MSDS6372 Project 2 - Osteoporosis in Women

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Objective 1 - EDA and logistic regression model

Introduction

The Global Longitudinal Study of Osteoporosis in Women (GLOW) (2005-2014) was a prospective cohort study of physician practices in the provision of prophylaxis and treatment against osteoporotic fractures. The goal of this research was to improve understanding of the risk and prevention of osteoporosis-related fractures among female residents of 10 countries who were 55 years of age and older. GLOW enrolled over 60,000 women through over 700 physicians in 10 countries, and conducted annual follow-up for up to 5 years through annual patient questionnaires.

The aim of the GLOW study was to collect uniform data to help describe the distribution of risk factors for osteoporosis-related fracture. This analysis uses one dataset from this study to try to predict a fracture using these risk factors.

Data Description

The data set provided is about predicting whether a woman with osteoporosis will have another bone fracture. Of course getting a bone fracture is somewhat circumstantial, but with this disease every day life could trigger a break if the progression of the disease is strong.

The dataset included a total of 14 variables: 3 ID variables which tell us the subject, doctor and physical location of each record, 4 continuous variables (BMI, Weight, Height, and Age), 6 categorical variables (PRIORFRAC, PREMENO, MOMFRAC, PREMEO, MOMFRAC, ARMASSIST, SMOKE, RATERISK), and the response (FRACTURE). We were unable to find a mapping the subjects with their location to understand the mix of countries represented.

We have 500 subjects in the dataset of which 33% of the subjects have/had fractures.

Missing values were not detected in dataset. Special characters were removed from column headings. What we know/don't know about the sample (500)

Exploratory Analysis

Assumptions

This is a prospective study which means it's a study over time of a group of similar individuals who differ with respect to certain factors under a study and how these factors affect rates of a certain outcome (Fracture vs No-Fracture) Linearity - Independence of errors - Based on SUB_ID(Subject ID) we confirm each record is an independent sample. Multicollinearity - Weight and BMI are highly correlated but we will remove one from the analysis.

```
GLOW dataset:

Variable Name Type   #Unique

     SUB_ID  integer  500 - Identification Code (1 - n)
    SITE_ID  integer    6 - Study Site (1 - 6)
     PHY_ID  integer  127 - Physician ID code (128 unique codes)
 PRIORFRAC*   factor    2 - History of Prior Fracture (1: No, 2: Yes)
        AGE  integer   36 - Age at Enrollment (Years)
     WEIGHT  numeric  128 - Weight at enrollment (Kilograms)
     HEIGHT  integer   34 - Height at enrollment (Centimeters)
        BMI  numeric  409 - Body Mass Index (Kg/m^2)
```

```
  PREMENO*   factor     2 - Menopause before age 45 (1: No, 2: Yes)
  MOMFRAC*   factor     2 - Mother had hip fracture (1: No, 2: Yes)
ARMASSIST*   factor     2 - Arms are needed to stand from a chair (1: No, 2: Yes)
    SMOKE*   factor     2 - Former or current smoker (1: No, 2: Yes)
 RATERISK*   factor     3 - Self-reported risk of fracture (1: Less, 2: Same, 3: Greater)
 FRACSCORE  integer    12 - Fracture Risk Score (Composite Risk Score)
 FRACTURE*   factor     2 - Any fracture in first year (1: No, 2: Yes)
```

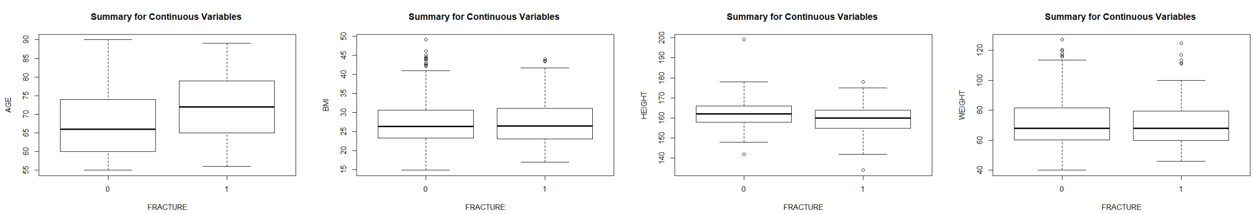


Figure 1 - Boxplots for Continuous Variables AGE, BMI, HEIGHT, WEIGHT

In Figure 1, we see the boxplots for the continous variables AGE, WEIGHT, HEIGHT, BMI.

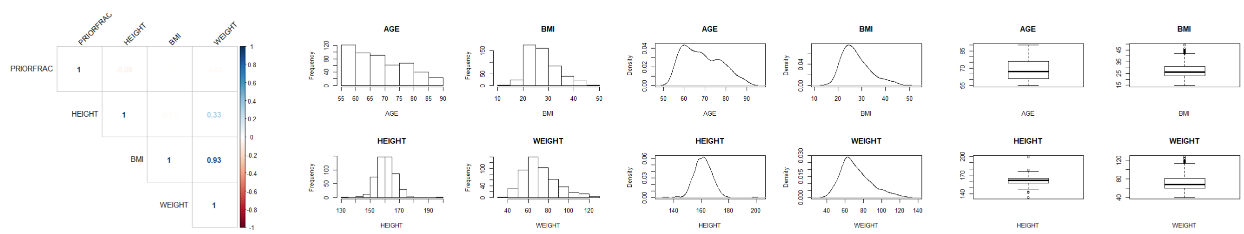


Figure 2 - Correlation, and Density plots for Continuous Variables AGE, BMI, HEIGHT, WEIGHT

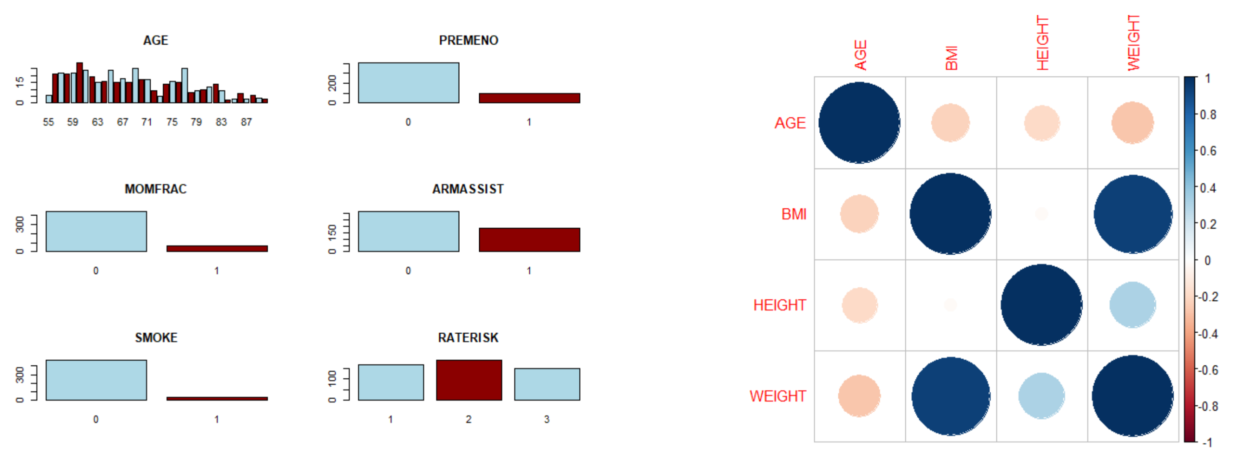


Figure 3 - Barplot (occurrances) and Multivariate Plots for Categorical and Continuous Variables

