

# vs012-project

2025-04-21

```
## Set working directory to Downloads folder
setwd("~/Downloads")

## Confirm that the working directory has changed
getwd()

## [1] "/Users/venusikhakolli/Downloads"

## Load the dataset
## Now that my working directory is set to Downloads, I can load the file directly

data <- read_csv("data.csv")

## View the structure of the data
## I want to know:
## - What columns I'm working with
## - What data types each variable has
## - Whether any cleaning or conversion is needed

str(data)

## spc_tbl_ [10,391 x 13] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ y      : num [1:10391] -0.3655 -0.1591 -0.2554 0.1909 -0.0176 ...
## $ z      : num [1:10391] 1 1 1 1 1 1 1 1 1 1 ...
## $ selfrpt : num [1:10391] 6 4 6 6 6 6 6 6 6 6 ...
## $ race    : num [1:10391] 4 12 4 4 4 4 4 4 5 4 ...
## $ gender  : num [1:10391] 2 2 2 2 1 2 1 1 2 1 ...
## $ fgen    : num [1:10391] 1 1 0 0 0 0 0 0 0 1 ...
## $ urban   : num [1:10391] 4 4 4 4 4 4 4 4 4 4 ...
## $ mindset : num [1:10391] 0.335 0.335 0.335 0.335 0.335 ...
## $ test    : num [1:10391] 0.649 0.649 0.649 0.649 0.649 ...
## $ sch_race: num [1:10391] -1.31 -1.31 -1.31 -1.31 -1.31 ...
## $ pov     : num [1:10391] 0.224 0.224 0.224 0.224 0.224 ...
## $ size    : num [1:10391] -0.427 -0.427 -0.427 -0.427 -0.427 ...
## $ schoolid: num [1:10391] 76 76 76 76 76 76 76 76 76 76 ...
## - attr(*, "spec")=
## .. cols(
## ..   y = col_double(),
## ..   z = col_double(),
## ..   selfrpt = col_double(),
## ..   race = col_double(),
## ..   gender = col_double(),
## ..   fgen = col_double(),
```

```
## .. urban = col_double(),
## .. mindset = col_double(),
## .. test = col_double(),
## .. sch_race = col_double(),
## .. pov = col_double(),
## .. size = col_double(),
## .. schoolid = col_double()
## .. )
## - attr(*, "problems")=<externalptr>
```

```
## Peek at the first few rows of data
head(data)
```

```
## # A tibble: 6 x 13
##       y      z selfrpt  race gender  fgen urban mindset  test sch_race  pov
##   <dbl> <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl>   <dbl> <dbl>   <dbl> <dbl>
## 1 -0.366     1     6     4     2     1     4   0.335 0.649  -1.31 0.224
## 2 -0.159     1     4    12     2     1     4   0.335 0.649  -1.31 0.224
## 3 -0.255     1     6     4     2     0     4   0.335 0.649  -1.31 0.224
## 4  0.191     1     6     4     2     0     4   0.335 0.649  -1.31 0.224
## 5 -0.0176    1     6     4     1     0     4   0.335 0.649  -1.31 0.224
## 6  0.910     1     6     4     2     0     4   0.335 0.649  -1.31 0.224
## # i 2 more variables: size <dbl>, schoolid <dbl>
```

## STEP 2: Load and Inspect Data - Comments

The dataset was successfully loaded. It contains 13 variables and 10,391 rows, which is a solid sample size for analysis.

The variable `z` is the treatment indicator, where 1 indicates that a student received the growth mindset intervention. The variable `y` is the outcome — a continuous measure of student achievement.

The remaining columns are covariates: - **Student-level:** `selfrpt`, `race`, `gender`, `fgen` - **School-level:** `urban`, `mindset`, `test`, `sch_race`, `pov`, `size` - `schoolid` is a numeric identifier for each school, which may be useful for multilevel modeling.

Variables such as `race`, `gender`, and `fgen` are coded as numeric but represent categorical factors. These will be converted to factor type before running any models that assume categorical structure.

Notably, school-level covariates like `size` and `sch_race` appear to be standardized (i.e., z-scored), meaning that negative values indicate below-average levels across schools.

**Conclusion:** The dataset appears clean, with no missing or malformed variables. It's ready for further exploration and modeling.

