D621 - Assignment 3

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DATA EXPLORATION

Summary Stats

```r
column_types <- sapply(df_training, class)
print(column_types)
```

```
##        zn     indus      chas       nox        rm       age       dis       rad
## "numeric" "numeric" "numeric" "numeric" "numeric" "numeric" "numeric" "numeric"
##       tax   ptratio     lstat      medv    target
## "numeric" "numeric" "numeric" "numeric" "numeric"
```

The following three columns were imported as numerical but should be factors: - chas: binomial - rad: ordinal - target: binomial

```r
# convert to factor
df_training <- df_training |>
  mutate(
    chas = as.factor(chas),
    rad = as.factor(rad),
    target = as.factor(target),
  )

numeric_cols <- c('zn', 'indus', 'nox', 'rm', 'age', 'dis', 'tax', 'ptratio', 'lstat', 'medv')

factor_cols <- c('chas', 'rad', 'target')

glimpse(df_training)
```

```
## Rows: 466
## Columns: 13
## $ zn      <dbl> 0, 0, 0, 30, 0, 0, 0, 0, 0, 80, 22, 0, 0, 22, 0, 0, 100, 20, 0~
## $ indus   <dbl> 19.58, 19.58, 18.10, 4.93, 2.46, 8.56, 18.10, 18.10, 5.19, 3.6~
## $ chas    <fct> 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ nox     <dbl> 0.605, 0.871, 0.740, 0.428, 0.488, 0.520, 0.693, 0.693, 0.515,~
## $ rm      <dbl> 7.929, 5.403, 6.485, 6.393, 7.155, 6.781, 5.453, 4.519, 6.316,~
## $ age     <dbl> 96.2, 100.0, 100.0, 7.8, 92.2, 71.3, 100.0, 100.0, 38.1, 19.1,~
## $ dis     <dbl> 2.0459, 1.3216, 1.9784, 7.0355, 2.7006, 2.8561, 1.4896, 1.6582~
## $ rad     <fct> 5, 5, 24, 6, 3, 5, 24, 24, 5, 1, 7, 5, 24, 7, 3, 3, 5, 5, 24, ~
## $ tax     <dbl> 403, 403, 666, 300, 193, 384, 666, 666, 224, 315, 330, 398, 66~
## $ ptratio <dbl> 14.7, 14.7, 20.2, 16.6, 17.8, 20.9, 20.2, 20.2, 20.2, 16.4, 19~
## $ lstat   <dbl> 3.70, 26.82, 18.85, 5.19, 4.82, 7.67, 30.59, 36.98, 5.68, 9.25~
## $ medv    <dbl> 50.0, 13.4, 15.4, 23.7, 37.9, 26.5, 5.0, 7.0, 22.2, 20.9, 24.8~
## $ target  <fct> 1, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0,~
```

A closer examination of the `rad` data shows that that our observations have a rad index value of 1-8 or 24 in this column. Below are the counts:

```
##
##   1   2   3   4   5   6   7   8  24
##  17  20  36 103 109  25  15  20 121
```

Means We can now calculate the summary statistics for the numeric parameters in our dataframe, including our mean, median, min/max, and standard deviations.

```
# only show summary stats for numeric values
for (param in numeric_cols) {
  cat("\nSummary for", param, ":\n")
  print(describe(df_training[[param]]))
}
```

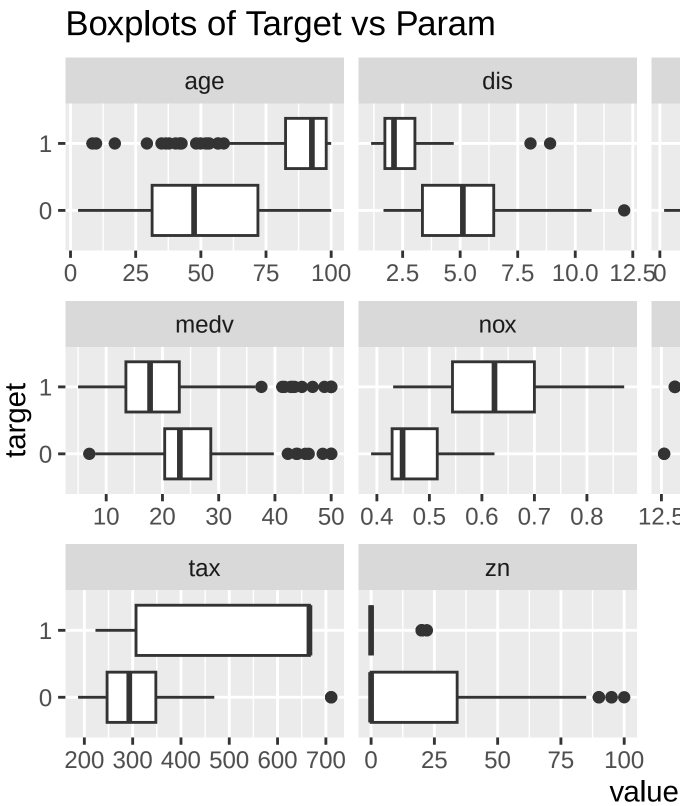
```
##
## Summary for zn :
##    vars   n  mean    sd median trimmed mad min max range skew kurtosis   se
## X1    1 466 11.58 23.36      0    5.35   0   0 100   100 2.18     3.81 1.08
##
## Summary for indus :
##    vars   n  mean   sd median trimmed  mad  min   max range skew kurtosis   se
## X1    1 466 11.11 6.85   9.69   10.91 9.34 0.46 27.74 27.28 0.29    -1.24 0.32
##
## Summary for nox :
##    vars   n mean   sd median trimmed  mad  min  max range skew kurtosis   se
## X1    1 466 0.55 0.12   0.54    0.54 0.13 0.39 0.87  0.48 0.75    -0.04 0.01
##
## Summary for rm :
##    vars   n mean  sd median trimmed  mad  min  max range skew kurtosis   se
## X1    1 466 6.29 0.7   6.21    6.26 0.52 3.86 8.78  4.92 0.48     1.54 0.03
##
## Summary for age :
##    vars   n  mean    sd median trimmed   mad min max range  skew kurtosis   se
## X1    1 466 68.37 28.32  77.15   70.96 30.02 2.9 100  97.1 -0.58    -1.01 1.31
##
## Summary for dis :
##    vars   n mean   sd median trimmed  mad  min   max range skew kurtosis  se
## X1    1 466  3.8 2.11   3.19    3.54 1.91 1.13 12.13    11    1     0.47 0.1
##
## Summary for tax :
##    vars   n  mean    sd median trimmed    mad min max range skew kurtosis   se
## X1    1 466 409.5 167.9  334.5  401.51 104.52 187 711   524 0.66    -1.15 7.78
##
## Summary for ptratio :
##    vars   n mean  sd median trimmed  mad  min max range  skew kurtosis  se
## X1    1 466 18.4 2.2   18.9    18.6 1.93 12.6  22   9.4 -0.75     -0.4 0.1
##
## Summary for lstat :
##    vars   n  mean  sd median trimmed  mad  min   max range skew kurtosis   se
## X1    1 466 12.63 7.1  11.35   11.88 7.07 1.73 37.97 36.24 0.91      0.5 0.33
##
## Summary for medv :
##    vars   n  mean   sd median trimmed mad min max range skew kurtosis   se
```

```
## X1     1 466 22.59 9.24    21.2    21.63    6    5   50     45  1.08      1.37 0.43
```

Plots of data

Boxplots Below is series of boxplots for all numeric parameters where target is our dependent variable.

```r
plot_boxplot(df_training, by = "target", title="Boxplots of Target vs Param")
```




```r
df_training_hi_crime <- df_training |>
  filter(target == 1) |>
  subset(select = -c(chas, rad, target))

df_training_lo_crime <- df_training |>
  filter(target == 0) |>
  subset(select = -c(chas, rad, target))

cat("\nIQR for High Crime Neighborhoods\n")
```

```
##
## IQR for High Crime Neighborhoods
```

```r
summary(df_training_hi_crime)
```

```
##        zn             indus            nox               rm
##  Min.   : 0.000   Min.   : 3.97   Min.   :0.4310   Min.   :3.863
##  1st Qu.: 0.000   1st Qu.: 9.90   1st Qu.:0.5440   1st Qu.:5.727
##  Median : 0.000   Median :18.10   Median :0.6240   Median :6.130
##  Mean   : 1.328   Mean   :15.31   Mean   :0.6404   Mean   :6.181
##  3rd Qu.: 0.000   3rd Qu.:18.10   3rd Qu.:0.7000   3rd Qu.:6.484
##  Max.   :22.000   Max.   :21.89   Max.   :0.8710   Max.   :8.780
```

```
##       age              dis              tax            ptratio
##  Min.   :  8.4   Min.   :1.130   Min.   :223.0   Min.   :13.00
##  1st Qu.: 82.5   1st Qu.:1.728   1st Qu.:307.0   1st Qu.:18.40
##  Median : 92.6   Median :2.125   Median :666.0   Median :20.20
##  Mean   : 86.5   Mean   :2.471   Mean   :513.8   Mean   :18.96
##  3rd Qu.: 98.1   3rd Qu.:3.033   3rd Qu.:666.0   3rd Qu.:20.20
##  Max.   :100.0   Max.   :8.907   Max.   :666.0   Max.   :21.20
##      lstat            medv
##  Min.   : 1.73   Min.   : 5.00
##  1st Qu.:11.10   1st Qu.:13.50
##  Median :15.39   Median :17.80
##  Mean   :16.02   Mean   :20.05
##  3rd Qu.:20.34   3rd Qu.:23.00
##  Max.   :37.97   Max.   :50.00
```

```
cat("\nIQR for Low Crime Neighborhoods\n")
```

```
##
## IQR for Low Crime Neighborhoods
```

```
summary(df_training_lo_crime)
```

```
##        zn             indus             nox               rm
##  Min.   :  0.00   Min.   : 0.460   Min.   :0.3890   Min.   :5.093
##  1st Qu.:  0.00   1st Qu.: 3.370   1st Qu.:0.4290   1st Qu.:5.985
##  Median :  0.00   Median : 5.640   Median :0.4490   Median :6.315
##  Mean   : 21.48   Mean   : 7.039   Mean   :0.4711   Mean   :6.396
##  3rd Qu.: 34.00   3rd Qu.: 9.690   3rd Qu.:0.5150   3rd Qu.:6.727
##  Max.   :100.00   Max.   :27.740   Max.   :0.6240   Max.   :8.069
##       age              dis              tax            ptratio
##  Min.   :  2.90   Min.   : 1.669   Min.   :187.0   Min.   :12.60
##  1st Qu.: 31.30   1st Qu.: 3.360   1st Qu.:247.0   1st Qu.:16.60
##  Median : 47.40   Median : 5.118   Median :293.0   Median :17.90
##  Mean   : 50.84   Mean   : 5.076   Mean   :308.8   Mean   :17.86
##  3rd Qu.: 71.90   3rd Qu.: 6.458   3rd Qu.:348.0   3rd Qu.:19.10
##  Max.   :100.00   Max.   :12.127   Max.   :711.0   Max.   :22.00
##      lstat            medv
##  Min.   : 1.98   Min.   : 7.00
##  1st Qu.: 5.70   1st Qu.:20.40
##  Median : 8.43   Median :23.10
##  Mean   : 9.36   Mean   :25.04
##  3rd Qu.:12.27   3rd Qu.:28.60
##  Max.   :30.81   Max.   :50.00
```

The boxplots show the distribution numerical parameters grouped by the dependent variable `target`. The plots are useful for getting a sense as to which parameters may be good predictors based on how different the parameter;s IQRs are. Conversely, similar IQRs may provide insight into which may not add much information to our model. Based on these box plots, we see that the IQR for `rm` are very similar where `target` is 0 and 1 and should be flagged for potential removal of our plot. `ptratio` and `medv` have some overlap All other variables appear somewhat

Further, we see that param *zn* has a median value around zero, suggesting that few neighborhoods have residential areas zoned for large plots as shown below. We should also consider omitting this variable from our model down the line

```
count_zeros <- sum(df_training_hi_crime$zn == 0)
cat("\nAbove Median Crime Rate Neighborhoods have ", count_zeros, " rows with a value of 0 for param zn
```

```
(count_zeros / nrow(df_training_hi_crime)), "%)\n")
```

```
##
## Above Median Crime Rate Neighborhoods have  214  rows with a value of 0 for param zn out of  229 obse
```

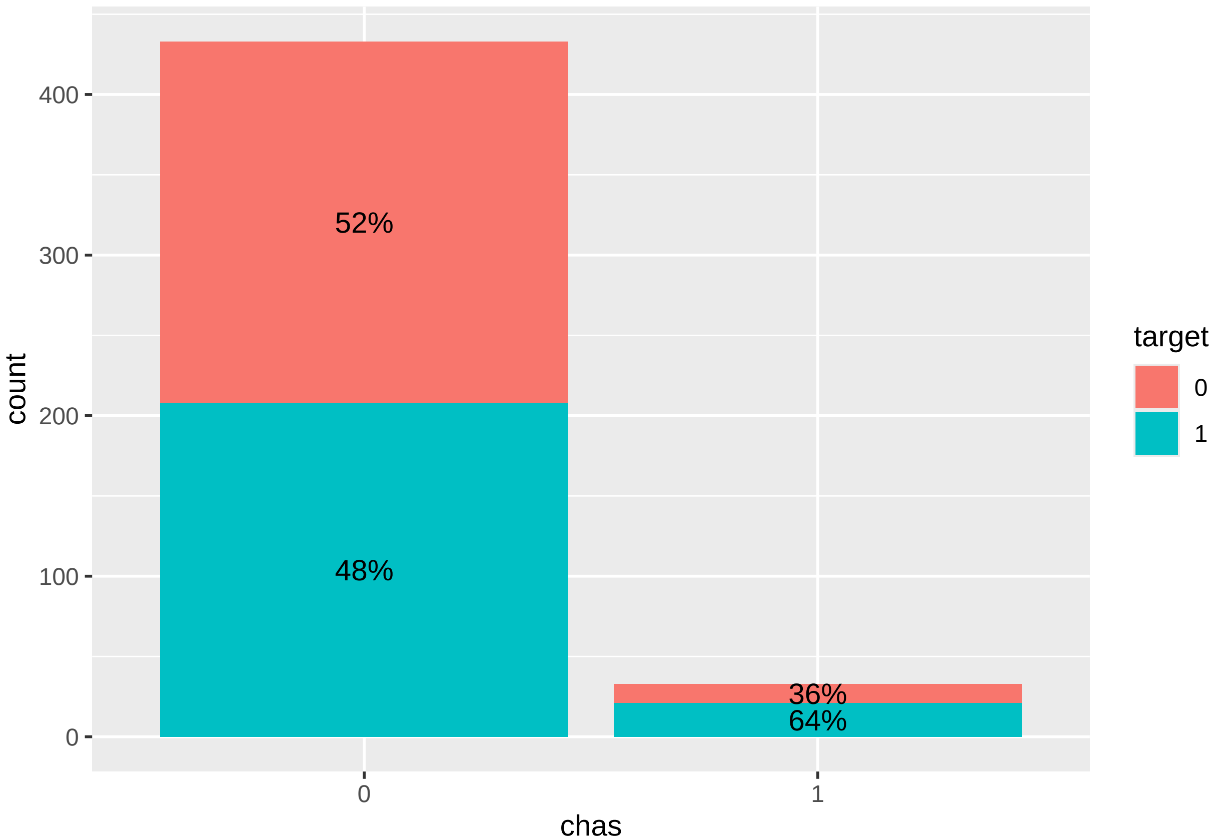
```
count_zeros <- sum(df_training_lo_crime$zn == 0)
cat("\nBelow Median Crime Rate Neighborhoods have ", count_zeros, " rows with a value of 0 for param zn
(count_zeros / nrow(df_training_lo_crime)), "%)\n")
```

```
##
## Below Median Crime Rate Neighborhoods have  125  rows with a value of 0 for param zn out of  237 obse
```

Categorical Variables

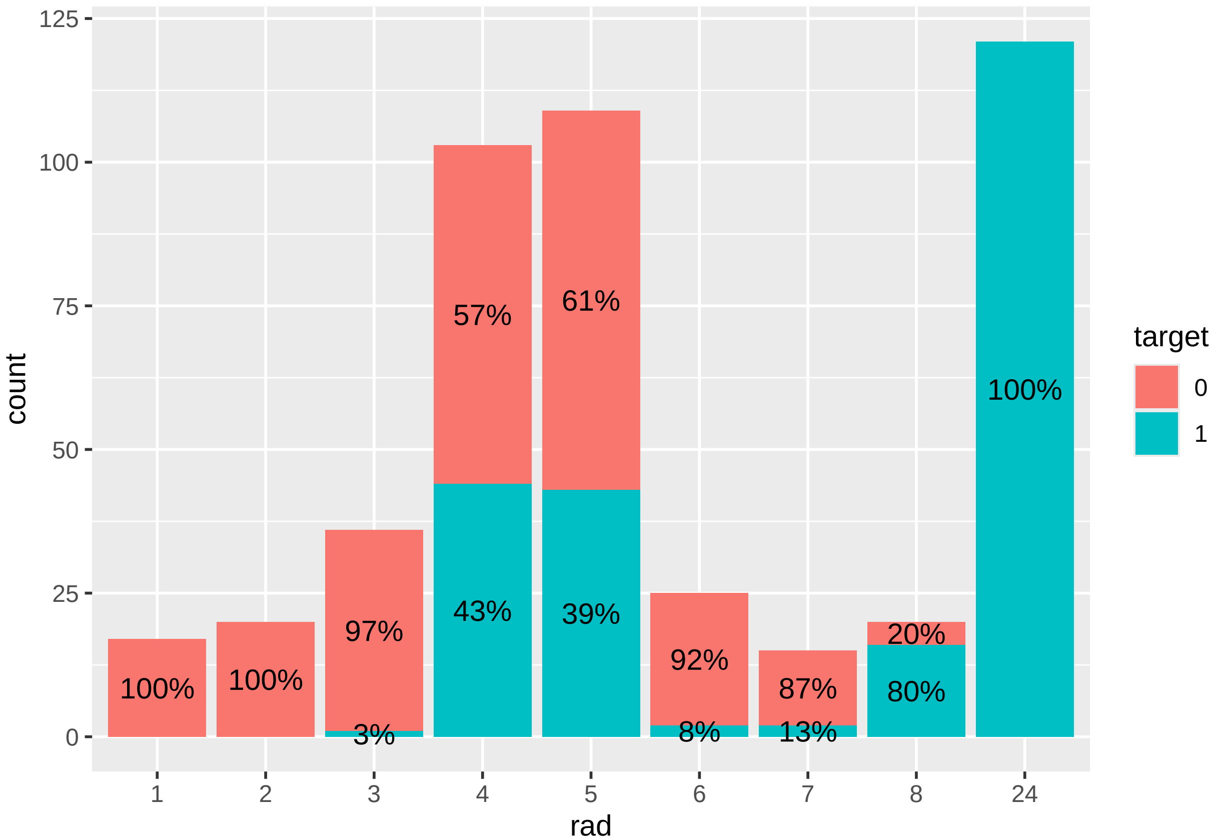
For our categorical variables, we can use barglaphs to get a sense of the parameter's impact on `target`.

```
df_training |>
  group_by(
    target,chas
  ) |>
  dplyr::summarise(
    count = n()
  ) |>
  ungroup() |>
  group_by(chas) |>
  mutate(
    percent = 100 * count / sum(count),
    label = paste0(round(percent),"%")
  ) |>
  ggplot() +
  aes(x = chas, y = count, label = label, fill=target) +
  geom_col() +
  geom_text(position = position_stack(0.5))
```



The bargraph for **chas** shows fairly equal values for 0 and 1 accross the **chas** values. This suggests that the variable will may have low impact on our model and we should consider removing it.

```
### rad
df_training |>
  group_by(
    target,rad
  ) |>
  dplyr::summarise(
    count = n()
  ) |>
  ungroup() |>
  group_by(rad) |>
  mutate(
    percent = 100 * count / sum(count),
    label = paste0(round(percent),"%")
  ) |>
  ggplot() +
  aes(x = rad, y = count, label = label, fill=target) +
  geom_col() +
  geom_text(position = position_stack(0.5))
```



The bargraphs for `rad` are somewhat more revealing. They suggest a strong relationship between low `rad` index values of 1-3 and below median crime rate, while an index value of 24 (the highest rad index) has a strong relationship with above median crime rate.

