

SS154 Assignment 3

```
# install.packages("janitor")
# install.packages('gridExtra')
# install.packages('cobalt')
```

```
library(cobalt)
```

```
## cobalt (Version 4.5.4, Build Date: 2024-02-26)
```

```
library(rgenoud)
```

```
## ## rgenoud (Version 5.9-0.10, Build Date: 2023-12-13)
## ## See http://sekhon.berkeley.edu/rgenoud for additional documentation.
## ## Please cite software as:
## ## Walter Mebane, Jr. and Jasjeet S. Sekhon. 2011.
## ## ``Genetic Optimization Using Derivatives: The rgenoud package for R.''
## ## Journal of Statistical Software, 42(11): 1-26.
## ##
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:stats':
##
## filter, lag
##
## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union
```

```
library(janitor)
```

```
##
## Attaching package: 'janitor'
##
## The following objects are masked from 'package:stats':
##
## chisq.test, fisher.test
```

```
library(lmtest)
```

```
## Loading required package: zoo
##
## Attaching package: 'zoo'
##
## The following objects are masked from 'package:base':
##
## as.Date, as.Date.numeric
```

```

library(gridExtra)

##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
##      combine
library(ggplot2)
library(stats)
library(MatchIt)

##
## Attaching package: 'MatchIt'
## The following object is masked from 'package:cobalt':
##
##      lalonde
library(car)

## Loading required package: carData
##
## Attaching package: 'car'
## The following object is masked from 'package:dplyr':
##
##      recode
library(stargazer)

##
## Please cite as:
## Hlavac, Marek (2022). stargazer: Well-Formatted Regression and Summary Statistics Tables.
## R package version 5.2.3. https://CRAN.R-project.org/package=stargazer
load("/Users/somto/Downloads/replication_data.RData", verbose=TRUE)

## Loading objects:
##      table
head(table)

## # A tibble: 6 x 22
##   year state statenam statenum fips      pop farsfats farsvmt mv330 pp0514
##   <dbl> <chr>   <chr>         <dbl> <dbl>   <dbl>   <dbl>   <dbl> <dbl>
## 1 1970 Alabama AL             1      1 3454557      NA      NA    1297 0.208
## 2 1971 Alabama AL             1      1 3497349      NA      NA    1320 0.204
## 3 1972 Alabama AL             1      1 3540003      NA      NA     678 0.198
## 4 1973 Alabama AL             1      1 3580759      NA      NA    1376 0.193
## 5 1974 Alabama AL             1      1 3627778      NA      NA    1118 0.188
## 6 1975 Alabama AL             1      1 3680495     902      NA    1087 0.184
## # i 12 more variables: pp1519 <dbl>, pp2024 <dbl>, pp2529 <dbl>, pp3034 <dbl>,
## #   pp3544 <dbl>, pp4554 <dbl>, pp5564 <dbl>, pp6500 <dbl>, auto <dbl>,
## #   bus <dbl>, truck <dbl>, mtrcycl <dbl>

```

```

filtered_data <- table %>%
  filter(year %in% c(2013))
dim(filtered_data)

## [1] 51 22
filtered_data

## # A tibble: 51 x 22
##   year state statenam statenum fips pop farsfats farsvmt mv330 pp0514
##   <dbl> <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 2013 Alabama AL 1 1 4.83e6 853 65046 NA 0.129
## 2 2013 Alaska AK 2 2 7.35e5 51 4848 NA 0.140
## 3 2013 Arizona AZ 3 4 6.63e6 849 60586 NA 0.138
## 4 2013 Arkansas AR 4 5 2.96e6 498 33493 NA 0.135
## 5 2013 California CA 5 6 3.83e7 3107 329534 NA 0.133
## 6 2013 Colorado CO 6 8 5.27e6 482 46968 NA 0.133
## 7 2013 Connecticut CT 7 9 3.60e6 286 30941 NA 0.125
## 8 2013 Delaware DE 8 10 9.26e5 99 9308 NA 0.123
## 9 2013 District of Columbia DC 9 11 6.46e5 20 3527 NA 0.0850
## 10 2013 Florida FL 10 12 1.96e7 2403 192702 NA 0.115
## # i 41 more rows
## # i 12 more variables: pp1519 <dbl>, pp2024 <dbl>, pp2529 <dbl>, pp3034 <dbl>,
## # pp3544 <dbl>, pp4554 <dbl>, pp5564 <dbl>, pp6500 <dbl>, auto <dbl>,
## # bus <dbl>, truck <dbl>, mtrcycl <dbl>

# get averages of youth accident percentages

av_dataset <- filtered_data %>%
  group_by(state) %>%
  mutate(average_percentage = mean(c(pp1519, pp2024), na.rm = TRUE))
head(av_dataset)

## # A tibble: 6 x 23
## # Groups: state [6]
##   year state statenam statenum fips pop farsfats farsvmt mv330 pp0514
##   <dbl> <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 2013 Alabama AL 1 1 4.83e6 853 65046 NA 0.129
## 2 2013 Alaska AK 2 2 7.35e5 51 4848 NA 0.140
## 3 2013 Arizona AZ 3 4 6.63e6 849 60586 NA 0.138
## 4 2013 Arkansas AR 4 5 2.96e6 498 33493 NA 0.135
## 5 2013 California CA 5 6 3.83e7 3107 329534 NA 0.133
## 6 2013 Colorado CO 6 8 5.27e6 482 46968 NA 0.133
## # i 13 more variables: pp1519 <dbl>, pp2024 <dbl>, pp2529 <dbl>, pp3034 <dbl>,
## # pp3544 <dbl>, pp4554 <dbl>, pp5564 <dbl>, pp6500 <dbl>, auto <dbl>,
## # bus <dbl>, truck <dbl>, mtrcycl <dbl>, average_percentage <dbl>

needed <- av_dataset %>%
  select(state, statenam, pp1519, pp2024, average_percentage)
# dim(needed)
head(needed)

## # A tibble: 6 x 5
## # Groups: state [6]
##   state statenam pp1519 pp2024 average_percentage
##   <chr> <chr> <dbl> <dbl> <dbl>