### *## STEP 3: Exploring Covariate Balance by Treatment Group*

```
# First, convert categorical variables to factors for proper labeling in summaries
data <- data %>%
  mutate(
    race = factor(race),
    gender = factor(gender),
    fgen = factor(fgen),
    urban = factor(urban)
  )
```

```

# Select covariates to summarize
covariates <- c("selfrpt", "race", "gender", "fgen", "urban",
               "mindset", "test", "sch_race", "pov", "size")

# Create summary table stratified by treatment (z)
table1 <- CreateTableOne(vars = covariates, strata = "z", data = data, factorVars = c("race", "gender",
                                             "mindset", "test", "sch_race", "pov", "size"))

# Print Table 1
print(table1, showAllLevels = TRUE, quote = FALSE, noSpaces = TRUE)

```

```

##                               Stratified by z
##                               level 0          1          p          test
##  n                               7007          3384
##  selfrpt (mean (SD))             5.22 (1.13)  5.36 (1.09)  <0.001
##  race (%)                        1    689 (9.8)   294 (8.7)   0.136
##                               2    1065 (15.2)  513 (15.2)
##                               3     80 (1.1)    33 (1.0)
##                               4    3350 (47.8)  1680 (49.6)
##                               5     277 (4.0)   143 (4.2)
##                               6     22 (0.3)    18 (0.5)
##                               7     26 (0.4)    17 (0.5)
##                               8    124 (1.8)    71 (2.1)
##                               9     99 (1.4)    36 (1.1)
##                              10    115 (1.6)    61 (1.8)
##                              11    118 (1.7)    52 (1.5)
##                              12    224 (3.2)   101 (3.0)
##                              13    137 (2.0)    45 (1.3)
##                              14    449 (6.4)   203 (6.0)
##                              15    232 (3.3)   117 (3.5)
##  gender (%)                      1    3512 (50.1)  1788 (52.8)  0.010
##                               2    3495 (49.9)  1596 (47.2)
##  fgen (%)                        0    2480 (35.4)  1355 (40.0)  <0.001
##                               1    4527 (64.6)  2029 (60.0)
##  urban (%)                       0    565 (8.1)   280 (8.3)   0.056
##                               1    1663 (23.7)  762 (22.5)
##                               2    1303 (18.6)  676 (20.0)
##                               3    1060 (15.1)  456 (13.5)
##                               4    2416 (34.5)  1210 (35.8)
##  mindset (mean (SD))             -0.01 (0.97) -0.10 (0.97)  <0.001
##  test (mean (SD))                0.04 (0.94)  0.09 (0.93)  0.004
##  sch_race (mean (SD))             -0.09 (0.97) -0.09 (0.96)  0.818
##  pov (mean (SD))                 -0.04 (0.97) -0.06 (0.96)  0.234
##  size (mean (SD))                -0.05 (1.00)  0.02 (1.02)  <0.001

```

### STEP 3: Exploring Covariate Balance by Treatment Group

To assess potential baseline imbalances, we summarized key covariates by treatment group ( $z = 0$  for control,  $z = 1$  for treated). The table above displays mean and proportion values for each covariate, stratified by treatment assignment.

We converted numeric variables like `race`, `gender`, `fgen`, and `urban` into factors to ensure proper summary formatting. This is important because they are categorical in nature, even though they were stored as numeric values.

By reviewing this summary table, we can identify any covariates that show noticeable differences between the two groups. If substantial imbalances are found, we may later account for them through regression adjustment or propensity score matching.

