(https://github.com/dd-consulting)

One-Stop Analytics: Predictive Modeling (Regression Models)

Case Study of Autism Spectrum Disorder (ASD) with R

ABOUT 1 IN 59 CHILDREN

WERE IDENTIFIED WITH AUTISM SPECTRUM DISORDER
AMONG A 2014 SAMPLE OF 8 YEAR OLDS FROM 11 US COMMUNITIES
IN CDC'S ADDM NETWORK

[United States]

Centers for Disease Control and Prevention (CDC) - Autism Spectrum Disorder (ASD)

Autism spectrum disorder (ASD) is a developmental disability that can cause significant social, communication and behavioral challenges. CDC is committed to continuing to provide essential data on ASD, search for factors that put children at risk for ASD and possible causes, and develop resources that help identify children with ASD as early as possible.

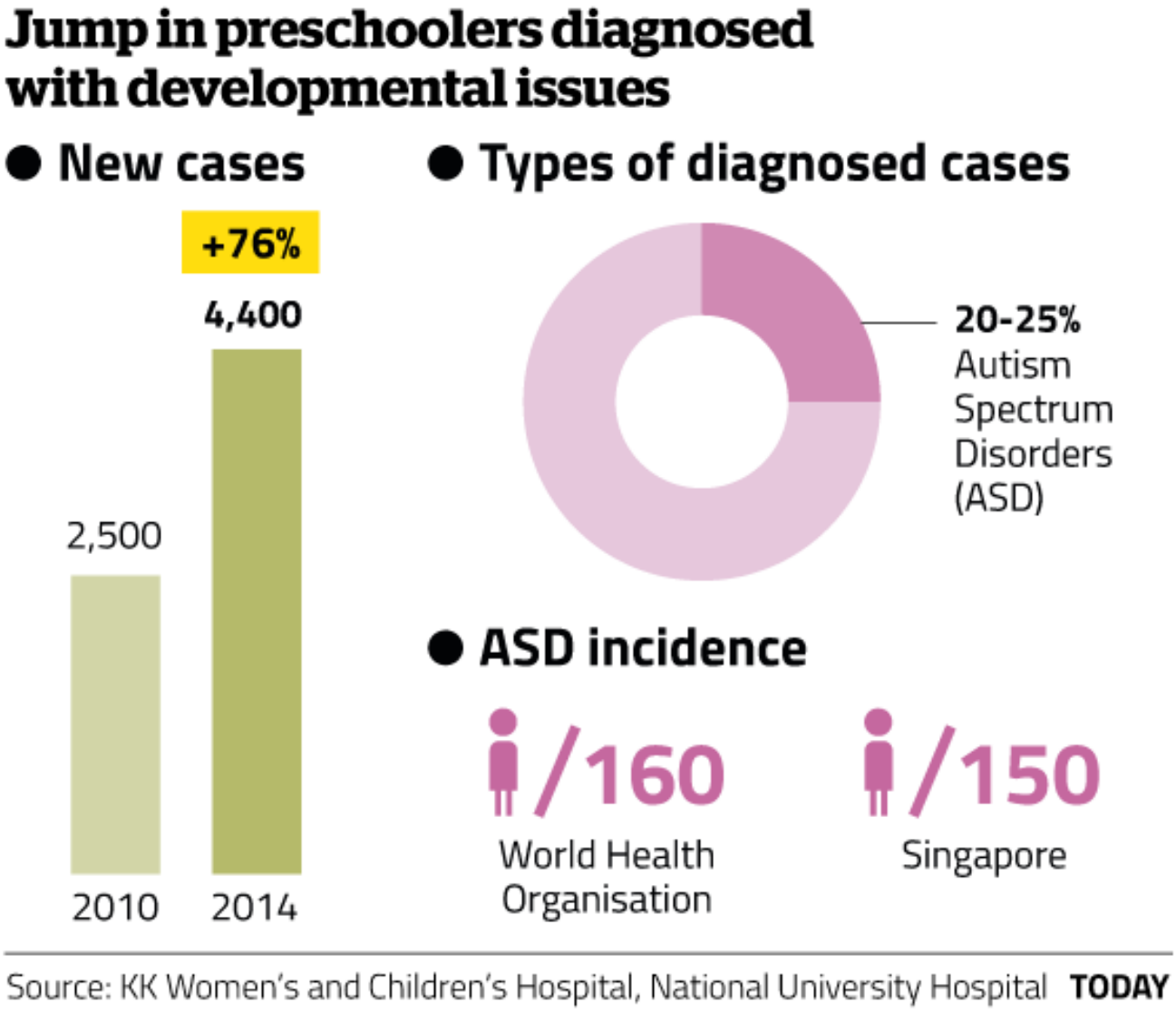
https://www.cdc.gov/ncbddd/autism/data/index.html (https://www.cdc.gov/ncbddd/autism/data/index.html)

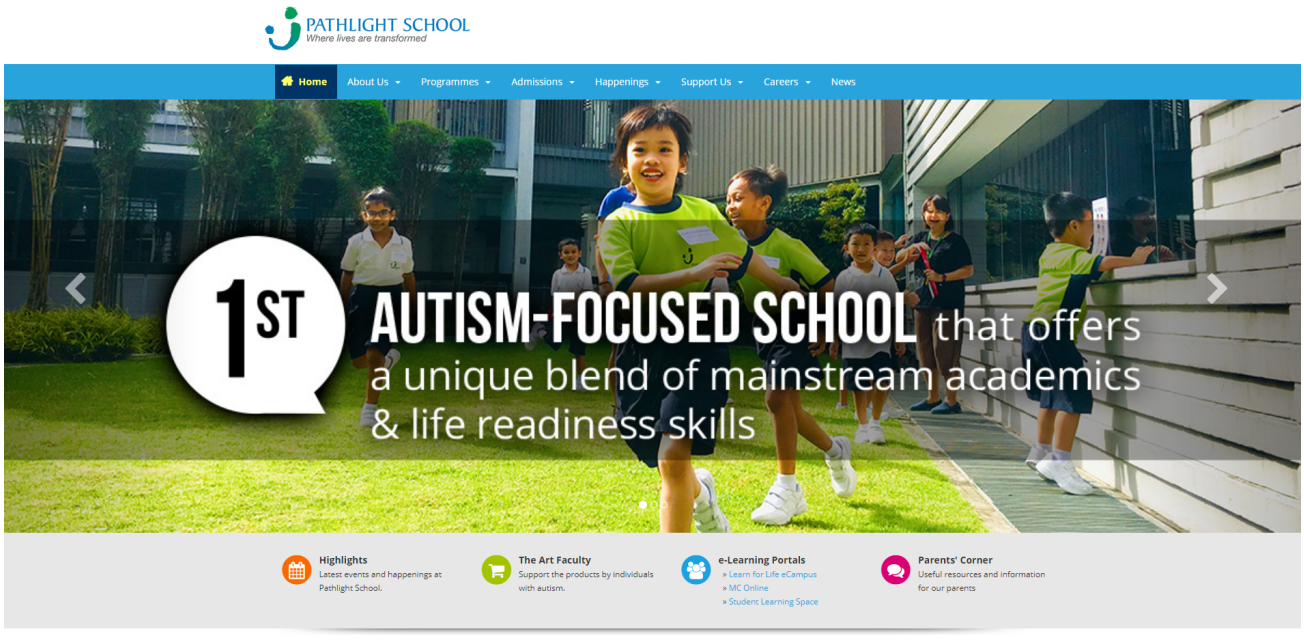
[Singapore]

TODAY Online - More preschoolers diagnosed with developmental issues

Doctors cited better awareness among parents and preschool teachers, leading to early referrals for diagnosis.

https://www.gov.sg/news/content/today-online-more-preschoolers-diagnosed-with-developmental-issues (https://www.gov.sg/news/content/today-online-more-preschoolers-diagnosed-with-developmental-issues)





https://www.pathlight.org.sg/ (https://www.pathlight.org.sg/)

()

Workshop Objective:

Use R to predict Autism Spectrum Disorder (ASD) prevalence.

https://www.cdc.gov/ncbddd/autism/data/index.html (https://www.cdc.gov/ncbddd/autism/data/index.html)

- **Linear Model: Simple Linear Regression (SLR)**
- **Linear Model: Multiple Linear Regression (MLR)**
- **Linear Model: Polynomial Regression (PLR)**
- **Linear Model: Logistic Regression (LR)**
- **Linear Model: Model Evaluation: Train/Test, K-Fold Cross Validation, Confusion Matrix**
- **Linear Model: Prevent Overfitting by Regularization Methods**
- **Workshop Submission**
- **Appendices**

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In [1]:
```
library("repr") # Show graphs in-line notebook
```

Obtain current R working directory

In [2]:
```
getwd()
```

'/media/sf_vm_shared_folder/DDC/DDC-ASD/model_R'

Set new R working directory

In [3]:
```
# setwd("/media/sf_vm_shared_folder/git/DDC/DDC-ASD/model_R")
# setwd('~/Desktop/admin-desktop/vm_shared_folder/git/DDC-ASD/model_R')
getwd()
```

'/media/sf_vm_shared_folder/DDC/DDC-ASD/model_R'

()

Linear Model: Simple Linear Regression (SLR)

Linear Model: Simple Linear Regression (SLR) - Workshop Task

Workshop Task:

1. a. Graph the data in a scatterplot to determine if there is a possible linear relationship.
2. b. Compute and interpret the linear correlation coefficient, r.
3. c. Determine the regression equation for the data.
4. d. Graph the regression equation and the data points.
5. e. Identify potential influential observations (outliers).
6. f. At the 5% significance level, do the data provide sufficient evidence to conclude that the slope of the population regression line is not 0 and, hence, that [Year] is useful as a predictor of ASD [Prevalence]?
7. g. Obtain the residuals and create a residual plot. Decide whether it is reasonable to consider that the assumptions for regression analysis are met by the variables in questions.
8. h. Compute and interpret the coefficient of determination, R^2.
9. i. Find the predicted ASD Prevalence of future Year.
10. j. Determine a 95% confidence interval for the predicted ASD Prevalence.

Use Case Data: "../dataset/ADV_ASD_State_R.csv"

Read in CSV data, storing as R dataframe

In [4]:
```
# Read back in above saved file:
ASD_State <- read.csv("../dataset/ADV_ASD_State_R.csv")
# Convert Year_Factor to ordered.factor
ASD_State$Year_Factor <- factor(ASD_State$Year_Factor, ordered = TRUE)
ASD_State$Prevalence_Risk2 = factor(ASD_State$Prevalence_Risk2, ordered=TRUE,
                                    levels=c("Low", "High"))
ASD_State$Prevalence_Risk4 = factor(ASD_State$Prevalence_Risk4, ordered=TRUE,
                                    levels=c("Low", "Medium", "High", "Very Hi
```

In [5]:
```
head(ASD_State)
```

State	Denominator	Prevalence	Lower.CI	Upper.CI	Year	Source	Source_Full1	State_Full1	State_F
AZ	45322	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Arizo
GA	43593	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Geo
MD	21532	5.5	4.6	6.6	2000	addm	Autism & Developmental Disabilities Monitoring Network	Maryland	Marylan

In [6]:
```
# Filter [ Source: ADDM ], including only two clomuns for SLR:
# Dependent variable: Prevalence
# independent variable: Year
ASD_State_4_SLR = subset(ASD_State, Source_UC == 'ADDM', select = c(Prevalence
#
dim(ASD_State_4_SLR)
head(ASD_State_4_SLR)
```

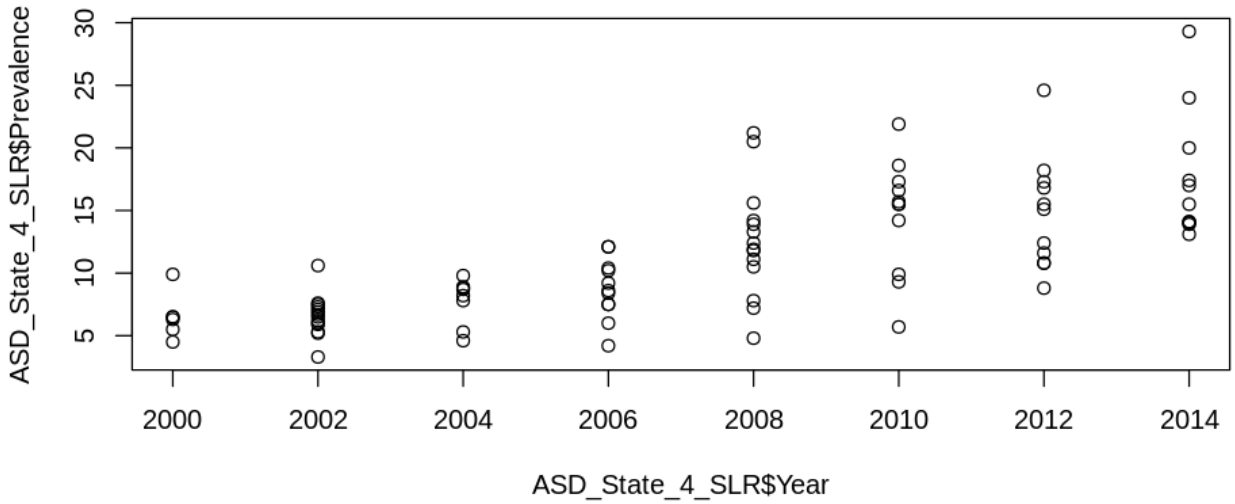
86 2

Prevalence	Year
6.5	2000
6.5	2000
5.5	2000
9.9	2000
6.3	2000
4.5	2000

SLR Workshop Task: 1. a. Graph the data in a scatterplot to determine if there is a possible linear relationship.

In [7]:
```
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=4)
```

In [8]:
```
plot(ASD_State_4_SLR$Year, ASD_State_4_SLR$Prevalence)
```



SLR Workshop Task: **2. b. Compute and interpret the linear correlation coefficient, r.**

Compute correlaion coefficient

In [9]:
```
cor(ASD_State_4_SLR$Year, ASD_State_4_SLR$Prevalence)
```

0.722409821134655

Apply correlation test (two tail: != 0)

In [10]:
```
cor.test(ASD_State_4_SLR$Year, ASD_State_4_SLR$Prevalence)
```

```
        Pearson's product-moment correlation

data:  ASD_State_4_SLR$Year and ASD_State_4_SLR$Prevalence
t = 9.5753, df = 84, p-value = 4.13e-15
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.6027995 0.8102653
sample estimates:
      cor
0.7224098
```

Apply correlation test (one tail: > 0)

In [11]:
```
cor.test(ASD_State_4_SLR$Year, ASD_State_4_SLR$Prevalence, alternative = "grea
```

```
        Pearson's product-moment correlation

data:  ASD_State_4_SLR$Year and ASD_State_4_SLR$Prevalence
t = 9.5753, df = 84, p-value = 2.065e-15
alternative hypothesis: true correlation is greater than 0
95 percent confidence interval:
 0.6243611 1.0000000
sample estimates:
      cor
0.7224098
```

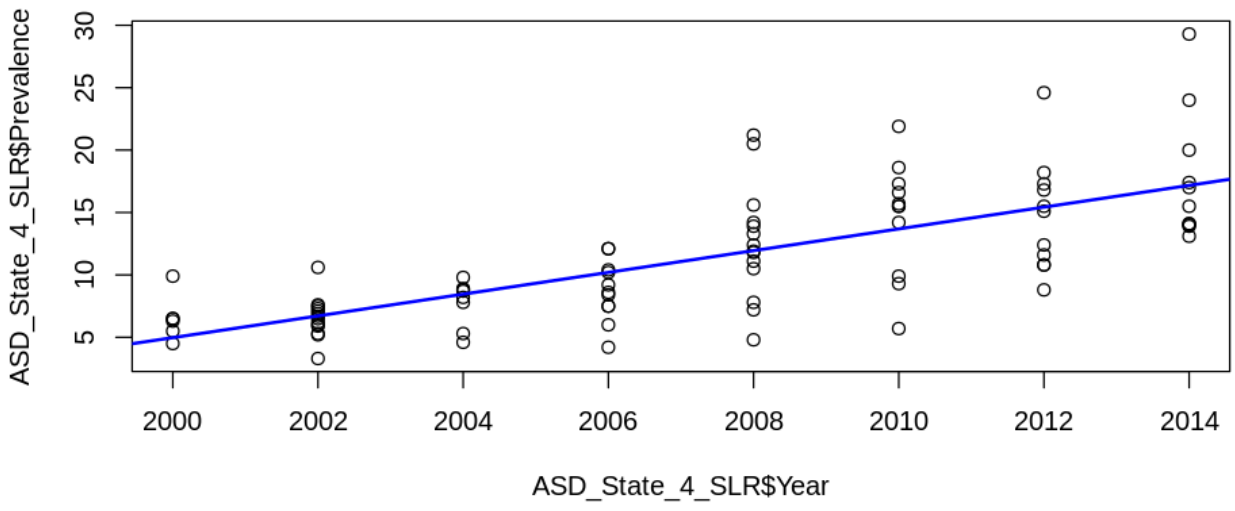
SLR Workshop Task: 3. c. Determine the regression equation for the data.