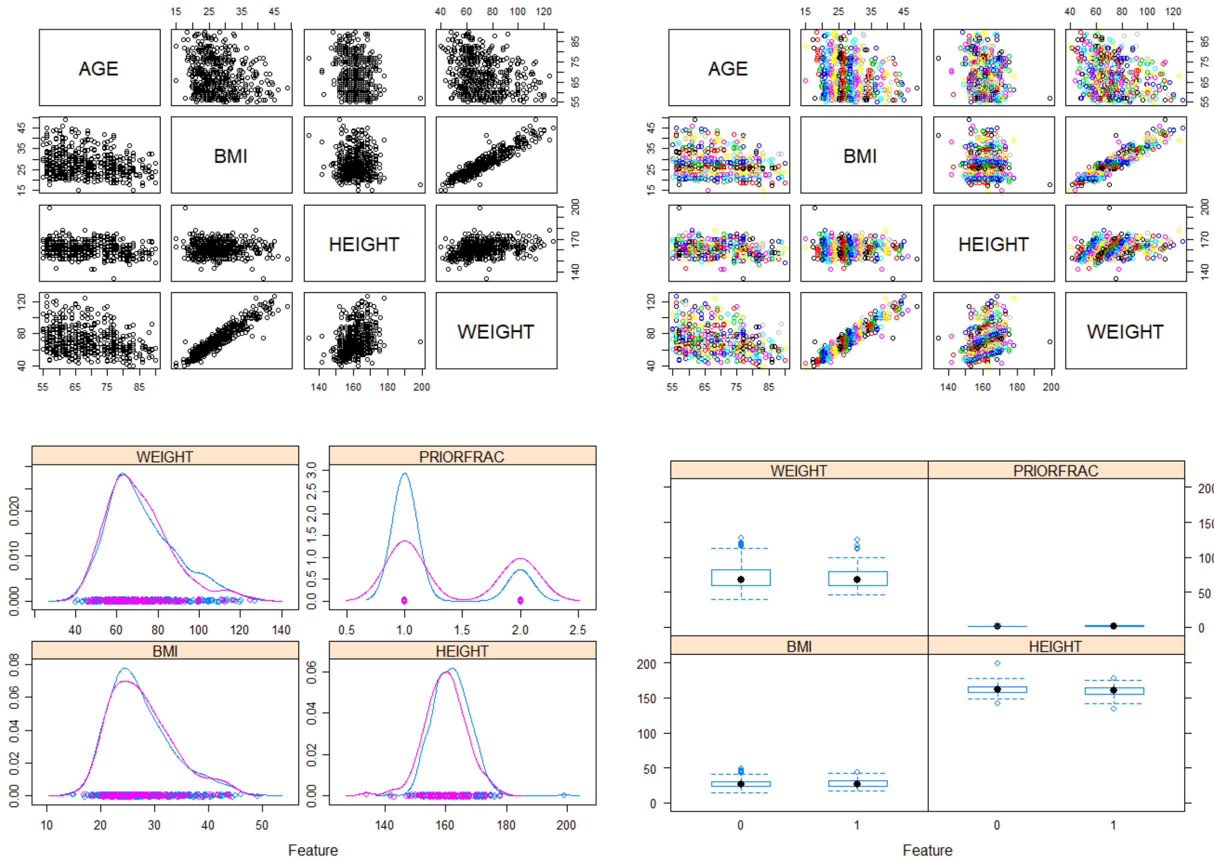


Figure 4 - Scatterplots

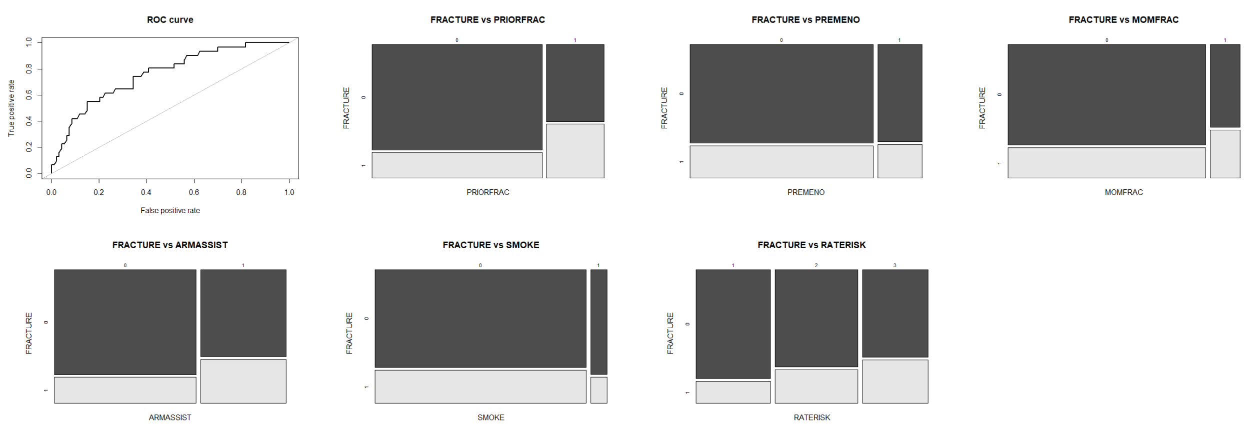


Figure 5 - ROC and 2-way Tables

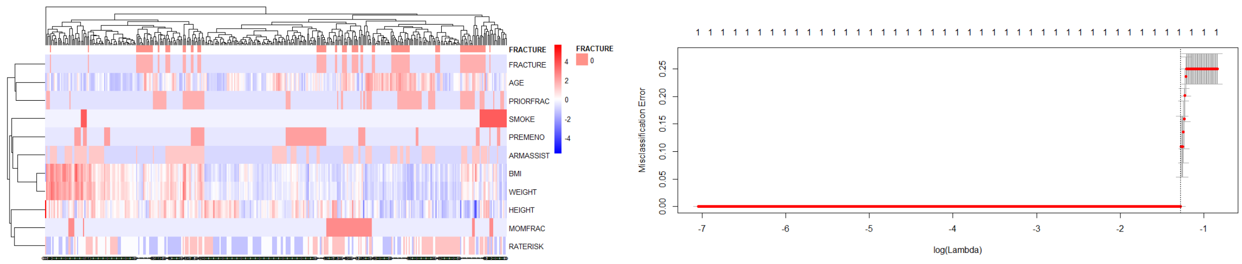


Figure 6 - Clustering

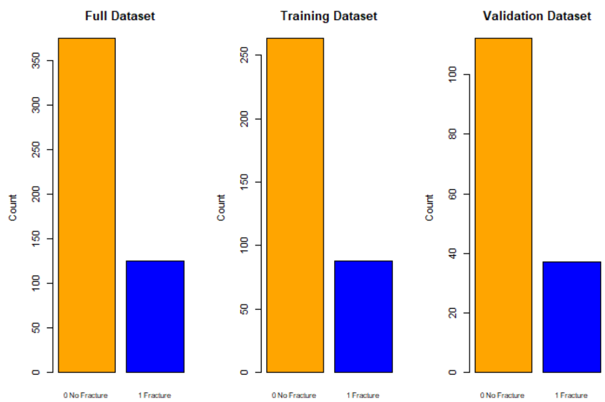


Figure 7 - Fracture Counts

Restatement of Problem and the overall approach to solve it.

Logistic regression is used to describe data and to explain the relationship between one dependent binary variable, in this case whether a woman will have a fracture related to osteoporosis, with one or more continuous or categorical variables. Using different modeling techniques, we will try to predict whether a sample will have a fracture related event.

Simple Logistic Model Selection

Model Considerations

For the purpose of feature selection for the simple logistic model, a lasso+logistic regression with cross validation (for 1000 lambda values) was performed on training data set in order to obtain the penalty value(lambda) that results in minimum misclassification rate. The result of this procedure is present in figure 7 below:

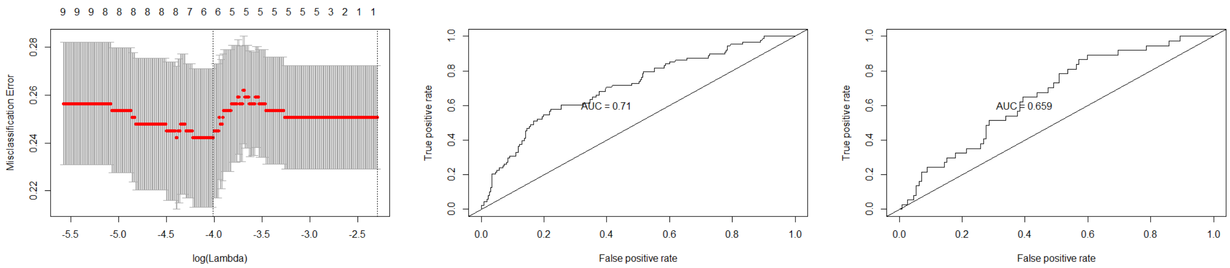


Figure 8 - Simple Logistic Regression lasso+logistic regression

```
Then the lasso+logistic model was rerun with best value of lambda obtained(lambda.min) from previous pro
12 x 1 sparse Matrix of class "dgCMatrix"
                                  1
(Intercept)                1.52902669
trainingData.AGE           0.03598544
trainingData.WEIGHT        .
trainingData.HEIGHT       -0.03340871
trainingData.BMI           .
trainingData.PRIORFRAC1    0.15180349
trainingData.PREMENO1      .
trainingData.MOMFRAC1      0.04035537
trainingData.ARMASSIST1    0.52512963
trainingData.SMOKE1        .
trainingData.RATERISK.L    0.33991586
trainingData.RATERISK.Q    .
```

Next, we went ahead and run simple logistic regression using this feature set of AGE, HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST and RATERISK.

Model Assumptions:

Assumption of binary response while running binary logistic regression.

The dependent variable is a factor with two defined levels (0 = No, 1 = Yes).

Assumption of independence among observations.

Since the method for selecting the subjects for this study and then formulation of given dataset from all of such population is not fully known, caution must be taken while generalizing the results from this analysis. Potential biases could be present among observations as selection bias, recall bias, serial and spatial correlation etc could be present. Generalizing the results from this analysis to whole population of such subjects is to be based upon assumption that subjects in given dataset are as representative of the underlying population as a random samples from such population are. For the purpose of our analysis, we assume observations in our dataset are independent of one another and proceed with the analysis.

Assumption of linearity of independent continuous predictors and their respective log odds

A scatter plot between two continuous predictors: AGE and HEIGHT as identified to be used in simple logistic model and their respective log odds is plotted and present as below.

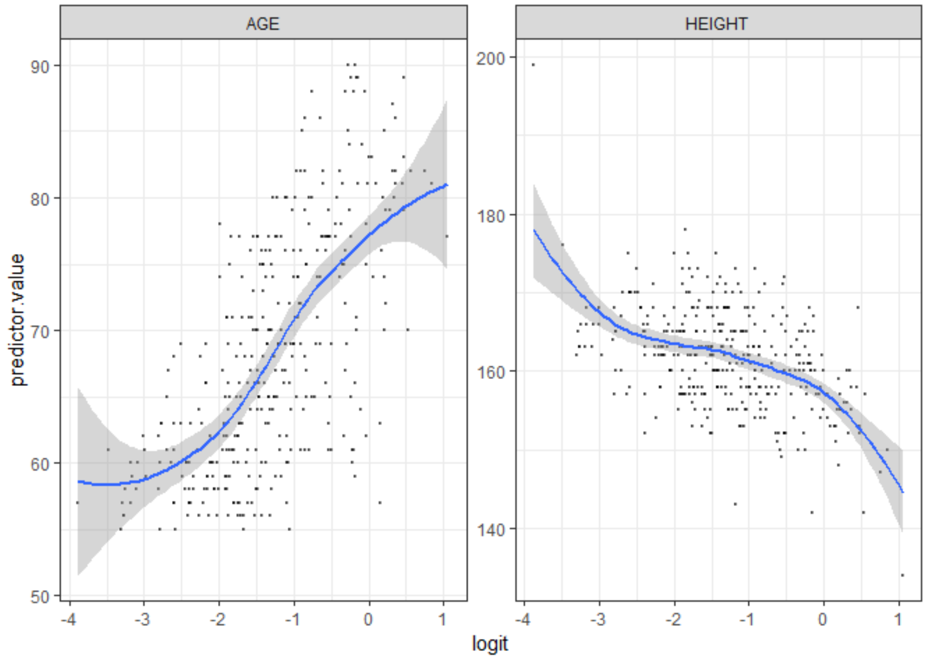


Figure 9 - Scatter Plot between AGE and HEIGHT and their log odds

Simple Logistic Model Fit:

The overall logistic regression model using selected variables came out significant and found AGE, HEIGHT, ARMASSIST and RATERISK as significant predictors at alpha=0.05 level for determining probability of getting a fracture in first year(response variable). The model output is as below:

```
Call:
glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
    ARMASSIST + RATERISK, family = binomial(link = "logit"),
    data = trainingData)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5491  -0.7377  -0.5763   0.2298   2.2214

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.33365    3.80104   0.877  0.38047
AGE          0.04347    0.01578   2.755  0.00587 **
HEIGHT      -0.04881    0.02165  -2.254  0.02418 *
PRIORFRAC1   0.22281    0.30097   0.740  0.45912
MOMFRAC1     0.33522    0.38263   0.876  0.38097
ARMASSIST1   0.68418    0.27861   2.456  0.01406 *
RATERISK.L   0.50762    0.24656   2.059  0.03951 *
RATERISK.Q  -0.06727    0.22219  -0.303  0.76209
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)
```

```
    Null deviance: 395.31  on 350  degrees of freedom
Residual deviance: 355.55  on 343  degrees of freedom
AIC: 371.55
```

A recursive model refinement process was performed by trying to add more variables that were not present in initial fit; and model performance in terms of AUC under ROC curve and accuracy via confusion matrix for validation dataset was assessed for each subsequent model. No subsequent model fit resulted in significant gains in terms of improved performance parameters. In fact, some resulted in decrease in accuracy on validation set as they were just acting as noise and didn't provide any valuable information about the response variable. Hence, initial fit was chosen as best fit and assessed further.

