The Lindner Example

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Contents

```
# Load packages
library(broom)
library(patchwork)
library(cobalt)
library(Matching)
library(tableone)
library(twang)
library(janitor)
library(here)
library(magrittr)
library(lme4)
library(tidyverse)
```

Note: we will also use the `broom.mixed` package, but we are not loading it as to prevent it conflicting with the functions of `broom`.

If you notice any errors or encounter any problems with this example, please contact Wyatt Bensken.

1 Load data

Information on the lindner dataset can be found at this site.[1,2]

[1] Rdocumentation. (n.d.). lindner: Lindner Center Data On 996 PCI Patients Analyzed By Kereiakes Et Al. (2000). Retrieved from https://www.rdocumentation.org/packages/MatchLinReg/versions/0.7.0/topics/lindner

[2] Kereiakes DJ, Obenchain RL, Barber BL, et al. Abciximab provides cost effective survival advantage in high volume interventional practice. Am Heart J 2000; 140: 603-610.

```
lindner_raw <- read.csv("data/lindner.csv")

lindner_raw %>%
  head(10)
```

```
   lifepres cardbill abcix stent height female diabetic acutemi ejecfrac
1       0.0    14301     1     0    163      1        1       0       56
2      11.6     3563     1     0    168      0        0       0       56
3      11.6     4694     1     0    188      0        0       0       50
4      11.6     7366     1     0    175      0        1       0       50
5      11.6     8247     1     0    168      1        0       0       55
6      11.6     8319     1     0    178      0        0       0       50
7      11.6     8410     1     0    185      0        0       0       58
8      11.6     8517     1     0    173      1        0       0       30
9      11.6     8763     1     0    152      1        0       0       60
10     11.6     8823     1     0    180      0        0       0       60
   ves1proc sixMonthSurvive
1         1           FALSE
2         1            TRUE
3         1            TRUE
4         1            TRUE
5         1            TRUE
6         1            TRUE
7         1            TRUE
8         1            TRUE
9         1            TRUE
10        1            TRUE
```

```
colSums(is.na(lindner_raw))
```

```
       lifepres        cardbill           abcix           stent          height
              0               0               0               0               0
         female        diabetic         acutemi        ejecfrac        ves1proc
              0               0               0               0               0
sixMonthSurvive
              0
```

After reading in the data, we can print the first 10 rows to get a sense of what our data looks like. We see it contains information on 996 participants, and there is no missing data.

2 Data managment

2.1 Managing binary variables

In the course of this example, we'll want both a numeric and factored version of each binary variable.

- In all numeric versions of binary variables: 1 indicates 'yes' to having trait/characteristic, 0 indicates 'no' to having trait/characteristic.

- Variable names with trailing "_f" denotes the factored version of each binary variable.

```
# Six month survival (turning logical variable to a factor)
lindner_raw$sixMonthSurvive_f <- factor(lindner_raw$sixMonthSurvive, levels = c(TRUE,FALSE),
                                        labels = c("yes", "no"))

# Creating numeric (1/0) version of six month survival variable
lindner_raw$sixMonthSurvive <- factor(lindner_raw$sixMonthSurvive_f, levels = c("yes","no"),
                                      labels = c(1, 0))

lindner_raw$sixMonthSurvive <- ifelse(lindner_raw$sixMonthSurvive == "1", 1, 0)

#Add variable named treated (same values as abcix variable)
lindner_raw$treated <- lindner_raw$abcix

# Factoring the exposure of interest variable. Change the name to 'treated' too.
lindner_raw$treated_f <- factor(lindner_raw$abcix, levels = c(1,0),
                                labels = c("treated", "control"))

# Factor version of stent variable
lindner_raw$stent_f <- factor(lindner_raw$stent, levels = c(1,0),
                              labels = c("yes", "no"))

# Factoring the female variable
lindner_raw$female_f <- factor(lindner_raw$female, levels = c(1,0),
                               labels = c("female", "male"))

# Factoring the diabetic variable
lindner_raw$diabetic_f <- factor(lindner_raw$diabetic, levels = c(1,0),
                                 labels = c("yes", "no"))

# Factoring the acutemi variable
lindner_raw$acutemi_f <- factor(lindner_raw$acutemi, levels = c(1,0),
                                labels = c("yes", "no"))

# Make lindner dataset with "clean" name.
lindner_clean <- lindner_raw
```

2.2 Inspecting the clean data

```
mosaic::inspect(lindner_clean)
```

```
Registered S3 method overwritten by 'mosaic':
  method                           from
  fortify.SpatialPolygonsDataFrame ggplot2

categorical variables:
               name  class levels   n missing
1 sixMonthSurvive_f factor      2 996       0
2         treated_f factor      2 996       0
3           stent_f factor      2 996       0
4          female_f factor      2 996       0
5        diabetic_f factor      2 996       0
6         acutemi_f factor      2 996       0
```

```
                                          distribution
1 yes (97.4%), no (2.6%)
2 treated (70.1%), control (29.9%)
3 yes (66.9%), no (33.1%)
4 male (65.3%), female (34.7%)
5 no (77.6%), yes (22.4%)
6 no (85.6%), yes (14.4%)

quantitative variables:
                 name   class  min       Q1  median      Q3      max
...1         lifepres numeric    0    11.60    11.6    11.6     11.6
...2         cardbill integer 2216 10218.75 12458.0 16660.0 178534.0
...3            abcix integer    0     0.00     1.0     1.0      1.0
...4            stent integer    0     0.00     1.0     1.0      1.0
...5           height integer  108   165.00   173.0   178.0    196.0
...6           female integer    0     0.00     0.0     1.0      1.0
...7         diabetic integer    0     0.00     0.0     0.0      1.0
...8          acutemi integer    0     0.00     0.0     0.0      1.0
...9         ejecfrac integer    0    45.00    55.0    56.0     90.0
...10        ves1proc integer    0     1.00     1.0     2.0      5.0
...11 sixMonthSurvive numeric    0     1.00     1.0     1.0      1.0
...12         treated integer    0     0.00     1.0     1.0      1.0
               mean           sd   n missing
...1  1.129719e+01 1.850501e+00 996       0
...2  1.567416e+04 1.118226e+04 996       0
...3  7.008032e-01 4.581362e-01 996       0
...4  6.686747e-01 4.709262e-01 996       0
...5  1.714438e+02 1.065813e+01 996       0
...6  3.473896e-01 4.763800e-01 996       0
...7  2.238956e-01 4.170623e-01 996       0
...8  1.435743e-01 3.508337e-01 996       0
...9  5.096687e+01 1.041326e+01 996       0
...10 1.385542e+00 6.573525e-01 996       0
...11 9.738956e-01 1.595259e-01 996       0
...12 7.008032e-01 4.581362e-01 996       0
```

3 Codebook

Information was copy/pasted from here [1,2] (with some changes to reflect this analysis)

- `cardbill` (**Quantitative Outcome**): "Cardiac related costs incurred within 6 months of patient's initial PCI; numeric value in 1998 dollars; costs were truncated by death for the 26 patients with lifepres == 0."
- `sixMonthSurvive/sixMonthSurvive_f` (**Binary Outcome**): "Survival at six months a recoded version of lifepres."
- `treated/treated_f` (**Exoisure**): "Numeric treatment selection indicator; 0 implies usual PCI care alone; 1 implies usual PCI care deliberately augmented by either planned or rescue treatment with abciximab."
- `stent/stent_f`: "Coronary stent deployment; numeric, with 1 meaning YES and 0 meaning NO."
- `height`: "Height in centimeters; numeric integer from 108 to 196."

- `female/female_f`: "Female gender; numeric, with 1 meaning YES and 0 meaning NO."
- `diabetic/diabetic_f`: "Diabetes mellitus diagnosis; numeric, with 1 meaning YES and 0 meaning NO."
- `acutemi/acutemi_f`: "Acute myocardial infarction within the previous 7 days; numeric, with 1 meaning YES and 0 meaning NO."
- `ejecfrac`: "Left ejection fraction; numeric value from 0 percent to 90 percent."
- `ves1proc`: "Number of vessels involved in the patient's initial PCI procedure; numeric integer from 0 to 5."
- Note: Percutaneous Coronary Intervention (PCI)

[1] Rdocumentation. (n.d.). lindner: Lindner Center Data On 996 PCI Patients Analyzed By Kereiakes Et Al. (2000). Retrieved from https://www.rdocumentation.org/packages/MatchLinReg/versions/0.7.0/topics/lindner

[2] Kereiakes DJ, Obenchain RL, Barber BL, et al. Abciximab provides cost effective survival advantage in high volume interventional practice. Am Heart J 2000; 140: 603-610.

4 Table 1

```
var_list = c("cardbill", "sixMonthSurvive_f", "stent_f", "height", "female_f", "diabetic_f",
             "acutemi_f", "ejecfrac", "ves1proc")

factor_list = c("sixMonthSurvive_f", "stent_f", "female_f", "diabetic_f", "acutemi_f")

CreateTableOne(vars = var_list, strata = "treated_f",
               data = lindner_clean, factorVars = factor_list)
```

```
                             Stratified by treated_f
                              treated            control             p      test
  n                                698                298                     
  cardbill (mean (SD))        16126.68 (9383.83) 14614.22 (14514.00)  0.051     
  sixMonthSurvive_f = no (%)        11 ( 1.6)          15 ( 5.0)      0.004     
  stent_f = no (%)                 206 (29.5)         124 (41.6)     <0.001     
  height (mean (SD))            171.44 (10.69)     171.45 (10.59)     0.996     
  female_f = male (%)              467 (66.9)         183 (61.4)      0.111     
  diabetic_f = no (%)              555 (79.5)         218 (73.2)      0.034     
  acutemi_f = no (%)               573 (82.1)         280 (94.0)     <0.001     
  ejecfrac (mean (SD))           50.40 (10.42)      52.29 (10.30)     0.009     
  ves1proc (mean (SD))            1.46 (0.71)        1.20 (0.48)     <0.001     
```

As we can see, The mean `cardbill` was higher in the treated population and a larger percentage of controls did not survive through 6 months.

5 Task 1: Ignoring covariates, estimate the effect of treatment vs. control on the two outcomes

5.1 Quantitative outcome: `cardbill`

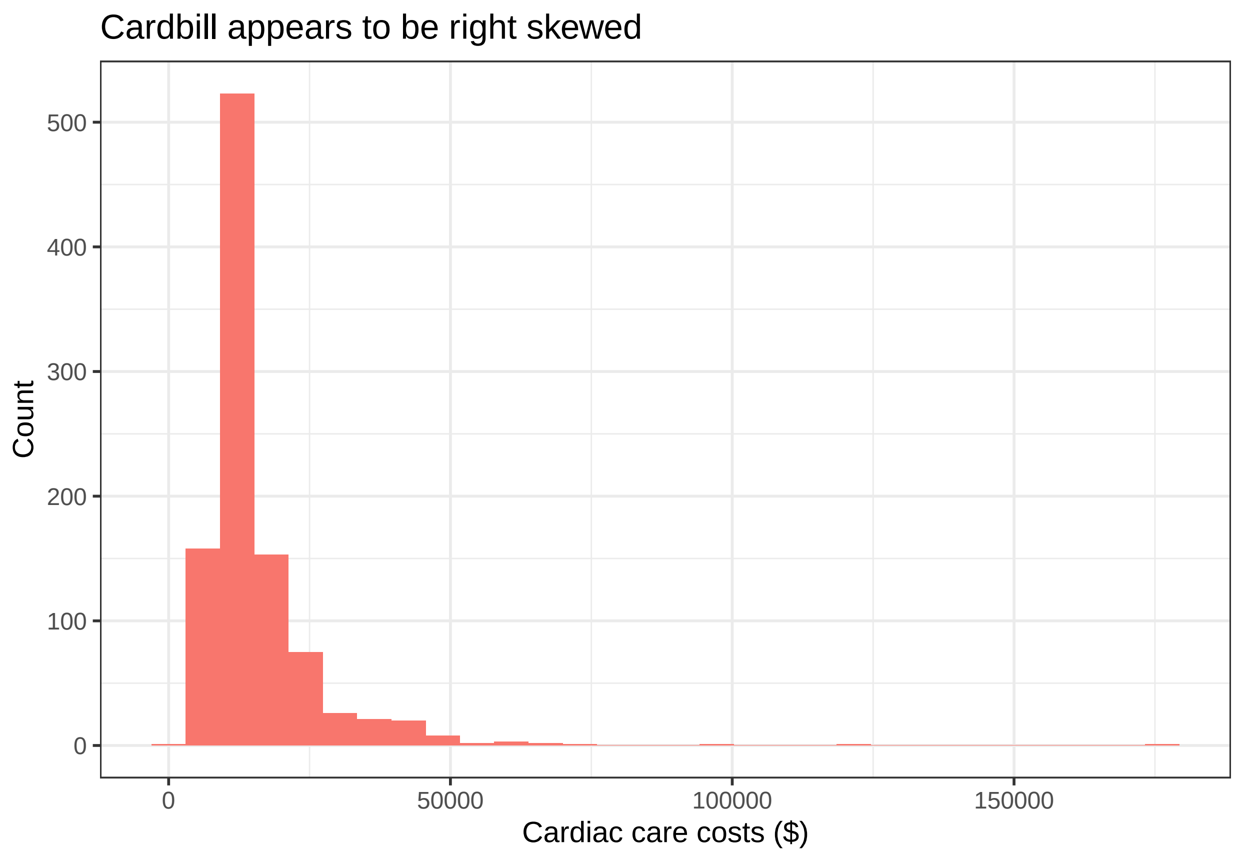
```
lindner_clean %$%
  mosaic::favstats(cardbill ~ treated_f)
```

```
  treated_f  min       Q1 median       Q3    max     mean        sd   n missing
1   treated 3563 10902.25  12944 17080.75  96741 16126.68  9383.825 698       0
2   control 2216  8300.00  10423 15895.75 178534 14614.22 14513.996 298       0
```

- Across the entire sample, the mean ($16,127 vs. $14,614) and median ($12,944 vs. $10,423) cardiac care costs were higher in treated individuals than non-treated controls.

```
ggplot(lindner_clean, aes(x = cardbill, fill = "cardbill")) +
  geom_histogram() +
  theme_bw() +
  labs(y = "Count",
       x = "Cardiac care costs ($)",
       title = "Cardbill appears to be right skewed") +
  guides(fill = FALSE)
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



As we can see in this figure, `cardbill` appears to be right/positively skewed.

```
unadjust_quant_outcome <- lm(cardbill ~ treated, data = lindner_clean)

unadjust_quant_outcome_tidy <- tidy(unadjust_quant_outcome, conf.int = TRUE, conf.level = 0.95) %>%
    filter(term == "treated")

unadjust_quant_outcome_tidy
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated    1512.      773.      1.96  0.0506    -3.83     3029.
```

Treated individuals were estimated to spend 1512.46 (95%CI: -3.83, 3028.76) more dollars than non-treated controls

5.2 Binary outcome: `sixMonthSurvive`

```
Epi::twoby2(table(lindner_clean$treated_f, lindner_clean$sixMonthSurvive_f))
```

```
2 by 2 table analysis:
------------------------------------------------------
Outcome   : yes
Comparing : treated vs. control

        yes no    P(yes) 95% conf. interval
treated 687 11    0.9842    0.9718   0.9913
control 283 15    0.9497    0.9182   0.9694

                                   95% conf. interval
             Relative Risk: 1.0364    1.0080   1.0656
         Sample Odds Ratio: 3.3103    1.5020   7.2957
Conditional MLE Odds Ratio: 3.3057    1.3992   8.0624
    Probability difference: 0.0346    0.0115   0.0664

             Exact P-value: 0.0037
        Asymptotic P-value: 0.0030
------------------------------------------------------
```

The odds treated individuals were alive after 6 months was roughly 3.31 times the odds that non-treated individuals were alive after 6 months.

```
unadjust_binary_outcome <- glm(sixMonthSurvive ~ treated, data = lindner_clean, family = binomial())

unadjust_binary_outcome_tidy <- tidy(unadjust_binary_outcome, conf.int = TRUE, conf.level = 0.95, expone
    filter(term == "treated")

unadjust_binary_outcome_tidy
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated     3.31     0.403      2.97 0.00299     1.51      7.48
```

The odds of being alive after six months in treated individuals was 3.31 (95%CI: 1.51, 7.48) times higher than the odds that a non-treated control would be alive after six months.

6 Task 2: Fitting the propensity score model

We will now fit the propensity score, which predicts treatment status based on available covariates. Remember, we're not worried about overfitting (including too many covariates) when calculating the propensity scores.

```
psmodel <- glm(treated ~ stent + height + female + diabetic + acutemi + ejecfrac + ves1proc, family = bi

summary(psmodel)
```

```
Call:
glm(formula = treated ~ stent + height + female + diabetic +
    acutemi + ejecfrac + ves1proc, family = binomial(), data = lindner_clean)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.5211  -1.2109   0.6399   0.8827   1.5259

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.965651   1.731085   1.713  0.08668 .
stent        0.573018   0.150454   3.809  0.00014 ***
height      -0.015366   0.009534  -1.612  0.10700
female      -0.359060   0.206904  -1.735  0.08267 .
diabetic    -0.406810   0.170623  -2.384  0.01711 *
acutemi      1.199548   0.270468   4.435 9.20e-06 ***
ejecfrac    -0.014789   0.007403  -1.998  0.04574 *
ves1proc     0.760502   0.138437   5.493 3.94e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1215.5  on 995  degrees of freedom
Residual deviance: 1124.3  on 988  degrees of freedom
AIC: 1140.3

Number of Fisher Scoring iterations: 4
```

Store the raw and linear propensity scores below.