In [12]:
```
fit_model = lm(formula = Prevalence ~ Year, data = ASD_State_4_SLR)
print(fit_model)
```

```
Call:
lm(formula = Prevalence ~ Year, data = ASD_State_4_SLR)

Coefficients:
(Intercept)         Year
 -1737.8464       0.8714
```

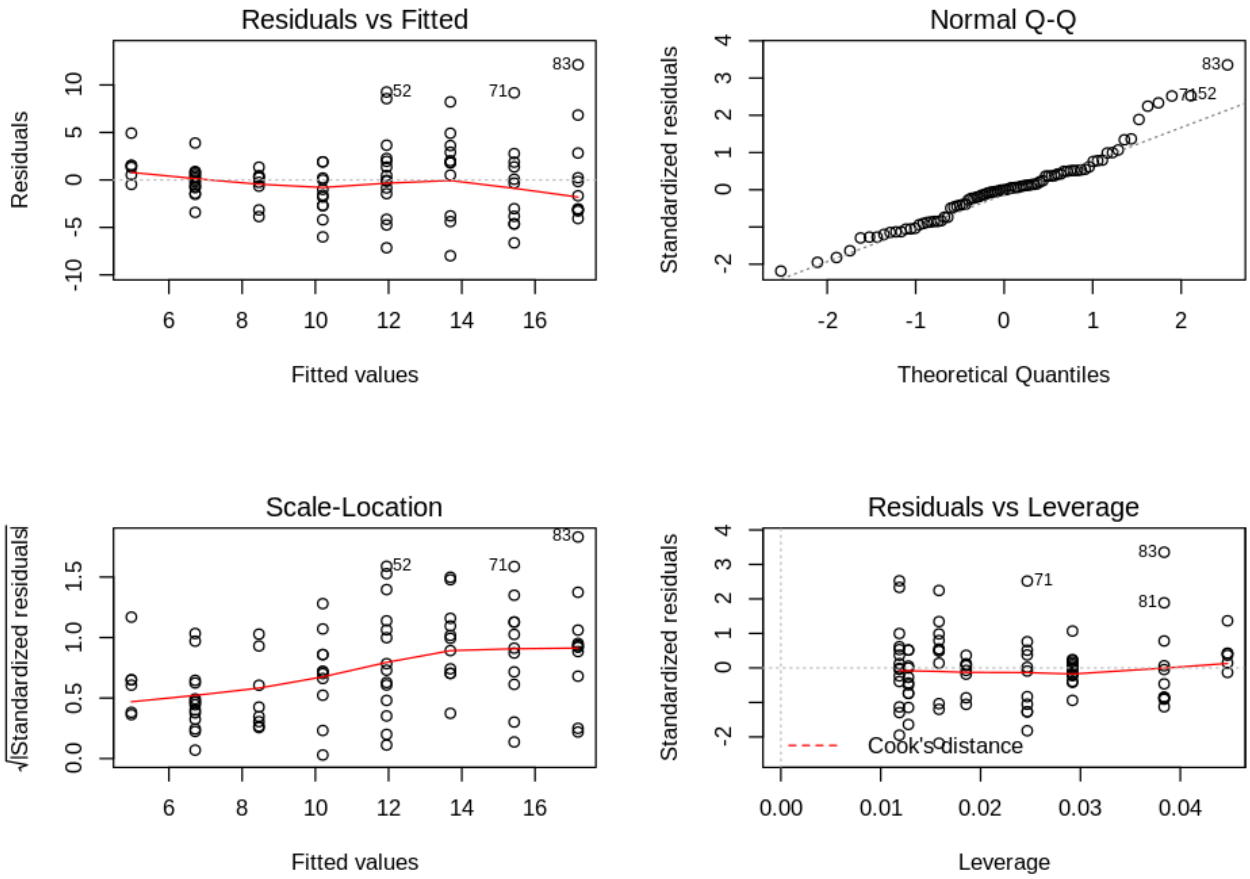
SLR Workshop Task: 4. d. Graph the regression equation and the data points.

In [13]:
```
plot(ASD_State_4_SLR$Year, ASD_State_4_SLR$Prevalence)
abline(fit_model, col="blue", lwd=2)
```



SLR Workshop Task: 5. e. Identify potential influential observations (outliers).

In [14]:
```
# library(repr)
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=6)
par(mfrow=c(2, 2))
plot(fit_model)
par(mfrow=c(1, 1))
```



[Tips] We notice:

- Based on **Residual vs Leverage** chart, there seems no potential influential observations (outliers)

SLR Workshop Task: 6. f. At the 5% significance level, do the data provide sufficient evidence to conclude that the slope of the population regression line is not 0 and, hence, that [Year] is useful as a predictor of ASD [Prevalence]?

In [15]:
```
summary(fit_model)
```

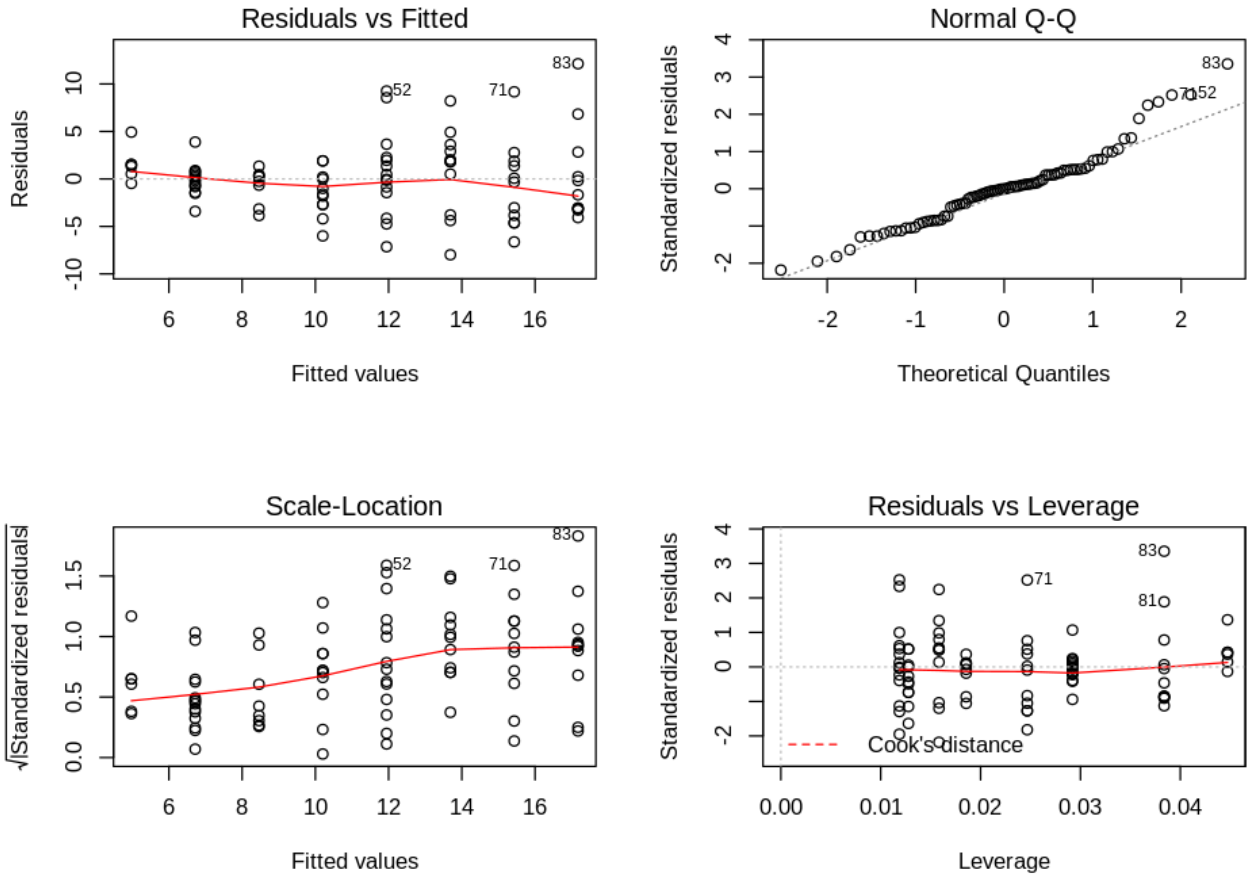
```
Call:
lm(formula = Prevalence ~ Year, data = ASD_State_4_SLR)

Residuals:
    Min      1Q  Median      3Q     Max 
-7.9888 -2.7032 -0.0104  1.7397 12.1255 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1.738e+03  1.827e+02  -9.513 5.51e-15 ***
Year         8.714e-01  9.101e-02   9.575 4.13e-15 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.688 on 84 degrees of freedom
Multiple R-squared:  0.5219,    Adjusted R-squared:  0.5162 
F-statistic: 91.69 on 1 and 84 DF,  p-value: 4.13e-15
```

[Tips] We notice:

2. F-test's p-value is 4.13e-15, which is smaller than 0.05, thus above 95% confidence.

SLR Workshop Task: 7. g. Obtain the residuals and create a residual plot. Decide whether it is reasonable to consider that the assumptions for regression analysis are met by the variables in questions.

In [16]:
```
# library(repr)
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=6)
par(mfrow=c(2, 2))
plot(fit_model)
par(mfrow=c(1, 1))
```



[Tips] We notice:

- Based on **Residual vs Fitted, Sacle-Location, and Normal Q-Q** charts, the residuals (vs fitted) are following linear assumption, with slightly "fan-shape" at larger Year values (Heteroscedasticity). https://statisticsbyjim.com/regression/heteroscedasticity-regression/ (https://statisticsbyjim.com/regression/heteroscedasticity-regression/)
- We are to explore polynomial regression method for this issue later.

SLR Workshop Task: 8. h. Compute and interpret the coefficient of determination, R^2.

In [17]:
```
summary(fit_model)
```

```
Call:
lm(formula = Prevalence ~ Year, data = ASD_State_4_SLR)

Residuals:
    Min      1Q  Median      3Q     Max 
-7.9888 -2.7032 -0.0104  1.7397 12.1255 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1.738e+03  1.827e+02  -9.513 5.51e-15 ***
Year         8.714e-01  9.101e-02   9.575 4.13e-15 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.688 on 84 degrees of freedom
Multiple R-squared:  0.5219,    Adjusted R-squared:  0.5162 
F-statistic: 91.69 on 1 and 84 DF,  p-value: 4.13e-15
```

[Tips] We notice:

- R^2 is 0.5219
- Adjusted R^2 is 0.5162

SLR Workshop Task: 9. i. Find the predicted ASD Prevalence of future Year.

In [18]:
```
future_year = 2025
newdata = data.frame(Year = future_year)
predict(fit_model,newdata)
#
cat("Predicted ASD Prevalence of Year [", future_year, "] is", round(predict(f
```

1: 26.7599815890101

```
Predicted ASD Prevalence of Year [ 2025 ] is 26.8 per 1,000 Children
```

SLR Workshop Task: 10. j. Determine a 95% confidence interval for the predicted ASD Prevalence.

In [19]:
```
predict(fit_model, newdata, interval = "predict")
```

fit	lwr	upr
26.75998	18.72351	34.79645

In [20]:
```
cat("\nPredicted ASD Prevalence of Year [", future_year, "] (95% Upper CI) is"
    round(predict(fit_model,newdata, interval = "predict")[3], 1), "per 1,000

cat("\nPredicted ASD Prevalence of Year [", future_year, "] (95% Lower CI) is"
    round(predict(fit_model,newdata, interval = "predict")[2], 1), "per 1,000
```

```
Predicted ASD Prevalence of Year [ 2025 ] (95% Upper CI) is 34.8 per 1,000 Ch
ildren
Predicted ASD Prevalence of Year [ 2025 ] (95% Lower CI) is 18.7 per 1,000 Ch
ildren
```

Quiz:

Create Prevalence ~ Year SLR model for Data Source: SPED

In [21]:
```
# Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

<!-- Your answer is below:
() -->

Linear Model: Multiple Linear Regression (MLR)

Linear Model: Multiple Linear Regression (MLR) - Workshop Task

Workshop Task:

1. a. Get the data.
2. b. Discover and visualize the data to gain insights (Is there missing Value in the dataframe, then how to deal with the missing value)
3. c. Visualize Data and trends
4. d. Compute correlation between variables and apply multiple regression.
5. e. Check multicollinearity, then how to remove multicollinearity.
6. f. How is your final model looks like?

MLR Workshop Task: 1. a. Get the data.

Use Case Data: "../dataset/ADV_ASD_State_R.csv"

Read in CSV data, storing as R dataframe

In [22]:
```
# Read back in above saved file:
# ASD_State <- read.csv("../dataset/ADV_ASD_State_R.csv")
# ASD_State$Year_Factor <- factor(ASD_State$Year_Factor, ordered = TRUE) # Con
# ASD_State$Prevalence_Risk2 = factor(ASD_State$Prevalence_Risk2, ordered=TRUE
# ASD_State$Prevalence_Risk4 = factor(ASD_State$Prevalence_Risk4, ordered=TRUE
```

In [23]:
```
head(ASD_State)
```

State	Denominator	Prevalence	Lower.CI	Upper.CI	Year	Source	Source_Full1	State_Full1	State_F
AZ	45322	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Arizo
GA	43593	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Geo
MD	21532	5.5	4.6	6.6	2000	addm	Autism & Developmental Disabilities Monitoring Network	Maryland	Marylan

In [24]:
```
names(ASD_State)
```

'State' 'Denominator' 'Prevalence' 'Lower.CI' 'Upper.CI' 'Year' 'Source' 'Source_Full1' 'State_Full1' 'State_Full2' 'Numerator_ASD' 'Numerator_NonASD' 'Proportion' 'Chi_Wilson_Corrected_Lower.CI' 'Chi_Wilson_Corrected_Upper.CI' 'Male.Prevalence' 'Male.Lower.CI' 'Male.Upper.CI' 'Female.Prevalence' 'Female.Lower.CI' 'Female.Upper.CI' 'Non.hispanic.white.Prevalence' 'Non.hispanic.white.Lower.CI' 'Non.hispanic.white.Upper.CI' 'Non.hispanic.black.Prevalence' 'Non.hispanic.black.Lower.CI' 'Non.hispanic.black.Upper.CI' 'Hispanic.Prevalence' 'Hispanic.Lower.CI' 'Hispanic.Upper.CI' 'Asian.or.Pacific.Islander.Prevalence' 'Asian.or.Pacific.Islander.Lower.CI' 'Asian.or.Pacific.Islander.Upper.CI' 'State_Region' 'Source_UC' 'Source_Full3' 'Prevalence_Risk2' 'Prevalence_Risk4' 'Year_Factor'

In [25]:
```
# Filter to include relevant clomuns for MLR:
# Dependent variable: Prevalence
# independent variable: Let's include all at the moment
ASD_State_4_MLR = ASD_State
#
dim(ASD_State_4_MLR)
head(ASD_State_4_MLR)
```

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State	Denominator	Prevalence	Lower.CI	Upper.CI	Year	Source	Source_Full1	State_Full1	State_F
AZ	45322	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Ariz
GA	43593	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Geo
MD	21532	5.5	4.6	6.6	2000	addm	Autism & Developmental Disabilities	Maryland	Maryla

MLR Workshop Task: 2. b. Discover and visualize the data to gain insights (Is there missing Value in the dataframe, then how to deal with the missing value).

In [26]:
```
summary(ASD_State_4_MLR)
```

```
     State         Denominator        Prevalence       Lower.CI     
 AZ     :  40   Min.   :    965   Min.   : 0.400   Min.   : 0.30  
 MD     :  40   1st Qu.: 107151   1st Qu.: 3.100   1st Qu.: 2.80  
 GA     :  39   Median : 353328   Median : 5.600   Median : 5.30  
 MO     :  39   Mean   : 604689   Mean   : 7.191   Mean   : 6.42  
 NC     :  39   3rd Qu.: 767928   3rd Qu.: 9.200   3rd Qu.: 8.60  
 WI     :  39   Max.   :5824922   Max.   :42.700   Max.   :29.90  
 (Other):1456                                                     
    Upper.CI           Year       Source    
 Min.   : 0.600   Min.   :2000   addm: 86  
 1st Qu.: 3.300   1st Qu.:2003   medi:655  
 Median : 5.900   Median :2007   nsch: 98  
 Mean   : 8.262   Mean   :2007   sped:853  
 3rd Qu.: 9.700   3rd Qu.:2011             
 Max.   :69.000   Max.   :2016             