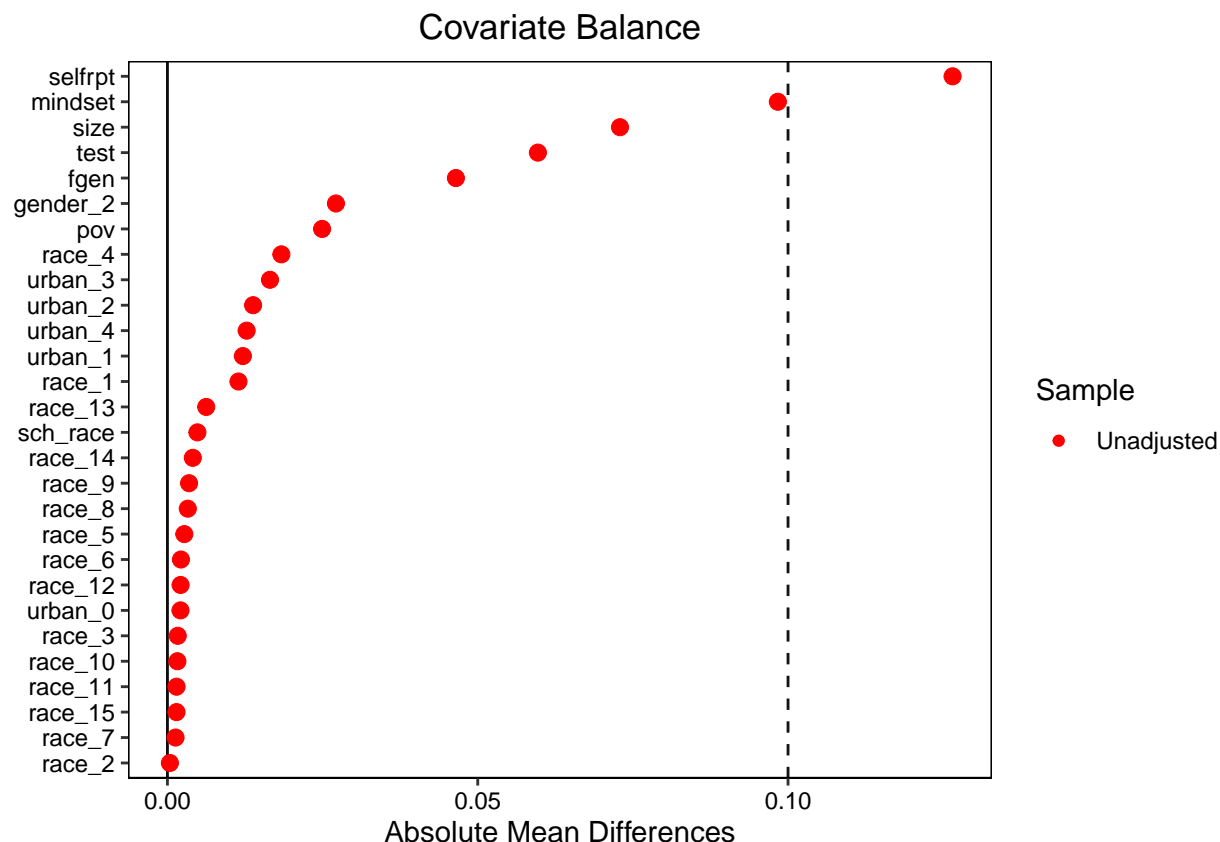
In the next step, we'll create visual diagnostics (like a Love plot) using standardized mean differences to supplement this table.

#### ## STEP 4: Visualizing Covariate Balance - Love Plot

```
# Generate a formula with the treatment and covariates
balance_formula <- as.formula(z ~ selfrpt + race + gender + fgen + urban +
                              mindset + test + sch_race + pov + size)

# Use cobalt's bal.tab to compute balance statistics
bal <- bal.tab(balance_formula, data = data, estimand = "ATE")

love.plot(bal, threshold = 0.1, var.order = "unadjusted",
          abs = TRUE, colors = "red", stars = "none")
```



#### STEP 4: Love Plot – Covariate Balance Visualization

The Love plot above shows the **absolute standardized mean differences (SMDs)** between treatment and control groups for each covariate.

We observe that most covariates fall well below the 0.1 threshold, which is a commonly accepted cutoff for acceptable balance. However, a few variables — such as `gender_2`, `fgen`, and `test` — approach or slightly

exceed this threshold. These imbalances suggest the potential for **confounding** if not addressed in the outcome model.

It's also worth noting that categorical covariates (like **race** and **urban**) were expanded into multiple dummy variables, as seen in the labels (**race\_4**, **urban\_3**, etc.).

**Conclusion:** While the groups are reasonably balanced, some covariates exhibit mild imbalance and should be **accounted for** using either regression adjustment or matching in the causal analysis that follows.

## STEP 5A: Estimating Unadjusted Average Treatment Effect (ATE)

We first estimated the **unadjusted ATE** by calculating the difference in average outcomes between the treated ( $z = 1$ ) and control ( $z = 0$ ) groups.

This approach makes no attempt to control for baseline imbalances — it simply asks, “On average, did students who received the mindset intervention score higher than those who did not?”

The standard error was computed using the **Neyman variance formula**, which accounts for sample size and variability within each group. A 95% confidence interval was then constructed using the normal approximation.