```
lindner_clean$ps <- psmodel$fitted
lindner_clean$linps <- psmodel$linear.predictors
```

6.1 Comparing distribution of propensity scores across treatment groups

6.2 Numerically

```
lindner_clean %$%
  mosaic::favstats(ps ~ treated_f)
```

```
  treated_f       min        Q1    median        Q3       max      mean
1   treated 0.3121753 0.6402644 0.7158289 0.8259514 0.9800181 0.7265015
2   control 0.2323431 0.5558665 0.6462761 0.7093624 0.9583296 0.6406106
         sd   n missing
```

```
1 0.1299570 698       0
2 0.1230138 298       0
```

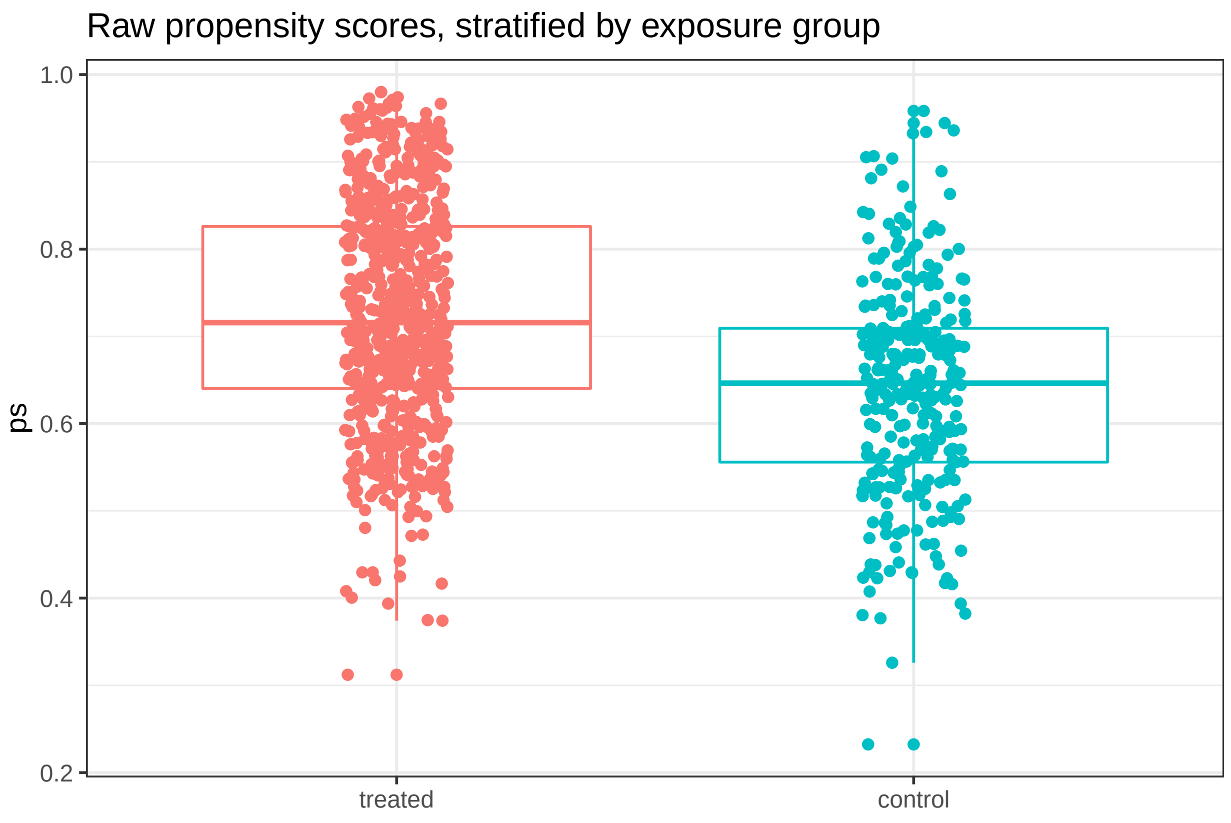
We can see there are no propensity scores equal to, or very close to, 0 or 1.

6.3 Visually

6.3.1 Boxplot

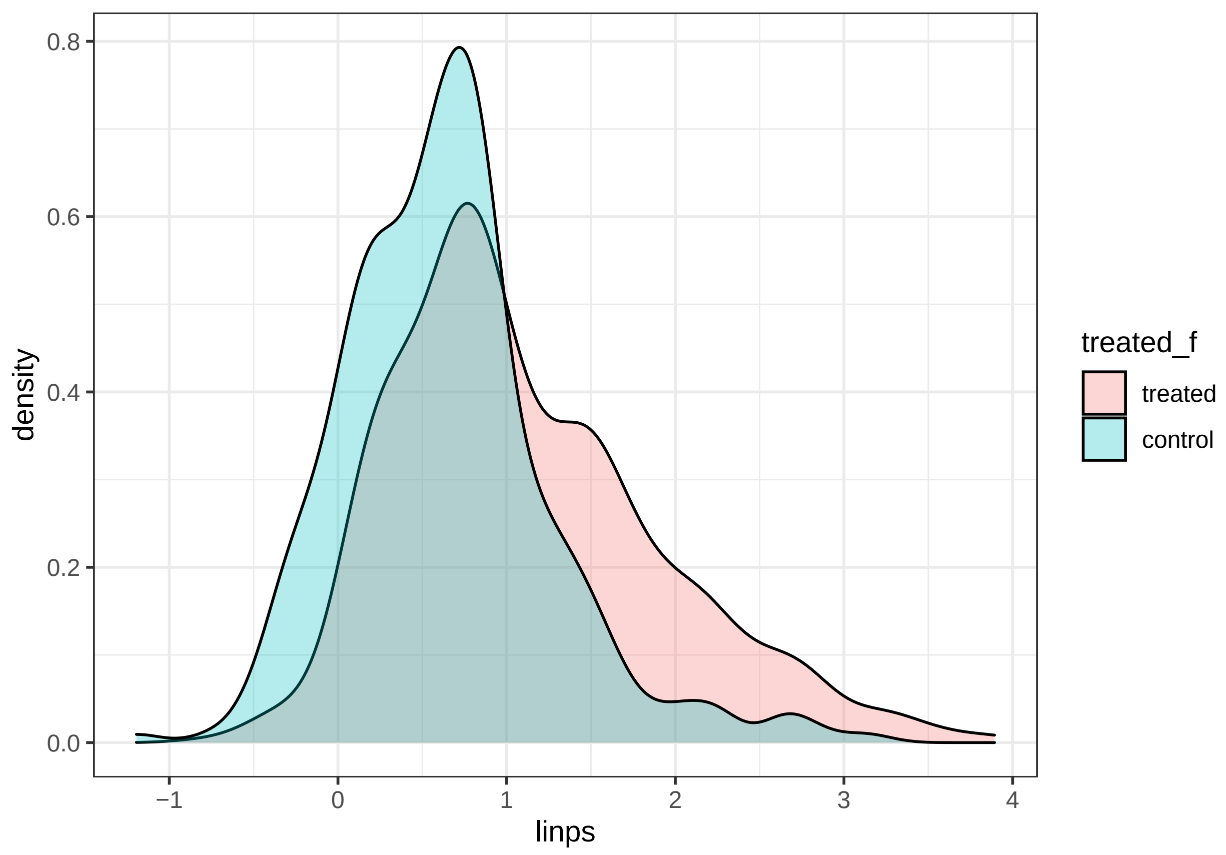
Now we'll visualize the distribution of the propensity scores stratified by treatment status.

```r
ggplot(lindner_clean, aes(x = treated_f, y = ps, color = treated_f)) +
geom_boxplot() +
geom_jitter(width = 0.1) +
guides(color = FALSE) +
theme_bw() +
labs(x = "",
     title = "Raw propensity scores, stratified by exposure group")
```



6.3.2 Density plot

```r
ggplot(lindner_clean, aes(x = linps, fill = treated_f)) +
geom_density(alpha = 0.3) +
  theme_bw()
```



Both of these plots demonstrate good overlap, suggesting a propensity score analysis may be appropriate.

7 Task 3: Rubin's Rules For Assessing Overlap Before Propensity Adjustment

7.1 Rubin's Rule 1

```
rubin1.unadj <- with(lindner_clean,
abs(100*(mean(linps[treated==1])-mean(linps[treated==0]))/sd(linps)))
rubin1.unadj
```

```
[1] 61.86668
```

As you can see, we fail Rubin's Rule 1 - in which we want below 50%.

7.2 Rubin's Rule 2

```
rubin2.unadj <-with(lindner_clean, var(linps[treated==1])/var(linps[treated==0]))
rubin2.unadj
```

```
[1] 1.672048
```

We also "fail" Rubin's Rule 2 wherewe are looking for value between 0.8 - 1.2 (ideally, 1).

8 Task 4: Greedy 1:1 matching on the linear PS

The first type of match we will conduct is greedy 1:1 matching, without replacement. As we had only 298 controls, we will not match all of the 698 treated patients.

```
X <- lindner_clean$linps ## matching on the linear propensity score
Tr <- as.logical(lindner_clean$treated)
match1 <- Match(Tr=Tr, X=X, M = 1, replace=FALSE, ties=FALSE)
```

```
Warning in Match(Tr = Tr, X = X, M = 1, replace = FALSE, ties = FALSE):
replace==FALSE, but there are more (weighted) treated obs than control obs. Some
treated obs will not be matched. You may want to estimate ATC instead.
```

```
summary(match1)
```

```
Estimate...  0
SE.........  0
T-stat.....  NaN
p.val......  NA

Original number of observations..............  996
Original number of treated obs...............  698
Matched number of observations...............  298
Matched number of observations  (unweighted).  298
```

Below we'll assess the match balance from the 1:1 matching.

```
set.seed(2021)
mb1 <- MatchBalance(treated ~ stent + height + female + diabetic + acutemi + ejecfrac + ves1proc + ps +
match.out = match1, nboots=500)
```

```
***** (V1) stent *****
                       Before Matching        After Matching
mean treatment........     0.70487           0.60738
mean control..........     0.58389           0.58389
std mean diff.........      26.505            4.8022

mean raw eQQ diff.....     0.12081           0.02349
med  raw eQQ diff.....           0                 0
max  raw eQQ diff.....           1                 1

mean eCDF diff........    0.060489          0.011745
med  eCDF diff........    0.060489          0.011745
max  eCDF diff........     0.12098           0.02349

var ratio (Tr/Co).....     0.85457           0.98151
T-test p-value........ 0.00032255           0.49878


***** (V2) height *****
                       Before Matching        After Matching
mean treatment........      171.44            171.77
mean control..........      171.45            171.45
std mean diff......... -0.033804            3.1486

mean raw eQQ diff.....     0.56376           0.88591
```

```
med  raw eQQ diff.....          0               0
max  raw eQQ diff.....         20              36

mean eCDF diff........  0.0078996        0.013639
med  eCDF diff........  0.0060095        0.010067
max  eCDF diff........   0.024971        0.053691

var ratio (Tr/Co).....     1.0201         0.93356
T-test p-value........    0.99608         0.70602
KS Bootstrap p-value..      0.938           0.554
KS Naive p-value......    0.99947         0.78362
KS Statistic..........   0.024971        0.053691


***** (V3) female *****
                       Before Matching       After Matching
mean treatment........    0.33095         0.37584
mean control..........    0.38591         0.38591
std mean diff.........    -11.672          -2.075

mean raw eQQ diff.....   0.053691        0.010067
med  raw eQQ diff.....          0               0
max  raw eQQ diff.....          1               1

mean eCDF diff........    0.02748       0.0050336
med  eCDF diff........    0.02748       0.0050336
max  eCDF diff........    0.05496        0.010067

var ratio (Tr/Co).....    0.93253         0.98988
T-test p-value........    0.10045         0.79492


***** (V4) diabetic *****
                       Before Matching       After Matching
mean treatment........    0.20487         0.25503
mean control..........    0.26846         0.26846
std mean diff.........    -15.743         -3.0743

mean raw eQQ diff.....   0.063758        0.013423
med  raw eQQ diff.....          0               0
max  raw eQQ diff.....          1               1

mean eCDF diff........   0.031793       0.0067114
med  eCDF diff........   0.031793       0.0067114
max  eCDF diff........   0.063585        0.013423

var ratio (Tr/Co).....    0.82788         0.96743
T-test p-value........    0.03402         0.69509


***** (V5) acutemi *****
                       Before Matching       After Matching
mean treatment........    0.17908       0.0033557
mean control..........   0.060403        0.060403
```

```
std mean diff.........     30.931           -98.478

mean raw eQQ diff.....    0.11745          0.057047
med  raw eQQ diff.....          0                 0
max  raw eQQ diff.....          1                 1

mean eCDF diff........    0.05934          0.028523
med  eCDF diff........    0.05934          0.028523
max  eCDF diff........    0.11868          0.057047

var ratio (Tr/Co).....     2.5853          0.058929
T-test p-value........ 4.6617e-09         7.888e-05


***** (V6) ejecfrac *****
                       Before Matching       After Matching
mean treatment........     50.403            53.349
mean control..........     52.289            52.289
std mean diff.........    -18.102            13.166

mean raw eQQ diff.....     2.0503            1.8255
med  raw eQQ diff.....          1                 0
max  raw eQQ diff.....         20                20

mean eCDF diff........   0.035602          0.026577
med  eCDF diff........   0.011423          0.033557
max  eCDF diff........    0.11383          0.053691

var ratio (Tr/Co).....     1.0238           0.61178
T-test p-value........  0.0085806           0.15759
KS Bootstrap p-value..      0.006             0.448
KS Naive p-value......  0.0089219           0.78362
KS Statistic..........    0.11383          0.053691


***** (V7) ves1proc *****
                       Before Matching       After Matching
mean treatment........     1.4628            1.0403
mean control..........     1.2047            1.2047
std mean diff.........     36.545           -67.707

mean raw eQQ diff.....     0.2651           0.16443
med  raw eQQ diff.....          0                 0
max  raw eQQ diff.....          1                 2

mean eCDF diff........   0.043323          0.032886
med  eCDF diff........  0.0090671         0.0067114
max  eCDF diff........    0.18842           0.13087

var ratio (Tr/Co).....     2.1614           0.25567
T-test p-value........   4.21e-11        5.2489e-08
KS Bootstrap p-value.. < 2.22e-16        < 2.22e-16
KS Naive p-value...... 7.2635e-07          0.012144
KS Statistic..........    0.18842           0.13087
```

```
***** (V8) ps *****
                       Before Matching       After Matching
mean treatment........     0.7265            0.60662
mean control..........    0.64061            0.64061
std mean diff.........     66.092            -45.866

mean raw eQQ diff.....   0.085216           0.046911
med  raw eQQ diff.....   0.081353           0.035726
max  raw eQQ diff.....    0.12087            0.23215

mean eCDF diff........    0.17141            0.10312
med  eCDF diff........    0.17768           0.083893
max  eCDF diff........    0.27599            0.23154

var ratio (Tr/Co).....     1.1161            0.36304
T-test p-value........ < 2.22e-16         4.5755e-12
KS Bootstrap p-value.. < 2.22e-16         < 2.22e-16
KS Naive p-value......  3.042e-14         2.3042e-07
KS Statistic..........    0.27599            0.23154


***** (V9) linps *****
                       Before Matching       After Matching
mean treatment........     1.1148            0.44175
mean control..........    0.63332            0.63332
std mean diff.........     60.484            -61.383

mean raw eQQ diff.....     0.4787             0.2442
med  raw eQQ diff.....    0.35992            0.15424
max  raw eQQ diff.....     1.0113             2.1601

mean eCDF diff........    0.17141            0.10312
med  eCDF diff........    0.17768           0.083893
max  eCDF diff........    0.27599            0.23154

var ratio (Tr/Co).....      1.672            0.25702
T-test p-value........ < 2.22e-16         6.4948e-13
KS Bootstrap p-value.. < 2.22e-16         < 2.22e-16
KS Naive p-value......  3.042e-14         2.3042e-07
KS Statistic..........    0.27599            0.23154


Before Matching Minimum p.value: < 2.22e-16
Variable Name(s): ves1proc ps linps  Number(s): 7 8 9

After Matching Minimum p.value: < 2.22e-16
Variable Name(s): ves1proc ps linps  Number(s): 7 8 9
```

```
covnames <- c("stent", "height", "female", "diabetic", "acutemi", "ejecfrac", "ves1proc", "ps", "linps"
```

This is Dr. Love's code to extract the standardized differences.

```
pre.szd <- NULL; post.szd <- NULL
for(i in 1:length(covnames)) {
pre.szd[i] <- mb1$BeforeMatching[[i]]$sdiff.pooled
post.szd[i] <- mb1$AfterMatching[[i]]$sdiff.pooled
}
```

We can now print our table of standardized differences.

```
match_szd <- data.frame(covnames, pre.szd, post.szd, row.names=covnames)
print(match_szd, digits=3)
```

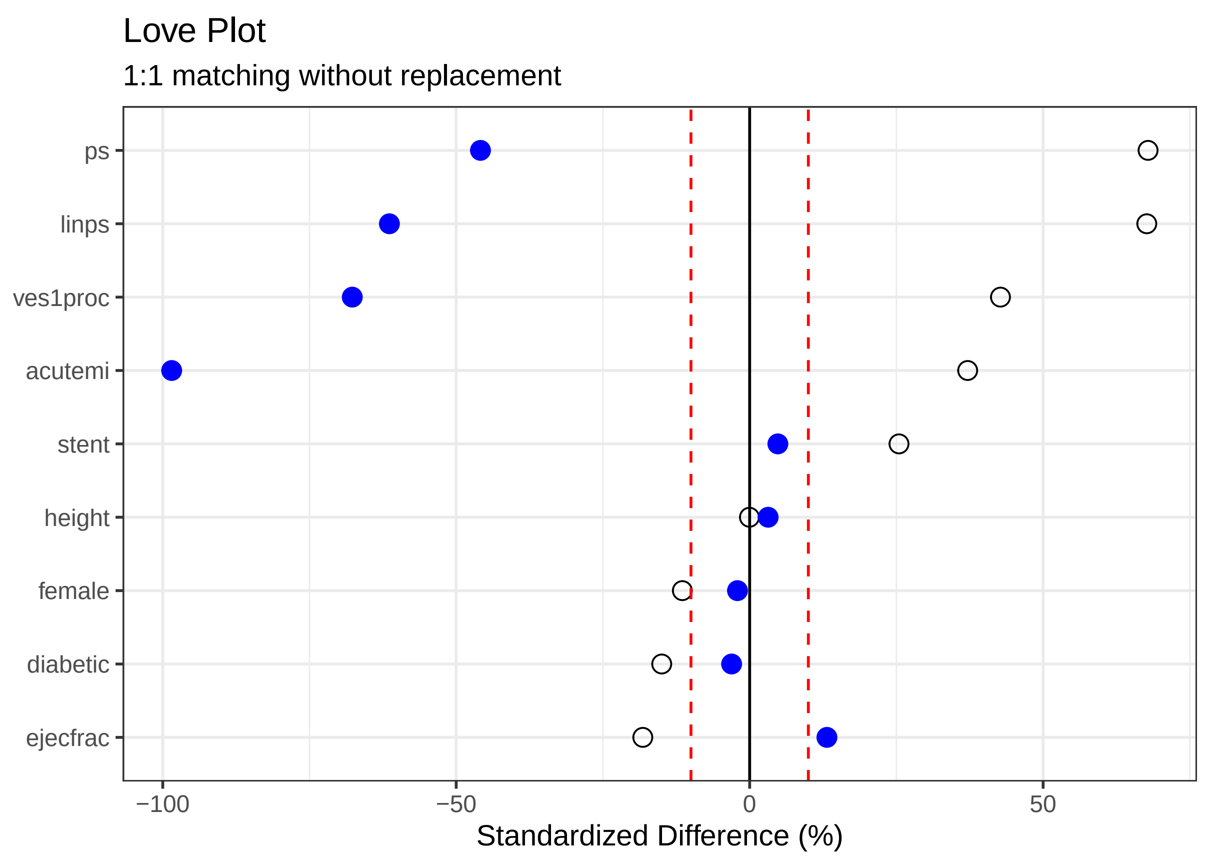
```
         covnames pre.szd post.szd
stent       stent  25.445     4.80
height     height  -0.034     3.15
female     female -11.466    -2.08
diabetic diabetic -14.983    -3.07
acutemi   acutemi  37.145   -98.48
ejecfrac ejecfrac -18.208    13.17
ves1proc ves1proc  42.734   -67.71
ps             ps  67.880   -45.87
linps       linps  67.664   -61.38
```

8.1 Love Plot of standardized differences before and after 1:1 matching

8.2 Using ggplot

In this figure, blue points are post-matching while white are pre-match