                                                 Source_Full1
 Autism & Developmental Disabilities Monitoring Network: 86  
 Medicaid                                                :655
```

In [27]:
```
# Check whether each columns got missing value:
lapply(ASD_State_4_MLR, function(col_x)sum(is.na(col_x)))

# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=3)
barplot(apply(ASD_State_4_MLR, 2, function(col_x)sum(is.na(col_x))))
```

$State
0
$Denominator
0
$Prevalence
0
$Lower.CI
0
$Upper.CI
0
$Year
0
$Source
0
$Source_Full1
0
$State_Full1

In [28]:
```
dim(ASD_State_4_MLR)
```

1692 39

In [29]:
```
#Get all the column variables which contains missing value
NA_Column_Names <- names(ASD_State_4_MLR[0, colSums(is.na(ASD_State_4_MLR)) >
#
NA_Column_Names
```

'Male.Prevalence' 'Male.Lower.CI' 'Male.Upper.CI' 'Female.Prevalence' 'Female.Lower.CI' 'Female.Upper.CI' 'Non.hispanic.white.Prevalence' 'Non.hispanic.white.Lower.CI' 'Non.hispanic.white.Upper.CI' 'Non.hispanic.black.Prevalence' 'Non.hispanic.black.Lower.CI' 'Non.hispanic.black.Upper.CI' 'Hispanic.Prevalence' 'Hispanic.Lower.CI' 'Hispanic.Upper.CI' 'Asian.or.Pacific.Islander.Prevalence' 'Asian.or.Pacific.Islander.Lower.CI' 'Asian.or.Pacific.Islander.Upper.CI'

In [30]:
```
# Remove these columns from dataframe
ASD_State_4_MLR <- ASD_State_4_MLR[ , !(names(ASD_State_4_MLR) %in% NA_Column_
#
head(ASD_State_4_MLR)
```

State	Denominator	Prevalence	Lower.CI	Upper.CI	Year	Source	Source_Full1	State_Full1	State_F
AZ	45322	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Arizo
GA	43593	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Geo
MD	21532	5.5	4.6	6.6	2000	addm	Autism & Developmental Disabilities Monitoring Network	Maryland	Marylan

No missing values, as they have been handled earlier. Hurrah!

But some varialbe contains "leaky" information, which can be used to directly calculate the dependent variable: Prevalence. This won't happen in real world scenario, thus they need to be removed.

In [31]:
```
cbind(names(ASD_State_4_MLR), c(1:length(names(ASD_State_4_MLR))))
```

State	1
Denominator	2
Prevalence	3
Lower.CI	4
Upper.CI	5
Year	6
Source	7
Source_Full1	8
State_Full1	9
State_Full2	10
Numerator_ASD	11
Numerator_NonASD	12
Proportion	13

In [32]:
```
Leaky_Column_Names = c('Lower.CI', 'Upper.CI', 'Numerator_ASD', 'Numerator_Non
                       'Chi_Wilson_Corrected_Lower.CI', 'Chi_Wilson_Corrected_
                       'Prevalence_Risk2', 'Prevalence_Risk4')
```

In [33]:
```
# Remove these columns from dataframe
ASD_State_4_MLR <- ASD_State_4_MLR[ , !(names(ASD_State_4_MLR) %in% Leaky_Colu
#
head(ASD_State_4_MLR)
```

State	Denominator	Prevalence	Year	Source	Source_Full1	State_Full1	State_Full2	State_Region
AZ	45322	6.5	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Arizona	D8 Mountain
GA	43593	6.5	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Georgia	D5 South Atlantic
MD	21532	5.5	2000	addm	Autism & Developmental Disabilities Monitoring Network	Maryland	MD-Maryland	D5 South Atlantic

Remove redundant/duplicate variables (aliased coefficients), retaining one for each type of information is enough:

https://en.wikipedia.org/wiki/Multicollinearity (https://en.wikipedia.org/wiki/Multicollinearity)

https://stats.stackexchange.com/questions/112442/what-are-aliased-coefficients (https://stats.stackexchange.com/questions/112442/what-are-aliased-coefficients)

In [34]:
```
Redundant_Column_Names = c('State', 'Source_Full1', 'State_Full1', 'State_Regi
```

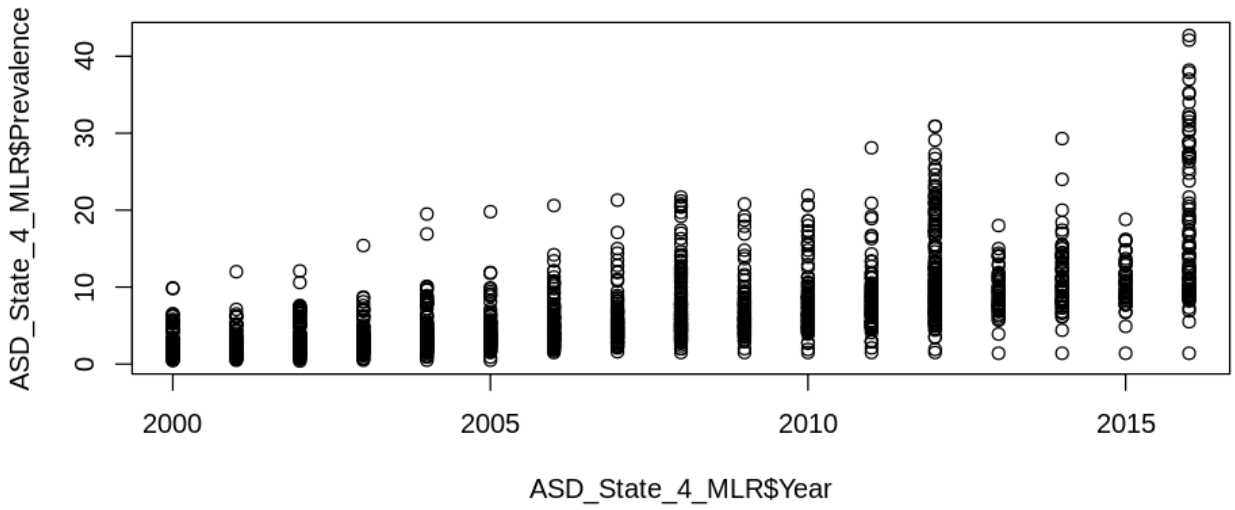
In [35]:
```
# Remove these columns from dataframe
ASD_State_4_MLR <- ASD_State_4_MLR[ , !(names(ASD_State_4_MLR) %in% Redundant_
#
head(ASD_State_4_MLR)
```

Denominator	Prevalence	Year	Source	State_Full2
45322	6.5	2000	addm	AZ-Arizona
43593	6.5	2000	addm	GA-Georgia
21532	5.5	2000	addm	MD-Maryland
29714	9.9	2000	addm	NJ-New Jersey
24535	6.3	2000	addm	SC-South Carolina
23065	4.5	2000	addm	WV-West Virginia

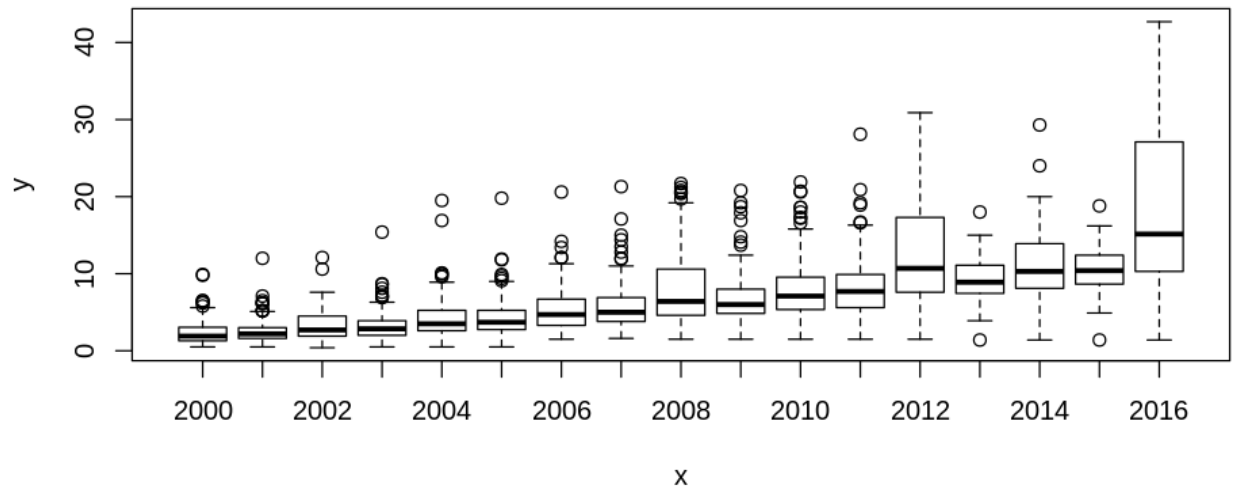
MLR Workshop Task: 3. c. Visualize the data to gain insights

In [36]:
```
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=4)
```

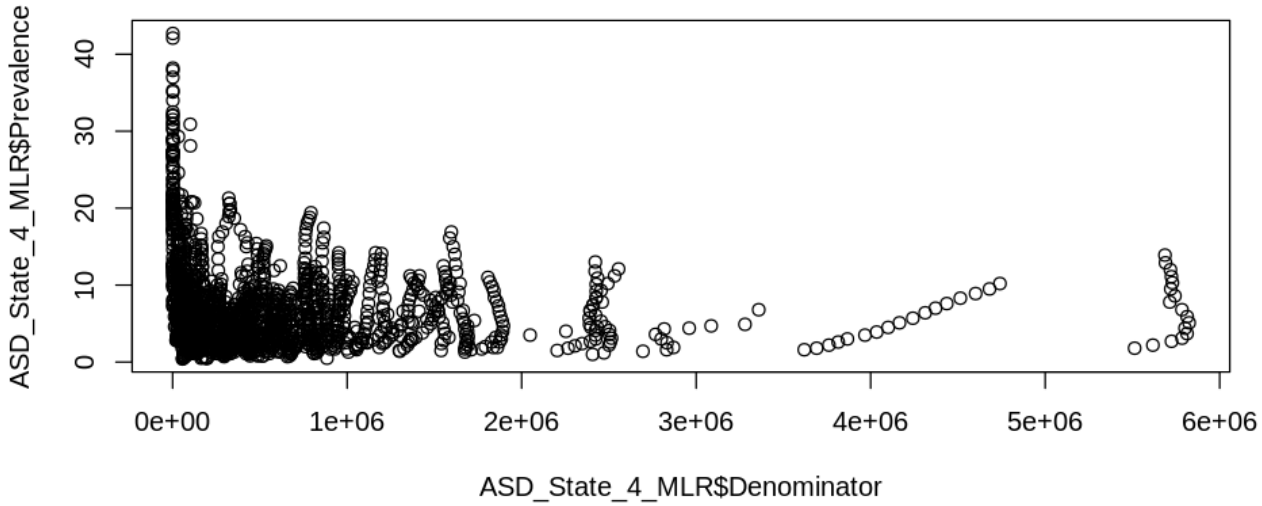
In [37]:
```
plot(ASD_State_4_MLR$Year, ASD_State_4_MLR$Prevalence)
```



In [38]:
```
plot(as.factor(ASD_State_4_MLR$Year), ASD_State_4_MLR$Prevalence)
```

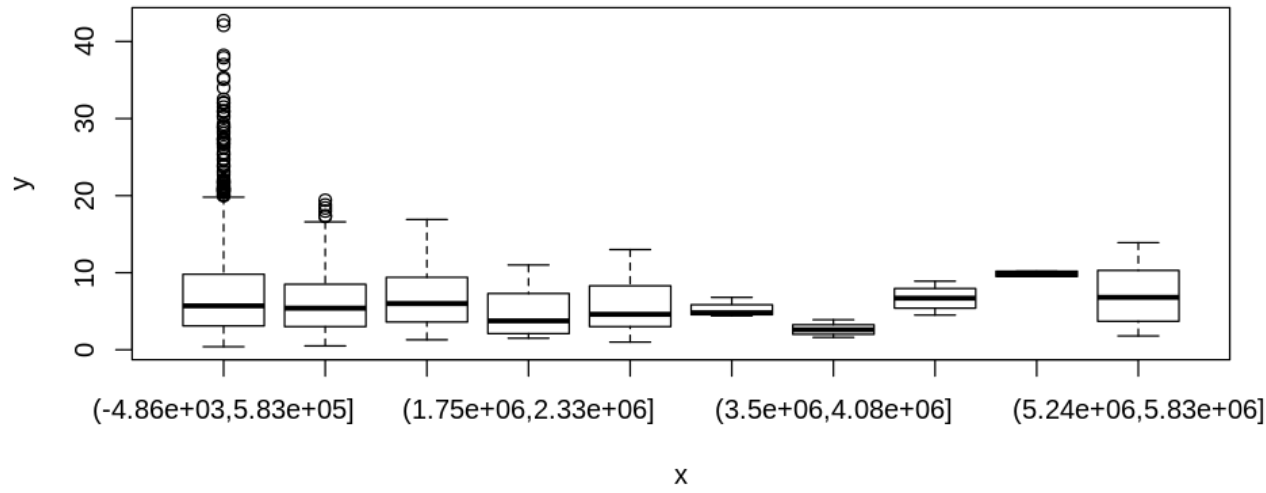


In [39]:
```
plot(ASD_State_4_MLR$Denominator, ASD_State_4_MLR$Prevalence)
```

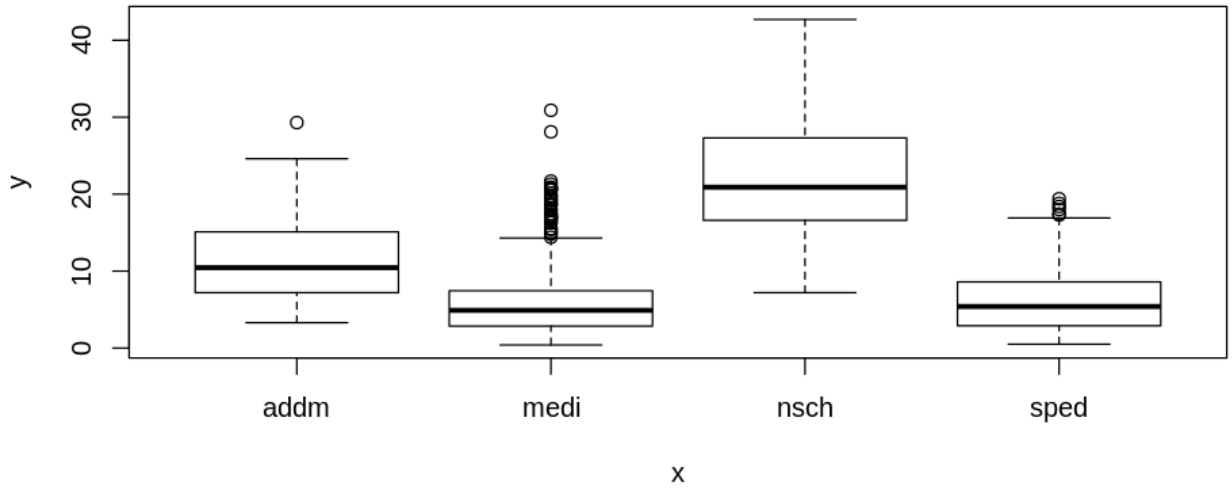


In [40]:
```
# To use bin() function
# https://www.rdocumentation.org/packages/OneR/versions/2.2/topics/bin
if(!require(OneR)){install.packages("OneR")}
library('OneR')