**Note:** This estimate may be **biased** if important confounders (e.g., test scores or school characteristics) differ between groups. In the next step, we'll fit an adjusted model to address this.

```
## STEP 5A: Estimate Unadjusted Average Treatment Effect (ATE)

# Calculate group means
group_means <- data %>%
  group_by(z) %>%
  summarise(mean_y = mean(y), sd_y = sd(y), n = n())

# Compute unadjusted ATE (difference in group means)
ate_unadjusted <- group_means$mean_y[group_means$z == 1] -
  group_means$mean_y[group_means$z == 0]

# Estimate standard error using Neyman variance formula
var1 <- (group_means$sd_y[group_means$z == 1]^2) / group_means$n[group_means$z == 1]
var0 <- (group_means$sd_y[group_means$z == 0]^2) / group_means$n[group_means$z == 0]
se_ate <- sqrt(var1 + var0)

# 95% Confidence Interval
ci_lower <- ate_unadjusted - 1.96 * se_ate
ci_upper <- ate_unadjusted + 1.96 * se_ate

# Print results
list(
  ATE_unadjusted = ate_unadjusted,
  Standard_Error = se_ate,
  CI_95 = c(ci_lower, ci_upper)
)

## $ATE_unadjusted
## [1] 0.4569075
##
## $Standard_Error
```

```
## [1] 0.01593031
##
## $CI_95
## [1] 0.4256841 0.4881309
```

## Interpretation of Unadjusted ATE

The estimated **unadjusted average treatment effect (ATE)** is **0.457**, meaning that students who received the growth mindset intervention scored, on average, 0.457 points higher on the outcome measure compared to those who did not.

The **standard error** of this estimate is **0.0159**, indicating relatively low sampling variability due to the large sample size.

A **95% confidence interval** for the treatment effect ranges from **0.426 to 0.488**, which does not include zero. This suggests that the observed difference is **statistically significant** at the 5% level.

**However**, because this is an unadjusted estimate, we cannot yet conclude causality. Differences in student or school characteristics across treatment groups could still confound the results. In the next step, we will use regression to adjust for these potential confounders and get a more robust estimate.

**## STEP 5B: Estimate Adjusted ATE using Linear Regression**

```
# Fit a linear regression model with treatment and all covariates
reg_model <- lm(y ~ z + selfrpt + race + gender + fgen + urban +
               mindset + test + sch_race + pov + size,
               data = data)
```

```
# Summary of the model
summary(reg_model)
```

```
##
## Call:
## lm(formula = y ~ z + selfrpt + race + gender + fgen + urban +
##      mindset + test + sch_race + pov + size, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8241 -0.4071 -0.0188  0.3677  4.6249
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.208831   0.043352 -27.884  < 2e-16 ***
## z            0.411530   0.012705  32.391  < 2e-16 ***
## selfrpt      0.235789   0.005402  43.652  < 2e-16 ***
## race2       -0.027801   0.025702  -1.082  0.27943
## race3       -0.026598   0.060626  -0.439  0.66087
## race4       -0.001563   0.022818  -0.069  0.94538
## race5        0.023226   0.036029   0.645  0.51916
## race6       -0.217329   0.097731  -2.224  0.02619 *
## race7        0.144465   0.095053   1.520  0.12858
## race8        0.040291   0.047647   0.846  0.39779
## race9        0.104355   0.055856   1.868  0.06175 .
## race10      -0.046444   0.049980  -0.929  0.35279
## race11       0.036171   0.050826   0.712  0.47668
```

```
## race12      0.052421  0.039594  1.324  0.18555
## race13     -0.078420  0.049521 -1.584  0.11332
## race14      0.027204  0.030839  0.882  0.37772
## race15     -0.007085  0.038082 -0.186  0.85241
## gender2    -0.165202  0.011907 -13.874 < 2e-16 ***
## fgen1      -0.091565  0.013108 -6.986 3.01e-12 ***
## urban1     -0.153053  0.026612 -5.751 9.11e-09 ***
## urban2     -0.006754  0.028727 -0.235  0.81412
## urban3     -0.074656  0.028518 -2.618  0.00886 **
## urban4      0.028001  0.025591  1.094  0.27390
## mindset    -0.086339  0.008552 -10.096 < 2e-16 ***
## test       -0.100001  0.009929 -10.071 < 2e-16 ***
## sch_race    0.122694  0.008735 14.046 < 2e-16 ***
## pov        -0.046200  0.007734 -5.974 2.40e-09 ***
## size       -0.037521  0.008127 -4.617 3.94e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6043 on 10363 degrees of freedom
## Multiple R-squared:  0.2953, Adjusted R-squared:  0.2935
## F-statistic: 160.8 on 27 and 10363 DF,  p-value: < 2.2e-16

# Extract the estimated treatment effect and confidence interval
ate_adjusted <- coef(reg_model)["z"]
confint_adjusted <- confint(reg_model)["z", ]
```