On the initial model fit, VIFs and influential observation analysis was then performed and results can be seen below as:

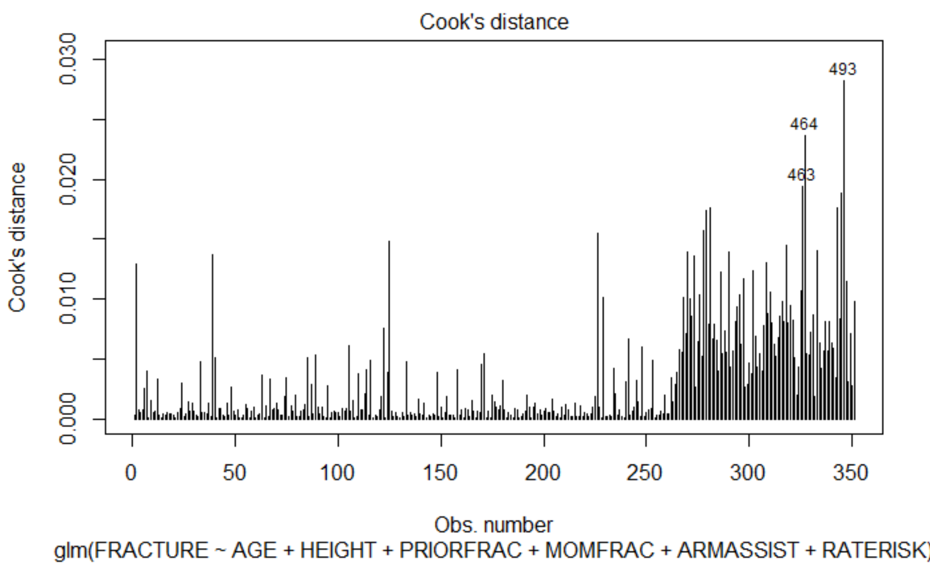


Figure 10 - Logistic Regression - Cook's D

```
              GVIF Df GVIF^(1/(2*Df))
AGE       1.209972  1        1.099987
HEIGHT    1.084342  1        1.041317
PRIORFRAC 1.172110  1        1.082640
MOMFRAC   1.010590  1        1.005281
ARMASSIST 1.124261  1        1.060312
RATERISK  1.096380  2        1.023270
```

As seen from above results that multiclonality is not seen and no substantially influential observation is found as seen from Cook's d plot. Hence, we proceeded with current model for model equation formulation and coefficients interpretations.

Model Equation

$log(\pi) = 3.33365 + 0.04347$ * AGE - 0.04881 * HEIGHT + 0.22281 * PRIORFRAC + 0.33522 * MOMFRAC + 0.68418 * ARMASSIST + 0.50762 * RATERISK_2 - 0.06727 * RATERISK_3

```
Next, we converted model coefficients and their respective 95% Confidence Intervals to Normal Scale and
```

```
            ODDs_Ratio      2.5 %        97.5 %
(Intercept) 28.0403767 0.0172620 5.378401e+04
AGE          1.0444253 1.0128322 1.077662e+00
HEIGHT       0.9523628 0.9118527 9.929059e-01
PRIORFRAC1   1.2495774 0.6857875 2.237992e+00
MOMFRAC1     1.3982464 0.6449924 2.917750e+00
ARMASSIST1   1.9821443 1.1469582 3.428352e+00
RATERISK.L   1.6613370 1.0283916 2.713240e+00
RATERISK.Q   0.9349462 0.6060378 1.451499e+00
```

Interpretation of the Coefficients:

For AGE: All the other variables being constant, for every one-year increase in age of women, the odds of being getting a fracture in first year (versus not getting a fracture in first year) increases by a factor of 1.04(4% increase). The 95% Confidence Interval for this multiplicative factor is from 1.01(1% increase) to 1.08(8% increase).

For HEIGHT: All the other variables being constant, for every one unit increase in height of women, the odds of being getting a fracture in first year (versus not getting a fracture in first year) decreases by a factor of 0.95(5% decrease). The 95% Confidence Interval for this multiplicative factor is from 0.91(9% decrease) to 0.99(1% decrease).

** All the below coefficients are of format: The estimated odds for Person X with/without characteristic are M times the odds (of developing fracture in first year), for another Person Y without/with that characteristic. **

For PRIORFRAC: All the other variables being constant, the estimated odds for a woman, who has history of prior fracture, are 1.25 (25% more) times the odds of having fracture again in first year, for a woman who didn't have prior history of fracture. The 95% Confidence Interval for this estimated odds ratio is from 0.69 times to 2.23 times.

For MOMFRAC: All the other variables being constant, the estimated odds for a woman, whose mother had hip fracture, are 1.40 (40% more) times the odds of having fracture in first year, for a woman whose mother didn't have hip fracture. The 95% Confidence Interval for this estimated odds ratio is from 0.64 times to 2.91 times.

For ARMASSIST: All the other variables being constant, the estimated odds for a woman, who needed arms to stand from a chair, are 1.98 (98% more) times the odds of having fracture in first year, for a woman who didn't need arms to stand from a chair. The 95% Confidence Interval for this estimated odds ratio is from 1.15 times to 3.43 times.

For RATERISK.2: All the other variables being constant, the estimated odds for a woman, who self-reported that her risk for developing fracture is same as others of the same age, are 1.66 (66% more) times the odds of having fracture in first year, for a woman who self-reported that her risk for developing fracture is less than others of the same age. The 95% Confidence Interval for this estimated odds ratio is from 1.03 times to 2.71 times.

For RATERISK.3: All the other variables being constant, the estimated odds for a woman, who self-reported that her risk for developing fracture is greater than others of the same age, are 0.93 (7% less) times the odds of having fracture in first year, for a woman who self-reported that her risk for developing fracture is less than others of the same age. The 95% Confidence Interval for this estimated odds ratio is from 0.61 times to 1.45 times.

Model Assessment:

Model performance was assessed on validation data using following parameters:

1. AUC under ROC curve

2. Overall Accuracy, Sensitivity and Specificity values obtained from confusion matrix.

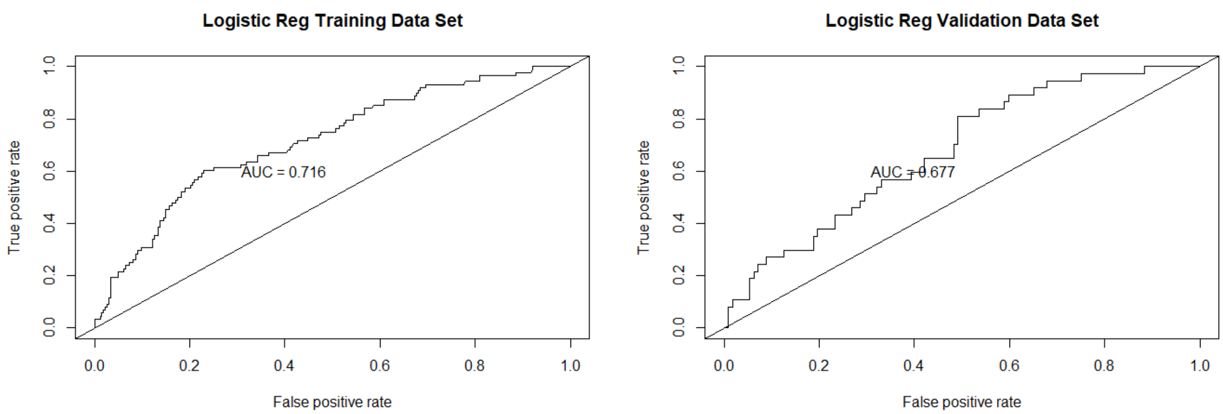


Figure 10 - Simple Logistic Regression - Performance

```
## Confusion Matrix and Statistics
##
## Reference
## Prediction 0 1
## 0 108 35
## 1 4 2
##
## Accuracy : 0.7383
## 95% CI : (0.66, 0.8068)
## No Information Rate : 0.7517
## P-Value [Acc > NIR] : 0.6866
##
## Kappa : 0.0255
## Mcnemar's Test P-Value : 1.556e-06
##
## Sensitivity : 0.96429
## Specificity : 0.05405
## Pos Pred Value : 0.75524
## Neg Pred Value : 0.33333
## Prevalence : 0.75168
## Detection Rate : 0.72483
## Detection Prevalence : 0.95973
## Balanced Accuracy : 0.50917
##
## 'Positive' Class : 0
##
```

Figure 11 - Simple Logistic Regression - Confusion Matrix

As seen from above ROC curves and confusion matrix:

1. Training set AUC is 71.6% and that for validation data set is about 67.7%. This is understandable since model was created using data training data set.
2. Overall Accuracy of the model is at 74.5% with high sensitivity 94.64% but very low specificity 13.51 %.
3. There relative low values of overall AUC and accuracy could be due to:

   a. Lack of complexity in the current model (in terms of higher order terms, transformations, interactions) etc.

   b. The available feature set and number of samples available are not sufficient enough to accurate model most of the trends in actual population data.

   c. Class imbalance that is present in original, training and validation data set. Especially, the number of true positive cases are very much under represented in both the training and test datasets and this could be the cause of low specificity values obtained from this model.
4. Specificity for the model could be improved by lower the cutoff for classification from its initial value of 0.5. This should be warranted since cost of not predicting true positive outweighs cost of predicting false positive in the current situation.

Final conclusions from the analysis of Objective 1

To improve the accuracy and AUC for the model, we would next increase complexity in current model by adding interactions to it.

Objective 2 - Additional Competing Models

- The performance of the Simple Logistic Regression model developed earlier has performance characteristics described in Figure X and Figure X with the AUC under ROC curve and Confusion Matrix.

Logistic Regression Model with Interactions

Model Considerations:

Since simple model was lacking in terms of complexity, hence interaction terms were added to the initial simple model in the hope of improving its predictive capability. After the recursive EDA process, three potential interactions were found from the dataset: AGE * PRIORFRAC, MOMFRAC * ARMASSIST and AGE * RATERISK. These could improve model performance as seen from below graphs that distribution for AGE variable among PRIOR FRAC groups is different for FRACTURE and NON-FRACTURE group and same is observed for MOMFRAC and ARMASSIST for levels of FRACTURE group as seen below:

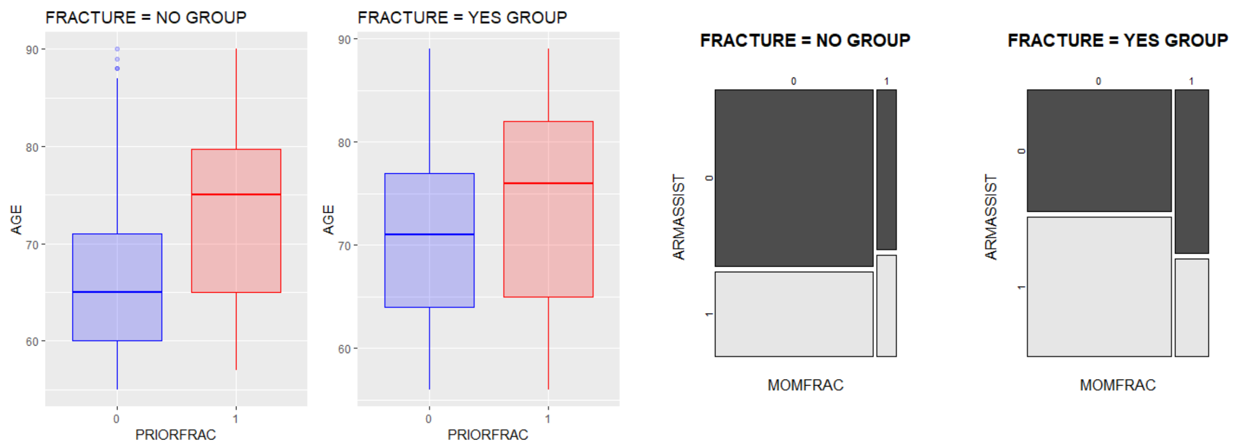


Figure 12 - Logistic Regression - Interactions

Model Assumptions:

Model assumptions are satisfied as we have seen from assumption section in simple logistic model section.