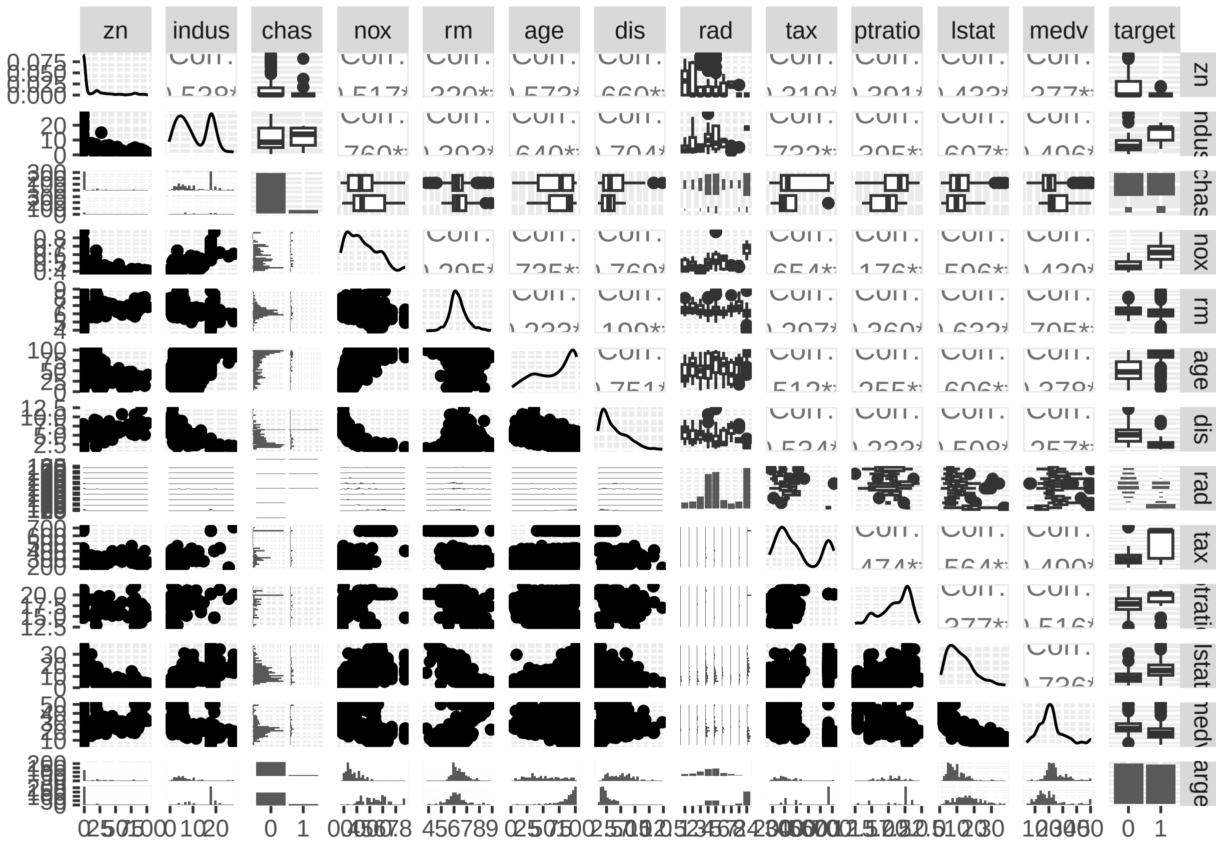
Pairs Using the pair function, we can print scatterplots comparing each of the variables to the others.

```
png("scatterplot_matrix.png", width = 800, height = 800)

pairs(df_training, main="")
dev.off()
```

```
## pdf
##   2
```

GGpairs plots take this a step further and show normal distribution and boxplots to get a fuller sense of how the data parameters relate to one another.

```
ggpairs(df_training)
```



Missing data

The training set contains no missing values.

```
introduce(df_training)
```

```
## # A tibble: 1 x 9
##    rows columns discrete_columns continuous_columns all_missing_columns
##   <int>   <int>            <int>              <int>               <int>
## 1   466      13                3                 10                   0
## # i 4 more variables: total_missing_values <int>, complete_rows <int>,
## #   total_observations <int>, memory_usage <dbl>
```

```
missing_values_count <- sapply(data, function(x) sum(is.na(x)))
print(missing_values_count)
```

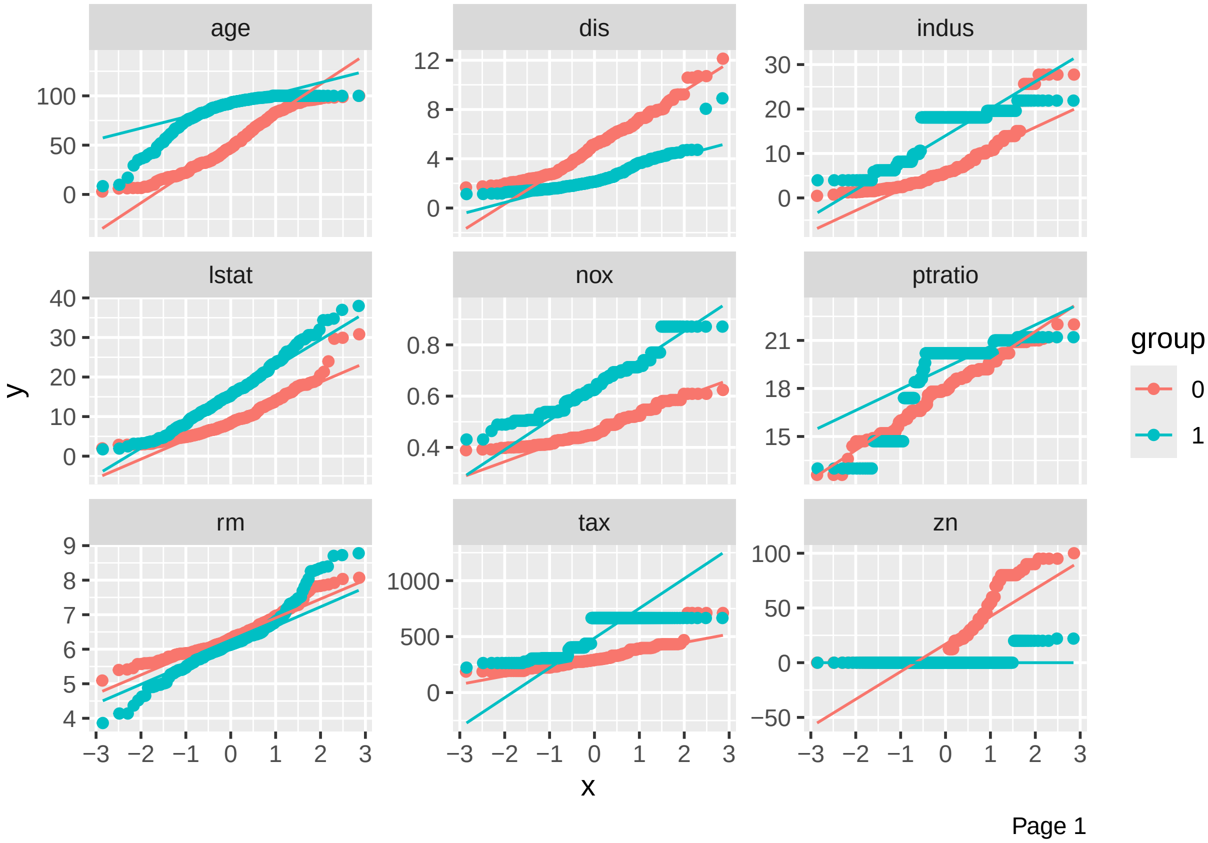
```
##       ...      list   package   lib.loc   verbose     envir overwrite
##         0         0         0         0         0         0         0         0
```

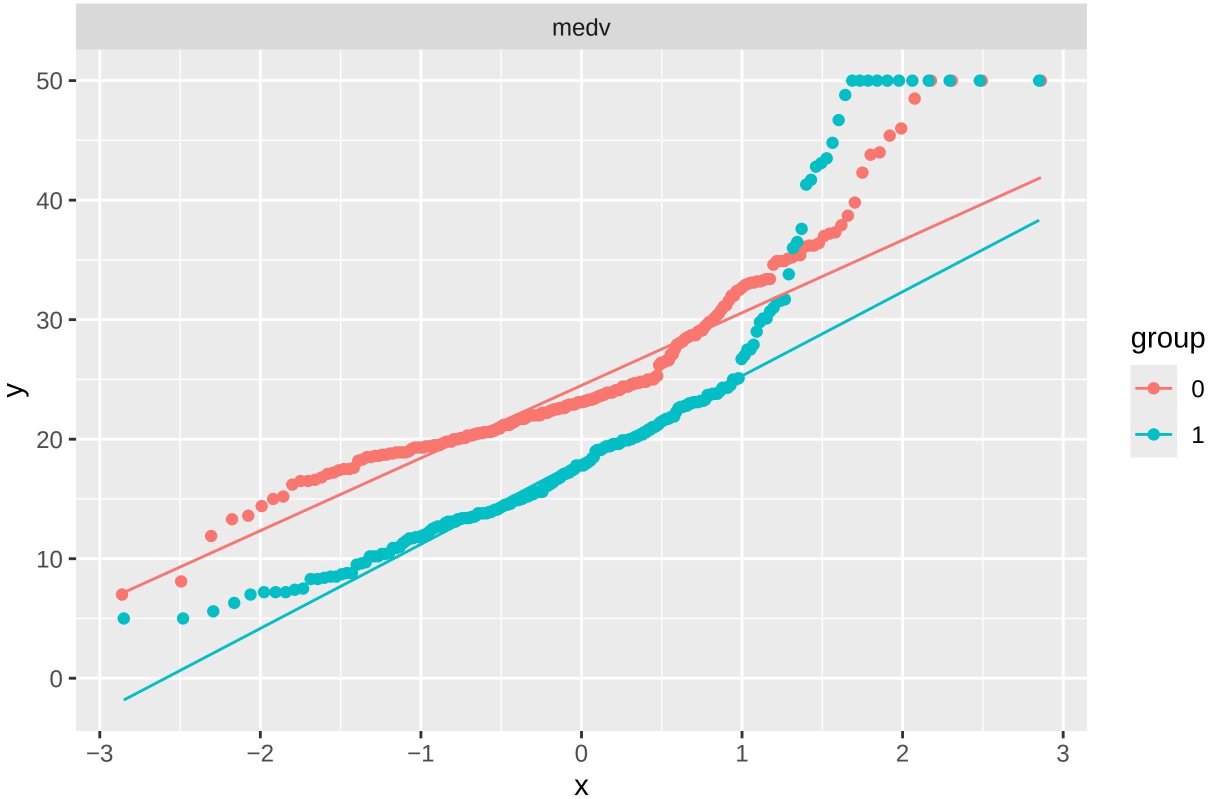
Distribution

Scatterplots of y=`target` plotted against each of the parameters confirm that the dependent variable is binomial. Therefore, linear regression is not be the best fit for this data and we should explore logistic regression such as logit and probit.

```
# scatter plot doesn't show much
# plot_scatterplot(df_training, by = "target")
# plot_qq(df_training, sampled_rows = 1000L)
```

```r
plot_qq(df_training, by="target", sampled_rows = 1000L)
```

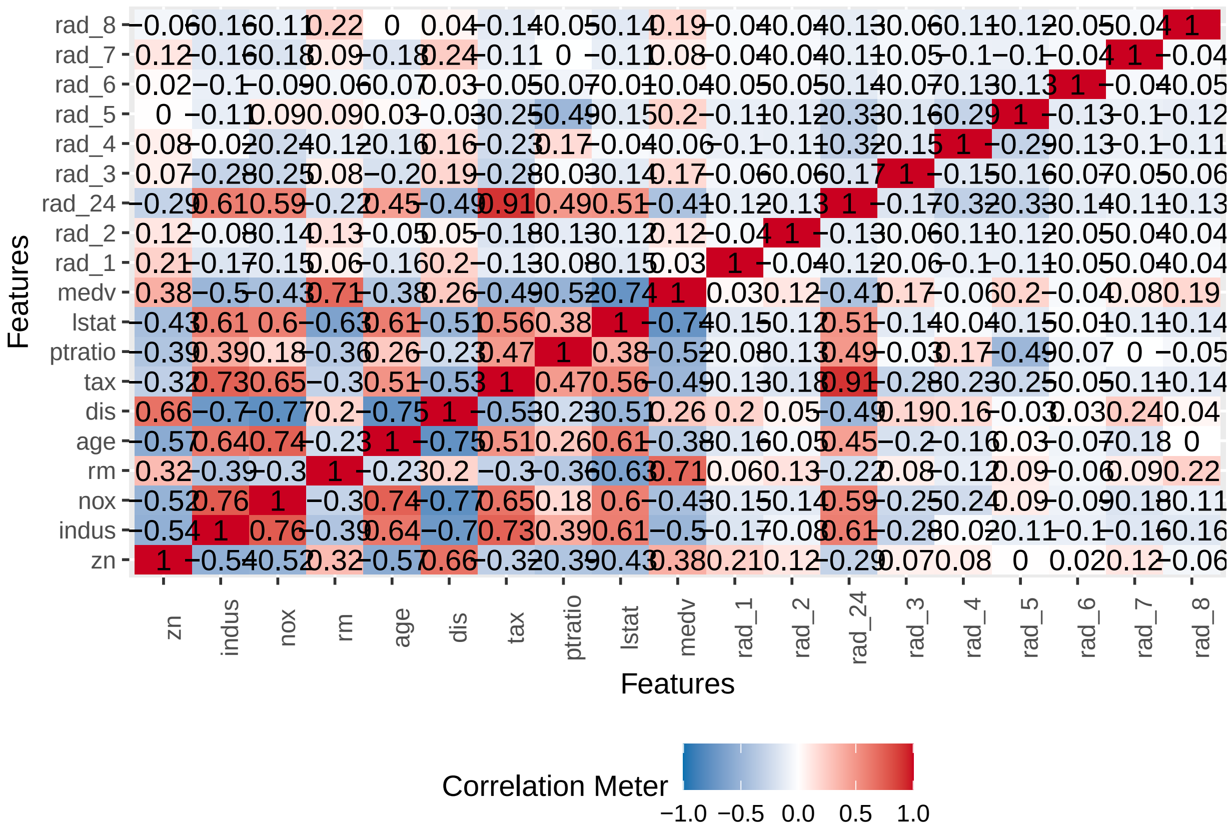




Page 2

Correlation

```
df_training |>
  subset(select=-c(target, chas)) |>
  plot_correlation(type = "all")
```



DATA PREPARATION

Fixing missing values

Luckily, there are no missing values in the training set.

Transforming data by bucketing and combining variables

The variable `rad` contains an ordinal factor that represents an index of accessibility to radial highways with values ranging from 1-24. A count of the rad values reveals that the `rad` column contains only values 1-8 and 24. This data set does not include any rows with a `rad` value of 9-23.

Since this column is contains values for an index value where 1 is assigned to neighborhoods with the poorest accessibility to a highway and 24 is assigned to neighborhoods with the most accessibility, we can simplify our variables by binning our rad values. Here we are using quantiles to bin the values into three buckets of nearly equal sizes for low, moderate and high accessibility. This method ensures a more balanced distribution of rows across the bins over using equal sized bins (1-8, 9-16, 17-24). This especially useful when the data is not uniformly distributed across the range such as in our case where we do not have any rad values of 1-23.

```
rad_counts
```

```
##
##   1   2   3   4   5   6   7   8  24
##  17  20  36 103 109  25  15  20 121
```

```
quantile_breaks <- quantile(as.numeric(df_training$rad), probs = c(0, 1/3, 2/3, 1))

df_training$radq <- cut(as.numeric(df_training$rad),
                   breaks = quantile_breaks,
                   labels = c('_low', '_mid', '_hi'),
```

```
                    include.lowest = TRUE,
                    right = TRUE)

table(df_training$radq)
```

```
##
## _low _mid  _hi
##  176  149  141
```

While the `glm` function should automatically perform one-hot encoding to factors, we should consider one-hot encoding on the `rad_quantile` parameter to perform other operations, such as calculating correlation using the spearman test.

We will drop one of the one-hot encoded params as the presence of this additional param will result in correlation issues down the line. `radq_mid` was selected, as it seemed to have the most mixed results in our plots above.

```
# one-hot encode rad values
rad_one_hot <- model.matrix(~ radq - 1, data = df_training)

# combine new columns
df_training_one_hot <- cbind(df_training[ , !names(df_training) %in% "rad"], rad_one_hot) |>
  subset(select=-c(radq, radq_mid))

glimpse(df_training_one_hot)
```

```
## Rows: 466
## Columns: 14
## $ zn       <dbl> 0, 0, 0, 30, 0, 0, 0, 0, 0, 80, 22, 0, 0, 22, 0, 0, 100, 20, ~
## $ indus    <dbl> 19.58, 19.58, 18.10, 4.93, 2.46, 8.56, 18.10, 18.10, 5.19, 3.~
## $ chas     <fct> 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## $ nox      <dbl> 0.605, 0.871, 0.740, 0.428, 0.488, 0.520, 0.693, 0.693, 0.515~
## $ rm       <dbl> 7.929, 5.403, 6.485, 6.393, 7.155, 6.781, 5.453, 4.519, 6.316~
## $ age      <dbl> 96.2, 100.0, 100.0, 7.8, 92.2, 71.3, 100.0, 100.0, 38.1, 19.1~
## $ dis      <dbl> 2.0459, 1.3216, 1.9784, 7.0355, 2.7006, 2.8561, 1.4896, 1.658~
## $ tax      <dbl> 403, 403, 666, 300, 193, 384, 666, 666, 224, 315, 330, 398, 6~
## $ ptratio  <dbl> 14.7, 14.7, 20.2, 16.6, 17.8, 20.9, 20.2, 20.2, 20.2, 16.4, 1~
## $ lstat    <dbl> 3.70, 26.82, 18.85, 5.19, 4.82, 7.67, 30.59, 36.98, 5.68, 9.2~
## $ medv     <dbl> 50.0, 13.4, 15.4, 23.7, 37.9, 26.5, 5.0, 7.0, 22.2, 20.9, 24.~
## $ target   <fct> 1, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0~
## $ radq_low <dbl> 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1~
## $ radq_hi  <dbl> 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0~
```

We will use the one-hot encoded dataframe to diagnose a preliminary model with all of the predictors.

```
model_full <- glm(target ~., binomial(link = "logit"), data=df_training_one_hot)
summary(model_full)
```

```
##
## Call:
## glm(formula = target ~ ., family = binomial(link = "logit"),
##     data = df_training_one_hot)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.736e+01  6.617e+00  -5.646 1.65e-08 ***
## zn          -8.026e-02  4.105e-02  -1.955 0.050551 .
```

```
## indus       -1.724e-01  4.986e-02  -3.457 0.000547 ***
## chas1        1.179e+00  8.097e-01   1.456 0.145311
## nox          5.946e+01  9.038e+00   6.579 4.74e-11 ***
## rm          -9.564e-01  6.992e-01  -1.368 0.171345
## age          2.030e-02  1.322e-02   1.536 0.124585
## dis          8.131e-01  2.456e-01   3.310 0.000931 ***
## tax          9.619e-04  2.291e-03   0.420 0.674583
## ptratio      1.190e-01  1.333e-01   0.893 0.372038
## lstat        5.447e-02  5.231e-02   1.041 0.297705
## medv         1.760e-01  5.907e-02   2.980 0.002887 **
## radq_low     1.563e+00  5.254e-01   2.975 0.002931 **
## radq_hi      5.118e+00  9.416e-01   5.436 5.46e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 180.97  on 452  degrees of freedom
## AIC: 208.97
##
## Number of Fisher Scoring iterations: 8
```

Reviewing the summary statistics for full model indicates that the variable `indus`, `nox`, `dis`, and `radq_hi` has very strong statistically signification. Two additional variables, `medv`, `dis` and `radq_mid`, have high statistical significance while `zn` has weak statistical significance. `chas1`, `rm`, `age`, `tax`, `ptratio` and `lstat` have weak statistical significance values.

Note: had we one-hot encoded all of the values for `rad` instead of binning them first, all `rad` params would have very weak statistical significance, as their p-values are nearly 1.0.

Multicollinearity

To test if correlation exists between the dependent and independent variables, we used a Pearson's Correlation test. The function below loops through each of our columns and prints out the correlation of the dependent variable `target` with each of the predictors. For predictors where Pearson's Correlation coefficient is close to zero, we can determine that collinearity does not exist.

```r
# is above .7 would be too highly correlated
cor_results <- data.frame(name = character(0), value = numeric(0))
for (param in colnames(df_training_one_hot)) {
  cat("\nPearson Test score for", param, ":\n")
  x <- as.numeric(df_training_one_hot$target)
  y <- as.numeric(df_training_one_hot[[param]])
  pearsons <- cor.test(x, y, method = "pearson")
  print(pearsons)
  # calc pearson cor value only
  cor_object <-  data.frame(name = param, value = cor(x, y))
  assign("cor_results", rbind(cor_results, cor_object), envir = .GlobalEnv)
}
```

```
##
## Pearson Test score for zn :
##
##  Pearson's product-moment correlation
##
```

```
## data:  x and y
## t = -10.309, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.5028019 -0.3547564
## sample estimates:
##        cor
## -0.4316818
##
##
## Pearson Test score for indus :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 16.361, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5438976 0.6594549
## sample estimates:
##       cor
## 0.6048507
##
##
## Pearson Test score for chas :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 1.7297, df = 464, p-value = 0.08435
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.01087336  0.16964461
## sample estimates:
##        cor
## 0.08004187
##
##
## Pearson Test score for nox :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 22.748, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.6801291 0.7663936
## sample estimates:
##       cor
## 0.7261062
##
##
## Pearson Test score for rm :
##
```

```
##  Pearson's product-moment correlation
##
## data:  x and y
## t = -3.325, df = 464, p-value = 0.0009542
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.24006288 -0.06258443
## sample estimates:
##        cor
## -0.1525533
##
##
## Pearson Test score for age :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 17.479, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5720099 0.6819122
## sample estimates:
##       cor
## 0.6301062
##
##
## Pearson Test score for dis :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = -16.963, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.6717579 -0.5592666
## sample estimates:
##        cor
## -0.6186731
##
##
## Pearson Test score for tax :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 16.631, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5508558 0.6650327
## sample estimates:
##       cor
## 0.6111133
##
##
```

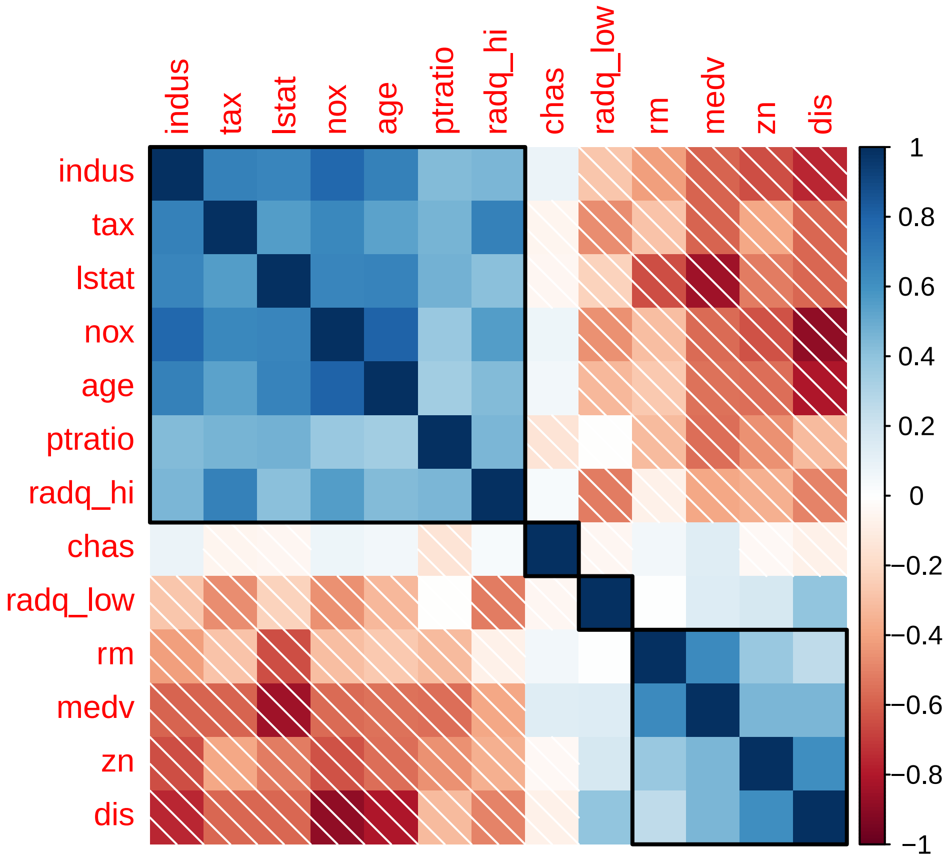
```
## Pearson Test score for ptratio :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 5.5819, df = 464, p-value = 4.053e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.1637438 0.3340729
## sample estimates:
##       cor
## 0.2508489
##
##
## Pearson Test score for lstat :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 11.443, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.3951287 0.5370764
## sample estimates:
##      cor
## 0.469127
##
##
## Pearson Test score for medv :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = -6.0536, df = 464, p-value = 2.925e-09
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.3527185 -0.1842424
## sample estimates:
##        cor
## -0.2705507
##
##
## Pearson Test score for target :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = Inf, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  1 1
## sample estimates:
## cor
##   1
```

```
##
##
## Pearson Test score for radq_low :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = -8.5077, df = 464, p-value = 2.466e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.4433864 -0.2860542
## sample estimates:
##        cor
## -0.3673453
##
##
## Pearson Test score for radq_hi :
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 17.599, df = 464, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5749042 0.6842126
## sample estimates:
##       cor
## 0.6326995
```

```r
print(cor_results)
```

```
##        name       value
## 1        zn -0.43168176
## 2     indus  0.60485074
## 3      chas  0.08004187
## 4       nox  0.72610622
## 5        rm -0.15255334
## 6       age  0.63010625
## 7       dis -0.61867312
## 8       tax  0.61111331
## 9   ptratio  0.25084892
## 10    lstat  0.46912702
## 11     medv -0.27055071
## 12   target  1.00000000
## 13 radq_low -0.36734528
## 14  radq_hi  0.63269952
```

Correlation Clusters Next we can visualize the correlations in clusters.