```
lp_wo_rep <- ggplot(match_szd, aes(x = pre.szd, y = reorder(covnames, pre.szd))) +
  geom_point(col = "black", size = 3, pch = 1) +
  geom_point(aes(x = post.szd, y = reorder(covnames, pre.szd)), size = 3, col = "blue") +
  theme_bw() +
  geom_vline(aes(xintercept = 0)) +
  geom_vline(aes(xintercept = 10), linetype = "dashed", col = "red") +
  geom_vline(aes(xintercept = -10), linetype = "dashed", col = "red") +
  labs(x = "Standardized Difference (%)",
     y = "",
     title = "Love Plot",
     subtitle = "1:1 matching without replacement")

lp_wo_rep
```



Just visually, we can see this match isn't all that great.

8.3 Using `cobalt` to make the Love Plot

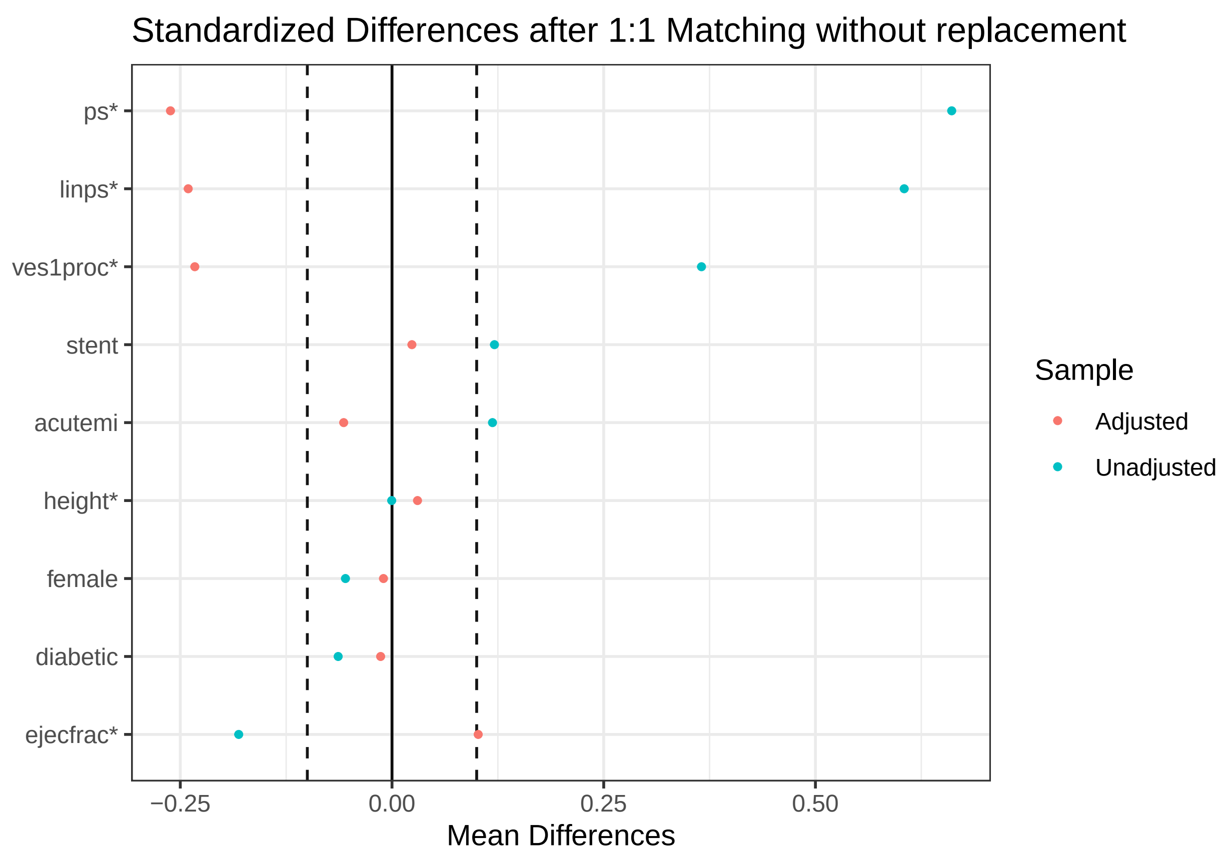
There's a more automated way to build the Love Plot - as we see here.

```
cobalt_tab <- bal.tab(match1, treated ~ stent + height + female + diabetic + acutemi + ejecfrac + ves1p

cobalt_tab
```

```
Balance Measures
            Type Diff.Un Diff.Adj
stent     Binary  0.1210   0.0235
height   Contin. -0.0003   0.0301
female    Binary -0.0550  -0.0101
diabetic  Binary -0.0636  -0.0134
acutemi   Binary  0.1187  -0.0570
ejecfrac Contin. -0.1810   0.1018
ves1proc Contin.  0.3654  -0.2329
ps       Contin.  0.6609  -0.2616
linps    Contin.  0.6048  -0.2407

Sample sizes
          Control Treated
All           298     698
Matched       298     298
```

```
Unmatched       0     400
```

```
p <- love.plot(cobalt_tab, threshold = .1, size = 1.5,
               var.order = "unadjusted",
               title = "Standardized Differences after 1:1 Matching without replacement",
               stars = "std")

p + theme_bw()
```



8.4 Extracting Variance Ratios

We can also look at variance ratios.

```
pre.vratio <- NULL; post.vratio <- NULL
for(i in 1:length(covnames)) {
pre.vratio[i] <- mb1$BeforeMatching[[i]]$var.ratio
post.vratio[i] <- mb1$AfterMatching[[i]]$var.ratio
}
## Table of Variance Ratios
match_vrat <- data.frame(names = covnames, pre.vratio, post.vratio, row.names=covnames)
print(match_vrat, digits=2)
```

```
            names pre.vratio post.vratio
stent       stent       0.85       0.982
height     height       1.02       0.934
female     female       0.93       0.990
```

```
diabetic diabetic       0.83       0.967
acutemi   acutemi       2.59       0.059
ejecfrac ejecfrac       1.02       0.612
ves1proc ves1proc       2.16       0.256
ps             ps       1.12       0.363
linps       linps       1.67       0.257
```

8.5 Creating a dataframe containing the matched sample

We will created a dataframe which includes our matched sample, and do a quick count for a sanity check.

```
matches <- factor(rep(match1$index.treated, 2))
lindner_clean.matchedsample <- cbind(matches, lindner_clean[c(match1$index.control, match1$index.treate

lindner_clean.matchedsample %>% count(treated_f)
```

```
  treated_f   n
1   treated 298
2   control 298
```

8.6 Reassessing Rubin's Rules after 1:1 matching without replacement

8.6.1 Rubin's Rule 1

```
rubin1.match <- with(lindner_clean.matchedsample,
abs(100*(mean(linps[treated==1])-mean(linps[treated==0]))/sd(linps)))
rubin1.match
```

```
[1] 38.54801
```

The new value for Rubin's Rule 1 is 38.55. While not ideal this technically passes Rubin's Rule 1 and is an improvement from the pre-match value of 61.87.

8.6.2 Rubin's Rule 2

```
rubin2.match <- with(lindner_clean.matchedsample, var(linps[treated==1])/var(linps[treated==0]))
rubin2.match
```

```
[1] 0.2570156
```

The new value for Rubin's Rule 2 is 0.26. This does not pass Rubin's Rule 2 and is not an improvement from the pre-match value of 1.67.

9 Task 5: Estimating the causal effect of the treatment on both outcomes after 1:1 matching without replacement

9.1 The Quantitative Outcome

We'll use a mixed model to estimate the effect of the treatment on `cardbill`. The matches will be treated as a random effect in the model (syntax "(1| matches.f)", and the treatment group will be treated as a fixed effect. We will use restricted maximum likelihood (REML) to estimate coefficient values.

```
#to appease lme4, factor the matches
lindner_clean.matchedsample$matches.f <- as.factor(lindner_clean.matchedsample$matches)

# fit the mixed model
matched_mixedmodel.out1 <- lmer(cardbill ~ treated + (1 | matches.f), REML = TRUE, data=lindner_clean.ma

summary(matched_mixedmodel.out1)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: cardbill ~ treated + (1 | matches.f)
   Data: lindner_clean.matchedsample

REML criterion at convergence: 12815.2

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.0495 -0.4295 -0.2546  0.0770 13.7835

Random effects:
 Groups    Name        Variance  Std.Dev.
 matches.f (Intercept)   6179257  2486
 Residual              128507597 11336
Number of obs: 596, groups:  matches.f, 298

Fixed effects:
            Estimate Std. Error t value
(Intercept)  14614.2      672.3  21.738
treated       -385.5      928.7  -0.415

Correlation of Fixed Effects:
        (Intr)
treated -0.691
```

```
confint(matched_mixedmodel.out1)
```

```
Computing profile confidence intervals ...

                2.5 %    97.5 %
.sig01          0.000  4670.945
.sigma      10465.897 12214.793
(Intercept) 13296.649 15931.794
treated     -2208.503  1437.530
```

```
tidy_mixed_matched <- broom.mixed::tidy(matched_mixedmodel.out1, conf.int = TRUE, conf.level = 0.95) %>%
  filter(term == "treated")

tidy_mixed_matched
```

```
# A tibble: 1 x 8
  effect group term    estimate std.error statistic conf.low conf.high
  <chr>  <chr> <chr>      <dbl>     <dbl>     <dbl>    <dbl>     <dbl>
1 fixed  <NA>  treated    -385.      929.    -0.415   -2206.     1435.
```

Treated individuals were estimated to spend $-385.49 (95%CI: -2205.69, 1434.71) less than non-treated individuals. As this result is not significant at an α of 0.05, a sensitivity analysis on the quantitative outcome will not make sense.

```
#check the mean cardbill in the matched sample
lindner_clean.matchedsample %>% group_by(treated_f) %>% summarise(mean = mean(cardbill))
```

```
# A tibble: 2 x 2
  treated_f   mean
* <fct>      <dbl>
1 treated   14229.
2 control   14614.
```

```
#check the mean cardbill in the entire sample
lindner_clean %>% group_by(treated_f) %>% summarise(mean = mean(cardbill))
```

```
# A tibble: 2 x 2
  treated_f   mean
* <fct>      <dbl>
1 treated   16127.
2 control   14614.
```

In treated individuals, the mean `cardbill` was lower within the matched sample than the entire sample (note the mean within the control group was the same as every control participant is in the matched sample. The mean changed in the treated group as only 298/698 treated patients are in the matched sample). This is a sanity check to assess if the mixed model results make sense; and it looks like they do.

9.2 The Binary Outcome

We will use conditional logistic regression to estimate the log odds (and ORs) of being alive after 6 months based on treatment status.

```
binary_outcome_adjusted <- survival::clogit(sixMonthSurvive ~ treated + strata(matches), data=lindner_cl

summary(binary_outcome_adjusted)
```

```
Call:
coxph(formula = Surv(rep(1, 596L), sixMonthSurvive) ~ treated +
    strata(matches), data = lindner_clean.matchedsample, method = "exact")

  n= 596, number of events= 578

          coef exp(coef) se(coef)     z Pr(>|z|)
treated 1.6094    5.0000   0.6325 2.545   0.0109 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

        exp(coef) exp(-coef) lower .95 upper .95
treated         5        0.2     1.448     17.27

Concordance= 0.833  (se = 0.124 )
Likelihood ratio test= 8.73  on 1 df,   p=0.003
Wald test            = 6.48  on 1 df,   p=0.01
Score (logrank) test = 8  on 1 df,   p=0.005
```

```
#Tidy model
tidy_binary_outcome_adjusted <- tidy(binary_outcome_adjusted, exponentiate = TRUE, conf.int = 0.95)
```

The odds of being alive after six months were 5 times higher in treated individuals than non-treated individuals (95%CI 1.45, 17.27)

10 Task 6 1:1 Matching With replacement

- As we saw in the 1:1 matching without replacement, 400 treated participants were excluded from the sample. This is a waste of data and we'll address this by again matching 1 treated participant to 1 control participant. However, this time we'll match with replacement, meaning each time a control participant is matched to a treated participant, the control participant will be placed back into the pool of possible patients a treated individual can be matched to. Thus, some control participants will be matched multiple times (not all control participants have to be matched to a treated participant). In the Lindner dataset 1:1 matching with replacement is a more reasonable choice.

```
X <- lindner_clean$linps ## matching on the linear propensity score
Tr <- as.logical(lindner_clean$treated)
match1 <- Match(Tr=Tr, X=X, M = 1, replace=TRUE, ties=FALSE) # notice replace =  TRUE
summary(match1)
```

```
Estimate...  0
SE.........  0
T-stat.....  NaN
p.val......  NA

Original number of observations..............  996
Original number of treated obs...............  698
Matched number of observations...............  698
Matched number of observations  (unweighted).  698
```

As you can see, this time we matched 698 treated individuals with 698 control participants. To reiterate, as we matched with replacement, and there were less control participants than treated participants, some control participants were matched multiple times.

Below we'll assess the match balance from the 1:1 matching with replacement.

```
set.seed(202102)
mb1 <- MatchBalance(treated ~ stent + height + female + diabetic + acutemi + ejecfrac + ves1proc + ps +
match.out = match1, nboots=500)
```

```
***** (V1) stent *****
                       Before Matching        After Matching
mean treatment........     0.70487            0.70487
mean control..........     0.58389            0.72779
std mean diff.........      26.505            -5.0222

mean raw eQQ diff.....     0.12081           0.022923
med  raw eQQ diff.....           0                  0
max  raw eQQ diff.....           1                  1

mean eCDF diff........    0.060489           0.011461
med  eCDF diff........    0.060489           0.011461
max  eCDF diff........     0.12098           0.022923

var ratio (Tr/Co).....     0.85457             1.0501
T-test p-value........ 0.00032255            0.23555


***** (V2) height *****
                       Before Matching        After Matching
mean treatment........      171.44             171.44
mean control..........     171.45            171.62
std mean diff.........  -0.033804           -1.6209

mean raw eQQ diff.....    0.56376           0.83811
med  raw eQQ diff.....          0                 0
max  raw eQQ diff.....         20                22

mean eCDF diff........  0.0078996          0.010261
med  eCDF diff........  0.0060095          0.008596
max  eCDF diff........   0.024971          0.038682

var ratio (Tr/Co).....     1.0201           0.80936
T-test p-value........    0.99608            0.7661
KS Bootstrap p-value..      0.968             0.396
KS Naive p-value......    0.99947           0.67329
KS Statistic..........   0.024971          0.038682


***** (V3) female *****
                       Before Matching       After Matching
mean treatment........    0.33095           0.33095
mean control..........    0.38591           0.29943
std mean diff.........    -11.672            6.6934

mean raw eQQ diff.....   0.053691          0.031519
med  raw eQQ diff.....          0                 0
max  raw eQQ diff.....          1                 1

mean eCDF diff........    0.02748          0.015759
med  eCDF diff........    0.02748          0.015759
max  eCDF diff........    0.05496          0.031519

var ratio (Tr/Co).....    0.93253            1.0555
T-test p-value........    0.10045            0.1537


***** (V4) diabetic *****
                       Before Matching       After Matching
mean treatment........    0.20487           0.20487
mean control..........    0.26846           0.22923
std mean diff.........    -15.743           -6.0301

mean raw eQQ diff.....   0.063758          0.024355
med  raw eQQ diff.....          0                 0
max  raw eQQ diff.....          1                 1

mean eCDF diff........   0.031793          0.012178
med  eCDF diff........   0.031793          0.012178
max  eCDF diff........   0.063585          0.024355

var ratio (Tr/Co).....    0.82788           0.92199
T-test p-value........    0.03402           0.21126
```

```
***** (V5) acutemi *****
                       Before Matching       After Matching
mean treatment........    0.17908          0.17908
mean control..........  0.060403           0.16762
std mean diff.........    30.931            2.9871

mean raw eQQ diff.....    0.11745         0.011461
med  raw eQQ diff.....          0                0
max  raw eQQ diff.....          1                1

mean eCDF diff........    0.05934        0.0057307
med  eCDF diff........    0.05934        0.0057307
max  eCDF diff........    0.11868         0.011461

var ratio (Tr/Co).....     2.5853           1.0537
T-test p-value........ 4.6617e-09          0.44149


***** (V6) ejecfrac *****
                       Before Matching       After Matching
mean treatment........     50.403           50.403
mean control..........     52.289           50.812
std mean diff.........    -18.102          -3.9327

mean raw eQQ diff.....     2.0503          0.80516
med  raw eQQ diff.....          1                0
max  raw eQQ diff.....         20               20

mean eCDF diff........   0.035602         0.012247
med  eCDF diff........   0.011423         0.008596
max  eCDF diff........    0.11383          0.06447

var ratio (Tr/Co).....     1.0238           1.1088
T-test p-value........  0.0085806          0.43271
KS Bootstrap p-value..      0.004            0.044
KS Naive p-value......  0.0089219           0.1099
KS Statistic..........    0.11383          0.06447


***** (V7) ves1proc *****
                       Before Matching       After Matching
mean treatment........     1.4628           1.4628
mean control..........     1.2047           1.4642
std mean diff.........     36.545         -0.20289

mean raw eQQ diff.....     0.2651         0.044413
med  raw eQQ diff.....          0                0
max  raw eQQ diff.....          1                1

mean eCDF diff........   0.043323        0.0074021
med  eCDF diff........  0.0090671         0.004298
max  eCDF diff........    0.18842         0.018625

var ratio (Tr/Co).....     2.1614           1.0942
```

```
T-test p-value........   4.21e-11          0.95523
KS Bootstrap p-value.. < 2.22e-16            0.594
KS Naive p-value...... 7.2635e-07          0.99973
KS Statistic..........    0.18842         0.018625


***** (V8) ps *****
                       Before Matching       After Matching
mean treatment........     0.7265            0.7265
mean control..........    0.64061            0.7262
std mean diff.........     66.092           0.23256

mean raw eQQ diff.....   0.085216         0.0014016
med  raw eQQ diff.....   0.081353        0.00063595
max  raw eQQ diff.....    0.12087          0.021689

mean eCDF diff........    0.17141         0.0031873
med  eCDF diff........    0.17768         0.0014327
max  eCDF diff........    0.27599          0.024355

var ratio (Tr/Co).....     1.1161            1.0083
T-test p-value........ < 2.22e-16         0.0032848
KS Bootstrap p-value.. < 2.22e-16            0.978
KS Naive p-value......  3.042e-14          0.98578
KS Statistic..........    0.27599          0.024355


***** (V9) linps *****
                       Before Matching       After Matching
mean treatment........     1.1148            1.1148
mean control..........    0.63332             1.108
std mean diff.........     60.484             0.859

mean raw eQQ diff.....     0.4787          0.016276
med  raw eQQ diff.....    0.35992         0.0028864
max  raw eQQ diff.....     1.0113           0.75735

mean eCDF diff........    0.17141         0.0031873
med  eCDF diff........    0.17768         0.0014327
max  eCDF diff........    0.27599          0.024355

var ratio (Tr/Co).....      1.672            1.0466
T-test p-value........ < 2.22e-16         0.0016161
KS Bootstrap p-value.. < 2.22e-16            0.978
KS Naive p-value......  3.042e-14          0.98578
KS Statistic..........    0.27599          0.024355


Before Matching Minimum p.value: < 2.22e-16
Variable Name(s): ves1proc ps linps  Number(s): 7 8 9

After Matching Minimum p.value: 0.0016161
Variable Name(s): linps  Number(s): 9
```

```
covnames <- c("stent", "height", "female", "diabetic", "acutemi", "ejecfrac", "ves1proc", "ps", "linps"
```

Dr. Love's code to extract the standardized differences.