Model Fit:

The overall logistic regression model using selected variables and interactions came out significant. But, since interactions were added, multicollinearity is created and VIF for the model increased as seen below:

```
                         GVIF Df GVIF^(1/(2*Df))
AGE                  1.997142  1        1.413203
HEIGHT               1.102446  1        1.049975
PRIORFRAC           67.052577  1        8.188564
MOMFRAC              1.872604  1        1.368431
ARMASSIST            1.292878  1        1.137048
RATERISK          4440.469420  2        8.163140
AGE:PRIORFRAC       71.017561  1        8.427192
AGE:RATERISK      4423.340582  2        8.155256
MOMFRAC:ARMASSIST    2.037634  1        1.427457
```

This issue was dealt by centering the AGE variable and re-running the model. The VIFs came back to normal values after centering on AGE variable was performed as seen below from VIFs after centering:

```
AGE                1.997142  1        1.413203
HEIGHT             1.102446  1        1.049975
PRIORFRAC          1.293722  1        1.137419
MOMFRAC            1.872604  1        1.368431
ARMASSIST          1.292878  1        1.137048
RATERISK           1.354533  2        1.078816
AGE:PRIORFRAC      2.076106  1        1.440870
AGE:RATERISK       1.295266  2        1.066816
MOMFRAC:ARMASSIST  2.037634  1        1.427457
```

The model output is as below:

```
glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
    ARMASSIST + RATERISK + AGE:PRIORFRAC + RATERISK:AGE + MOMFRAC:ARMASSIST,

    family = binomial(link = "logit"), data = trainingData)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5521  -0.7592  -0.5543   0.2845   2.3802

Coefficients:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)          6.25924    3.51520   1.781  0.07497 .
AGE                  0.60346    0.18440   3.273  0.00107 **
HEIGHT              -0.04913    0.02191  -2.242  0.02495 *
PRIORFRAC1           0.38979    0.31394   1.242  0.21438
MOMFRAC1             0.74167    0.50795   1.460  0.14426
ARMASSIST1           0.80585    0.29990   2.687  0.00721 **
RATERISK.L           0.58312    0.26591   2.193  0.02831 *
RATERISK.Q          -0.13762    0.23352  -0.589  0.55566
AGE:PRIORFRAC1      -0.45140    0.27996  -1.612  0.10688
AGE:RATERISK.L      -0.13870    0.24978  -0.555  0.57869
AGE:RATERISK.Q       0.14622    0.22380   0.653  0.51355
MOMFRAC1:ARMASSIST1 -0.74229    0.76220  -0.974  0.33011
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)
```

Although no interaction was significant at alpha=0.05 level, interaction between AGE*PriorFrac looks promising (p-value = 0.10688). Hence, using the above model for model equation formulation.

Model Equation:

Model Assessment.

Model performance was assessed on validation data using following parameters:

1. AUC under ROC curve
2. Overall Accuracy, Sensitivity and Specificity values obtained from confusion matrix.

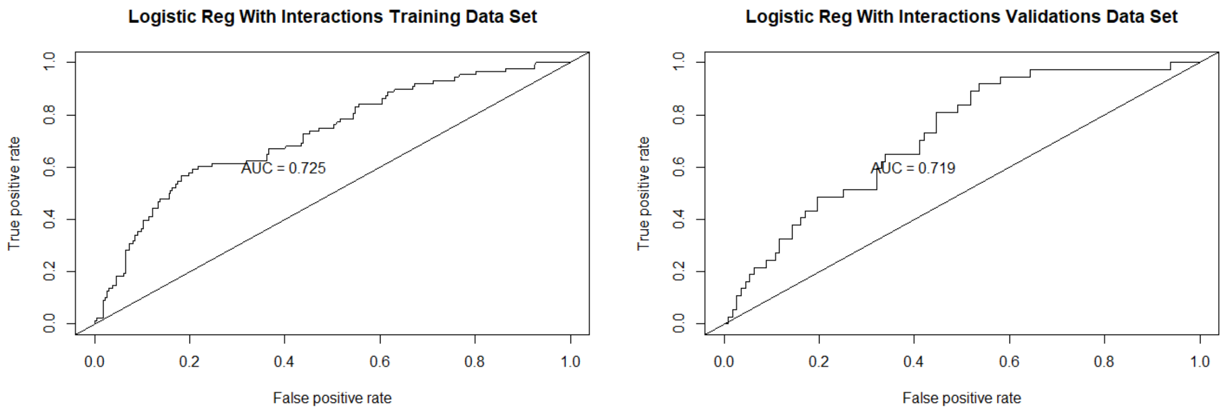


Figure 13 - Logistic Regression with Interactions - Performance

```
## Confusion Matrix and Statistics
##
## Reference
## Prediction 0 1
## 0 105 30
## 1 7 7
##
## Accuracy : 0.7517
## 95% CI : (0.6743, 0.8187)
## No Information Rate : 0.7517
## P-Value [Acc > NIR] : 0.5440183
##
## Kappa : 0.16
## Mcnemar's Test P-Value : 0.0002983
##
## Sensitivity : 0.9375
## Specificity : 0.1892
## Pos Pred Value : 0.7778
## Neg Pred Value : 0.5000
## Prevalence : 0.7517
## Detection Rate : 0.7047
## Detection Prevalence : 0.9060
## Balanced Accuracy : 0.5633
##
## 'Positive' Class : 0
##
```

Figure 14 - Logistic Regression with Interactions - Confusion Matrix

As seen from above ROC curves and confusion matrix:
1. Training set AUC is 72.5% and that for validation data set is about 72.2%. This is understandable since model was created using data training data set.
2. Overall Accuracy of the model is at 75.17% with high sensitivity 93.75% but low specificity 18.92 %.
3. This model performed little better over simple model with AUC increasing from 67.7% to 72.2% and overall accuracy increasing from 74.5% to 75.17%.
4. These slight increases in accuracy are consistent with the outcome received from model fit that none of

the interactions added were highly significant. So, added complexity did increase the overall AUC by about 5 % but was not improved performance significantly.
5. There relative low values of overall AUC and accuracy could be due to:
a. Still Missing complexity in the current model (in terms of higher order terms, transformations, further interactions) etc. b. The available feature set and number of samples available are not sufficient enough to accurate model most of the trends in actual population data.
c. Class imbalance that is present in original, training and validation data set. Especially, the number of true positive cases are very much underrepresented in both the training and test datasets and this could be the cause of low specificity values obtained from this model.
6. Specificity for the model could be improved by lower the cutoff for classification from its initial value of 0.5. This should be warranted since cost of not predicting true positive outweighs cost of predicting false positive in the current situation.

Random Forest and Conditional Random Forest Models

Model Considerations.

To further account for the remaining complexity and improve model predictive ability, we ran the ensemble based random forest model. We ran both flavors of random forest model that is normal one and conditional random forest one. Normal random forest model is biased towards predictors with more levels since knowing these would decrease the entropy the most and provide more information. Hence, normal random forest favors predictors with more levels. Whereas, conditional random forest takes this into account and produce more unbiased trees than normal random forest by assigning more weights to certain nodes at the time of aggregation.

A recursive process was performed to tune the random forest model for ntee, mtry and maxnodes parameters. Without pruning the tree length, random forest overfitted on our relatively small training data set but performed poorly as compared to logistic regression on validation data set as seen below:

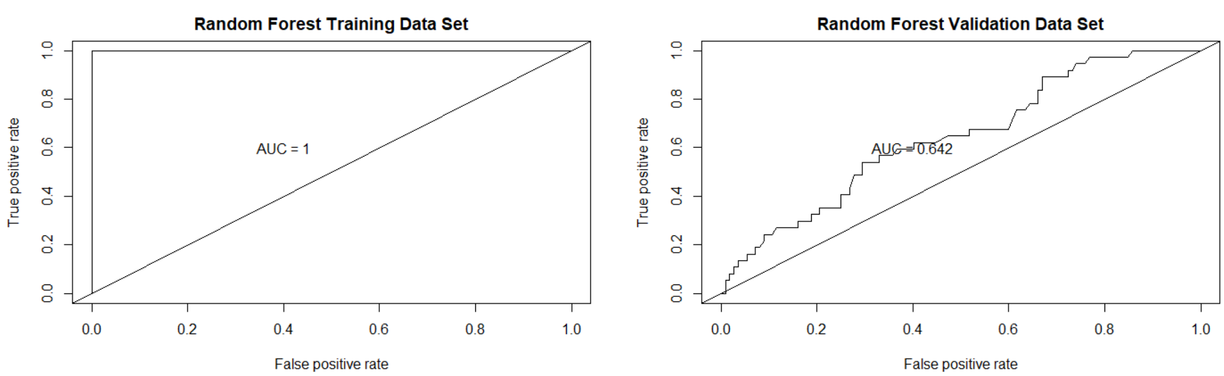


Figure 15 - Random Forests - Performance

Maxnodes parameter along with ntree and mtry parameters was adjusted so as to achieve better performance and then we proceeded with fitting the random forest model.

Model Assumptions:

Since random forest is a non-parametric test which relies upon ensemble techniques, it doesn't require model assumptions to be satisfied before running the model.

Model Fit.

```
Call:
 randomForest(formula = FRACTURE ~ ., data = trainingData, mtry = 4,      ntree = 500, maxnodes = 12, i
```

```
                Type of random forest: classification
                      Number of trees: 500
No. of variables tried at each split: 4

        OOB estimate of  error rate: 24.79%
Confusion matrix:
    0 1 class.error
0 260 3  0.01140684
1  84 4  0.95454545
```

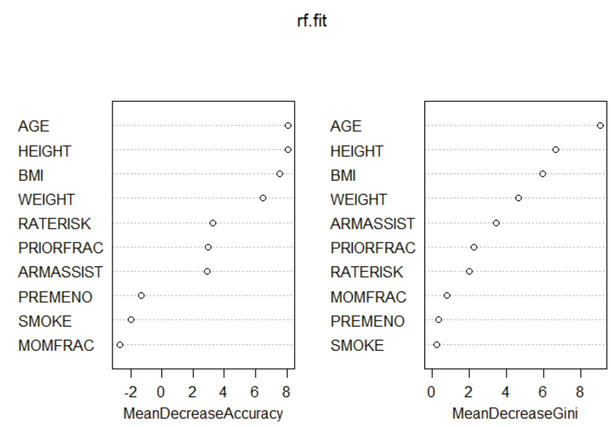


Figure 16 - Random Forest

As predicted, random forest is assigning more importance to predictors with more levels.