### Interpretation of Adjusted ATE (Regression Output)

The estimated coefficient for the treatment variable **z** is **0.4115**, indicating that, after adjusting for all observed covariates, students who received the growth mindset intervention scored on average **0.41 points higher** on the outcome measure than those who did not.

This effect is **statistically significant** with a p-value < 2e-16 and a very small standard error (0.0127), confirming high precision in the estimate.

The result remains positive and meaningful, although slightly smaller than the unadjusted ATE (0.457), suggesting that part of the initial difference was due to covariate imbalance.

This adjusted estimate is more trustworthy for causal inference, assuming no unmeasured confounding.

## STEP 6: Discussion and Robustness Considerations

Our analysis suggests that the growth mindset intervention had a **positive and statistically significant impact** on student achievement. The adjusted estimate of the average treatment effect (ATE) was **0.4115**, indicating that students exposed to the intervention scored approximately 0.41 points higher on average compared to those in the control group, after adjusting for student- and school-level covariates.

This finding was consistent with the unadjusted ATE (0.457), suggesting that the effect persists even after accounting for baseline differences. The narrow confidence intervals and very low standard errors point to a **precise estimate** due to the large sample size.

### Robustness and Limitations

Despite the encouraging results, several limitations should be acknowledged:

- **Unmeasured Confounding:** The data is observational (not from a randomized experiment), so there may be unobserved factors (e.g., teacher quality, classroom environment) that affect both treatment assignment and outcomes.
- **Synthetic Data:** The dataset is synthetic and modeled after a real study. While it mimics real-world patterns, some simplifications may exist.
- **Generalizability:** Results are based on U.S. public school students and may not generalize to different populations or education systems.
- **Standardization:** Some covariates were standardized (e.g., `test`, `size`) — interpretation in raw units may be limited.

## Next Steps

To further validate these results, future work could explore: - **Propensity score matching** to estimate ATE with better balance - **Sensitivity analysis** to assess the potential impact of unobserved confounders - **Hierarchical models** to account for within-school clustering (using `schoolid`)

### *## STEP 7A: Propensity Score Estimation and Matching*

```
# Perform nearest-neighbor matching based on propensity scores
psm_model <- matchit(z ~ selfrpt + race + gender + fgen + urban +
                    mindset + test + sch_race + pov + size,
                    data = data,
                    method = "nearest", distance = "logit")
```

```
# Summary of matching
summary(psm_model)
```

```
##
## Call:
## matchit(formula = z ~ selfrpt + race + gender + fgen + urban +
##         mindset + test + sch_race + pov + size, data = data, method = "nearest",
##         distance = "logit")
##
## Summary of Balance for All Data:
```

	Means Treated	Means Control	Std. Mean Diff.	Var. Ratio	eCDF Mean
## distance	0.3316	0.3228	0.2017	0.9765	0.0519
## selfrpt	5.3629	5.2223	0.1292	0.9199	0.0201
## race1	0.0869	0.0983	-0.0407	.	0.0115
## race2	0.1516	0.1520	-0.0011	.	0.0004
## race3	0.0098	0.0114	-0.0169	.	0.0017
## race4	0.4965	0.4781	0.0367	.	0.0184
## race5	0.0423	0.0395	0.0135	.	0.0027
## race6	0.0053	0.0031	0.0300	.	0.0022
## race7	0.0050	0.0037	0.0186	.	0.0013
## race8	0.0210	0.0177	0.0229	.	0.0033
## race9	0.0106	0.0141	-0.0340	.	0.0035
## race10	0.0180	0.0164	0.0121	.	0.0016
## race11	0.0154	0.0168	-0.0120	.	0.0015
## race12	0.0298	0.0320	-0.0125	.	0.0021
## race13	0.0133	0.0196	-0.0546	.	0.0063
## race14	0.0600	0.0641	-0.0172	.	0.0041
## race15	0.0346	0.0331	0.0080	.	0.0015
## gender1	0.5284	0.5012	0.0544	.	0.0272