Using "hclust", our corrplot shows four distinct groups, each with strong correlation between the parameters within each group. This suggests that we may want to select specific parameters from within these groups or conduct principal component analysis on each of these groups.

```r
car::vif(model_full) |> sort()
```

Variance Inflation Factor

```
##     chas radq_low       zn  radq_hi      age      tax  ptratio    lstat
## 1.208878 1.939100 1.979366 2.126242 2.146346 2.205786 2.314164 2.561351
##    indus      dis       rm      nox     medv
## 3.388295 4.138425 4.732821 5.329898 5.983892
```

A VIF test suggests that we should remove nox and medv.

Presence of Outliers

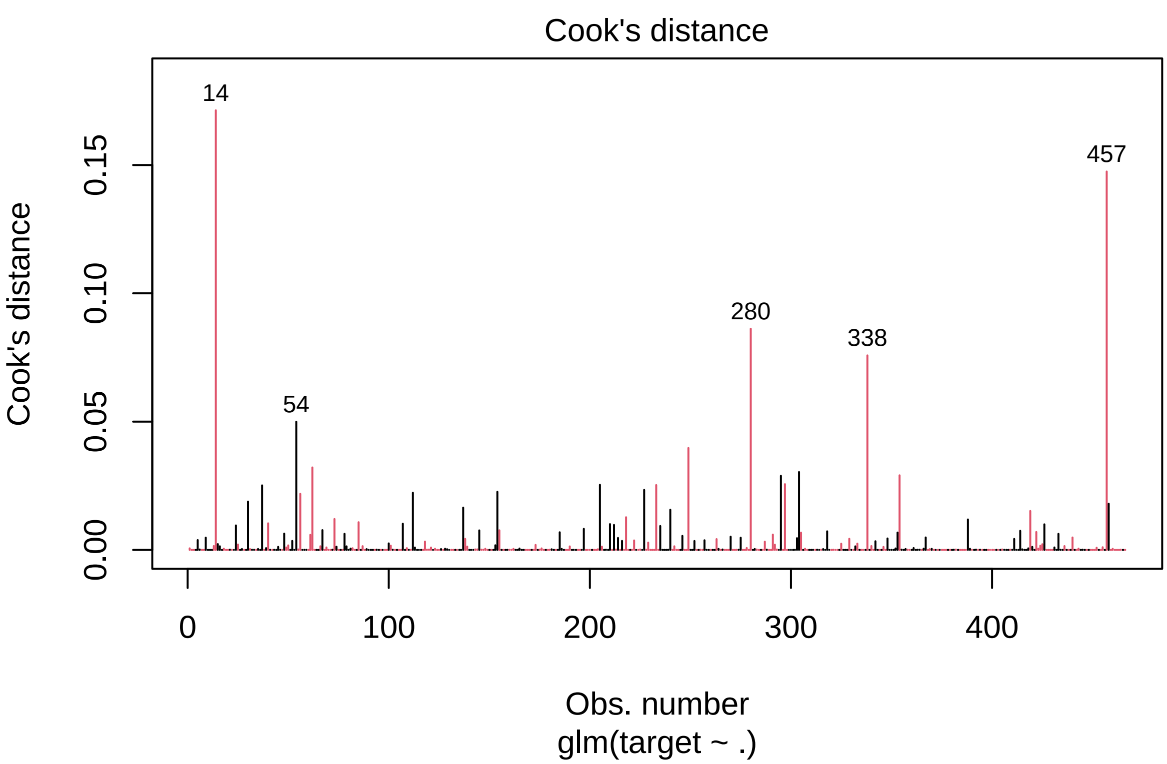
We can examine our diagnostic plots to find potential outliers and leverage. First we will examine the Cook's Distance and Cook's Distance vs Leverage plots. Cook's Distance measures the influence of an observation on the fitted values of the model.

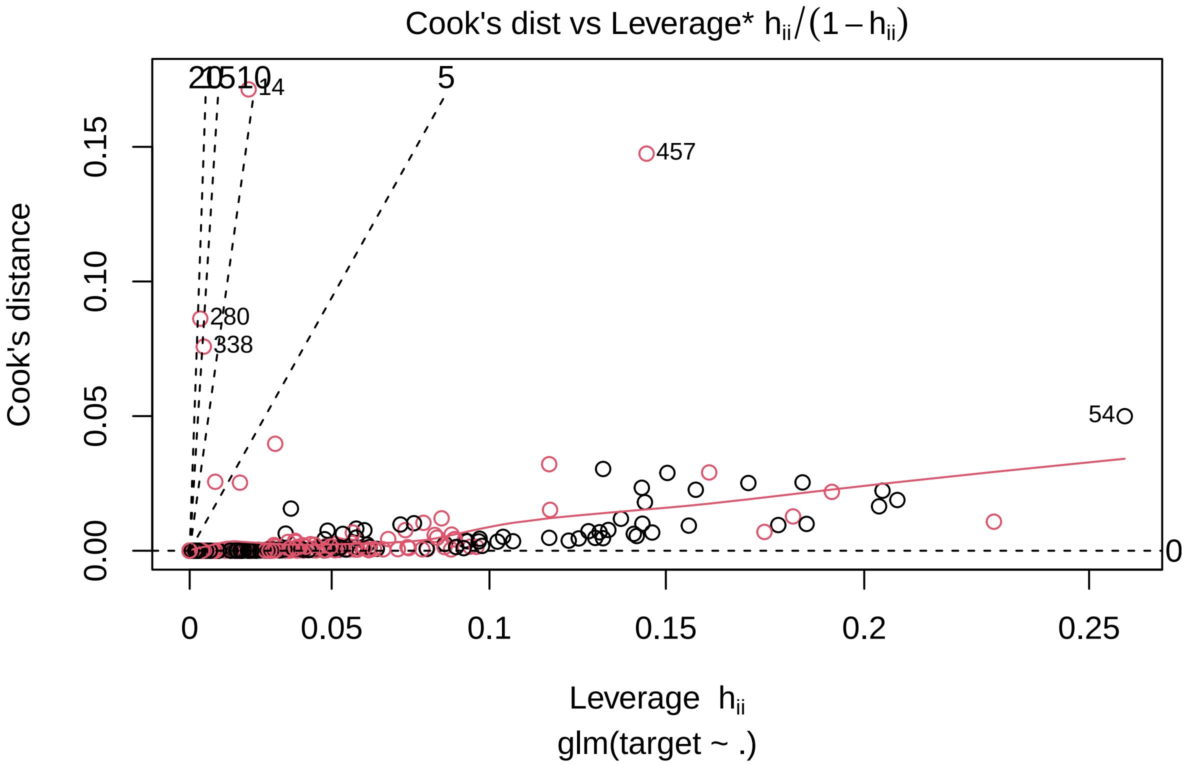
```
## Rows: 5
## Columns: 21
## $ index      <int> 14, 457, 280, 338, 54
## $ target     <chr> "Hi", "Hi", "Hi", "Hi", "Lo"
## $ zn         <dbl> 22, 0, 22, 20, 0
## $ indus      <dbl> 5.86, 10.59, 5.86, 6.96, 1.89
## $ chas       <fct> 0, 0, 0, 0, 0
```

```
## $ nox        <dbl> 0.431, 0.489, 0.431, 0.464, 0.518
## $ rm         <dbl> 8.259, 5.412, 6.108, 5.856, 6.540
## $ age        <dbl> 8.4, 9.8, 34.9, 42.1, 59.7
## $ dis        <dbl> 8.9067, 3.5875, 8.0555, 4.4290, 6.2669
## $ tax        <dbl> 330, 277, 330, 223, 422
## $ ptratio    <dbl> 19.1, 18.6, 19.1, 18.6, 15.9
## $ lstat      <dbl> 3.54, 29.55, 9.16, 13.00, 8.65
## $ medv       <dbl> 42.8, 23.7, 24.3, 21.1, 16.5
## $ radq_low   <dbl> 0, 1, 0, 1, 1
## $ radq_hi    <dbl> 0, 0, 0, 0, 0
## $ .fitted    <dbl> -4.6773398, -2.3444828, -5.7239448, -5.3060581, 0.4048362
## $ .resid     <dbl> 3.061568, 2.207286, 3.384437, 3.259143, -1.353450
## $ .hat       <dbl> 0.021373959, 0.144810967, 0.003911828, 0.005210891, 0.25736~
## $ .sigma     <dbl> 0.6164625, 0.6234026, 0.6129971, 0.6144815, 0.6291214
## $ .cooksd    <dbl> 0.17134297, 0.14748407, 0.08620525, 0.07580775, 0.04996881
## $ .std.resid <dbl> 3.094821, 2.386863, 3.391076, 3.267668, -1.570564
```

The calculation above shows that points 14, 457, 280, 338, and 54 have the highest Cook's distance values (ordered from highest to lowest) and should be investigated as potential outliers.

```
par(mar = c(5, 4, 4, 2) + 0.1)
plot(model_full, which = c(4, 6), col=df_training_one_hot$target,  id.n = 5)
```



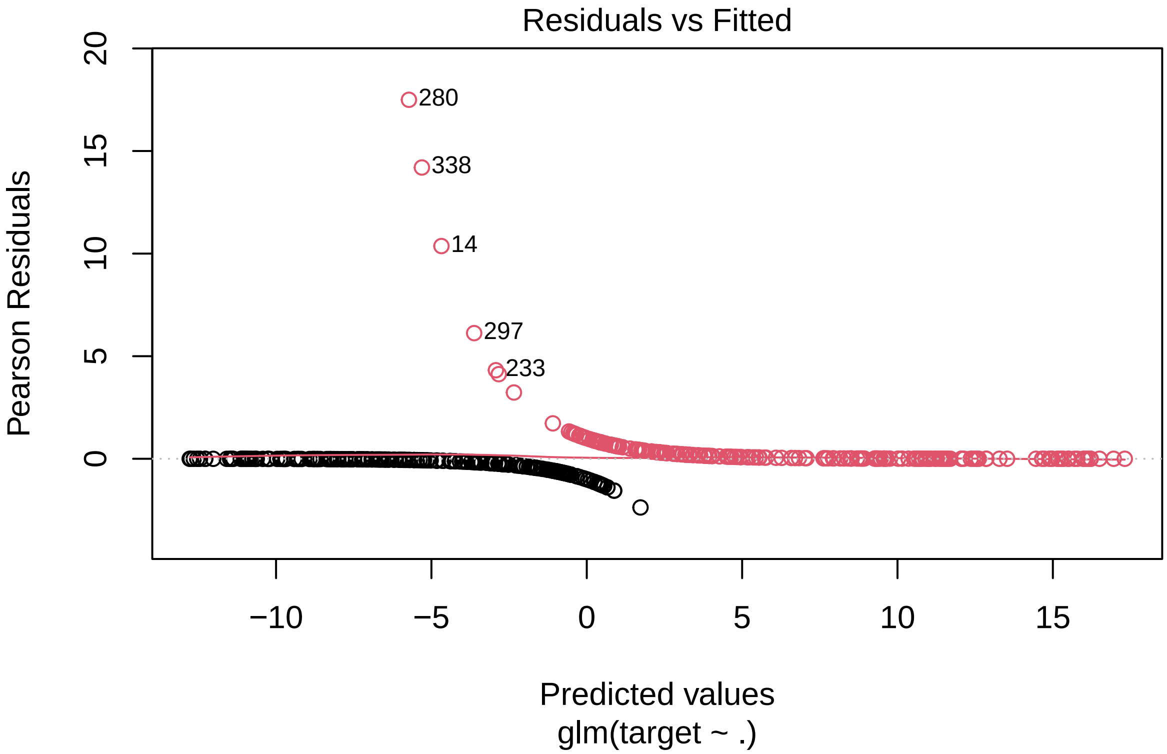


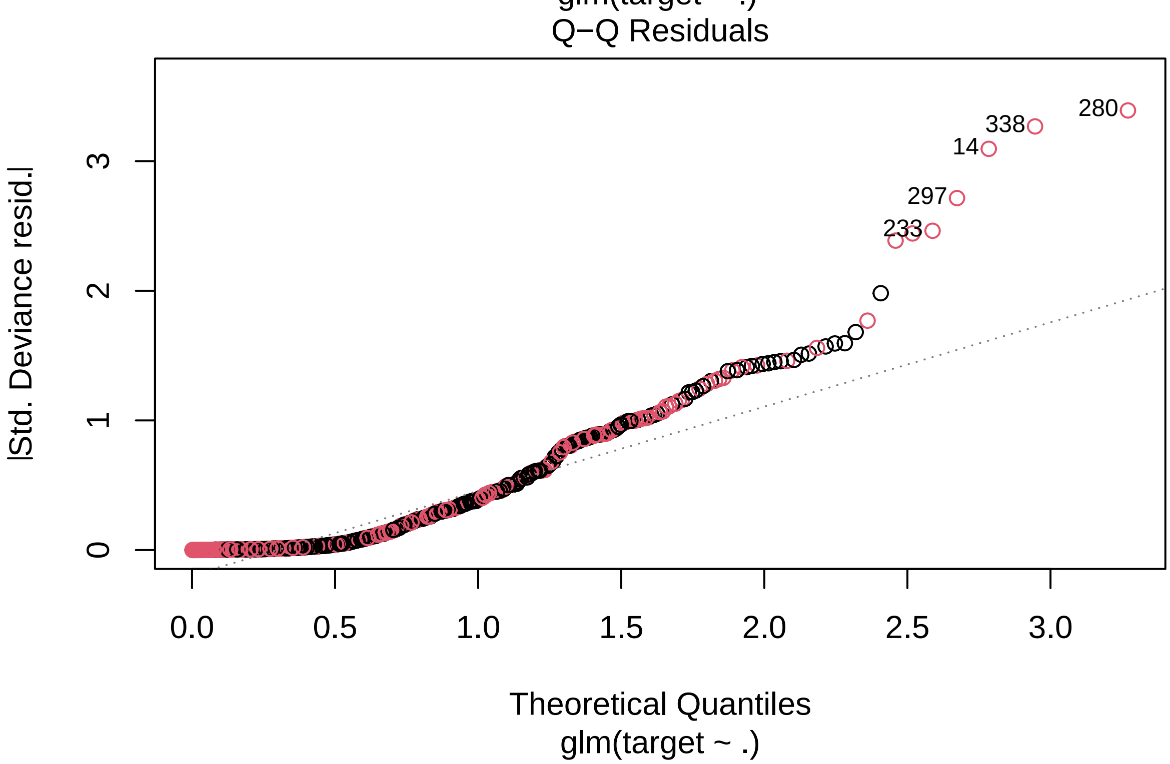
We see on the Cook's dist vs Leverage plot that points 280 and 338 may have very high leverage on our model, followed by point 14. Point 457 also stand out and should be investigated but appears to have less leverage.

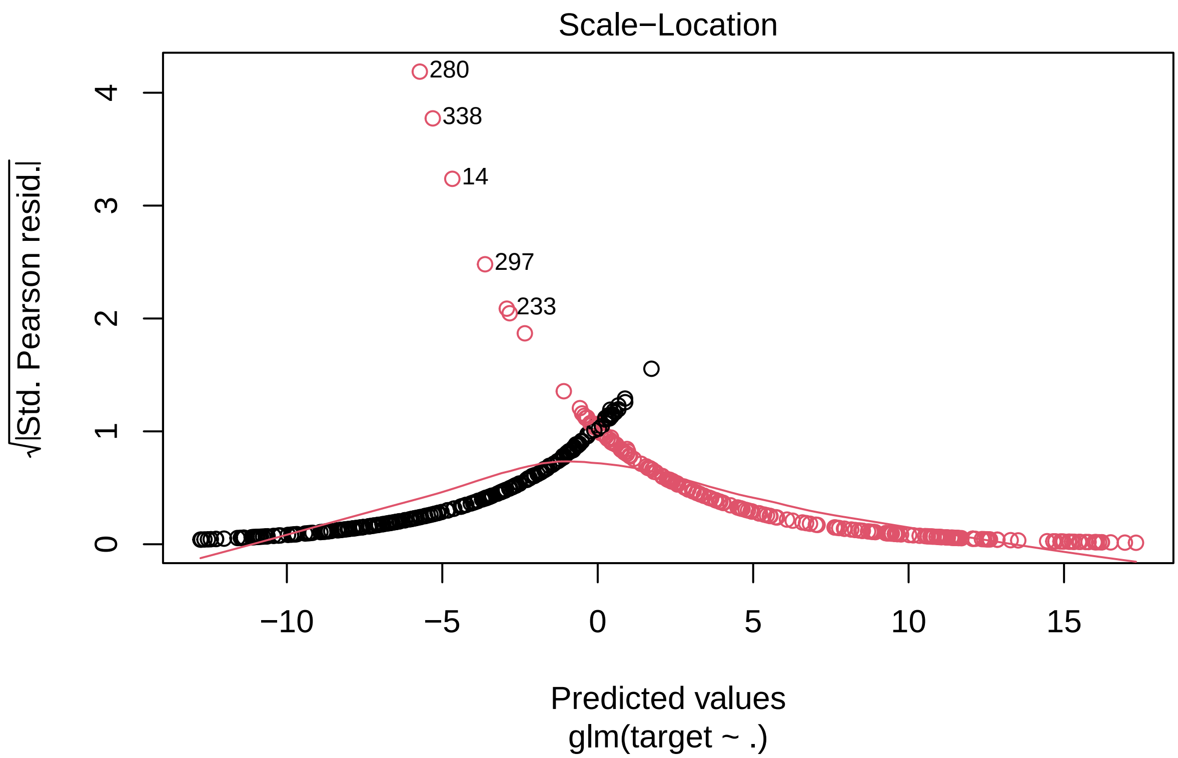
```
# print influential points using cooks-distance
cooksd <- cooks.distance(model_full)
influential <- which(cooksd > (4 / length(cooksd)))
print(influential)
```

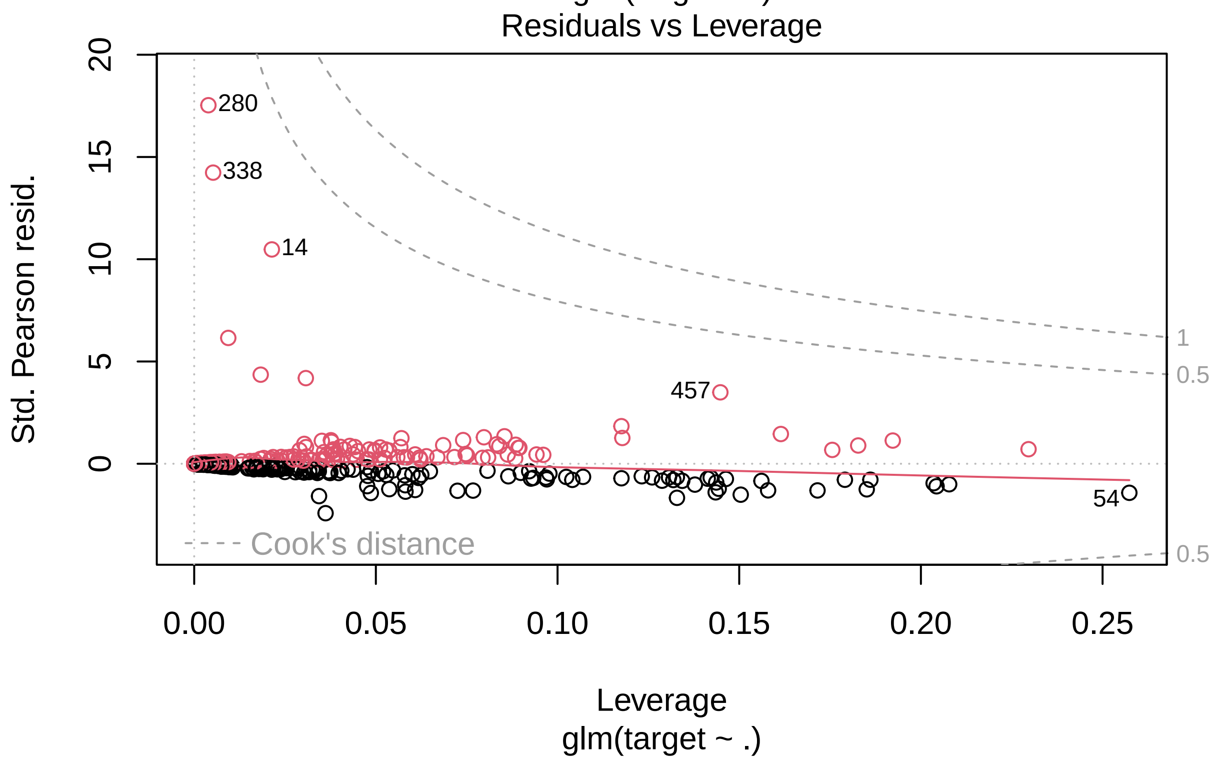
```
##  14  24  30  37  40  54  56  62  73  85 107 112 137 154 205 210 212 218 227 233
##  14  24  30  37  40  54  56  62  73  85 107 112 137 154 205 210 212 218 227 233
## 235 240 249 280 295 297 304 338 354 388 419 426 457 458
## 235 240 249 280 295 297 304 338 354 388 419 426 457 458
```

The formula above is used to idential influential points defined as points Cook's Distance value is greater than 4 / length of cooksd. This contains all three points (280, 338, and 14) as being influential.


