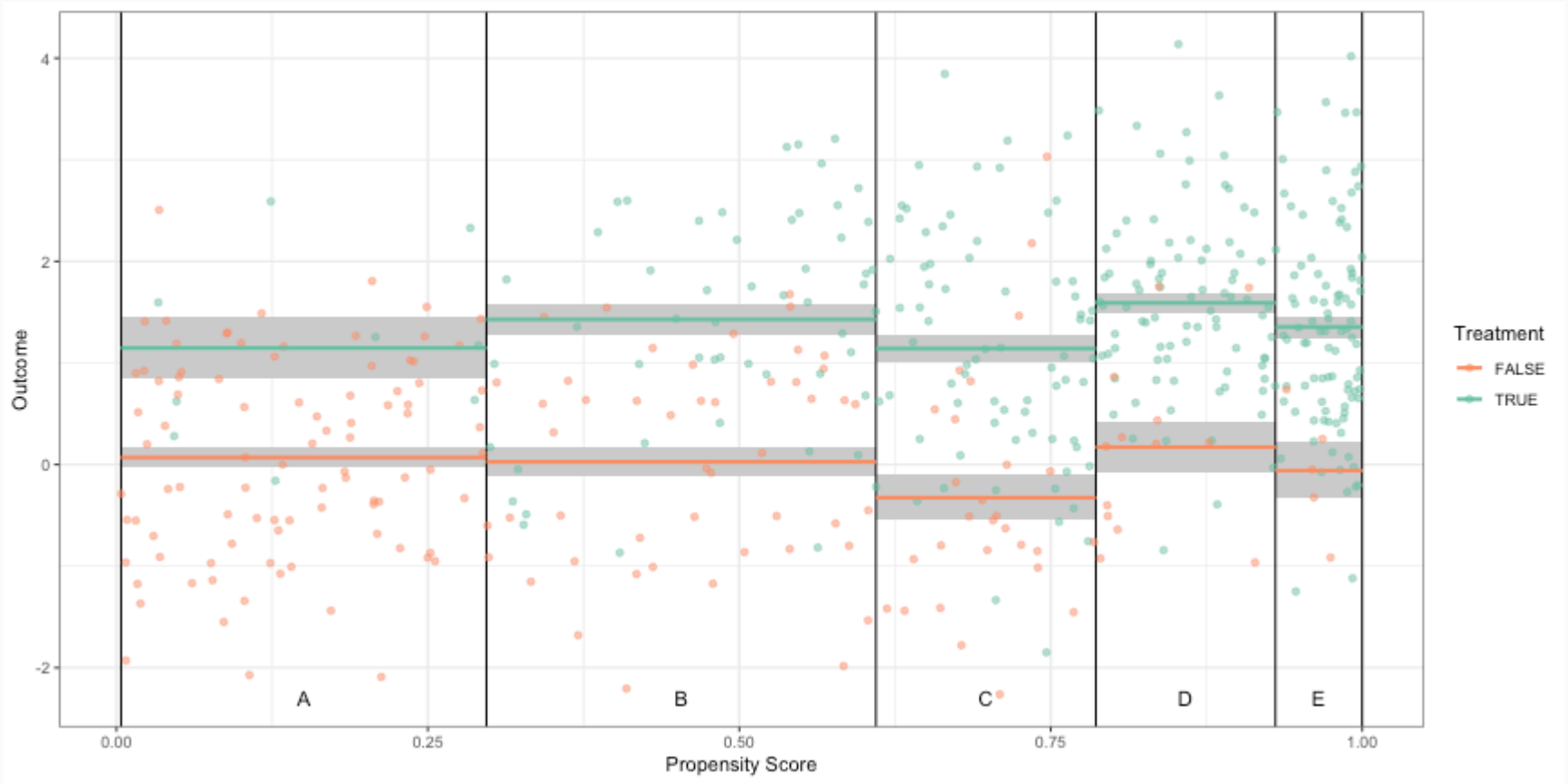
Stratification

Stratification involves dividing (or stratifying) the observations into subgroups based upon the propensity score. Here, we used quintiles on the propensity scores where were estimated using logistic regression. For classification trees the stratum is determined by the leaf nodes.



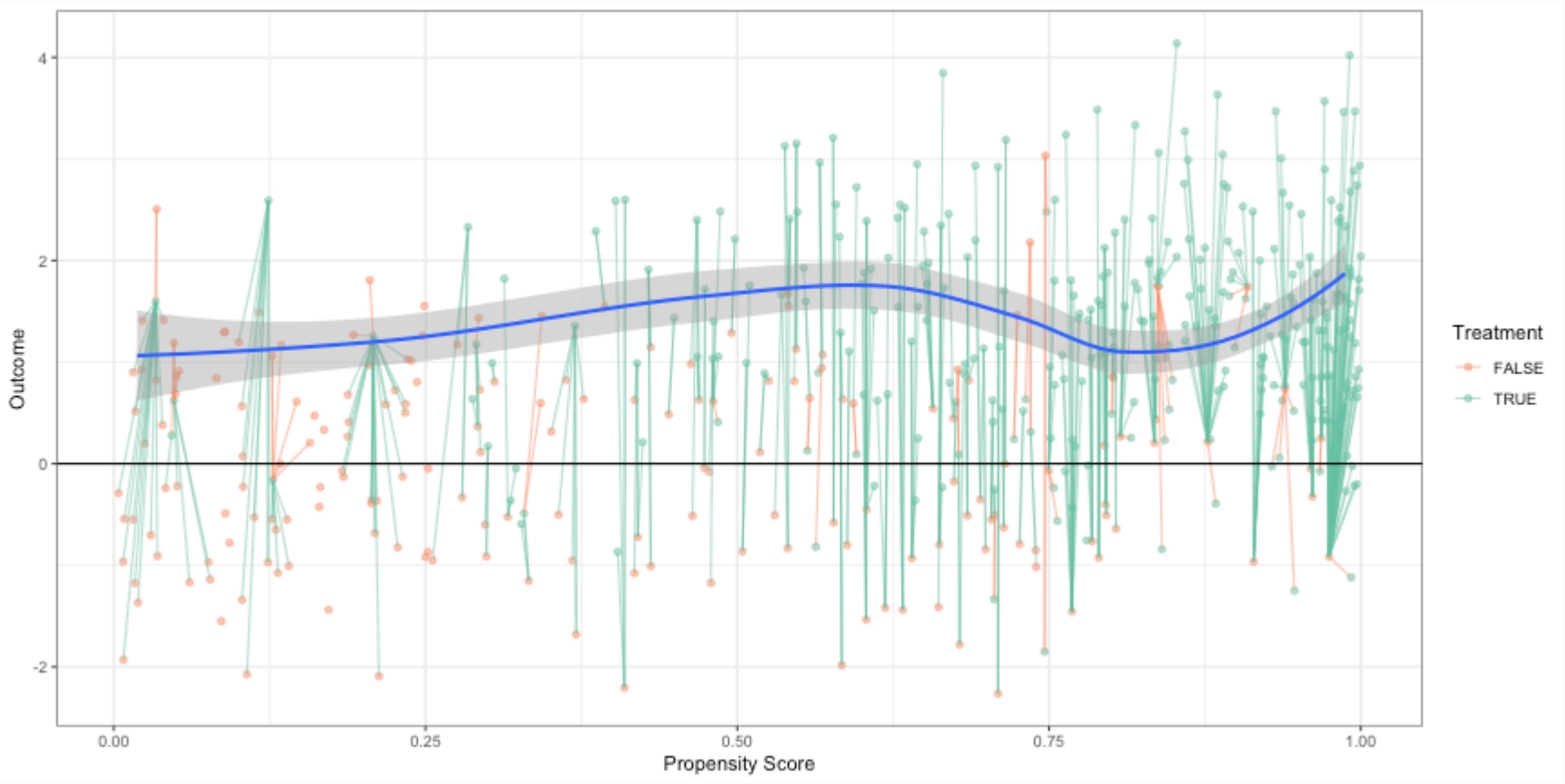
Stratification (cont.)

Independent sample tests (e.g. *t*-tests) are conducted within each stratum and pooled to provide an overall estimate.



Matching

Dependent sample tests (e.g. *t*-tests) are conducted using match pairs to provide a treatment.



Matching Methods

There are many choices and approaches to matching, including:

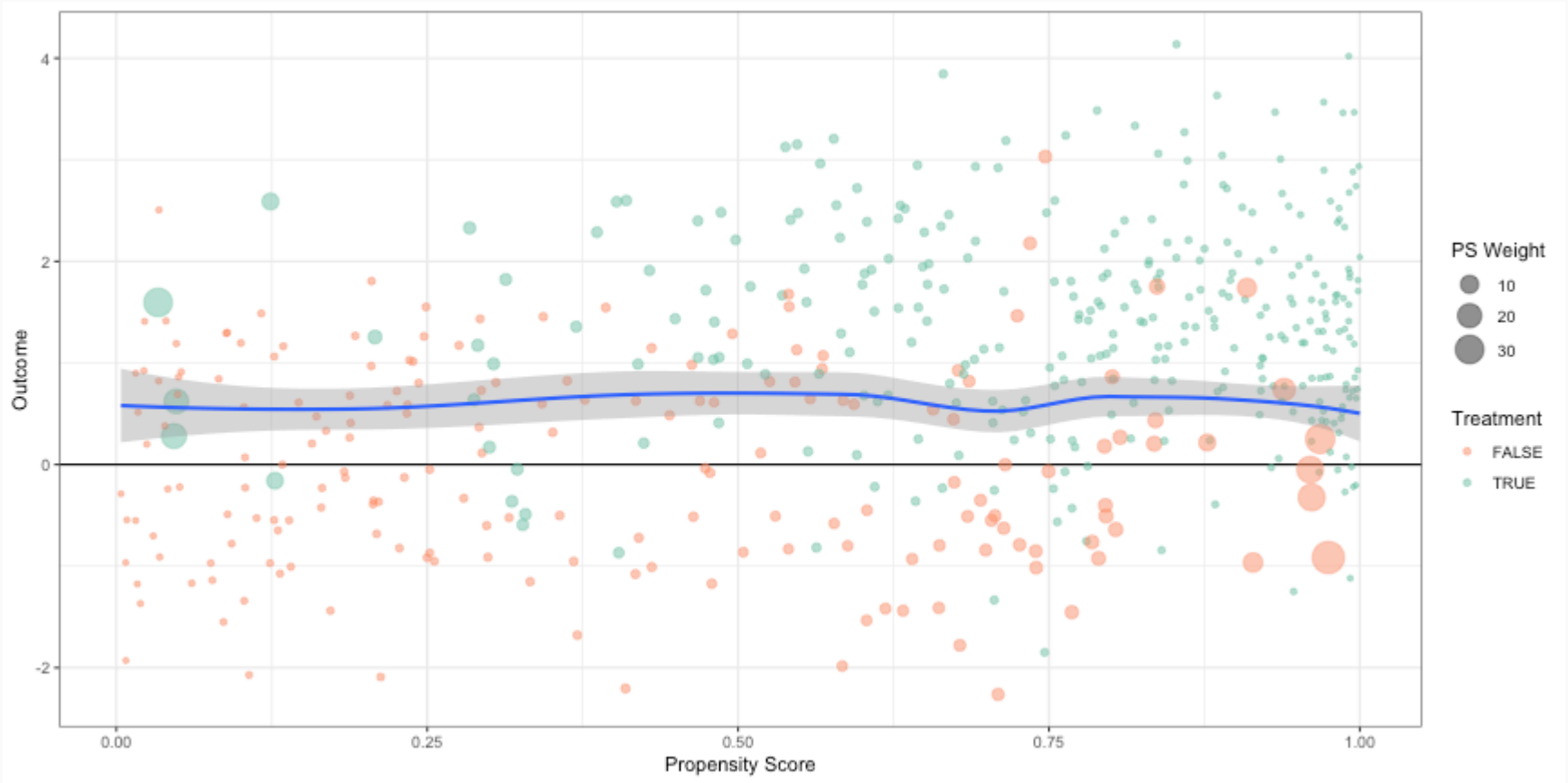
- Propensity score matching.
- Limited exact matching.
- Full matching.
- Nearest neighbor matching.
- Optimal/Genetic matching.
- Mahalanobis distance matching (for quantitative covariates only).
- Matching with and without replacement.
- One-to-one or one-to-many matching.

Which method should you use?

Whichever one gives the best balance!

