DATA 621 - HW3

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Homework 3 - Logistic Regression

Analysis of Factors that Influence Crime Rates:

In this homework assignment, we explore, analyze, and model a dataset containing information on crime for various neighborhoods of a major city. Each record has a response variable indicating whether or not the crime rate is above the median crime rate (1) or not (0).

Our objective is to build a binary logistic regression model on the training dataset to predict whether the neighborhood will be at risk for high crime levels.

Below is a short description of the variables of interest in the dataset:

Column	Description
zn	proportion of residential land zoned for large lots (over 25000 square feet) (*predictor variable*)
indus	proportion of non-retail business acres per suburb (*predictor variable*)
chas	a dummy var. for whether the suburb borders the Charles River (1) or not (0) (*predictor variable*)
nox	nitrogen oxides concentration (parts per 10 million) (*predictor variable*)
rm	average number of rooms per dwelling (*predictor variable*)
age	proportion of owner-occupied units built prior to 1940 (*predictor variable*)
dis	weighted mean of distances to five Boston employment centers (*predictor variable*)
rad	index of accessibility to radial highways (*predictor variable*)
tax	full-value property-tax rate per $10,000 (*predictor variable*)
ptratio	pupil-teacher ratio by town (*predictor variable*)
lstat	lower status of the population (percent) (*predictor variable*)
medv	median value of owner-occupied homes in $1000s (*predictor variable*)
target	**whether the crime rate is above the median crime rate (1) or not (0) (*response variable*)**

Data Exploration:

```
## [1] 466  13
```

The dataset consists of 466 observations of 13 variables. There are 12 predictor variables and one response variable (`target`).

```
## 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    <int> 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, 1.6582~
## $ rad     <int> 5, 5, 24, 6, 3, 5, 24, 24, 5, 1, 7, 5, 24, 7, 3, 3, 5, 5, 24, ~
## $ tax     <int> 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  <int> 1, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0,~
```

All of the columns in the dataset are numeric, but the predictor variable `chas` is a dummy variable, as is the response variable `target`. We re-code them as factors.

Let's take a look at the summary statistics for the variables in the dataset.

```
##       zn            indus            chas         nox               rm
##  Min.   :  0.00   Min.   : 0.460   0:433   Min.   :0.3890   Min.   :3.863
##  1st Qu.:  0.00   1st Qu.: 5.145   1: 33   1st Qu.:0.4480   1st Qu.:5.887
##  Median :  0.00   Median : 9.690           Median :0.5380   Median :6.210
##  Mean   : 11.58   Mean   :11.105           Mean   :0.5543   Mean   :6.291
##  3rd Qu.: 16.25   3rd Qu.:18.100           3rd Qu.:0.6240   3rd Qu.:6.630
##  Max.   :100.00   Max.   :27.740           Max.   :0.8710   Max.   :8.780
##       age             dis              rad             tax
##  Min.   :  2.90   Min.   : 1.130   Min.   : 1.00   Min.   :187.0
##  1st Qu.: 43.88   1st Qu.: 2.101   1st Qu.: 4.00   1st Qu.:281.0
##  Median : 77.15   Median : 3.191   Median : 5.00   Median :334.5
##  Mean   : 68.37   Mean   : 3.796   Mean   : 9.53   Mean   :409.5
##  3rd Qu.: 94.10   3rd Qu.: 5.215   3rd Qu.:24.00   3rd Qu.:666.0
##  Max.   :100.00   Max.   :12.127   Max.   :24.00   Max.   :711.0
##     ptratio         lstat            medv          target
##  Min.   :12.6   Min.   : 1.730   Min.   : 5.00   0:237
##  1st Qu.:16.9   1st Qu.: 7.043   1st Qu.:17.02   1:229
##  Median :18.9   Median :11.350   Median :21.20
##  Mean   :18.4   Mean   :12.631   Mean   :22.59
##  3rd Qu.:20.2   3rd Qu.:16.930   3rd Qu.:25.00
##  Max.   :22.0   Max.   :37.970   Max.   :50.00
```

```
##          zn        indus          nox           rm          age          dis
##  23.3646511    6.8458549    0.1166667    0.7048513   28.3213784    2.1069496
##         rad          tax      ptratio        lstat         medv
##   8.6859272  167.9000887    2.1968447    7.1018907    9.2396814
```

We can see the mean, median, standard deviations, etc. for each of the variables in the dataset.

For the `target` variable, there are 229 instances where crime level is above the median level (`target = 1`) and 237 instances where crime is not above the median level (`target = 0`). Since the response variable is fairly balanced between its two levels, the data will not require any resampling to weight the distributions for each level.

The minimum, first quantile, and median values for `zn` are all 0. This variable refers to the proportion of residential land zoned for large lots. Most of the neighborhoods in this dataset do not have land that is zoned for large lots.

For the `age` variable, the median is higher than the mean. This indicates the data is left-skewed, meaning there is a greater proportion of homes that were built prior to 1940 in the dataset.

There do not appear to be any missing values to address. Let's validate this.

```
## [1] 0
```

There are in fact no missing values in the dataset.

To check whether the predictor variables are correlated with the target variable, we produce a correlation funnel that visualizes the strength of the relationships between our predictors and our response.
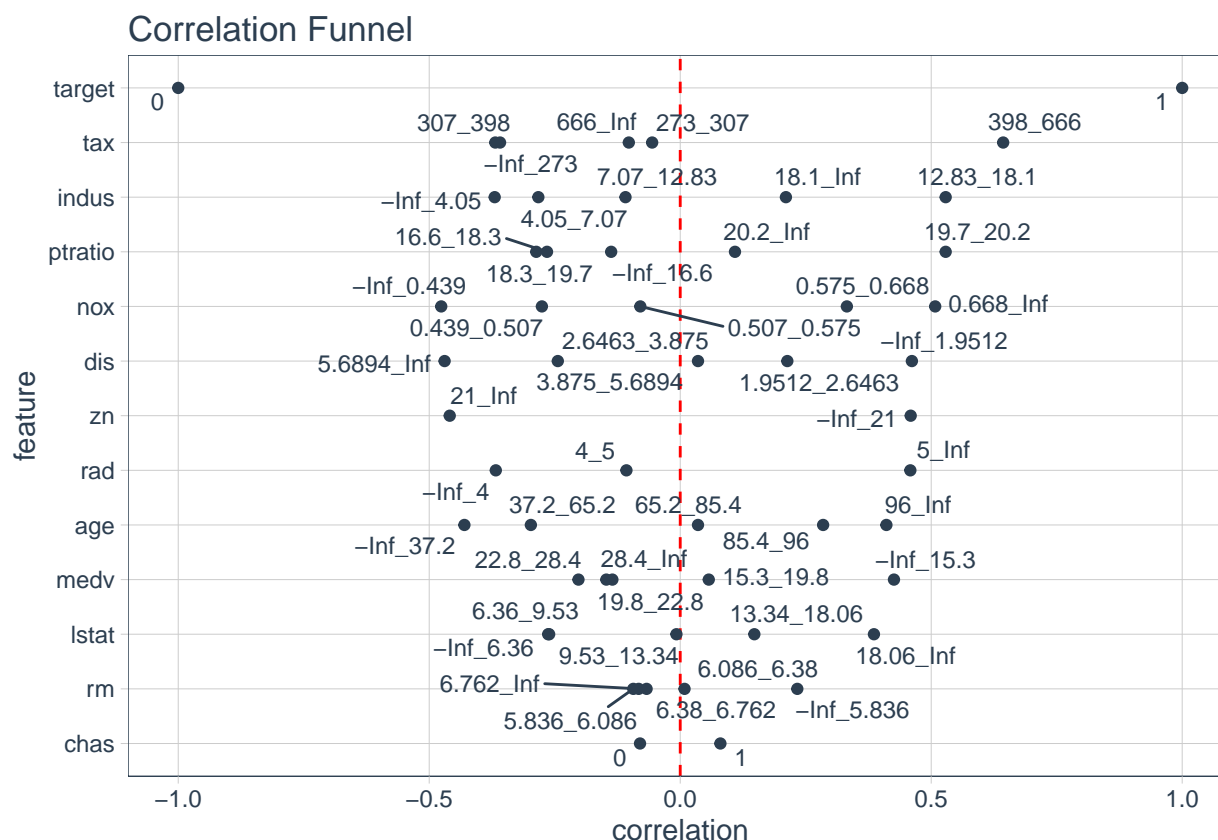
The correlation funnel plots the most important features towards the top. In our dataset, the four most important features correlated with the response variable are `tax`, `indus`, `ptratio`, and `nox`.

Looking at the features towards the bottom, the four least important features correlated with the response variable are `medv`, `lstat`, `rm`, and `chas`, with `chas` being the least correlated to `target`. These correlations are measured by the Pearson Correlation coefficient by default.

Since both `chas` and `target` are binary categorical variables, the correct coefficient to use to understand the strength of their relationship is actually the ϕ coefficient. If either of these categorical variables had more than two categories, we would need to calculate ϕ using the formula for Cramer's V (also called Cramer's ϕ) coefficient. However, in the special case that both categorical variables are binary, the value of Cramer's V coefficient will actually be equal to the value of the Pearson Correlation coefficient. So either formula actually results in the same value for ϕ. We prove this below.

[1] TRUE

The value for ϕ is 0.08004 regardless of the formula used to calculate it, and this very low value proves the very small amount of correlation between `chas` and `target` estimated by the correlation funnel is accurate.

Now we check for multicollinearity between predictor variables.
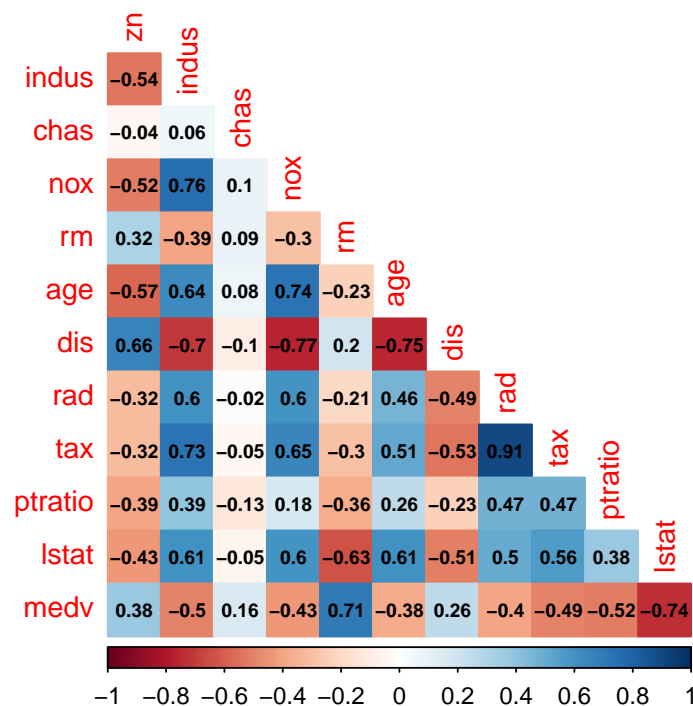
It is clear that the predictor variables `rad` and `tax` are very highly correlated (more than 0.9). We will attempt to account for this when we prepare the data.

There are some smaller, but still high correlations between other predictor variables as well. `indus` is highly correlated (more than 0.7) with `nox`, `dis`, and `tax`. `nox` is also highly correlated with `age` and `dis`. `rm` is highly correlated with `medv`. `lstat` is highly correlated with `medv`.