Residuals vs Fitted
Pearson Residuals
Predicted values
glm(target ~ .)
280
338
14
297
233


Q−Q Residuals
|Std. Deviance resid.|
Theoretical Quantiles
glm(target ~ .)
280
338
14
297
233



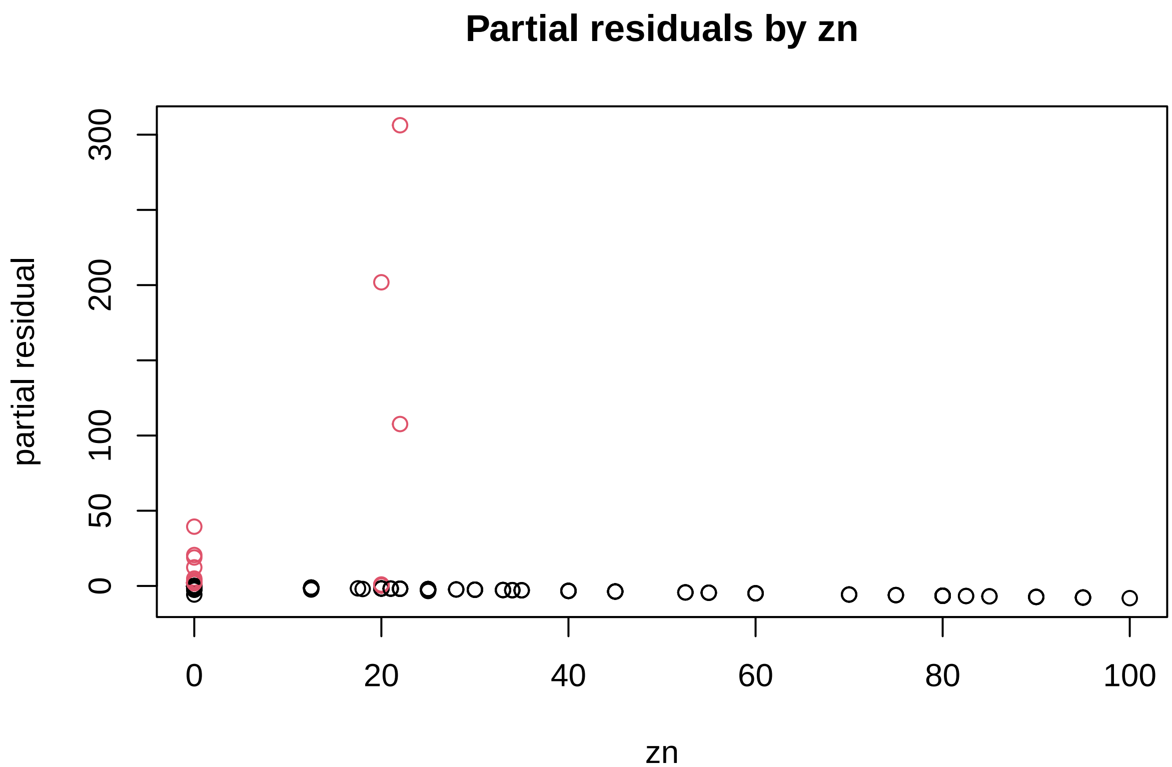


Our residual vs fitted, QQ, Scale-Location and Residual vs Leverage plots all confirm that points 280, 338, and 14 should be investigated and could be outliers with high influence. Points 457 appear to have less leverage and does not stand out in these plots.

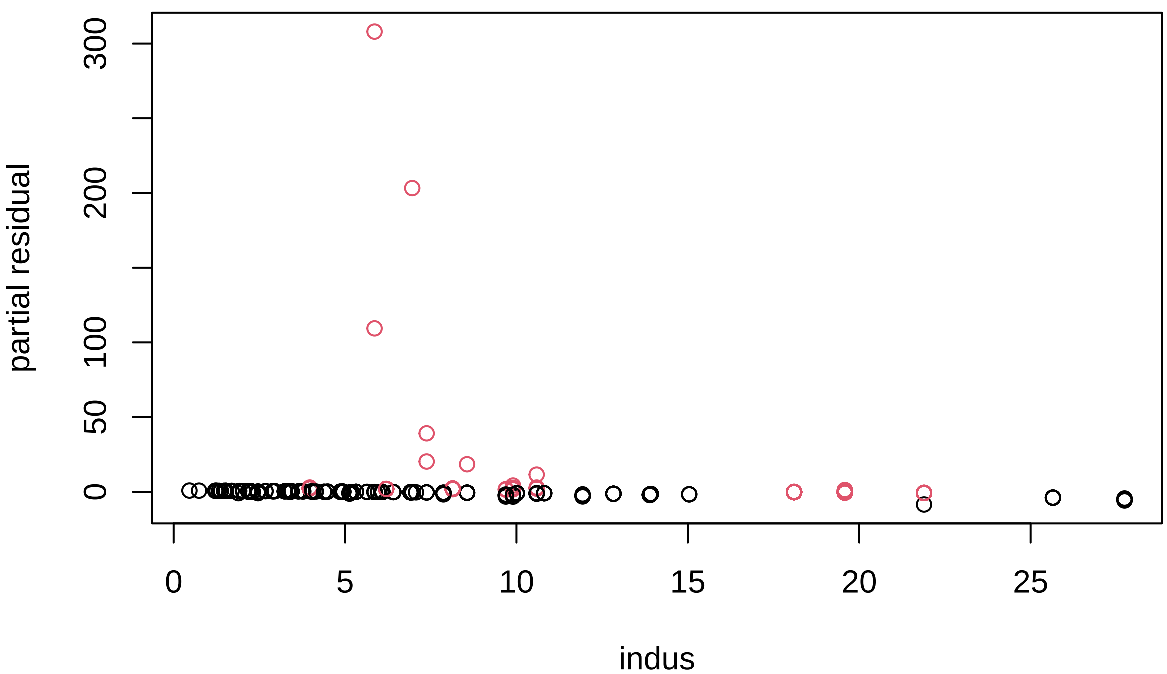
Below is the output for the three points identified as potential outliers in our diagnostic plots. A quick review of the data doesn't reveal anything that stands out as being out of the ordinary.

Partial residual plots

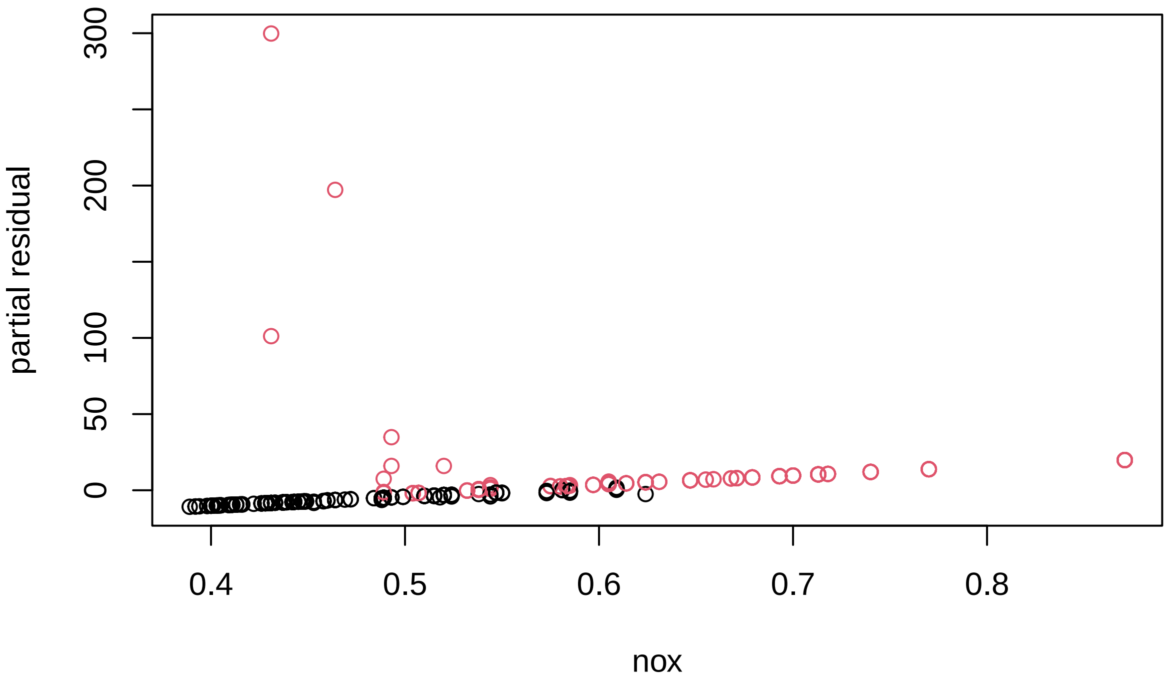
```
for (j in names(coef(model_full))[-1]) {
  if (j != 'chas1' && j != 'chas2'){
    plot(
      x = df_training_one_hot[,j],
      y = residuals(model_full, "partial")[,j],
    col = df_training_one_hot$target,
    main = paste0("Partial residuals by ", j),
    xlab = j,
    ylab = "partial residual"
    )
  }
}
```