Weighting

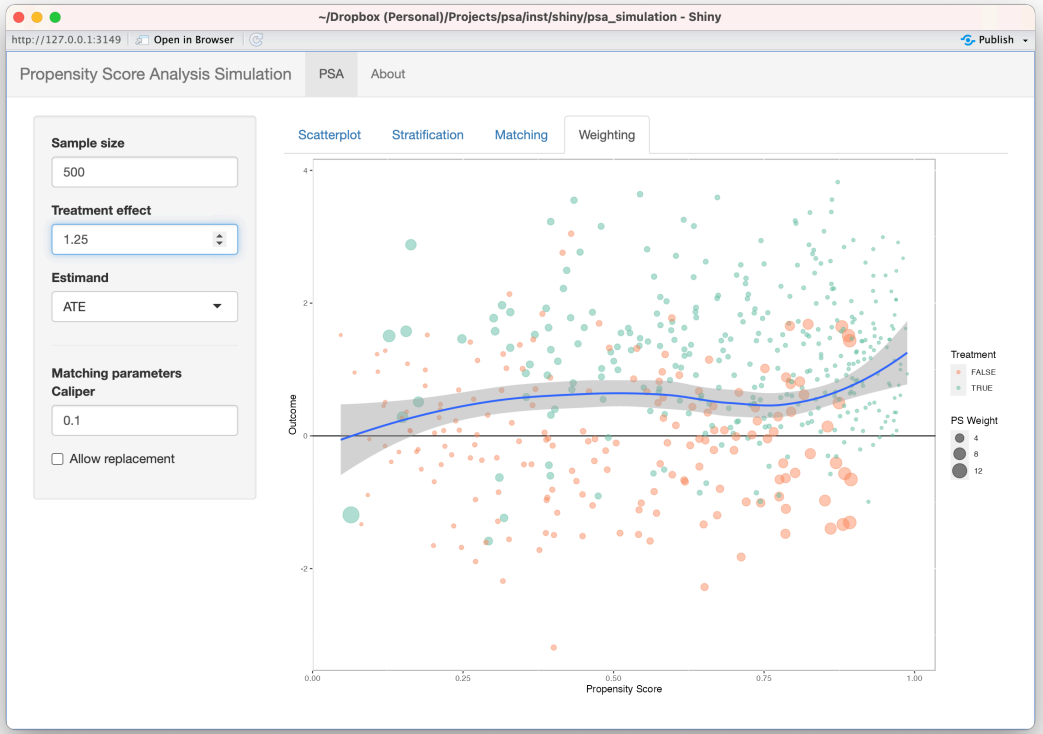
Propensity score weights can be used as regression weights, the specific weights depend on the desired estimand and will be provided in later slides.



Shiny Application

We can explore how these three plots change as the treatment effects change using the `psa::psa_simulation_shiny()` application.

```
psa::psa_simulation_shiny()
```



Phase I: Estimate Propensity Scores

In this example we will use logistic regression to estimate the propensity scores.

```
lr.out <- glm(
    treatment ~ x1 + x2 + x3,
    data = dat,
    family = binomial(link='logit'))
dat$ps <- fitted(lr.out) # Propensity scores
```

For stratification we will use quintiles to split the observations into five equal groups.

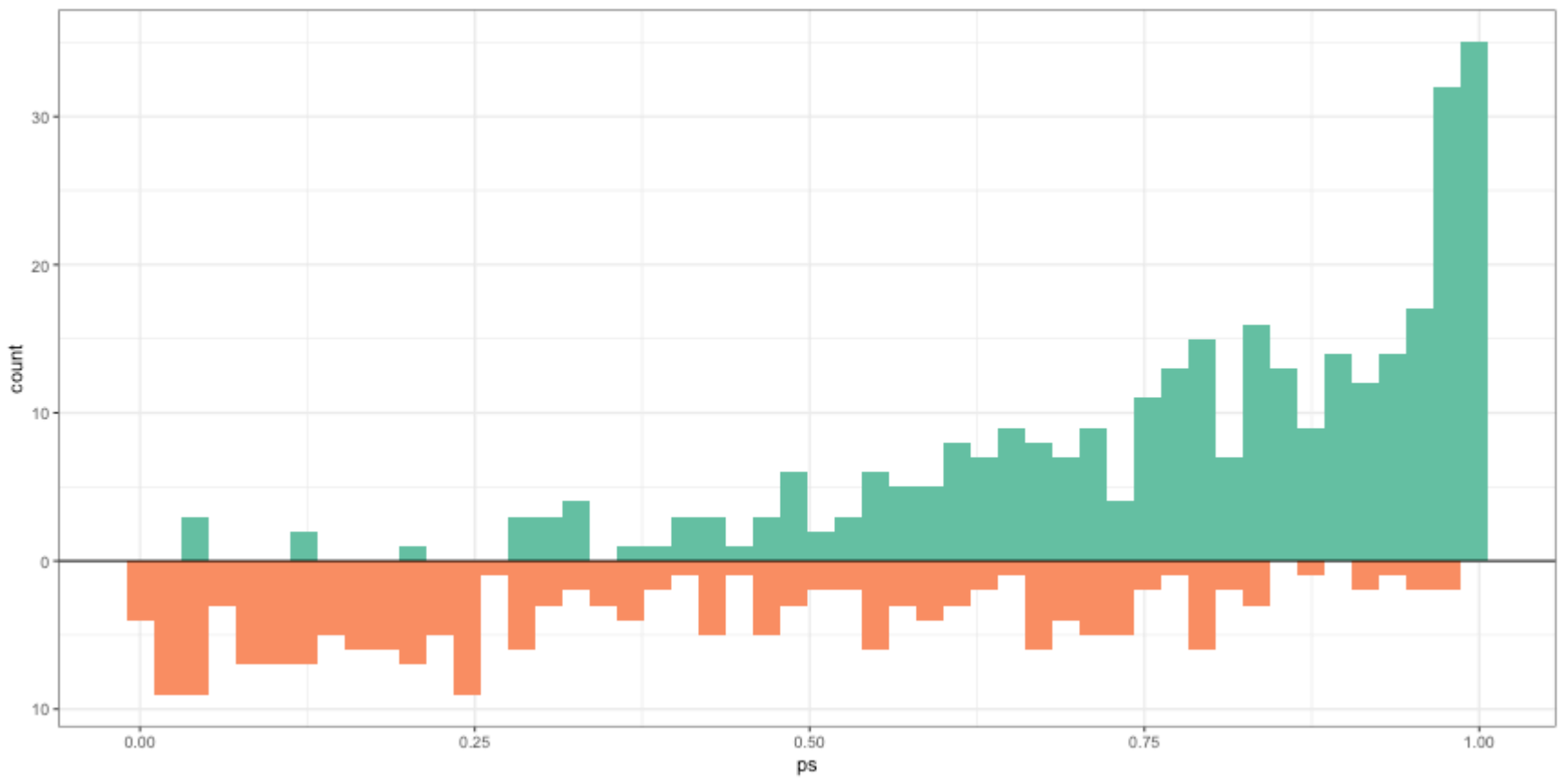
```
breaks5 <- psa::get_strata_breaks(dat$ps)
dat$strata5 <- cut(
    x = dat$ps,
    breaks = breaks5$breaks,
    include.lowest = TRUE,
    labels = breaks5$labels$strata)
```

```
summary(lr.out)
```

```
##
## Call:
## glm(formula = treatment ~ x1 + x2 + x3, family = binomial(link = "logit"),
##     data = dat)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.1006     0.2069  -5.319 1.04e-07 ***
## x1            0.4399     0.1266   3.476  0.00051 ***
## x2            1.9818     0.3404   5.823 5.79e-09 ***
## x3TRUE       -0.7166     0.4087  -1.753  0.07955 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 658.96  on 499  degrees of freedom
## Residual deviance: 432.95  on 496  degrees of freedom
## AIC: 440.95
##
## Number of Fisher Scoring iterations: 5
```

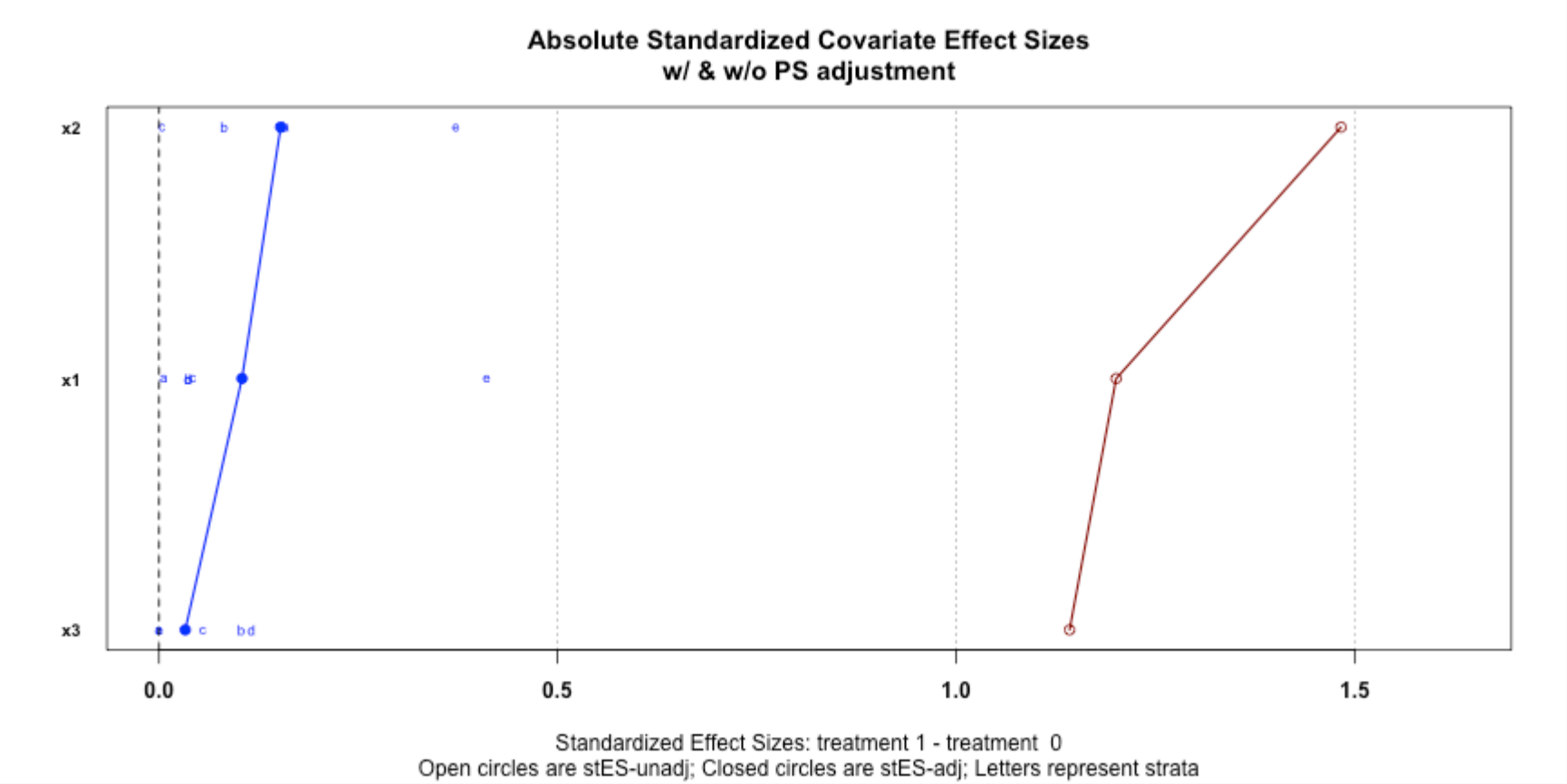
Distribution of Propensity Scores

```
ggplot(dat) +
    geom_histogram(data = dat[dat$treatment == 1,], aes(x = ps, y = after_stat(count)), bins = 50, fill = cols[2]) +
    geom_histogram(data = dat[dat$treatment == 0,], aes(x = ps, y = -after_stat(count)), bins = 50, fill = cols[1]) +
    geom_hline(yintercept = 0, lwd = 0.5) +    scale_y_continuous(label = abs)
```



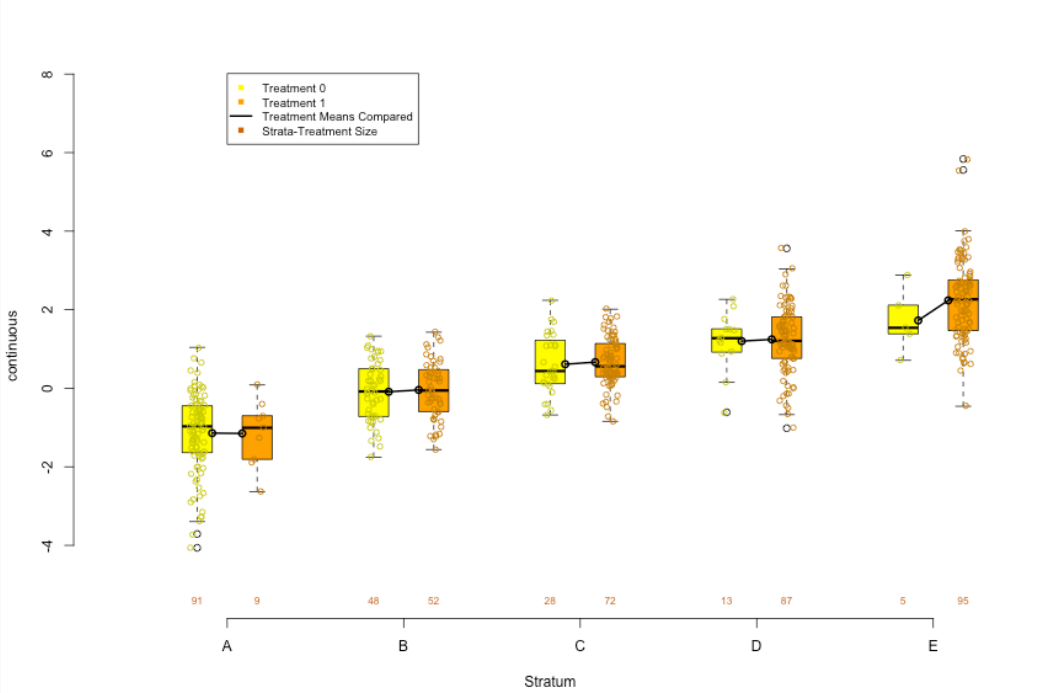
Check Balance: Multiple Covariates

```
PSAgraphics::cv.bal.psa(dat[,1:3], dat$treatment, dat$ps, strata = 5)
```