# Bin 'Denominator'
plot(bin(ASD_State_4_MLR$Denominator, nbins = 10), ASD_State_4_MLR$Prevalence)
```

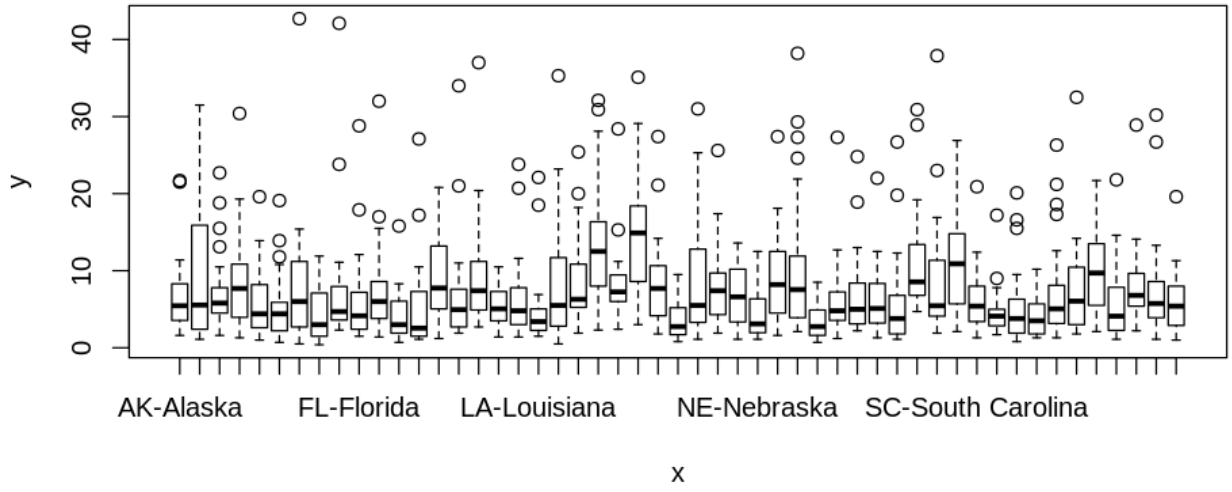
```
Loading required package: OneR
```



In [41]:
```
plot(ASD_State_4_MLR$Source, ASD_State_4_MLR$Prevalence)
```



In [42]:
```
plot(ASD_State_4_MLR$State_Full2, ASD_State_4_MLR$Prevalence)
```



MLR Workshop Task: **4. d. Compute correlation between variables and apply multiple regression.**

Recode categorical variable to dummy (numeric) variable using one-hot encoding:

In [43]:
```
# To use select_if() function
if(!require(dplyr)){install.packages("dplyr")}
library("dplyr")

summary(select_if(ASD_State_4_MLR, is.numeric))
```

```
Loading required package: 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


  Denominator        Prevalence          Year     
 Min.   :    965   Min.   : 0.400   Min.   :2000  
 1st Qu.: 107151   1st Qu.: 3.100   1st Qu.:2003  
 Median : 353328   Median : 5.600   Median :2007  
 Mean   : 604689   Mean   : 7.191   Mean   :2007  
 3rd Qu.: 767928   3rd Qu.: 9.200   3rd Qu.:2011  
 Max.   :5824922   Max.   :42.700   Max.   :2016  
```

In [44]:
```
correlation = cor(select_if(ASD_State_4_MLR, is.numeric))
correlation
```

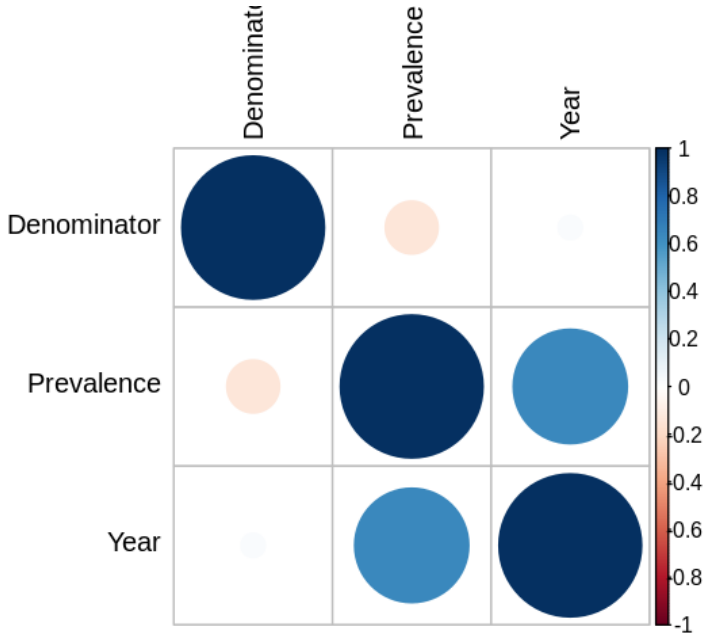
	Denominator	Prevalence	Year
Denominator	1.00000000	-0.1374662	0.02851671
Prevalence	-0.13746621	1.0000000	0.64002950
Year	0.02851671	0.6400295	1.00000000

In [45]:
```
# Variable's correlation against target dependent variable:
correlation[, 2]
```

Denominator	-0.137466206927898
Prevalence	1
Year	0.640029495747179

In [46]:
```
if(!require(corrplot)){install.packages("corrplot")}
library("corrplot")
corrplot(correlation, tl.col="black", tl.pos = "lt")
```

```
Loading required package: corrplot
corrplot 0.84 loaded
```



In [47]:
```
str(ASD_State_4_MLR)
```

```
'data.frame':   1692 obs. of  5 variables:
 $ Denominator: int  45322 43593 21532 29714 24535 23065 35472 45113 36472 11
020 ...
 $ Prevalence : num  6.5 6.5 5.5 9.9 6.3 4.5 3.3 6.2 6.9 5.9 ...
 $ Year       : int  2000 2000 2000 2000 2000 2000 2002 2002 2002 2002 ...
 $ Source     : Factor w/ 4 levels "addm","medi",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ State_Full2: Factor w/ 51 levels "AK-Alaska","AL-Alabama",..: 4 11 21 32 4
1 50 2 4 3 6 ...
```

In [48]:
```
# To build (National level) ASD Prevalence predictive model for all state's:
# In situations that we won't know the US. State name, we can also fit a model
fit_model = lm(Prevalence ~ . - State_Full2, data = ASD_State_4_MLR) # Exclude
#
summary(fit_model)
```

```
Call:
lm(formula = Prevalence ~ . - State_Full2, data = ASD_State_4_MLR)

Residuals:
     Min       1Q   Median       3Q      Max
-11.4476  -1.9332  -0.2786   1.2479  21.0130

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.310e+03  3.819e+01 -34.306   <2e-16 ***
Denominator -1.139e-07  1.057e-07  -1.078    0.281
Year         6.583e-01  1.902e-02  34.606   <2e-16 ***
Sourcemedi  -4.550e+00  3.964e-01 -11.478   <2e-16 ***
Sourcensch   6.699e+00  5.171e-01  12.956   <2e-16 ***
Sourcesped  -5.611e+00  3.984e-01 -14.085   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.43 on 1686 degrees of freedom
Multiple R-squared:  0.6585,    Adjusted R-squared:  0.6575
F-statistic: 650.2 on 5 and 1686 DF,  p-value: < 2.2e-16
```

Adjusted R^2 = 0.6575

In [49]:
```
# To build (US. State level) ASD Prevalence predictive model for specific stat
# In situations that we shall know the US. State name. (A state name is requir
fit_model = lm(Prevalence ~ . , data = ASD_State_4_MLR) # "~." means all other
#
summary(fit_model)
```

```
Call:
lm(formula = Prevalence ~ ., data = ASD_State_4_MLR)

Residuals:
     Min       1Q   Median       3Q      Max
-11.3326  -1.3626  -0.0689   1.2558  19.0273

Coefficients:
                                Estimate Std. Error t value Pr(>|t|)

(Intercept)                   -1.305e+03  3.144e+01 -41.498  < 2e-16 *
**
Denominator                    1.152e-06  2.252e-07   5.115 3.50e-07 *
**
Year                           6.558e-01  1.566e-02  41.889  < 2e-16 *
**
Sourcemedi                    -4.997e+00  3.557e-01 -14.048  < 2e-16 *
**
Sourcensch                     6.100e+00  4.404e-01  13.853  < 2e-16 *
```

Adjusted R^2 = 0.7697

MLR Workshop Task: 5. e. Check multicollinearity, then how to remove multicollinearity.

< Detection of multicollinearity >

Some authors have suggested a formal detection-tolerance or the variance inflation factor (VIF) for multicollinearity. A VIF of 5 or 10 and above indicates a multicollinearity problem.

In [50]:
```
# To use select_if() function
if(!require(car)){install.packages("car")}
library("car")
```

```
Loading required package: car
Loading required package: carData

Attaching package: ‘car’

The following object is masked from ‘package:dplyr’:

    recode
```

In [51]:
```
vif(fit_model)
```

	GVIF	Df	GVIF^(1/(2*Df))
Denominator	7.737921	1	2.781712
Year	1.146987	1	1.070975
Source	2.502245	3	1.165167
State_Full2	7.768262	50	1.020712

[Tips] We notice VIF of Denominator and State_Full2 are high. Let's exclude them one at a time.

Retain: State; Remove: Denominator then re-build model:

In [52]:
```
# To build (National level) ASD Prevalence predictive model for all state's:
# In situations that we won't know the US. State name, we can also fit a model
fit_model_with_State = lm(Prevalence ~ . - Denominator, data = ASD_State_4_MLR
#
summary(fit_model_with_State)
```

```
State_Full2KY-Kentucky             -4.094e-01  7.084e-01  -0.578 0.563423

State_Full2LA-Louisiana            -2.034e+00  7.084e-01  -2.872 0.004134 *
*
State_Full2MA-Massachusetts         1.337e+00  7.031e-01   1.901 0.057418 .

State_Full2MD-Maryland              8.308e-01  6.754e-01   1.230 0.218796

State_Full2ME-Maine                 6.458e+00  7.409e-01   8.716  < 2e-16 *
**
State_Full2MI-Michigan              1.516e+00  7.084e-01   2.139 0.032544 *

State_Full2MN-Minnesota             7.094e+00  6.980e-01  10.164  < 2e-16 *
**
State_Full2MO-Missouri              7.645e-01  6.785e-01   1.127 0.259995

State_Full2MS-Mississippi          -1.940e+00  7.204e-01  -2.692 0.007164 *
*
```

In [53]:
```
vif(fit_model_with_State)
```

	GVIF	Df	GVIF^(1/(2*Df))
Year	1.139247	1	1.067355
Source	1.306350	3	1.045546
State_Full2	1.149997	50	1.001399

Adjusted R^2 = 0.7662

Retain: Denominator; Remove: State; then re-build model:

In [54]:
```
# To build (National level) ASD Prevalence predictive model for all state's:
# In situations that we won't know the US. State name, we can also fit a model
fit_model_with_Denominator = lm(Prevalence ~ . - State_Full2, data = ASD_State
#
summary(fit_model_with_Denominator)
```

```
Call:
lm(formula = Prevalence ~ . - State_Full2, data = ASD_State_4_MLR)

Residuals:
     Min       1Q   Median       3Q      Max
-11.4476  -1.9332  -0.2786   1.2479  21.0130

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.310e+03  3.819e+01 -34.306   <2e-16 ***
Denominator -1.139e-07  1.057e-07  -1.078    0.281
Year         6.583e-01  1.902e-02  34.606   <2e-16 ***
Sourcemedi  -4.550e+00  3.964e-01 -11.478   <2e-16 ***
Sourcensch   6.699e+00  5.171e-01  12.956   <2e-16 ***
Sourcesped  -5.611e+00  3.984e-01 -14.085   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.43 on 1686 degrees of freedom
Multiple R-squared:  0.6585,    Adjusted R-squared:  0.6575
F-statistic: 650.2 on 5 and 1686 DF,  p-value: < 2.2e-16
```

In [55]:
```
vif(fit_model_with_Denominator)
```

	GVIF	Df	GVIF^(1/(2*Df))
Denominator	1.145505	1	1.070283
Year	1.138674	1	1.067086
Source	1.301973	3	1.044962

Adjusted R^2 = 0.6575

MLR Workshop Task: 6. f. How is your final model looks like?

- During prediction, if US. State name will be known, then the **fit_model_with_State** can be better because it has higher R^2 value.
- During prediction, if US. State name will NOT be known, then the **fit_model_with_Denominator** can be adopted because it doesn't require state name as input for prediciton.

MLR Prediciton 1

Let's use **fit_model_with_State** to predict CA-California ASD Prevalence of Year 2016 if ADDM would have conducted a survey

In [56]:
```
newdata = ASD_State_4_MLR[1,] # Copy datastructure
newdata$Prevalence = NA
newdata$Denominator = 50000
newdata$Year = 2016
newdata$Source = "addm"
#newdata$State_Full2 = "CA-California"
newdata$State_Full2 = "AZ-Arizona"

newdata
```

Denominator	Prevalence	Year	Source	State_Full2
50000	NA	2016	addm	AZ-Arizona

In [57]:
```
predict(fit_model_with_State, newdata, interval = "predict")
#
cat("Predicted ASD Prevalence is", round(predict(fit_model_with_State, newdata
```

fit	lwr	upr
17.54292	11.88535	23.20049

```
Predicted ASD Prevalence is 17.5 per 1,000 Children
```

MLR Prediciton 2

Let's use **fit_model_with_Denominator** to predict National level ASD Prevalence of Year 2016 if ADDM would have conducted a survey

In [58]:
```
predict(fit_model_with_Denominator, newdata, interval = "predict")
#
cat("Predicted ASD Prevalence is", round(predict(fit_model_with_Denominator, n
```

fit	lwr	upr
17.07629	10.30306	23.84952

```
Predicted ASD Prevalence is 17.1 per 1,000 Children
```

MLR Prediciton 2

Let's use **fit_model** to predict FL-Florida State level ASD Prevalence of Year 2025 if SPED will conduct a record review/survey of 2,600,000 children.

In [59]:
```
newdata = ASD_State_4_MLR[1,] # Copy datastructure
newdata$Prevalence = NA
newdata$Denominator = 2600000
newdata$Year = 2025
newdata$Source = "sped"
newdata$State_Full2 = "FL-Florida"

newdata
```

Denominator	Prevalence	Year	Source	State_Full2
2600000	NA	2025	sped	FL-Florida

In [60]:
```
predict(fit_model, newdata, interval = "predict")
#
cat("Predicted ASD Prevalence is", round(predict(fit_model, newdata), 1), "per
```

fit	lwr	upr
16.63773	11.00985	22.2656

```
Predicted ASD Prevalence is 16.6 per 1,000 Children
```

()

Linear Model: Polynomial (Linear) Regression (PLR)

Linear Model: Polynomial (Linear) Regression (PLR) - Workshop Task

Workshop Task:

1. a. Get the data.
2. b. Discover and visualize the data to gain insights (Is there missing Value in the dataframe, then how to deal with the missing value)
3. c. Visualize Data and trends
4. d. Compute correlation between variables and apply multiple regression.
5. e. Multiple polynomial regression.

PLR Workshop Task: 1. a. Get the data.

Use Case Data: "../dataset/ADV_ASD_State_R.csv"

Read in CSV data, storing as R dataframe

In [61]:
```
# Read back in above saved file:
ASD_State <- read.csv("../dataset/ADV_ASD_State_R.csv")
ASD_State$Year_Factor <- factor(ASD_State$Year_Factor, ordered = TRUE) # Conve
ASD_State$Prevalence_Risk2 = factor(ASD_State$Prevalence_Risk2, ordered=TRUE,
ASD_State$Prevalence_Risk4 = factor(ASD_State$Prevalence_Risk4, ordered=TRUE,
```

In [62]:
```
head(ASD_State)
```

State	Denominator	Prevalence	Lower.CI	Upper.CI	Year	Source	Source_Full1	State_Full1	State_F
AZ	45322	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Arizo
GA	43593	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Geo
MD	21532	5.5	4.6	6.6	2000	addm	Autism & Developmental Disabilities Monitoring Network	Maryland	Marylan

In [63]:
```
names(ASD_State)
```

'State' 'Denominator' 'Prevalence' 'Lower.CI' 'Upper.CI' 'Year' 'Source' 'Source_Full1' 'State_Full1' 'State_Full2' 'Numerator_ASD' 'Numerator_NonASD' 'Proportion' 'Chi_Wilson_Corrected_Lower.CI' 'Chi_Wilson_Corrected_Upper.CI' 'Male.Prevalence' 'Male.Lower.CI' 'Male.Upper.CI' 'Female.Prevalence' 'Female.Lower.CI' 'Female.Upper.CI' 'Non.hispanic.white.Prevalence' 'Non.hispanic.white.Lower.CI' 'Non.hispanic.white.Upper.CI' 'Non.hispanic.black.Prevalence' 'Non.hispanic.black.Lower.CI' 'Non.hispanic.black.Upper.CI' 'Hispanic.Prevalence' 'Hispanic.Lower.CI' 'Hispanic.Upper.CI' 'Asian.or.Pacific.Islander.Prevalence' 'Asian.or.Pacific.Islander.Lower.CI' 'Asian.or.Pacific.Islander.Upper.CI' 'State_Region' 'Source_UC' 'Source_Full3' 'Prevalence_Risk2' 'Prevalence_Risk4' 'Year_Factor'

In [64]:
```
# Filter [ Source: SPED ], including only two clomuns for SLR:
# Dependent variable: Prevalence
# independent variable: Year
# ASD_State_4_PLR = subset(ASD_State, Source_UC == 'SPED' & State_Full2 == 'MN
# ASD_State_4_PLR = subset(ASD_State, Source_UC == 'SPED' & State_Full2 == 'MS
ASD_State_4_PLR = subset(ASD_State, Source_UC == 'SPED' & State_Full2 == 'FL-F
#
dim(ASD_State_4_PLR)
head(ASD_State_4_PLR)
```

17 2

	Prevalence	Year
849	1.5	2000
900	1.8	2001
951	2.1	2002
1002	2.4	2003
1052	2.7	2004
1100	3.0	2005

PLR Workshop Task: 2. b. Discover and visualize the data to gain insights (Is there missing Value in the dataframe, then how to deal with the missing value).

In [65]:
```
summary(ASD_State_4_PLR)
```