Let's take a look at the distributions for the predictor variables.
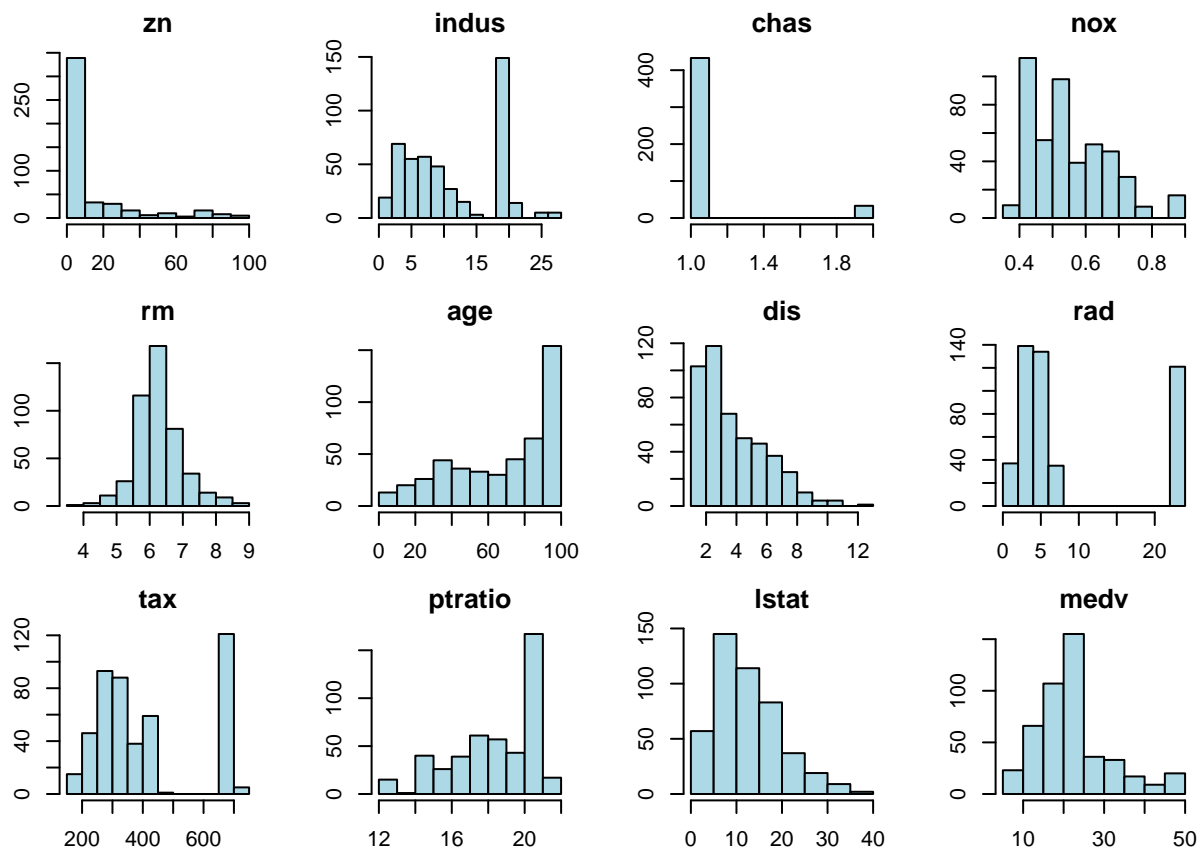
The distribution for `rm` appears to be normal, and the distribution for `medv` is nearly normal. The distributions for `zn`, `dis`, `lstat`, and `nox` are right-skewed. The distributions for `age` and `ptratio` are left-skewed.

The distributions for the remaining variables are multimodal, including the distribution for `chas`, which appears degenerate at first glance. It looks like a near-zero variance predictor, which we can confirm using the `nearZeroVar` function from the `caret` package.

	freqRatio	percentUnique	zeroVar	nzv
zn	16.142857	5.5793991	FALSE	FALSE
indus	4.321429	15.6652361	FALSE	FALSE
chas	13.121212	0.4291845	FALSE	FALSE
nox	1.176471	16.9527897	FALSE	FALSE
rm	1.000000	89.9141631	FALSE	FALSE
age	10.500000	71.4592275	FALSE	FALSE
dis	1.000000	81.5450644	FALSE	FALSE
rad	1.110092	1.9313305	FALSE	FALSE
tax	3.457143	13.5193133	FALSE	FALSE
ptratio	4.000000	9.8712446	FALSE	FALSE
lstat	1.000000	90.9871245	FALSE	FALSE
medv	2.142857	46.7811159	FALSE	FALSE

The percentage of unique values, `percentUnique`, in the sample for this predictor is less than the typical threshold of 10 percent, but there is a second criterion to consider: the `freqRatio`. This measures the frequency of the most common value (0 in this case) to the frequency of the second most common value (1 in this case). The `freqRatio` value for this predictor is less than the typical threshold of 19 (i.e. 95 occurrences

of the most frequent value for every 5 occurrences of the second most frequent value). So it is not considered a near-zero variance predictor. Neither are any of the other predictors.

Next we analyze boxplots to determine the spread of the numeric predictor variables. This will also reveal any outliers.
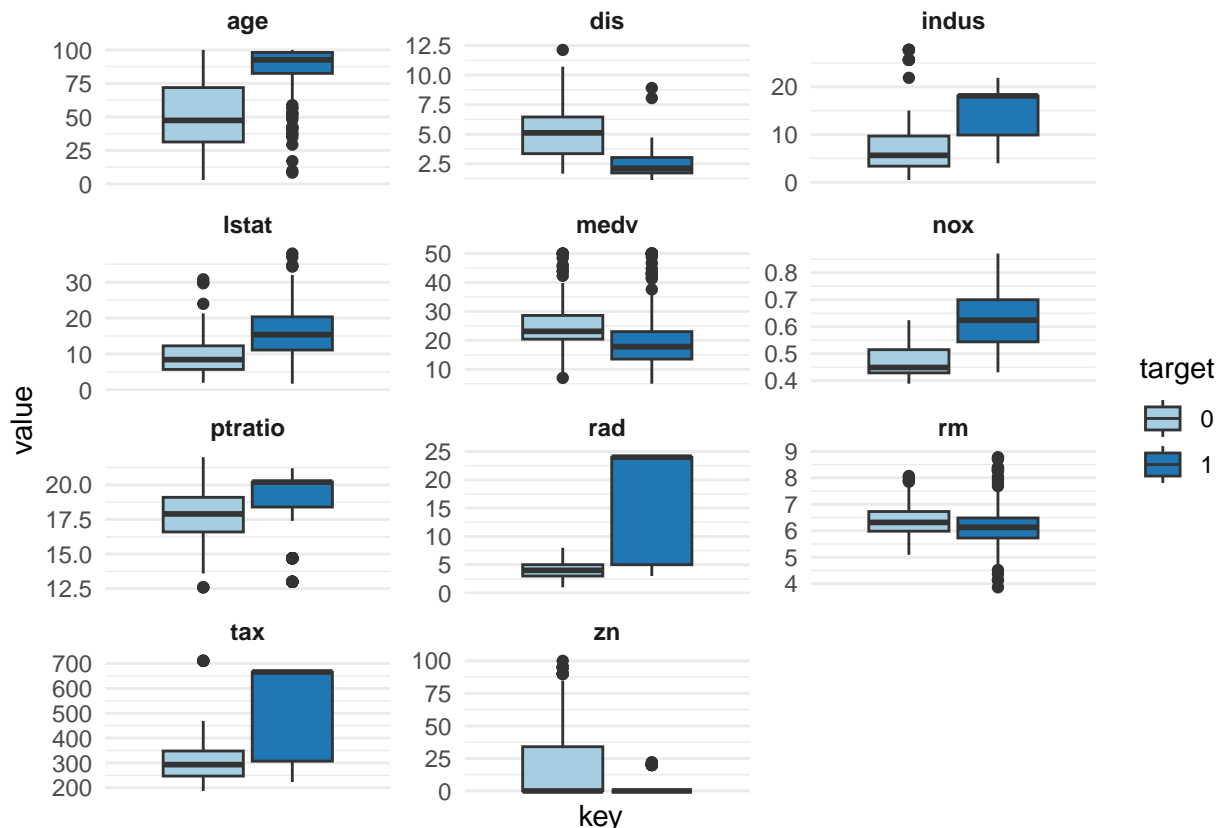
For certain predictors, the variance between the two categories of the response variable differs largely: `age`, `dis`, `nox`, `rad`, `indus`, and `zn`. Many of these variables also have almost no overlap in the interquartile ranges for each level of the response.

We also see some outliers in one or both levels of the response for some variables. We have no reason to conclude the outliers represent anything other than accurately recorded information that could be important to our model.

Data Preparation:

We confirmed earlier that there are no missing values to impute and no near-zero variance variables to remove. We also decided against winsorizing the outliers, which is a method of outlier imputation that replaces any value of a variable above or below percentile k with the value of the kth percentile itself. (We tested building a model using winsorized data, and it did not result in a model with different predictors or coefficients than building a model with non-winsorized data, so we scrapped it.)

We check whether our predictor variables with skewed distributions would benefit from transformations.

| Skewed Variable	Ideal Lambda Proposed by Box-Cox	Reasonable Alternative Transformation
zn	-0.3	log
dis	-0.15	log

Skewed Variable	Ideal Lambda Proposed by Box-Cox	Reasonable Alternative Transformation
lstat	0.25	log
nox	-0.95	inverse
age	1.3	no transformation
ptratio	2	square

Some of the skewed variables might benefit from transformations, so we create transformed versions of our train and test data. We will incorporate these transformed predictors into one of our models in the next section: Model 2.

We now consider modifying the `rad` and `tax` variables in an attempt to minimize the very high correlation we identified earlier between these two predictors. First, we look at the `rad` distribution more closely.
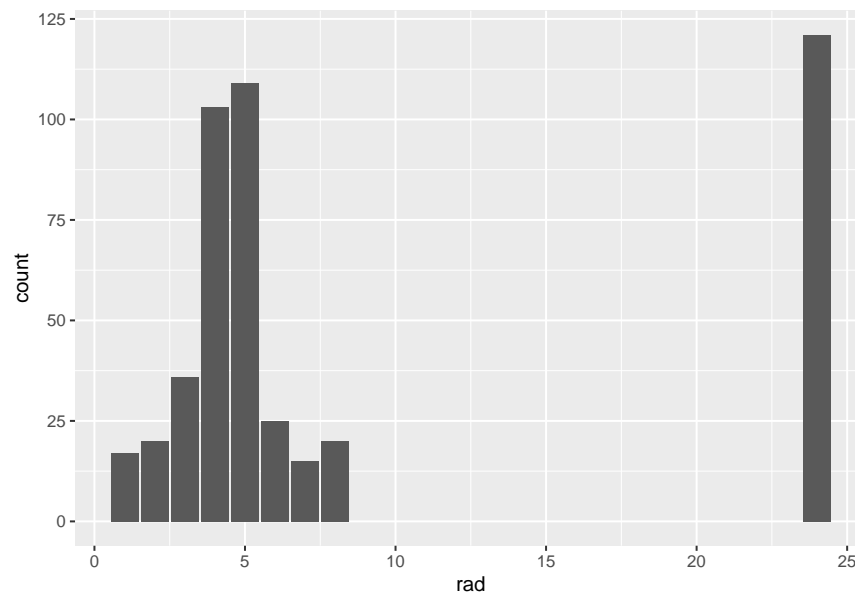
It is apparent that this variable may be more useful as a dummy variable given the limited potential values for this predictor. We bin the values and create the `rad_less5` dummy variable indicating 1 if the value for `rad` is < 5 and 0 if not. Using the same logic, we also bin the values in the `tax` variable into three levels (low is < 300, middle is 300 to 400, high is 400+), then create two dummy variables: `middle_tax` and `high_tax`.
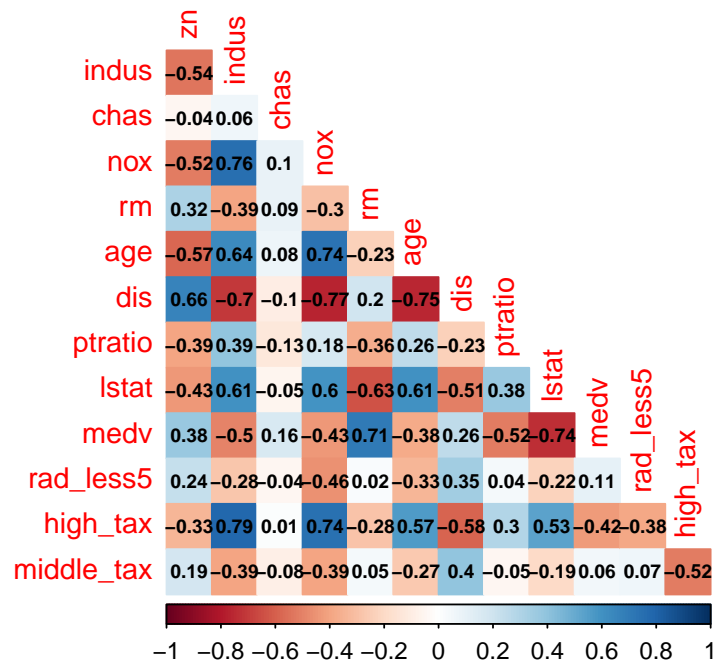
Both binned dummy columns address the correlation concerns that were previously identified. We will attempt to incorporate these binned predictors into one of our models in the next section: Model 3.