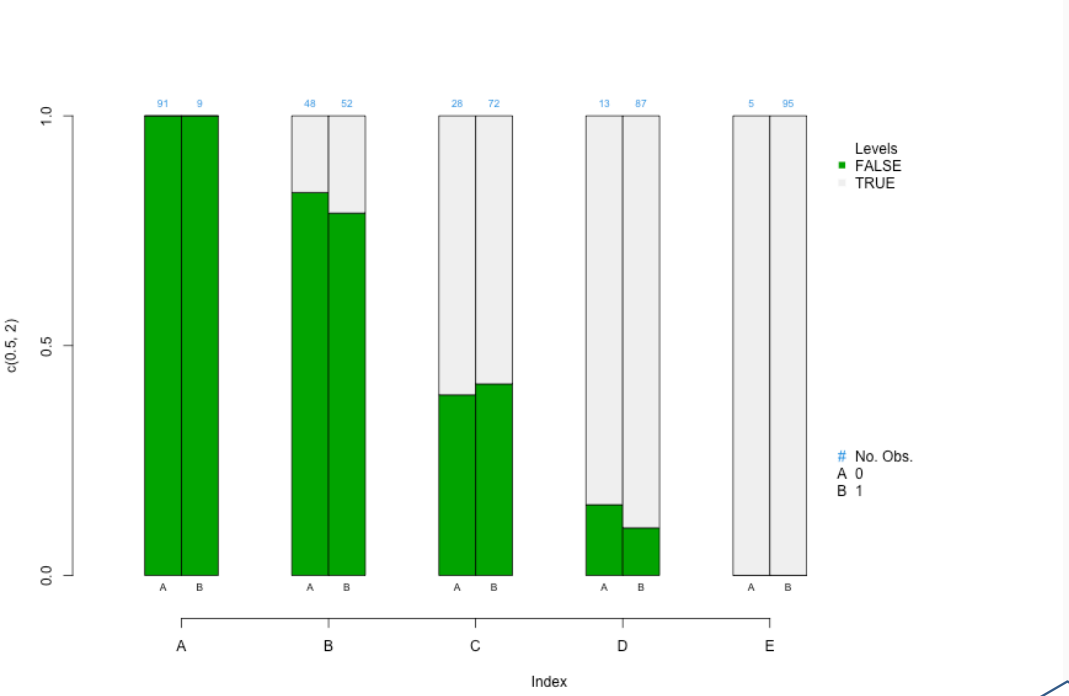


Check Balance: Single Covariate

```
PSAgraphics::box.psa(dat$x1,
                     dat$treatment,
                     dat$strata5)
```




```
PSAgraphics::cat.psa(dat$x3,
                     dat$treatment,
                     dat$strata5)
```

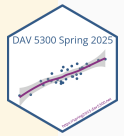


PS Weights for Understanding Treatment Effects

Given that the distribution of treatment and control observations across the propensity score range are not the same, there are a number of alternative estimates of treatment effect. We will explore three additional esimates in addition to the classic average treatment effect.

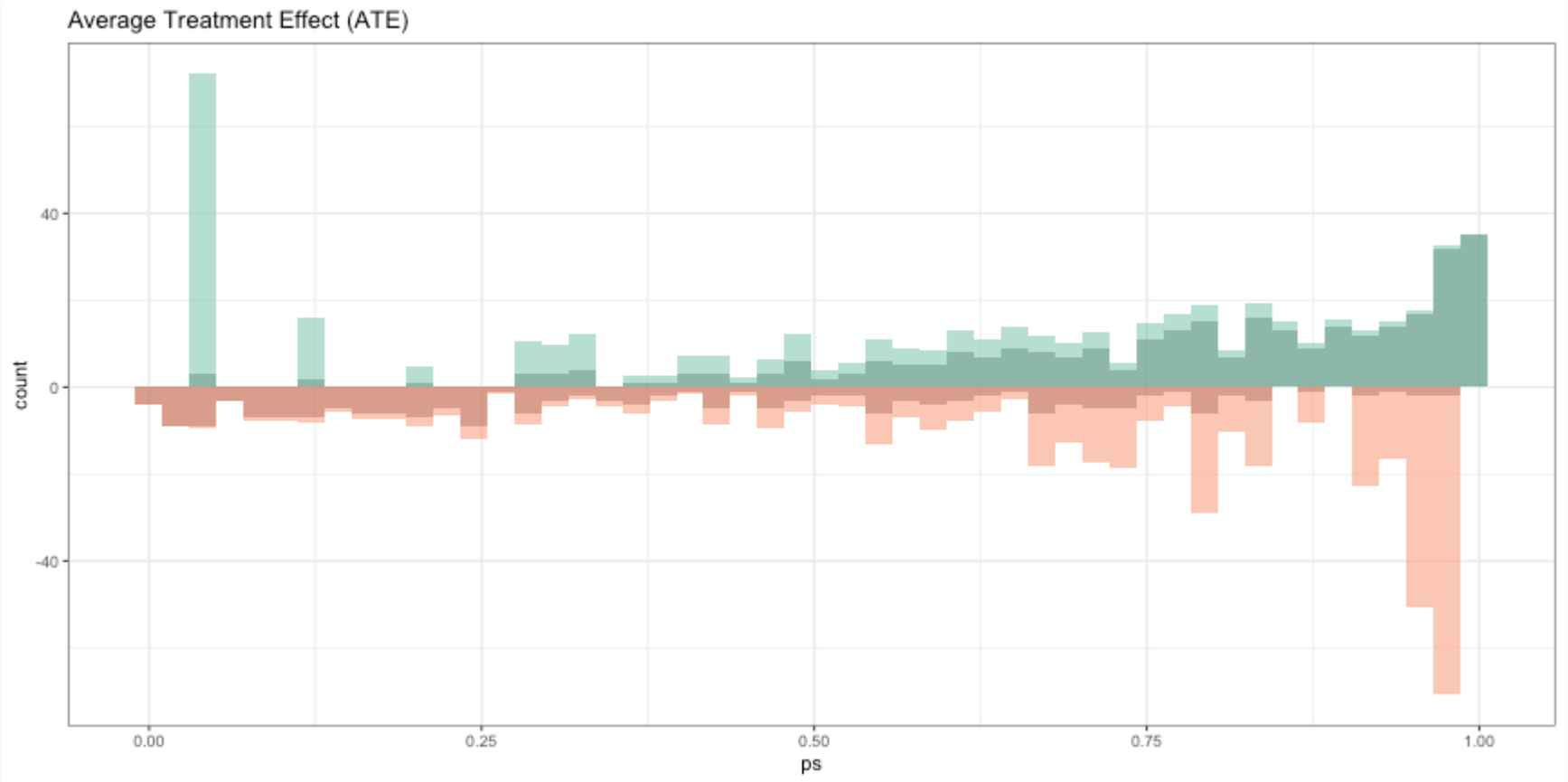
```
dat <- dat |> mutate(
    ate_weight = psa::calculate_ps_weights(treatment, ps, estimand = 'ATE'),
    att_weight = psa::calculate_ps_weights(treatment, ps, estimand = 'ATT'),
    atc_weight = psa::calculate_ps_weights(treatment, ps, estimand = 'ATC'),
    atm_weight = psa::calculate_ps_weights(treatment, ps, estimand = 'ATM')
)
dat |> head(n = 4)
```

```
## # A tibble: 4 × 11
##       x1    x2 x3    treatment outcome    ps strata5 ate_weight att_weight
##    <dbl> <dbl> <lgl>     <dbl>   <dbl> <dbl> <fct>        <dbl>      <dbl>
## 1 1.35  0.744 FALSE         0  1.46   0.725 C             3.63       2.63
## 2 0.149 1.55  TRUE          0 -0.924  0.790 D             4.76       3.76
## 3 2.47  2.39  TRUE          1 -0.0527 0.982 E             1.02       1
## 4 2.29  1.66  TRUE          1  1.05   0.922 D             1.08       1
## # ℹ 2 more variables: atc_weight <dbl>, atm_weight <dbl>
```



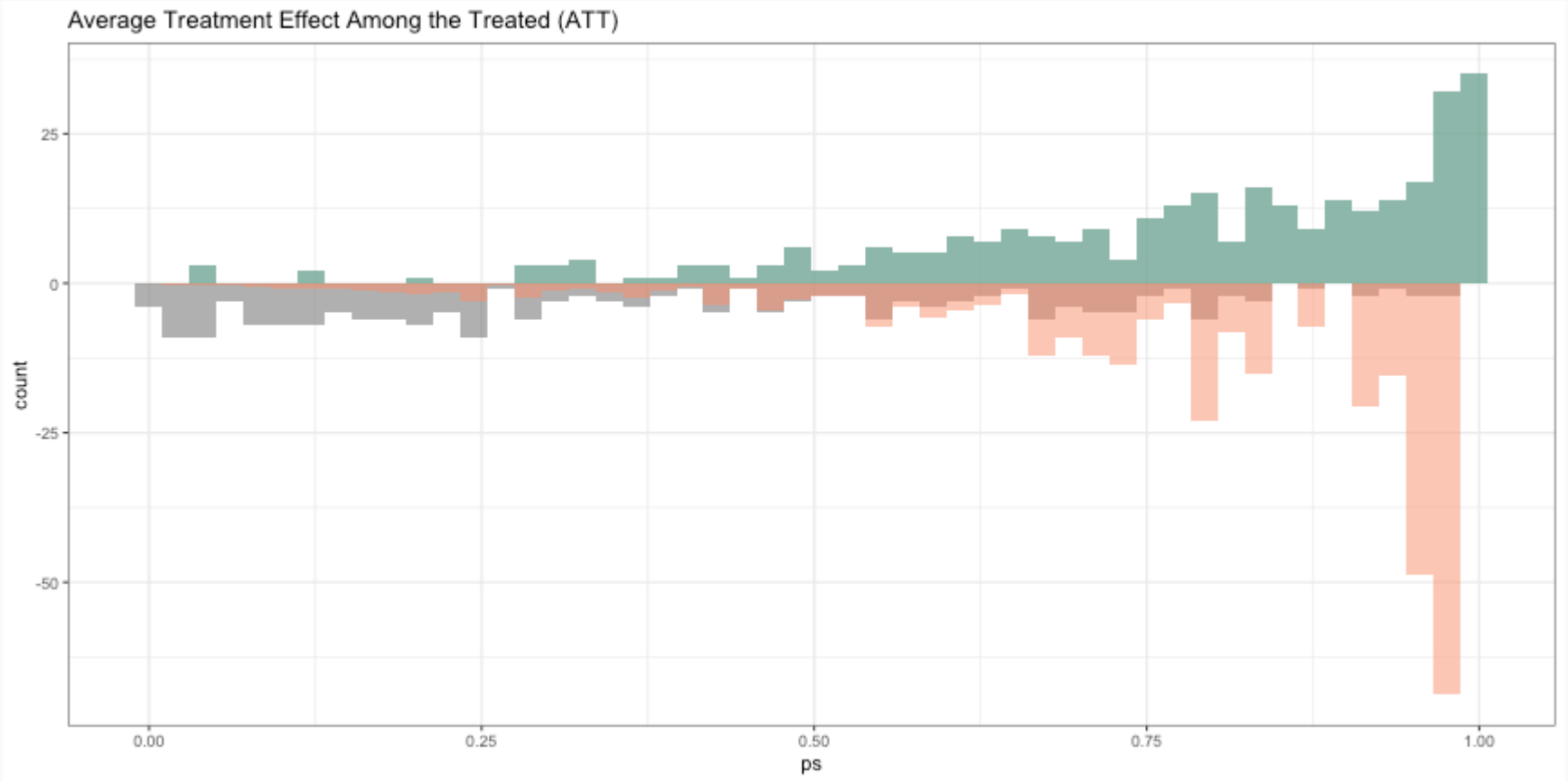
Average Treatment Effect (ATE)

$$ATE = E(Y_1 - Y_0|X) = E(Y_1|X) - E(Y_0|X)$$



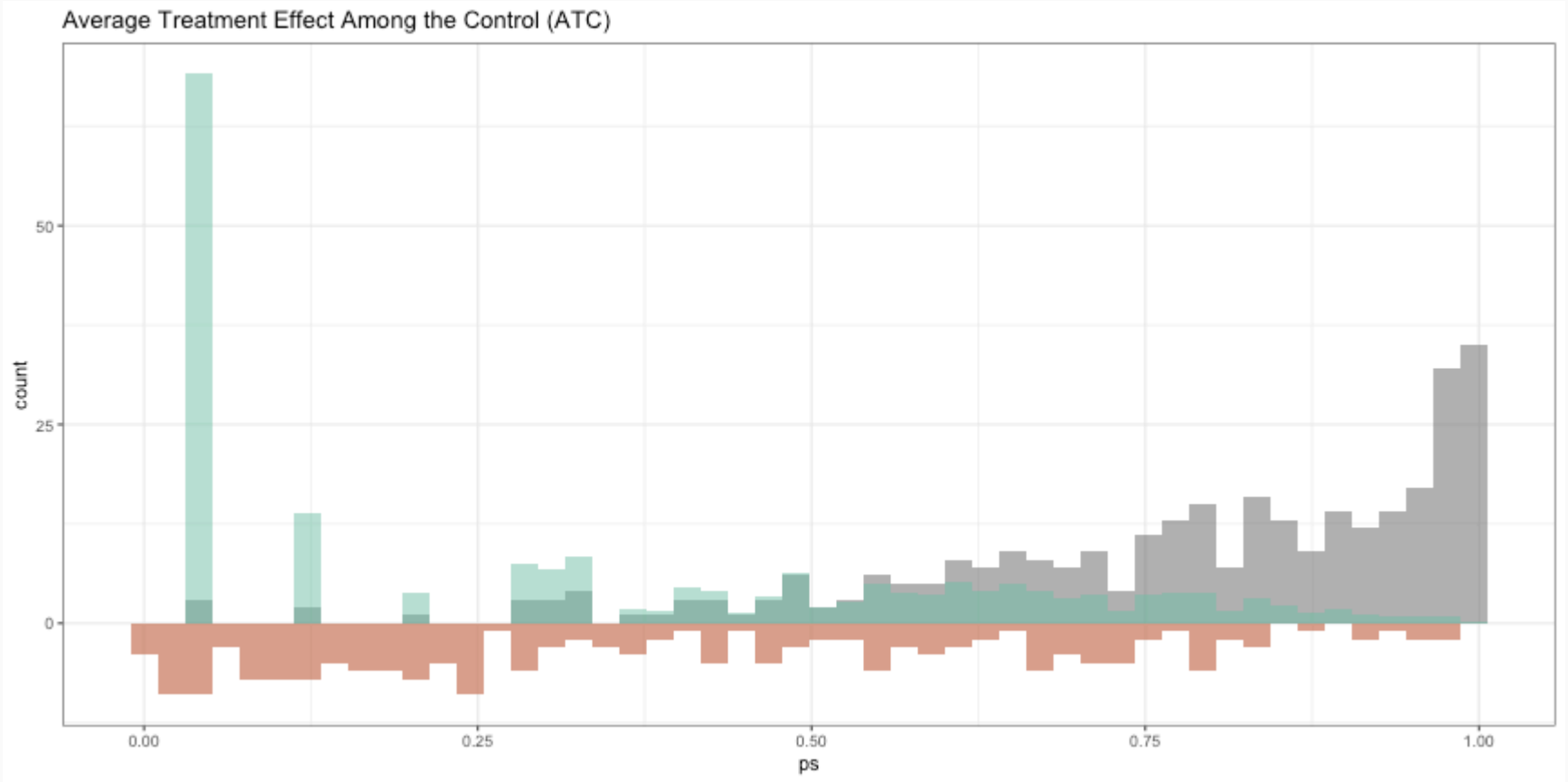
Average Treatment Effect Among the Treated (ATT)