```
pre.szd <- NULL; post.szd <- NULL
for(i in 1:length(covnames)) {
pre.szd[i] <- mb1$BeforeMatching[[i]]$sdiff.pooled
post.szd[i] <- mb1$AfterMatching[[i]]$sdiff.pooled
}
```

Table of standardized differences

```
match_szd <- data.frame(covnames, pre.szd, post.szd, row.names=covnames)
print(match_szd, digits=3)
```

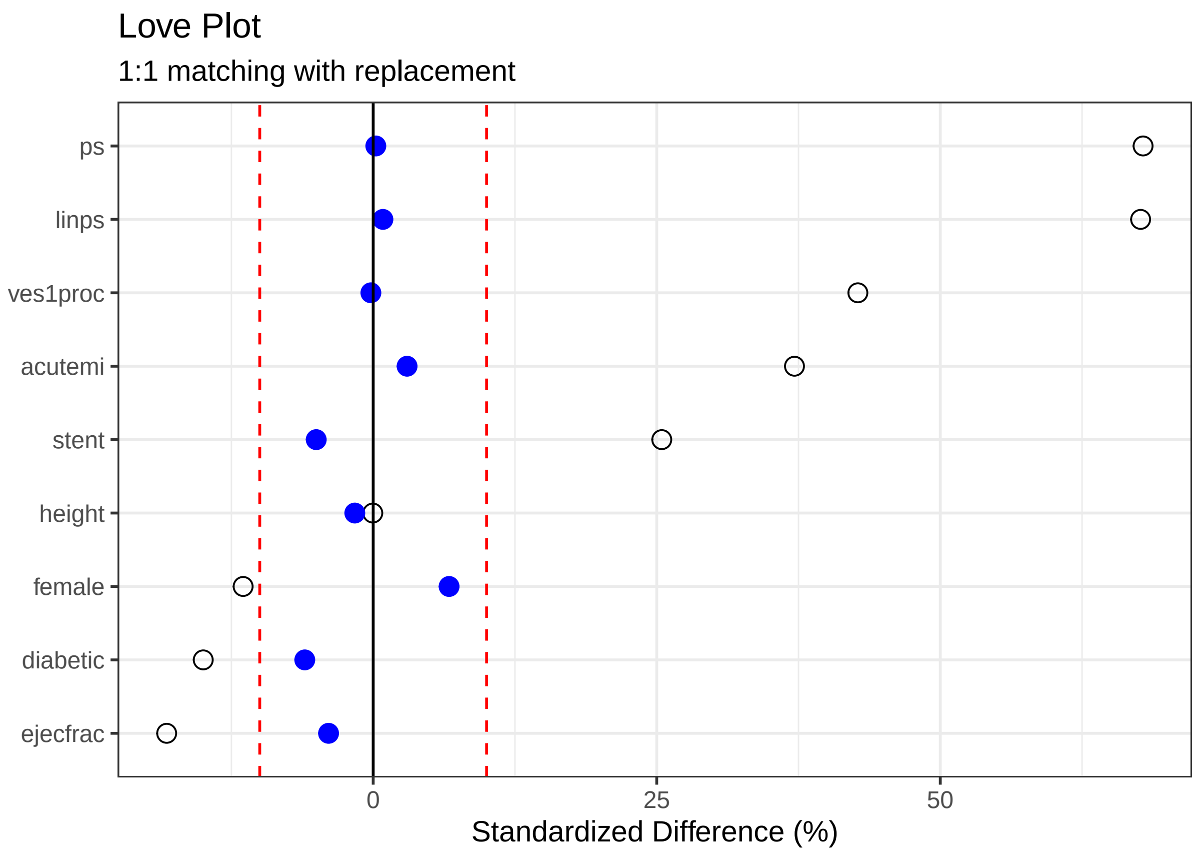
```
         covnames pre.szd post.szd
stent       stent  25.445   -5.022
height     height  -0.034   -1.621
female     female -11.466    6.693
diabetic diabetic -14.983   -6.030
acutemi   acutemi  37.145    2.987
ejecfrac ejecfrac -18.208   -3.933
ves1proc ves1proc  42.734   -0.203
ps             ps  67.880    0.233
linps       linps  67.664    0.859
```

10.1 Love Plot of standardized differences before and after 1:1 matching

10.2 Using ggplot

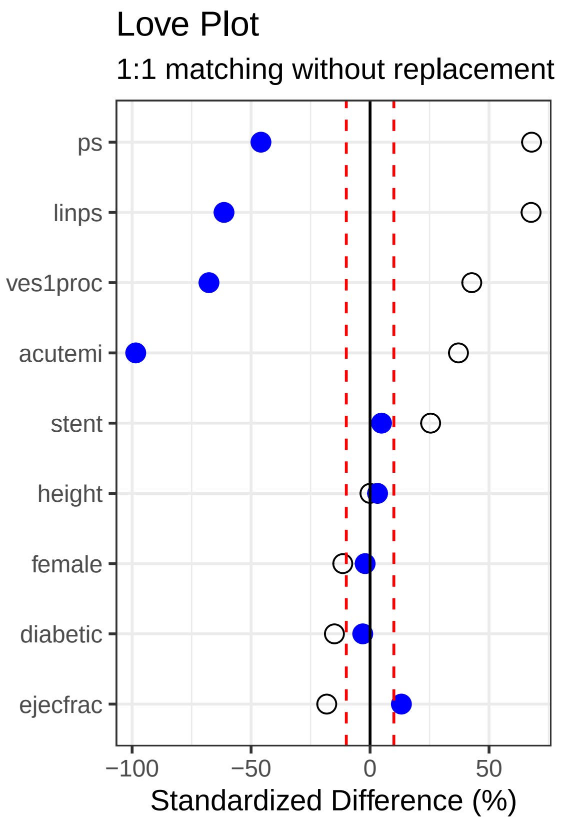
In this figure, blue points are post-matching while white are pre-match.

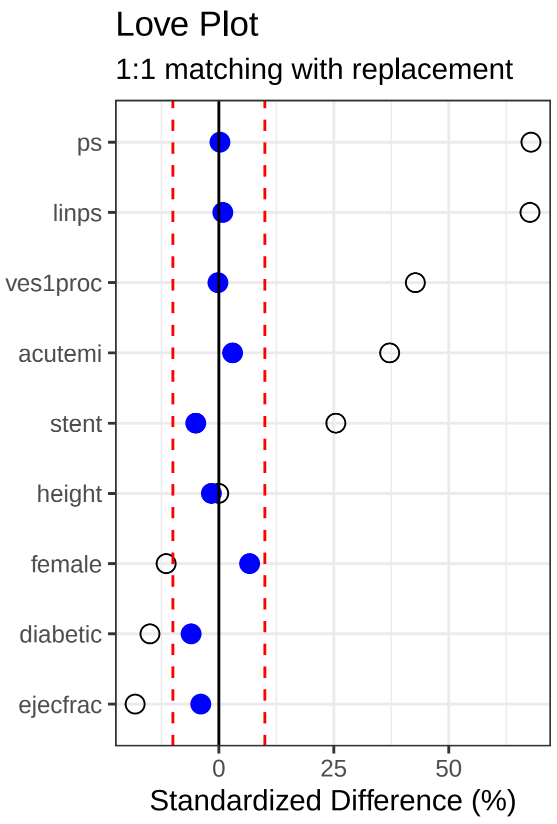
```
lp_w_rep <- ggplot(match_szd, aes(x = pre.szd, y = reorder(covnames, pre.szd))) +
  geom_point(col = "black", size = 3, pch = 1) +
  geom_point(aes(x = post.szd, y = reorder(covnames, pre.szd)), size = 3, col = "blue") +
  theme_bw() +
  geom_vline(aes(xintercept = 0)) +
  geom_vline(aes(xintercept = 10), linetype = "dashed", col = "red") +
  geom_vline(aes(xintercept = -10), linetype = "dashed", col = "red") +
  labs(x = "Standardized Difference (%)",
     y = "",
     title = "Love Plot",
     subtitle = "1:1 matching with replacement")

lp_w_rep
```



- Visually, the Love Plot using 1:1 matching with replacement looks pretty good.

```
# comparison of love plots with and without replacement
lp_wo_rep +  lp_w_rep
```





When we look at the plots without replacement and with replacement side-by-side, it definitely looks better than the 1:1 matching without replacement.

10.3 Using `cobalt` to make the Love Plot

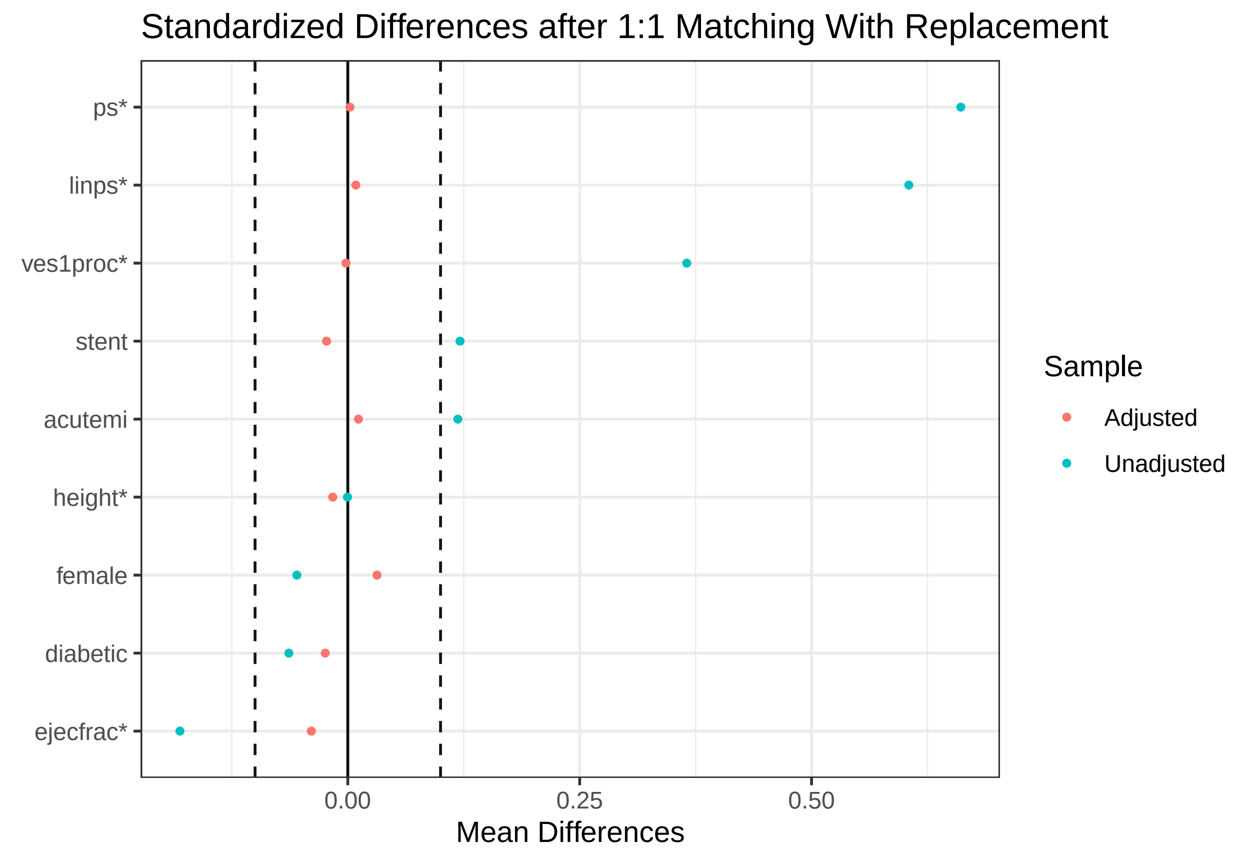
Again, we can also use an automated way to make the Love Plot.

```
cobalt_tab <- bal.tab(match1, treated ~ stent + height + female + diabetic + acutemi + ejecfrac + ves1p

cobalt_tab
```

```
Balance Measures
             Type Diff.Un Diff.Adj
stent      Binary  0.1210  -0.0229
height    Contin. -0.0003  -0.0162
female     Binary -0.0550   0.0315
diabetic   Binary -0.0636  -0.0244
acutemi    Binary  0.1187   0.0115
ejecfrac  Contin. -0.1810  -0.0393
ves1proc  Contin.  0.3654  -0.0020
ps        Contin.  0.6609   0.0023
linps     Contin.  0.6048   0.0086

Sample sizes
                     Control Treated
All                   298.       698
```

```
Matched (ESS)          112.16     698
Matched (Unweighted)  229.       698
Unmatched               69.         0
```

```
p <- love.plot(cobalt_tab, threshold = .1, size = 1.5,
               var.order = "unadjusted",
               title = "Standardized Differences after 1:1 Matching With Replacement",
               stars = "std")

p + theme_bw()
```



10.4 Extracting Variance Ratios

```
pre.vratio <- NULL; post.vratio <- NULL
for(i in 1:length(covnames)) {
pre.vratio[i] <- mb1$BeforeMatching[[i]]$var.ratio
post.vratio[i] <- mb1$AfterMatching[[i]]$var.ratio
}
## Table of Variance Ratios
match_vrat <- data.frame(names = covnames, pre.vratio, post.vratio, row.names=covnames)
print(match_vrat, digits=2)
```

```
            names pre.vratio post.vratio
stent       stent       0.85        1.05
height     height       1.02        0.81
```

```
female     female       0.93        1.06
diabetic diabetic       0.83        0.92
acutemi   acutemi       2.59        1.05
ejecfrac ejecfrac       1.02        1.11
ves1proc ves1proc       2.16        1.09
ps             ps       1.12        1.01
linps       linps       1.67        1.05
```

10.5 Creating a dataframe containing the matched sample

```
matches <- factor(rep(match1$index.treated, 2))
lindner_clean.matchedsample <- cbind(matches, lindner_clean[c(match1$index.control, match1$index.treate

lindner_clean.matchedsample %>% count(treated_f)
```

```
  treated_f   n
1   treated 698
2   control 698
```

10.6 Reassessing Rubin's Rules after 1:1 matching with replacement

10.6.1 Rubin's Rule 1

```
rubin1.match.rep <- with(lindner_clean.matchedsample,
abs(100*(mean(linps[treated==1])-mean(linps[treated==0]))/sd(linps)))
rubin1.match.rep
```

```
[1] 0.8690187
```

The new value for Rubin's Rule 1 is 0.87. This value passes Rubin's Rule 1 and is an improvement from the Rubin's Rule 1 value obtained during 1:1 matching without replacement, 38.55. The pre-match value was 61.87.

10.6.2 Rubin's Rule 2

```
rubin2.match.rep <- with(lindner_clean.matchedsample, var(linps[treated==1])/var(linps[treated==0]))
rubin2.match.rep
```

```
[1] 1.046553
```

The new value for Rubin's Rule 2 is 1.05. This passes Rule 2 and is an improvement from the Rubin's Rule 2 value obtained during 1:1 matching without replacement, 0.26. The pre-match value was 1.67.

10.7 Estimating the causal effect of the treatment on both outcomes after 1:1 matching with replacement

10.7.1 The Quantitative Outcome

Again, we'll use a mixed model to estimate the effect of the treatment on `cardbill`. The matches will be treated as a random effect in the model (syntax "(1| matches.f)". and the treatment group will be treated as a fixed effect. We will use restricted maximum likelihood (REML) to estimate coefficient values.

```
#to appease lme4, factor the matches
lindner_clean.matchedsample$matches.f <- as.factor(lindner_clean.matchedsample$matches)

# fit the mixed model
matched_mixedmodel.rep.out1 <- lmer(cardbill ~ treated + (1 | matches.f), REML = TRUE, data=lindner_clea

summary(matched_mixedmodel.rep.out1)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: cardbill ~ treated + (1 | matches.f)
   Data: lindner_clean.matchedsample

REML criterion at convergence: 30148

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.1569 -0.4789 -0.2828  0.1116 13.2194

Random effects:
 Groups    Name        Variance  Std.Dev.
 matches.f (Intercept)   7604218  2758
 Residual              135785615 11653
Number of obs: 1396, groups:  matches.f, 698

Fixed effects:
            Estimate Std. Error t value
(Intercept)  16337.4      453.2  36.046
treated       -210.7      623.8  -0.338

Correlation of Fixed Effects:
        (Intr)
treated -0.688
```

```
confint(matched_mixedmodel.rep.out1)
```

```
Computing profile confidence intervals ...

                2.5 %    97.5 %
.sig01          0.000  4287.944
.sigma      11059.236 12282.671
(Intercept) 15449.068 17225.702
treated     -1434.047  1012.643
```

```
tidy_mixed_matched_rep <- broom.mixed::tidy(matched_mixedmodel.rep.out1, conf.int = TRUE, conf.level = 
  filter(term == "treated")

tidy_mixed_matched_rep
```

```
# A tibble: 1 x 8
  effect group term    estimate std.error statistic conf.low conf.high
  <chr>  <chr> <chr>      <dbl>     <dbl>     <dbl>    <dbl>     <dbl>
1 fixed  <NA>  treated    -211.      624.    -0.338   -1433.     1012.
```

Treated individuals were estimated to spend $-210.7 less (95%CI -1433.24, 1011.84) than non-treated individuals. This finding is not significant at an α of 0.05, thus, the sensitivity analysis on the Quantitative outcome will still not make sense.

```
#sanity check for model
lindner_clean.matchedsample %>% group_by(treated_f) %>% summarise(mean_card = mean(cardbill))
```

```
# A tibble: 2 x 2
  treated_f mean_card
* <fct>         <dbl>
1 treated      16127.
2 control      16337.
```

- The mixed model above predicted treated individuals would spend roughly $-210.7 less than control participants. After doing a quick check of the mean `cardbill` within the matched sample, the mixed model results make sense.

10.7.2 The Binary Outcome

We will use conditional logistic regression to estimate the log odds (and ORs) of being alive after 6 months based on treatment status.