Model Assessment:

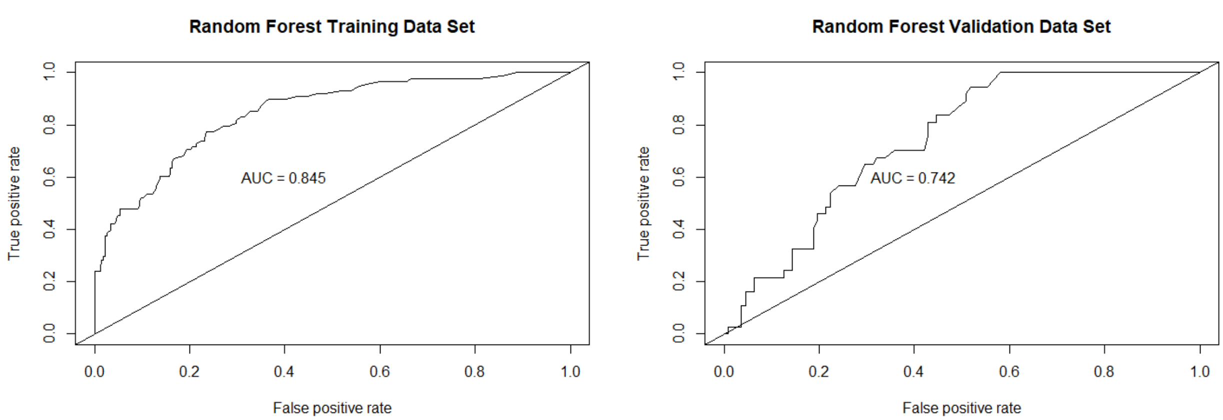


Figure 17 - Conditional Random Forests

```
Confusion Matrix and Statistics

          Reference
Prediction   0   1
         0 111  37
         1   1   0
```

```
               Accuracy : 0.745
                 95% CI : (0.6672, 0.8128)
    No Information Rate : 0.7517
    P-Value [Acc > NIR] : 0.6175

                  Kappa : -0.0132
 Mcnemar's Test P-Value : 1.365e-08

            Sensitivity : 0.9911
            Specificity : 0.0000
         Pos Pred Value : 0.7500
         Neg Pred Value : 0.0000
             Prevalence : 0.7517
         Detection Rate : 0.7450
   Detection Prevalence : 0.9933
      Balanced Accuracy : 0.4955
```

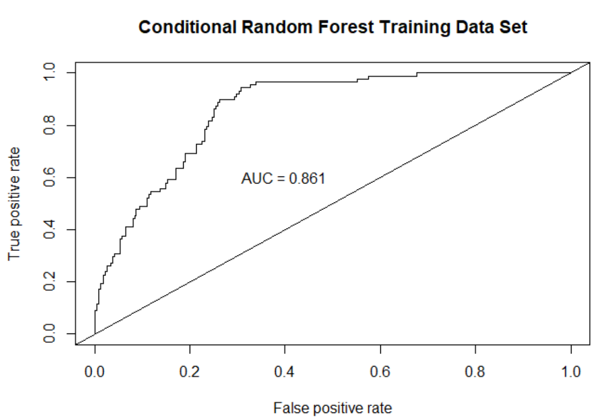
Figure 18 - Conditional Random Forest Confusion Matrix

As seen from above ROC curves and confusion matrix: 1. Random Forest model improves on overall AUC performance slightly and takes it to 74.2% as compared to logistic regression with interaction model that had 72.5% AUC. So it did model some extra remaining complexity.

2. This model performed really badly as compared to other models in classifying true positives and have specificity value of zero.

3. This could be due to the fact that our training and test datasets have slight proportion of positive cases and model is unable to capture trends in positive observations as accurately as it captured for negative observations. Small sample sizes in training and validation sets and class unbalance is appearing to contribute to this discrepancy, since random forest model is prone to overfitting when sample sizes are relatively small.

4. Conditional random forest model performed better than this model in terms of overall accuracy and specificity values as seen from below results but it suffered on overall AUC. But again, this could be caused due to random variation and biases in data sets.



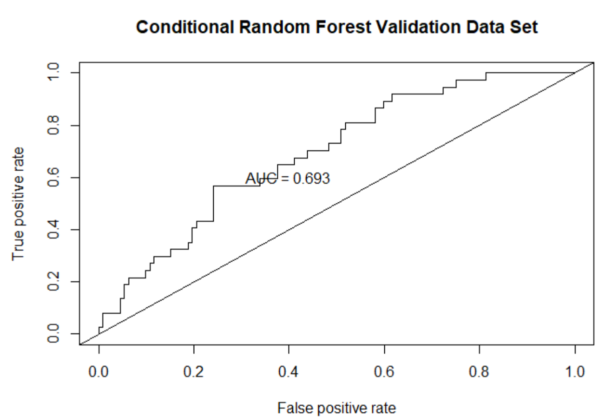


Figure 19 - Conditional Random Forest using Conditional Inference Trees

```
     Random Forest using Conditional Inference Trees

Number of trees:  500

Response:  FRACTURE
Inputs:  PRIORFRAC, AGE, WEIGHT, HEIGHT, BMI, PREMENO, MOMFRAC, ARMASSIST, SMOKE, RATERISK
Number of observations:  351

Confusion Matrix and Statistics

          Reference
Prediction   0   1
         0 106  31
         1   6   6

               Accuracy : 0.7517
                 95% CI : (0.6743, 0.8187)
    No Information Rate : 0.7517
    P-Value [Acc > NIR] : 0.544

                  Kappa : 0.1403
 Mcnemar's Test P-Value : 7.961e-05

            Sensitivity : 0.9464
            Specificity : 0.1622

Variable Importance as predicted by conditional random forest

AGE        HEIGHT     ARMASSIST           BMI     PRIORFRAC        WEIGHT      RATERISK         SMOKE
```

Linear Discriminant Analysis Model

Model Considerations.

LDA can only be done with continuous predictors and in our dataset we have only four continuous predictors: AGE, HEIGHT, WEIGHT and BMI. As we have seen in EDA part that categorical variables appear to be significant in classifying the response, throwing away the information they provide could result in decrease in overall performance of the model (and BMI and WEIGHT not been so significant as seen from logistic model) as compared to rest of the models.

Model Assumptions:

Assumption of Equal Variance / CoVariance.

We computed the amount of the between-group variance that is explained by each linear discriminate. In this dataset, we tested whether the variance in each continuous variable is the same for all subjects with/without Fractures.

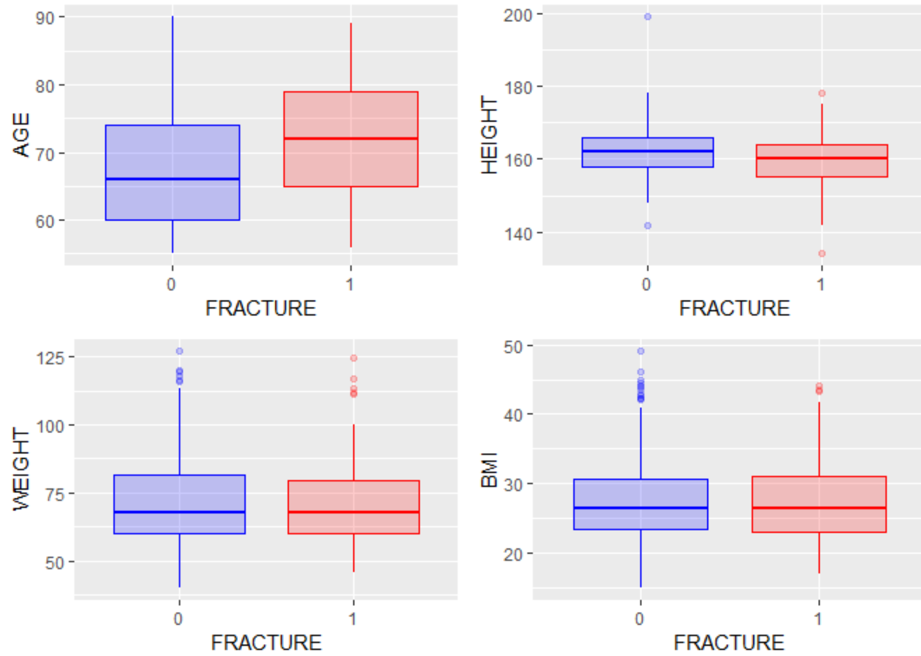


Figure 20 - LDA Equal Variance

```
Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group   1   1.522 0.2179
      498
Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group   1  0.9566 0.3285
      498
Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group   1  0.9475 0.3308
      498
Levene's Test for Homogeneity of Variance (center = median)
       Df F value Pr(>F)
group   1  0.0188 0.8911
```

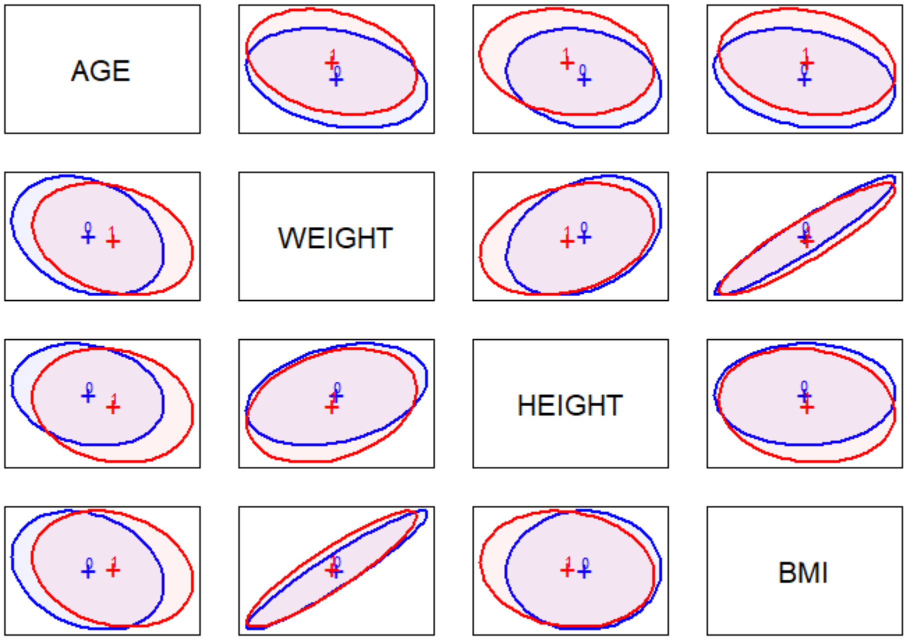


Figure 21 - LDA Ellipse Plots

From the boxplots and ellipse plots above we can didn't observe difference in spread of eclipses and axis of eclipses are fairly aligned for each pair. We also ran a Levene's Test between each predictor and response and result confirms that spread for each predictor is not differing for levels of response

Assumption of independence among observations.

Since the method for selecting the subjects for this study and then formulation of given dataset from all of such population is not fully known, caution must be taken while generalizing the results from this analysis. Potential biases could be present among observations as selection bias, recall bias, serial and spatial correlation etc could be present. Generalizing the results from this analysis to whole population of such subjects is to be based upon assumption that subjects in given dataset are as representative of the underlying population as a random samples from such population are. For the purpose of our analysis, we assume observations in our dataset are independent of one another and proceed with the analysis.