$$ATT = E(Y_1 - Y_0|X, C = 1) = E(Y_1|X, C = 1) - E(Y_0|X, C = 1)$$



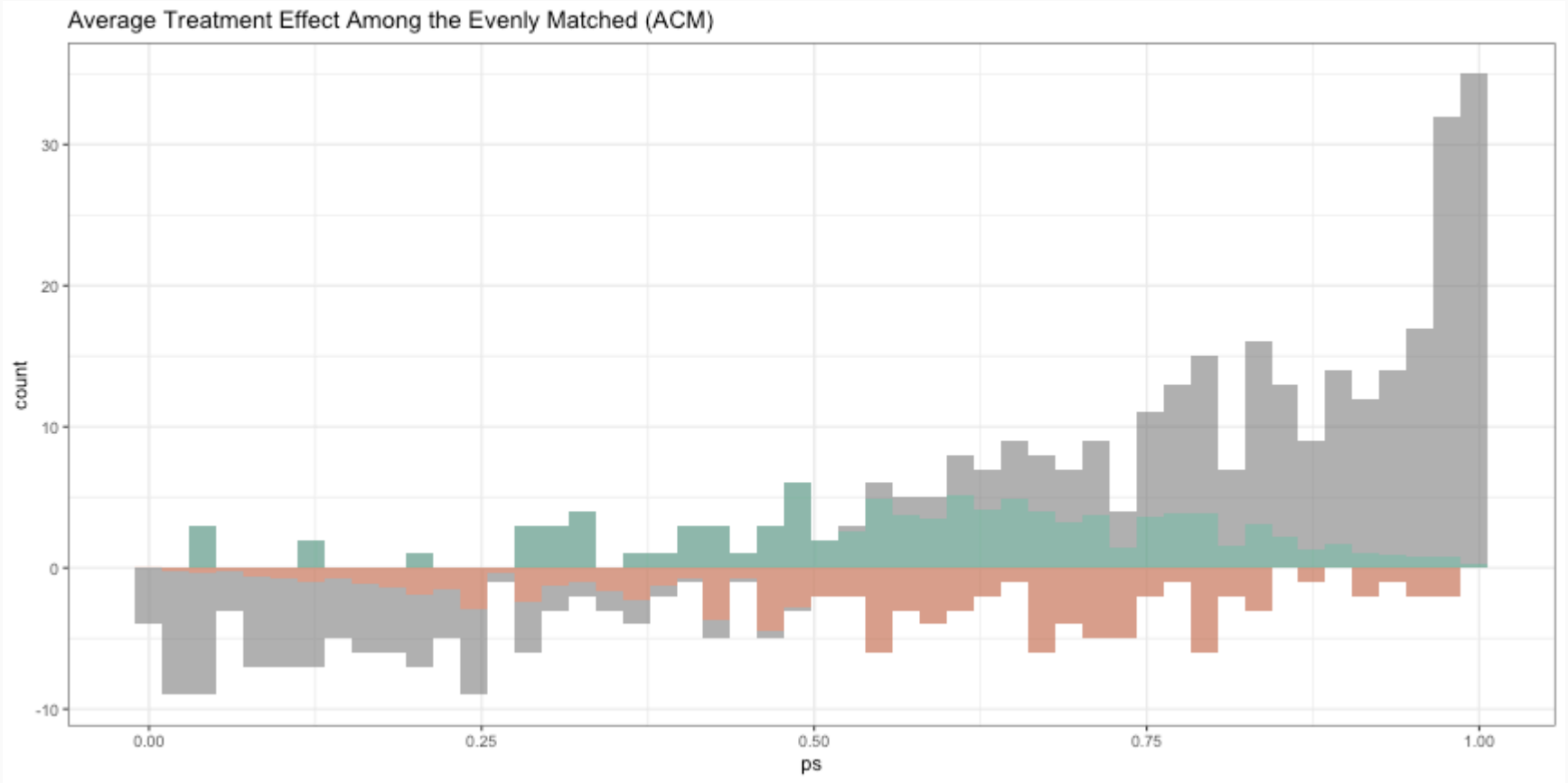
Average Treatment Effect Among the Control (ATC)

$$ATC = E(Y_1 - Y_0|X = 0) = E(Y_1|X = 0) - E(Y_0|X = 0)$$



Average Treatment Effect Among the Evenly Matched

$$ATM_d = E(Y_1 - Y_0 | M_d = 1)$$



Treatment Effects for Weighting

$$Treatment\ Effect = \frac{\sum Y_i Z_i w_i}{\sum Z_i w_i} - \frac{\sum Y_i (1 - Z_i) w_i}{\sum (1 - Z_i) w_i}$$

Where w is the weight (as defined in the following sections), Z_i is the treatment assignment such that $Z = 1$ is treatment and $Z = 0$ is control, and Y_i is the outcome

$$w_{ATE} = \frac{Z_i}{\pi_i} + \frac{1 - Z_i}{1 - \pi_i}$$

$$w_{ATC} = \frac{(1 - \pi_i) Z_i}{\pi_i} + \frac{(1 - e_i)(1 - Z_i)}{1 - \pi_i}$$

$$w_{ATT} = \frac{\pi_i Z_i}{\pi_i} + \frac{\pi_i (1 - Z_i)}{1 - \pi_i}$$

$$w_{ATM} = \frac{min\{\pi_i, 1 - \pi_i\}}{Z_i \pi_i (1 - Z_i)(1 - \pi_i)}$$

Treatment Effects

Average Treatment Effect

```
psa::treatment_effect(
    treatment = dat$treatment,
    outcome = dat$outcome,
    weights = dat$ate_weight)
```

```
## [1] 1.336979
```

```
lm(outcome ~ treatment,
   data = dat,
   weights = dat$ate_weight)
```

```
##
## Call:
## lm(formula = outcome ~ treatment, data = dat, weights =
##
## Coefficients:
## (Intercept)    treatment
##      -0.044        1.337
```

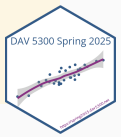
Average Treatment Effect Among the Treated

```
psa::treatment_effect(
    treatment = dat$treatment,
    outcome = dat$outcome,
    weights = dat$att_weight)
```

```
## [1] 1.447406
```

```
lm(outcome ~ treatment,
   data = dat,
   weights = dat$att_weight)
```

```
##
## Call:
## lm(formula = outcome ~ treatment, data = dat, weights =
##
## Coefficients:
## (Intercept)    treatment
##    -0.07002      1.44741
```



Treatment Effects (cont.)

Average Treatment Effect Among the Control

```
psa::treatment_effect(
    treatment = dat$treatment,
    outcome = dat$outcome,
    weights = dat$atc_weight)
```

```
## [1] 1.157861
```

```
lm(outcome ~ treatment,
   data = dat,
   weights = dat$atc_weight)
```

```
##
## Call:
## lm(formula = outcome ~ treatment, data = dat, weights =
##
## Coefficients:
## (Intercept)    treatment
##    0.002491     1.157861
```

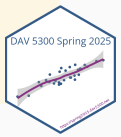
Average Treatment Effect Among the Evenly Matched

```
psa::treatment_effect(
    treatment = dat$treatment,
    outcome = dat$outcome,
    weights = dat$atm_weight)
```

```
## [1] 1.370067
```

```
lm(outcome ~ treatment,
   data = dat,
   weights = dat$atm_weight)
```

```
##
## Call:
## lm(formula = outcome ~ treatment, data = dat, weights =
##
## Coefficients:
## (Intercept)    treatment
##    -0.02388      1.37007
```



Example: National Supported Work Demonstration

National Supported Work

The National Supported Work (NSW) Demonstration was a federally and privately funded randomized experiment done in the 1970s to estimate the effects of a job training program for disadvantaged workers.

- Participants were randomly selected to participate in the training program.
- Both groups were followed up to determine the effect of the training on wages.
- Analysis of the mean differences (unbiased given randomization), was approximately $800.

Lalonde (1986) used data from the Panel Survey of Income Dynamics (PSID) and the Current Population Survey (CPS) to investigate whether non-experimental methods would result in similar results to the randomized experiment. He found results ranging from $700 to $16,000.

National Supported Work (cont.)

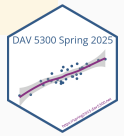
Dehejia and Wahba (1999) later used propensity score matching to analyze the data. The found that,

- Comparison groups selected by Lalonde were very dissimilar to the treated group.
- By restricting the comparison group to those that were similar to the treated group, they could replicate the original NSW results.
- Using the CPS data, the range of treatment effect was between $1,559 to $1,681. The experimental results for the sample sample was approximately $1,800.

The covariates available include: age, education level, high school degree, marital status, race, ethnicity, and earning sin 1974 and 1975.

Outcome of interest is earnings in 1978.

```
data(lalonde, package='Matching')
```



Estimating Propensity Scores

Estimate propensity scores using logistic regression.

```
lalonde.formu <- treat ~ age + educ + black + hisp +
    married + nodegr + re74 + re75
glm1 <- glm(lalonde.formu,
            data = lalonde,
            family = binomial(link = 'logit'))
```

Get the propensity scores:

```
lalonde$ps <- fitted(glm1)
```

Define the stratification:

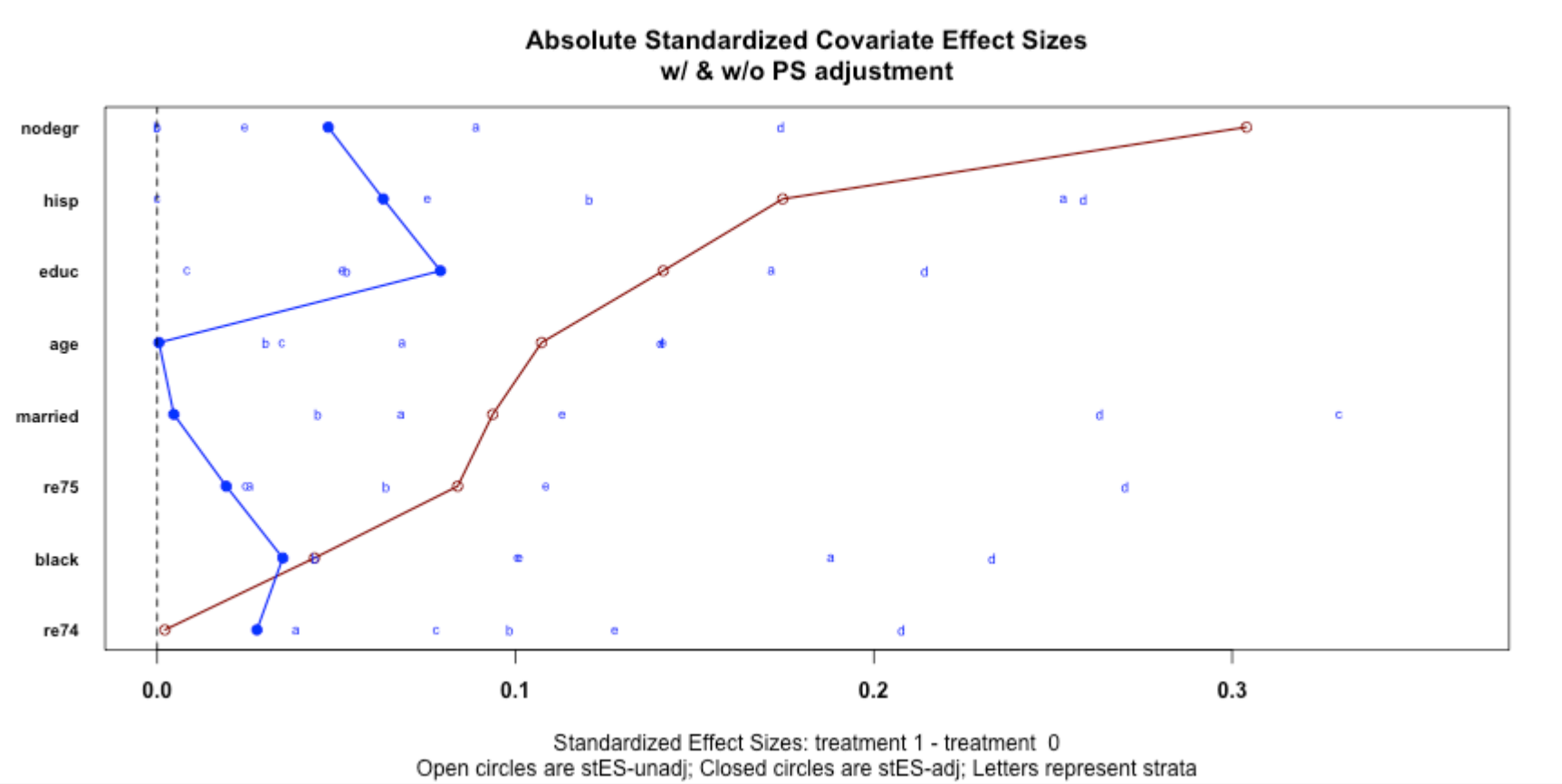
```
strata5 <- cut(lalonde$ps,
               quantile(lalonde$ps, seq(0, 1, 1/5)),
               include.lowest = TRUE,
               labels = letters[1:5])
```

```
summary(glm1)
```

```
##
## Call:
## glm(formula = lalonde.formu, family = binomial(link = "logit"),
##     data = lalonde)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.178e+00  1.056e+00   1.115  0.26474
## age          4.698e-03  1.433e-02   0.328  0.74297
## educ        -7.124e-02  7.173e-02  -0.993  0.32061
## black       -2.247e-01  3.655e-01  -0.615  0.53874
## hisp        -8.528e-01  5.066e-01  -1.683  0.09228 .
## married      1.636e-01  2.769e-01   0.591  0.55463
## nodegr      -9.035e-01  3.135e-01  -2.882  0.00395 **
## re74        -3.161e-05  2.584e-05  -1.223  0.22122
## re75         6.161e-05  4.358e-05   1.414  0.15744
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 604.20  on 444  degrees of freedom
## Residual deviance: 587.22  on 436  degrees of freedom
## AIC: 605.22
##
## Number of Fisher Scoring iterations: 4
```