```
   Prevalence          Year     
 Min.   : 1.500   Min.   :2000  
 1st Qu.: 2.700   1st Qu.:2004  
 Median : 4.900   Median :2008  
 Mean   : 5.694   Mean   :2008  
 3rd Qu.: 8.300   3rd Qu.:2012  
 Max.   :12.100   Max.   :2016  
```

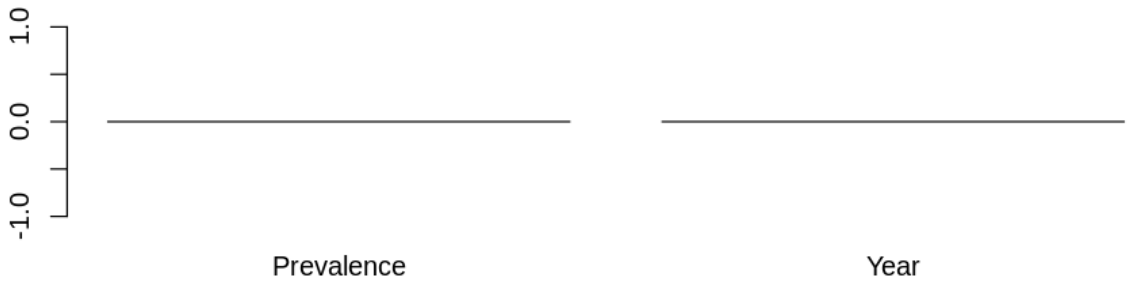
In [66]:
```
# Check whether each columns got missing value:
lapply(ASD_State_4_PLR, function(col_x)sum(is.na(col_x)))

# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=3)
barplot(apply(ASD_State_4_PLR, 2, function(col_x)sum(is.na(col_x))))
```

$Prevalence

0

$Year

0

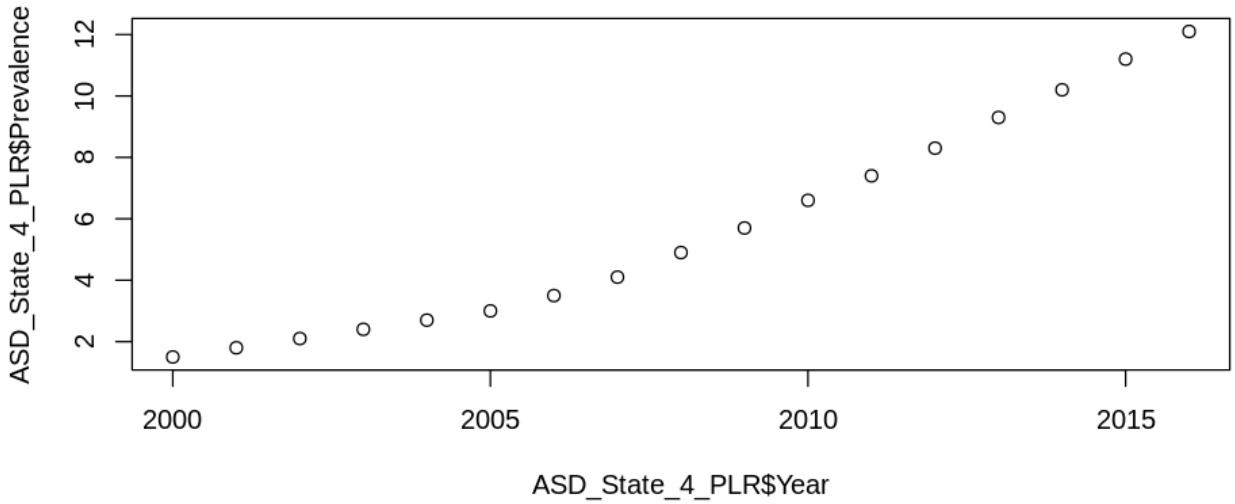


No missing values

PLR Workshop Task: 3. c. Visualize the data to gain insights

In [67]:
```
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=4)
```

In [68]:
```
plot(ASD_State_4_PLR$Year, ASD_State_4_PLR$Prevalence)
```



PLR Workshop Task: **4. d. Compute correlation between variables and apply multiple regression.**

Recode categorical variable to dummy (numeric) variable using one-hot encoding:

In [69]:
```
# To use select_if() function
if(!require(dplyr)){install.packages("dplyr")}
library("dplyr")

summary(select_if(ASD_State_4_PLR, is.numeric))
```

```
   Prevalence          Year
 Min.   : 1.500   Min.   :2000
 1st Qu.: 2.700   1st Qu.:2004
 Median : 4.900   Median :2008
 Mean   : 5.694   Mean   :2008
 3rd Qu.: 8.300   3rd Qu.:2012
 Max.   :12.100   Max.   :2016
```

In [70]:
```
correlation = cor(select_if(ASD_State_4_PLR, is.numeric))
correlation
```

	Prevalence	Year
Prevalence	1.000000	0.980119
Year	0.980119	1.000000

In [71]:
```
# Variable's correlation against target dependent variable:
correlation[, 1]
```

Prevalence	1
Year	0.980118967682229

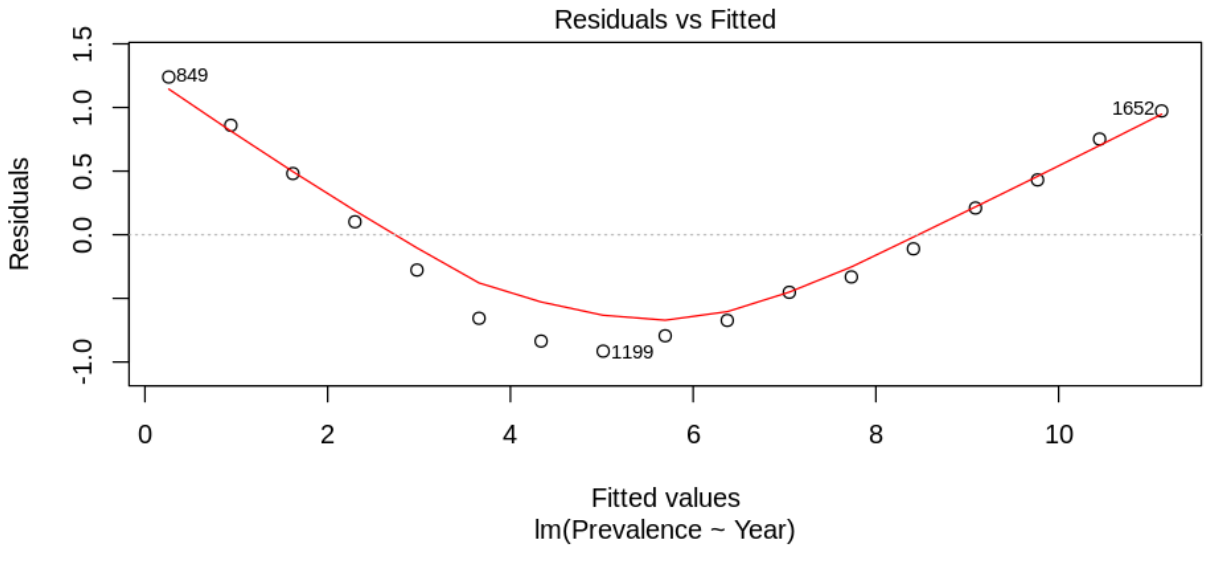
In [72]:
```
str(ASD_State_4_PLR)
```

```
'data.frame':   17 obs. of  2 variables:
 $ Prevalence: num  1.5 1.8 2.1 2.4 2.7 3 3.5 4.1 4.9 5.7 ...
 $ Year      : int  2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 ...
```

In [73]:
```
# SLR
fit_model_SLR = lm(Prevalence ~ Year , data = ASD_State_4_PLR)
#
summary(fit_model_SLR)
```

```
Call:
lm(formula = Prevalence ~ Year, data = ASD_State_4_PLR)

Residuals:
    Min      1Q  Median      3Q     Max
-0.9150 -0.6566 -0.1108  0.4809  1.2392

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -1358.0726    71.2824  -19.05 6.37e-12 ***
Year            0.6792     0.0355   19.13 6.00e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.717 on 15 degrees of freedom
Multiple R-squared:  0.9606,    Adjusted R-squared:  0.958
F-statistic:   366 on 1 and 15 DF,  p-value: 5.995e-12
```

In [74]:
```
plot(fit_model_SLR)
```



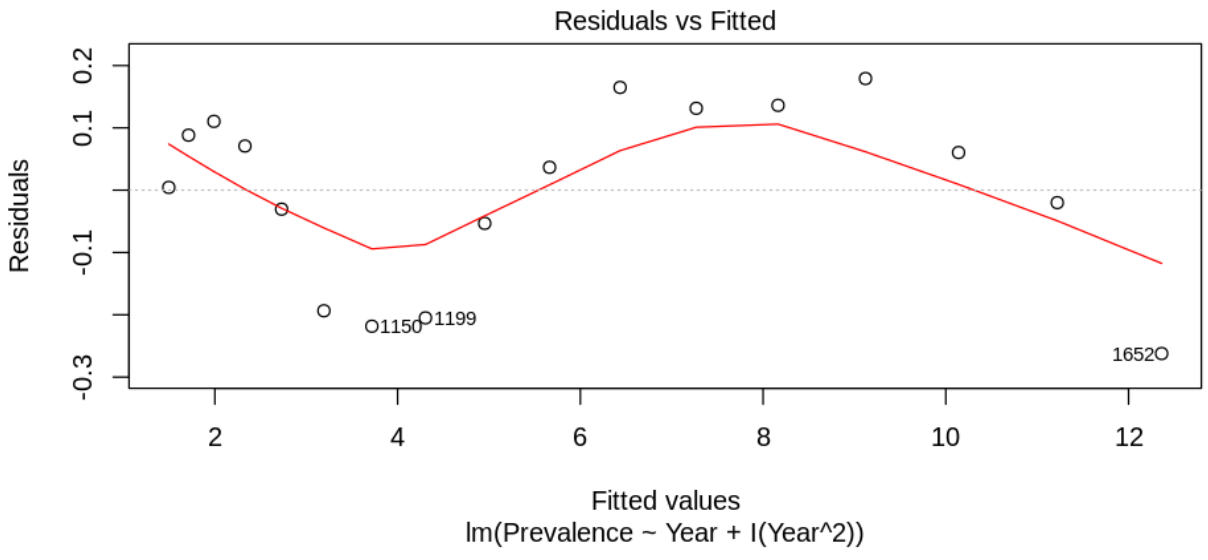
Adjusted R^2 = 0.958

In [75]:
```
# PLR (quadratic)
fit_model_PLR = lm(Prevalence ~ Year + I(Year^2), data = ASD_State_4_PLR)
#
summary(fit_model_PLR)
```

```
Call:
lm(formula = Prevalence ~ Year + I(Year^2), data = ASD_State_4_PLR)

Residuals:
     Min       1Q   Median       3Q      Max
-0.26223 -0.05325  0.03671  0.11045  0.17918

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.231e+05  6.980e+03   17.64 5.87e-11 ***
Year        -1.233e+02  6.953e+00  -17.73 5.45e-11 ***
I(Year^2)    3.087e-02  1.731e-03   17.83 5.07e-11 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.1524 on 14 degrees of freedom
Multiple R-squared:  0.9983,    Adjusted R-squared:  0.9981
F-statistic:  4209 on 2 and 14 DF,  p-value: < 2.2e-16
```

Abount I() function: https://stackoverflow.com/questions/8055508/in-r-formulas-why-do-i-have-to-use-the-i-function-on-power-terms-like-y-i (https://stackoverflow.com/questions/8055508/in-r-formulas-why-do-i-have-to-use-the-i-function-on-power-terms-like-y-i)

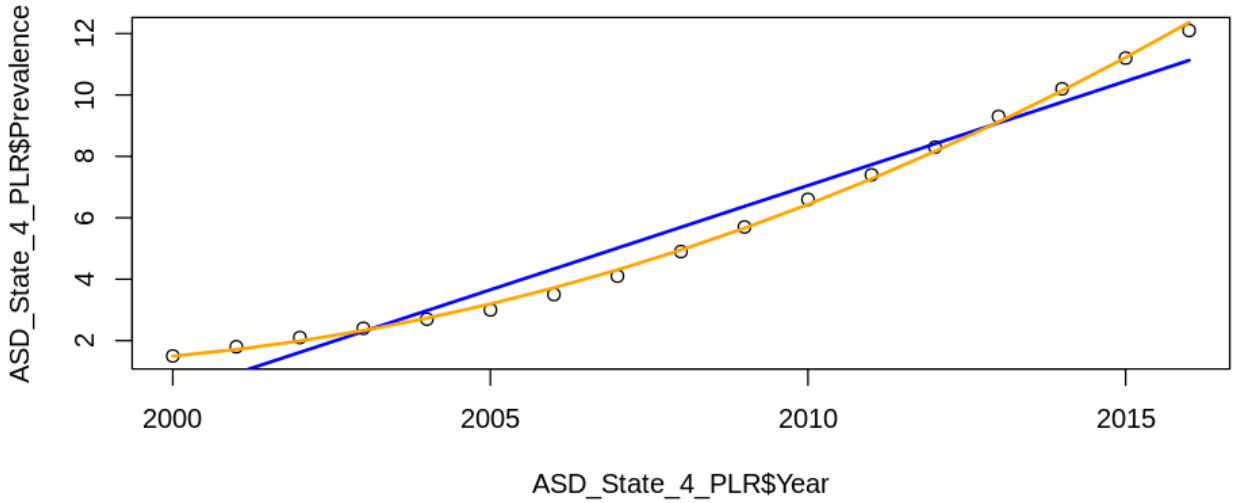
In [76]:
```
plot(fit_model_PLR)
```



Adjusted R^2 = 0.9981

Visualise the difference between SLR & PLR:

In [77]:
```
plot(ASD_State_4_PLR$Year, ASD_State_4_PLR$Prevalence)
# add SLR line
lines(ASD_State_4_PLR$Year, predict(fit_model_SLR, ASD_State_4_PLR), col="blue
# add PLR line
lines(ASD_State_4_PLR$Year, predict(fit_model_PLR, ASD_State_4_PLR), col="oran
```



PLR Prediciton

In [78]:
```
newdata = ASD_State_4_PLR[1,] # Copy datastructure
newdata$Prevalence = NA
newdata$Year = 2025

newdata
```

	Prevalence	Year
849	NA	2025

In [79]:
```
predict(fit_model_PLR, newdata, interval = "predict")
#
cat("Predicted ASD Prevalence of Year [", newdata$Year, "] is", round(predict(
```

	fit	lwr	upr
849	25.42036	24.34469	26.49602

```
Predicted ASD Prevalence of Year [ 2025 ] is 25.4 per 1,000 Children
```

Multiple PLR Workshop Task: **5. e. Multiple polynomial regression (MPR).** (Enhance MLR by adding higher order transformed variables.)

Resuse MLR data: **ASD_State_4_MLR** Cop to new dataframe: ASD_State_4_MPR

In [80]:
```
ASD_State_4_MPR = ASD_State_4_MLR

dim(ASD_State_4_MPR)
```

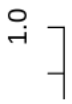
```
1692  5
```

In [81]:
```
summary(ASD_State_4_MPR)
```

```
  Denominator        Prevalence          Year       Source    
 Min.   :    965   Min.   : 0.400   Min.   :2000   addm: 86  
 1st Qu.: 107151   1st Qu.: 3.100   1st Qu.:2003   medi:655  
 Median : 353328   Median : 5.600   Median :2007   nsch: 98  
 Mean   : 604689   Mean   : 7.191   Mean   :2007   sped:853  
 3rd Qu.: 767928   3rd Qu.: 9.200   3rd Qu.:2011             
 Max.   :5824922   Max.   :42.700   Max.   :2016             