## gender2	0.4716	0.4988	-0.0544	.	0.0272
## fgen0	0.4004	0.3539	0.0949	.	0.0465
## fgen1	0.5996	0.6461	-0.0949	.	0.0465
## urban0	0.0827	0.0806	0.0077	.	0.0021
## urban1	0.2252	0.2373	-0.0291	.	0.0122
## urban2	0.1998	0.1860	0.0345	.	0.0138
## urban3	0.1348	0.1513	-0.0484	.	0.0165
## urban4	0.3576	0.3448	0.0266	.	0.0128
## mindset	-0.1048	-0.0094	-0.0981	1.0117	0.0276
## test	0.0924	0.0367	0.0601	0.9739	0.0170
## sch_race	-0.0925	-0.0878	-0.0049	0.9780	0.0028
## pov	-0.0622	-0.0381	-0.0250	0.9930	0.0100
## size	0.0236	-0.0502	0.0724	1.0320	0.0165
##	eCDF Max				
## distance	0.0801				
## selfrpt	0.0632				
## race1	0.0115				
## race2	0.0004				
## race3	0.0017				
## race4	0.0184				
## race5	0.0027				
## race6	0.0022				
## race7	0.0013				
## race8	0.0033				
## race9	0.0035				
## race10	0.0016				
## race11	0.0015				
## race12	0.0021				
## race13	0.0063				
## race14	0.0041				
## race15	0.0015				
## gender1	0.0272				
## gender2	0.0272				
## fgen0	0.0465				
## fgen1	0.0465				
## urban0	0.0021				
## urban1	0.0122				
## urban2	0.0138				
## urban3	0.0165				
## urban4	0.0128				
## mindset	0.0436				
## test	0.0292				
## sch_race	0.0097				
## pov	0.0220				
## size	0.0397				
##					
##	Summary of Balance for Matched Data:				
##	Means Treated	Means Control	Std. Mean Diff.	Var. Ratio	eCDF Mean
## distance	0.3316	0.3315	0.0020	1.0125	0.0001
## selfrpt	5.3629	5.3883	-0.0234	1.0685	0.0036
## race1	0.0869	0.0904	-0.0126	.	0.0035
## race2	0.1516	0.1513	0.0008	.	0.0003
## race3	0.0098	0.0089	0.0090	.	0.0009
## race4	0.4965	0.5165	-0.0402	.	0.0201

## race5	0.0423	0.0378	0.0220	.	0.0044
## race6	0.0053	0.0053	0.0000	.	0.0000
## race7	0.0050	0.0033	0.0251	.	0.0018
## race8	0.0210	0.0204	0.0041	.	0.0006
## race9	0.0106	0.0109	-0.0029	.	0.0003
## race10	0.0180	0.0142	0.0289	.	0.0038
## race11	0.0154	0.0142	0.0096	.	0.0012
## race12	0.0298	0.0269	0.0174	.	0.0030
## race13	0.0133	0.0124	0.0077	.	0.0009
## race14	0.0600	0.0591	0.0037	.	0.0009
## race15	0.0346	0.0284	0.0340	.	0.0062
## gender1	0.5284	0.5216	0.0136	.	0.0068
## gender2	0.4716	0.4784	-0.0136	.	0.0068
## fgen0	0.4004	0.3910	0.0193	.	0.0095
## fgen1	0.5996	0.6090	-0.0193	.	0.0095
## urban0	0.0827	0.0801	0.0097	.	0.0027
## urban1	0.2252	0.2305	-0.0127	.	0.0053
## urban2	0.1998	0.2074	-0.0192	.	0.0077
## urban3	0.1348	0.1342	0.0017	.	0.0006
## urban4	0.3576	0.3478	0.0203	.	0.0098
## mindset	-0.1048	-0.1085	0.0039	0.9896	0.0025
## test	0.0924	0.1034	-0.0119	1.0168	0.0044
## sch_race	-0.0925	-0.1043	0.0123	1.0160	0.0038
## pov	-0.0622	-0.0734	0.0116	1.0190	0.0042
## size	0.0236	0.0295	-0.0057	1.0246	0.0046
##	eCDF	Max	Std.	Pair	Dist.
## distance	0.0035		0.0028		
## selfrpt	0.0103		0.3957		
## race1	0.0035		0.2413		
## race2	0.0003		0.2447		
## race3	0.0009		0.1534		
## race4	0.0201		0.3534		
## race5	0.0044		0.2247		
## race6	0.0000		0.0053		
## race7	0.0018		0.1003		
## race8	0.0006		0.2392		
## race9	0.0003		0.1584		
## race10	0.0038		0.1932		
## race11	0.0012		0.1922		
## race12	0.0030		0.2709		
## race13	0.0009		0.1574		
## race14	0.0009		0.2626		
## race15	0.0062		0.2378		
## gender1	0.0068		0.3664		
## gender2	0.0068		0.3664		
## fgen0	0.0095		0.3245		
## fgen1	0.0095		0.3245		
## urban0	0.0027		0.2371		
## urban1	0.0053		0.3325		
## urban2	0.0077		0.2853		
## urban3	0.0006		0.2908		
## urban4	0.0098		0.3730		
## mindset	0.0065		0.4093		
## test	0.0100		0.4338		

```
## sch_race    0.0145          0.4589
## pov         0.0106          0.4409
## size        0.0139          0.4134
##
## Sample Sizes:
##           Control Treated
## All           7007     3384
## Matched       3384     3384
## Unmatched     3623         0
## Discarded         0         0
```