```
binary_outcome_adjusted_rep <- survival::clogit(sixMonthSurvive ~ treated + strata(matches), data=lindn

summary(binary_outcome_adjusted_rep)
```

```
Call:
coxph(formula = Surv(rep(1, 1396L), sixMonthSurvive) ~ treated +
    strata(matches), data = lindner_clean.matchedsample, method = "exact")

  n= 1396, number of events= 1321

          coef exp(coef) se(coef)     z Pr(>|z|)
treated 1.8405    6.3000   0.3404 5.407 6.41e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

        exp(coef) exp(-coef) lower .95 upper .95
treated       6.3     0.1587     3.233     12.28

Concordance= 0.863  (se = 0.057 )
Likelihood ratio test= 42.88  on 1 df,   p=6e-11
Wald test            = 29.24  on 1 df,   p=6e-08
Score (logrank) test = 38.48  on 1 df,   p=6e-10
```

```
#Tidy model
tidy_binary_outcome_adjusted_rep <- tidy(binary_outcome_adjusted_rep, exponentiate = TRUE, conf.int = 0

tidy_binary_outcome_adjusted_rep
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic      p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>        <dbl>    <dbl>     <dbl>
1 treated     6.30     0.340      5.41 0.0000000641     3.23      12.3
```

The odds of being alive after six months were 6.3 times higher in treated individuals than non-treated controls (95%CI 3.23, 12.28)

11 Task 7: Subclassification by Propensity Score Quintile

```
#cut into quintiles
lindner_clean$stratum <- Hmisc::cut2(lindner_clean$ps, g=5)
lindner_clean$quintile <- factor(lindner_clean$stratum, labels=1:5)

#Sanity check: check to make sure quntiles are evenish, numbers make sense, etc.
lindner_clean %>% count(stratum, quintile)
```

```
        stratum quintile   n
1 [0.232,0.581)        1 200
2 [0.581,0.669)        2 199
3 [0.669,0.726)        3 200
4 [0.726,0.826)        4 199
5 [0.826,0.980]        5 198
```

11.1 Check Balance and Propensity Score Overlap in Each Quintile

11.1.1 Numerically

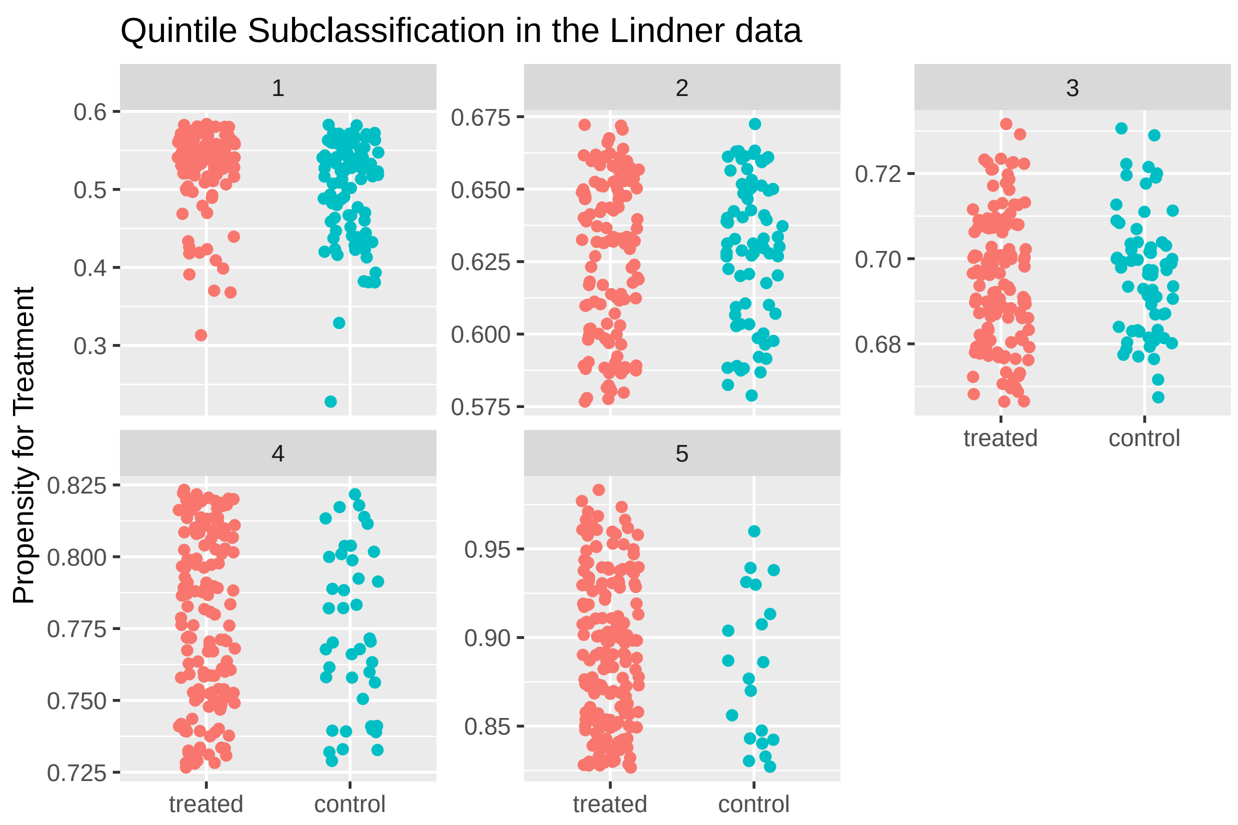
Only 20 controls were were in the largest quintile, which seems a bit low.

```
lindner_clean %>% count(quintile, treated_f)
```

```
   quintile treated_f   n
1         1   treated 105
2         1   control  95
3         2   treated 124
4         2   control  75
5         3   treated 135
6         3   control  65
7         4   treated 156
8         4   control  43
9         5   treated 178
10        5   control  20
```

11.1.2 Graphically

```
ggplot(lindner_clean, aes(x = treated_f, y = round(ps,2), group = quintile, color = treated_f)) +
geom_jitter(width = 0.2) +
guides(color = FALSE) +
facet_wrap(~ quintile, scales = "free_y") +
labs(x = "", y = "Propensity for Treatment",
title = "Quintile Subclassification in the Lindner data")
```



11.2 Creating a Standardized Difference Calculation Function

Here we implement Dr. Love's function to calculate the standardizes differences is utilized below.

```
szd <- function(covlist, g) {
covlist2 <- as.matrix(covlist)
g <- as.factor(g)
res <- NA
for(i in 1:ncol(covlist2)) {
cov <- as.numeric(covlist2[,i])
num <- 100*diff(tapply(cov, g, mean, na.rm=TRUE))
den <- sqrt(mean(tapply(cov, g, var, na.rm=TRUE)))
res[i] <- round(num/den,2)
}
names(res) <- names(covlist)
res
}
```

Now we'll split data into quintiles - and give them each their own dataframe.

```
quin1 <- filter(lindner_clean, quintile==1)
quin2 <- filter(lindner_clean, quintile==2)
quin3 <- filter(lindner_clean, quintile==3)
quin4 <- filter(lindner_clean, quintile==4)
quin5 <- filter(lindner_clean, quintile==5)
```

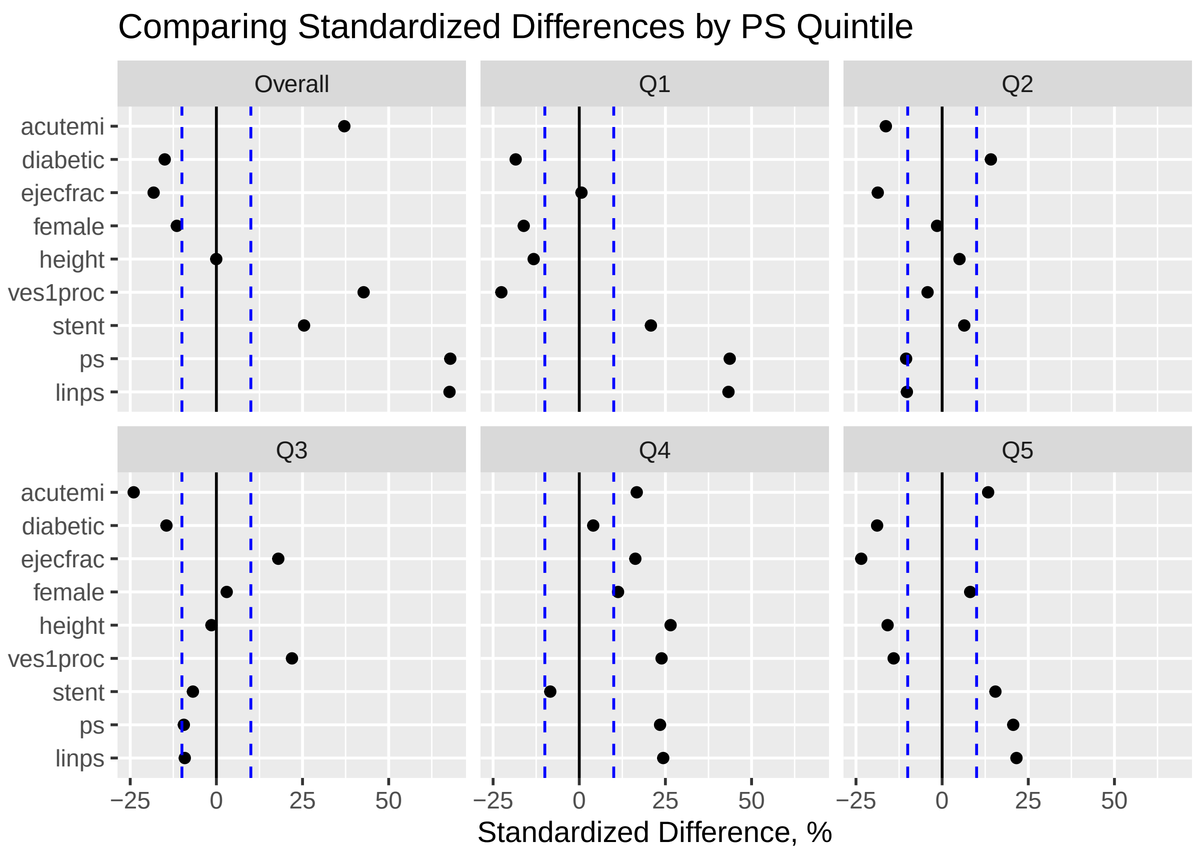
Now we'll run the function above to calculate the standardized differences for each covariate in each quintile.

```r
covs <- c("stent", "height", "female", "diabetic", "acutemi", "ejecfrac", "ves1proc", "ps", "linps")
d.q1 <- szd(quin1[covs], quin1$treated)
d.q2 <- szd(quin2[covs], quin2$treated)
d.q3 <- szd(quin3[covs], quin3$treated)
d.q4 <- szd(quin4[covs], quin4$treated)
d.q5 <- szd(quin5[covs], quin5$treated)
d.all <- szd(lindner_clean[covs], lindner_clean$treated)
lindner_clean.szd <- tibble(covs, Overall = d.all, Q1 = d.q1, Q2 = d.q2, Q3 = d.q3, Q4 = d.q4, Q5 = d.q5
lindner_clean.szd <- gather(lindner_clean.szd, "quint", "sz.diff", 2:7)
```

11.3 Plotting the post-subclassification standardized differences

```r
ggplot(lindner_clean.szd, aes(x = sz.diff, y = reorder(covs, -sz.diff), group = quint)) +
  geom_point() +
geom_vline(xintercept = 0) +
geom_vline(xintercept = c(-10,10), linetype = "dashed", col = "blue") +
facet_wrap(~ quint) +
labs(x = "Standardized Difference, %", y = "",
title = "Comparing Standardized Differences by PS Quintile")
```

```
Warning: Removed 1 rows containing missing values (geom_point).
```



The results of the standardized differences by quintile are fairly variable.

11.4 Rubin's Rules post subclassification

11.4.1 Rule 1

```
rubin1.q1 <- with(quin1, abs(100*(mean(linps[treated==1]) - mean(linps[treated==0]))/sd(linps)))

rubin1.q2 <- with(quin2, abs(100*(mean(linps[treated==1]) -mean(linps[treated==0]))/sd(linps)))

rubin1.q3 <- with(quin3, abs(100*(mean(linps[treated==1]) -mean(linps[treated==0]))/sd(linps)))

rubin1.q4 <- with(quin4, abs(100*(mean(linps[treated==1]) -mean(linps[treated==0]))/sd(linps)))

rubin1.q5 <- with(quin5, abs(100*(mean(linps[treated==1]) -mean(linps[treated==0]))/sd(linps)))

rubin1.sub <- c(rubin1.q1, rubin1.q2, rubin1.q3, rubin1.q4, rubin1.q5)
names(rubin1.sub)=c("Q1", "Q2", "Q3", "Q4", "Q5")

rubin1.sub
```

```
       Q1        Q2        Q3        Q4        Q5
42.633282 10.122973  9.054266 23.662028 20.717673
```

All are under 50. Not great, but OK. For comparison, the original Rubin's Rule 1 value was 61.87.

11.4.2 Rule 2

```
rubin2.q1 <- with(quin1, var(linps[treated==1])/var(linps[treated==0]))
rubin2.q2 <- with(quin2, var(linps[treated==1])/var(linps[treated==0]))
rubin2.q3 <- with(quin3, var(linps[treated==1])/var(linps[treated==0]))
rubin2.q4 <- with(quin4, var(linps[treated==1])/var(linps[treated==0]))
rubin2.q5 <- with(quin5, var(linps[treated==1])/var(linps[treated==0]))

rubin2.sub <- c(rubin2.q1, rubin2.q2, rubin2.q3, rubin2.q4, rubin2.q5)
names(rubin2.sub)=c("Q1", "Q2", "Q3", "Q4", "Q5")
rubin2.sub
```

```
       Q1        Q2        Q3        Q4        Q5
0.6582169 1.2083230 1.1754770 1.2154060 1.2353984
```

All but Q1 are at least close to passing Rule 2. For comparison, the original Rubin's Rule 2 value was 1.67.

12 Task 8: Estimated effect after subclassification

12.1 Quantitative outcome

```
quin1.out1 <- lm(cardbill ~ treated, data=quin1)
quin2.out1 <- lm(cardbill ~ treated, data=quin2)
quin3.out1 <- lm(cardbill ~ treated, data=quin3)
quin4.out1 <- lm(cardbill ~ treated, data=quin4)
quin5.out1 <- lm(cardbill ~ treated, data=quin5)

coef(summary(quin1.out1)); coef(summary(quin2.out1)); coef(summary(quin3.out1)); coef(summary(quin4.out
                Estimate Std. Error     t value     Pr(>|t|)
(Intercept) 14262.49474   1083.197 13.16704155 7.497113e-29
treated       -67.69474   1494.953 -0.04528217 9.639280e-01
```

```
              Estimate Std. Error  t value     Pr(>|t|)
(Intercept) 15038.427   1794.884 8.378497 1.000329e-14
treated      1412.154   2273.799 0.621055 5.352814e-01
```

```
              Estimate Std. Error  t value     Pr(>|t|)
(Intercept) 13259.415   1099.734 12.05693 1.846022e-25
treated      2837.814   1338.554  2.12006 3.524616e-02
```

```
             Estimate Std. Error  t value     Pr(>|t|)
(Intercept) 14474.19   1620.396 8.932501 2.966193e-16
treated      2979.16   1830.144 1.627828 1.051596e-01
```

```
              Estimate Std. Error   t value     Pr(>|t|)
(Intercept) 19398.350   1967.305  9.860368 7.011002e-19
treated     -3498.063   2074.886 -1.685906 9.340509e-02
```

The mean of the five quintile-specific estimated regression coefficients is below.

```
est.st <- (coef(quin1.out1)[2] + coef(quin2.out1)[2] + coef(quin3.out1)[2] +
coef(quin4.out1)[2] + coef(quin5.out1)[2])/5

est.st
```

```
treated
732.674
```

The mean SE is below.

```
se.q1 <- summary(quin1.out1)$coefficients[2,2]
se.q2 <- summary(quin2.out1)$coefficients[2,2]
se.q3 <- summary(quin3.out1)$coefficients[2,2]
se.q4 <- summary(quin4.out1)$coefficients[2,2]
se.q5 <- summary(quin5.out1)$coefficients[2,2]

se.st <- sqrt((se.q1^2 + se.q2^2 + se.q3^2 + se.q4^2 + se.q5^2)*(1/25))
se.st
```

```
[1] 821.008
```

The mean estimate, with a 95% CI, is below.

```
strat.result1 <- data_frame(estimate = est.st,
conf.low = est.st - 1.96*se.st,
conf.high = est.st + 1.96*se.st)
```

```
Warning: `data_frame()` is deprecated as of tibble 1.1.0.
Please use `tibble()` instead.
This warning is displayed once every 8 hours.
Call `lifecycle::last_warnings()` to see where this warning was generated.
```

```
strat.result1
```

```
# A tibble: 1 x 3
  estimate conf.low conf.high
     <dbl>    <dbl>     <dbl>
```

```
1     733.    -877.     2342.
```

So treated individuals were estimated to spend $732.67 more (95%CI -876.5, 2341.85) than non treated individuals.

12.2 Binary Outcome

```
quin1.out2 <- glm(sixMonthSurvive ~ treated, data=quin1, family=binomial())
quin2.out2 <- glm(sixMonthSurvive ~ treated, data=quin2, family=binomial())
quin3.out2 <- glm(sixMonthSurvive ~ treated, data=quin3, family=binomial())
quin4.out2 <- glm(sixMonthSurvive ~ treated, data=quin4, family=binomial())
quin5.out2 <- glm(sixMonthSurvive ~ treated, data=quin5, family=binomial())

coef(summary(quin1.out2)); coef(summary(quin2.out2)); coef(summary(quin3.out2)); coef(summary(quin4.out
```

```
            Estimate Std. Error  z value     Pr(>|z|)
(Intercept) 3.124565  0.5108708 6.116155 9.586018e-10
treated     1.519826  1.1272001 1.348319 1.775557e-01

            Estimate Std. Error  z value     Pr(>|z|)
(Intercept) 2.876386  0.5138915 5.597262 2.177636e-08
treated     1.935799  1.1278865 1.716306 8.610597e-02

            Estimate Std. Error  z value     Pr(>|z|)
(Intercept) 3.028522  0.5911534 5.123073 3.005960e-07
treated     1.869318  1.1648042 1.604834 1.085303e-01

            Estimate Std. Error   z value     Pr(>|z|)
(Intercept) 3.737670   1.011815 3.6940239 0.0002207331
treated     0.194156   1.167726 0.1662684 0.8679457146

            Estimate Std. Error  z value    Pr(>|z|)
(Intercept) 1.734601  0.6262243 2.769936 0.005606735
treated     1.809253  0.7732630 2.339764 0.019295953
```

Estimated log-odds (averaged over the quintiles).

```
est.st.log <- (coef(quin1.out2)[2] + coef(quin2.out2)[2] + coef(quin3.out2)[2] +
coef(quin4.out2)[2] + coef(quin5.out2)[2])/5

est.st.log
```

```
treated
1.46567
```

Estimated odds ratio (averaged over the quintiles).

```
exp(est.st.log)
```

```
 treated
4.330444
```

The average SE (averaged over the quintiles).