```

```
## 1 Alabama      AL      0.0660 0.0740      0.0700
## 2 Alaska       AK      0.0670 0.0860      0.0765
## 3 Arizona      AZ      0.0680 0.0730      0.0705
## 4 Arkansas     AR      0.0660 0.0710      0.0685
## 5 California   CA      0.0690 0.0760      0.0725
## 6 Colorado     CO      0.0640 0.0710      0.0675
```

```
write.csv(needed, file = "marijuana_x_accidents.csv", row.names = FALSE)
getwd()
```

```
## [1] "/Users/somto"
```

```
# using augmented data from Google sheets
```

```
data <- read.csv("https://docs.google.com/spreadsheets/d/e/2PACX-1vQSb1NQnsUppe-H4FrbliXT-nuUIy5RTJq-b0I")
```

```
names(data)
```

```
## [1] "state"
## [2] "statenam"
## [3] "marijuana..medical.or.recreational..legalized.by.2011"
## [4] "X2013_pp1519"
## [5] "X2013_pp2024"
## [6] "X2013_average_percentage"
## [7] "X2013_public_transport_percentage"
## [8] "X2013_unemployment_rate"
## [9] "X2013_gdp"
## [10] "X2013_pop"
## [11] "X2013_per_capita_gdp"
```

```
data <- data %>% clean_names()
names(data)
```

```
## [1] "state"
## [2] "statenam"
## [3] "marijuana_medical_or_recreational_legalized_by_2011"
## [4] "x2013_pp1519"
## [5] "x2013_pp2024"
## [6] "x2013_average_percentage"
## [7] "x2013_public_transport_percentage"
## [8] "x2013_unemployment_rate"
## [9] "x2013_gdp"
## [10] "x2013_pop"
## [11] "x2013_per_capita_gdp"
```

```
head(data)
```

```
##      state statenam marijuana_medical_or_recreational_legalized_by_2011
## 1  Alabama      AL      0
## 2  Alaska       AK      1
## 3  Arizona      AZ      1
## 4  Arkansas     AR      0
## 5  California   CA      1
## 6  Colorado     CO      1
##  x2013_pp1519 x2013_pp2024 x2013_average_percentage
## 1      0.066      0.074      0.0700
## 2      0.067      0.086      0.0765
```

## 3	0.068	0.073	0.0705		
## 4	0.066	0.071	0.0685		
## 5	0.069	0.076	0.0725		
## 6	0.064	0.071	0.0675		
##	x2013_public_transport_percentage	x2013_unemployment_rate	x2013_gdp	x2013_pop	
## 1		0.0048	0.072	180,727	4833722
## 2		0.0184	0.062	51,542	735132
## 3		0.0236	0.079	261,924	6626624
## 4		0.0047	0.072	115,745	2959373
## 5		0.0531	0.094	2,050,693	38332521
## 6		0.0335	0.071	273,721	5268367
##	x2013_per_capita_gdp				
## 1	37388.79				
## 2	70112.58				
## 3	39526.01				
## 4	39111.33				
## 5	53497.47				
## 6	51955.57				