Before we build the models in the next section, we have decided that none of the models will be trained on the variable `chas`, as we have deemed this predictor irrelevant based on the earlier conclusion that its correlation with the response variable is very low.

Build Models

We build three models. Model 1 will be trained using untransformed data, Model 2 will be trained using transformed data for skewed predictors, and Model 3 will be trained using binned data for highly correlated predictors. For Models 1 and 2, stepwise model selection will be used to pick the model with the lowest AIC. For Model 3, an alternative exhaustive search method will be used to pick two sub-models based on different criteria: one with the lowest AIC and one with the lowest BIC.

Model 1: Stepwise AIC Selection on Untransformed Data We start with a full model using the untransformed data and then perform stepwise model selection to select the model with the smallest AIC value using the `stepAIC()` function from the `MASS` package.

```
##
## Call:
## glm(formula = target ~ zn + nox + age + dis + rad + tax + ptratio +
##     medv, family = "binomial", data = train_df)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -37.415922   6.035013  -6.200 5.65e-10 ***
```

```
## zn           -0.068648    0.032019   -2.144   0.03203 *
## nox          42.807768    6.678692    6.410 1.46e-10 ***
## age           0.032950    0.010951    3.009   0.00262 **
## dis           0.654896    0.214050    3.060   0.00222 **
## rad           0.725109    0.149788    4.841 1.29e-06 ***
## tax          -0.007756    0.002653   -2.924   0.00346 **
## ptratio       0.323628    0.111390    2.905   0.00367 **
## medv          0.110472    0.035445    3.117   0.00183 **
## ---
## 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: 197.32  on 457  degrees of freedom
## AIC: 215.32
##
## Number of Fisher Scoring iterations: 9
```

Model 1, the stepwise untransformed model, consists of 8 predictor variables and has an AIC of 215.32.

To interpret the model coefficients other than the Intercept, we first need to exponentiate them.

Feature	Coefficient
zn	9.336551e-01
nox	3.901012e+18
age	1.033499e+00
dis	1.924943e+00
rad	2.064956e+00
tax	9.922739e-01
ptratio	1.382133e+00
medv	1.116805e+00

The coefficients are now easier to interpret. Features with coefficients less than 1 indicate the odds of the crime rate being above the median crime rate decrease as that feature increases, while coefficients greater than 1 indicate the odds of the crime rate being above the median crime rate increases as that feature increases. How much the odds increase or decrease per 1 unit increase in the feature is the difference between that feature's coefficient and 1, multiplied by 100 so we can understand it as a percentage increase or decrease.

The coefficient for `nox` is extremely large. If we look back at the boxplots, we can see that the spreads for each category of the `target` value have no overlap in their interquartile ranges for this predictor. Almost all measures greater than 0.5 are associated with above median crime rates, and since this variable is measured on a scale less than 1, an increase of 1 in its value makes any measurement a large enough value to associate it with above median crime rates.

Now that we understand that, let's exclude `nox` from the features so that we can look at the rest of their coefficients more closely.

Feature	Coefficient	Percentage Change in Odds Crime Rate Above Median
rad	2.0649560	106.5
dis	1.9249425	92.5
ptratio	1.3821333	38.2
medv	1.1168050	11.7

Feature	Coefficient	Percentage Change in Odds Crime Rate Above Median
age	1.0334994	3.3
tax	0.9922739	-0.8
zn	0.9336551	-6.6

It's interesting that variables that did not have as strong of a linear relationship in the correlation funnel have an estimated larger percentage impact in the model given the exponentiated coefficients outside of nox.

Here, we see that increasing `rad` by 1 unit increases the odds of being above the median crime rate by 106.5 percent, increasing `zn` by 1 unit decreases the odds of being above the median crime rate by 6.6 percent, and so forth.

It is not so obvious what the perceived strength of the statistical relationship between radial highways and crime might be. Perhaps it has to do with neighborhoods that are closer to locations where a visitor could easily come and go from a city or are more industrial areas that are less desirable places to live due to their proximity to highways.

More Discussion of These Coefficients/Inference TK

Let's check for possible multicollinearity within this model.

```
##       zn      nox      age      dis      rad      tax  ptratio     medv
## 1.789037 3.172660 1.701974 3.595939 1.697110 1.754274 1.865085 2.193689
```

All of the variance inflation factors are less than 5 so there are no issues of multicollinearity within this model.

Model 2: Stepwise AIC Selection on Transformed Data We build our second model using the transformed data. We again start with a full model, then use the same stepwise lowest-AIC selection process we used for the first model to get a reduced model.

```
##
## Call:
## glm(formula = target ~ rm + age + rad + tax + ptratio + medv +
##     log_zn + log_dis + inverse_nox + ptratio_sq, family = "binomial",
##     data = train_df_trans)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  57.953075  16.505867   3.511 0.000446 ***
## rm           -1.112460   0.691852  -1.608 0.107848
## age           0.039927   0.013075   3.054 0.002261 **
## rad           0.771059   0.160598   4.801 1.58e-06 ***
## tax          -0.004776   0.003080  -1.551 0.120935
## ptratio      -5.631650   1.953687  -2.883 0.003944 **
## medv          0.198305   0.072945   2.719 0.006557 **
## log_zn       -0.233077   0.091993  -2.534 0.011288 *
## log_dis       3.327668   0.990327   3.360 0.000779 ***
## inverse_nox -10.240584   2.222121  -4.608 4.06e-06 ***
## ptratio_sq    0.164595   0.053176   3.095 0.001966 **
## ---
## 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: 182.17  on 455  degrees of freedom
## AIC: 204.17
##
## Number of Fisher Scoring iterations: 9
```

Model 2, the stepwise transformed model, consists of 10 predictor variables and has an AIC of 204.17.

To interpret the model coefficients, we first need to exponentiate them again to discuss how 1 unit increases in each of these predictors would affect the odds of the crime rate being above the median.

Feature	Coefficient	Percentage Change in Odds Crime Rate Above Median
log_dis	27.8732635	2687.3
rad	2.1620549	116.2
medv	1.2193343	21.9
ptratio_sq	1.1789157	17.9
age	1.0407348	4.1
tax	0.9952353	-0.5
log_zn	0.7920925	-20.8
rm	0.3287494	-67.1
ptratio	0.0035827	-99.6
inverse_nox	0.0000357	-100.0

A 1 unit increase in the transformed predictor `log_dis` results in a 2687.3 percent increase in the odds of being above the median crime rate, a 1 unit increase in the the transformed predictor `log_zn` results in a 20.8 percent decrease in the odds of being above the median crime rate, and so forth.

Note that since Model 2 uses the transformed predictor `inverse_nox` instead of the original predictor `nox`, the exponentiated coefficient for the transformed predictor is very small instead of very large, and therefore a 1 unit increase in `inverse_nox` logically results in a 100 percent decrease in the odds of being above the median crime rate.

Note also that the coefficient for the transformed predictor `ptratio_sq` is positive, where as the coefficient for its untransformed lower order term `ptratrio` is negative. This falls within expected behavior when adding a quadratic term, and visually the relationship between the response and these predictors would look like a concave upward parabola that decreases to a minimum, then increases.

We check for possible multicollinearity within this model.

```
##          rm         age         rad         tax     ptratio        medv
##    4.344643    2.141214    1.614811    2.046894  476.759375    7.221909
##      log_zn     log_dis inverse_nox  ptratio_sq
##    2.195675    4.183535    3.930079  461.852610
```

We see very high variance inflation factors for `ptratio` and `ptratio_sq`. This is expected since we've included a higher order term and its lower order term in the model. We want to keep both, as keeping just the higher order term would be us insisting the lower order term has no effect on the model, and we have no reason to do that.

The only other variance inflation factor higher than 5 is for `medv`. We will remove this variable from Model 2.

11

```
## 
## Call:
## glm(formula = target ~ rm + age + rad + tax + ptratio + log_zn +
##     log_dis + inverse_nox + ptratio_sq, family = "binomial",
##     data = train_df_trans)
## 
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 60.140668  16.253255   3.700 0.000215 ***
## rm           0.494090   0.372585   1.326 0.184803
## age          0.020514   0.010356   1.981 0.047602 *
## rad          0.767895   0.155308   4.944 7.64e-07 ***
## tax         -0.006503   0.003029  -2.147 0.031770 *
## ptratio     -6.270963   1.882200  -3.332 0.000863 ***
## log_zn      -0.246547   0.087797  -2.808 0.004983 **
## log_dis      2.169973   0.856591   2.533 0.011301 *
## inverse_nox -8.517841   1.979060  -4.304 1.68e-05 ***
## ptratio_sq   0.176822   0.051446   3.437 0.000588 ***
## ---
## 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: 190.28  on 456  degrees of freedom
## AIC: 210.28
## 
## Number of Fisher Scoring iterations: 9
```

This increased the AIC for Model 2 to 210.28. This is still lower than the AIC from model 1.

Model 3: Utilizing Dummy Variables with Best Subset   The stepwise lowest-AIC selection method was utilized to optimize the previous two models' performance. For Model 3, we will use an alternative approach, the `bestglm` function from the `bestglm` package, which attempts to find the best subset model by comparing all permutations for model optimization. This package also allows us to use an alternative criterion to evaluate the model performance. So we will evaluate using AIC in one iteration and BIC in another. (This function has a limitation of 15 predictors given the computational power needed for all variations of the model.)

One nice feature of the `bestglm` output is it includes the best criterion version of each model size, which can allow us to evaluate if certain combinations make intuitive sense.


```
## 
## Call:
## glm(formula = y ~ ., family = family, data = Xi, weights = weights)
## 
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -34.89257    5.19589  -6.715 1.88e-11 ***
## zn           -0.06141    0.02780  -2.209  0.02717 *
## indus        -0.07595    0.04544  -1.671  0.09463 .
## nox          42.22695    6.09505   6.928 4.27e-12 ***
## dis           0.48597    0.18853   2.578  0.00995 **
```

```
## ptratio         0.24496      0.10466    2.340  0.01926 *
## lstat           0.07749      0.04403    1.760  0.07838 .
## medv            0.18040      0.04026    4.480 7.45e-06 ***
## high_tax1       2.43610      0.60410    4.033 5.52e-05 ***
## middle_tax1     2.46552      0.48470    5.087 3.64e-07 ***
## ---
## 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: 220.53  on 456  degrees of freedom
## AIC: 240.53
##
## Number of Fisher Scoring iterations: 8
```

For Model 3, the model with the lowest AIC returned by the `bestglm` function has nine predictors and an AIC of 232.43. We will refer to this model as Model 3A: Binned (Best AIC) hereafter.