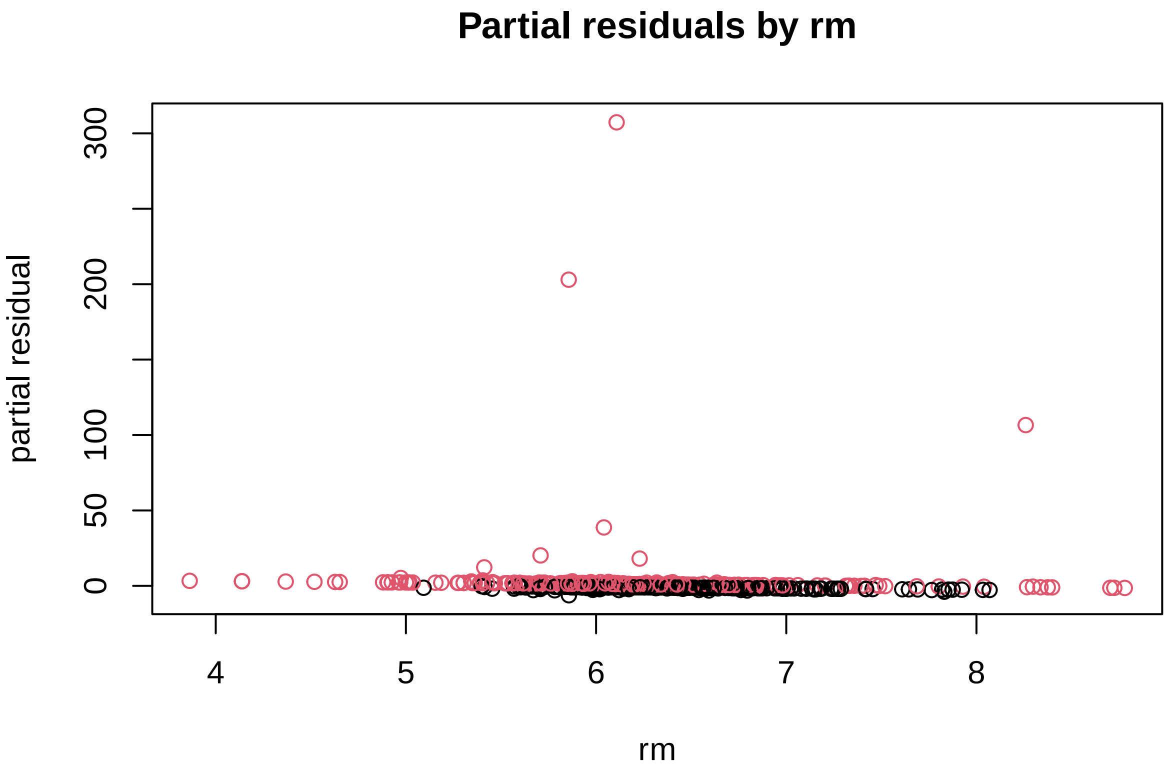


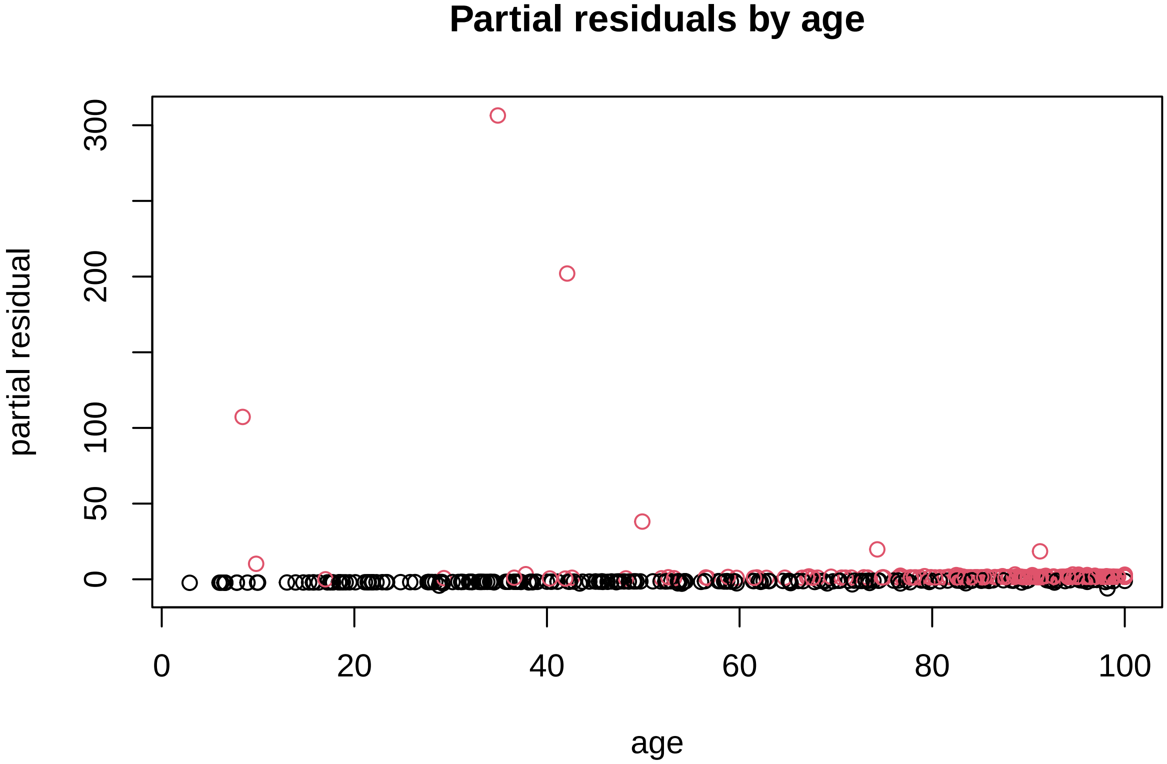
Partial residuals by indus

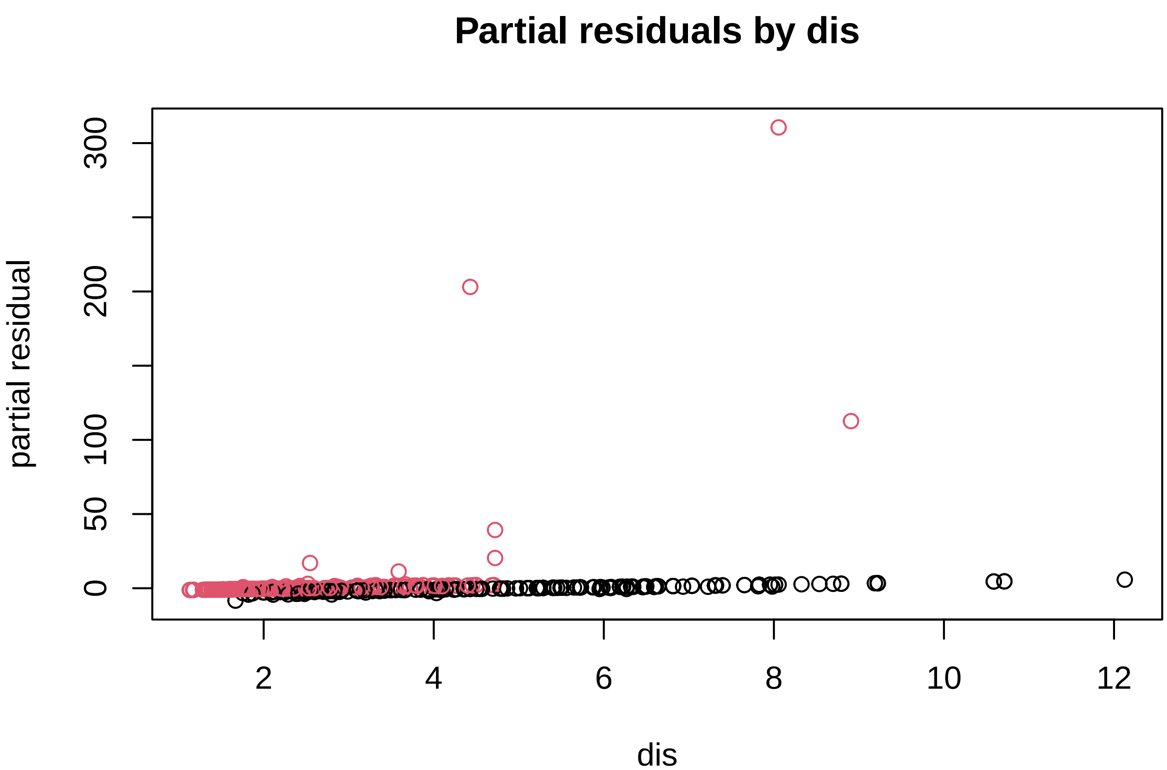


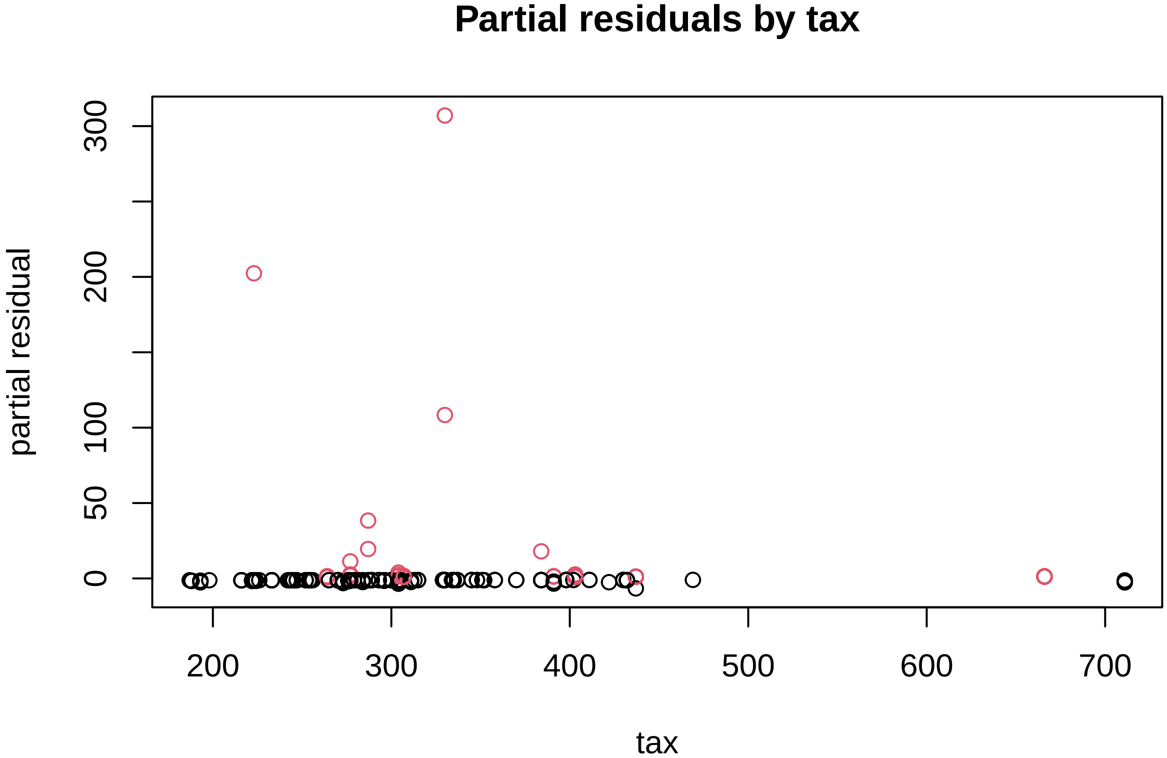
Partial residuals by nox

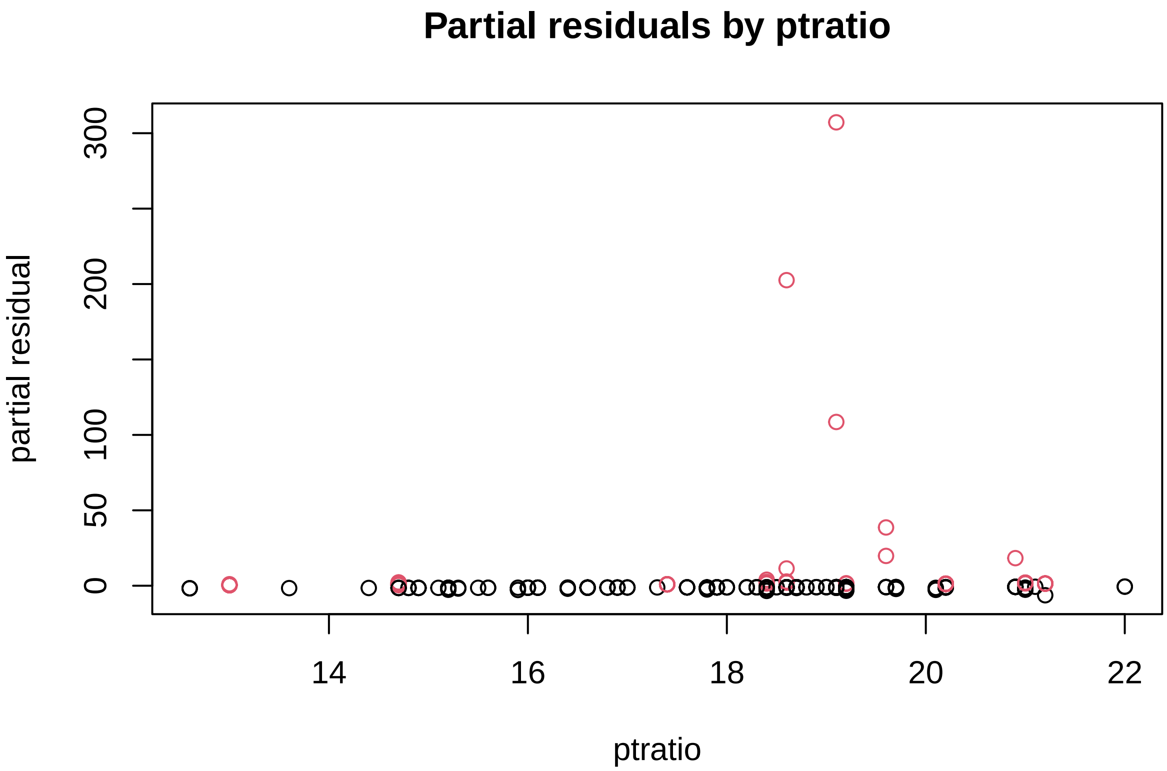



Partial residuals by rm
partial residual
0
50
100
200
300
4
5
6
7
8
rm

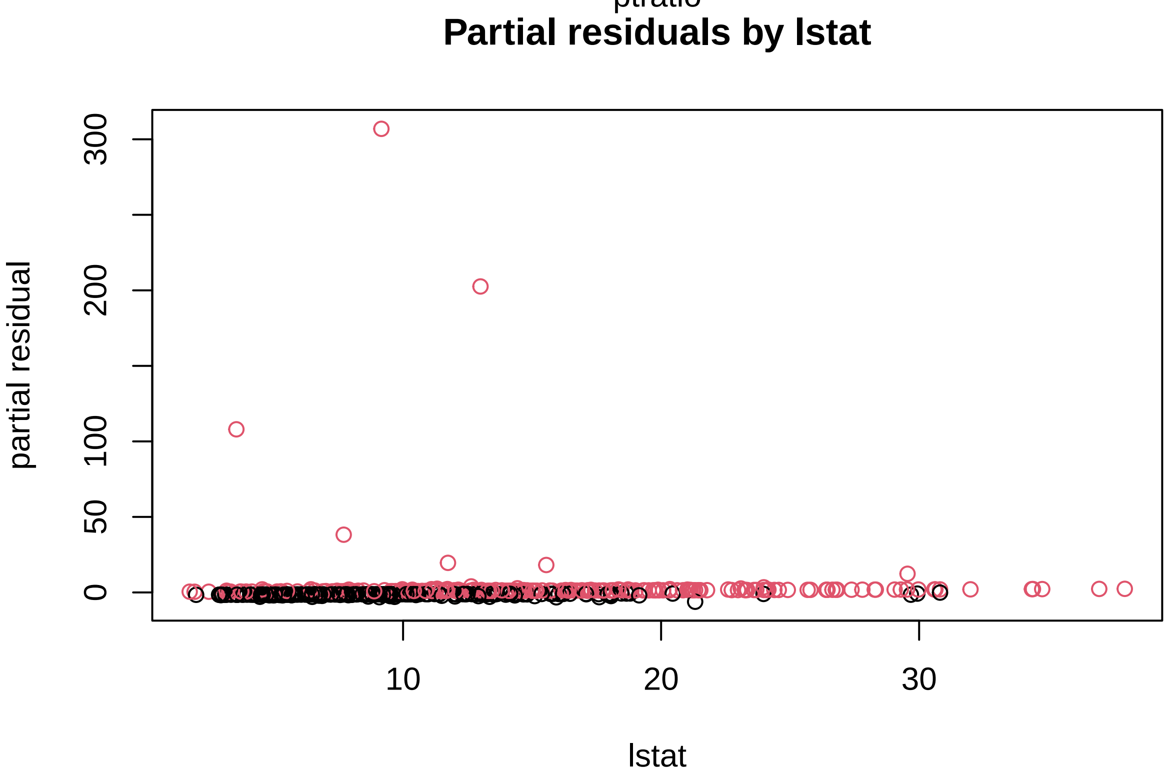

Partial residuals by age
partial residual
0
50
100
200
300
0
20
40
60
80
100
age


Partial residuals by dis
partial residual
0
50
100
200
300
2
4
6
8
10
12
dis

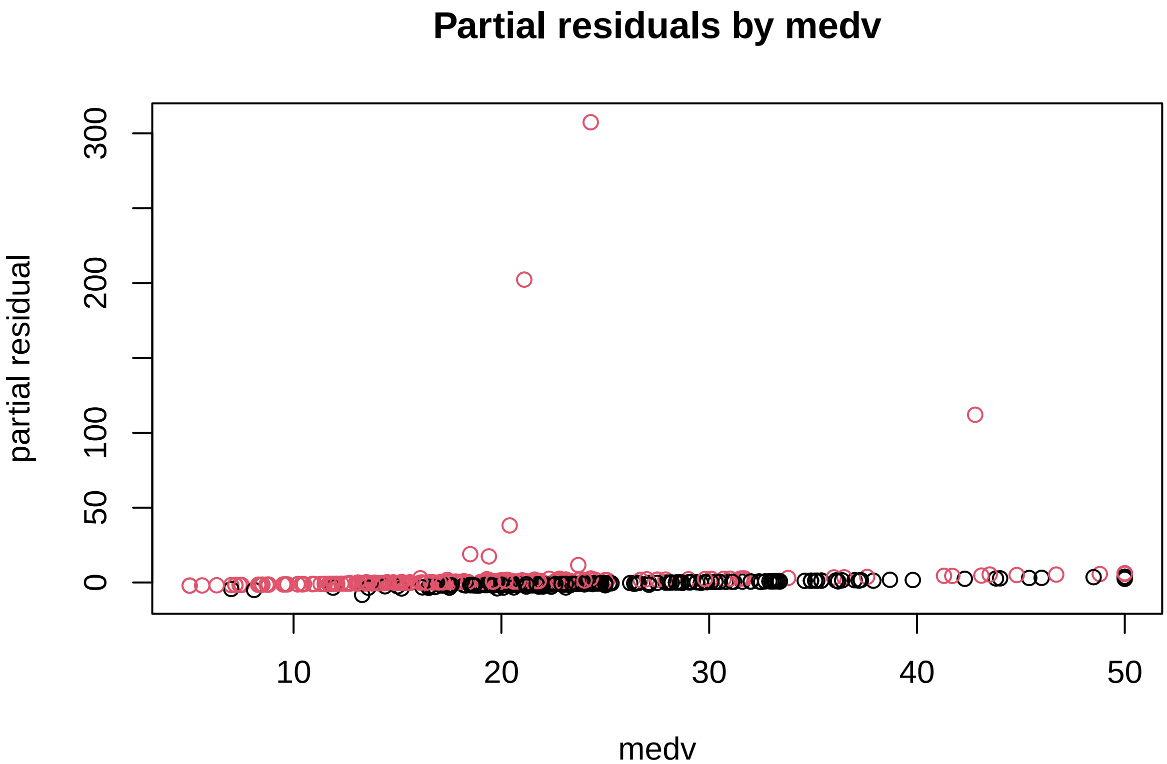

Partial residuals by tax
partial residual
0
50
100
200
300
200
300
400
500
600
700
tax

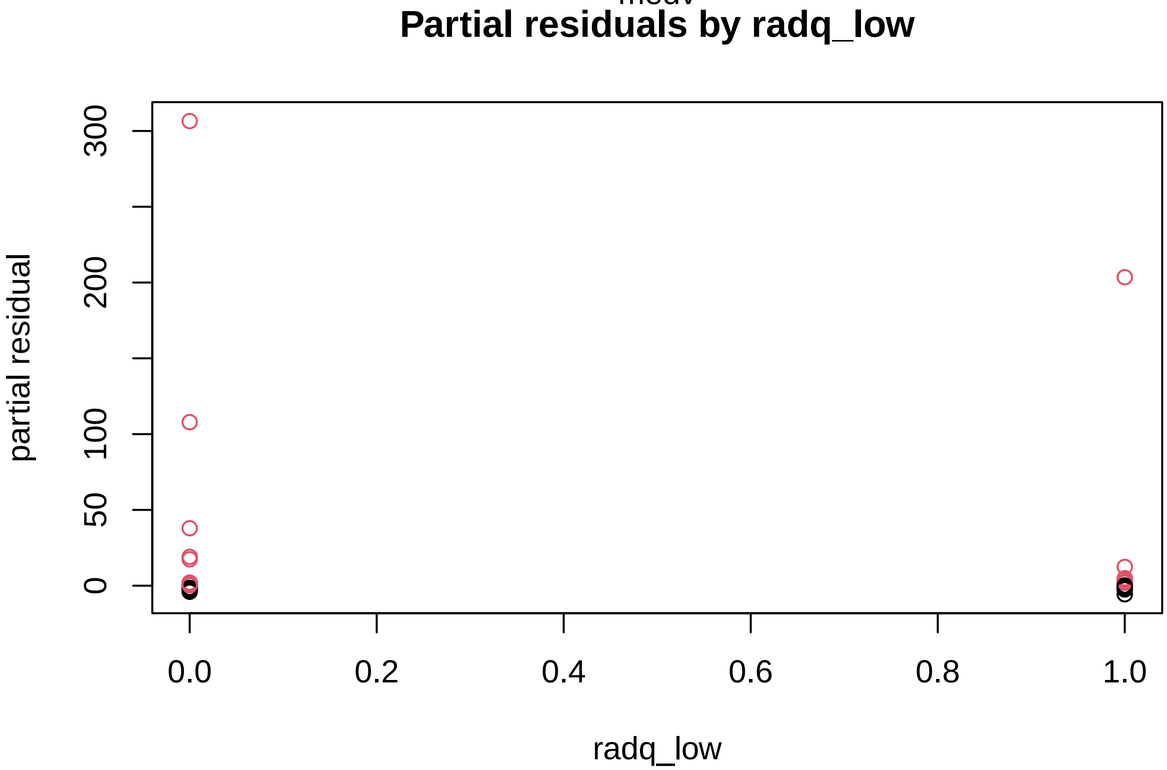


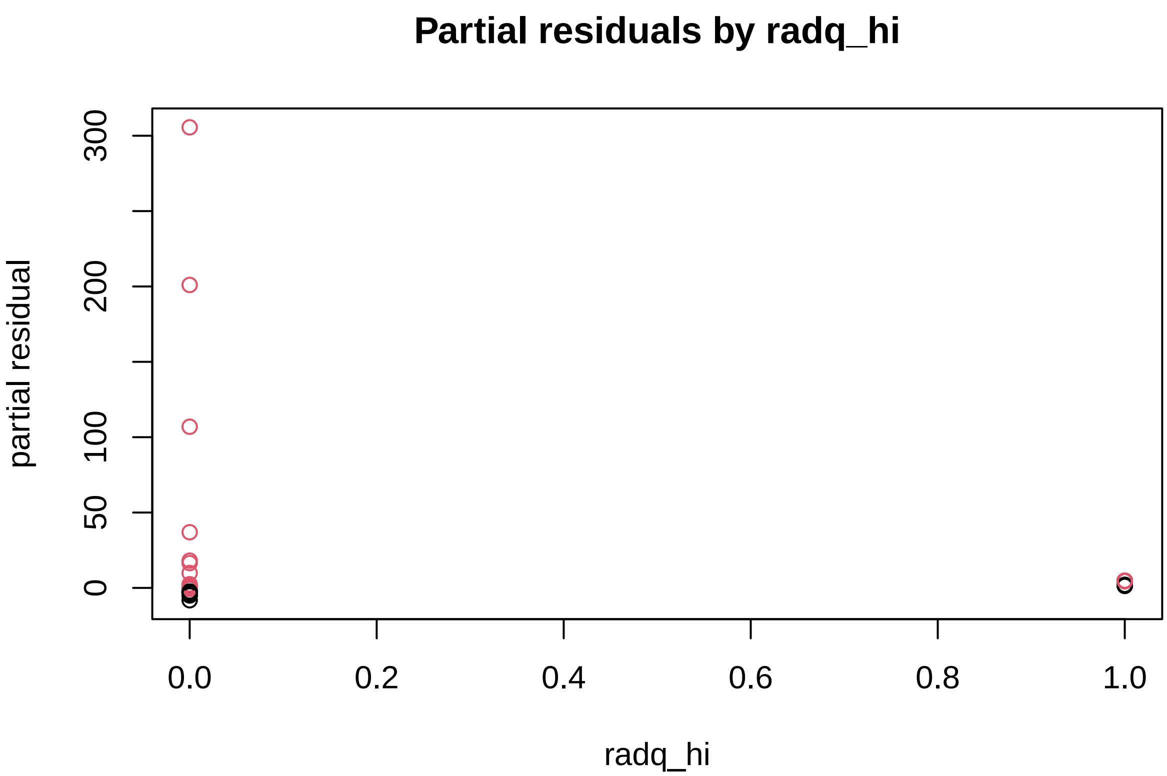
Partial residuals by ptratio
partial residual
0
50
100
200
300
14
16
18
20
22
ptratio



Partial residuals by lstat
partial residual
0
50
100
200
300
10
20
30
lstat


Partial residuals by medv
partial residual
0
50
100
200
300
10
20
30
40
50
medv

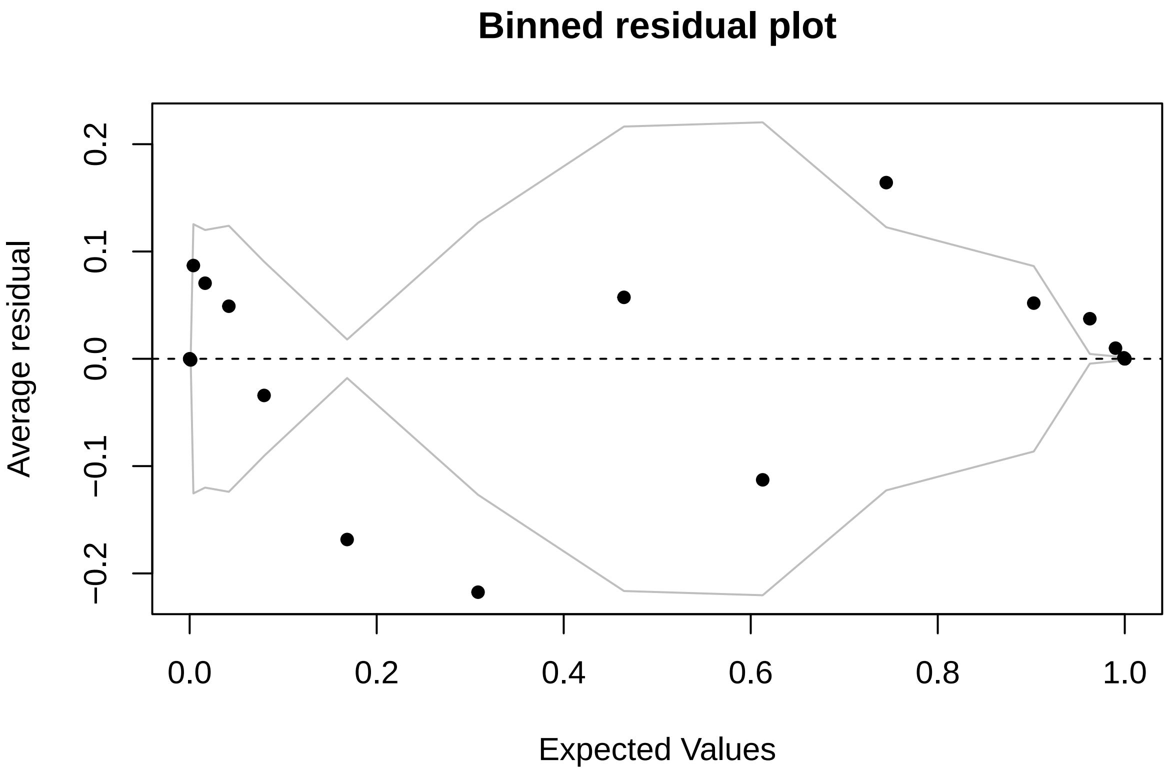

Partial residuals by radq_low
partial residual
0
50
100
200
300
0.0
0.2
0.4
0.6
0.8
1.0
radq_low



Binned Residuals Plot

Below is a Binned Residuals Plot. The binned residuals plot divide the data into categories (bins) based on their fitted values, then plot the average residual versus the average fitted value for each bin.

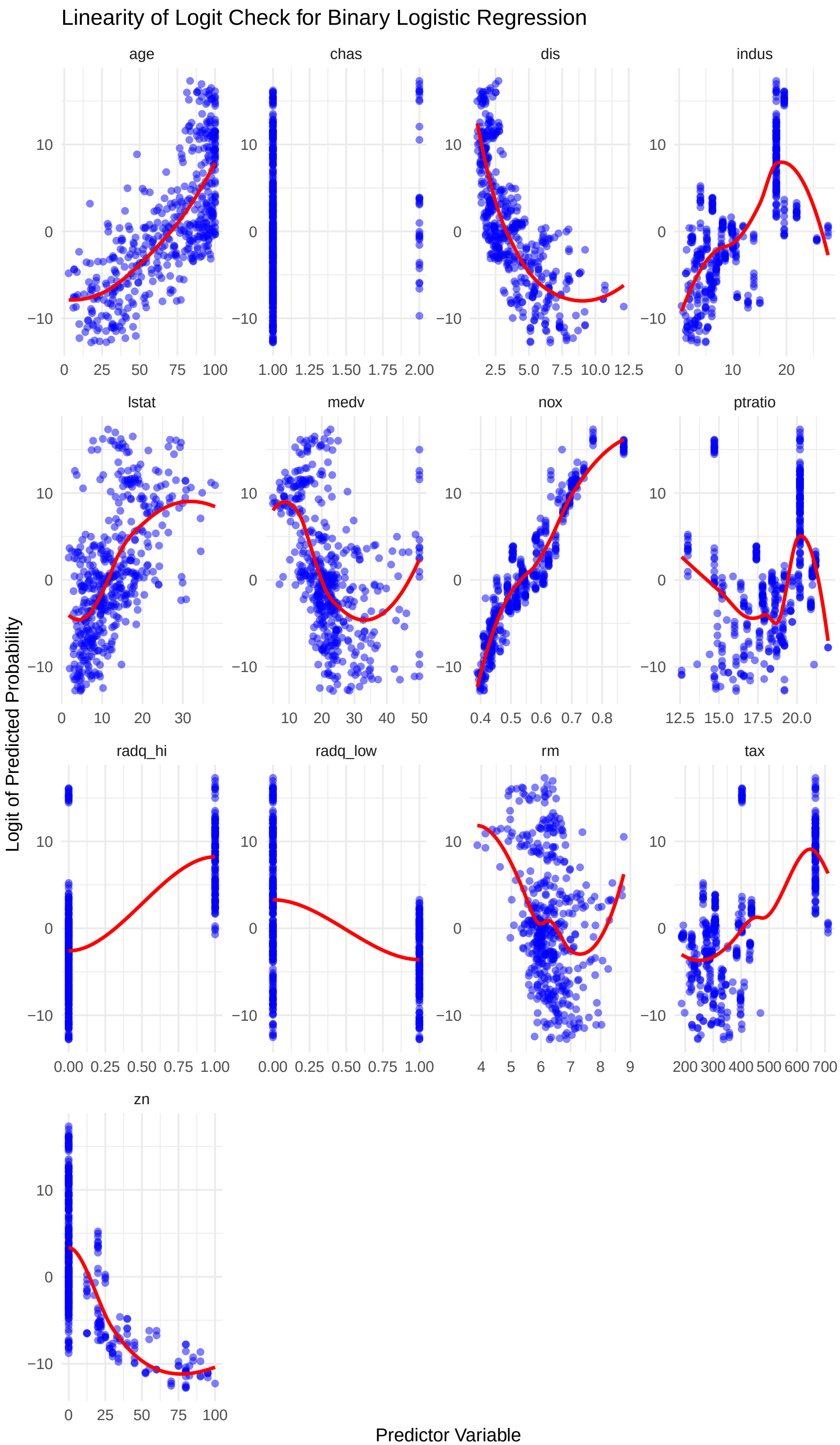
```
binnedplot(
  x = predict(model_full, newdata=df_training_one_hot, type="response"),
  y = residuals(model_full, type="response")
)
```



In a Binned Residuals Plot, the gray lines indicate plus and minus 2 standard-error bounds. We would expect about 95% of the binned residuals to fall within these lines. Several points fall outside of the 95% interval, but three points are more obviously outside.

Linearity

To check this condition, I created a scatterplot with a loess line to check that there is a linear relationship between the logit of the dependent variable and the independent variables.



Linearity of Logit Check for Binary Logistic Regression
age
chas
dis
indus
lstat
medv
nox
ptratio
radq_hi
radq_low
rm
tax
zn
Logit of Predicted Probability
Predictor Variable

Using mathematical transformations

To reduce the influence of outliers and better align the data with the assumptions of logistic regression, log-transformations were applied to tax, zn, dis, and lstat. This transformation helps normalize the data, reduce variance, and enhance model interpretability. A small constant was added to zn before the transformation to account for zero values.