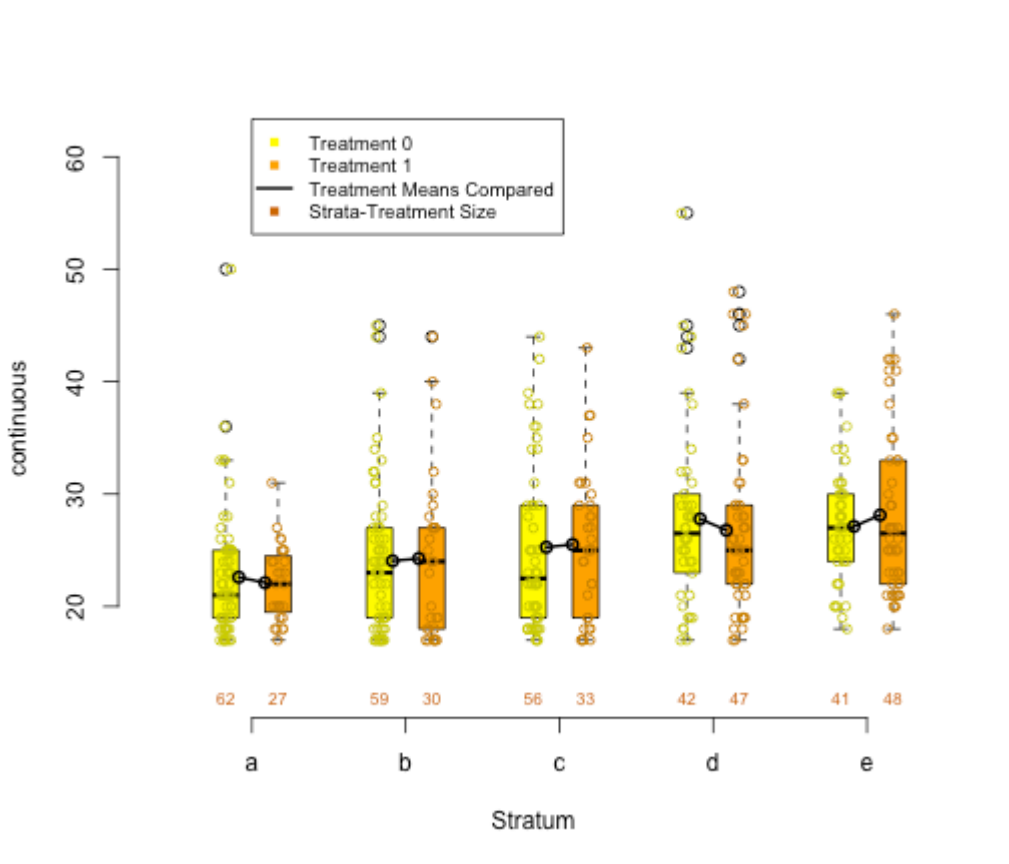
Checking Balance: Covariate Balance Plot

```
covars <- all.vars(lalonde.formu)
covars <- lalonde[,covars[2:length(covars)]]
cv.bal.psa(covars, lalonde$treat, lalonde$ps, strata = 5)
```

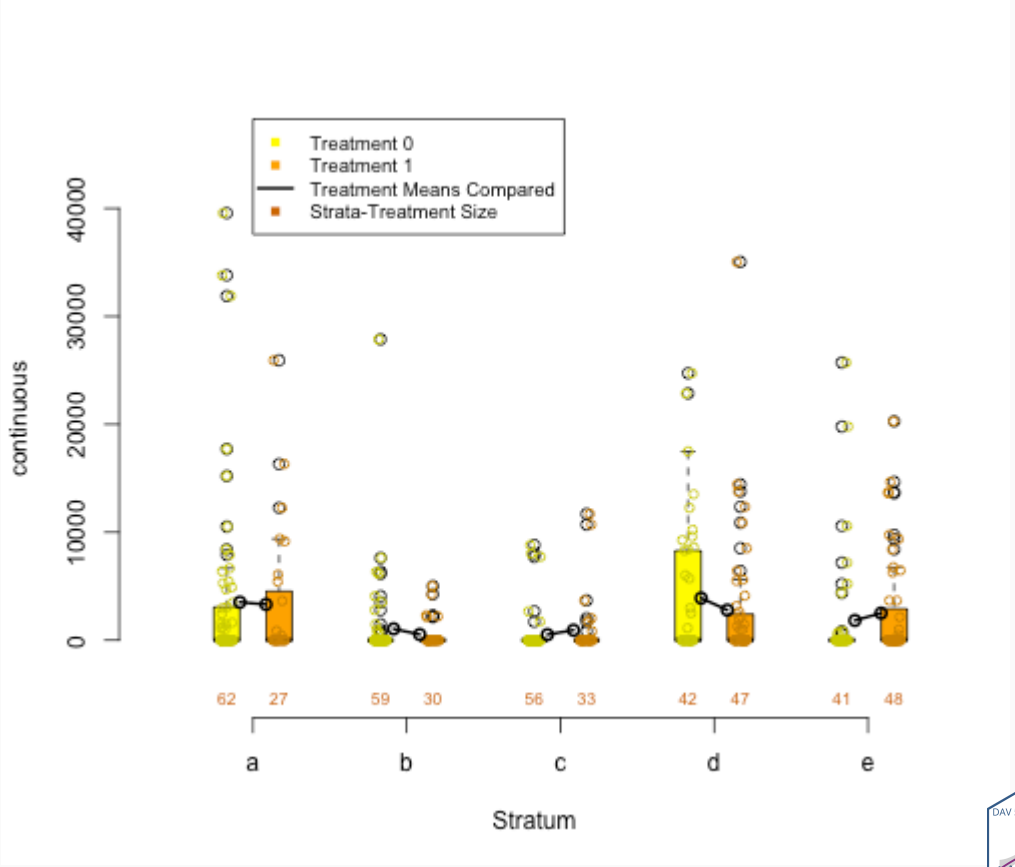


Checking Balance: Continuous Covariates

```
box.psa(lalonde$age, lalonde$treat, strata5)
```

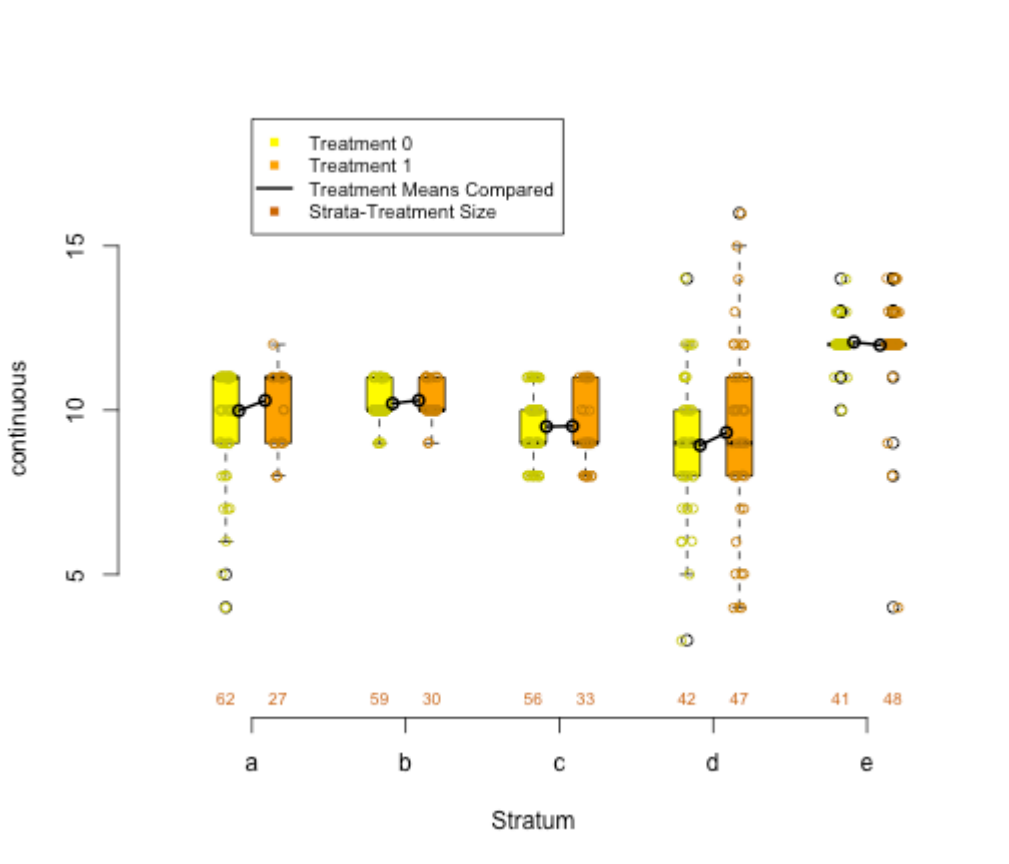



```
box.psa(lalonde$re74, lalonde$treat, strata5)
```

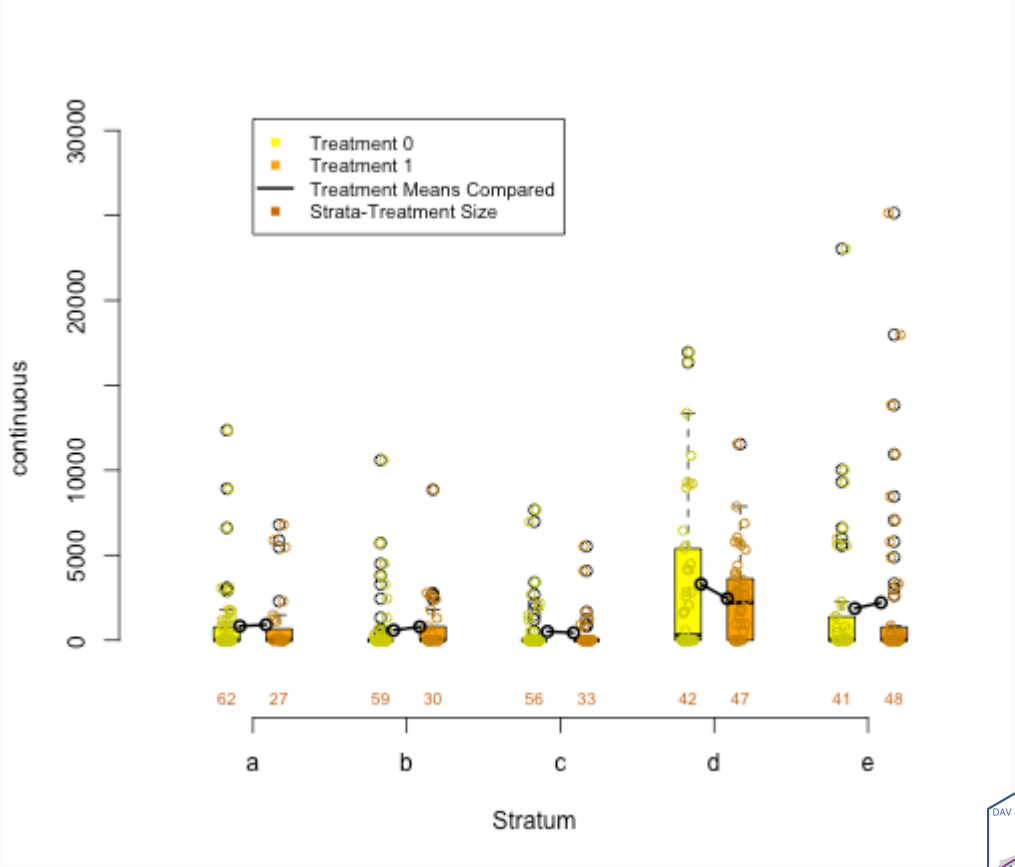


Checking Balance: Continuous Covariates (cont.)

```
box.psa(lalonde$educ, lalonde$treat, strata5)
```