To interpret the model coefficients, we first need to exponentiate them again to discuss how 1 unit increases in each of these predictors would affect the odds of the crime rate being above the median. Since the coefficient for `nox` is again very large, and we know why, we omit it from this discussion.

Feature	Coefficient	Percentage Change in Odds Crime Rate Above Median
middle_tax1	11.7695493	1077.0
high_tax1	11.4284198	1042.8
dis	1.6257472	62.6
ptratio	1.2775687	27.8
medv	1.1977016	19.8
lstat	1.0805744	8.1
zn	0.9404404	-6.0
indus	0.9268601	-7.3

```
##
## Call:
## glm(formula = y ~ ., family = family, data = Xi, weights = weights)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -20.75803    2.42265  -8.568  < 2e-16 ***
## zn           -0.04425    0.02050  -2.158 0.030917 *
## nox          30.82843    3.76920   8.179 2.86e-16 ***
## medv          0.10629    0.02742   3.877 0.000106 ***
## high_tax1     2.12259    0.54002   3.931 8.47e-05 ***
## middle_tax1   2.79677    0.48744   5.738 9.60e-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: 235.46  on 460  degrees of freedom
## AIC: 247.46
```

```
##
## Number of Fisher Scoring iterations: 7
```

The lowest BIC model returned by the `bestglm` function has only six predictors. We will refer to this model as Model 3B: Binned (Best BIC) hereafter. As expected the BIC criterion measure preferred a model with less predictors than AIC as it's penalty function more heavily penalizes model complexity.

To interpret the model coefficients, we first need to exponentiate them again to discuss how 1 unit increases in each of these predictors would affect the odds of the crime rate being above the median. Since the coefficient for `nox` is again very large, and we know why, we omit it from this discussion.
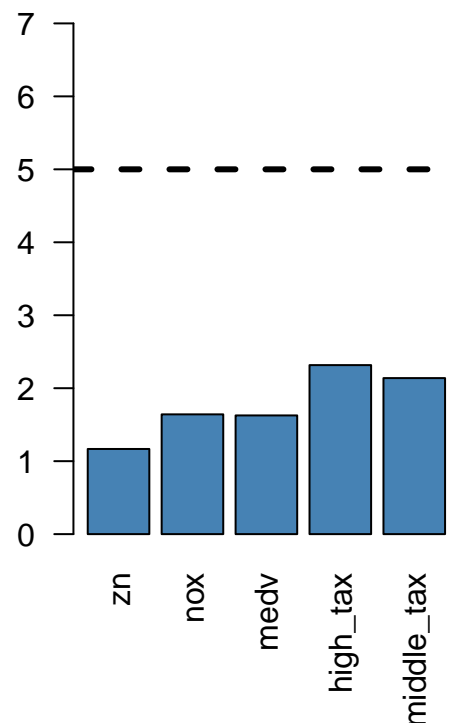
Feature	Coefficient	Percentage Change in Odds Crime Rate Above Median
middle_tax1	16.3915419	1539.2
high_tax1	8.3527231	735.3
medv	1.1121435	11.2
zn	0.9567148	-4.3

Let's review the models for any multicollinearity concerns:

Model 3A: Binned (Best AIC) VIF
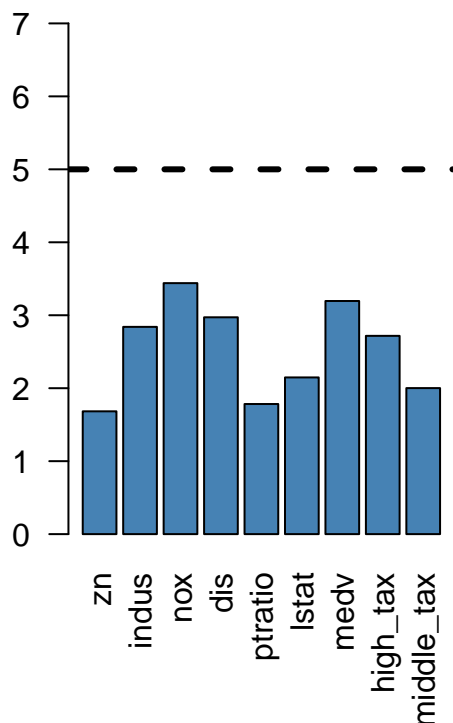
Model 3B: Binned (Best BIC) VIF

Neither Model 3A nor Model 3B has correlation concerns that would require further revision of the underlying selected predictors.

Select Models:

The main criterion we will use to select the model with the best performance is the ROC curve, but we need to check for goodness of fit issues prior to that. We will not select a model with a better ROC curve if we

determine there is a suggestion of lack of fit for that model. The main criteria we will use to determine lack of fit are binned residual plots, marginal model plots, and the Hosmer-Lemeshow statistic.

To check for goodness of fit, we first plot the residuals for each model against their fitted values.
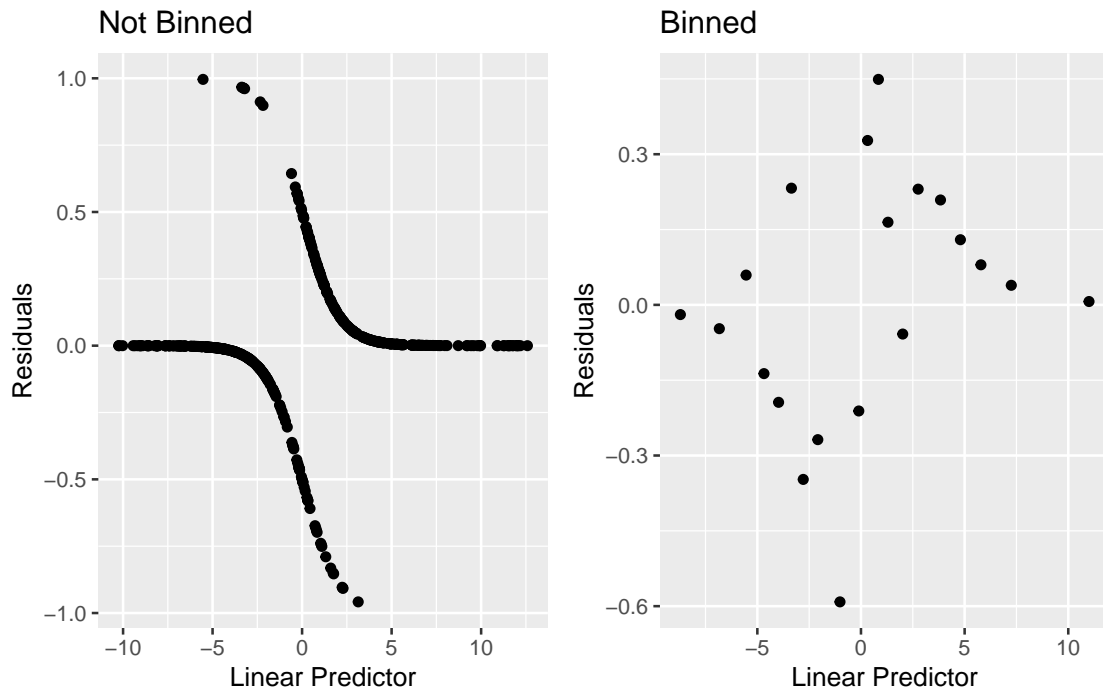
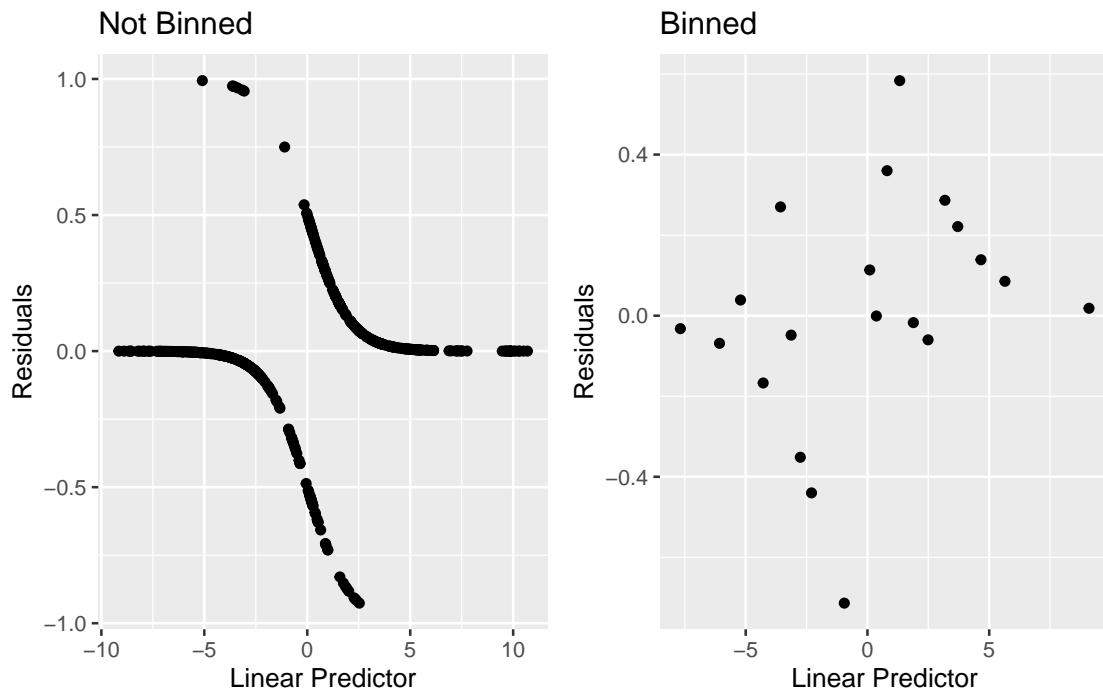## Model 1: Stepwise Untransformed