Linear Regression Analysis

```
# linear regression models (no matching)

model1 = lm(x2013_average_percentage ~
  marijuana_medical_or_recreational_legalized_by_2011 +
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  x2013_per_capita_gdp,
  data=data)

model2 = lm(x2013_average_percentage ~
  marijuana_medical_or_recreational_legalized_by_2011 +
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  log(x2013_per_capita_gdp),
  data=data)

model3 = lm(x2013_average_percentage ~
  marijuana_medical_or_recreational_legalized_by_2011 +
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  log(x2013_per_capita_gdp) +
  x2013_unemployment_rate:log(x2013_per_capita_gdp),
  data=data)

model4 = lm(x2013_average_percentage ~
  marijuana_medical_or_recreational_legalized_by_2011 +
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  x2013_per_capita_gdp +
  x2013_unemployment_rate:x2013_per_capita_gdp,
  data=data)
```

```

model5 = lm(x2013_average_percentage ~
            marijuana_medical_or_recreational_legalized_by_2011 +
            x2013_public_transport_percentage +
            x2013_unemployment_rate +
            log(x2013_per_capita_gdp) +
            x2013_public_transport_percentage:x2013_unemployment_rate,
            data=data)

# stargazer(model1, model2, model3, model4, model5, type='html', out='ols_models_comparison.html')
stargazer(model1, model2, model3, model4, model5, type='text')

##
## =====
##
##
##
##
## (1) (2) x20
## -----
## marijuana_medical_or_recreational_legalized_by_2011 -0.001 -0.001
## (0.001) (0.001)
##
## x2013_public_transport_percentage -0.024* -0.016
## (0.014) (0.013)
##
## x2013_unemployment_rate -0.027 -0.026
## (0.035) (0.036)
##
## x2013_per_capita_gdp 0.00000***
## (0.00000)
##
## log(x2013_per_capita_gdp) 0.007**
## (0.003)
##
## x2013_unemployment_rate:log(x2013_per_capita_gdp)
##
##
## x2013_unemployment_rate:x2013_per_capita_gdp
##
##
## x2013_public_transport_percentage:x2013_unemployment_rate
##
##
## Constant 0.066*** -0.008
## (0.004) (0.036)
##
## -----
## Observations 51 51
## R2 0.206 0.172
## Adjusted R2 0.137 0.100
## Residual Std. Error 0.003 (df = 46) 0.004 (df = 46)
## F Statistic 2.987** (df = 4; 46) 2.393* (df = 4; 46) 2
## =====
## Note:

```

```

# residual plot to check linearity and homoskedasticity assumptions

# Function to calculate Goldfeld-Quandt test p-value
gq_test_p <- function(model) {
  gq_test_result <- gqtest(model)
  p_value <- gq_test_result$p.value
  return(p_value)
}

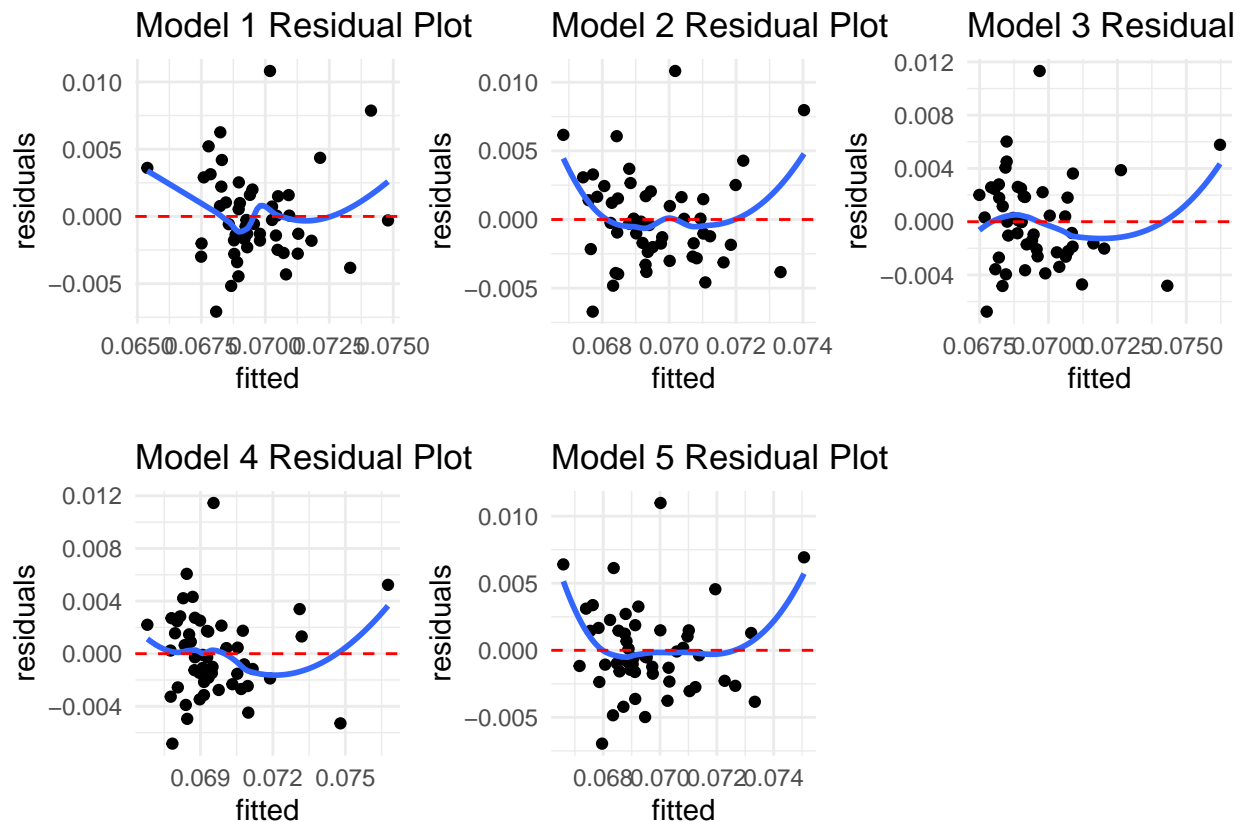
# Create residual plots for multiple models
residual_plots <- lapply(1:5, function(i) {
  model <- get(paste0("model", i))

  ggplot(data.frame(residuals = residuals(model), fitted = fitted(model)), aes(x = fitted, y = residuals)) +
    geom_point() + geom_smooth(method = "loess", se=FALSE) +
    geom_hline(yintercept = 0, linetype = "dashed", color = "red") +
    ggtitle(paste("Model", i, "Residual Plot")) +
    theme_minimal() +
    theme(aspect.ratio = 1)
})

# Arrange plots in a grid
grid.arrange(grobs = residual_plots, ncol = 3)

## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'