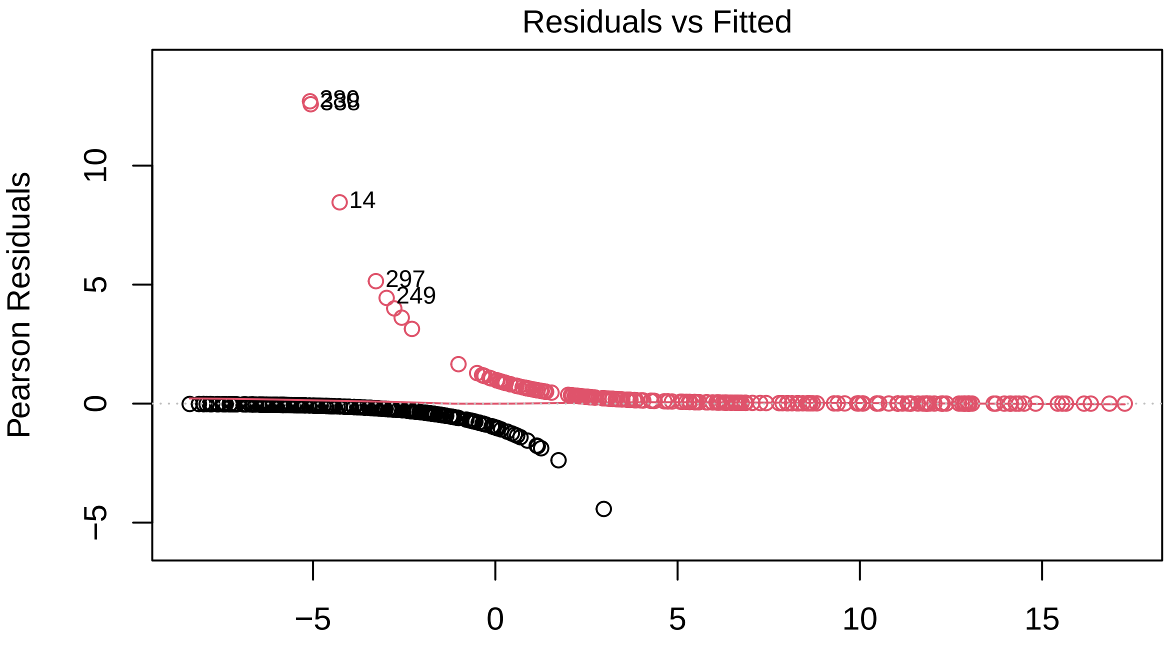
```r
df_training_1h_log <- df_training_one_hot |>
  mutate(
    log_tax = log(tax),
    log_dis = log(dis),
    log_zn = log(zn + 1),
    log_lstat = log(lstat),
    log_medv = log(medv),
    log_indus = log(indus),
    log_ptratio = log(ptratio),
  ) |>
  subset(select = -c(tax, dis, zn, lstat, medv, indus, ptratio))


model_full_log <- glm(target ~., binomial(link = "logit"), data=df_training_1h_log)
summary(model_full_log)
```

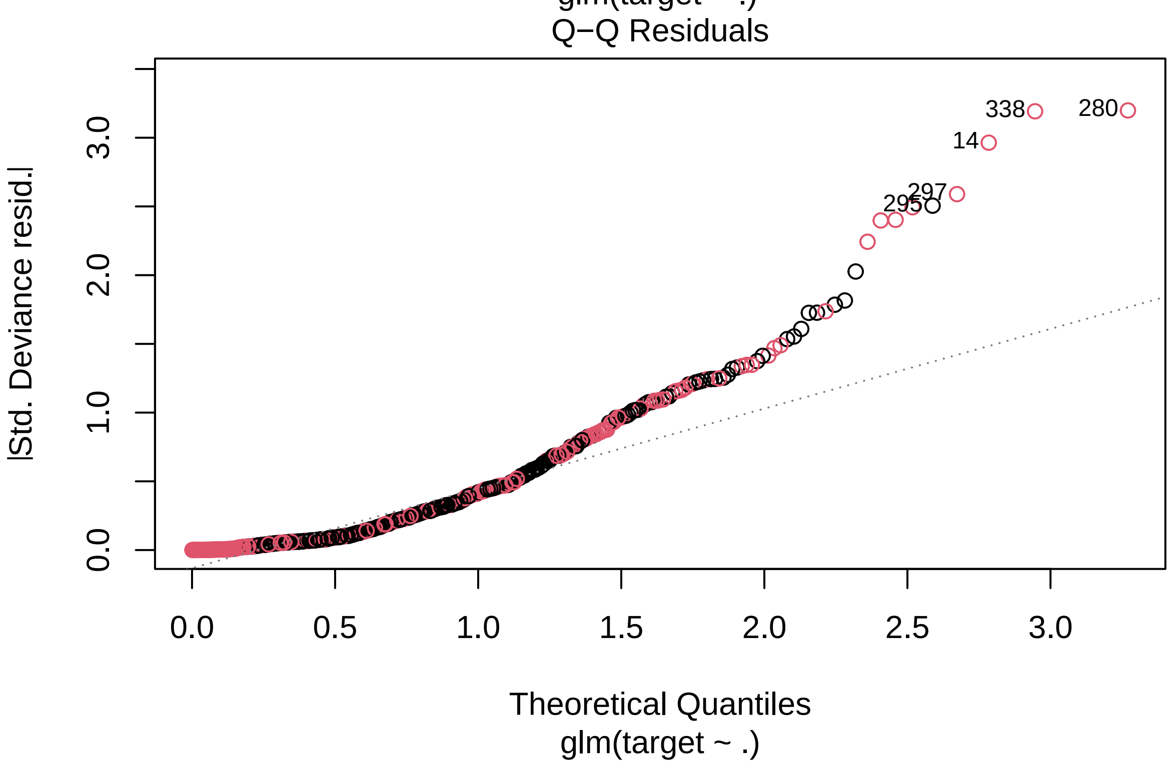
```
##
## Call:
## glm(formula = target ~ ., family = binomial(link = "logit"),
##     data = df_training_1h_log)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -61.55667   14.07134  -4.375 1.22e-05 ***
## chas1         0.76611    0.78810   0.972  0.33100
## nox          55.42383    8.35816   6.631 3.33e-11 ***
## rm           -0.44042    0.60357  -0.730  0.46557
## age           0.02181    0.01234   1.768  0.07708 .
## radq_low      1.54137    0.52446   2.939  0.00329 **
## radq_hi       4.56152    0.81652   5.587 2.32e-08 ***
## log_tax       1.42973    0.92183   1.551  0.12091
## log_dis       4.30622    0.96710   4.453 8.48e-06 ***
## log_zn       -0.46306    0.23731  -1.951  0.05102 .
## log_lstat     0.59773    0.64866   0.921  0.35680
## log_medv      4.37118    1.39379   3.136  0.00171 **
## log_indus    -0.45813    0.46068  -0.994  0.32000
## log_ptratio   1.43430    2.38065   0.602  0.54685
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 186.45  on 452  degrees of freedom
## AIC: 214.45
##
```

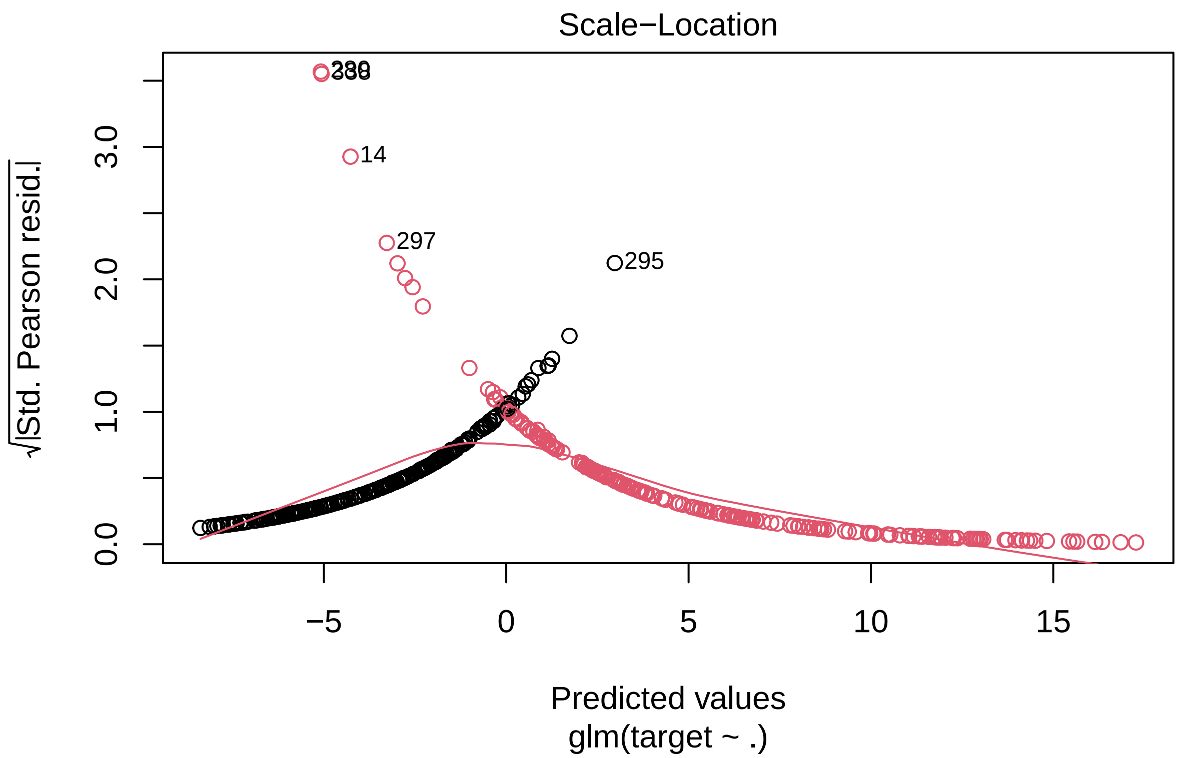
```
## Number of Fisher Scoring iterations: 8
```

Outlier Applying the log transformation didn't make too much of a difference with our questionable points (280, 338, and 14)

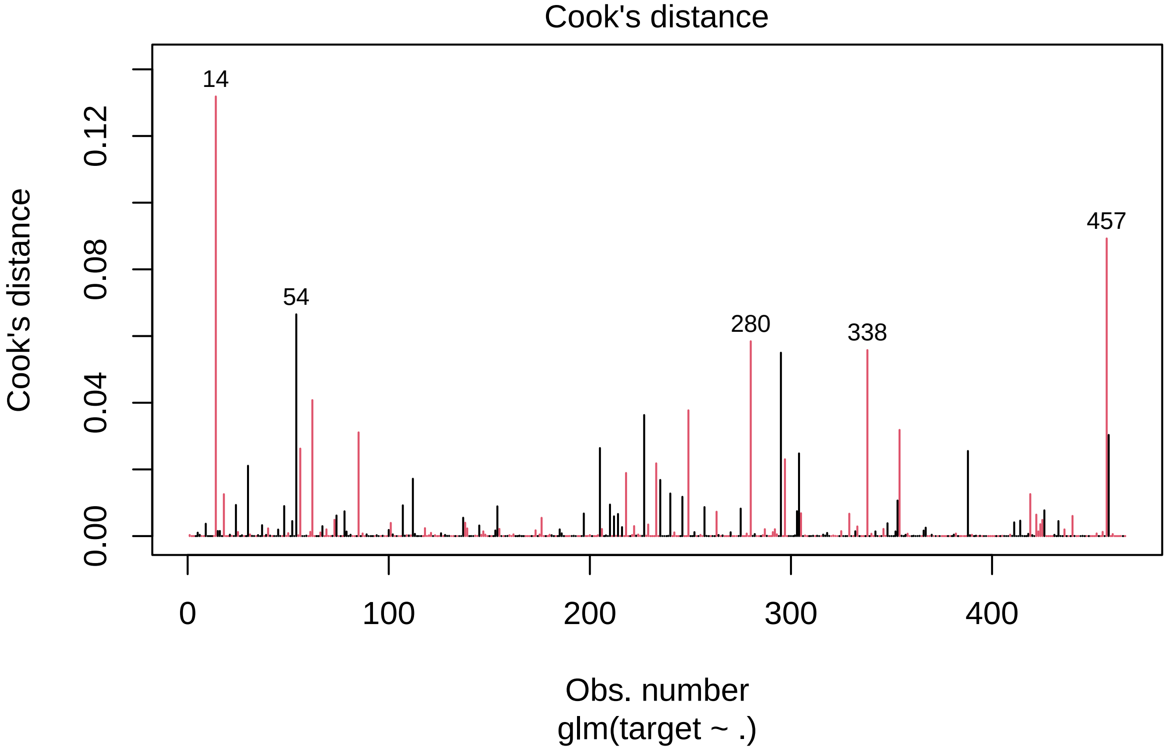
```r
par(mar = c(5, 4, 4, 2) + 0.1)
plot(model_full_log, which = c(4, 6, 1, 2, 3, 5), col=df_training_1h_log$target,  id.n = 5)
```



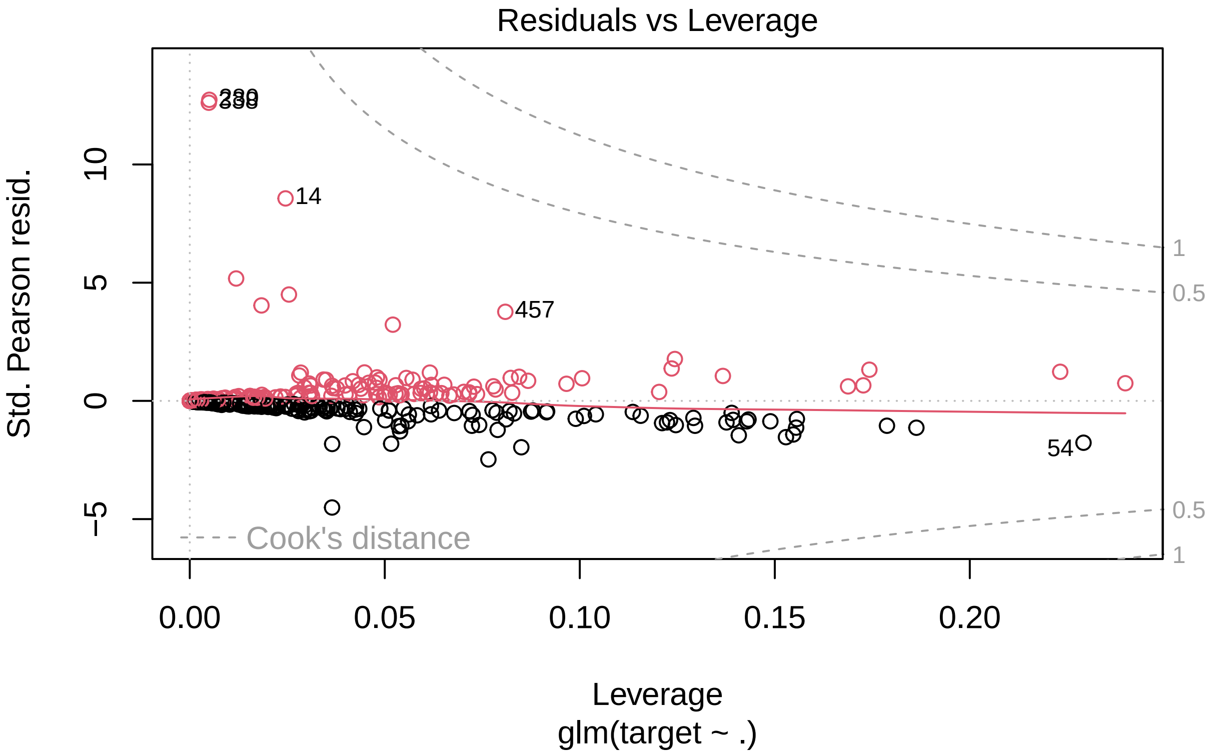


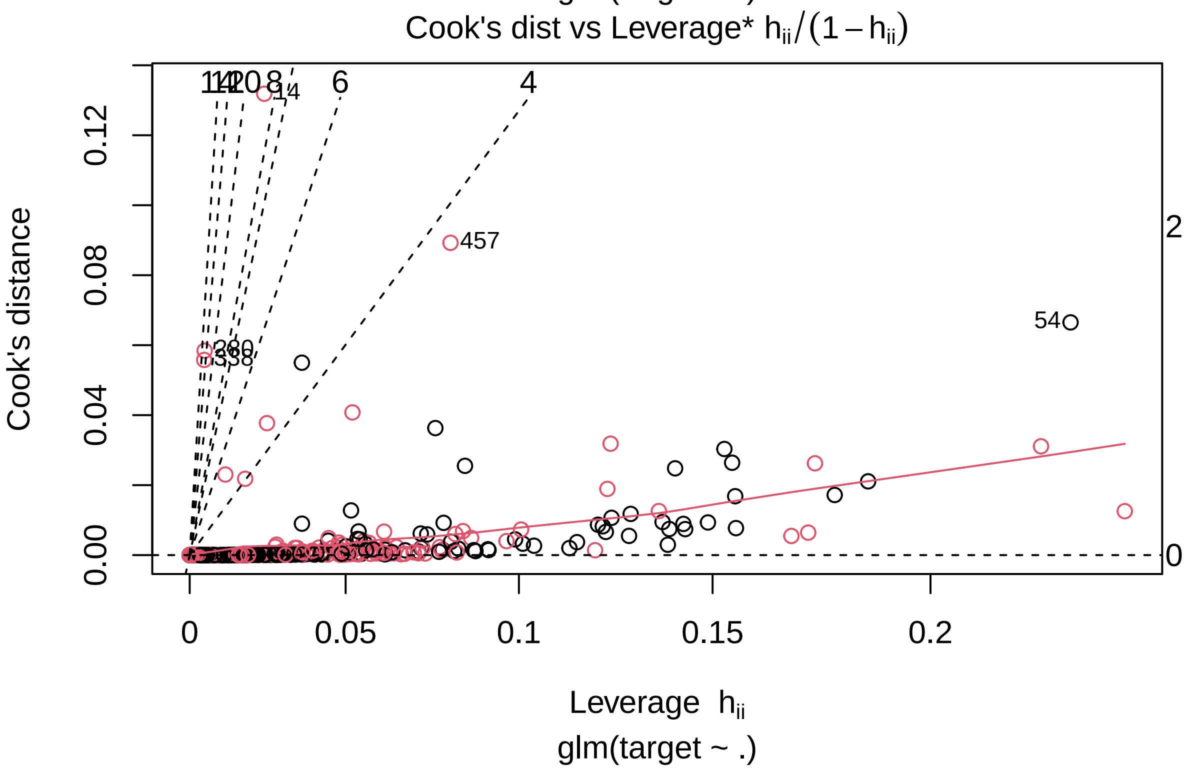


Scale−Location
√|Std. Pearson resid.|
0.0
1.0
2.0
3.0
−5
0
5
10
15
Predicted values
glm(target ~ .)
14
297
295

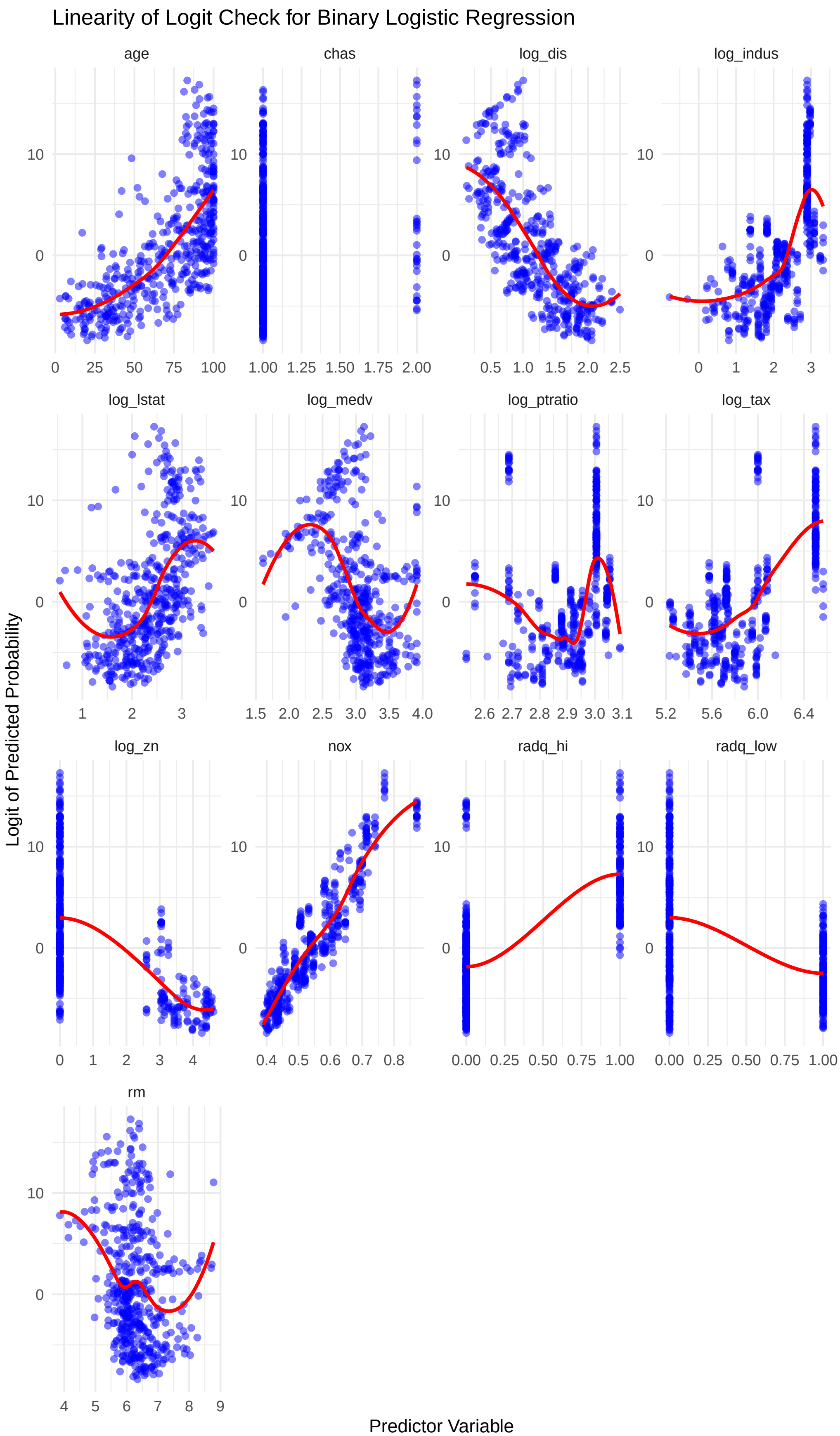


Cook's distance
Cook's distance
0.00
0.04
0.08
0.12
0
100
200
300
400
Obs. number
glm(target ~ .)
14
54
280
338
457





Linearity Applying the log transformation helped the linearity for some of the variables. It had less of an effect on medv, indus, and ptratio


Linearity of Logit Check for Binary Logistic Regression
age
chas
log_dis
log_indus
log_lstat
log_medv
log_ptratio
log_tax
log_zn
nox
radq_hi
radq_low
rm
Logit of Predicted Probability
Predictor Variable

Colinearity A Variance Inflation Factor test on our model with logged predictors shows that `nox` and `medv` should be considered for removal. `rm` and `log_dis` may also need to considered.

```
car::vif(model_full_log) |> sort()
```

```
##        chas     radq_hi    radq_low     log_tax      log_zn         age
##    1.231235    1.652783    1.964114    1.989751    2.016719    2.036268
##   log_indus log_ptratio   log_lstat          rm     log_dis         nox
##    2.704867    2.745159    3.199281    3.993171    4.738826    5.340565
##    log_medv
##    6.182031
```

MODEL BUILDING

Using a binomial (`target`) for our dependent variable would violate the common assumptions for linear regression. Specifically:

- the observations will not be normally distributed as they are binary
- the variance of error may be heteroskedastic instead of homoskedastic
- R-squared may not a good fit

To account for these violations, we wil use a Generalized Linear Model (GLM) to conduct logistic regression.