```
se.q1.log <- summary(quin1.out2)$coefficients[2,2]
se.q2.log <- summary(quin2.out2)$coefficients[2,2]
se.q3.log <- summary(quin3.out2)$coefficients[2,2]
se.q4.log <- summary(quin4.out2)$coefficients[2,2]
se.q5.log <- summary(quin5.out2)$coefficients[2,2]
se.st.log <- sqrt((se.q1.log^2 + se.q2.log^2 + se.q3.log^2 + se.q4.log^2 + se.q5.log^2)*(1/25))
se.st.log #log odds
```

```
[1] 0.4841899
```

```
strat.result2 <- data_frame(estimate = exp(est.st.log),
conf.low = exp(est.st.log - 1.96*se.st.log),
conf.high = exp(est.st.log + 1.96*se.st.log))

strat.result2
```

```
# A tibble: 1 x 3
  estimate conf.low conf.high
     <dbl>    <dbl>     <dbl>
1     4.33     1.68      11.2
```

The odds of being alive after 6 months was 4.33 (95%CI 1.68, 11.19) times higher in treated individuals than non-treated individuals.

13 Task 9: Weighting

13.1 Calculating the ATT and ATE weights

13.1.1 ATT weights

First, we can use tge average treatment effect on the treated (ATT) approach where we weight treated subjects as 1 and controls as ps/(1-ps)

```
lindner_clean$wts1 <- ifelse(lindner_clean$treated==1, 1, lindner_clean$ps/(1-lindner_clean$ps))
```

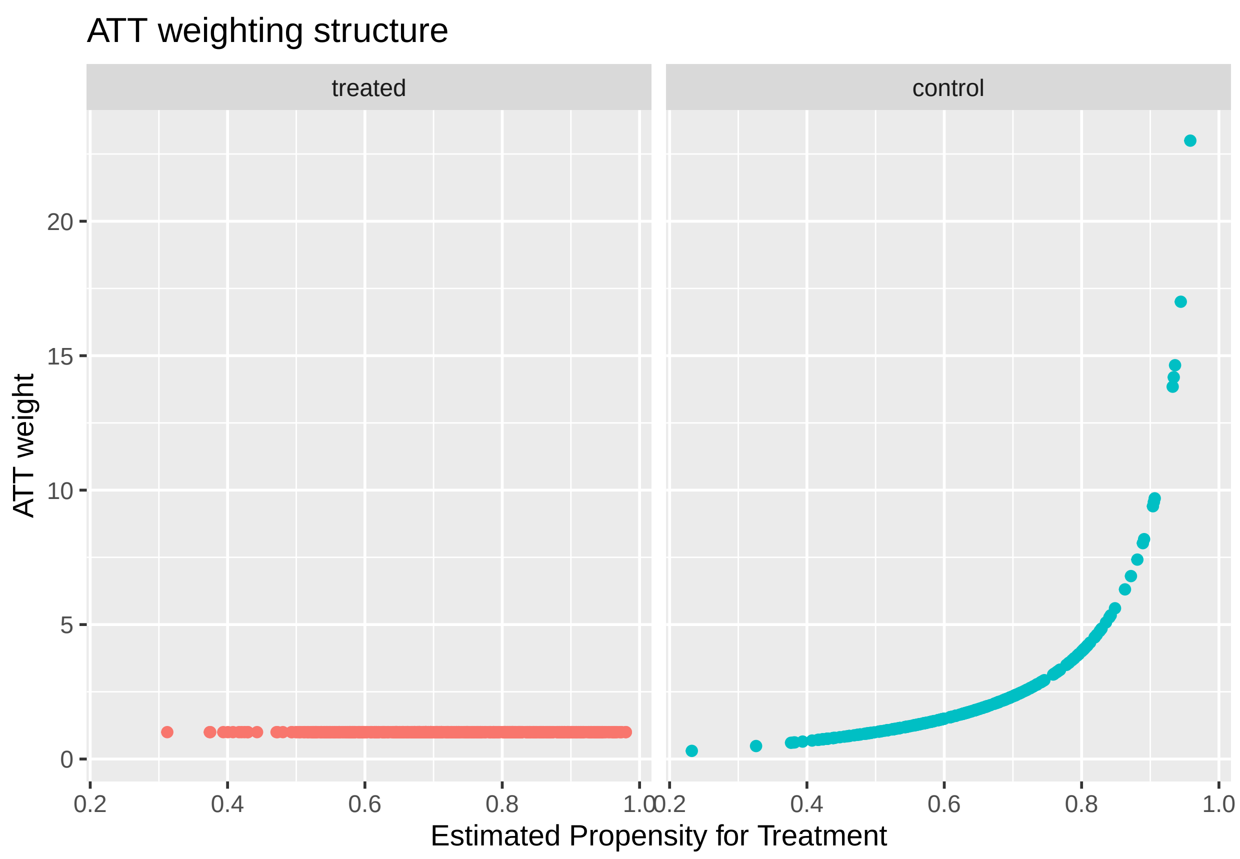
13.1.2 ATE weights

We can also use the average treatment effect (ATE) weights where we weight treated subjects by 1/ps and controls by 1/(1-PS)

```
lindner_clean$wts2 <- ifelse(lindner_clean$treated==1, 1/lindner_clean$ps, 1/(1-lindner_clean$ps))
```

13.2 Working with the ATT weights

```
ggplot(lindner_clean, aes(x = ps, y = wts1, color = treated_f)) +
geom_point() +
guides(color = FALSE) +
facet_wrap(~ treated_f) +
labs(x = "Estimated Propensity for Treatment",
y = "ATT weight",
title = "ATT weighting structure")
```



```r
#turn dataset into a dataframe for twang (its a tibble now)
lindner_clean_df <- data.frame(lindner_clean)

#name covariates
covlist <- c("stent", "height", "female", "diabetic", "acutemi", "ejecfrac", "ves1proc", "ps", "linps")
```

```r
bal.wts1 <- dx.wts(x=lindner_clean_df$wts1, data=lindner_clean_df, vars=covlist,
treat.var="treated", estimand="ATT")

bal.wts1
```

```
  type n.treat n.ctrl ess.treat ess.ctrl      max.es     mean.es      max.ks
1  unw     698    298       698 298.0000 0.66091743 0.29567509 0.27599469
2          698    298       698 149.4503 0.08471131 0.03315857 0.06089807
     mean.ks iter
1 0.13749095   NA
2 0.03182485   NA
```

```r
bal.table(bal.wts1)
```

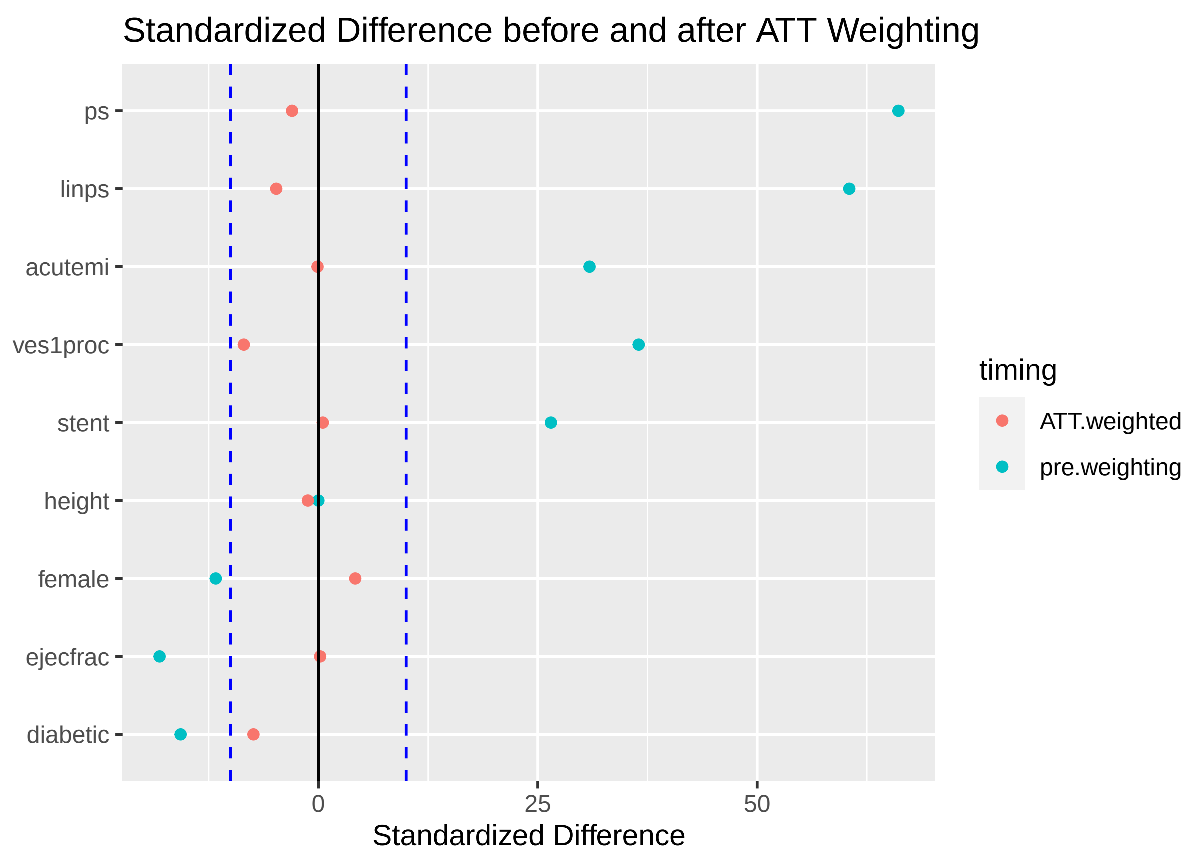
```
$unw
           tx.mn  tx.sd   ct.mn  ct.sd std.eff.sz   stat     p    ks ks.pval
stent      0.705  0.456   0.584  0.494      0.265  3.624 0.000 0.121   0.004
height   171.443 10.695 171.446 10.589      0.000 -0.005 0.996 0.025   0.999
female     0.331  0.471   0.386  0.488     -0.117 -1.647 0.100 0.055   0.531
diabetic   0.205  0.404   0.268  0.444     -0.157 -2.127 0.034 0.064   0.349
acutemi    0.179  0.384   0.060  0.239      0.309  5.923 0.000 0.119   0.005
ejecfrac  50.403 10.419  52.289 10.297     -0.181 -2.640 0.008 0.114   0.008
```

```
ves1proc     1.463  0.706   1.205  0.480       0.365  6.693 0.000 0.188   0.000
ps           0.727  0.130   0.641  0.123       0.661  9.928 0.000 0.276   0.000
linps        1.115  0.796   0.633  0.616       0.605 10.321 0.000 0.276   0.000

[[2]]
           tx.mn  tx.sd   ct.mn  ct.sd std.eff.sz   stat     p    ks ks.pval
stent      0.705  0.456   0.702  0.458      0.005  0.065 0.948 0.002   1.000
height   171.443 10.695 171.568 11.934     -0.012 -0.102 0.919 0.042   0.974
female     0.331  0.471   0.311  0.464      0.042  0.497 0.620 0.020   1.000
diabetic   0.205  0.404   0.235  0.425     -0.074 -0.716 0.474 0.030   1.000
acutemi    0.179  0.384   0.180  0.385     -0.001 -0.011 0.991 0.001   1.000
ejecfrac  50.403 10.419  50.384 10.358      0.002  0.019 0.985 0.032   0.999
ves1proc   1.463  0.706   1.523  0.749     -0.085 -0.647 0.518 0.038   0.990
ps         0.727  0.130   0.730  0.134     -0.030 -0.273 0.785 0.061   0.725
linps      1.115  0.796   1.153  0.839     -0.048 -0.360 0.719 0.061   0.725
```

```
bal.before.wts1 <- bal.table(bal.wts1)[1]
bal.after.wts1 <- bal.table(bal.wts1)[2]
balance.att.weights <- data_frame(names = rownames(bal.before.wts1$unw),
pre.weighting = 100*bal.before.wts1$unw$std.eff.sz,
ATT.weighted = 100*bal.after.wts1[[1]]$std.eff.sz)
balance.att.weights <- gather(balance.att.weights, timing, szd, 2:3)
```

Now we can plot the standardized differences after ATT weighting.

```
ggplot(balance.att.weights, aes(x = szd, y = reorder(names, szd), color = timing)) +
  geom_point() +
  geom_vline(xintercept = 0) +
  geom_vline(xintercept = c(-10,10), linetype = "dashed", col = "blue") +
  labs(x = "Standardized Difference",
       y = "",
       title = "Standardized Difference before and after ATT Weighting")
```



The standardized differences look much better here in this approach.

13.2.1 Rubin's Rules

13.2.1.1 Rule 1

Numbers from balance table above: (-0.048 * 100) = 4.8%. So passes Rule 1.

13.2.1.2 Rule 2

Numbers from balance table above:$(0.796^2)/(0.839^2) = 0.9001237$. Passes Rule 2

13.2.2 Estimated effect on outcomes after ATT weighting

13.2.2.1 Quantitative outcome

To estimate the effect of the treatment on `cardbill`, we'll use svyglm from the `survey` package to apply the ATT weights in a linear model.

```
lindnerwt1.design <- svydesign(ids=~1, weights=~wts1, data=lindner_clean) # using ATT weights

adjout1.wt1 <- svyglm(cardbill ~ treated, design=lindnerwt1.design)

wt_att_results1 <- tidy(adjout1.wt1, conf.int = TRUE) %>% filter(term == "treated")

wt_att_results1
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated    -239.     1417.    -0.169   0.866   -3017.     2538.
```

Estimate (95%CI) -239.28 (-3016.54, 2537.99)

13.2.2.2 Binary outcome

We'll do similar coding for the binary outcome.

```
adjout2.wt1 <- svyglm(sixMonthSurvive ~ treated, design=lindnerwt1.design, family=quasibinomial())

wt_att_results2 <- tidy(adjout2.wt1, conf.int = TRUE, exponentiate = TRUE) %>%
filter(term == "treated")
wt_att_results2
```

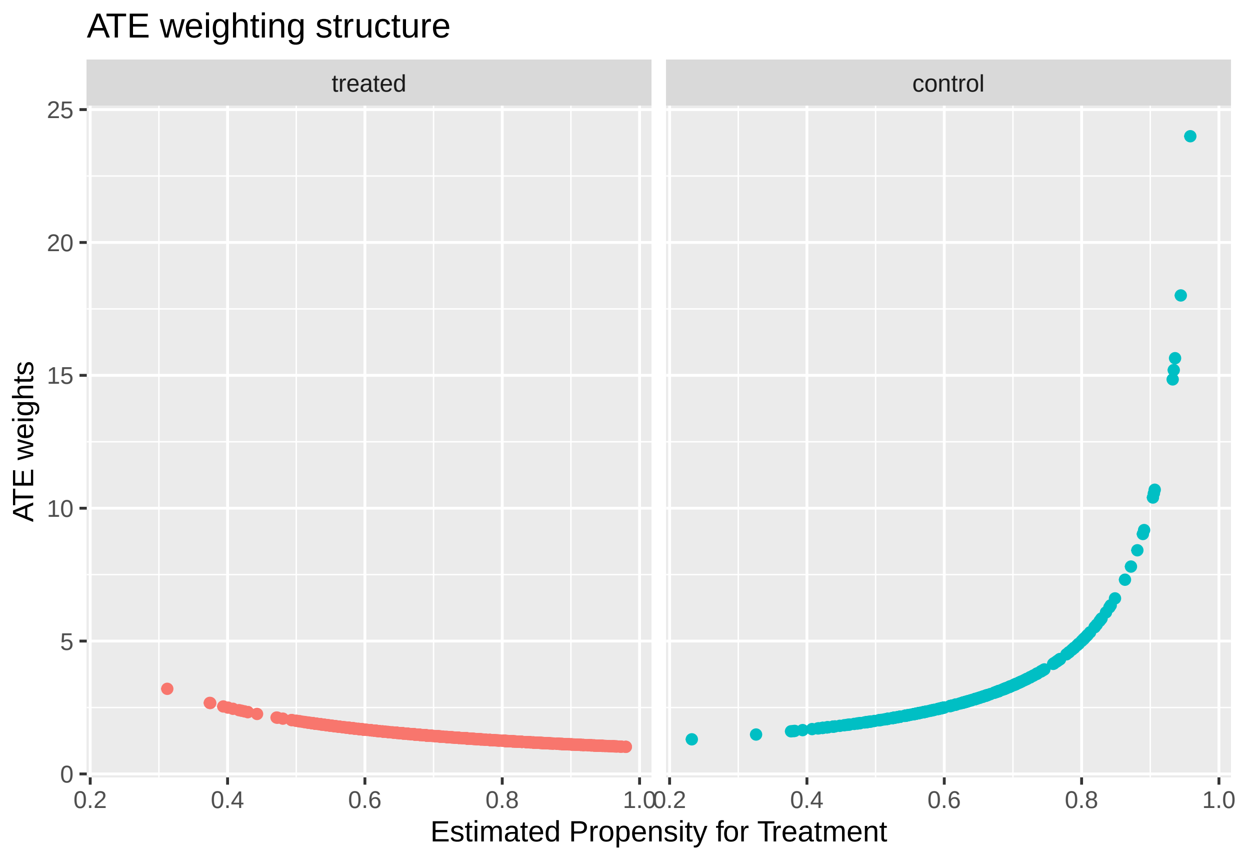
```
# A tibble: 1 x 7
  term    estimate std.error statistic  p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 treated     6.50     0.537      3.49 0.000509     2.27      18.6
```

Estimate (95%CI) 6.5 (2.27, 18.63)

13.3 Working with the ATE weights

Now, we'll go through the same steps with the ATE weights.