```

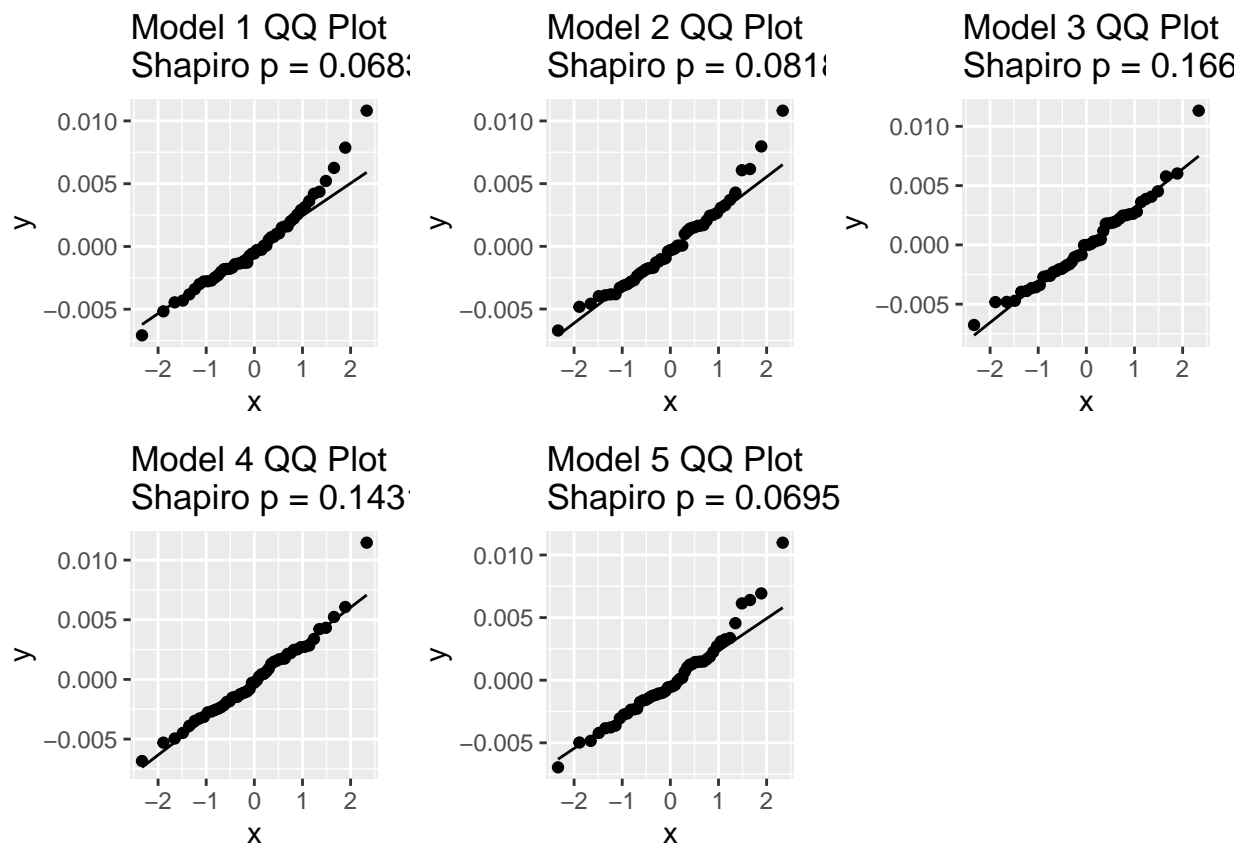


```
# QQ Plot - to check normality of errors assumption

# Function to calculate p-value from Shapiro-Wilk test
get_shapiro_p <- function(model) {
  shapiro_result <- shapiro.test(residuals(model))
  p_value <- shapiro_result$p.value
  return(p_value)
}

# Create QQ plots for multiple models
qqplots <- lapply(1:5, function(i) {
  model <- get(paste0("model", i))
  ggplot(data.frame(residuals = residuals(model)), aes(sample = residuals)) +
    stat_qq() +
    stat_qq_line() +
    ggtitle(paste("Model", i, "QQ Plot \nShapiro p =", round(get_shapiro_p(model), 4))) +
    theme(aspect.ratio = 1) # Set aspect ratio to make plots more square
})

# Arrange plots in a grid
grid.arrange(grobs = qqplots, ncol = 3, main = "QQ Plots for Models 1 through 5")
```

```
# VIF plot - to check no multicollinearity assumption
```

```
# Set up multi-panel layout
```

```
par(mfrow = c(2, 3)) # 2 rows and 3 columns grid
```

```
# List of model names
```

```
model_names <- paste0("model", 1:5)
```

```
# Loop over each model
```

```
for (model_name in model_names) {
```

```
  # Get predictor names
```

```
  predictor_names <- names(coef(get(model_name)))[-1]
```

```
  # Create a numbered vector for the x-axis
```

```
  x_labels <- 1:length(predictor_names)
```

```
  # Plot with numbered labels
```

```
  barplot(vif(get(model_name)), col = "skyblue", main = paste("Variance Inflation Factor (VIF) -", model_name),  
    names.arg = x_labels, las = 1)
```

```
  # Create modified legend labels
```

```
  legend_labels <- paste0(x_labels, ". ", predictor_names) # Combine number and name
```

```
  # Create and position the legend
```

```
  legend("topleft", legend = legend_labels,  
    title = "Predictor Number & Name",  
    col = "skyblue", bty = "n", cex = 0.95)
```