Backward Selection Model (BIC)

```
# Backward stepwise regression
backward_model <- stepAIC(model_full, direction = "backward", k=log(nrow(df_training_one_hot)))
```

```
## Start:  AIC=266.99
## target ~ zn + indus + chas + nox + rm + age + dis + tax + ptratio +
##     lstat + medv + radq_low + radq_hi
##
##            Df Deviance    AIC
## - tax       1   181.15 261.02
## - ptratio   1   181.76 261.64
## - lstat     1   182.04 261.92
## - rm        1   182.84 262.72
## - chas      1   183.04 262.92
## - age       1   183.46 263.33
## - zn        1   186.29 266.16
## <none>          180.97 266.99
## - medv      1   190.89 270.76
## - radq_low  1   190.93 270.81
## - dis       1   192.90 272.77
## - indus     1   194.95 274.82
## - radq_hi   1   233.24 313.11
## - nox       1   272.51 352.39
##
## Step:  AIC=261.02
## target ~ zn + indus + chas + nox + rm + age + dis + ptratio +
##     lstat + medv + radq_low + radq_hi
##
##            Df Deviance    AIC
## - ptratio   1   181.90 255.63
## - lstat     1   182.38 256.11
## - rm        1   182.89 256.62
```

```
## - chas      1   183.10 256.83
## - age       1   183.52 257.25
## - zn        1   186.43 260.16
## <none>          181.15 261.02
## - radq_low  1   190.96 264.69
## - medv      1   190.97 264.70
## - dis       1   192.90 266.63
## - indus     1   195.66 269.39
## - radq_hi   1   246.52 320.25
## - nox       1   273.18 346.91
##
## Step:  AIC=255.63
## target ~ zn + indus + chas + nox + rm + age + dis + lstat + medv +
##     radq_low + radq_hi
##
##            Df Deviance    AIC
## - rm        1   183.31 250.90
## - lstat     1   183.32 250.91
## - chas      1   183.57 251.16
## - age       1   183.76 251.34
## <none>          181.90 255.63
## - zn        1   188.59 256.18
## - medv      1   191.14 258.73
## - dis       1   193.32 260.90
## - indus     1   196.68 264.26
## - radq_low  1   197.70 265.29
## - radq_hi   1   258.34 325.92
## - nox       1   276.37 343.95
##
## Step:  AIC=250.9
## target ~ zn + indus + chas + nox + age + dis + lstat + medv +
##     radq_low + radq_hi
##
##            Df Deviance    AIC
## - age       1   184.18 245.62
## - chas      1   185.38 246.82
## - lstat     1   186.68 248.13
## <none>          183.31 250.90
## - zn        1   190.50 251.94
## - medv      1   193.27 254.71
## - dis       1   193.78 255.22
## - indus     1   197.50 258.94
## - radq_low  1   198.16 259.60
## - radq_hi   1   260.41 321.85
## - nox       1   276.66 338.10
##
## Step:  AIC=245.62
## target ~ zn + indus + chas + nox + dis + lstat + medv + radq_low +
##     radq_hi
##
##            Df Deviance    AIC
## - chas      1   186.52 241.82
## - lstat     1   188.79 244.09
## <none>          184.18 245.62
```

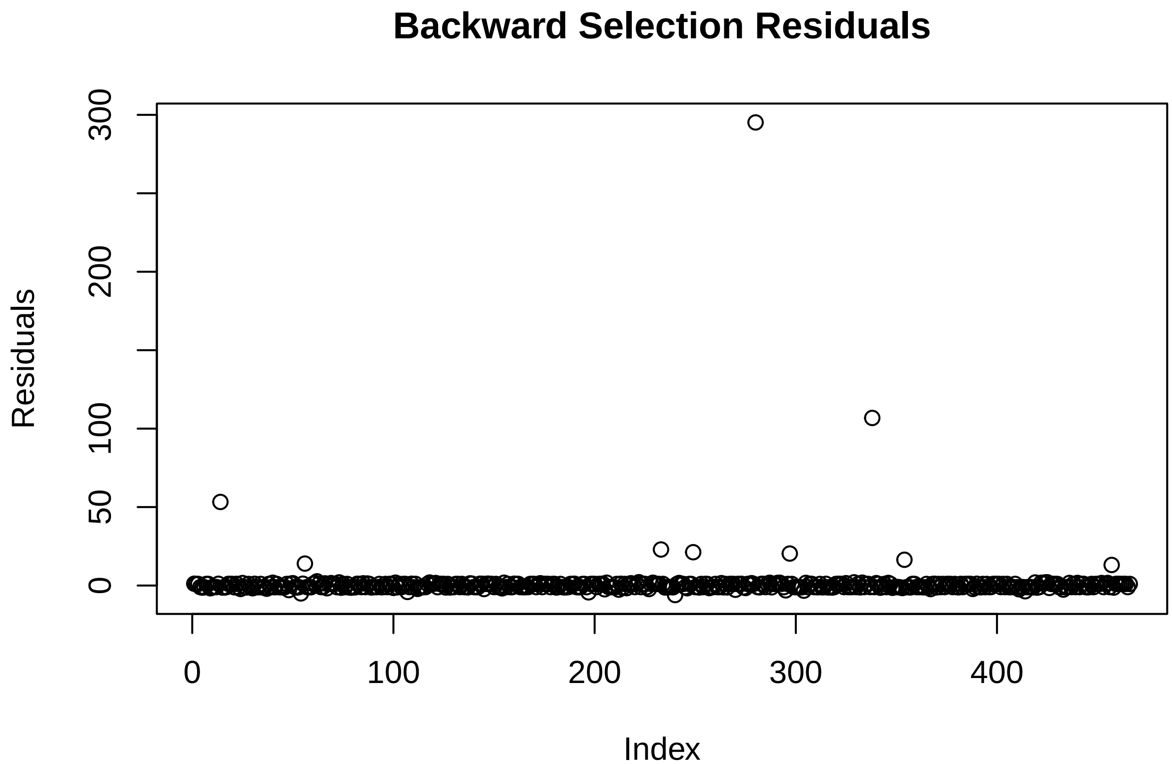
```
## - zn        1   191.45 246.75
## - dis       1   193.99 249.28
## - medv      1   194.41 249.70
## - indus     1   198.41 253.71
## - radq_low  1   200.10 255.40
## - radq_hi   1   262.55 317.84
## - nox       1   289.78 345.08
##
## Step:  AIC=241.82
## target ~ zn + indus + nox + dis + lstat + medv + radq_low + radq_hi
##
##            Df Deviance    AIC
## - lstat     1   191.97 241.13
## <none>          186.52 241.82
## - zn        1   194.01 243.17
## - dis       1   195.90 245.05
## - medv      1   198.71 247.87
## - indus     1   199.42 248.57
## - radq_low  1   200.88 250.03
## - radq_hi   1   265.34 314.50
## - nox       1   289.83 338.99
##
## Step:  AIC=241.13
## target ~ zn + indus + nox + dis + medv + radq_low + radq_hi
##
##            Df Deviance    AIC
## <none>          191.97 241.13
## - zn        1   198.69 241.70
## - medv      1   198.73 241.74
## - dis       1   199.72 242.73
## - indus     1   202.54 245.55
## - radq_low  1   206.64 249.65
## - radq_hi   1   270.27 313.28
## - nox       1   298.32 341.33
```

```
summary(backward_model)
```

```
##
## Call:
## glm(formula = target ~ zn + indus + nox + dis + medv + radq_low +
##     radq_hi, family = binomial(link = "logit"), data = df_training_one_hot)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -33.35748    5.01546  -6.651 2.91e-11 ***
## zn           -0.08021    0.03682  -2.178 0.029380 *
## indus        -0.13193    0.04263  -3.095 0.001968 **
## nox          55.14154    8.02184   6.874 6.25e-12 ***
## dis           0.60188    0.22176   2.714 0.006645 **
## medv          0.06570    0.02705   2.429 0.015141 *
## radq_low      1.58049    0.43618   3.623 0.000291 ***
## radq_hi       4.95421    0.77313   6.408 1.47e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

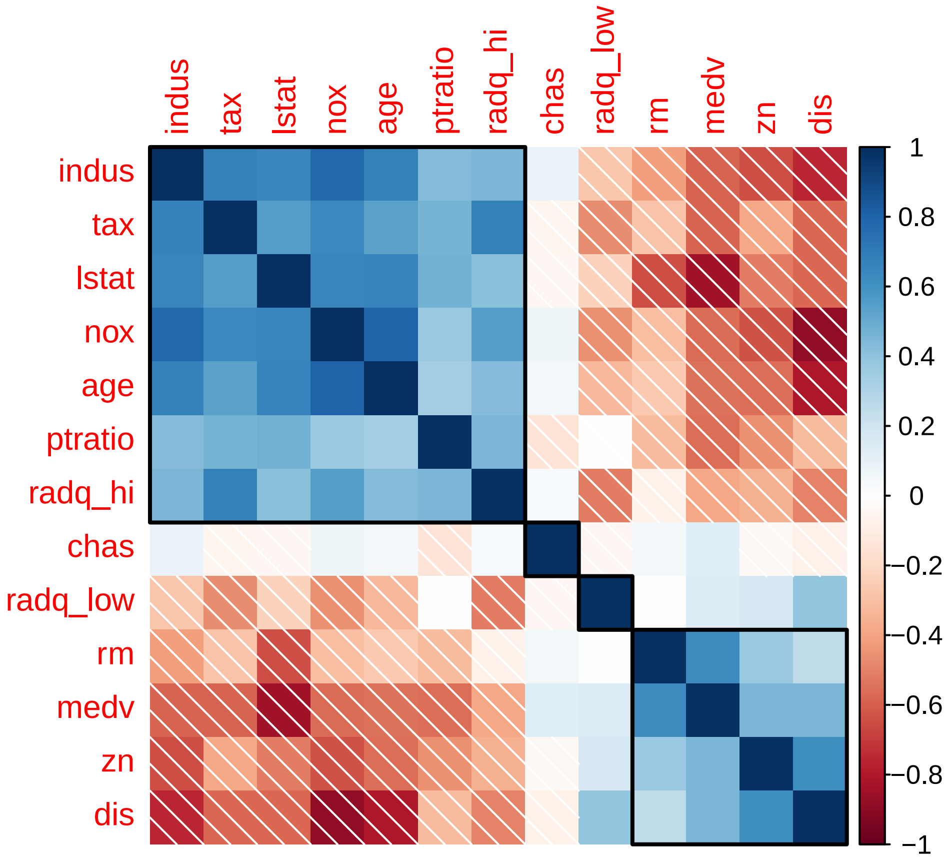
```
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 191.97  on 458  degrees of freedom
## AIC: 207.97
##
## Number of Fisher Scoring iterations: 8
```

```r
plot(backward_model$residuals, main = "Backward Selection Residuals", ylab = "Residuals")
```



Models Cased on Predictor Correlation

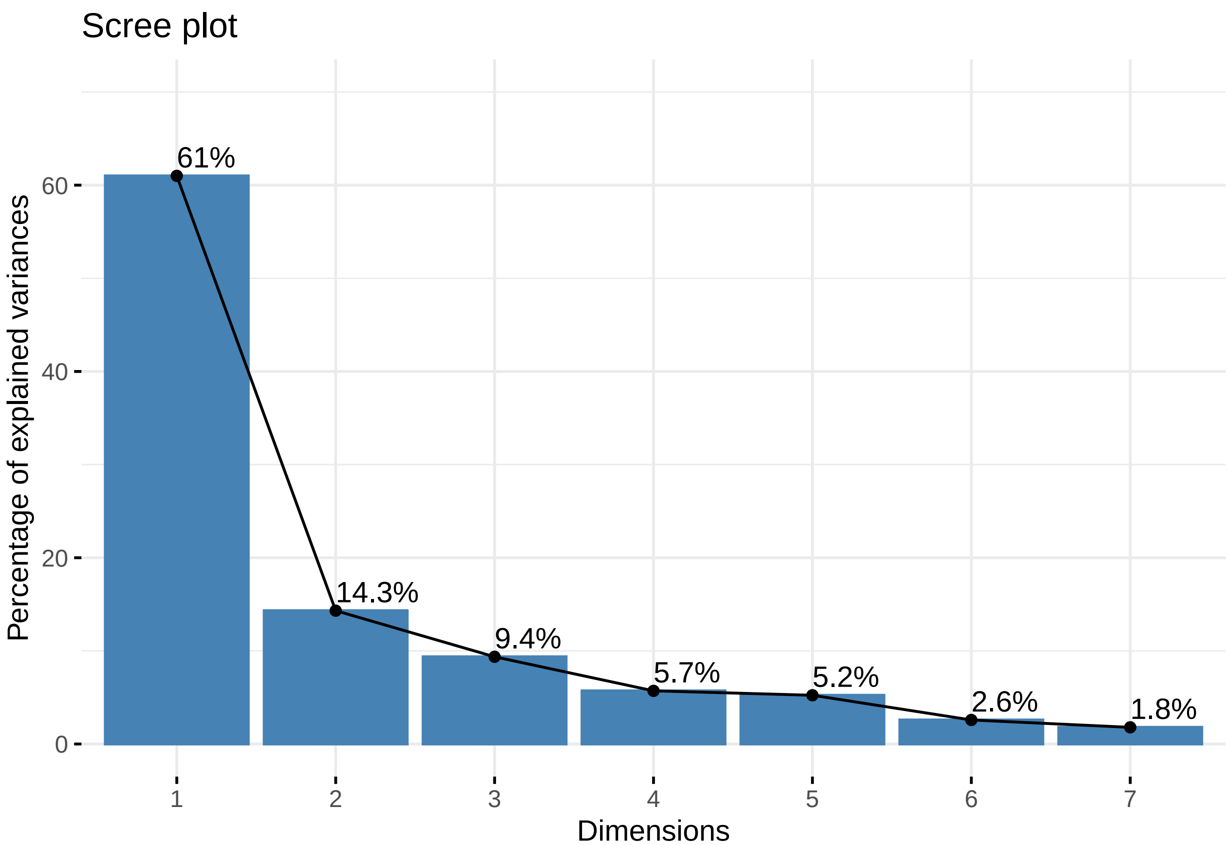
These models were guided by the results of our correlation plot. The correlation plot shows strong correlation among predictors in two large clusters suggesting that selecting one variable from each cluster might be sufficient within our model.



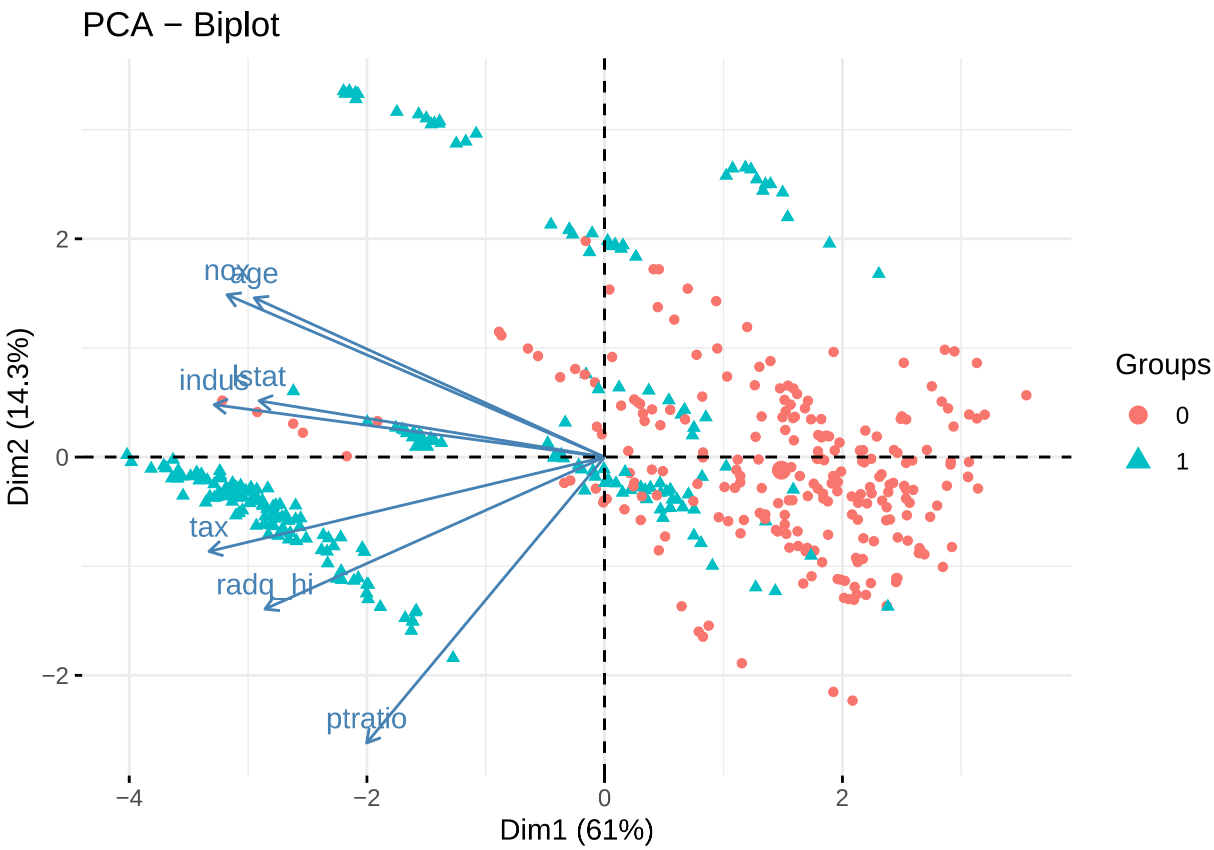

```
##
## Call:
## glm(formula = target ~ indus + chas + radq_low + medv, family = binomial(link = "logit"),
##     data = df_training_one_hot)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.185085   0.577111  -3.786 0.000153 ***
## indus        0.215890   0.023736   9.095  < 2e-16 ***
## chas1        0.508463   0.484696   1.049 0.294162
## radq_low    -1.274556   0.261075  -4.882 1.05e-06 ***
## medv         0.008922   0.016893   0.528 0.597415
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 426.57  on 461  degrees of freedom
## AIC: 436.57
##
## Number of Fisher Scoring iterations: 4
```

Model using Principal Components This section uses the correlation plot to perform Principal Component Analysis on the two large variable clusters shown in the plot. We will then substiture the variables in each of the two clusters with their respective PC scores in our model.

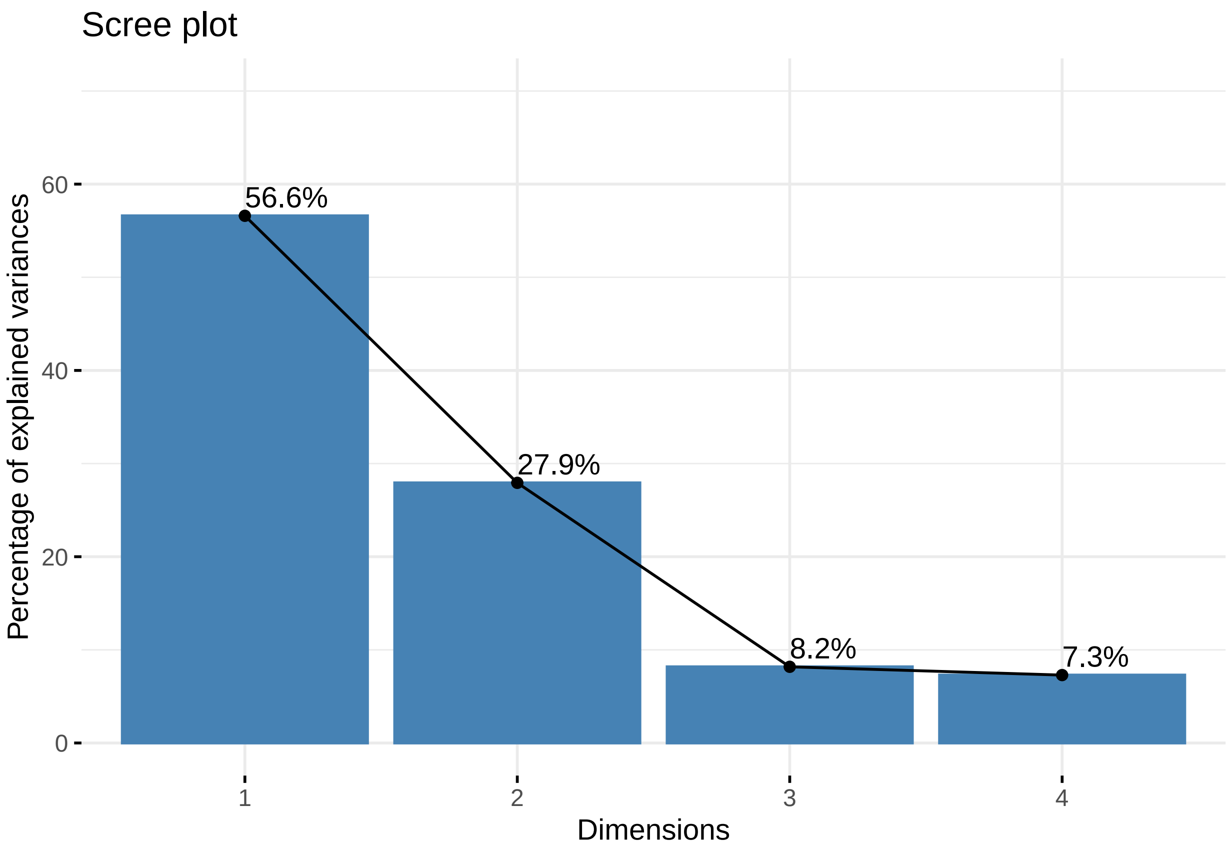
```r
# Create PCA from first cluster in our correlation plot
df_pca_subset1 <- df_training_one_hot |>
  subset(select = c(indus, tax, lstat, nox, age, ptratio, radq_hi))