Assumption of Normality

Density plots were plotted for each predictor for both levels of response as seen below:

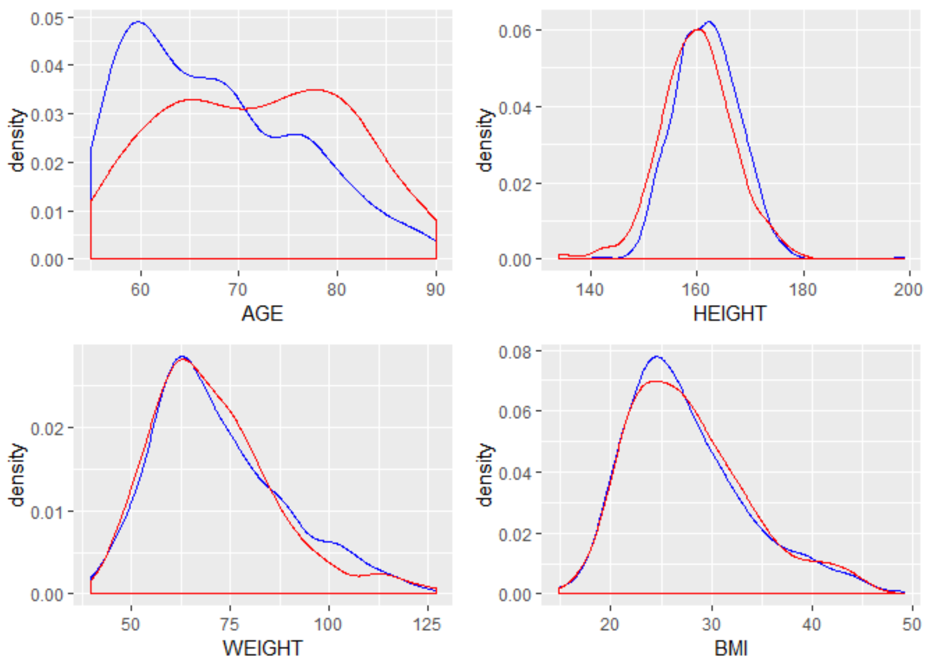


Figure 22 - LDA Density Plots

Distribution of all predictors except AGE looks sufficiently normal and have about similar spread. To check on AGE variable a QQ Plot for AGE for both levels of response variable was plotted as seen below:

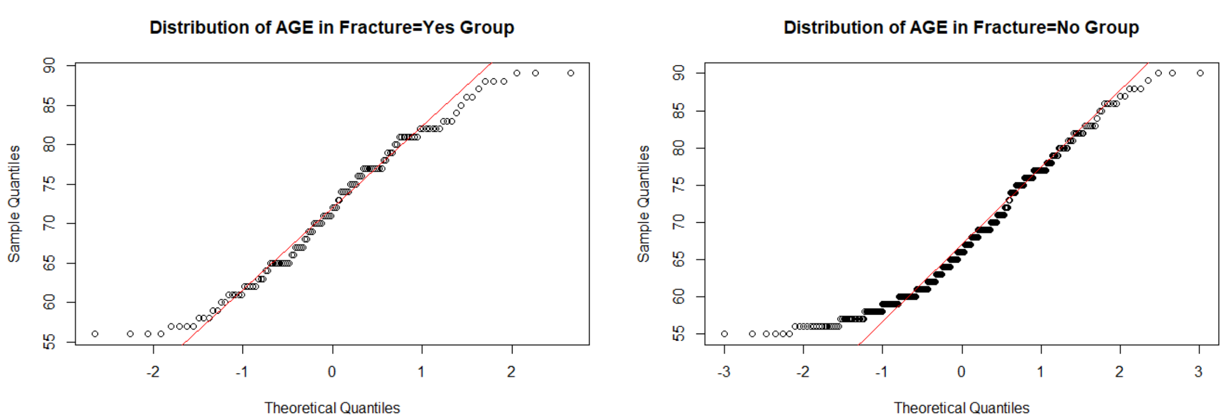


Figure 23 - LDA QQ Plots

As seen from the above QQ plots and presence of sufficient sample size, distribution of AGE looks sufficiently Normal for both levels of response variable.

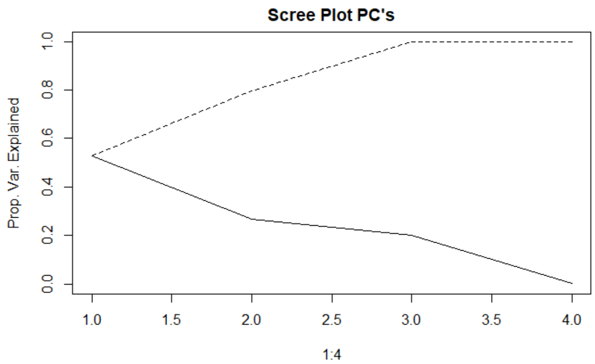
Since all the assumptions for LDA have been met, we would now go ahead and run the LDA model.

Model Fit.

Note on PCA

Our dataset had only 4 continuous predictors so PCA would not help us much in terms of dimensionality reduction. We ran initial PCA model to see if data separates out well. But as seen from below output from

Scree plot that 4 Principal Components were required to explain all variance and that's equal to number of predictors used. Also, data didn't separate out well between PC1 and PC2.



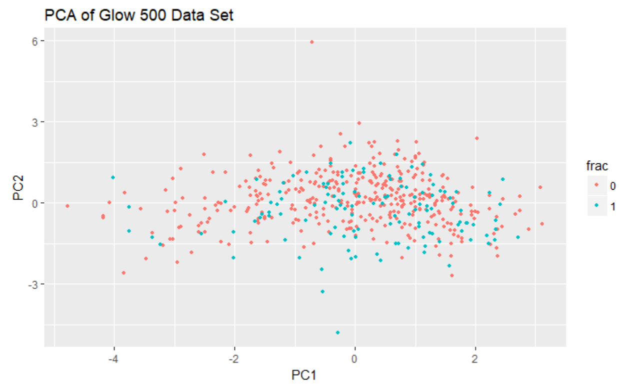


Figure 24 - LDA PCA Notes

"'

Summary table of performance

Model	Predictors	Accuracy	95% CI	Sensitivity	Specificity	AUC
Logistic Regression (logit)	7	74.5%	(66.7%, 81.3%)	94.6%	13.5%	67.8%
Logistic Regression w/Interactions (logit)	7 + 3 interactions	75.2%	(67.4%, 81.9%)	92.9%	21.6%	72.2%
Random Forest*	10	74.5%	(66.7%, 81.3%)	99.1%	0.0%	74.2%
*RF Lower Cutoff (decreasing the probability from 50% to 30%)	10	73.8%	(66%, 80.7%)	91.1%	21.6%	
Conditional Random Forest	10	75.2%	(67.4%, 81.9%)	94.6%	16.2%	69.3%
LDA	4	73.2%	(65.3%, 80.1%)	94.6%	8.1%	60.2%

Conclusion/Discussion

In summary, as seen from above table with performance metrices:

Simple logistic model suffers in terms of prediction accuracy since its not complex enough to model all trends present in dataset. Logistic regression model with interactions added did a better job in improving the overall AUC and accuracy over the simple logistic model. Random Forest increased the overall AUC but performed really badly in terms of specificity and looks to overfit the trends in dataset on true negative side and hence predicting badly on true positive side since our training/validation dataset was unbalanced in favor of true negative observations. LDA, as expected performed poorly as compared to other models in terms of overall AUC since it didn't consider categorical variables and it can be seen from EDA that most of categorical variables looked promising for separating the response. And also, two of continuous predictors: Weight and BMI were not significant as seen by the logistic model fit. Hence, all in all, in our given dataset, we think logistic model with interactions performed better than rest of the models since it didn't overfit on true negative side and had enough complexity as compared to rest of the models to make informed predictions.

Appendix ==

*** *Appendix A:* EDA - Analysis ========================

Data Set 1: Osteoporosis in Women

From Hosmer, Lemeshow, and Sturdivant (2013), Applied Logistic Regression, 3rd Edition. The Global Longitudinal Study of Osteoporosis in Women (GLOW) is an international study of osteoporosis in women aged 55 years and over. The major goals of the study are to examine prevention and treatment of fractures and distribution of risk factors among older women. Complete details on the study as well as a list of GLOW publications may be found at the Center for Outcomes Research web site, http://www.outcomes-umassmed.org/glow. There are over 60K observations in the original data set. This data set contains a sample of 500 of them. The link below is to a website with the data set and description of the variables. The data set in question is called "glow500".

https://www.umass.edu/statdata/statdata/data/glow/index.html Note: If you choose this data set, you MAY NOT use the Hosmer, Lemeshow, and Sturdivant text to help you in your analysis. You may only use Chapter 1 in order to obtain a description of the data.

Of course if you dont have the book

https://www.umass.edu/statdata/statdata/data/glow/glow.pdf provides definitions to the variables.

The Global Longitudinal Study of Osteoporosis in Women (GLOW) (2005-2014) was a prospective cohort study of physician practices in the provision of prophylaxis and treatment against osteoporotic fractures. The goal of this research was to improve understanding of the risk and prevention of osteoporosis-related fractures among female residents of 10 countries who were 55 years of age and older. GLOW enrolled over 60,000 women through over 700 physicians in 10 countries, and conducted annual follow-up for up to 5 years through annual patient questionnaires.

Setup:

Data Import and Cleaning

Missing values were not detected in dataset. Special characters were removed from column headings. What we know/don't know about the sample (500): 1. We do not know if the subjects are distributed equally around the world. We will assume that the same percentage from each region was selected for the sample in this dataset. 2. Based on the Sub_ID(Subject ID), we can assume that the datat is independent sample of participants.

```
glow_data_file <- here::here("data", "glow500.csv")
dataset_loc <-
dataset <- read.csv(glow_data_file, sep=",", stringsAsFactors = TRUE, header=TRUE,na.strings=c(""))

# List rows of data that have missing values
Missing_values <- dataset[!complete.cases(dataset),]

# Create new dataset without missing data
dataset <- na.omit(dataset)

#remove FRACSCORE feature per professor Turner
drops <- c("FRACSCORE")
dataset <- dataset[ , !(names(dataset) %in% drops)]
```

```r
#Cleanup column names
colnames(dataset)[colnames(dataset)=="ï..SUB_ID"] <- "SUB_ID"

#set categorical variables as factors
dataset$PRIORFRAC <- factor(dataset$PRIORFRAC,labels=c("0","1"))
dataset$PREMENO <- factor(dataset$PREMENO,labels=c("0","1"))
dataset$MOMFRAC <- factor(dataset$MOMFRAC,labels=c("0","1"))
dataset$ARMASSIST <- factor(dataset$ARMASSIST,labels=c("0","1"))
dataset$SMOKE <- factor(dataset$SMOKE,labels=c("0","1"))
dataset$RATERISK <- factor(dataset$RATERISK,labels=c("1","2","3"))
dataset$FRACTURE <- factor(dataset$FRACTURE,labels=c("0","1"))

#rearrange columns
dataset <- dataset[c("SUB_ID","SITE_ID","PHY_ID","AGE","BMI","HEIGHT","WEIGHT","PRIORFRAC","PREMENO","M

str(dataset)
```

```
## 'data.frame':    500 obs. of  14 variables:
##  $ SUB_ID   : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ SITE_ID  : int  1 4 6 6 1 5 5 1 1 4 ...
##  $ PHY_ID   : int  14 284 305 309 37 299 302 36 8 282 ...
##  $ AGE      : int  62 65 88 82 61 67 84 82 86 58 ...
##  $ BMI      : num  28.2 34 20.6 24.3 29.4 ...
##  $ HEIGHT   : int  158 160 157 160 152 161 150 153 156 166 ...
##  $ WEIGHT   : num  70.3 87.1 50.8 62.1 68 68 50.8 40.8 62.6 63.5 ...
##  $ PRIORFRAC: Factor w/ 2 levels "0","1": 1 1 2 1 1 2 1 2 2 1 ...
##  $ PREMENO  : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ MOMFRAC  : Factor w/ 2 levels "0","1": 1 1 2 1 1 1 1 1 1 1 ...
##  $ ARMASSIST: Factor w/ 2 levels "0","1": 1 1 2 1 1 1 1 1 1 1 ...
##  $ SMOKE    : Factor w/ 2 levels "0","1": 1 1 1 1 1 2 1 1 1 1 ...
##  $ RATERISK : Factor w/ 3 levels "1","2","3": 2 2 1 1 2 2 1 2 2 1 ...
##  $ FRACTURE : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
```