Not Binned

Binned

Model 2: Stepwise Transformed

Not Binned
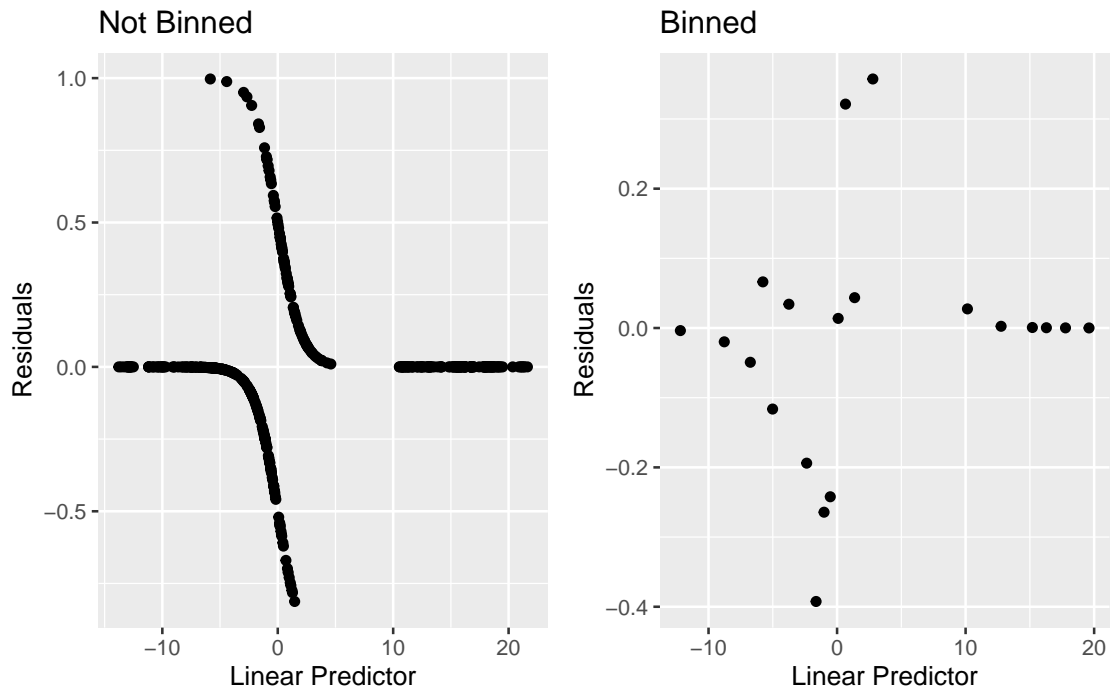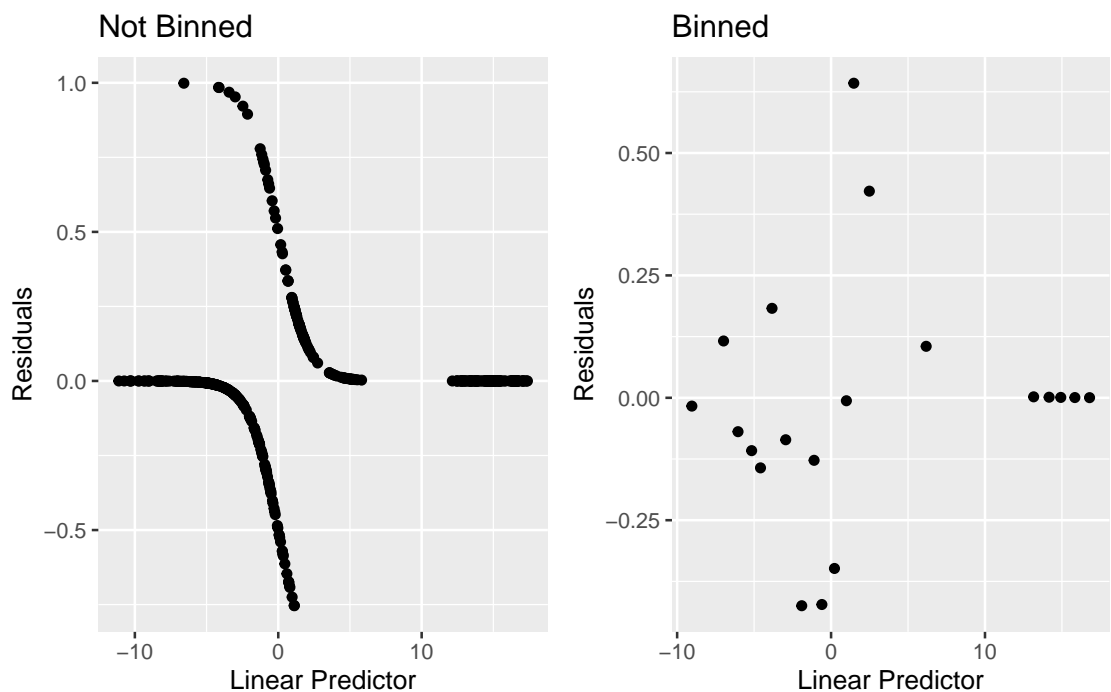
Binned

Model 3A: Binned (Best AIC)
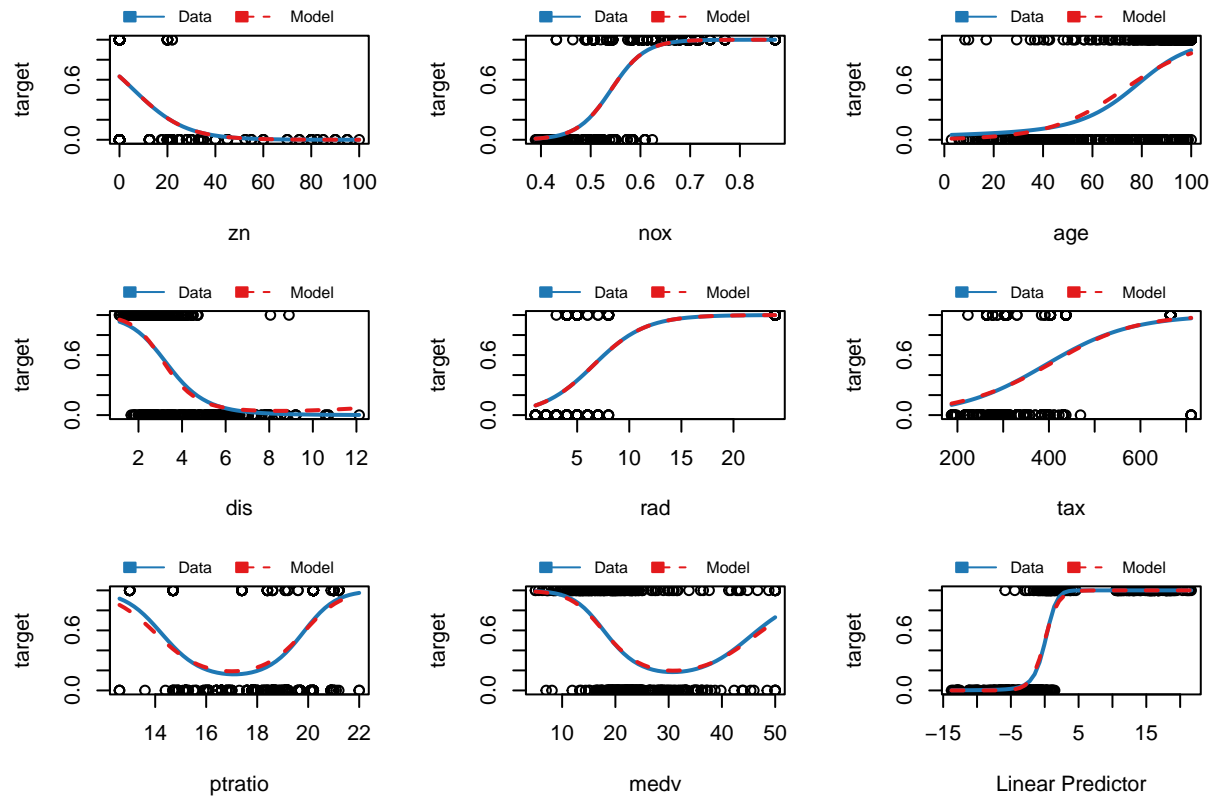

Model 3B: Binned (Best BIC)

The binned residual plots don't quite eliminate the patterns in the raw residuals as we expected. We refrain from concluding anything determinant about the fit for each model just by looking at these plots.

Next we create marginal model plots for the response and each predictor in each model. (Note that the `mmps` function from the `car` package used to generate these plots skips any factors and interaction terms

within the model intentionally. So for Models 3A and 3B, which include dummy variables we created, fewer predictors are plotted than are present within the models.)
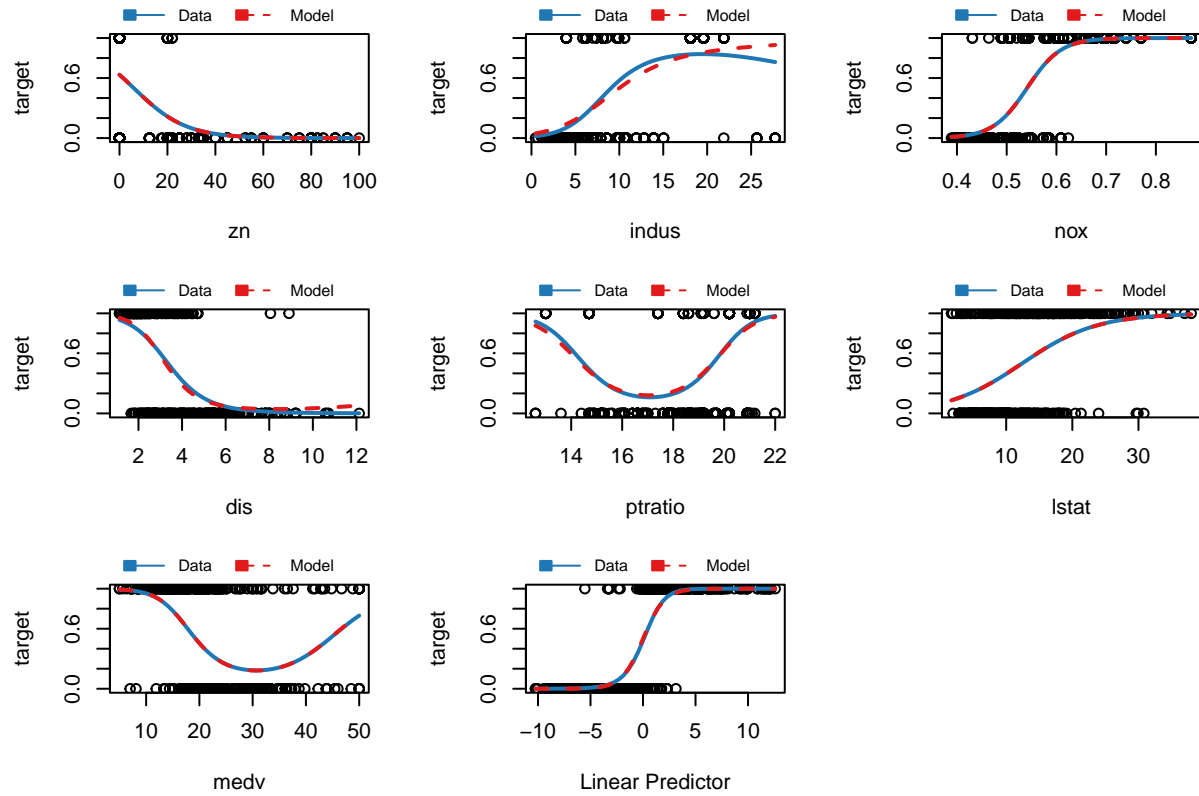
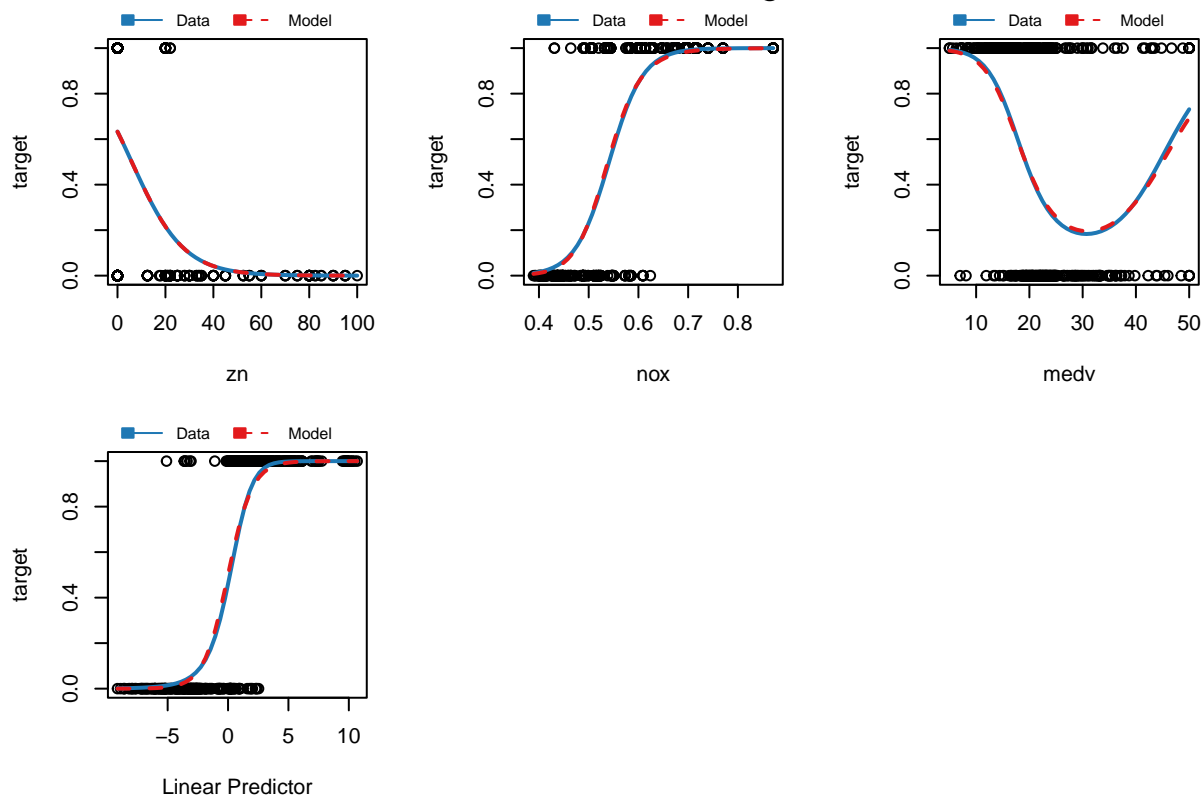## Model 1: Stepwise Untransformed: Marginal Model Plots