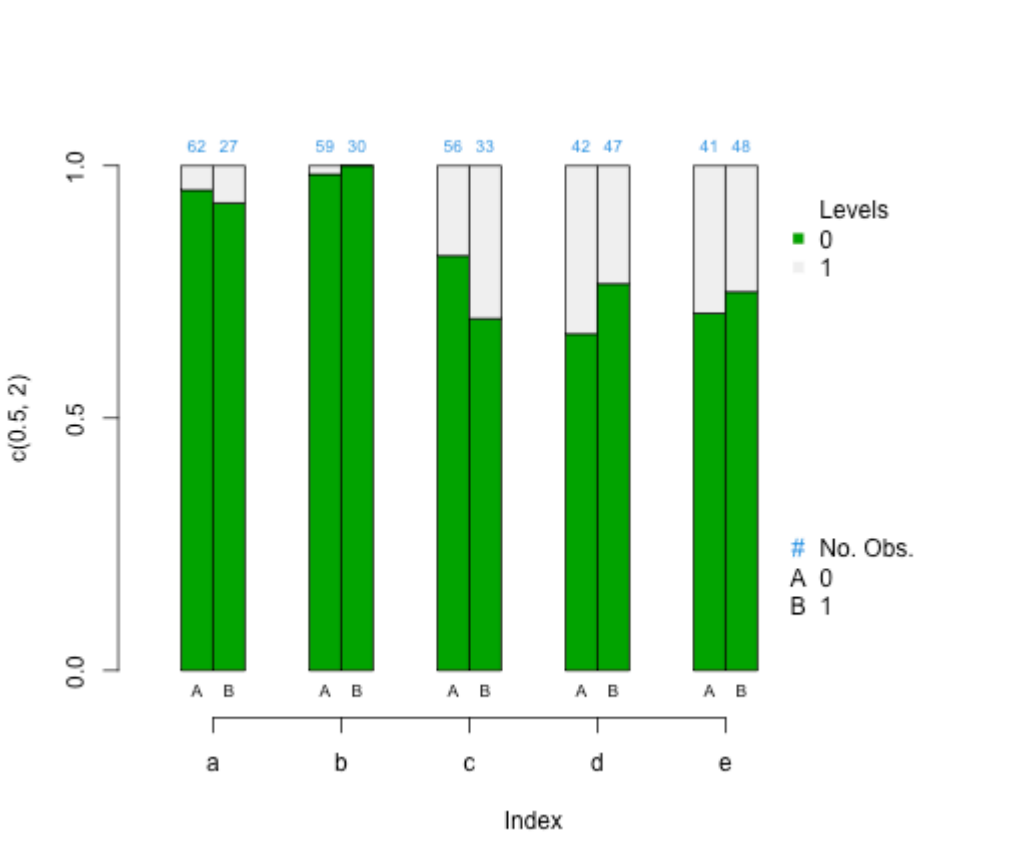



```
box.psa(lalonde$re75, lalonde$treat, strata5)
```

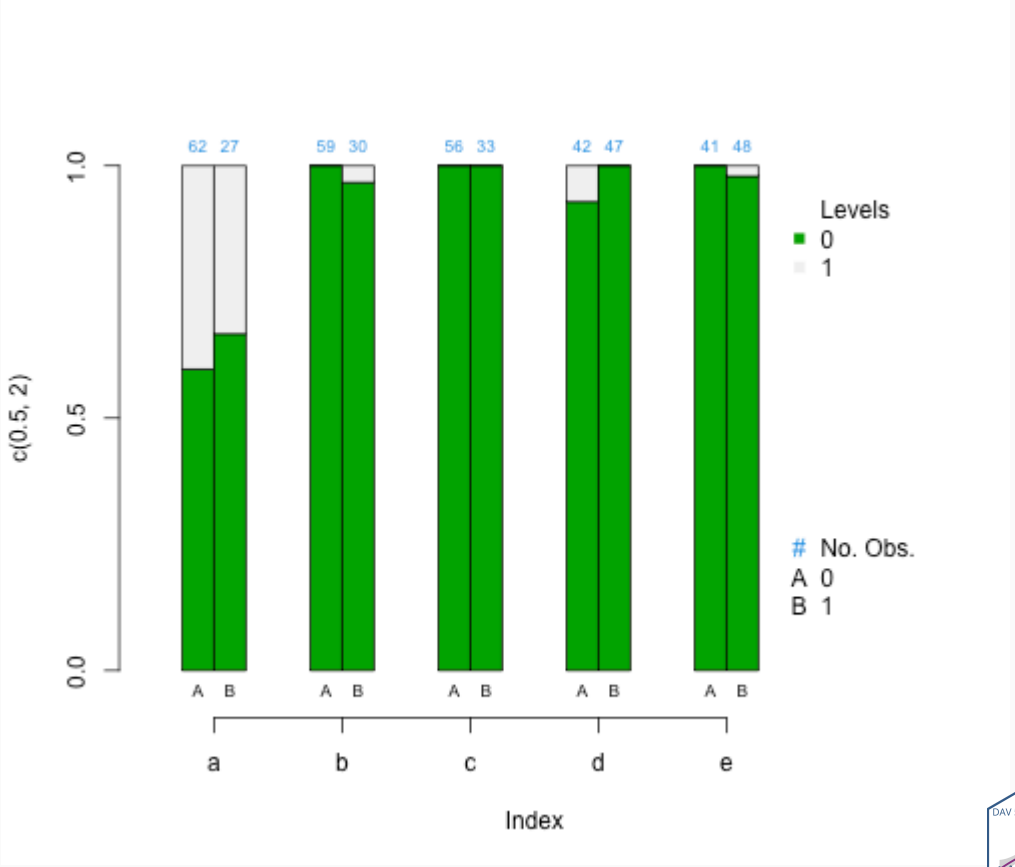


Checking Balance: Categorical Covariates

```
cat.psa(lalonde$married, lalonde$treat, strata5)
```

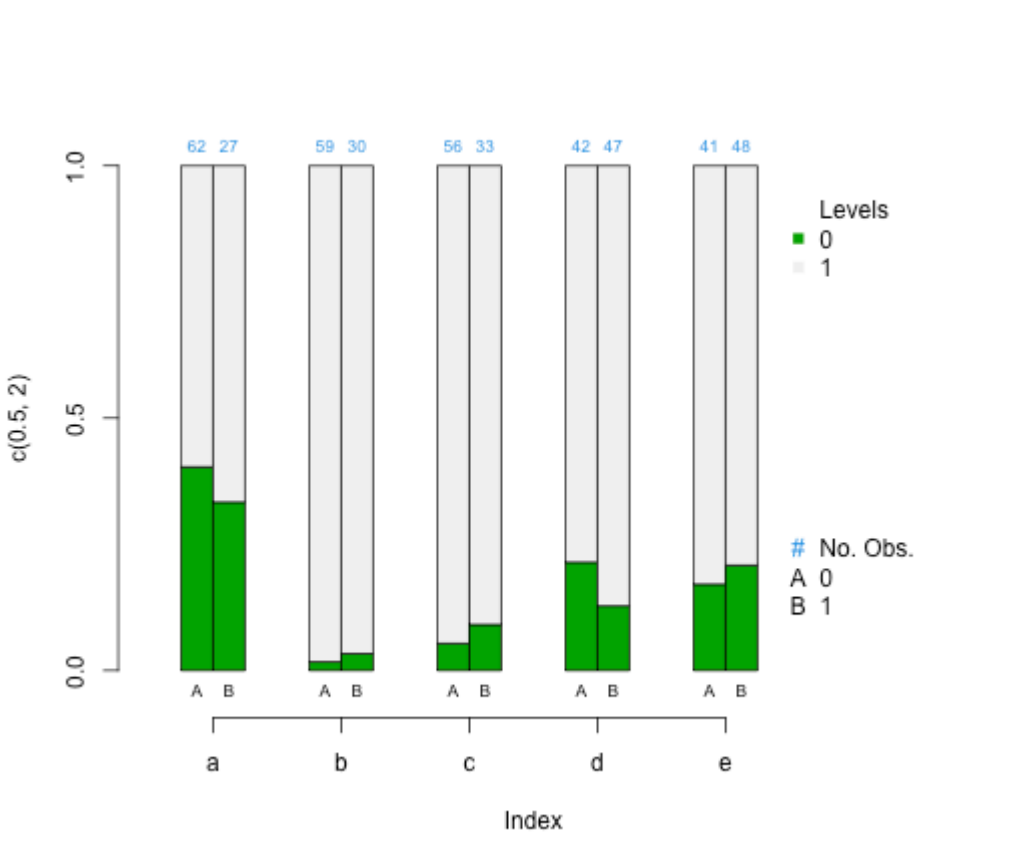



```
cat.psa(lalonde$hisp, lalonde$treat, strata5)
```

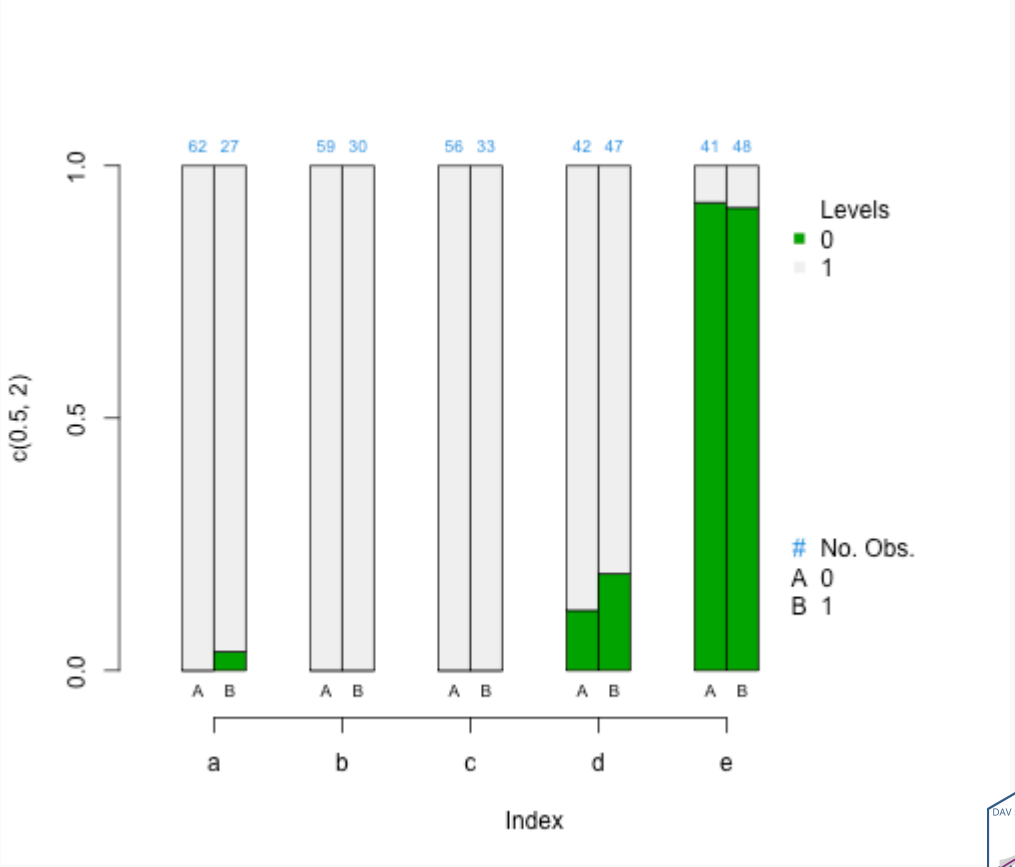


Checking Balance: Categorical Covariates (cont.)