Exploratory Data Analysis

Grouping Variables as Continuous, Categorical, and ID

```r
numericVar <- dataset[,4:7]
ID_var <- dataset[,c(1:3)]
set_noID <- dataset[4:14]
categoricalVar <- dataset[8:14]
```

Create Train and Validation Datasets

```r
validation_index = createDataPartition(dataset$FRACTURE, p=0.70, list=FALSE)
validationData = dataset[-validation_index,c(4:14)]
trainingData = dataset[validation_index,c(4:14)]
```

Summary Statistics

Assumptions This is a prospective study which means its a study over time of a group of similar individuals who differ with respect to certain factors under a study and how these factors affect rates of a certain outcome (Fracture vs No-Fracture) Linearity - Independence of errors - Based on SUB_ID(Subject ID) we confirm each record is an independent sample. Multicollinearity - Weight and BMI are highly correlated but we will remove one from the

```r
#Summary stats by groups for continous predictors
t(aggregate(AGE~FRACTURE,data=dataset,summary))
```

```
##              [,1]       [,2]
## FRACTURE     "0"        "1"
## AGE.Min.     "55.00000" "56.00000"
## AGE.1st Qu.  "60.00000" "65.00000"
## AGE.Median   "66.00000" "72.00000"
## AGE.Mean     "67.48533" "71.79200"
## AGE.3rd Qu.  "74.00000" "79.00000"
## AGE.Max.     "90.00000" "89.00000"
```

```r
t(aggregate(BMI~FRACTURE,data=dataset,summary))
```

```
##              [,1]       [,2]
## FRACTURE     "0"        "1"
## BMI.Min.     "14.87637" "17.04223"
## BMI.1st Qu.  "23.32087" "23.04688"
## BMI.Median   "26.36709" "26.43080"
## BMI.Mean     "27.50140" "27.70793"
## BMI.3rd Qu.  "30.61756" "31.09282"
## BMI.Max.     "49.08241" "44.03628"
```

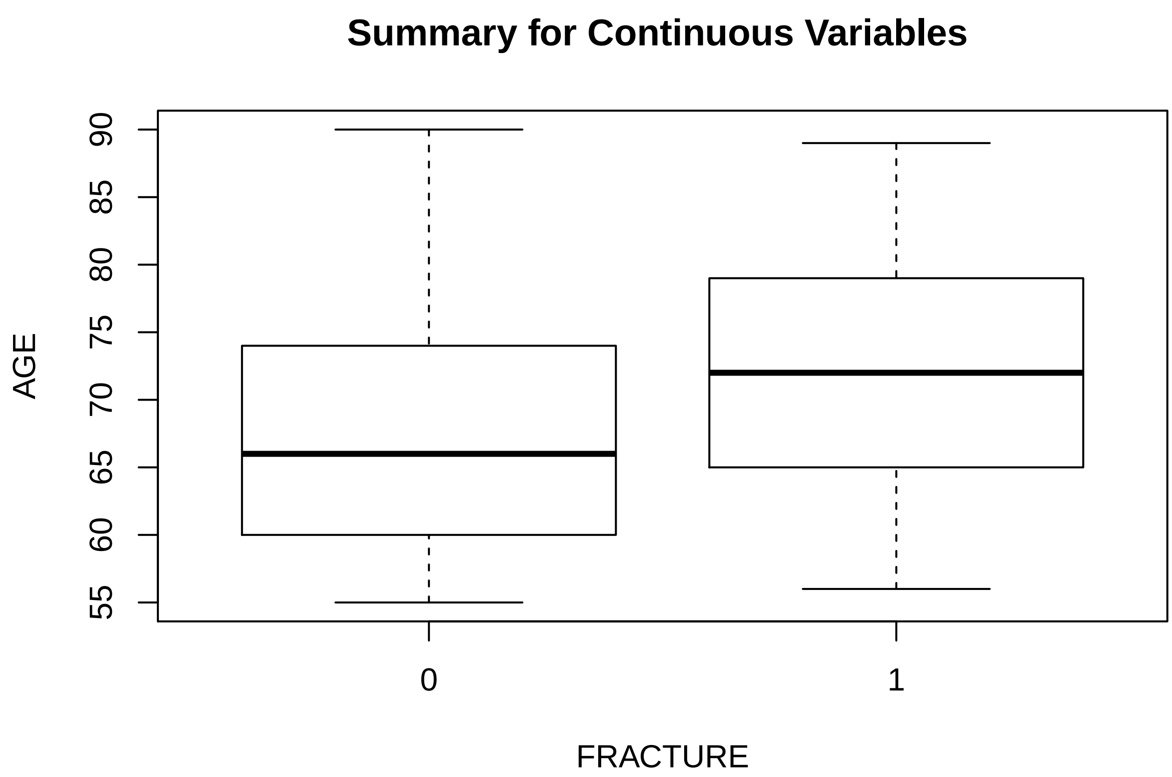
```r
t(aggregate(WEIGHT~FRACTURE,data=dataset,summary))
```

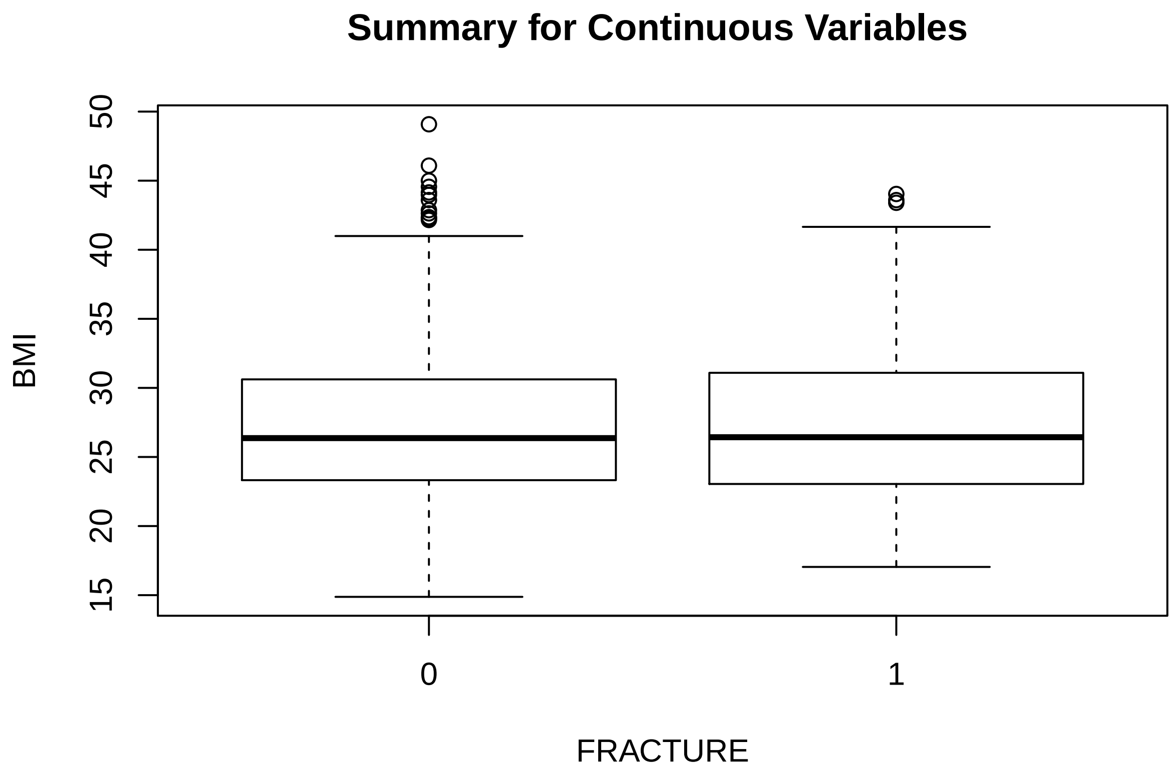
```
##                 [,1]        [,2]
## FRACTURE        "0"         "1"
## WEIGHT.Min.     " 39.90000" " 45.80000"
## WEIGHT.1st Qu.  " 60.30000" " 59.90000"
## WEIGHT.Median   " 68.00000" " 68.00000"
## WEIGHT.Mean     " 72.16693" " 70.79200"
## WEIGHT.3rd Qu.  " 81.60000" " 79.40000"
## WEIGHT.Max.     "127.00000" "124.70000"
```

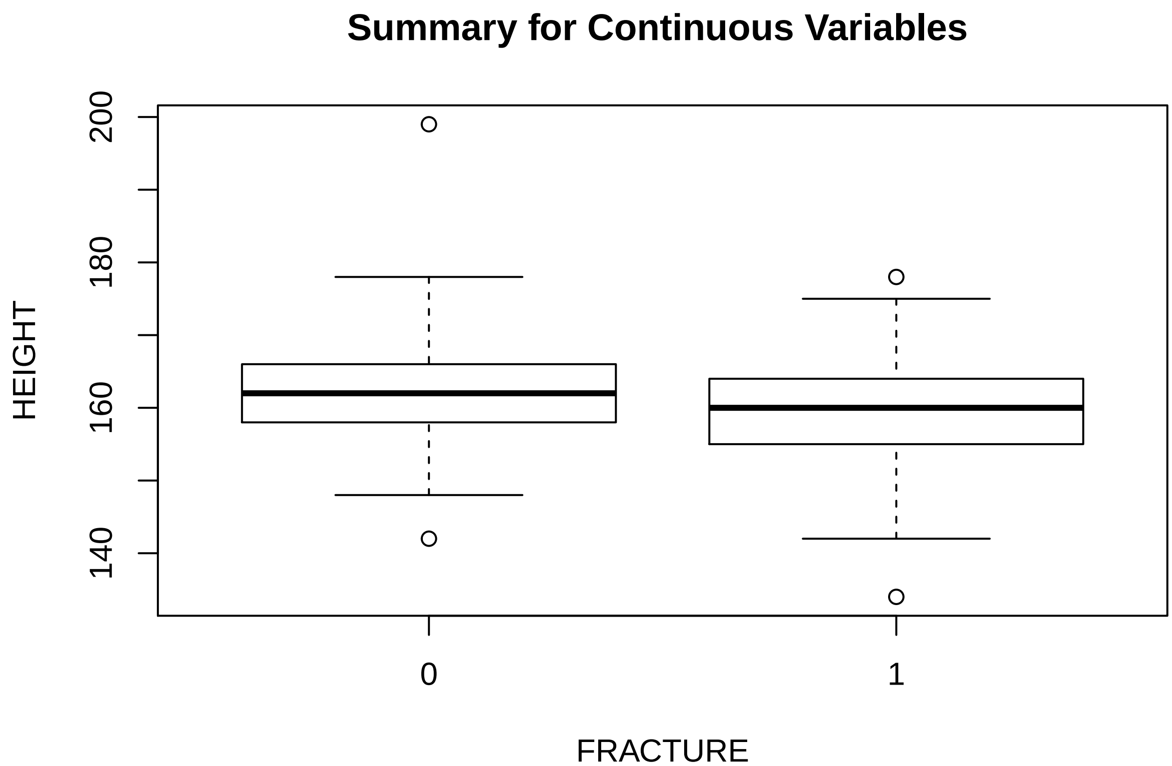
```r
t(aggregate(HEIGHT~FRACTURE,data=dataset,summary))
```