Model 2: Stepwise Transformed: Marginal Model Plots
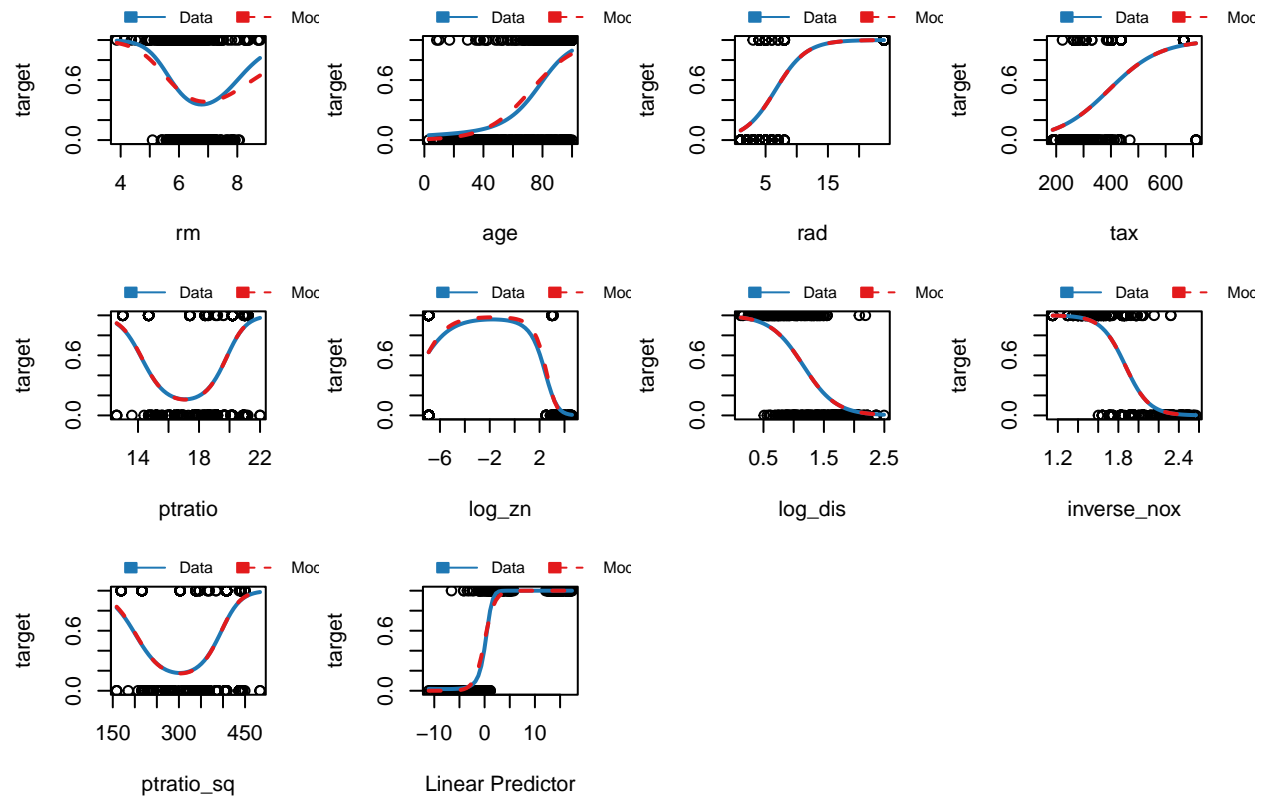
Model 3A: Binned: Best AIC: Marginal Model Plots

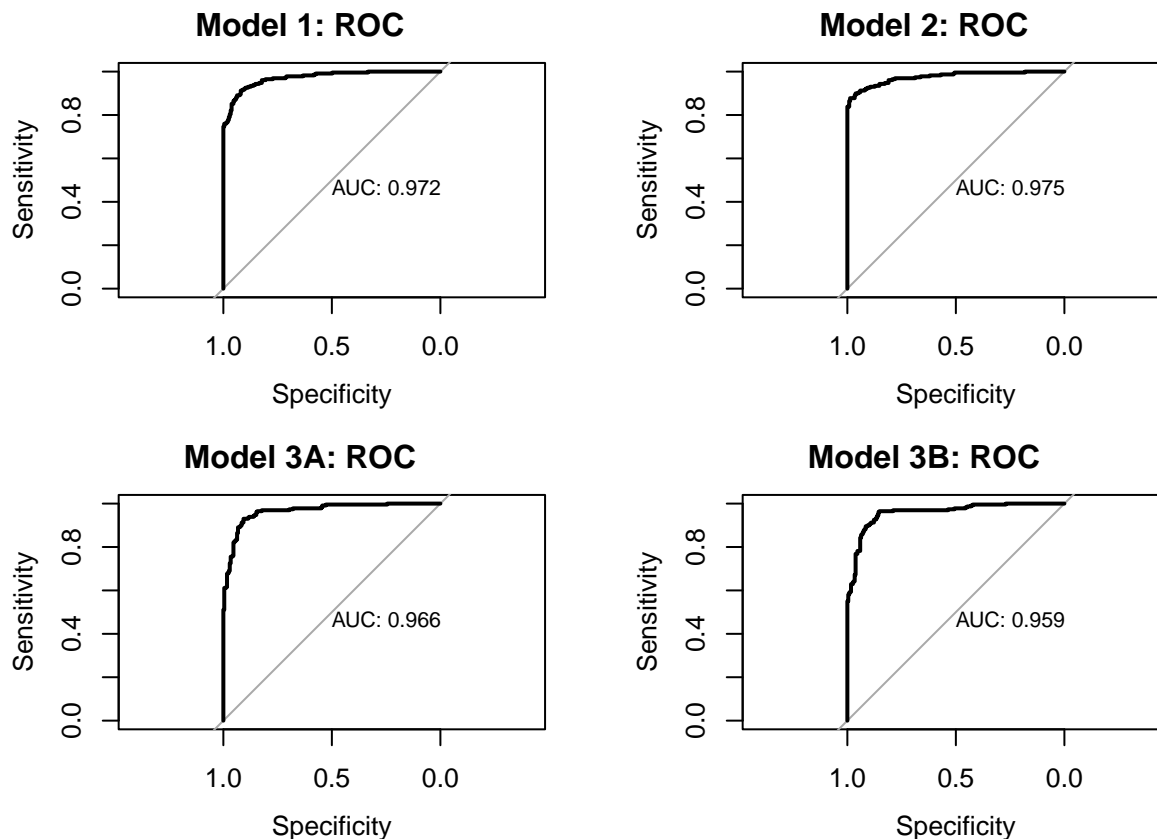## Model 3B: Binned: Best BIC: Marginal Model Plots

There is very good agreement between the two fits for all of the predictors in the marginal model plots for Models 1 and 3B. There is one notable deviation of fit for the relationship between `target` and `rm` for Model 2, and one notable deviation of fit for the relationship between `target` and `indus` in Model 3A.

We calculate the Hosmer-Lemeshow statistic for each model to further check for lack of fit.

Model	HL Statistic	DoF	P Value
Model 1: Stepwise Untransformed	12.57643	8	0.1272784
Model 2: Stepwise Transformed	52.0694	8	1.631963e-08
Model 3A: Binned (Best AIC)	13.97434	8	0.08243674
Model 3B: Binned (Best BIC)	19.66757	8	0.01166965

The moderate p-values here for Models 1 and 3A suggest no lack of fit, while the low p-values for Models 2 and 3B do. This is a little surprising for Models 3A and 3B given the marginal models plots issues for the former and the lack thereof for the latter. Note that this statistic can't tell us whether any of the models are overfitting the data though.

We produce ROC curves for each model to determine which performs better on the training data.

Model 1: ROC   **Model 2: ROC**

AUC: 0.972   AUC: 0.975

Model 3A: ROC   **Model 3B: ROC**

AUC: 0.966   AUC: 0.959

Model 2 performs best on the training data based on its ROC curve, but the only model for which there was no suggestion of lack of fit in both the marginal models plots and the HL statistics was Model 1. Its ROC curve is very similar that of Model 2 anyway, so we prefer Model 1 and select it for final evaluation.

Evaluation

Confusion Tables: Model 1:

```
##           Reference
## Prediction   0    1
##          0 218   22
##          1  19  207
```

Model 2:

```
##           Reference
## Prediction   0    1
##          0 219   20
##          1  18  209
```

Model 3a:

```
##           Reference
## Prediction   0   1
```

21

```
##           0 211  16
##           1  26 213
```

Model 3b:

```
##          Reference
## Prediction  0   1
##           0 203  11
##           1  34 218
```

Training Data Evaluation Metrics

	Model 1	Model 2	Model 3a	Model 3b
Sensitivity	0.9039301	0.9126638	0.9301310	0.9519651
Specificity	0.9198312	0.9240506	0.8902954	0.8565401
Pos Pred Value	0.9159292	0.9207048	0.8912134	0.8650794
Neg Pred Value	0.9083333	0.9163180	0.9295154	0.9485981
Precision	0.9159292	0.9207048	0.8912134	0.8650794
Recall	0.9039301	0.9126638	0.9301310	0.9519651
F1	0.9098901	0.9166667	0.9102564	0.9064449
Prevalence	0.4914163	0.4914163	0.4914163	0.4914163
Detection Rate	0.4442060	0.4484979	0.4570815	0.4678112
Detection Prevalence	0.4849785	0.4871245	0.5128755	0.5407725
Balanced Accuracy	0.9118807	0.9183572	0.9102132	0.9042526