                State_Full2
 AZ-Arizona         :  40  
 MD-Maryland        :  40  
 GA-Georgia         :  39  
 MO-Missouri        :  39  
 NC-North Carolina  :  39  
 WI-Wisconsin       :  39  
 (Other)            :1456  
```

In [82]:
```
# Check whether each columns got missing value:
lapply(ASD_State_4_MLR, function(col_x)sum(is.na(col_x)))

# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=3)
barplot(apply(ASD_State_4_MLR, 2, function(col_x)sum(is.na(col_x))))
```

$Denominator
0
$Prevalence
0
$Year
0
$Source
0
$State_Full2
0



Build Multiple PLR model: + I(Year^2) + I(log(Denominator)

In [83]:
```
fit_model_MPR = lm(Prevalence ~ . + I(Year^2) + I(log(Denominator)), data = AS
#
summary(fit_model_MPR)
```

```
Call:
lm(formula = Prevalence ~ . + I(Year^2) + I(log(Denominator)),
    data = ASD_State_4_MPR)

Residuals:
   Min     1Q Median     3Q    Max
-9.697 -1.238  0.007  1.157 19.672

Coefficients:
                                  Estimate Std. Error t value Pr(>|t|)

(Intercept)                      7.908e+04  1.309e+04   6.044 1.86e-09 *
**
Denominator                      2.074e-06  2.340e-07   8.863  < 2e-16 *
**
Year                            -7.943e+01  1.304e+01  -6.093 1.38e-09 *
**
Sourcemedi                       8.189e-01  6.860e-01   1.194 0.232812
```

Adjusted R^2 = 0.7884

Mutiple PLR Prediciton

In [84]:
```
# Copy datastructure
newdata = subset(ASD_State_4_MPR, ASD_State_4_MPR$Year == 2016 &
                                  ASD_State_4_MPR$State_Full2 == 'FL-Florida' &
                                  ASD_State_4_MPR$Source == 'sped')
newdata
```

	Denominator	Prevalence	Year	Source	State_Full2
1652	2555399	12.1	2016	sped	FL-Florida

In [85]:
```
newdata = ASD_State_4_MPR[1,] # Copy datastructure
newdata$Prevalence = NA
newdata$Denominator = 2600000
newdata$Year = 2025
newdata$Source = "sped"
newdata$State_Full2 = "FL-Florida"

newdata
```

Denominator	Prevalence	Year	Source	State_Full2
2600000	NA	2025	sped	FL-Florida

In [86]:
```
predict(fit_model_MPR, newdata, interval = "predict")
#
cat("Predicted ASD Prevalence of Year [", newdata$Year, "] is", round(predict(
```

fit	lwr	upr
22.70557	17.01847	28.39267

```
Predicted ASD Prevalence of Year [ 2025 ] is 22.7 per 1,000 Children
```

Quiz:

Compare predicted ASD prevalence and model R^2 between: Multiple Linear Rregression and Multiple Polynomial Rregression.

Which prediction result would you use? Provide yor justifications.

In [87]:
```
# Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

()

Linear Model: Logistic Regression (LR)

Linear Model: Logistic Regression (LR) - Workshop Task

Workshop Task:

1. a. Get the data.
2. b. Logistic regression - Binary Class.
3. c. Logistic regression - Multi-Class.

LR Workshop Task: 1. a. Get the data.

Use Case Data: "../dataset/ADV_ASD_State_R.csv"

Read in CSV data, storing as R dataframe

In [88]:
```
# Read back in above saved file:
# ASD_State <- read.csv("../dataset/ADV_ASD_State_R.csv")
# ASD_State$Year_Factor <- factor(ASD_State$Year_Factor, ordered = TRUE) # Con
# ASD_State$Prevalence_Risk2 = factor(ASD_State$Prevalence_Risk2, ordered=TRUE
# ASD_State$Prevalence_Risk4 = factor(ASD_State$Prevalence_Risk4, ordered=TRUE
```

In [89]:
```
head(ASD_State)
```

State	Denominator	Prevalence	Lower.CI	Upper.CI	Year	Source	Source_Full1	State_Full1	State_F
AZ	45322	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Arizo
GA	43593	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Geo
MD	21532	5.5	4.6	6.6	2000	addm	Autism & Developmental Disabilities Monitoring Network	Maryland	Marylan

In [90]:
```
Column_Names = c("Prevalence_Risk2", "Denominator", "Year", "Source", "State_F
ASD_State_4_LR_Risk2 <- ASD_State[ , (names(ASD_State) %in% Column_Names)]
dim(ASD_State_4_LR_Risk2)
head(ASD_State_4_LR_Risk2)
```

1692 5

Denominator	Year	Source	State_Full2	Prevalence_Risk2
45322	2000	addm	AZ-Arizona	High
43593	2000	addm	GA-Georgia	High
21532	2000	addm	MD-Maryland	High
29714	2000	addm	NJ-New Jersey	High
24535	2000	addm	SC-South Carolina	High
23065	2000	addm	WV-West Virginia	Low

In [91]:
```
Column_Names = c("Prevalence_Risk4", "Denominator", "Year", "Source", "State_F
ASD_State_4_LR_Risk4 <- ASD_State[ , (names(ASD_State) %in% Column_Names)]
dim(ASD_State_4_LR_Risk4)
head(ASD_State_4_LR_Risk4)
```

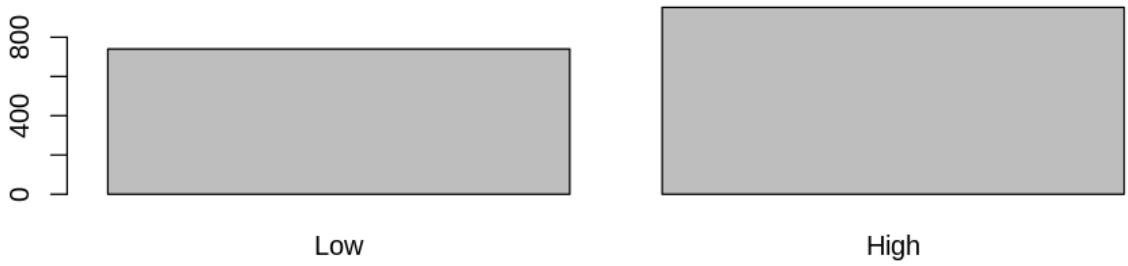
```
1692  5
```

Denominator	Year	Source	State_Full2	Prevalence_Risk4
45322	2000	addm	AZ-Arizona	Medium
43593	2000	addm	GA-Georgia	Medium
21532	2000	addm	MD-Maryland	Medium
29714	2000	addm	NJ-New Jersey	Medium
24535	2000	addm	SC-South Carolina	Medium
23065	2000	addm	WV-West Virginia	Low

LR Workshop Task: 2. b. Logistic regression (LR) Binary Class. (Reuse Multiple Polynomial Model on categorical dependent variable.)

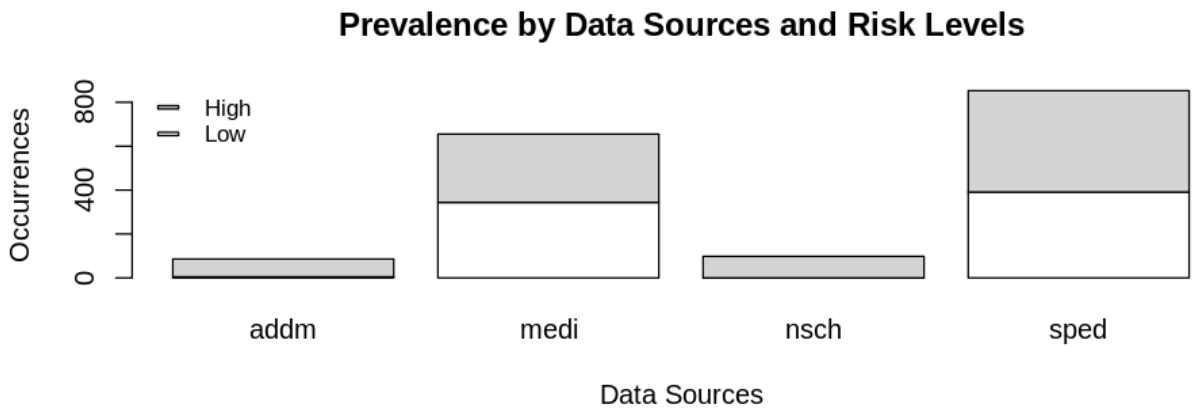
In [92]:
```
table(ASD_State_4_LR_Risk2$Prevalence_Risk2)
barplot(table(ASD_State_4_LR_Risk2$Prevalence_Risk2))
```

```
Low High
740  952
```



In [93]:
```
counts = table(ASD_State_4_LR_Risk2$Prevalence_Risk2, ASD_State_4_LR_Risk2$Sou
counts
barplot(counts,
        main="Prevalence by Data Sources and Risk Levels",
        xlab="Data Sources",
        ylab="Occurrences",
        col=c("white", "lightgrey"),
        legend = rownames(counts),
        args.legend = list(x = "topleft", bty = "n", cex = 0.85, y.intersp = 4
```

```
      addm medi nsch sped
Low      5  344    0  391
High    81  311   98  462
```



In [94]:
```
str(ASD_State_4_LR_Risk2)
```

```
'data.frame':   1692 obs. of  5 variables:
 $ Denominator     : int  45322 43593 21532 29714 24535 23065 35472 45113 364
72 11020 ...
 $ Year            : int  2000 2000 2000 2000 2000 2000 2002 2002 2002 2002
...
 $ Source          : Factor w/ 4 levels "addm","medi",..: 1 1 1 1 1 1 1 1 1 1
...
 $ State_Full2     : Factor w/ 51 levels "AK-Alaska","AL-Alabama",..: 4 11 21
32 41 50 2 4 3 6 ...
 $ Prevalence_Risk2: Ord.factor w/ 2 levels "Low"<"High": 2 2 2 2 2 1 1 2 2 2
...
```

Build model

In [95]:
```
# Binary Classification:
fit_model_LR_Risk2 = glm(Prevalence_Risk2 ~ Denominator + Year + Source + Stat
                         family=binomial(link='logit'), data = ASD_State_4_LR_
#
summary(fit_model_LR_Risk2)
```

```
Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”
```

Evaluate model

In [96]:
```
# Likelihood ratio test: significance of the difference between the full model
pchisq(fit_model_LR_Risk2$null.deviance - fit_model_LR_Risk2$deviance,
       fit_model_LR_Risk2$df.null - fit_model_LR_Risk2$df.residual, lower.tail
```

1.53354721010441e-271

Check whether above value is very small (the smaller the more significant), e.g. < 0.05.

< How to perform a Logistic Regression in R > Michy Alice

https://www.r-bloggers.com/how-to-perform-a-logistic-regression-in-r/ (https://www.r-bloggers.com/how-to-perform-a-logistic-regression-in-r/)

In [97]:
```
# null deviance and the residual deviance
anova(fit_model_LR_Risk2, test="Chisq")
```

```
Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”
```

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL	NA	NA	1691	2318.9775	NA
Denominator	1	3.537393	1690	2315.4401	5.999971e-02
Year	1	799.973390	1689	1515.4667	5.468229e-176
Source	3	130.380991	1686	1385.0857	4.476806e-28
State_Full2	50	503.146385	1636	881.9393	4.071306e-76
I(Year^2)	1	3.124751	1635	878.8146	7.711166e-02
I(log(Denominator))	1	37.914698	1634	840.8999	7.390635e-10

In [98]:
```
# R^2 equivalent
if(!require(pscl)){install.packages("pscl")}
library("pscl")
```

```
Loading required package: pscl
Classes and Methods for R developed in the
Political Science Computational Laboratory
Department of Political Science
Stanford University
Simon Jackman
hurdle and zeroinfl functions by Achim Zeileis
```

While no exact equivalent to the R^2 of linear regression exists, the **McFadden** R^2 index can be used to assess the model fit.

In [99]:
```
# R^2 equivalent
pR2(fit_model_LR_Risk2)[4]
```

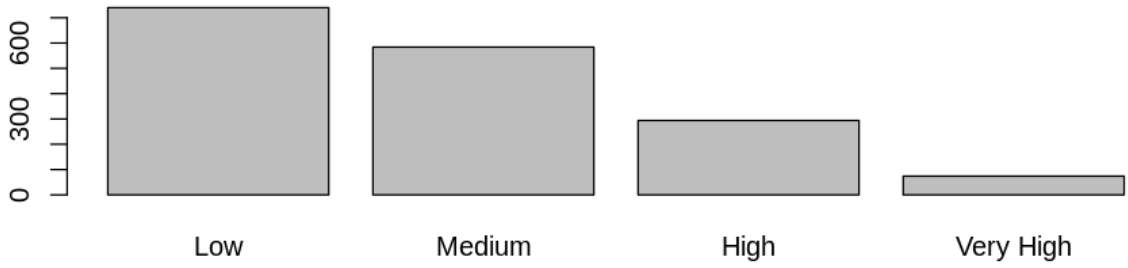
McFadden: 0.637383340253751

McFadden R^2 = 0.6374

LR Workshop Task: **3. c. Logistic regression (LR) Muti-Class.** (Reuse Multiple Polynomial Model on categorical dependent variable.)

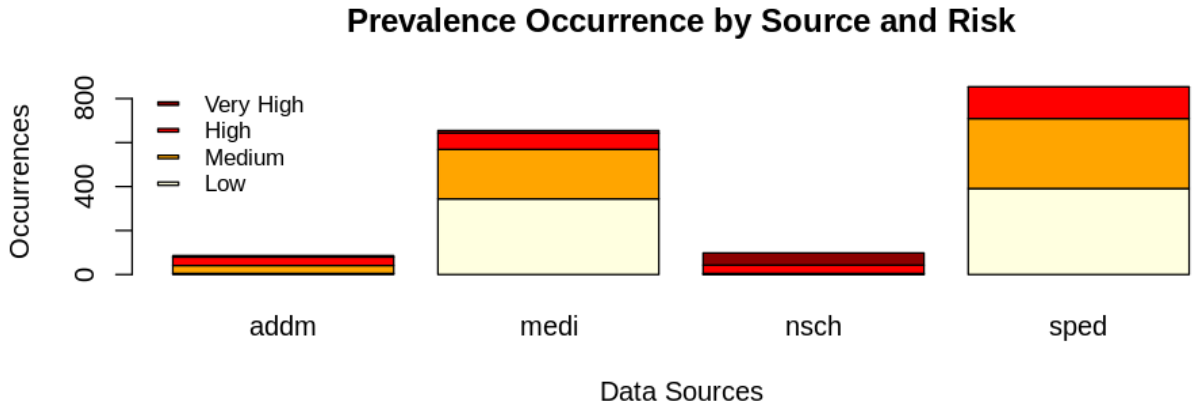
In [100]:
```
table(ASD_State_4_LR_Risk4$Prevalence_Risk4)
barplot(table(ASD_State_4_LR_Risk4$Prevalence_Risk4))
```

```
      Low    Medium      High Very High 
      740       584       294        74 
```



In [101]:
```
counts = table(ASD_State_4_LR_Risk4$Prevalence_Risk4, ASD_State_4_LR_Risk4$Sou
counts
barplot(counts,
        main="Prevalence Occurrence by Source and Risk",
        xlab="Data Sources",
        ylab="Occurrences",
        col=c("lightyellow", "orange", "red","darkred"),
        legend = rownames(counts),
        args.legend = list(x = "topleft", bty = "n", cex = 0.85, y.intersp = 4
```

```
           addm medi nsch sped
Low           5  344    0  391
Medium       36  225    5  318
High         38   74   38  144
Very High     7   12   55    0
```



Build model

In [102]:
```
# multinom function from the nnet package
if(!require(nnet)){install.packages("nnet")}
library("nnet")
```

```
Loading required package: nnet
```

In [103]:
```
# Multi-Class Classification:
fit_model_LR_Risk4 = multinom(Prevalence_Risk4 ~ Denominator + Year + Source +
                      data = ASD_State_4_LR_Risk4, maxit=1000) # maxit https://

summary(fit_model_LR_Risk4)
```

```
iter 150 value 784.905675
iter 160 value 784.812617
iter 160 value 784.812617
iter 170 value 784.774742
iter 170 value 784.774742
iter 180 value 784.759309
iter 180 value 784.759309
iter 190 value 784.753016
iter 190 value 784.753016
iter 200 value 784.750451
iter 200 value 784.750451
iter 210 value 784.749404
iter 210 value 784.749404
iter 220 value 784.748978
iter 220 value 784.748978
iter 230 value 784.748804
iter 230 value 784.748804
final  value 784.748760
converged
```