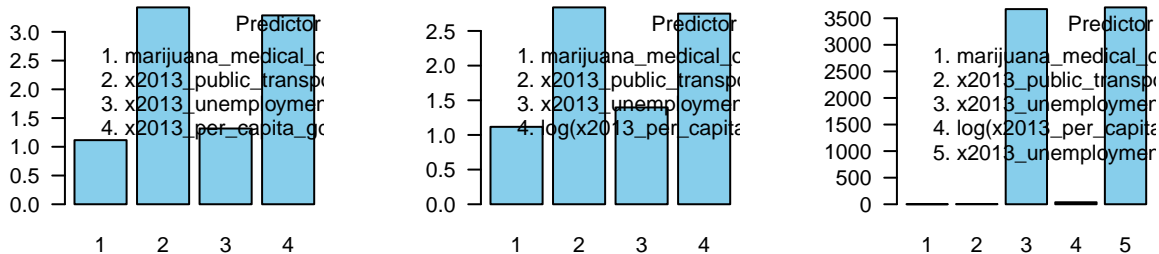
```
}
```

```
## there are higher-order terms (interactions) in this model
## consider setting type = 'predictor'; see ?vif
## there are higher-order terms (interactions) in this model
## consider setting type = 'predictor'; see ?vif
## there are higher-order terms (interactions) in this model
## consider setting type = 'predictor'; see ?vif
```

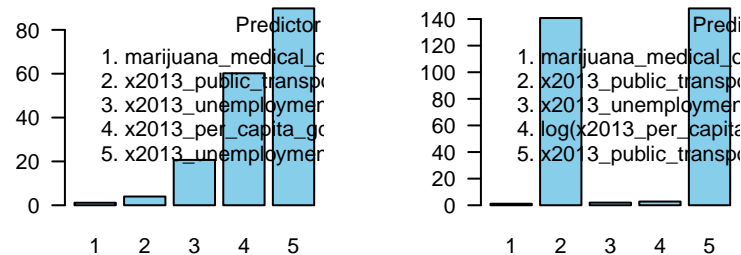
```
# Reset the plotting layout
```

```
par(mfrow = c(1, 1))
```

ariance Inflation Factor (VIF) – mariance Inflation Factor (VIF) – mariance Inflation Factor (VIF) – m



ariance Inflation Factor (VIF) – mariance Inflation Factor (VIF) – m



Matching Analysis

```
# full matching with propensity scores
```

```
m.out1 <- matchit(marijuana_medical_or_recreational_legalized_by_2011 ~
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  x2013_per_capita_gdp,
  data = data,
  method = "full", distance = "glm")
```

```
# Checking balance after matching
```

```
summary(m.out1)
```

```
##
```

```
## Call:
```

```
## matchit(formula = marijuana_medical_or_recreational_legalized_by_2011 ~
```

```
## x2013_public_transport_percentage + x2013_unemployment_rate +
```

```
## x2013_per_capita_gdp, data = data, method = "full", distance = "glm")
```

```
##
## Summary of Balance for All Data:
##
```