All of the models appear to perform somewhat similarly although number 2 has the highest AUC, F1 score, precision and accuracy which on that basis would make it seem like the preferred choice to select out of the reviewed approaches.
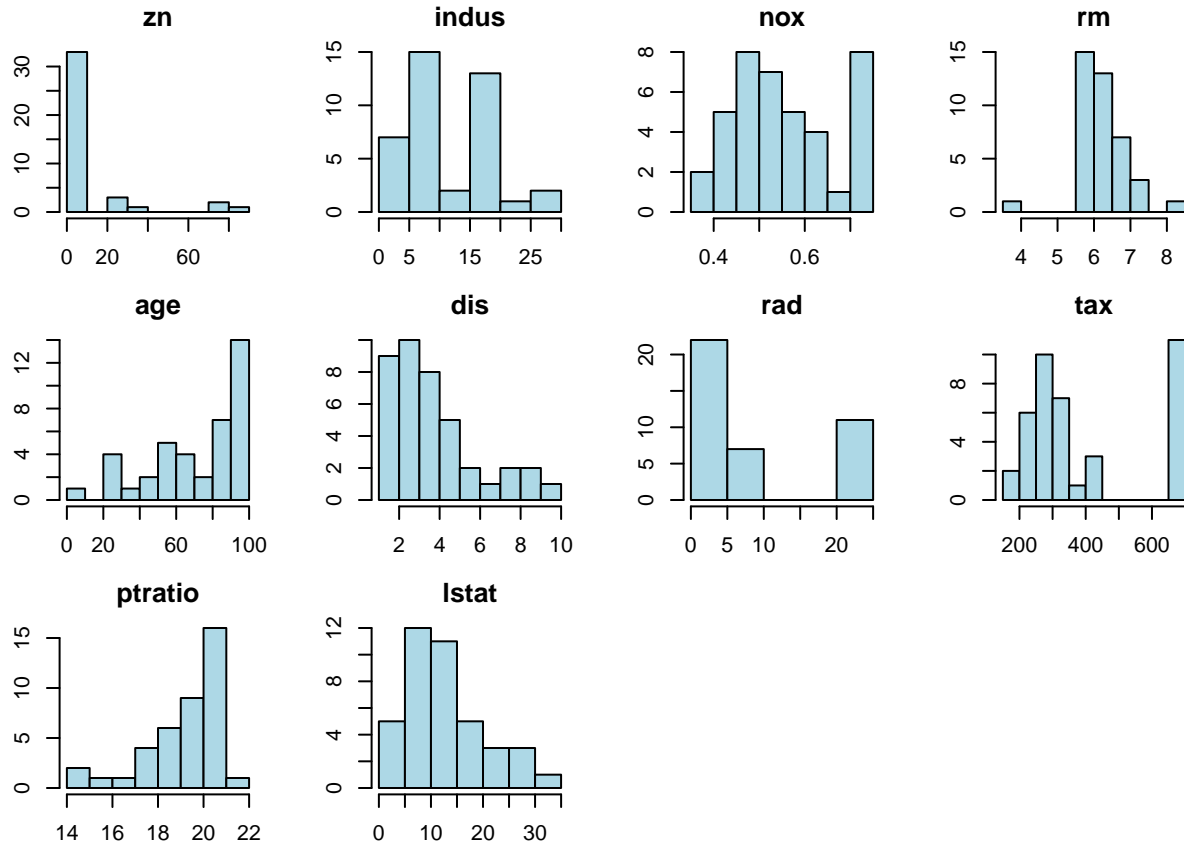
The evaluation set's distributions appear to be similar enough to the training data that would not prevent the use of transformations to mirror the modeling approach taken in model 2.

```
## # A tibble: 2 x 2
##   predictions   cnt
##         <dbl> <int>
## 1           0    20
## 2           1    20
```

The predictions are evenly split at 50% between the two binary responses and that result does not diverge much from the training set. With the available data in the training and test set the model has performed as expected and additional target information would be helpful to further evaluate and refine the underlying model to minimize any overfitting.