< MULTINOMIAL LOGISTIC REGRESSION | R DATA ANALYSIS EXAMPLES >

https://stats.idre.ucla.edu/r/dae/multinomial-logistic-regression/
(https://stats.idre.ucla.edu/r/dae/multinomial-logistic-regression/)

In [104]:
```
## extract the coefficients from the model and exponentiate
exp(coef(fit_model_LR_Risk4))
# Uncomment below to display all p values:
# paste(exp(coef(fit_model)))
```

	(Intercept)	Denominator	Year	Sourcemedi	Sourcensch	Sourcesped	State_Full2AL-Alabama	Sta
Medium	0.9995993	1.000002	0.5391502	0.67139922	3.62644214	0.563177522	1.296484	
High	0.9987223	1.000004	0.3065507	0.07997104	1.29768902	0.015604143	6.007789	
Very High	0.9988990	1.000005	0.1954550	11.39221703	0.02789111	0.001129263	785.348612	

In [105]:
```
# Test the significance/importance of each coefficient (check if p values < 0.

# z score for coefficients
z <- summary(fit_model_LR_Risk4)$coefficients/summary(fit_model_LR_Risk4)$stan
cat('\n< Talbe of coefficient z scores>')
z

# p value of 2-tailed z test
p <- (1 - pnorm(abs(z), 0, 1)) * 2
cat('\n< Talbe of coefficient p values>')
p
# Uncomment below to display all p values:
# paste(p)
```

```
< Talbe of coefficient z scores>
```

	(Intercept)	Denominator	Year	Sourcemedi	Sourcensch	Sourcesped	State_
Medium	-61605204332	22.77665	-47431585791	-3.574096e+11	5.516405e+12	-9.518100e+11	5.631
High	-103347504827	29.75500	-56434165146	-1.080017e+12	9.680944e+10	-8.591119e+12	3.547
Very High	-70795238650	2.72952	-50871679968	7.376106e+11	-1.223631e+12	-9.905923e+13	6.225

```
< Talbe of coefficient p values>
```

	(Intercept)	Denominator	Year	Sourcemedi	Sourcensch	Sourcesped	State_Full2AL-Alabama	State_Ful Arka
Medium	0	0.000000000	0	0	0	0	0	
High	0	0.000000000	0	0	0	0	0	
Very High	0	0.006342669	0	0	0	0	0	

While no exact equivalent to the R^2 of linear regression exists, the **McFadden** R^2 index can be used to assess the model fit.

In [106]:
```
# R^2 equivalent
pR2(fit_model_LR_Risk4)[4]
```

```
fitting null model for pseudo-r2
# weights:  8 (3 variable)
initial  value 2345.610059
iter  10 value 1979.347988
final  value 1979.347206
converged
```

McFadden: 0.603531528984306

McFadden R^2 = 0.6035

()

Linear Model: Model Evaluation

Linear Model: Linear Model: Model Evaluation - Workshop Task

Workshop Task:

1. a. Train/Test Dataset Split
2. b. Confusion Matrix & Accuracy for Classification
3. c. K-Fold Cross Validation
4. d. R^2, MSE, RMSE for Regression for Regression

Model Evaluation Workshop Task: 1. a. Train/Test Dataset Split

In [107]:
```
if(!require(caTools)){install.packages("caTools")}
library("caTools")
```

```
Loading required package: caTools
```

In [108]:
```
# Generate a random number sequence that can be reproduced to check results th
set.seed(88)

# Stratified Random Sampling: split dataset into two sets in predefined propor
# while preserving differnt class ratios of dependent variable. (e.g. Proporti
split <- sample.split(ASD_State_4_LR_Risk2$Prevalence_Risk2, SplitRatio = 0.7)
```

In [109]:
```
# Get training and test data
trainset <- subset(ASD_State_4_LR_Risk2, split == TRUE)
testset <- subset(ASD_State_4_LR_Risk2, split == FALSE)
```

Build a binary classification model to predict (categorical) Prevalence Risk Level using Logistic Regression (LR)

In [110]:
```
# Binary Classification:
fit_model_LR_Risk2 = glm(Prevalence_Risk2 ~ Denominator + Year + Source + Stat
                         family=binomial(link='logit'), data = trainset) # dat

summary(fit_model_LR_Risk2)
```

```
Call:
glm(formula = Prevalence_Risk2 ~ Denominator + Year + Source +
    State_Full2 + I(Year^2) + I(log(Denominator)), family = binomial(link =
"logit"),
    data = trainset)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.2887  -0.2840   0.0000   0.2573   2.9945

Coefficients:
                                    Estimate Std. Error z value Pr(>|z|)

(Intercept)                        5.763e+04  3.538e+04   1.629 0.103311

Denominator                        4.162e-06  6.157e-07   6.760 1.38e-11 *
```

Model Evaluation Workshop Task: 2. b. Confusion Matrix & Accuracy for Classification

https://en.wikipedia.org/wiki/Confusion_matrix (https://en.wikipedia.org/wiki/Confusion_matrix)

In [111]:
```
# Confusion matrix on Trainset
probTrainset <- predict(fit_model_LR_Risk2, type = 'response')
# One way is to use the proportion of High risk in the *Training* data.
threshold2 <- sum(trainset$Prevalence_Risk2 == "High")/length(trainset$Prevale
cat('Trainset High Risk Threshold = ', threshold2)
# If logistic regression probability > threshold, predict High, else predict L
predictTrainset <- ifelse(probTrainset > threshold2, "High", "Low")
# Create a contingency table (Confusion Matrix) with actuals on rows and predi
table(trainset$Prevalence_Risk2, predictTrainset)

# Accuracy on Trainset
AccuracyTrain <- mean(predictTrainset == trainset$Prevalence_Risk2)
cat('Trainset Accuracy = ', AccuracyTrain)
```

```
Trainset High Risk Threshold =  0.5625

      predictTrainset
       High Low
  Low    46 472
  High  593  73

Trainset Accuracy =  0.8994932
```

In [112]:
```
# Confusion matrix on Testset
probTestset <- predict(fit_model_LR_Risk2, newdata = testset, type = 'response
# One way is to use the proportion of High risk in the *Training* data.
cat('Reused Trainset High Risk Threshold = ', threshold2)
# If logistic regression probability > threshold, predict High, else predict L
predictTestset <- ifelse(probTestset > threshold2, "High", "Low")
# Create a contingency table (Confusion Matrix) with actuals on rows and predi
table(testset$Prevalence_Risk2, predictTestset)

# Accuracy on Trainset
AccuracyTest <- mean(predictTestset == testset$Prevalence_Risk2)
cat('Testset Accuracy = ', AccuracyTest)
```

```
Reused Trainset High Risk Threshold =  0.5625

      predictTestset
       High Low
  Low    30 192
  High  258  28

Testset Accuracy =  0.8858268
```

Model Evaluation Workshop Task: 3. c. K-Fold Cross Validation

R caret package

The caret package (short for Classification And REgression Training) is a set of functions that attempt to streamline the process for creating predictive models. The package contains tools for:

- data splitting
- pre-processing
- feature selection
- model tuning using resampling
- variable importance estimation

http://topepo.github.io/caret/index.html (http://topepo.github.io/caret/index.html)

In [113]:
```
if(!require(caret)){install.packages("caret")}
library("caret")
```

```
Loading required package: caret
Loading required package: lattice
Loading required package: ggplot2
Registered S3 methods overwritten by 'ggplot2':
  method         from
  [.quosures     rlang
  c.quosures     rlang
  print.quosures rlang
```

In [114]:
```
if(!require(e1071)){install.packages("e1071")}
library("e1071")
```

```
Loading required package: e1071
```

In [115]:
```
# Caret train/test split method:
set.seed(88)
caret_idx = createDataPartition(ASD_State_4_LR_Risk2$Prevalence_Risk2, p = 0.8
caret_trainset = ASD_State_4_LR_Risk2[caret_idx, ]
caret_testset  = ASD_State_4_LR_Risk2[-caret_idx, ]

#caret_threshold <- sum(caret_trainset$Prevalence_Risk2 == "Low")/length(caret
#caret_threshold
```

In [116]:
```
# Caret logistic regresion
set.seed(88)
cv_control = trainControl(method = "cv", number = 5)

caret_model_LR_Risk2 = train(form = Prevalence_Risk2 ~ ., data = caret_trainse
                             trControl = cv_control, method = "glm", family =
#
caret_model_LR_Risk2
```

```
Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”Warning message:
“glm.fit: fitted probabilities numerically 0 or 1 occurred”

Generalized Linear Model

1439 samples
   4 predictor
   2 classes: 'Low', 'High'

No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 1151, 1151, 1151, 1151, 1152
Resampling results:

  Accuracy   Kappa
  0.8638018  0.7237422
```

In [117]:
```
# Get predicted class label
caret_model_LR_Risk2_Pred <- predict(caret_model_LR_Risk2, caret_testset)

# Uncomment below to get class probability
# caret_model_LR_Risk2_Pred <- predict(caret_model_LR_Risk2, caret_testset, ty
```

https://topepo.github.io/caret/using-your-own-model-in-train.html#Illustration5
(https://topepo.github.io/caret/using-your-own-model-in-train.html#Illustration5)

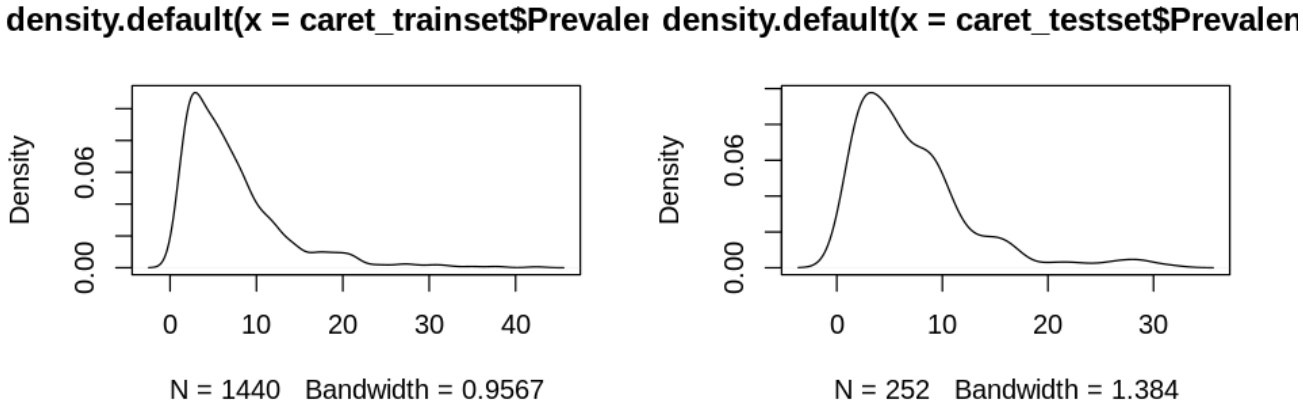
In [118]:
```
# CM & Acc
cm_table <- table(as.factor(caret_model_LR_Risk2_Pred), caret_testset$Prevalen
confusionMatrix(cm_table)
```

```
Confusion Matrix and Statistics


          Low High
  Low      92   11
  High     19  131

                Accuracy : 0.8814
                  95% CI : (0.8351, 0.9185)
    No Information Rate : 0.5613
    P-Value [Acc > NIR] : <2e-16

                   Kappa : 0.7573

 Mcnemar's Test P-Value : 0.2012

            Sensitivity : 0.8288
            Specificity : 0.9225
         Pos Pred Value : 0.8932
         Neg Pred Value : 0.8733
             Prevalence : 0.4387
         Detection Rate : 0.3636
   Detection Prevalence : 0.4071
      Balanced Accuracy : 0.8757

       'Positive' Class : Low
```

Model Evaluation Workshop Task: 4. d. R^2, MSE, RMSE for Regression

In [119]:
```
# Caret train/test split method:
set.seed(88)
caret_idx = createDataPartition(ASD_State_4_MLR$Prevalence, p = 0.85, list = F
caret_trainset = ASD_State_4_MLR[caret_idx, ]
caret_testset  = ASD_State_4_MLR[-caret_idx, ]
```

In [120]:
```
# Look at below plots of train and test, shape of distribution are similar, wh
par(mfrow=c(1, 2))
plot(density(caret_trainset$Prevalence))
plot(density(caret_testset$Prevalence))
par(mfrow=c(1, 1))
```



Build a regression model to predict (numeric) Prevalanece using Multiple Linear Regression

(MLR)

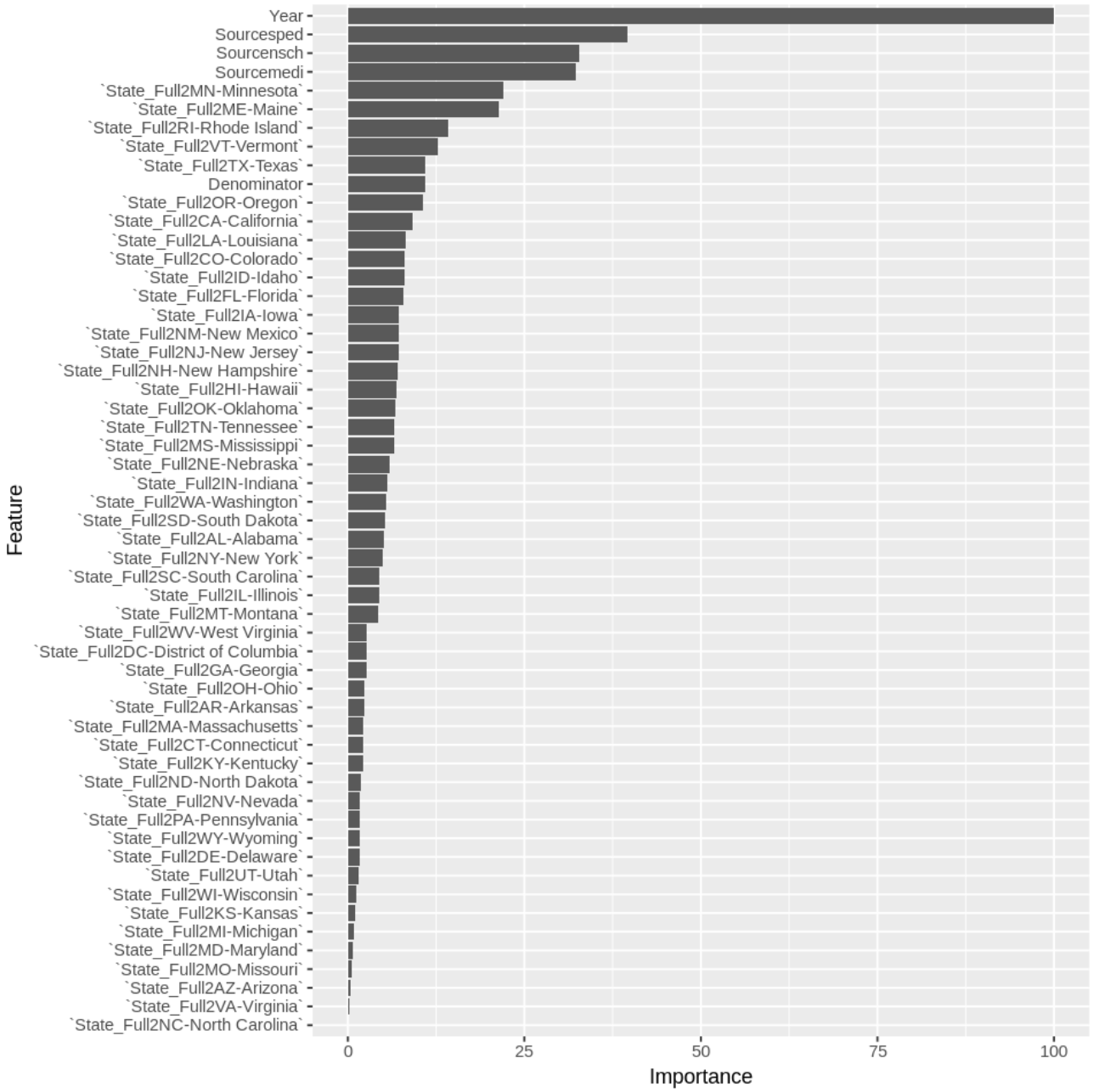
In [121]:
```
if(!require(elasticnet)){install.packages("elasticnet")}
library("elasticnet")
```

```
Loading required package: elasticnet
Loading required package: lars
Loaded lars 1.2
```