# calculate PCA
df_training_pca1 <- prcomp(df_pca_subset1, scale=TRUE)

# use eigen vectors to plot % of data explained by PCA1
fviz_eig(df_training_pca1, addlabels=TRUE, ylim=c(0, 70))
```



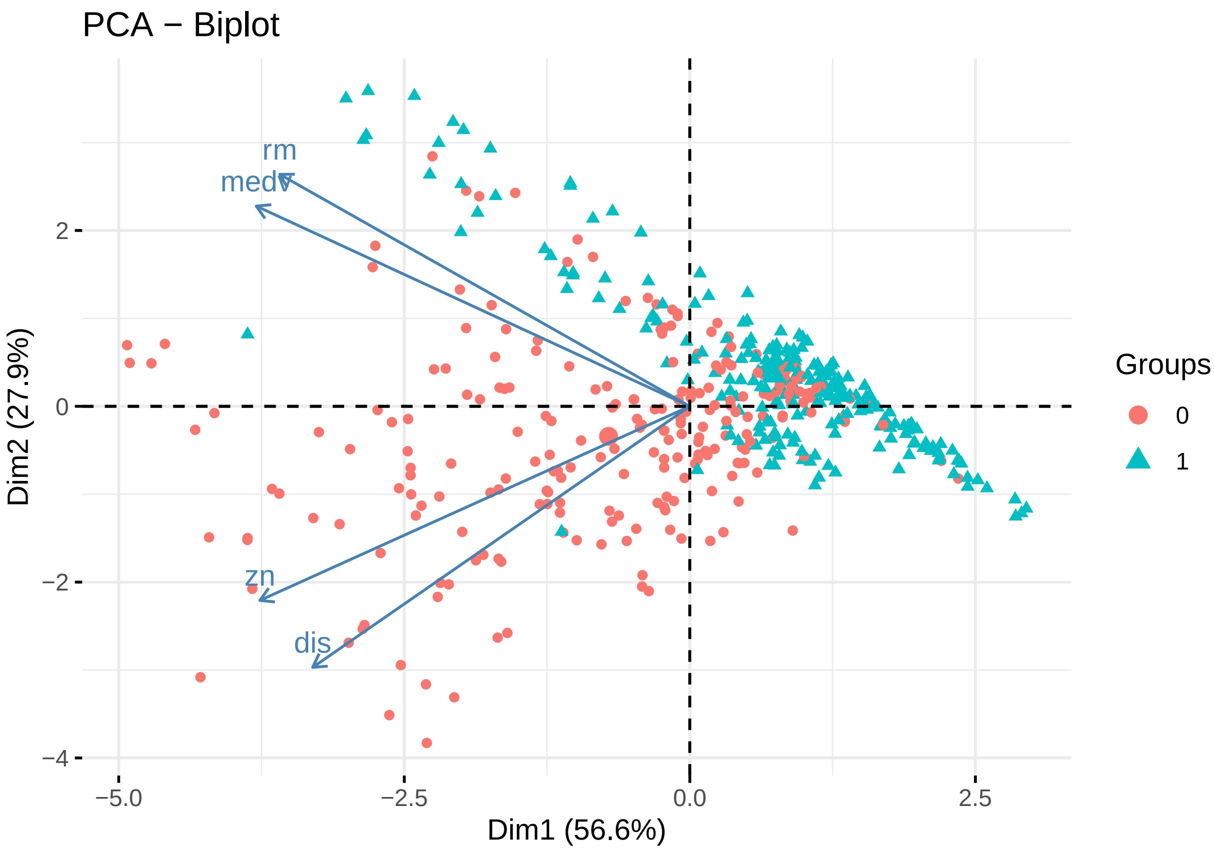

```r
# plot PCA biplot
fviz_pca_biplot(df_training_pca1, label="var", habillage =  df_training_one_hot$target)
```




```
# Create PCA from second cluster in our correlation plot
df_pca_subset2 <- df_training_one_hot |>
  subset(select = c(rm, medv, zn, dis))

# calculate PCA
df_training_pca2 <- prcomp(df_pca_subset2, scale=TRUE)

# use eigen vectors to plot % of data explained by PCA1
fviz_eig(df_training_pca2, addlabels=TRUE, ylim=c(0, 70))
```




```r
# plot PCA biplot
fviz_pca_biplot(df_training_pca2, label="var", habillage =  df_training_one_hot$target)
```




```r
# add pca's to our dataset
df_training_one_hot_pca <- df_training_one_hot |>
  subset(select = c(target, chas, radq_low)) |>
  mutate(
    group1_pc1 = df_training_pca1$x[,"PC1"],
    group1_pc2 = df_training_pca1$x[,"PC2"],
    group2_pc1 = df_training_pca2$x[,"PC1"],
    group2_pc2 = df_training_pca2$x[,"PC2"],
  )

#ggpairs(df_training_one_hot_pca |> subset(select = -c(target)))

model_pca <- glm(target ~., binomial(link = "logit"), data=df_training_one_hot_pca)
summary(model_pca)
```

```
##
## Call:
## glm(formula = target ~ ., family = binomial(link = "logit"),
##     data = df_training_one_hot_pca)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.14990    0.22856   0.656 0.511908
## chas1          0.35486    0.52302   0.678 0.497468
## radq_low      -0.04425    0.32215  -0.137 0.890753
## group1_pc1    -1.45138    0.18342  -7.913 2.52e-15 ***
## group1_pc2     0.17208    0.15573   1.105 0.269166
```

```
## group2_pc1  -0.30550    0.20533  -1.488 0.136790
## group2_pc2   0.67822    0.18654   3.636 0.000277 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 289.25  on 459  degrees of freedom
## AIC: 303.25
##
## Number of Fisher Scoring iterations: 6
```

Interestingly, only the primary principal component from group1 and the secondary principal component from group two have strong statistical significance. `radq_low` has a particularly high p-value and should be considered for removal.

```r
model_pca2 <- update(model_pca, . ~ . - radq_low)
summary(model_pca2)
```

```
##
## Call:
## glm(formula = target ~ chas + group1_pc1 + group1_pc2 + group2_pc1 +
##     group2_pc2, family = binomial(link = "logit"), data = df_training_one_hot_pca)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.1331     0.1933   0.689 0.491070
## chas1         0.3545     0.5219   0.679 0.497018
## group1_pc1   -1.4576     0.1779  -8.194 2.53e-16 ***
## group1_pc2    0.1751     0.1541   1.136 0.256022
## group2_pc1   -0.3094     0.2032  -1.523 0.127809
## group2_pc2    0.6808     0.1856   3.668 0.000244 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 289.27  on 460  degrees of freedom
## AIC: 301.27
##
## Number of Fisher Scoring iterations: 6
```

```r
model_pca2 <- update(model_pca2, . ~ . - chas)
summary(model_pca2)
```

```
##
## Call:
## glm(formula = target ~ group1_pc1 + group1_pc2 + group2_pc1 +
##     group2_pc2, family = binomial(link = "logit"), data = df_training_one_hot_pca)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.1640     0.1881   0.871 0.383506
## group1_pc1   -1.4598     0.1780  -8.201 2.38e-16 ***
```

```
## group1_pc2    0.1848     0.1532   1.206 0.227758
## group2_pc1   -0.3124     0.2027  -1.542 0.123190
## group2_pc2    0.6823     0.1845   3.697 0.000218 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 289.73  on 461  degrees of freedom
## AIC: 299.73
##
## Number of Fisher Scoring iterations: 6
```

```r
model_pca2 <- update(model_pca2, . ~ . - group1_pc2)
summary(model_pca2)
```

```
##
## Call:
## glm(formula = target ~ group1_pc1 + group2_pc1 + group2_pc2,
##     family = binomial(link = "logit"), data = df_training_one_hot_pca)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.1950     0.1905   1.024    0.306
## group1_pc1   -1.4594     0.1818  -8.027 9.99e-16 ***
## group2_pc1   -0.2843     0.2034  -1.398    0.162
## group2_pc2    0.7457     0.1783   4.181 2.90e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 291.22  on 462  degrees of freedom
## AIC: 299.22
##
## Number of Fisher Scoring iterations: 6
```

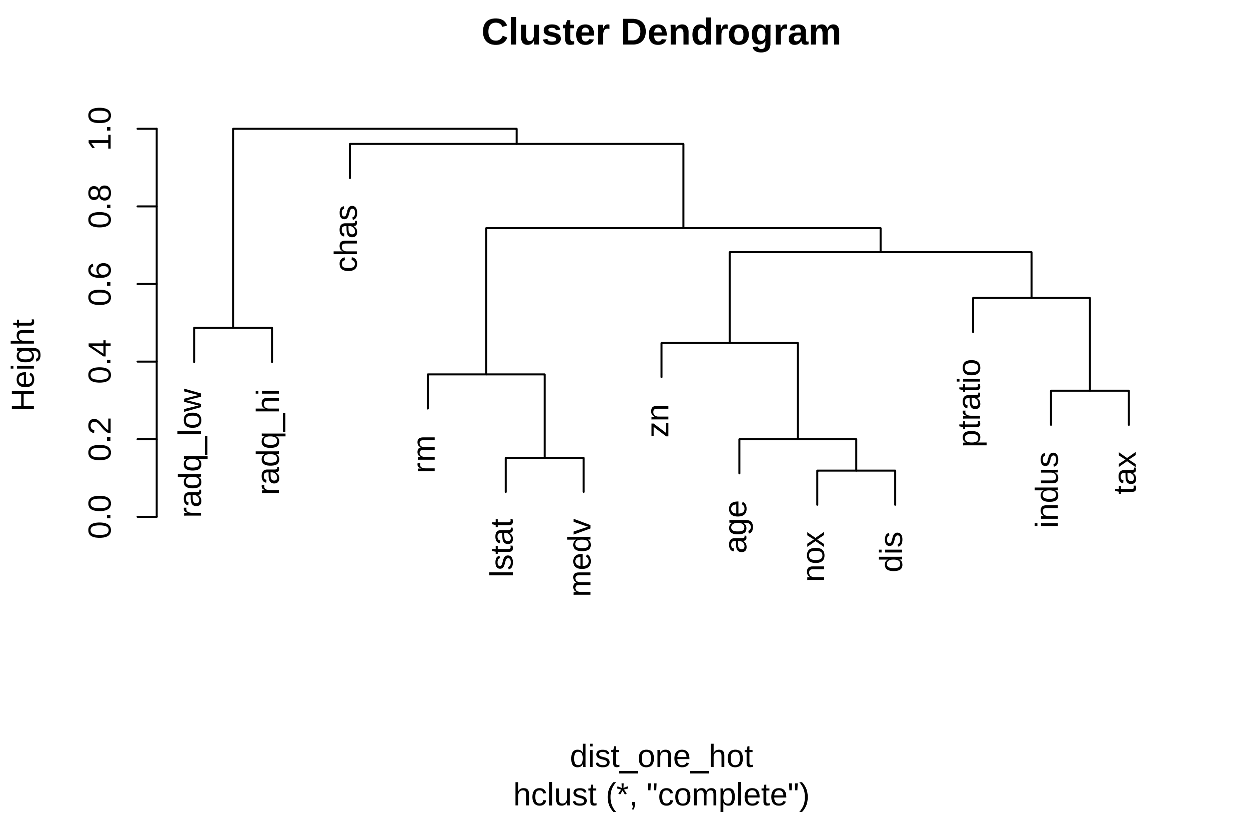
```r
model_pca2 <- update(model_pca2, . ~ . - group2_pc1)
summary(model_pca2)
```

```
##
## Call:
## glm(formula = target ~ group1_pc1 + group2_pc2, family = binomial(link = "logit"),
##     data = df_training_one_hot_pca)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.05301    0.16131   0.329    0.742
## group1_pc1  -1.28804    0.12063 -10.678  < 2e-16 ***
## group2_pc2   0.87594    0.16084   5.446 5.15e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 293.06  on 463  degrees of freedom
## AIC: 299.06
##
## Number of Fisher Scoring iterations: 6
```

Model based on Variable Clustering The dendogram is a variable clustering technique that shows how the parameters progressively come together at different levels of similarity. It offers another way to visualize correlations between our parameters. In this model, we will use the dedogram to prune parameters that are similar from the lower branches. In this model, we used the results from a T and Wilcox pairwise test to assist with the parameter selection.

```r
dist_one_hot = as.dist(m = 1 - abs(df_training_cor))
par(mar = c(5, 4, 4, 2) + 0.1)
plot(hclust(dist_one_hot))
```




```r
sapply(numeric_cols, function(param) {
  pairwise.t.test(
    x = df_training_one_hot[, param],
    g = df_training_one_hot$target,
    pool.sd = FALSE,
    paired = FALSE,
    alternative = "two.sided"
  )$p.value
}) |> sort()
```

```
##          nox          age          dis        indus          tax        lstat
```

```
## 1.486824e-70 3.953661e-52 1.762618e-48 7.522700e-48 2.028465e-45 4.663092e-26
##           zn         medv      ptratio           rm
## 1.545946e-21 3.868621e-09 4.851822e-08 1.036364e-03
```

```
sapply(numeric_cols, function(param) {
  pairwise.wilcox.test(
    x = df_training_one_hot[, param],
    g = df_training_one_hot$target,
    pool.sd = FALSE,
    paired = FALSE,
    alternative = "two.sided"
  )$p.value
}) |> sort()
```

```
##          nox          dis          age        indus          tax        lstat
## 1.505559e-59 7.713151e-46 4.570642e-44 1.169101e-40 8.311193e-38 4.704275e-25
##           zn         medv      ptratio           rm
## 1.999127e-24 4.781087e-18 1.305775e-14 1.331368e-04
```

```
model_dendo <- glm(target ~ radq_hi + chas + lstat + indus + age, binomial(link = "logit"), data=df_trai
summary(model_dendo)
```

```
##
## Call:
## glm(formula = target ~ radq_hi + chas + lstat + indus + age,
##     family = binomial(link = "logit"), data = df_training_one_hot)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -5.090764   0.560770  -9.078  < 2e-16 ***
## radq_hi      3.827787   0.576717   6.637 3.20e-11 ***
## chas1        0.266750   0.554497   0.481   0.6305
## lstat        0.003477   0.028225   0.123   0.9020
## indus        0.061046   0.025708   2.375   0.0176 *
## age          0.050076   0.008265   6.059 1.37e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 645.88  on 465  degrees of freedom
## Residual deviance: 297.52  on 460  degrees of freedom
## AIC: 309.52
##
## Number of Fisher Scoring iterations: 6
```

Model Using Quasi-Logit

Model comparison

```
library(pscl)
#models <- list(model_full, model_full_log, backward_model, model_corr, model_pca, model_dendo)

stats <- LRstats(model_full, model_full_log,
        backward_model, model_corr, model_pca, model_dendo)
```

```
stats$McFaddenR2 <- NA
stats$Accuracy <- NA
stats$Precision <- NA
stats$Recall <- NA
stats$Sensitivity <- NA
stats$Specificity <- NA
stats$F1_score <- NA
stats$AUC <- NA
stats$CV_est_prediction_error <- NA
stats$CV_adj_estimate <- NA

enhanceEvaluationMetrics <- function(df, model_name) {
  model <- get(model_name)

  if (model_name == "model_full_log") {
    model_data <- df_training_1h_log
  } else if (model_name == "model_pca") {
    model_data <- df_training_one_hot_pca
  } else {
    model_data <- df_training_one_hot
  }

  df[model_name, "McFaddenR2"] <- pR2(model)["McFadden"]

  pred_probs <- predict(model, type = "response")

  pred_probs_factor <- as.factor(ifelse(pred_probs > 0.5, 1, 0))
  conf_matrix <- confusionMatrix(pred_probs_factor, model_data$target)
  df[model_name, "Accuracy"] <- conf_matrix$overall['Accuracy']
  df[model_name, "Precision"] <- conf_matrix$byClass['Precision']
  df[model_name, "Recall"] <- conf_matrix$byClass['Recall']
  df[model_name, "F1_score"] <- conf_matrix$byClass['F1']
  df[model_name, "Sensitivity"] <- conf_matrix$byClass["Sensitivity"]
  df[model_name, "Specificity"] <- conf_matrix$byClass["Specificity"]

  #roc_model <- roc(as.factor(model_data$target), pred_probs)
  #plot(roc_model, main = "ROC Curve using pROC", col = "red", lwd = 2)
  # roc_auc not working, so use MLmetrics
  df[model_name, "AUC"] <- MLmetrics::AUC(y_true = model_data$target, y_pred = pred_probs)

  # Cross-Validation using 10 folsds
  cv_result <- boot::cv.glm(model_data, model, K= 10)
  df[model_name, "CV_est_prediction_error"] <- cv_result$delta[1]
  df[model_name, "CV_adj_estimate"] <- cv_result$delta[2]

  return(df)
}


# Loop through the list of models and update the dataframe for each
for (model_name in rownames(stats)) {

  stats <- enhanceEvaluationMetrics(stats, model_name)
```

```
}
```

```
## fitting null model for pseudo-r2
## fitting null model for pseudo-r2
## fitting null model for pseudo-r2
## fitting null model for pseudo-r2
## fitting null model for pseudo-r2
## fitting null model for pseudo-r2
```

```
stats
```

```
## Likelihood summary table:
##                   AIC    BIC LR Chisq  Df Pr(>Chisq) McFaddenR2 Accuracy
## model_full     208.97 266.99   180.97 452    1.00000    0.71981  0.92275
## model_full_log 214.45 272.47   186.45 452    1.00000    0.71132  0.92918
## backward_model 207.97 241.13   191.97 458    1.00000    0.70277  0.92704
## model_corr     436.57 457.29   426.57 461    0.87313    0.33955  0.78326
## model_pca      303.25 332.26   289.25 459    1.00000    0.55216  0.85193
## model_dendo    309.52 334.39   297.52 460    1.00000    0.53935  0.85837
##                Precision  Recall Sensitivity Specificity F1_score     AUC
## model_full       0.92405 0.92405     0.92405     0.92140  0.92405 0.97771
## model_full_log   0.93220 0.92827     0.92827     0.93013  0.93023 0.97483
## backward_model   0.93939 0.91561     0.91561     0.93886  0.92735 0.97291
## model_corr       0.75564 0.84810     0.84810     0.71616  0.79920 0.84462
## model_pca        0.83871 0.87764     0.87764     0.82533  0.85773 0.94054
## model_dendo      0.84615 0.88186     0.88186     0.83406  0.86364 0.93288
##                CV_est_prediction_error CV_adj_estimate
## model_full                    0.064875        0.064216
## model_full_log                0.066332        0.065778
## backward_model                0.063653        0.063330
## model_corr                    0.152090        0.151907
## model_pca                     0.099415        0.099234
## model_dendo                   0.103802        0.103593
```

For logistic regression, the "prediction error" is the mean squared error (difference between the predicted probabilities and the actual outcomes).

Checking the Model's Conditions We will examine the following key conditions for fitting a logistic model:

1. dependent variable is binary
2. large enough sample
3. observations are independent, not matched
4. independent (predictor) variables do not correlate too strongly with each other
5. linearity of independent variables and log odds
6. no outliers in data

Confidence Interval

```
##                    2.5 %       97.5 %
## (Intercept) -51.220070886 -25.123420900
## zn           -0.167059221  -0.009805196
## indus        -0.277621666  -0.079569873
## chas1        -0.437329365   2.774890137
```

```
## nox          43.146882327  78.772474084
## rm           -2.343126185   0.413916124
## age          -0.004788160   0.047225213
## dis           0.345497559   1.314977464
## tax          -0.003432766   0.005692181
## ptratio      -0.145335266   0.382263413
## lstat        -0.049284710   0.156305233
## medv          0.064587356   0.297709207
## radq_low      0.575629081   2.654531102
## radq_hi       3.463840203   7.223064642
```

```r
exp(coef(model_full))
```

Odds Ratio

```
##  (Intercept)           zn        indus        chas1          nox           rm
## 5.965983e-17 9.228761e-01 8.416752e-01 3.251869e+00 6.638993e+25 3.842654e-01
##          age          dis          tax      ptratio        lstat         medv
## 1.020511e+00 2.254949e+00 1.000962e+00 1.126409e+00 1.055980e+00 1.192431e+00
##     radq_low      radq_hi
## 4.772780e+00 1.670461e+02
```

```r
model_summary <- summary(model_full)
#param_pvalue <- model_summary$coefficients["target", "Pr(>|z|)"]
anova(model_full, test = "Chisq")
```

ANOVA Test

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: target
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                       465     645.88
## zn        1  127.411       464     518.46 < 2.2e-16 ***
## indus     1   86.433       463     432.03 < 2.2e-16 ***
## chas      1    1.274       462     430.76 0.2589811
## nox       1  150.804       461     279.95 < 2.2e-16 ***
## rm        1    6.755       460     273.20 0.0093493 **
## age       1    0.217       459     272.98 0.6415150
## dis       1    7.981       458     265.00 0.0047265 **
## tax       1   14.205       457     250.80 0.0001639 ***
## ptratio   1    3.659       456     247.14 0.0557589 .
## lstat     1    0.640       455     246.50 0.4236364
## medv      1   12.753       454     233.74 0.0003555 ***
## radq_low  1    0.504       453     233.24 0.4775972
## radq_hi   1   52.270       452     180.97 4.838e-13 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```