```
ggplot(lindner_clean, aes(x = ps, y = wts2, color = treated_f)) +
geom_point() +
guides(color = FALSE) +
facet_wrap(~ treated_f) +
labs(x = "Estimated Propensity for Treatment",
y = "ATE weights",
title = "ATE weighting structure")
```



```
bal.wts2 <- dx.wts(x=lindner_clean_df$wts2, data=lindner_clean_df, vars=covlist,
treat.var="treated", estimand="ATE")

bal.wts2
```

```
  type n.treat n.ctrl ess.treat ess.ctrl      max.es     mean.es      max.ks
1  unw     698    298   698.000 298.0000 0.64205075 0.29974928 0.27599469
2          698    298   671.093 199.6805 0.06759172 0.02390944 0.04595042
     mean.ks iter
1 0.13749095   NA
2 0.02622715   NA
```

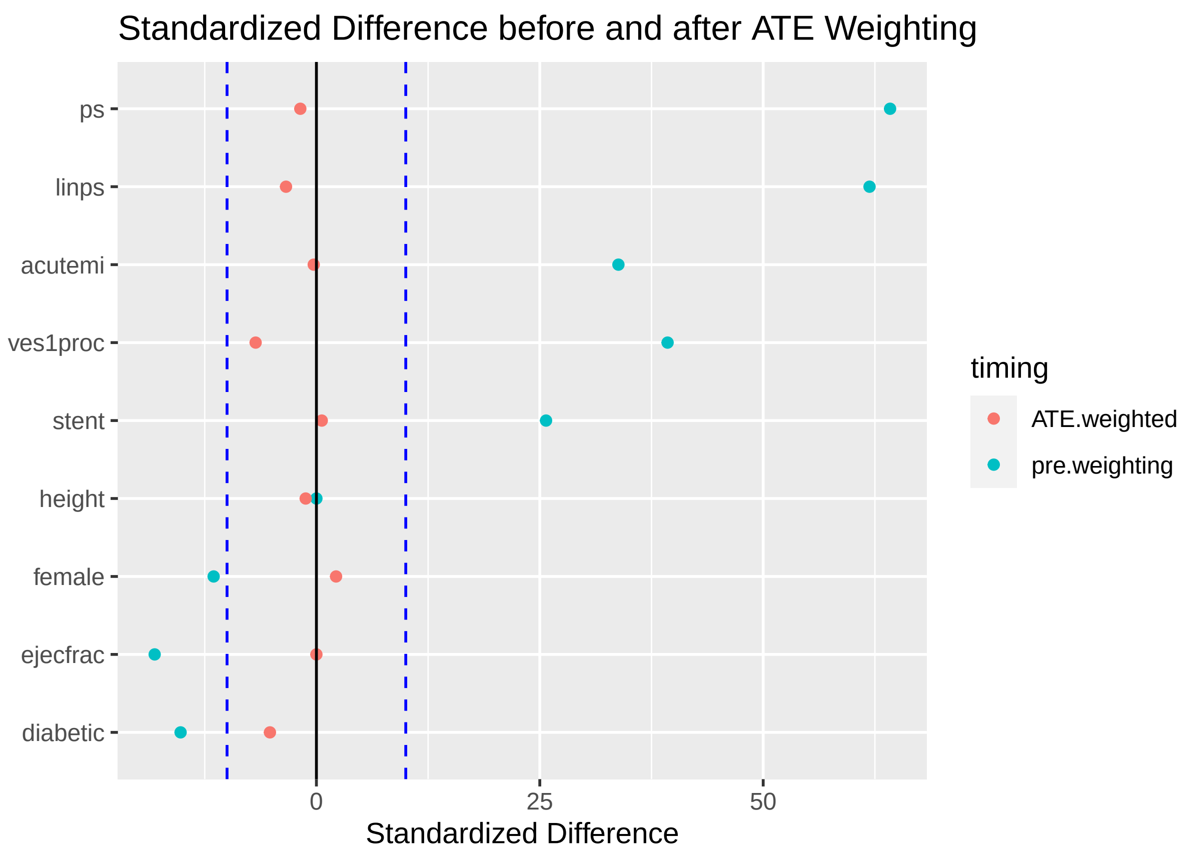
```
bal.table(bal.wts2)
```

```
$unw
           tx.mn  tx.sd   ct.mn  ct.sd std.eff.sz   stat     p    ks ks.pval
stent      0.705  0.456   0.584  0.494      0.257  3.624 0.000 0.121   0.004
height   171.443 10.695 171.446 10.589      0.000 -0.005 0.996 0.025   0.999
female     0.331  0.471   0.386  0.488     -0.115 -1.647 0.100 0.055   0.531
diabetic   0.205  0.404   0.268  0.444     -0.152 -2.127 0.034 0.064   0.349
acutemi    0.179  0.384   0.060  0.239      0.338  5.923 0.000 0.119   0.005
ejecfrac  50.403 10.419  52.289 10.297     -0.181 -2.640 0.008 0.114   0.008
ves1proc   1.463  0.706   1.205  0.480      0.393  6.693 0.000 0.188   0.000
ps         0.727  0.130   0.641  0.123      0.642  9.928 0.000 0.276   0.000
linps      1.115  0.796   0.633  0.616      0.619 10.321 0.000 0.276   0.000

[[2]]
```

```
           tx.mn  tx.sd   ct.mn  ct.sd std.eff.sz   stat     p    ks ks.pval
stent      0.670  0.470   0.667  0.472      0.006  0.081 0.936 0.003   1.000
height   171.404 10.602 171.532 11.552     -0.012 -0.124 0.902 0.038   0.974
female     0.344  0.475   0.333  0.472      0.022  0.283 0.777 0.010   1.000
diabetic   0.223  0.416   0.245  0.431     -0.052 -0.601 0.548 0.022   1.000
acutemi    0.143  0.351   0.144  0.352     -0.003 -0.026 0.979 0.001   1.000
ejecfrac  50.943 10.109  50.948 10.377      0.000 -0.006 0.995 0.042   0.934
ves1proc   1.384  0.663   1.428  0.696     -0.068 -0.586 0.558 0.028   0.999
ps         0.701  0.133   0.704  0.137     -0.018 -0.185 0.853 0.046   0.884
linps      0.973  0.774   0.999  0.815     -0.034 -0.292 0.771 0.046   0.884
```

```
bal.before.wts2 <- bal.table(bal.wts2)[1]
bal.after.wts2 <- bal.table(bal.wts2)[2]
balance.ate.weights <- data_frame(names = rownames(bal.before.wts2$unw),
pre.weighting = 100*bal.before.wts2$unw$std.eff.sz,

ATE.weighted = 100*bal.after.wts2[[1]]$std.eff.sz)
balance.ate.weights <- gather(balance.ate.weights, timing, szd, 2:3)
```

```
ggplot(balance.ate.weights, aes(x = szd, y = reorder(names, szd), color = timing)) +
geom_point() +
geom_vline(xintercept = 0) +
geom_vline(xintercept = c(-10,10), linetype = "dashed", col = "blue") +
labs(x = "Standardized Difference", y = "",
title = "Standardized Difference before and after ATE Weighting")
```



Again, the standardized differences look good here.

13.3.1 Rubin's Rules

13.3.1.1 Rule 1
-0.033*100 = 3.3%. Passes Rule 1 (numbers from ATE weight balance table above).

13.3.1.2 Rule 2
$(0.774^2)/(0.815^2) = 0.9019173$. Passes Rule 2 (numbers from ATE weight balance table above).

13.3.2 Estimated effect on outcomes after ATE weighting

```
lindnerwt2.design <- svydesign(ids=~1, weights=~wts2, data=lindner_clean) # using ATE weights

adjout1.wt2 <- svyglm(cardbill ~ treated, design=lindnerwt2.design)

wt_ate_results1 <- tidy(adjout1.wt2, conf.int = TRUE) %>% filter(term == "treated")
wt_ate_results1
```

13.3.2.1 Quantitative outcome

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated     147.      1192.     0.124   0.902   -2190.     2484.
```

- **Estimate** 147.26 (95% CI: -2189.63, 2484.15)

```
adjout2.wt2 <- svyglm(sixMonthSurvive ~ treated, design=lindnerwt2.design, family=quasibinomial())

wt_ate_results2 <- tidy(adjout2.wt2, conf.int = TRUE, exponentiate = TRUE) %>%
filter(term == "treated")
wt_ate_results2
```

13.3.2.2 Binary outcome

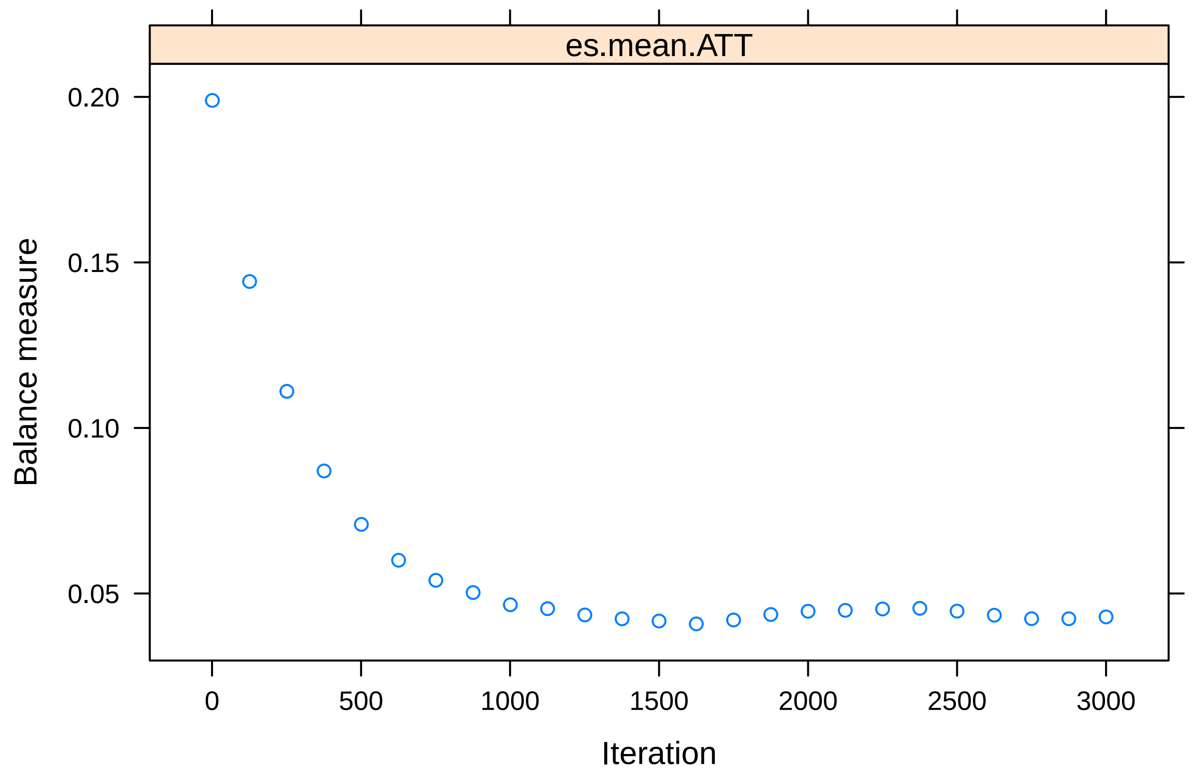
```
# A tibble: 1 x 7
  term    estimate std.error statistic  p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 treated     5.74     0.503      3.47 0.000538     2.14      15.4
```

- **Estimate** 5.74 (95% CI: 2.14, 15.38)

14 Task 10: Using TWANG for propensity score estimation and ATT weighting

```
ps.toy <- ps(treated ~ stent + height + female + diabetic + acutemi + ejecfrac + ves1proc,
data = lindner_clean_df,
n.trees = 3000,
interaction.depth = 2,
stop.method = c("es.mean"),
estimand = "ATT",
verbose = FALSE)
```

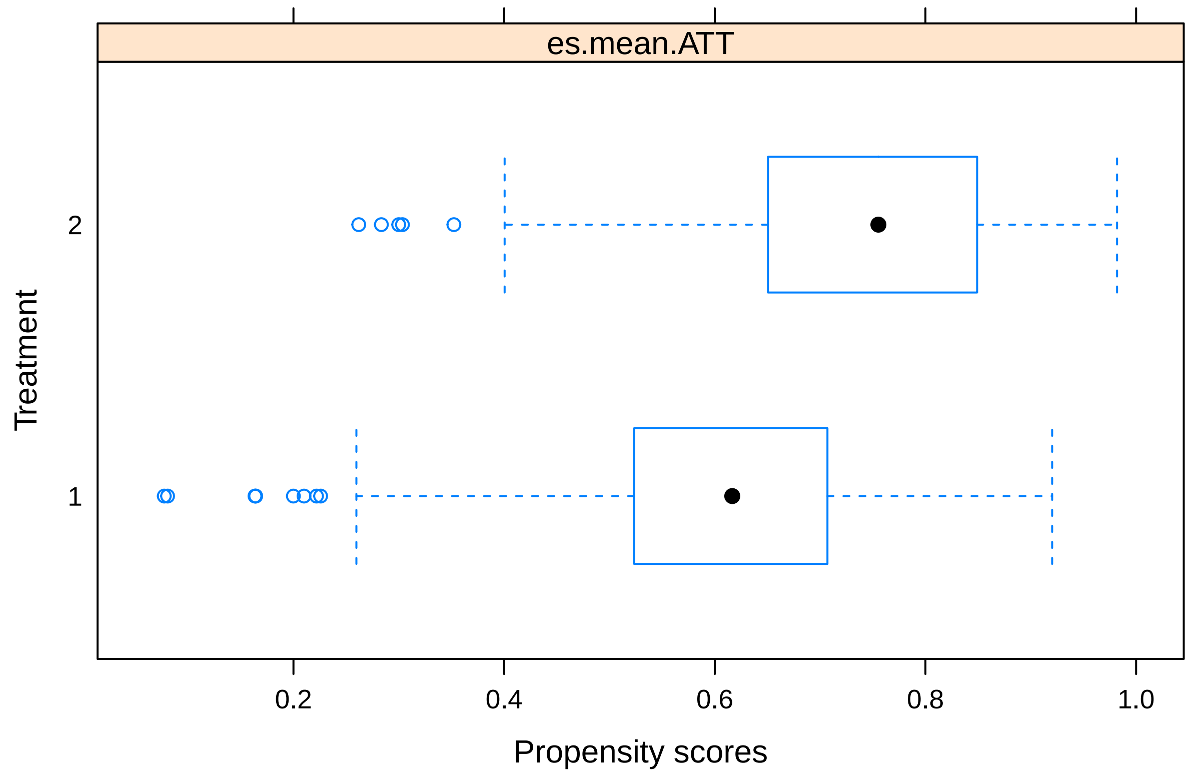
```
plot(ps.toy)
```



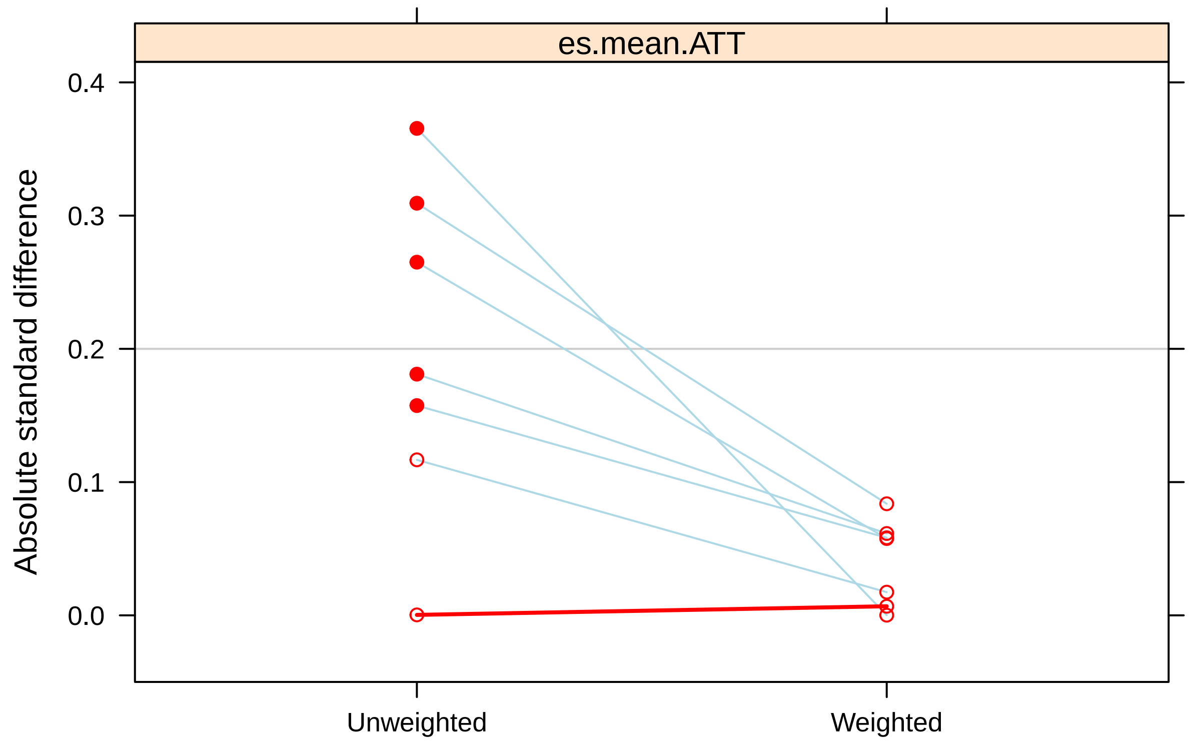
```
summary(ps.toy)
```

```
             n.treat n.ctrl ess.treat ess.ctrl     max.es    mean.es    max.ks
unw              698    298       698   298.00 0.36544982 0.19933096 0.1884195
es.mean.ATT      698    298       698   172.19 0.08373615 0.04075872 0.0388038
             max.ks.p    mean.ks iter
unw                NA 0.09791845   NA
es.mean.ATT        NA 0.02469335 1628
```

```
plot(ps.toy, plots = 2)
```



```r
plot(ps.toy, plots = 3)
```



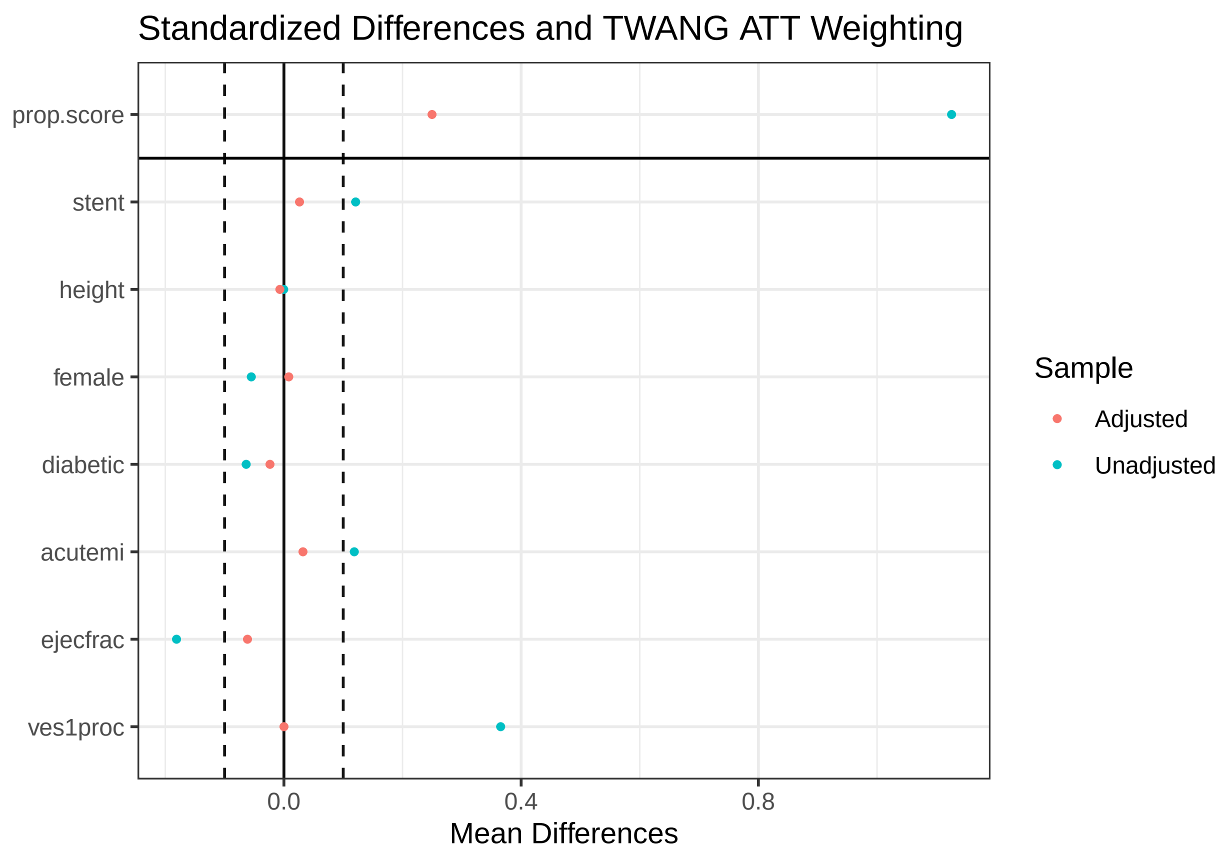
```
bal.tab(ps.toy, full.stop.method = "es.mean.att")
```

```
Call
 ps(formula = treated ~ stent + height + female + diabetic + acutemi +
    ejecfrac + ves1proc, data = lindner_clean_df, n.trees = 3000,
    interaction.depth = 2, verbose = FALSE, estimand = "ATT",
    stop.method = c("es.mean"))

Balance Measures
               Type Diff.Adj
prop.score Distance   0.2497
stent        Binary   0.0263
height      Contin.  -0.0068
female       Binary   0.0082
diabetic     Binary  -0.0235
acutemi      Binary   0.0321
ejecfrac    Contin.  -0.0614
ves1proc    Contin.   0.0001

Effective sample sizes
           Control Treated
Unadjusted  298.       698
Adjusted    172.19     698
```

```
p <- love.plot(bal.tab(ps.toy),
threshold = .1, size = 1.5,
title = "Standardized Differences and TWANG ATT Weighting")
```

```
Warning: Standardized mean differences and raw mean differences are present in the same plot.
Use the 'stars' argument to distinguish between them and appropriately label the x-axis.
```

```
p + theme_bw()
```



Compared to the manual ATT/ATE weights, the standardized differences look a bit worse here.