In [122]:
```
# Caret MLR regresion
set.seed(88)
cv_control = trainControl(method = "cv", number = 5)
#
caret_model_MLR <- train(Prevalence ~ ., data = caret_trainset, trControl = cv
#
caret_model_MLR
```

```
Linear Regression

1440 samples
   4 predictor

No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 1151, 1152, 1151, 1154, 1152
Resampling results:

  RMSE      Rsquared   MAE
  2.974216  0.7446885  1.980013

Tuning parameter 'intercept' was held constant at a value of TRUE
```

In [123]:
```
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=8)
ggplot(varImp(caret_model_MLR))
# plot(varImp(caret_model_MLR))
```



In [124]:
```
caret_model_MLR_Pred <- predict(caret_model_MLR, caret_testset)
head(caret_model_MLR_Pred)
```

22	9.38901166070576
27	7.83151887672917
33	9.67043449997018
36	10.6096278033993
41	12.0705916087649
55	13.4026625975964

In [125]:
```
# MSE
mean((caret_testset$Prevalence - caret_model_MLR_Pred)^2)
```

5.83744775233841

In [126]:
```
# RMSE
sqrt(mean((caret_testset$Prevalence - caret_model_MLR_Pred)^2))
```

2.41608107321307

Calculate R^2 for entire train set (all folds) https://stackoverflow.com/questions/25691127/r-squared-on-test-data (https://stackoverflow.com/questions/25691127/r-squared-on-test-data)

In [127]:
```
caret_model_MLR_Pred_Train <- predict(caret_model_MLR, caret_trainset)

SS.total      <- sum((caret_trainset$Prevalence-mean(caret_trainset$Prevalence
SS.residual   <- sum(residuals(caret_model_MLR)^2)
SS.regression <- sum((caret_model_MLR_Pred_Train-mean(caret_trainset$Prevalenc

# fraction of variability explained by the model
cat("\nTrain R^2 fraction of variability explained by the model :", SS.regress

# caret_model_MLR_L2
```

```
Train R^2 fraction of variability explained by the model : 0.7699826
```

Calculate R^2 for test set https://stackoverflow.com/questions/25691127/r-squared-on-test-data (https://stackoverflow.com/questions/25691127/r-squared-on-test-data)

In [128]:
```
# True y values:
# head(caret_testset$Prevalence)

# Predicated y values (y hat):
# head(caret_model_MLR_Pred)

SS.total      <- sum((caret_testset$Prevalence - mean(caret_testset$Prevalence
SS.residual   <- sum((caret_testset$Prevalence - caret_model_MLR_Pred)^2)
SS.regression <- sum((caret_model_MLR_Pred - mean(caret_testset$Prevalence))^2

# NOT the fraction of variability explained by the model
test.rsq <- 1 - SS.residual/SS.total
# cat("\nNOT Test fraction of variability explained by the model :", test.rsq

# fraction of variability explained by the model
cat("\nTest R^2 fraction of variability explained by the model :", SS.regressi
```

```
Test R^2 fraction of variability explained by the model : 0.8988214
```

()

Linear Model: Prevent Overfitting by Regularization Methods

Linear Model: Prevent Overfitting by Regularization Methods - L1 Lasso

Regression & L2 Ridge regression

https://towardsdatascience.com/l1-and-l2-regularization-methods-ce25e7fc831c (https://towardsdatascience.com/l1-and-l2-regularization-methods-ce25e7fc831c)

- L1 Lasso Regression (Least Absolute Shrinkage and Selection Operator) adds “absolute value of magnitude” of coefficient as penalty term to the loss function.
- L2 Ridge regression adds “squared magnitude” of coefficient as penalty term to the loss function.

The key difference between these techniques is that L1 Lasso shrinks the less important feature’s coefficient to zero thus, removing some feature altogether. So, this works well for feature selection in case we have a huge number of features.

https://towardsdatascience.com/create-predictive-models-in-r-with-caret-12baf9941236 (https://towardsdatascience.com/create-predictive-models-in-r-with-caret-12baf9941236)

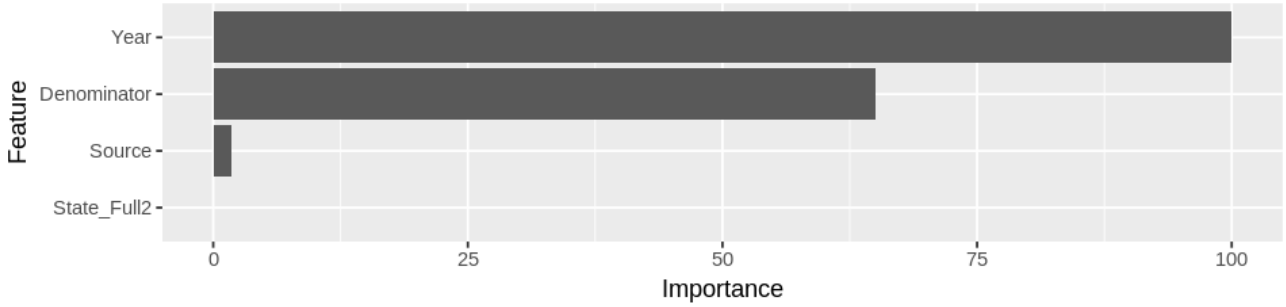
Enhanced MLR using Regularization: L1 Lasso

In [129]:
```
if(!require(elasticnet)){install.packages("elasticnet")}
library("elasticnet")
```

In [130]:
```
# Caret MLR with Regularization
# possible method: boot", "boot632", "cv", "repeatedcv", "LOOCV", "LGOCV"
cv_control <- trainControl(method = "repeatedcv",
                           number = 10,     # number of folds
                           repeats = 5)    # repeated N times

caret_model_MLR_L1 <- train(Prevalence ~ .,
               data = caret_trainset,
               method = "lasso",  # Try using "ridge"
               trControl = cv_control,
               preProcess = c('scale', 'center'))  # Auto pre-process data
#
caret_model_MLR_L1
```

```
The lasso

1440 samples
   4 predictor

Pre-processing: scaled (55), centered (55)
Resampling: Cross-Validated (10 fold, repeated 5 times)
Summary of sample sizes: 1296, 1295, 1296, 1296, 1296, 1296, ...
Resampling results across tuning parameters:

  fraction  RMSE      Rsquared   MAE
  0.1       4.586996  0.5968962  3.264324
  0.5       3.141998  0.7206010  2.138362
  0.9       2.925833  0.7546077  1.966103

RMSE was used to select the optimal model using the smallest value.
The final value used for the model was fraction = 0.9.
```

In [131]:
```
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=2)
ggplot(varImp(caret_model_MLR_L1))
# plot(varImp(caret_model_MLR_L1))
```



In [132]:
```
caret_model_MLR_Pred <- predict(caret_model_MLR_L1, caret_testset)
head(caret_model_MLR_Pred)
```

22	9.09559548122945
27	7.65758256776709
33	9.71165245354341
36	10.4202137443522
41	11.766911449798
55	13.0976251287959

In [133]:
```
# MSE
mean((caret_testset$Prevalence - caret_model_MLR_Pred)^2)
```

5.90034443032887

In [134]:
```
# RMSE
sqrt(mean((caret_testset$Prevalence - caret_model_MLR_Pred)^2))
```

2.42906245912469

Calculate R^2 for entire train set (all folds) https://stackoverflow.com/questions/25691127/r-squared-on-test-data (https://stackoverflow.com/questions/25691127/r-squared-on-test-data)

In [135]:
```
caret_model_MLR_Pred_Train <- predict(caret_model_MLR_L1, caret_trainset)

SS.total      <- sum((caret_trainset$Prevalence-mean(caret_trainset$Prevalence
SS.residual   <- sum(residuals(caret_model_MLR_L1)^2)
SS.regression <- sum((caret_model_MLR_Pred_Train-mean(caret_trainset$Prevalenc

# fraction of variability explained by the model
cat("\nTrain R^2 fraction of variability explained by the model :", SS.regress

# caret_model_MLR_L2
```

```
Train R^2 fraction of variability explained by the model : 0.7498116
```

Calculate R^2 for test set https://stackoverflow.com/questions/25691127/r-squared-on-test-data (https://stackoverflow.com/questions/25691127/r-squared-on-test-data)

In [136]:
```
# True y values:
# head(caret_testset$Prevalence)

# Predicated y values (y hat):
# head(caret_model_MLR_Pred)

SS.total      <- sum((caret_testset$Prevalence - mean(caret_testset$Prevalence
SS.residual   <- sum((caret_testset$Prevalence - caret_model_MLR_Pred)^2)
SS.regression <- sum((caret_model_MLR_Pred - mean(caret_testset$Prevalence))^2

# NOT the fraction of variability explained by the model
test.rsq <- 1 - SS.residual/SS.total
# cat("\nNOT Test fraction of variability explained by the model :", test.rsq

# fraction of variability explained by the model
cat("\nTest R^2 fraction of variability explained by the model :", SS.regressi
```

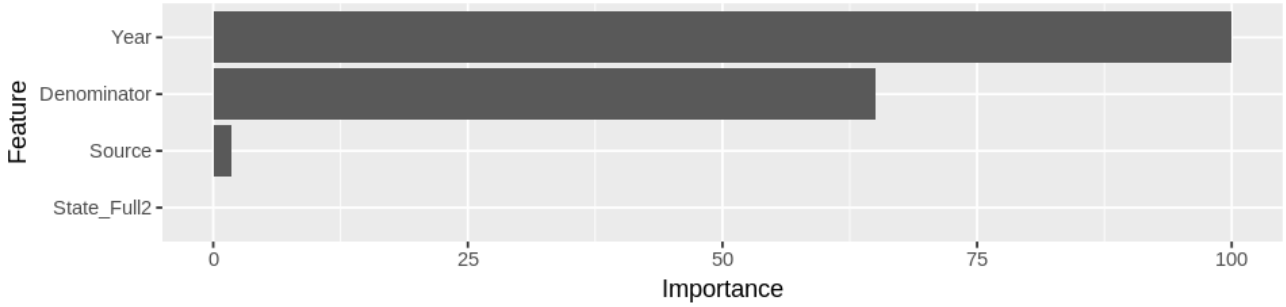
```
Test R^2 fraction of variability explained by the model : 0.8798161
```

Enhanced MLR using Regularization: L2 Ridge

In [137]:
```
# Caret MLR with Regularization
# possible method: boot", "boot632", "cv", "repeatedcv", "LOOCV", "LGOCV"
cv_control <- trainControl(method = "repeatedcv",
                           number = 10,     # number of folds
                           repeats = 5)    # repeated N times

caret_model_MLR_L2 <- train(Prevalence ~ .,
                data = caret_trainset,
                method = "ridge",  # Try using "lasso"
                trControl = cv_control,
                preProcess = c('scale', 'center'))  # Auto pre-process data
#
caret_model_MLR_L2
```

```
Ridge Regression

1440 samples
   4 predictor

Pre-processing: scaled (55), centered (55)
Resampling: Cross-Validated (10 fold, repeated 5 times)
Summary of sample sizes: 1296, 1297, 1296, 1297, 1295, 1296, ...
Resampling results across tuning parameters:

  lambda  RMSE      Rsquared   MAE
  0e+00   2.951386  0.7509153  1.966418
  1e-04   2.951369  0.7509168  1.966466
  1e-01   3.000216  0.7427197  2.048206

RMSE was used to select the optimal model using the smallest value.
The final value used for the model was lambda = 1e-04.
```

In [138]:
```
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=2)
ggplot(varImp(caret_model_MLR_L2))
# plot(varImp(caret_model_MLR_L2))
```



In [139]:
```
caret_model_MLR_Pred <- predict(caret_model_MLR_L2, caret_testset)
head(caret_model_MLR_Pred)
```

22	9.38476017497349
27	7.82653071659292
33	9.66714756932461
36	10.6063229876567
41	12.0663388797878
55	13.3984373159588

In [140]:
```
# MSE
mean((caret_testset$Prevalence - caret_model_MLR_Pred)^2)
```

5.83820592478024

In [141]:
```
# RMSE
sqrt(mean((caret_testset$Prevalence - caret_model_MLR_Pred)^2))
```

2.41623796940207

Calculate R^2 for entire train set (all folds) https://stackoverflow.com/questions/25691127/r-squared-on-test-data (https://stackoverflow.com/questions/25691127/r-squared-on-test-data)

In [142]:
```
caret_model_MLR_Pred_Train <- predict(caret_model_MLR_L2, caret_trainset)

SS.total      <- sum((caret_trainset$Prevalence-mean(caret_trainset$Prevalence
SS.residual   <- sum(residuals(caret_model_MLR_L2)^2)
SS.regression <- sum((caret_model_MLR_Pred_Train-mean(caret_trainset$Prevalenc

# fraction of variability explained by the model
cat("\nTrain R^2 fraction of variability explained by the model :", SS.regress

# caret_model_MLR_L2
```

```
Train R^2 fraction of variability explained by the model : 0.7699436
```

Calculate R^2 for test set https://stackoverflow.com/questions/25691127/r-squared-on-test-data (https://stackoverflow.com/questions/25691127/r-squared-on-test-data)

In [143]:
```
# True y values:
# head(caret_testset$Prevalence)

# Predicated y values (y hat):
# head(caret_model_MLR_Pred)

SS.total      <- sum((caret_testset$Prevalence - mean(caret_testset$Prevalence
SS.residual   <- sum((caret_testset$Prevalence - caret_model_MLR_Pred)^2)
SS.regression <- sum((caret_model_MLR_Pred - mean(caret_testset$Prevalence))^2

# NOT the fraction of variability explained by the model
test.rsq <- 1 - SS.residual/SS.total
# cat("\nNOT Test fraction of variability explained by the model :", test.rsq

# fraction of variability explained by the model
cat("\nTest R^2 fraction of variability explained by the model :", SS.regressi
```

```
Test R^2 fraction of variability explained by the model : 0.8987872
```

()

Workshop Submission

What to submit?

Create predictive model for Multi Class Classification of ASD Prevalence Risk Level (Low, Medium, High, Very High) using Caret package's multinom logistic regression algorithm.

References:

https://daviddalpiaz.github.io/r4sl/the-caret-package.html (https://daviddalpiaz.github.io/r4sl/the-caret-package.html)

http://topepo.github.io/caret/index.html (http://topepo.github.io/caret/index.html)

https://cran.r-project.org/web/packages/caret/caret.pdf (https://cran.r-project.org/web/packages/caret/caret.pdf)

In [144]:
```
# Code example of multinomial logistic regresion using Iris flower dataset
iris[c(1:3, 51:53, 101:103), ]
summary(iris)
iris_model = train(Species ~ ., data = iris, method = "multinom",
                   trControl = trainControl(method = "cv", number = 5), trac
iris_model
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
51	7.0	3.2	4.7	1.4	versicolor
52	6.4	3.2	4.5	1.5	versicolor
53	6.9	3.1	4.9	1.5	versicolor
101	6.3	3.3	6.0	2.5	virginica
102	5.8	2.7	5.1	1.9	virginica
103	7.1	3.0	5.9	2.1	virginica

```
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
 Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100
 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
 Median :5.800   Median :3.000   Median :4.350   Median :1.300
 Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
 3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
 Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
       Species
 setosa    :50
 versicolor:50
 virginica :50



Penalized Multinomial Regression

150 samples
  4 predictor
  3 classes: 'setosa', 'versicolor', 'virginica'

No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 120, 120, 120, 120, 120
Resampling results across tuning parameters:

  decay  Accuracy   Kappa
  0e+00  0.9533333  0.93
  1e-04  0.9600000  0.94
  1e-01  0.9733333  0.96

Accuracy was used to select the optimal model using the largest value.
The final value used for the model was decay = 0.1.
```

In [145]:
```
# Write your code below and press Shift+Enter to execute

```

Double-click **here** for the solution.

()

Excellent! You have completed the workshop notebook!

Connect with the author:

This notebook was written by GU Zhan (Sam) (https://sg.linkedin.com/in/zhan-gu-27a82823).

Sam (https://www.iss.nus.edu.sg/about-us/staff/detail/201/GU%20Zhan) is currently a lecturer in Institute of Systems Science (https://www.iss.nus.edu.sg/) in National University of Singapore (http://www.nus.edu.sg/). He devotes himself into pedagogy & andragogy, and is very passionate in inspiring next generation of artificial intelligence lovers and leaders.

()

Appendices

Interactive workshops: < Learning R inside R > using swirl() (in R/RStudio)

https://github.com/telescopeuser/S-SB-Workshop (https://github.com/telescopeuser/S-SB-Workshop)

https://github.com/dd-consulting (https://github.com/dd-consulting)