Appendix

```
knitr::opts_chunk$set(echo = TRUE, warning=FALSE)

library(tidyverse)
library(modelr)
library(DataExplorer)
library(correlationfunnel)
library(caret)
library(knitr)
```

```r
library(confintr)
library(psych)
library(car)
library(corrplot)
library(RColorBrewer)
library(MASS)
select <- dplyr::select
library(glmtoolbox)
library(cowplot)
library(pROC)
library(bestglm)

train_df <- read.csv("https://raw.githubusercontent.com/andrewbowen19/businessAnalyticsDataMiningDATA62
test_df <- read.csv("https://raw.githubusercontent.com/andrewbowen19/businessAnalyticsDataMiningDATA621,

dim(train_df)

train_df |>
    glimpse()

train_df <- train_df |>
    mutate(chas = as.factor(chas), target = as.factor(target))

summary(train_df)

# standard deviation
sapply((train_df |> select (-chas, -target)), sd)

sum(is.na(train_df))

train_df_binarized <- train_df |>
    binarize(n_bins = 5, thresh_infreq = 0.01, name_infreq = "OTHER",
            one_hot = TRUE)
train_df_corr <- train_df_binarized |>
    correlate(target__1)
train_df_corr |>
    plot_correlation_funnel()
rm(train_df_binarized, train_df_corr)

factors <- c("chas", "target")
cramersv <- round(cramersv(train_df |> select(all_of(factors))), 5)
pearson <- round(cor(as.numeric(train_df$chas), as.numeric(train_df$target), method = "pearson"), 5)
(cramersv == pearson)

corrplot(cor(train_df |> select(-target) |> mutate(chas = as.numeric(chas))),
        method="color",
        diag=FALSE,
        type="lower",
        addCoef.col = "black",
        number.cex=0.70)

par(mfrow=c(3,4))
par(mai=c(.3,.3,.3,.3))
```

```r
variables <- names(train_df)
for (i in 1:(length(variables)-1)) {
    if (variables[i] %in% factors){
        hist(as.numeric(train_df[[variables[i]]]), main = variables[i],
            col = "lightblue")
    }else{
        hist(train_df[[variables[i]]], main = variables[i], col = "lightblue")
    }
}

nzv <- nearZeroVar(train_df |> select(-target), saveMetrics = TRUE)
knitr::kable(nzv)

train_df |>
    dplyr::select(-chas) |>
    gather(key, value, -target) |>
    mutate(key = factor(key),
           target = factor(target)) |>
    ggplot(aes(x = key, y = value)) +
    geom_boxplot(aes(fill = target)) +
    scale_x_discrete(labels = NULL, breaks = NULL) +
    facet_wrap(~ key, scales = 'free', ncol = 3) +
    scale_fill_brewer(palette = "Paired") +
    theme_minimal() +
    theme(strip.text = element_text(face = "bold"))

skewed <- c("zn", "dis", "lstat", "nox", "age", "ptratio")
train_df_trans <- train_df
for (i in 1:(length(skewed))){
    #Add a small constant to columns with any 0 values
    if (sum(train_df_trans[[skewed[i]]] == 0) > 0){
        train_df_trans[[skewed[i]]] <-
            train_df_trans[[skewed[i]]] + 0.001
    }
}
for (i in 1:(length(skewed))){
    if (i == 1){
        lambdas <- c()
    }
    bc <- boxcox(lm(train_df_trans[[skewed[i]]] ~ 1),
                 lambda = seq(-2, 2, length.out = 81),
                 plotit = FALSE)
    lambda <- bc$x[which.max(bc$y)]
    lambdas <- append(lambdas, lambda)
}
lambdas <- as.data.frame(cbind(skewed, lambdas))
adj <- c("log", "log", "log", "inverse", "no transformation", "square")
lambdas <- cbind(lambdas, adj)
cols <- c("Skewed Variable", "Ideal Lambda Proposed by Box-Cox", "Reasonable Alternative Transformation"
colnames(lambdas) <- cols
kable(lambdas, format = "simple")

remove <- c("zn", "dis", "lstat", "nox")
```

```r
train_df_trans <- train_df_trans |>
    mutate(log_zn = log(zn),
           log_dis = log(dis),
           log_lstat = log(lstat),
           inverse_nox = nox^-1,
           ptratio_sq = ptratio^2) |>
    select(-all_of(remove))
test_df_trans <- test_df
for (i in 1:(length(skewed))){
    #Add a small constant to columns with any 0 values
    if (sum(test_df_trans[[skewed[i]]] == 0) > 0){
        test_df_trans[[skewed[i]]] <-
            test_df_trans[[skewed[i]]] + 0.001
    }
}
test_df_trans <- test_df_trans |>
    mutate(log_zn = log(zn),
           log_dis = log(dis),
           log_lstat = log(lstat),
           inverse_nox = nox^-1,
           ptratio_sq = ptratio^2) |>
    select(-all_of(remove))

ggplot(train_df,aes(x=rad)) +
    geom_bar()
remove <- c("rad", "tax")
train_df2 <- train_df |>
    mutate(rad_less5=as.factor(ifelse(rad<5,1,0)),
           high_tax=as.factor(ifelse(tax>400,1,0)),
           middle_tax=as.factor(ifelse(tax<400 & tax>=300,1,0))) |>
    select(-all_of(remove)) |>
    relocate(target,.after=last_col())
test_df2 <- test_df |>
    mutate(rad_less5=as.factor(ifelse(rad<5,1,0)),
           high_tax=as.factor(ifelse(tax>400,1,0)),
           middle_tax=as.factor(ifelse(tax<400 & tax>=300,1,0))) |>
    select(-all_of(remove))

corrplot(cor(train_df2 |> select(-target) |> mutate(chas = as.numeric(chas),
                                             rad_less5 = as.numeric(rad_less5),
                                             high_tax = as.numeric(high_tax),
                                             middle_tax = as.numeric(middle_tax))),
         method="color",
         diag=FALSE,
         type="lower",
         addCoef.col = "black",
         number.cex=0.70)
train_df <- train_df |>
    select(-chas)
train_df_trans <- train_df_trans |>
    select(-chas)
train_df2 <- train_df2 |>
    select(-chas)
```

```r
test_df <- test_df |>
    select(-chas)
test_df_trans <- test_df_trans |>
    select(-chas)
test_df2 <- test_df2 |>
    select(-chas)

glm_full <- glm(target~., family='binomial', data=train_df)
model_1 <- stepAIC(glm_full, trace=0)
summary(model_1)

beta <- coef(model_1)
beta_exp <- as.data.frame(exp(beta)) |>
    rownames_to_column()
cols <- c("Feature", "Coefficient")
colnames(beta_exp) <- cols
beta_exp <- beta_exp |>
    filter(Feature != "(Intercept)")
knitr::kable(beta_exp, format = "simple")

beta_exp <- beta_exp |>
    filter(Feature != "nox") |>
    mutate(diff = round(Coefficient - 1, 3) * 100) |>
    arrange(desc(diff))
cols <- c("Feature", "Coefficient", "Percentage Change in Odds Crime Rate Above Median")
colnames(beta_exp) <- cols
knitr::kable(beta_exp, format = "simple")

vif(model_1)

glm_full2 <- glm(target~., family='binomial', data=train_df_trans)
model_2 <- stepAIC(glm_full2, trace=0)
summary(model_2)

beta2 <- coef(model_2)
beta2_exp <- as.data.frame(exp(beta2)) |>
    rownames_to_column()
cols <- c("Feature", "Coefficient")
colnames(beta2_exp) <- cols
beta2_exp <- beta2_exp |>
    filter(Feature != "(Intercept)")
beta2_exp <- beta2_exp |>
    mutate(diff = round(Coefficient - 1, 3) * 100) |>
    arrange(desc(diff))
cols <- c("Feature", "Coefficient", "Percentage Change in Odds Crime Rate Above Median")
colnames(beta2_exp) <- cols
knitr::kable(beta2_exp, format = "simple")

vif(model_2)

model_2 <- update(model_2, ~ . - medv)
summary(model_2)
```

```r
model_3_aic <- bestglm(train_df2,IC="AIC",family=binomial)
model_3_bic <- bestglm(train_df2,IC="BIC",family=binomial)

#log_aic_tax$BestModels #commented out since I'm not sure what you want to extract from what object her
summary(model_3_aic$BestModel)

beta3a <- coef(model_3_aic$BestModel)
beta3a_exp <- as.data.frame(exp(beta3a)) |>
    rownames_to_column()
cols <- c("Feature", "Coefficient")
colnames(beta3a_exp) <- cols
remove <- c("nox", "(Intercept)")
beta3a_exp <- beta3a_exp |>
    filter(!Feature %in% remove)
beta3a_exp <- beta3a_exp |>
    mutate(diff = round(Coefficient - 1, 3) * 100) |>
    arrange(desc(diff))
cols <- c("Feature", "Coefficient", "Percentage Change in Odds Crime Rate Above Median")
colnames(beta3a_exp) <- cols
knitr::kable(beta3a_exp, format = "simple")

summary(model_3_bic$BestModel)

beta3b <- coef(model_3_bic$BestModel)
beta3b_exp <- as.data.frame(exp(beta3b)) |>
    rownames_to_column()
cols <- c("Feature", "Coefficient")
colnames(beta3b_exp) <- cols
remove <- c("nox", "(Intercept)")
beta3b_exp <- beta3b_exp |>
    filter(!Feature %in% remove)
beta3b_exp <- beta3b_exp |>
    mutate(diff = round(Coefficient - 1, 3) * 100) |>
    arrange(desc(diff))
cols <- c("Feature", "Coefficient", "Percentage Change in Odds Crime Rate Above Median")
colnames(beta3b_exp) <- cols
knitr::kable(beta3b_exp, format = "simple")

viz_vif <- function(model_input, title){
    barplot(vif(model_input), main = title, col = "steelblue",
            ylim=c(0,7), las = 2) #create horizontal bar chart to display each VIF value

abline(h = 5, lwd = 3, lty = 2)
}
par(mfrow=c(1,2))
viz_vif(model_3_aic$BestModel, "Model 3A: Binned (Best AIC) VIF")
viz_vif(model_3_bic$BestModel, "Model 3B: Binned (Best BIC) VIF")

linpred1 <- predict(model_1)
predprob1 <- predict(model_1, type = "response")
rawres1 <- residuals(model_1, type = "response")
res1 <- as.data.frame(cbind(linpred1, predprob1, rawres1))
linpred2 <- predict(model_2)
```

```
predprob2 <- predict(model_2, type = "response")
rawres2 <- residuals(model_2, type = "response")
res2 <- as.data.frame(cbind(linpred2, predprob2, rawres2))
pa <- res1 |>
    ggplot() +
    geom_point(aes(x = linpred1, y = rawres1)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Not Binned")
train_df_mod1 <- train_df |>
    mutate(residuals = residuals(model_1),
           linpred = predict(model_1),
           predprob = predict(model_1, type = "response"))
binned1 <- train_df_mod1 |>
    group_by(cut(linpred, breaks = unique(quantile(linpred,
                                            probs = seq(.05, 1, .05)))))
diag1 <- binned1 |>
    summarize(residuals = mean(residuals), linpred = mean(linpred))
pb <- diag1 |>
    ggplot() +
    geom_point(aes(x = linpred, y = residuals)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Binned")
pc <- res2 |>
    ggplot() +
    geom_point(aes(x = linpred2, y = rawres2)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Not Binned")
train_df_mod2 <- train_df_trans |>
    mutate(residuals = residuals(model_2),
           linpred = predict(model_2),
           predprob = predict(model_2, type = "response"))
binned2 <- train_df_mod2 |>
    group_by(cut(linpred, breaks = unique(quantile(linpred,
                                            probs = seq(.05, 1, .05)))))
diag2 <- binned2 |>
    summarize(residuals = mean(residuals), linpred = mean(linpred))
pd <- diag2 |>
    ggplot() +
    geom_point(aes(x = linpred, y = residuals)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Binned")
title1 <- ggdraw() +
    draw_label("Model 1: Stepwise Untransformed")
p1a <- plot_grid(pa, pb, ncol = 2, align = "h", axis = "b")
p1 <- plot_grid(title1, p1a, ncol = 1, rel_heights = c(0.1, 1))
title2 <- ggdraw() +
    draw_label("Model 2: Stepwise Transformed")
p2a <- plot_grid(pc, pd, ncol = 2, align = "h", axis = "b")
p2 <- plot_grid(title2, p2a, ncol = 1, rel_heights = c(0.1, 1))
p1
p2

linpred3a <- predict(model_3_aic$BestModel)
predprob3a <- predict(model_3_aic$BestModel, type = "response")
rawres3a <- residuals(model_3_aic$BestModel, type = "response")
res3a <- as.data.frame(cbind(linpred3a, predprob3a, rawres3a))
linpred3b <- predict(model_3_bic$BestModel)
```

```r
predprob3b <- predict(model_3_bic$BestModel, type = "response")
rawres3b <- residuals(model_3_bic$BestModel, type = "response")
res3b <- as.data.frame(cbind(linpred3b, predprob3b, rawres3b))
pe <- res3a |>
    ggplot() +
    geom_point(aes(x = linpred3a, y = rawres3a)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Not Binned")
train_df_mod3a <- train_df |>
    mutate(residuals = residuals(model_3_aic$BestModel),
           linpred = predict(model_3_aic$BestModel),
           predprob = predict(model_3_aic$BestModel, type = "response"))
binned3a <- train_df_mod3a |>
    group_by(cut(linpred, breaks = unique(quantile(linpred,
                                                   probs = seq(.05, 1, .05)))))
diag3a <- binned3a |>
    summarize(residuals = mean(residuals), linpred = mean(linpred))
pf <- diag3a |>
    ggplot() +
    geom_point(aes(x = linpred, y = residuals)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Binned")
pg <- res3b |>
    ggplot() +
    geom_point(aes(x = linpred3b, y = rawres3b)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Not Binned")
train_df_mod3b <- train_df |>
    mutate(residuals = residuals(model_3_bic$BestModel),
           linpred = predict(model_3_bic$BestModel),
           predprob = predict(model_3_bic$BestModel, type = "response"))
binned3b <- train_df_mod3b |>
    group_by(cut(linpred, breaks = unique(quantile(linpred,
                                                   probs = seq(.05, 1, .05)))))
diag3b <- binned3b |>
    summarize(residuals = mean(residuals), linpred = mean(linpred))
ph <- diag3b |>
    ggplot() +
    geom_point(aes(x = linpred, y = residuals)) +
    labs(x = "Linear Predictor", y = "Residuals", title = "Binned")
title3 <- ggdraw() +
    draw_label("Model 3A: Binned (Best AIC)")
p3a1 <- plot_grid(pe, pf, ncol = 2, align = "h", axis = "b")
p3a <- plot_grid(title3, p3a1, ncol = 1, rel_heights = c(0.1, 1))
title4 <- ggdraw() +
    draw_label("Model 3B: Binned (Best BIC)")
p3b1 <- plot_grid(pg, ph, ncol = 2, align = "h", axis = "b")
p3b <- plot_grid(title4, p3b1, ncol = 1, rel_heights = c(0.1, 1))
p3a
p3b

palette <- brewer.pal(n = 12, name = "Paired")
mmps(model_1, layout = c(3, 3), grid = FALSE, col.line = palette[c(2,6)],
     main = "Model 1: Stepwise Untransformed: Marginal Model Plots")
mmps(model_2, layout = c(3, 4), grid = FALSE, col.line = palette[c(2,6)],
     main = "Model 2: Stepwise Transformed: Marginal Model Plots")
```

```r
model_3_aic_for_mmps <- glm(formula(model_3_aic$BestModel), family = "binomial",
                            data = train_df2)
mmps(model_3_aic_for_mmps, layout = c(3, 3), grid = FALSE, col.line = palette[c(2,6)],
     main = "Model 3A: Binned: Best AIC: Marginal Model Plots", ylab = "target")
model_3_bic_for_mmps <- glm(formula(model_3_bic$BestModel), family = "binomial",
                            data = train_df2)
mmps(model_3_bic_for_mmps, layout = c(2, 3), grid = FALSE, col.line = palette[c(2,6)],
     main = "Model 3B: Binned: Best BIC: Marginal Model Plots", ylab = "target")
hlstat1 <- hltest(model_1, verbose = FALSE)
hlstat2 <- hltest(model_2, verbose = FALSE)
hlstat3a <- hltest(model_3_aic$BestModel, verbose = FALSE)
hlstat3b <- hltest(model_3_bic$BestModel, verbose = FALSE)
models <- c("Model 1: Stepwise Untransformed",
            "Model 2: Stepwise Transformed",
            "Model 3A: Binned (Best AIC)",
            "Model 3B: Binned (Best BIC)")
hl_tbl <- as.data.frame(cbind(models, rbind(hlstat1[2:4], hlstat2[2:4],
                                            hlstat3a[2:4], hlstat3b[2:4])))
cols <- c("Model", "HL Statistic", "DoF", "P Value")
colnames(hl_tbl) <- cols
knitr::kable(hl_tbl, format = "simple")

par(mfrow=c(2,2))
par(mai=c(.3,.3,.3,.3))
roc1 <- roc(train_df_mod1$target, train_df_mod1$predprob, plot = TRUE,
            print.auc = TRUE, show.thres = TRUE)
title(main = "Model 1: ROC")
roc2 <- roc(train_df_mod2$target, train_df_mod2$predprob, plot = TRUE,
            print.auc = TRUE, show.thres = TRUE)
title(main = "Model 2: ROC")
roc3a <- roc(train_df_mod3a$target, train_df_mod3a$predprob, plot = TRUE,
            print.auc = TRUE, show.thres = TRUE)
title(main = "Model 3A: ROC")
roc3b <- roc(train_df_mod3b$target, train_df_mod3b$predprob, plot = TRUE,
            print.auc = TRUE, show.thres = TRUE)
title(main = "Model 3B: ROC")

pred1_df <- as.data.frame(predprob1) |> mutate(predicted=as.factor(ifelse(predprob1>0.5,1,0))) |>select
pred2_df <- as.data.frame(predprob2) |> mutate(predicted=as.factor(ifelse(predprob2>0.5,1,0))) |>select
pred3a_df <- as.data.frame(predprob3a) |> mutate(predicted=as.factor(ifelse(predprob3a>0.5,1,0))) |>sel
pred3b_df <- as.data.frame(predprob3b) |> mutate(predicted=as.factor(ifelse(predprob3b>0.5,1,0))) |>sel

model_1_cm <- confusionMatrix(pred1_df$predicted,reference=train_df$target, positive='1')
model_2_cm <- confusionMatrix(pred2_df$predicted,reference=train_df$target, positive='1')
model_3a_cm <- confusionMatrix(pred3a_df$predicted,reference=train_df$target, positive='1')
model_3b_cm <- confusionMatrix(pred3b_df$predicted,reference=train_df$target, positive='1')

model_1_cm$table

model_2_cm$table
model_3a_cm$table
model_3b_cm$table
```

```r
preds <- as.data.frame(cbind(model_1_cm$byClass,model_2_cm$byClass,model_3a_cm$byClass,model_3b_cm$byCla
colnames(preds) <-c('Model 1','Model 2','Model 3a','Model 3b')
knitr::kable(preds, format = "simple")

par(mfrow=c(3,4))
par(mai=c(.3,.3,.3,.3))
variables <- names(test_df)
for (i in 1:(length(variables)-1)) {
    if (variables[i] %in% factors){
        hist(as.numeric(test_df[[variables[i]]]), main = variables[i],
            col = "lightblue")
    }else{
        hist(test_df[[variables[i]]], main = variables[i], col = "lightblue")
    }
}
eval_pred <- predict(model_2,test_df_trans,type = "response")
as.data.frame(eval_pred) |> mutate(predictions=ifelse(eval_pred>=0.5,1,0)) |> group_by(predictions) |> s
```