	Means Treated	Means Control	Std. Mean Diff.
distance	0.4096	0.2952	0.5553
x2013_public_transport_percentage	0.0552	0.0304	0.2795
x2013_unemployment_rate	0.0747	0.0671	0.4825
x2013_per_capita_gdp	56004.4134	47654.0888	0.2880

```
##
```

	Var. Ratio	eCDF Mean	eCDF Max
distance	3.7144	0.1915	0.4412
x2013_public_transport_percentage	3.0344	0.1887	0.4118
x2013_unemployment_rate	0.9408	0.1292	0.2647
x2013_per_capita_gdp	9.5880	0.0952	0.2353

```
##
## Summary of Balance for Matched Data:
##
```

	Means Treated	Means Control	Std. Mean Diff.
distance	0.4096	0.3880	0.1047
x2013_public_transport_percentage	0.0552	0.0382	0.1911
x2013_unemployment_rate	0.0747	0.0761	-0.0876
x2013_per_capita_gdp	56004.4134	49557.4793	0.2223

```
##
```

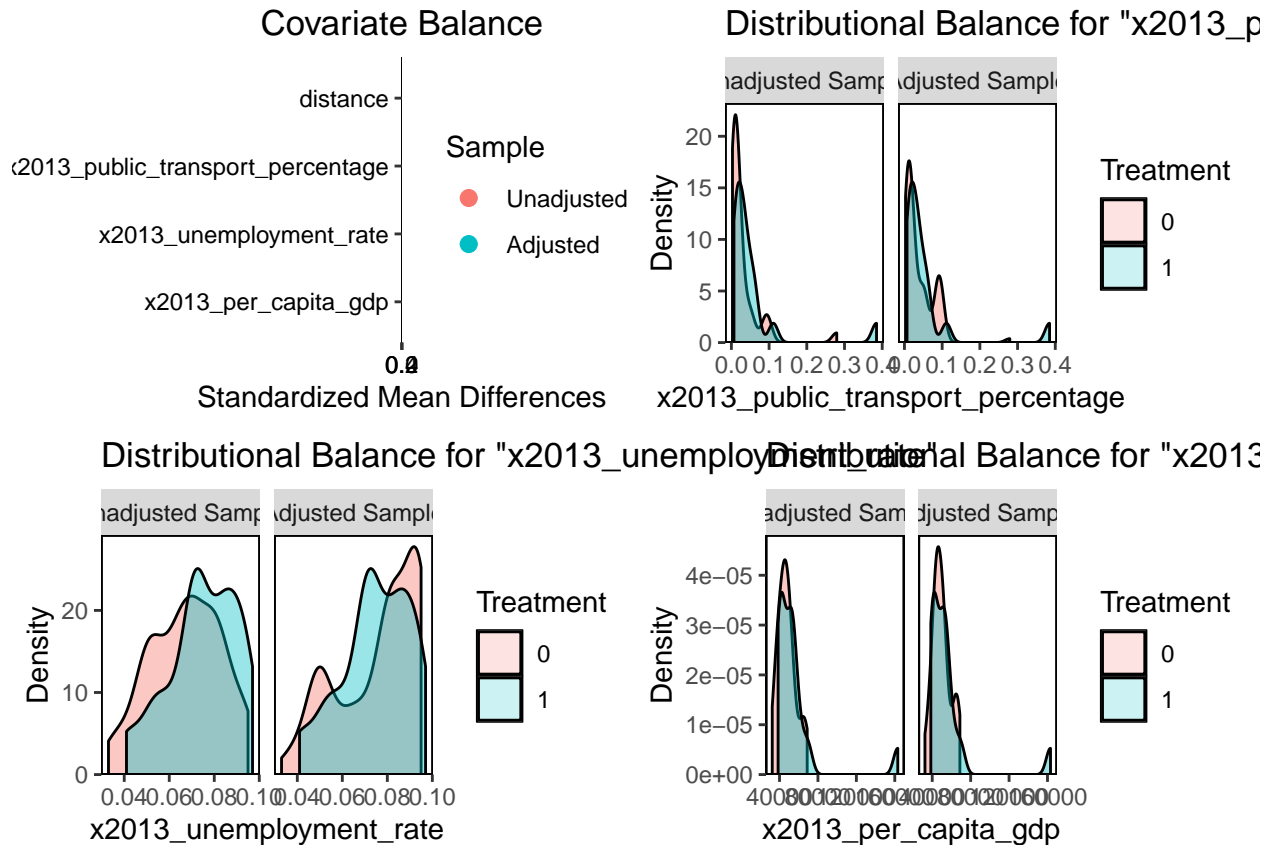
	Var. Ratio	eCDF Mean	eCDF Max	Std. Pair Dist.
distance	1.8664	0.0318	0.1176	0.1118
x2013_public_transport_percentage	4.2015	0.0944	0.2608	0.4404
x2013_unemployment_rate	0.7207	0.0766	0.2059	0.6349
x2013_per_capita_gdp	9.4694	0.0803	0.2137	0.3841

```
##
## Sample Sizes:
##
```