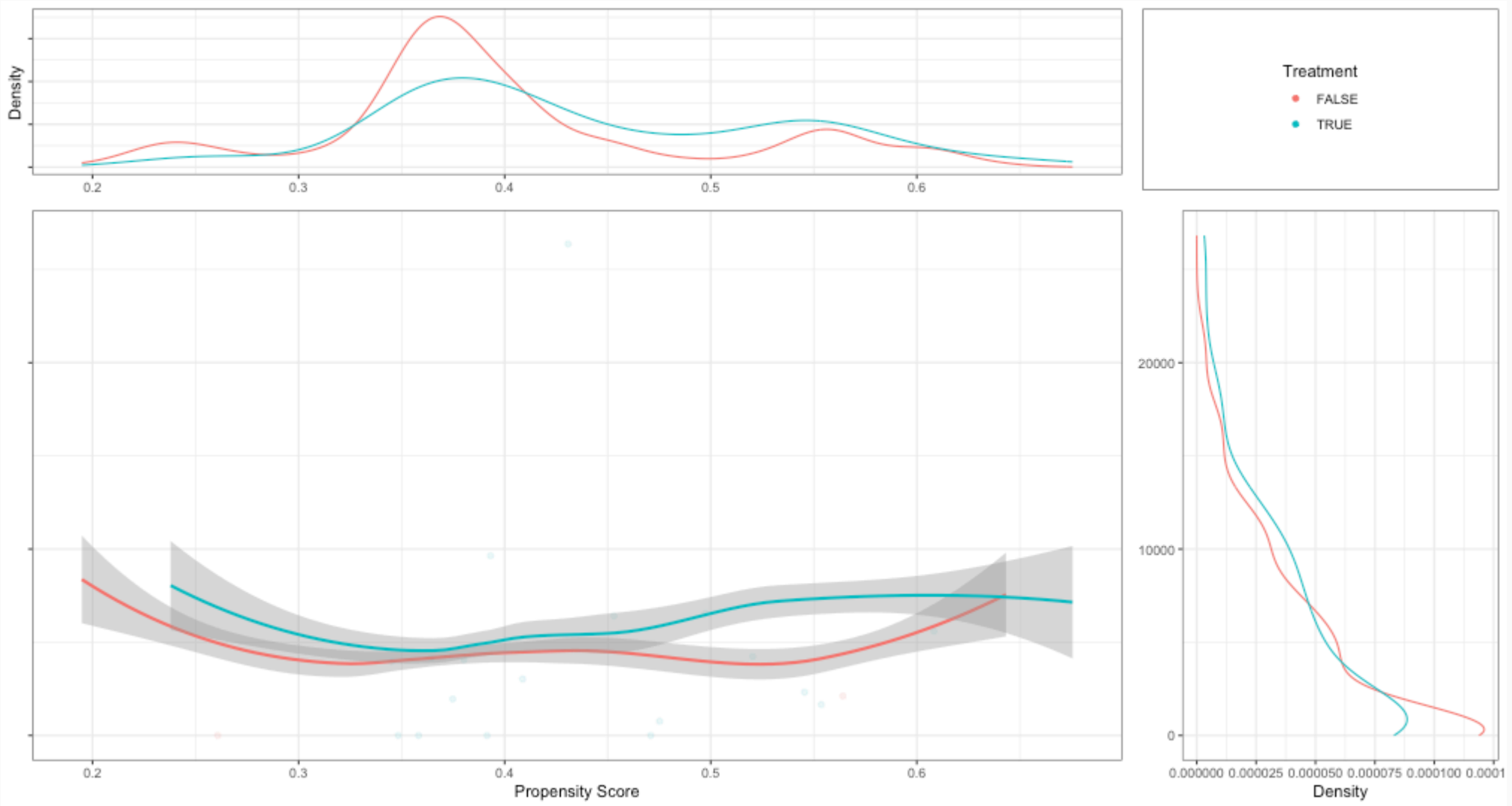
```
cat.psa(lalonde$black, lalonde$treat, strata5)
```




```
cat.psa(lalonde$nodegr, lalonde$treat, strata5)
```

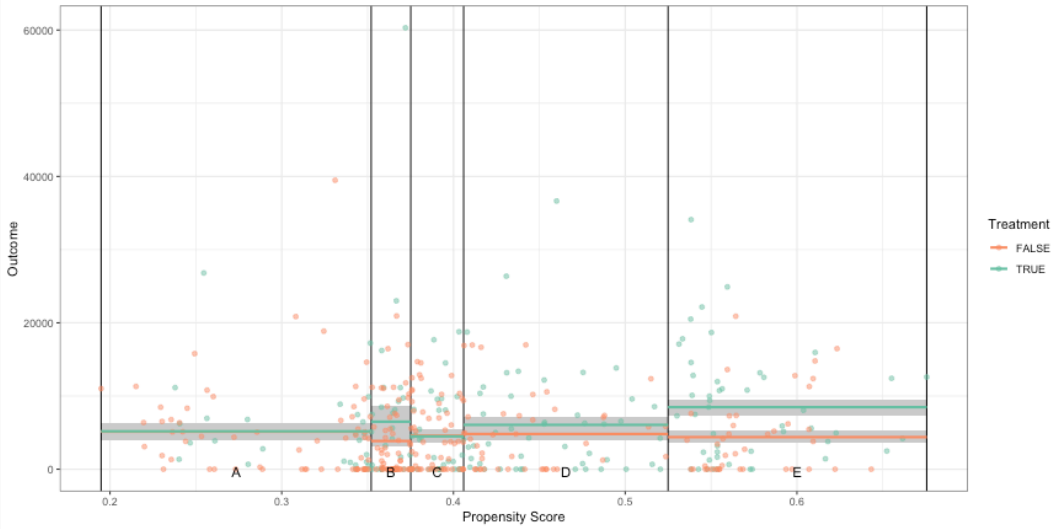


Loess Regression

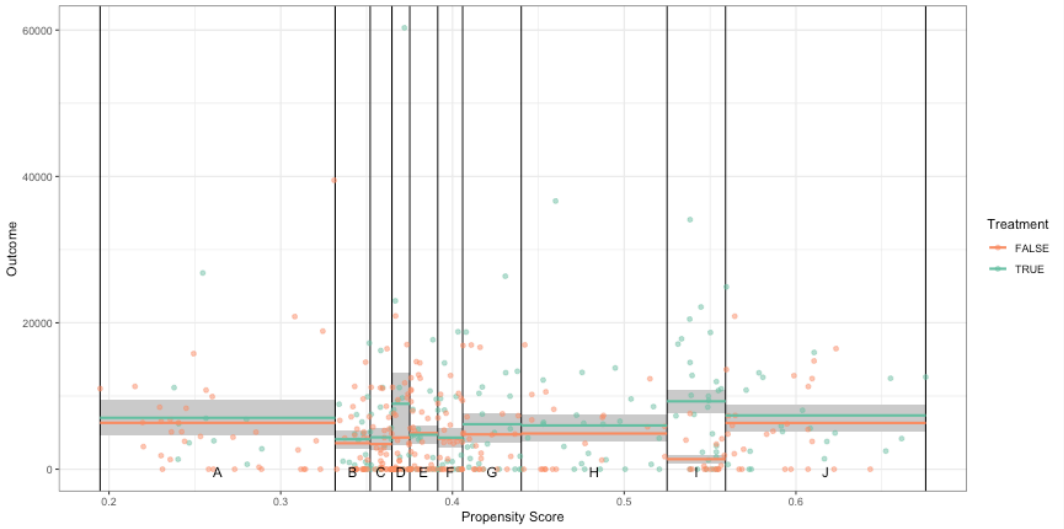


Stratification

```
psa::stratification_plot(ps = psadf$ps,
                         treatment = psadf$Tr,
                         outcome = psadf$Y,
                         n_strata = 5)
```

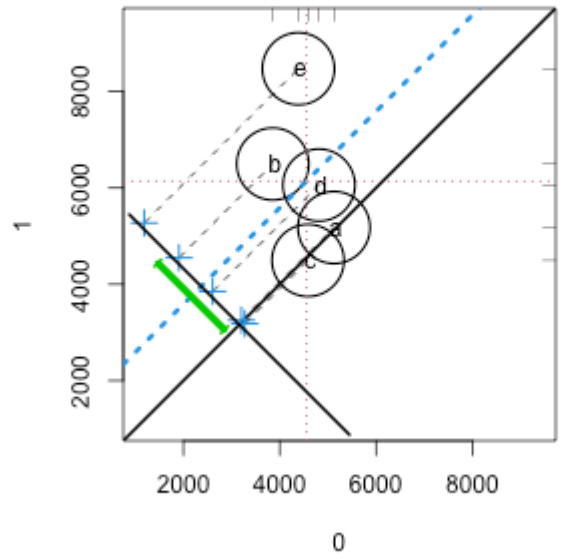



```
psa::stratification_plot(ps = psadf$ps,
                         treatment = psadf$Tr,
                         outcome = psadf$Y,
                         n_strata = 10)
```

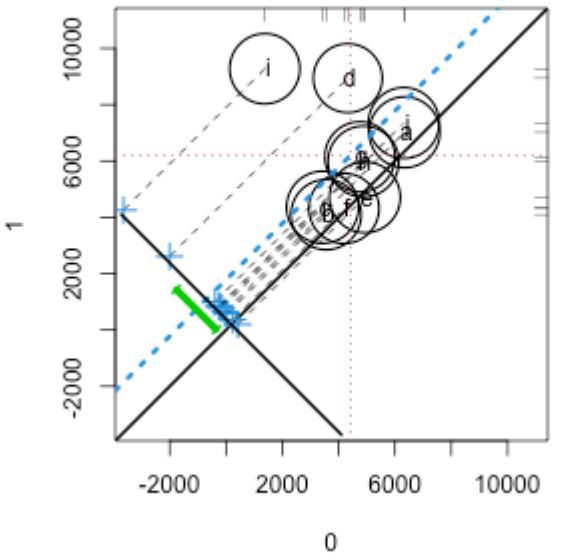


Stratification (cont.)

```
strata5 <- cut(lalonde$ps,
               quantile(lalonde$ps, seq(0, 1, 1/5)),
               include.lowest = TRUE,
               labels = letters[1:5])
circ.psa(lalonde$re78, lalonde$treat, strata5)
```



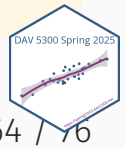

```
strata10 <- cut(lalonde$ps,
                quantile(lalonde$ps, seq(0, 1, 1/10)),
                include.lowest = TRUE,
                labels = letters[1:10])
circ.psa(lalonde$re78, lalonde$treat, strata10)
```



Stratification (cont.)

```
## $summary.strata
##   n.0 n.1  means.0  means.1
## a  62  27 5126.493 5178.073
## b  59  30 3855.200 6496.695
## c  56  33 4586.869 4495.076
## d  42  47 4814.028 6059.232
## e  41  48 4387.692 8474.201
##
## $wtd.Mn.0
## [1] 4554.056
##
## $wtd.Mn.1
## [1] 6140.655
##
## $ATE
## [1] 1586.599
##
## $se.wtd
## [1] 693.5067
##
## $approx.t
## [1] 2.287792
##
## $df
## [1] 435
##
## $CI.95
## [1]  223.5584 2949.6395
```

```
## $summary.strata
##   n.0 n.1  means.0  means.1
## a  35  10 6339.437 7019.962
## b  27  17 3554.157 4094.609
## c  31  16 3430.148 4356.532
## d  28  14 4325.792 8942.596
## e  30  15 4932.648 4710.588
## f  26  18 4187.895 4315.483
## g  22  22 4755.015 6148.795
## h  20  25 4878.944 5980.416
## i  16  28 1375.014 9276.448
## j  25  20 6315.806 7351.056
##
## $wtd.Mn.0
## [1] 4414.111
##
## $wtd.Mn.1
## [1] 6195.262
##
## $ATE
## [1] 1781.151
##
## $se.wtd
## [1] 710.5964
##
## $approx.t
## [1] 2.506559
##
## $df
## [1] 425
##
## $CI.95
## [1]  384.4306 3177.8724
```



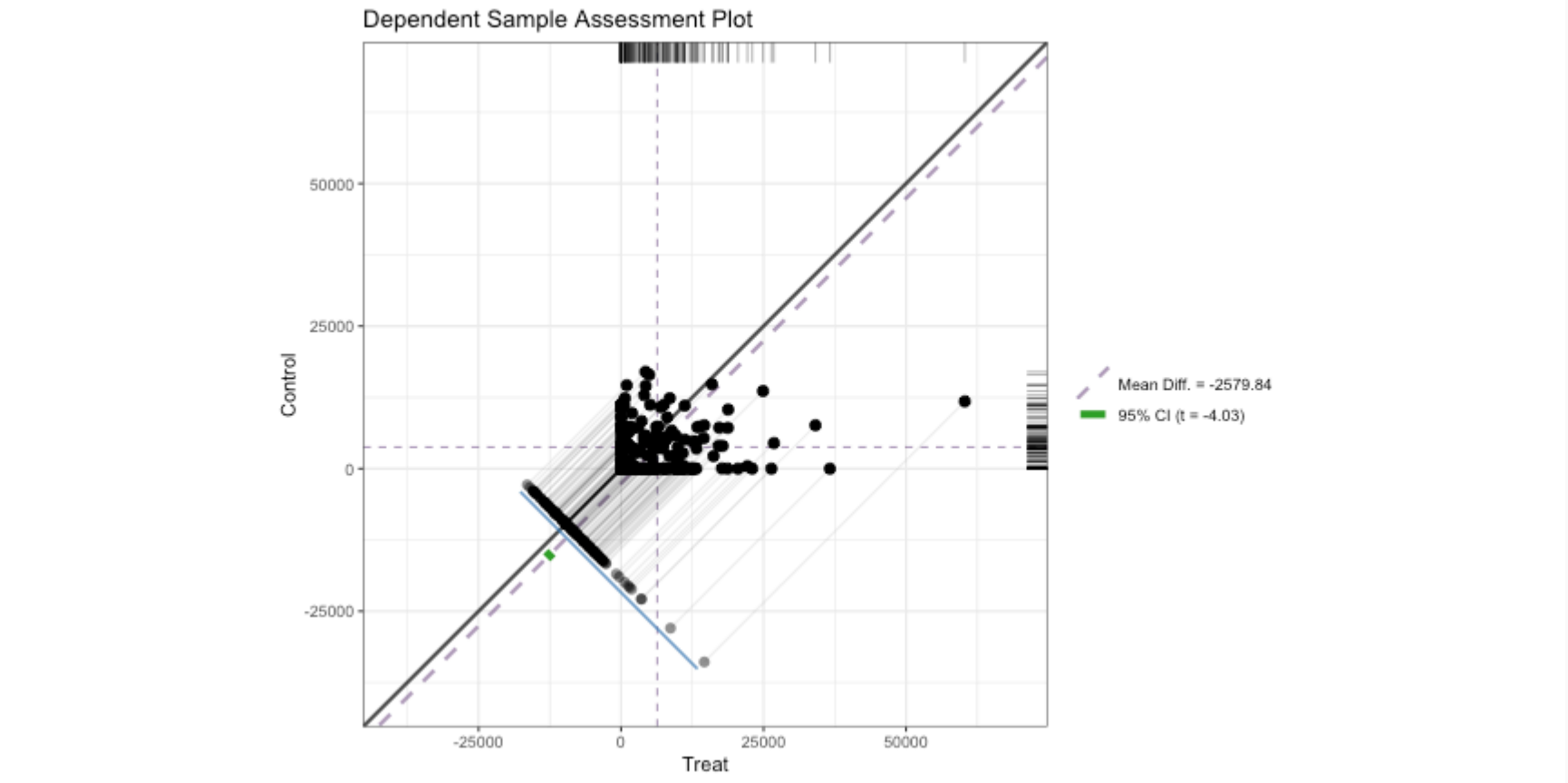
Matching

```
rr <- Match(Y = lalonde$re78,
            Tr = lalonde$treat,
            X = lalonde$ps,
            M = 1,
            estimand = 'ATT',
            ties = FALSE)
summary(rr)
```

```
##
## Estimate...  2579.8
## SE.........  637.69
## T-stat.....  4.0456
## p.val......  5.2189e-05
##
## Original number of observations..............  445
## Original number of treated obs...............  185
## Matched number of observations...............  185
## Matched number of observations  (unweighted).  185
```