14.1 Estimated effect on outcomes after TWANG ATT weighting

14.1.1 Quantitative outcome

```
toywt3.design <- svydesign(ids=~1,
weights=~get.weights(ps.toy,
stop.method = "es.mean"),
data=lindner_clean) # using twang ATT weights

adjout1.wt3 <- svyglm(cardbill ~ treated, design=toywt3.design)
wt_twangatt_results1 <- tidy(adjout1.wt3, conf.int = TRUE) %>% filter(term == "treated")
wt_twangatt_results1
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated     501.     1102.     0.454   0.650   -1660.     2661.
```

- **Estimate** 500.51 (95% CI: -1660.15, 2661.17)

14.1.2 Binary outcome

```
adjout2.wt3 <- svyglm(sixMonthSurvive ~ treated, design=toywt3.design,
family=quasibinomial())

wt_twangatt_results2 <- tidy(adjout2.wt3, conf.int = TRUE, exponentiate = TRUE) %>%
filter(term == "treated")
wt_twangatt_results2
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated     4.02     0.487      2.86 0.00438     1.55      10.4
```

- **Estimate** 4.02 (95% CI: 1.55, 10.44)

15 Task 11: After direct adjustment with linear PS

Here we'll directly adjust for the linear propensity score by including it as a covariate in the model.

15.1 Quantitative outcome

```
direct_out1 <- lm(cardbill ~ treated + linps, data=lindner_clean)

adj_out1 <- tidy(direct_out1, conf.int = TRUE) %>% filter(term == "treated")
adj_out1
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated    1168.      805.      1.45   0.147    -412.     2748.
```

- **Estimate** 1167.9 (95% CI:-412.22, 2748.02)

15.2 Binary outcome

```
direct_out2 <- glm(sixMonthSurvive ~ treated + linps, data=lindner_clean, family=binomial())

adj_out2 <- tidy(direct_out2, exponentiate = TRUE, conf.int = TRUE) %>%
filter(term == "treated")
adj_out2
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic  p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 treated     4.64     0.438      3.50 0.000463     1.99      11.3
```

- **Estimate** 4.64 (95% CI: 1.99, 11.27)

16 Task 12: "Double Robust" Approach: Weighting + Direct Adjustment

Here we'll adjust for the linear propensity score and the ATT/ATE/TWANG weights when predicting the quantitative outcome.

16.1 Quantitative outcome

16.1.1 ATT weights

```r
design_att <- svydesign(ids=~1, weights=~wts1, data=lindner_clean) # using ATT weights

dr.out1.wt1 <- svyglm(cardbill ~ treated + linps, design=design_att)
dr_att_out1 <- tidy(dr.out1.wt1, conf.int = TRUE) %>% filter(term == "treated")
dr_att_out1
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated    -127.     1217.    -0.104   0.917   -2511.     2258.
```

- **Estimate** -126.72 (95% CI: -2511.33, 2257.89)

16.1.2 ATE weights

```r
design_ate<- svydesign(ids=~1, weights=~wts2, data=lindner_clean) # using ATE weights

dr.out1.wt2 <- svyglm(cardbill ~ treated + linps, design=design_ate)
dr_ate_out1 <- tidy(dr.out1.wt2, conf.int = TRUE) %>% filter(term == "treated")
dr_ate_out1
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated     217.     1069.     0.203   0.839   -1879.     2312.
```

- **Estimate** 216.77 (95% CI: -1878.59, 2312.13)

16.1.3 TWANG ATT weights

```r
wts3 <- get.weights(ps.toy, stop.method = "es.mean")
twang.design <- svydesign(ids=~1, weights=~wts3, data=lindner_clean) # twang ATT weights

dr.out1.wt3 <- svyglm(cardbill ~ treated + linps, design=twang.design)
dr_twangatt_out1 <- tidy(dr.out1.wt3, conf.int = TRUE) %>% filter(term == "treated")
dr_twangatt_out1
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated     375.     1103.     0.340   0.734   -1787.     2537.
```

- **Estimate** 375.05 (95% CI: -1787.05, 2537.16)

16.2 Binary outcome

Now we'll adjust for the linear propensity score and the ATT/ATE/TWANG weights when predicting the binary outcome.

16.2.1 ATT weights

```r
dr.out2.wt1 <- svyglm(sixMonthSurvive ~ treated + linps, design=design_att,
family=quasibinomial())

dr_att_out2 <- tidy(dr.out2.wt1, exponentiate = TRUE, conf.int = TRUE) %>%
filter(term == "treated")
dr_att_out2
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic  p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 treated     6.90     0.563      3.43 0.000634     2.29      20.8
```

- **Estimate** 6.9 (95% CI: 2.29, 20.81)

16.2.2 ATE weights

```r
dr.out2.wt2 <- svyglm(sixMonthSurvive ~ treated + linps, design=design_ate,
family=quasibinomial())

dr_ate_out2 <- tidy(dr.out2.wt2, exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term == "treated")

dr_ate_out2
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic  p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 treated     5.95     0.517      3.45 0.000590     2.16      16.4
```

- **Estimate** 5.95 (95% CI: 2.16, 16.39)

16.2.3 TWANG ATT weights

```r
dr.out2.wt3 <- svyglm(sixMonthSurvive ~ treated + linps, design=twang.design,
family=quasibinomial())

dr_twangatt_out2 <- tidy(dr.out2.wt3, exponentiate = TRUE, conf.int = TRUE) %>%
filter(term == "treated")
dr_twangatt_out2
```

```
# A tibble: 1 x 7
  term    estimate std.error statistic p.value conf.low conf.high
  <chr>      <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 treated     4.87     0.554      2.86 0.00436     1.64      14.4
```

- **Estimate** 4.87 (95% CI: 1.64, 14.44)

```
sessioninfo::session_info()
```

```
- Session info ---------------------------------------------------------------
 setting  value
 version  R version 4.0.3 (2020-10-10)
 os       Windows 10 x64
 system   x86_64, mingw32
 ui       RTerm
 language (EN)
 collate  English_United States.1252
 ctype    English_United States.1252
 tz       America/New_York
 date     2021-02-17

- Packages -------------------------------------------------------------------
 ! package      * version    date       lib source
   assertthat     0.2.1      2019-03-21 [1] CRAN (R 4.0.0)
   backports      1.2.1      2020-12-09 [1] CRAN (R 4.0.3)
   base64enc      0.1-3      2015-07-28 [1] CRAN (R 4.0.0)
   boot           1.3-26     2021-01-25 [1] CRAN (R 4.0.3)
   broom        * 0.7.3      2020-12-16 [1] CRAN (R 4.0.3)
   broom.mixed    0.2.6      2020-05-17 [1] CRAN (R 4.0.3)
   cellranger     1.1.0      2016-07-27 [1] CRAN (R 4.0.0)
   checkmate      2.0.0      2020-02-06 [1] CRAN (R 4.0.0)
   class          7.3-17     2020-04-26 [2] CRAN (R 4.0.3)
   cli            2.2.0      2020-11-20 [1] CRAN (R 4.0.3)
   cluster        2.1.0      2019-06-19 [2] CRAN (R 4.0.3)
   cmprsk         2.2-10     2020-06-09 [1] CRAN (R 4.0.0)
   cobalt       * 4.2.4      2020-11-05 [1] CRAN (R 4.0.3)
   coda           0.19-4     2020-09-30 [1] CRAN (R 4.0.2)
   colorspace     2.0-0      2020-11-11 [1] CRAN (R 4.0.3)
   crayon         1.3.4      2017-09-16 [1] CRAN (R 4.0.0)
   crosstalk      1.1.1      2021-01-12 [1] CRAN (R 4.0.3)
   data.table     1.13.6     2020-12-30 [1] CRAN (R 4.0.3)
   DBI            1.1.1      2021-01-15 [1] CRAN (R 4.0.3)
   dbplyr         2.0.0      2020-11-03 [1] CRAN (R 4.0.3)
   digest         0.6.27     2020-10-24 [1] CRAN (R 4.0.3)
   dplyr        * 1.0.3      2021-01-15 [1] CRAN (R 4.0.3)
   e1071          1.7-4      2020-10-14 [1] CRAN (R 4.0.3)
   ellipsis       0.3.1      2020-05-15 [1] CRAN (R 4.0.0)
   Epi            2.43       2021-01-27 [1] CRAN (R 4.0.3)
   etm            1.1.1      2020-09-08 [1] CRAN (R 4.0.2)
   evaluate       0.14       2019-05-28 [1] CRAN (R 4.0.0)
   fansi          0.4.2      2021-01-15 [1] CRAN (R 4.0.3)
   farver         2.0.3      2020-01-16 [1] CRAN (R 4.0.0)
   forcats      * 0.5.1      2021-01-27 [1] CRAN (R 4.0.3)
   foreign        0.8-81     2020-12-22 [1] CRAN (R 4.0.3)
   Formula        1.2-4      2020-10-16 [1] CRAN (R 4.0.3)
   fs             1.5.0      2020-07-31 [1] CRAN (R 4.0.2)
   gbm          * 2.1.8      2020-07-15 [1] CRAN (R 4.0.2)
```

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generics       0.1.0      2020-10-31 [1] CRAN (R 4.0.3)
ggdendro       0.1.22     2020-09-13 [1] CRAN (R 4.0.2)
ggforce        0.3.2      2020-06-23 [1] CRAN (R 4.0.3)
ggformula    * 0.10.1     2021-01-13 [1] CRAN (R 4.0.3)
ggplot2      * 3.3.3      2020-12-30 [1] CRAN (R 4.0.3)
ggrepel        0.9.1      2021-01-15 [1] CRAN (R 4.0.3)
ggridges     * 0.5.3      2021-01-08 [1] CRAN (R 4.0.3)
ggstance     * 0.3.5      2020-12-17 [1] CRAN (R 4.0.3)
glue           1.4.2      2020-08-27 [1] CRAN (R 4.0.3)
gridExtra      2.3        2017-09-09 [1] CRAN (R 4.0.3)
gtable         0.3.0      2019-03-25 [1] CRAN (R 4.0.0)
haven          2.3.1      2020-06-01 [1] CRAN (R 4.0.0)
here         * 1.0.1      2020-12-13 [1] CRAN (R 4.0.3)
highr          0.8        2019-03-20 [1] CRAN (R 4.0.0)
Hmisc          4.4-2      2020-11-29 [1] CRAN (R 4.0.3)
hms            1.0.0      2021-01-13 [1] CRAN (R 4.0.3)
htmlTable      2.1.0      2020-09-16 [1] CRAN (R 4.0.2)
htmltools      0.5.0      2020-06-16 [1] CRAN (R 4.0.2)
htmlwidgets    1.5.3      2020-12-10 [1] CRAN (R 4.0.3)
httr           1.4.2      2020-07-20 [1] CRAN (R 4.0.2)
janitor      * 2.1.0      2021-01-05 [1] CRAN (R 4.0.3)
jpeg           0.1-8.1    2019-10-24 [1] CRAN (R 4.0.0)
jsonlite       1.7.2      2020-12-09 [1] CRAN (R 4.0.3)
knitr          1.31       2021-01-27 [1] CRAN (R 4.0.3)
labeling       0.4.2      2020-10-20 [1] CRAN (R 4.0.3)
labelled       2.7.0      2020-09-21 [1] CRAN (R 4.0.2)
lattice      * 0.20-41    2020-04-02 [1] CRAN (R 4.0.3)
latticeExtra * 0.6-29     2019-12-19 [1] CRAN (R 4.0.0)
leaflet        2.0.4.1    2021-01-07 [1] CRAN (R 4.0.3)
lifecycle      0.2.0      2020-03-06 [1] CRAN (R 4.0.0)
lme4         * 1.1-26     2020-12-01 [1] CRAN (R 4.0.3)
lubridate      1.7.9.2    2020-11-13 [1] CRAN (R 4.0.3)
magrittr     * 2.0.1      2020-11-17 [1] CRAN (R 4.0.3)
MASS         * 7.3-53     2020-09-09 [1] CRAN (R 4.0.3)
Matching     * 4.9-7      2020-02-06 [1] CRAN (R 4.0.0)
Matrix       * 1.2-18     2019-11-27 [2] CRAN (R 4.0.3)
mgcv           1.8-33     2020-08-27 [2] CRAN (R 4.0.3)
minqa          1.2.4      2014-10-09 [1] CRAN (R 4.0.0)
mitools        2.4        2019-04-26 [1] CRAN (R 4.0.0)
modelr         0.1.8      2020-05-19 [1] CRAN (R 4.0.0)
mosaic         1.8.3      2021-01-18 [1] CRAN (R 4.0.3)
mosaicCore     0.9.0      2021-01-16 [1] CRAN (R 4.0.3)
mosaicData   * 0.20.2     2021-01-16 [1] CRAN (R 4.0.3)
munsell        0.5.0      2018-06-12 [1] CRAN (R 4.0.0)
nlme           3.1-149    2020-08-23 [2] CRAN (R 4.0.3)
nloptr         1.2.2.2    2020-07-02 [1] CRAN (R 4.0.2)
nnet           7.3-15     2021-01-24 [1] CRAN (R 4.0.3)
numDeriv       2016.8-1.1 2019-06-06 [1] CRAN (R 4.0.0)
patchwork    * 1.1.1      2020-12-17 [1] CRAN (R 4.0.3)
pillar         1.4.7      2020-11-20 [1] CRAN (R 4.0.3)
pkgconfig      2.0.3      2019-09-22 [1] CRAN (R 4.0.0)
plyr           1.8.6      2020-03-03 [1] CRAN (R 4.0.0)
png            0.1-7      2013-12-03 [1] CRAN (R 4.0.0)
polyclip       1.10-0     2019-03-14 [1] CRAN (R 4.0.0)
```

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   purrr        * 0.3.4      2020-04-17 [1] CRAN (R 4.0.0)
   R6             2.5.0      2020-10-28 [1] CRAN (R 4.0.3)
   RColorBrewer   1.1-2      2014-12-07 [1] CRAN (R 4.0.0)
   Rcpp           1.0.6      2021-01-15 [1] CRAN (R 4.0.3)
   readr        * 1.4.0      2020-10-05 [1] CRAN (R 4.0.3)
   readxl         1.3.1      2019-03-13 [1] CRAN (R 4.0.0)
   reprex         1.0.0      2021-01-27 [1] CRAN (R 4.0.3)
   reshape2       1.4.4      2020-04-09 [1] CRAN (R 4.0.0)
   rlang          0.4.9      2020-11-26 [1] CRAN (R 4.0.3)
   rmarkdown      2.6        2020-12-14 [1] CRAN (R 4.0.3)
   rpart          4.1-15     2019-04-12 [2] CRAN (R 4.0.3)
   rprojroot      2.0.2      2020-11-15 [1] CRAN (R 4.0.3)
   rstudioapi     0.13       2020-11-12 [1] CRAN (R 4.0.3)
   rvest          0.3.6      2020-07-25 [1] CRAN (R 4.0.2)
   scales         1.1.1      2020-05-11 [1] CRAN (R 4.0.0)
   sessioninfo    1.1.1      2018-11-05 [1] CRAN (R 4.0.3)
   snakecase      0.11.0     2019-05-25 [1] CRAN (R 4.0.0)
   statmod        1.4.35     2020-10-19 [1] CRAN (R 4.0.3)
   stringi        1.5.3      2020-09-09 [1] CRAN (R 4.0.2)
   stringr      * 1.4.0      2019-02-10 [1] CRAN (R 4.0.0)
   survey       * 4.0        2020-04-03 [1] CRAN (R 4.0.0)
   survival     * 3.2-7      2020-09-28 [1] CRAN (R 4.0.3)
   tableone     * 0.12.0     2020-07-26 [1] CRAN (R 4.0.3)
   tibble       * 3.0.5      2021-01-15 [1] CRAN (R 4.0.3)
   tidyr        * 1.1.2      2020-08-27 [1] CRAN (R 4.0.2)
   tidyselect     1.1.0      2020-05-11 [1] CRAN (R 4.0.0)
   tidyverse    * 1.3.0      2019-11-21 [1] CRAN (R 4.0.3)
 D TMB            1.7.18     2020-07-27 [1] CRAN (R 4.0.3)
   twang        * 1.6        2020-02-27 [1] CRAN (R 4.0.0)
   tweenr         1.0.1      2018-12-14 [1] CRAN (R 4.0.0)
   utf8           1.1.4      2018-05-24 [1] CRAN (R 4.0.0)
   vctrs          0.3.6      2020-12-17 [1] CRAN (R 4.0.3)
   withr          2.4.1      2021-01-26 [1] CRAN (R 4.0.3)
   xfun           0.19       2020-10-30 [1] CRAN (R 4.0.3)
   xml2           1.3.2      2020-04-23 [1] CRAN (R 4.0.0)
   xtable       * 1.8-4      2019-04-21 [1] CRAN (R 4.0.0)
   yaml           2.2.1      2020-02-01 [1] CRAN (R 4.0.0)
   zoo            1.8-8      2020-05-02 [1] CRAN (R 4.0.0)

[1] C:/Users/Thomas/Documents/R/win-library/4.0
[2] C:/Program Files/R/R-4.0.3/library

 D -- DLL MD5 mismatch, broken installation.
```