	Control	Treated
All	34.	17
Matched (ESS)	13.12	17
Matched	34.	17
Unmatched	0.	0
Discarded	0.	0

```
##
m.out1_lp <- love.plot(m.out1)
m.out1_bp1 <- bal.plot(m.out1, "x2013_public_transport_percentage", which = "both")
m.out1_bp2 <- bal.plot(m.out1, "x2013_unemployment_rate", which = "both")
m.out1_bp3 <- bal.plot(m.out1, "x2013_per_capita_gdp", which = "both")
grid.arrange(m.out1_lp, m.out1_bp1, m.out1_bp2, m.out1_bp3, ncol = 2)

## Warning: No shared levels found between `names(values)` of the manual scale and the
## data's colour values.
## No shared levels found between `names(values)` of the manual scale and the
## data's colour values.
## No shared levels found between `names(values)` of the manual scale and the
## data's colour values.
```



```
m.genetic = matchit(marijuana_medical_or_recreational_legalized_by_2011 ~
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  x2013_per_capita_gdp,
  data = data, method="genetic", estimand = "ATT")
```

```
## Warning: (from Matching) The key tuning parameters for optimization were are
## all left at their default values. The 'pop.size' option in particular should
## probably be increased for optimal results. For details please see the help
## page and https://www.jsekhon.com
```

```
summary(m.genetic)

##
## Call:
## matchit(formula = marijuana_medical_or_recreational_legalized_by_2011 ~
##   x2013_public_transport_percentage + x2013_unemployment_rate +
##   x2013_per_capita_gdp, data = data, method = "genetic",
##   estimand = "ATT")
##
## Summary of Balance for All Data:
##
##           Means Treated Means Control Std. Mean Diff.
## distance           0.4096           0.2952           0.5553
## x2013_public_transport_percentage 0.0552           0.0304           0.2795
## x2013_unemployment_rate           0.0747           0.0671           0.4825
## x2013_per_capita_gdp           56004.4134           47654.0888           0.2880
##
##           Var. Ratio eCDF Mean eCDF Max
## distance           3.7144           0.1915           0.4412
```