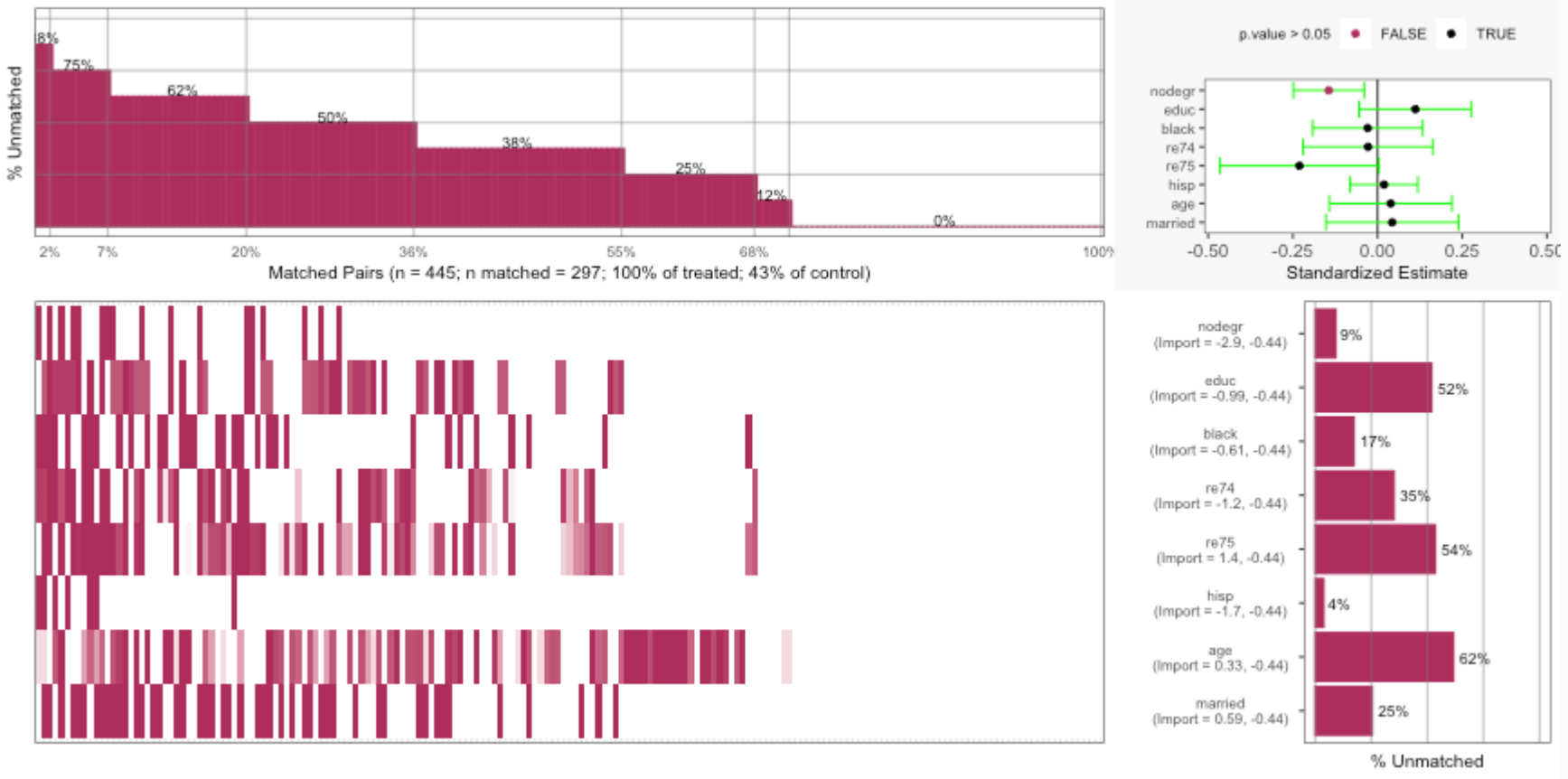
Visualizing Matching Results

```
matches <- data.frame(Treat = lalonde[rr$index.treated,'re78'],
                      Control = lalonde[rr$index.control,'re78'])
granovagg.ds(matches[,c('Control','Treat')], xlab = 'Treat', ylab = 'Control')
```



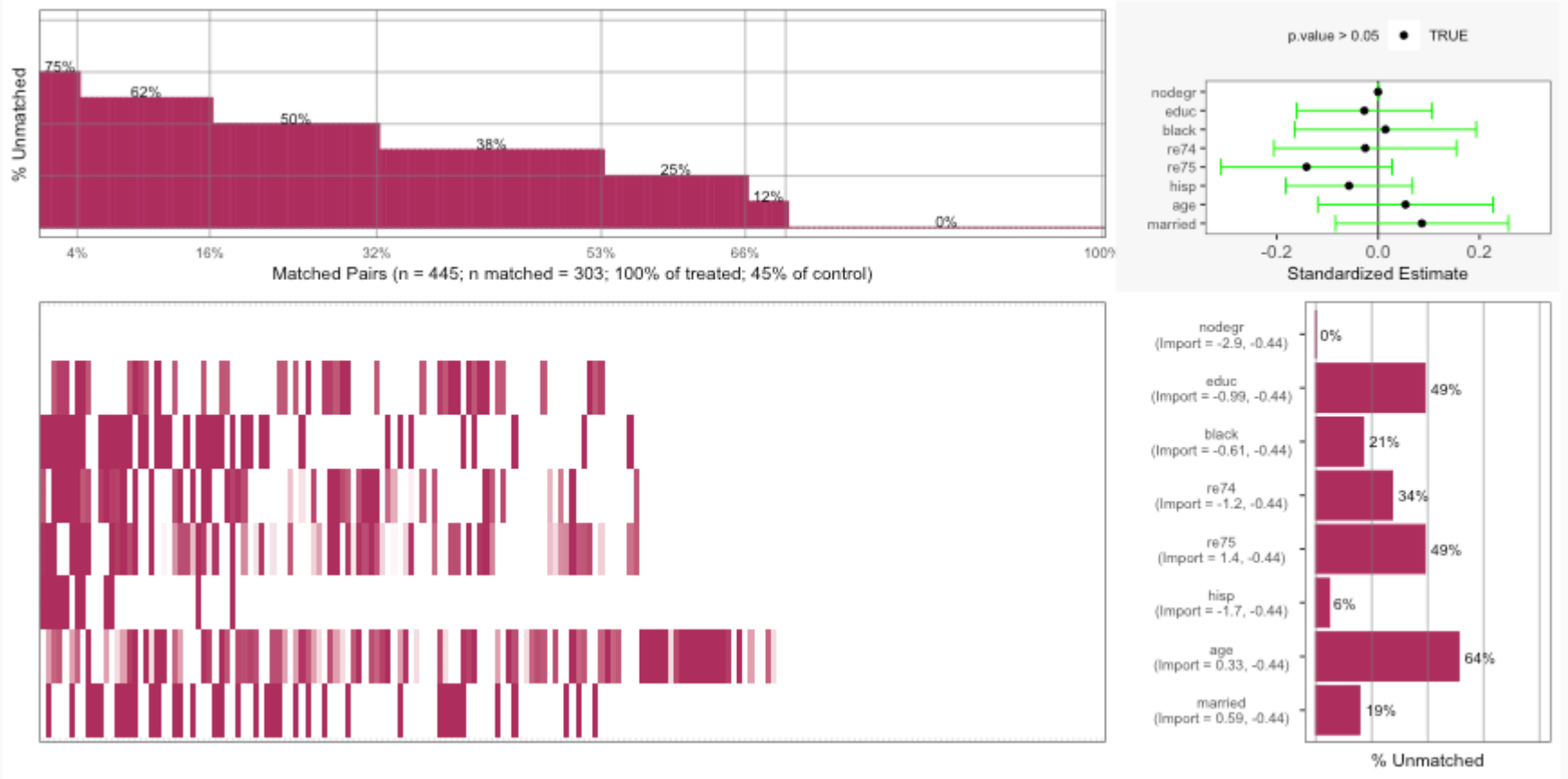
Balance for Matching

```
psa::MatchBalance(df = lalonde, formu = lalonde.formu,
                  formu.Y = update.formula(lalonde.formu, re78 ~ .),
                  M = 1, estimand = 'ATT', ties = FALSE) |> plot()
```



Balance for Matching (cont.)

```
psa::MatchBalance(df = lalonde, formu = lalonde.formu,
                  formu.Y = update.formula(lalonde.formu, re78 ~ .),
                exact.covs = c('nodegr'),
                  M = 1, estimand = 'ATT', ties = FALSE) |> plot()
```



Sensitivity Analysis

Sensitivity Analysis

- An observational study is free of hidden bias if the propensity scores for each subject depend only on the observed covariates.
- That is, the *p*-value is valid *if* there are no unobserved confounders.
- However, there are very likely covariates that would better model treatment. These introduce hidden bias.
- Hidden bias exists if two subjects have the same covariates, but different propensity scores.

$X_a = X_b$ but $\pi_a \neq \pi_b$ for some a and b.

Sensitivity Analysis

Each person in the treatment is matched to exactly one person in the control. The odds of being in the treatment for persons a and b are:

$O_a = \frac{\pi_a}{1-\pi_a}$ and $O_b = \frac{\pi_b}{1-\pi_b}$

The ratio of these odds, Γ, measures the bias after matching.

$$\Gamma = \frac{O_a}{O_b} = \frac{\pi_a/(1-\pi_a)}{\pi_b/(1-\pi_b)}$$

This is the ratio of the odds the treated unit being in the treatment group to the matched control unit being in the treatment group.

Sensitivity Analysis

Sensitivity analysis tests whether the results hold for various ranges of Γ. That is, we test how large the differences in π (i.e. propensity scores) would have to be to change our basic inference. Let p_a and p_b be the probability of each unit of the matched pair being treated, conditional on exactly one being treated. For example:

- If $\Gamma = 1$, the treatment and control unit within each pair has the same value of treatment assignment ($p_a = 0.5$ and $p_b = 0.5$).
- If $\frac{1}{2} \leq \Gamma \leq 2$, no unit can be more than twice as likely as its match to get treated ($0.33 \leq p_a, p_b \leq 0.66$).
- If $\frac{1}{3} \leq \Gamma \leq 3$, no unit can be more than three times as likely as its match to get treated ($0.25 \leq p_a, p_b \leq 0.75$)

To get the bounds:

$$\frac{1}{\Gamma + 1} \leq p_a, p_b \leq \frac{\Gamma}{\Gamma + 1}$$

Wilcoxon Signed Rank Test

- Drop pairs where the matches have the same outcome.
- Calculate the difference in outcomes within each pair.
- Rank the pairs from smallest absolute difference to largest absolute difference (i.e. the smallest = 1).
- Take the sum of the ranks where the treated unit had the higher outcome.

$$W = \left| \sum_{1}^{N_r} sgn(x_{T,i} - x_{C,i}) \cdot R_i \right|$$

Where N is the number of ranked pairs; R_i is the rank for pair *r*; $x_{T,i}$ and $x_{C,i}$ are the outcomes for the i^{th} treated and control pair, respectively.

Sensitivity Analysis

The process for sensitivity analysis:

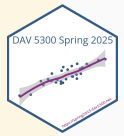
- Select a series of values for Γ. For social science research, values between 1 and 2 is an appropriate start.
- For each Γ, estimate the *p*-values to see how the *p*-values increase for larger values of Γ.
- For binary outcomes, use McNemar's test, for all others use Wilcoxon sign rank test and the Hodges-Lehmann point estimate. See Keele (2010) for more information.

Sensitivity Analysis

Children of parents who had worked in a factory where lead was used in making batteries were matched by age, exposure to traffic, and neighborhood with children whose parents did not work in lead-related industries. Whole blood was assessed for lead content yielding measurements in mg/dl

```
require(rbounds)
psens(lalonde$re78[rr$index.treated],
      lalonde$re78[rr$index.control],
      Gamma = 2, GammaInc = 0.1)
```

```
##
##  Rosenbaum Sensitivity Test for Wilcoxon Signed Rank P-Value
##
## Unconfounded estimate ....  2e-04
##
##  Gamma Lower bound Upper bound
##    1.0       2e-04      0.0002
##    1.1       0e+00      0.0016
##    1.2       0e+00      0.0069
##    1.3       0e+00      0.0215
##    1.4       0e+00      0.0527
```



One Minute Paper

1. What was the most important thing you learned during this class?
2. What important question remains unanswered for you?

https://forms.gle/sTwKB3HivjtbafBb7