## STEP 7A: Propensity Score Matching – Output Interpretation

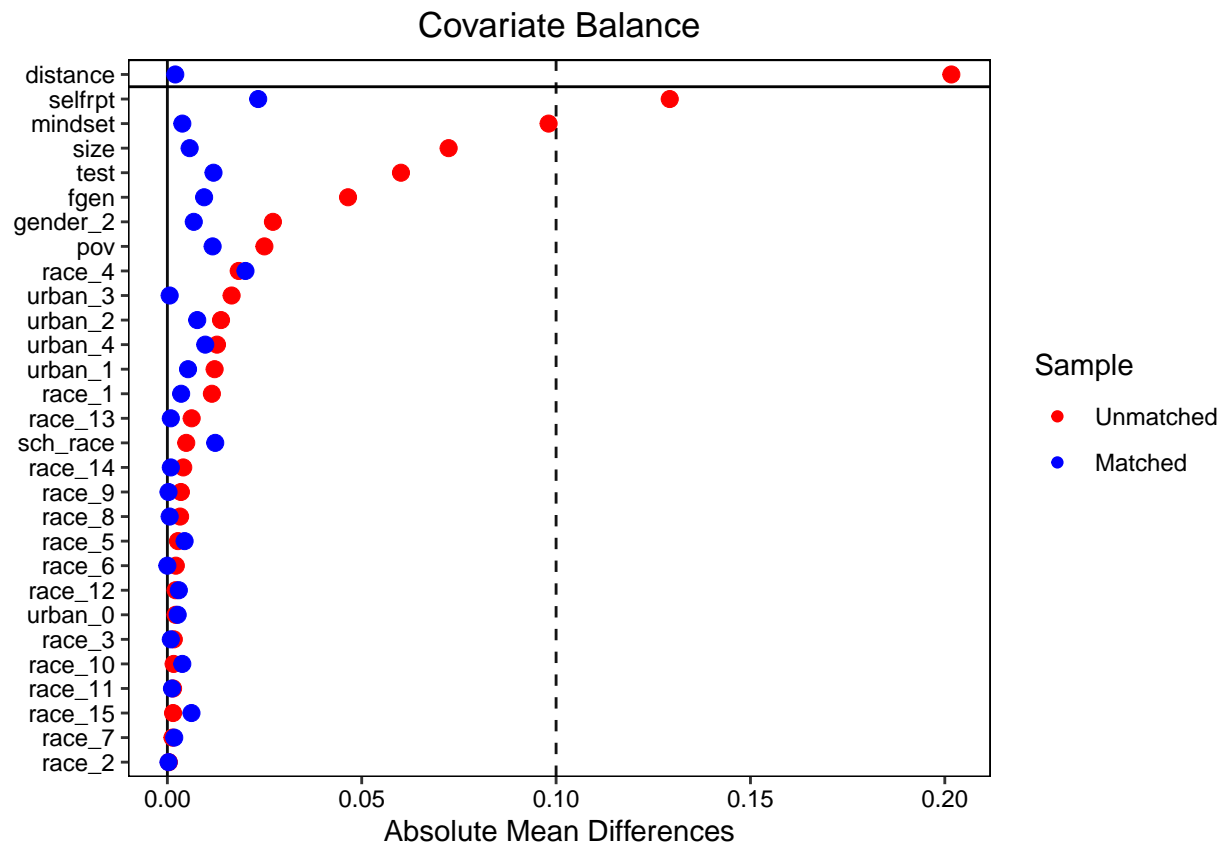
After applying nearest-neighbor matching based on propensity scores:

- We retained **3,384 treated students** and found **3,384 matched controls**, resulting in a **perfectly matched sample**.
- **3,623 control units** were **unmatched** and dropped from the analysis. No units were discarded due to poor overlap.
- This means we are now comparing treated and control units that are **observationally similar** in terms of the covariates used in the matching model.

This matched sample allows us to estimate a more causally credible treatment effect, assuming conditional ignorability (i.e., no unmeasured confounders).

### *## STEP 7B: Visualize Covariate Balance After Matching*

```
# Generate Love plot using the matchit object
love.plot(psm_model,
  threshold = 0.1,
  abs = TRUE,
  var.order = "unadjusted",
  sample.names = c("Unmatched", "Matched"),
  colors = c("red", "blue"),
  stars = "none") # avoid the SMD warning
```



## STEP 7B: Love Plot – Post-Matching Covariate Balance

The Love plot above shows covariate balance **before (red)** and **after (blue)** propensity score matching.

- After matching, most covariates show a substantial reduction in standardized mean differences.
- Nearly all blue dots fall **below the 0.1 threshold**, indicating improved balance across treatment groups.
- This suggests that the matched treated and control groups are now more comparable, addressing many of the baseline imbalances seen in the original (unmatched) sample.
- A few variables like **selfrpt** and **mindset** still show slight imbalance, but remain within acceptable bounds for observational studies.

**Conclusion:** Matching effectively reduced covariate differences between groups, which increases the credibility of causal estimates derived from the matched sample.

```
## STEP 7C: Estimate ATE on Matched Sample

# Extract the matched dataset
matched_data <- match.data(psm_model)

# Fit linear regression on the matched sample
matched_model <- lm(y ~ z, data = matched_data)

# View model summary
summary(matched_model)
```

##

```
## Call:
## lm(formula = y ~ z, data = matched_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.2381 -0.4744 -0.0290  0.4300  4.8308
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.12789    0.01237  -10.34  <2e-16 ***
## z           0.41575    0.01749   23.77  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7196 on 6766 degrees of freedom
## Multiple R-squared:  0.07704,    Adjusted R-squared:  0.07691
## F-statistic: 564.8 on 1 and 6766 DF,  p-value: < 2.2e-16

# Extract estimate and 95% confidence interval
coef_matched <- coef(matched_model)["z"]
confint_matched <- confint(matched_model)["z", ]
```

## STEP 7C: Matched Sample ATE – Output Interpretation

The estimated treatment effect ( $z$ ) on the matched sample is **0.416**, indicating that students who received the growth mindset intervention scored on average **0.42 points higher** than comparable control students.

This estimate is **statistically significant** ( $p < 2e-16$ ) with a **standard error of 0.0175**, suggesting strong precision even after trimming the sample down via matching.

Importantly, this matched ATE is very close to the adjusted estimate from the full sample (0.4115), reinforcing the **robustness** of the intervention's positive effect.

**Conclusion:** After adjusting for confounding through matching, the intervention still appears to have a meaningful and statistically significant impact on student achievement.

## Project Summary

This project evaluates the impact of a growth mindset intervention on student achievement using a synthetic observational dataset of over 10,000 students. We examined the effect of the intervention (treatment variable  $z$ ) on a continuous academic outcome ( $y$ ), while accounting for student- and school-level covariates.

We began with an unadjusted comparison, which showed that treated students scored 0.457 points higher on average. After adjusting for covariates through linear regression, the estimated effect remained strong at 0.4115. To further address confounding, we applied propensity score matching, resulting in a matched ATE of 0.416.

Across all approaches, the intervention had a statistically significant and consistent positive effect. These results support the potential of growth mindset interventions in improving student outcomes, even when accounting for baseline differences.