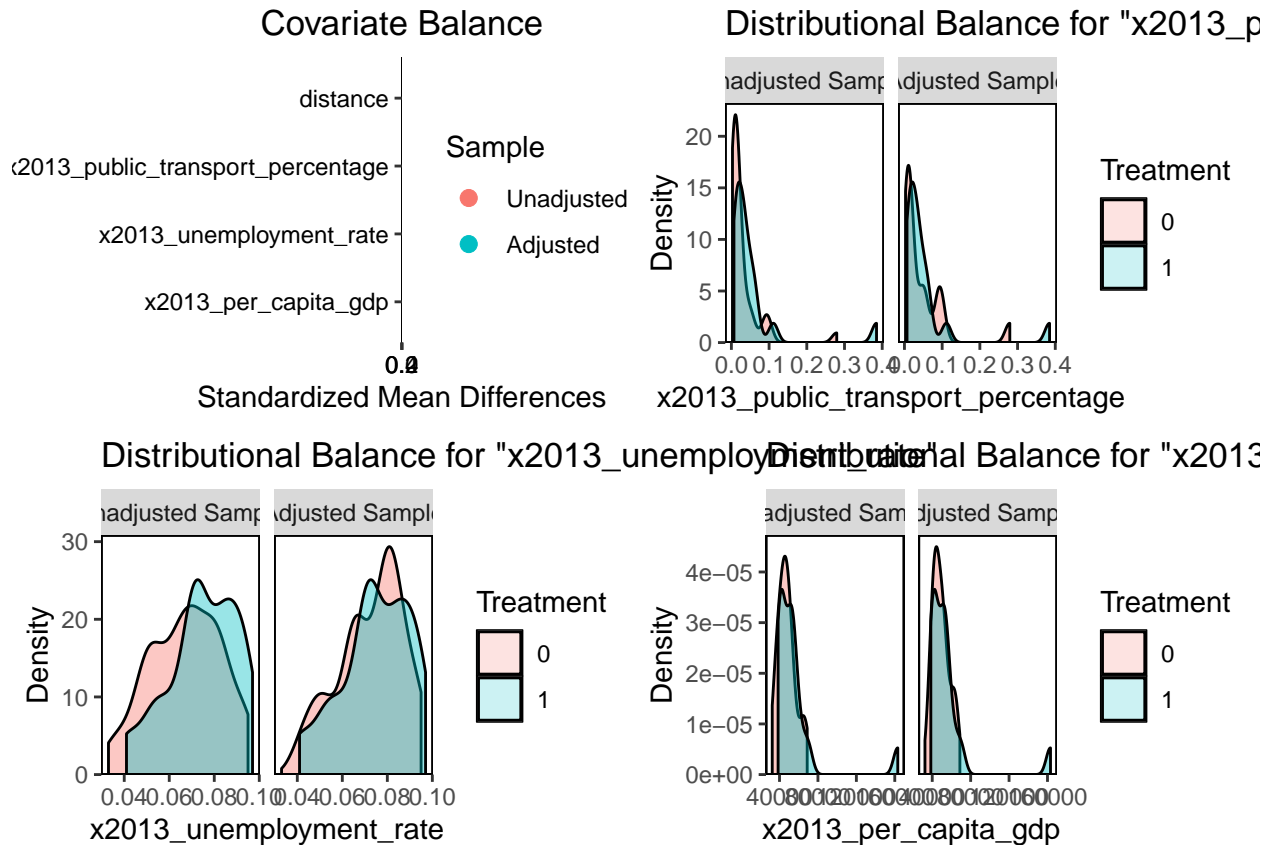
```
## x2013_public_transport_percentage      3.0344      0.1887      0.4118
## x2013_unemployment_rate                 0.9408      0.1292      0.2647
## x2013_per_capita_gdp                   9.5880      0.0952      0.2353
##
## Summary of Balance for Matched Data:
##
## Means Treated Means Control Std. Mean Diff.
## distance                0.4096            0.3354            0.3600
## x2013_public_transport_percentage      0.0552            0.0482            0.0796
## x2013_unemployment_rate                0.0747            0.0728            0.1239
## x2013_per_capita_gdp                56004.4134      48935.0393            0.2438
##
## Var. Ratio eCDF Mean eCDF Max Std. Pair Dist.
## distance                2.7762      0.1061      0.3529            0.4543
## x2013_public_transport_percentage      1.7079      0.1091      0.2353            0.2349
## x2013_unemployment_rate                1.1257      0.0553      0.1765            0.4167
## x2013_per_capita_gdp                11.7594      0.0681      0.1765            0.3188
##
## Sample Sizes:
##           Control Treated
## All           34      17
## Matched        17      17
## Unmatched       17       0
## Discarded        0       0

m.genetic_lp <- love.plot(m.genetic)
m.genetic_bp1 <- bal.plot(m.genetic, "x2013_public_transport_percentage", which = "both")
m.genetic_bp2 <- bal.plot(m.genetic, "x2013_unemployment_rate", which = "both")
m.genetic_bp3 <- bal.plot(m.genetic, "x2013_per_capita_gdp", which = "both")
grid.arrange(m.genetic_lp, m.genetic_bp1, m.genetic_bp2, m.genetic_bp3, ncol = 2)

## Warning: No shared levels found between `names(values)` of the manual scale and the
## data's colour values.

## Warning: No shared levels found between `names(values)` of the manual scale and the
## data's colour values.

## No shared levels found between `names(values)` of the manual scale and the
## data's colour values.
```



```
m1.data <- match.data(m.out1)
m.genetic.data <- match.data(m.genetic)

model2_full = lm(x2013_average_percentage ~
  marijuana_medical_or_recreational_legalized_by_2011 +
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  log(x2013_per_capita_gdp),
  data=m1.data)

model2_genetic = lm(x2013_average_percentage ~
  marijuana_medical_or_recreational_legalized_by_2011 +
  x2013_public_transport_percentage +
  x2013_unemployment_rate +
  log(x2013_per_capita_gdp),
  data=m.genetic.data)

# stargazer(model2_full, model2_genetic, type='html', out='ols_model2_matching_comparison.html')
stargazer(model2_full, model2_genetic, type='text')
```

```
##
## =====
##                               Dependent variable:
##                               -----
##                               x2013_average_percentage
##                               (1)                (2)
## -----
```

## marijuana_medical_or_recreational_legalized_by_2011	-0.001	-0.001
##	(0.001)	(0.001)
##		
## x2013_public_transport_percentage	-0.016	-0.016
##	(0.013)	(0.012)
##		
## x2013_unemployment_rate	-0.026	-0.002
##	(0.036)	(0.036)
##		
## log(x2013_per_capita_gdp)	0.007**	0.008**
##	(0.003)	(0.003)
##		
## Constant	-0.008	-0.013
##	(0.036)	(0.037)
##		
## -----		
## Observations	51	34
## R2	0.172	0.168
## Adjusted R2	0.100	0.054
## Residual Std. Error	0.004 (df = 46)	0.003 (df = 29)
## F Statistic	2.393* (df = 4; 46)	1.469 (df = 4; 29)
## =====		
## Note:	*p<0.1; **p<0.05; ***p<0.01	