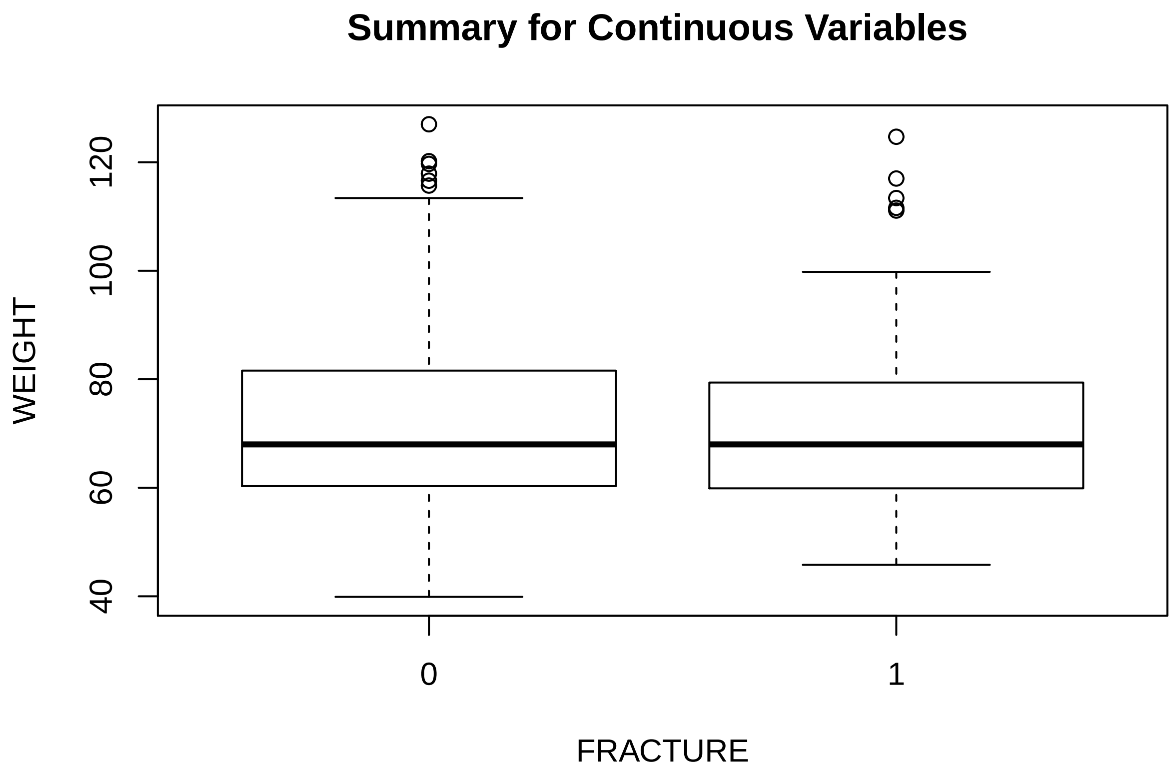
```
##                 [,1]      [,2]
## FRACTURE        "0"       "1"
## HEIGHT.Min.     "142.000" "134.000"
## HEIGHT.1st Qu.  "158.000" "155.000"
## HEIGHT.Median   "162.000" "160.000"
## HEIGHT.Mean     "161.864" "159.864"
## HEIGHT.3rd Qu.  "166.000" "164.000"
## HEIGHT.Max.     "199.000" "178.000"
```

```r
#par(mfrow=c(2,2)) # put four figures in a row (2*4)
for (i in 4:7) {
  boxplot(dataset[,i] ~ dataset$FRACTURE,ylab=names(dataset)[i],xlab="FRACTURE", main="Summary for Conti
}
```




Summary for Continuous Variables
BMI
50
45
40
35
30
25
20
15
0
1
FRACTURE


Summary for Continuous Variables
200
180
160
140
HEIGHT
0
1
FRACTURE




```
#create an nicer summary table
index<-which(sapply(dataset,is.numeric))
tab.cont<-c()
for (i in index){
  tab.cont<-rbind(tab.cont,summary(dataset[,i]))
}
rownames(tab.cont)<-names(dataset)[index]
View(tab.cont)
tab.cont
```

```
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## SUB_ID     1.00000 125.75000 250.50000 250.50000 375.25000 500.00000
## SITE_ID    1.00000   2.00000   3.00000   3.43600   5.00000   6.00000
## PHY_ID     1.00000  57.75000 182.50000 178.55000 298.00000 325.00000
## AGE       55.00000  61.00000  67.00000  68.56200  76.00000  90.00000
## BMI       14.87637  23.26889  26.41898  27.55303  30.79205  49.08241
## HEIGHT   134.00000 157.00000 161.50000 161.36400 165.00000 199.00000
## WEIGHT    39.90000  59.90000  68.00000  71.82320  81.30000 127.00000
```

```
# display the first 20 rows
print(head(dataset, n=20))
```

```
##    SUB_ID SITE_ID PHY_ID AGE      BMI HEIGHT WEIGHT PRIORFRAC PREMENO
## 1       1       1     14  62 28.16055    158   70.3         0       0
## 2       2       4    284  65 34.02344    160   87.1         0       0
```

```
## 3        3        6     305   88  20.60936     157    50.8           1        0
## 4        4        6     309   82  24.25781     160    62.1           0        0
## 5        5        1      37   61  29.43213     152    68.0           0        0
## 6        6        5     299   67  26.23356     161    68.0           1        0
## 7        7        5     302   84  22.57778     150    50.8           0        0
## 8        8        1      36   82  17.42919     153    40.8           1        0
## 9        9        1       8   86  25.72321     156    62.6           1        0
## 10      10        4     282   58  23.04398     166    63.5           0        0
## 11      11        6     315   67  28.87778     153    67.6           0        0
## 12      12        1      34   56  42.27473     167   117.9           0        0
## 13      13        6     315   59  25.56775     162    67.1           0        0
## 14      14        1      33   72  21.15702     165    57.6           0        0
## 15      15        1      23   64  23.90625     160    61.2           0        1
## 16      16        3     179   68  30.09143     161    78.0           0        0
## 17      17        4     284   67  38.82461     165   105.7           0        0
## 18      18        4     283   69  25.07240     162    65.8           0        0
## 19      19        3     179   78  31.09282     162    81.6           1        0
## 20      20        6     313   60  23.00296     157    56.7           0        0
##    MOMFRAC ARMASSIST SMOKE RATERISK FRACTURE
## 1        0         0     0        2        0
## 2        0         0     0        2        0
## 3        1         1     0        1        0
## 4        0         0     0        1        0
## 5        0         0     0        2        0
## 6        0         0     1        2        0
## 7        0         0     0        1        0
## 8        0         0     0        2        0
## 9        0         0     0        2        0
## 10       0         0     0        1        0
## 11       1         0     1        1        0
## 12       0         1     1        2        0
## 13       0         0     1        1        0
## 14       0         1     0        1        0
## 15       0         0     0        2        0
## 16       0         1     0        1        0
## 17       0         0     0        1        0
## 18       0         0     0        2        0
## 19       0         1     0        3        0
## 20       0         0     0        2        0
```

```r
# display the dimensions of the dataset
print(dim(dataset))
```

```
## [1] 500  14
```

```r
# list types for each attribute
print(sapply(dataset,class))
```

```
##    SUB_ID   SITE_ID    PHY_ID       AGE       BMI    HEIGHT    WEIGHT
## "integer" "integer" "integer" "integer" "numeric" "integer" "numeric"
## PRIORFRAC   PREMENO   MOMFRAC ARMASSIST     SMOKE  RATERISK  FRACTURE
##  "factor"  "factor"  "factor"  "factor"  "factor"  "factor"  "factor"
```

```r
# Standard Deviations for the non-categorical columns
std=sapply(set_noID,sd)
```

```
## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm = na.rm): Calling var(x)
##   Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm = na.rm): Calling var(x)
##   Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm = na.rm): Calling var(x)
##   Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm = na.rm): Calling var(x)
##   Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm = na.rm): Calling var(x)
##   Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm = na.rm): Calling var(x)
##   Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.

## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm = na.rm): Calling var(x)
##   Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.
```

```r
print('The standard deviations are:')
```

```
## [1] "The standard deviations are:"
```

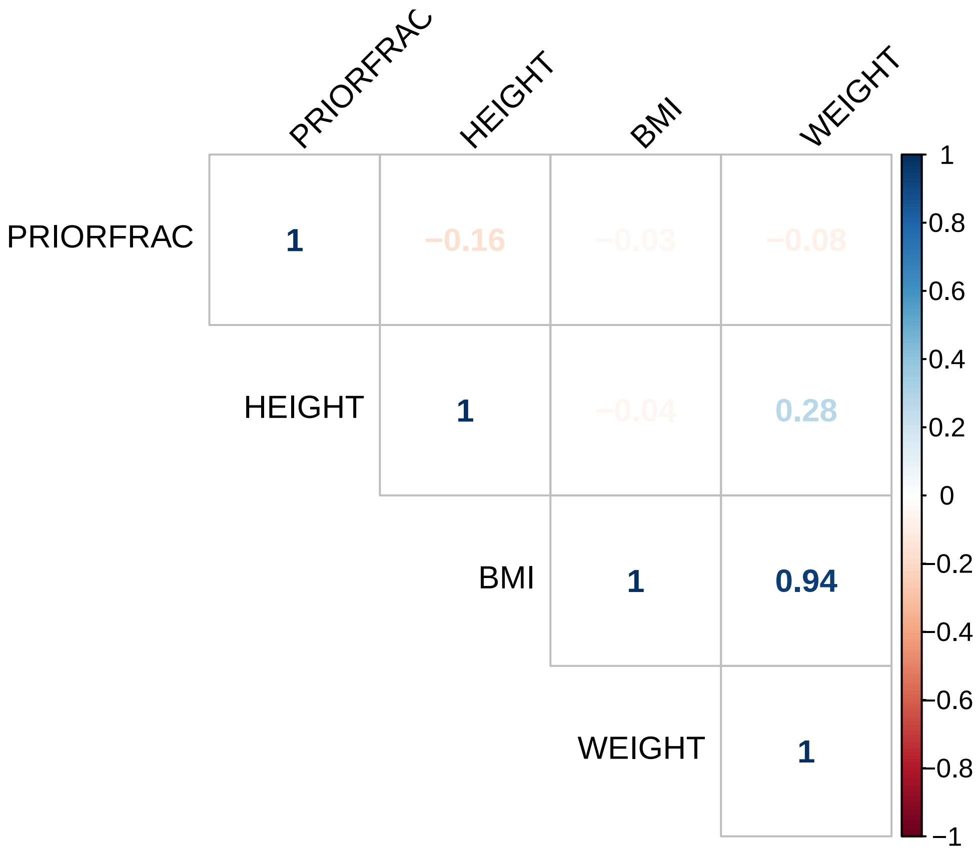
```r
print(std)
```

```
##        AGE        BMI     HEIGHT     WEIGHT  PRIORFRAC    PREMENO
##  8.9895372  5.9739583  6.3554928 16.4359918  0.4345961  0.3958249
##    MOMFRAC  ARMASSIST      SMOKE   RATERISK   FRACTURE
##  0.3366402  0.4848651  0.2554025  0.7922470  0.4334464
```

Correlations

BMI and Weight show to be highly correlation which makes sense since weight is a factor in calculation of BMI. We will remove Weight from models in order to meet assumptions.

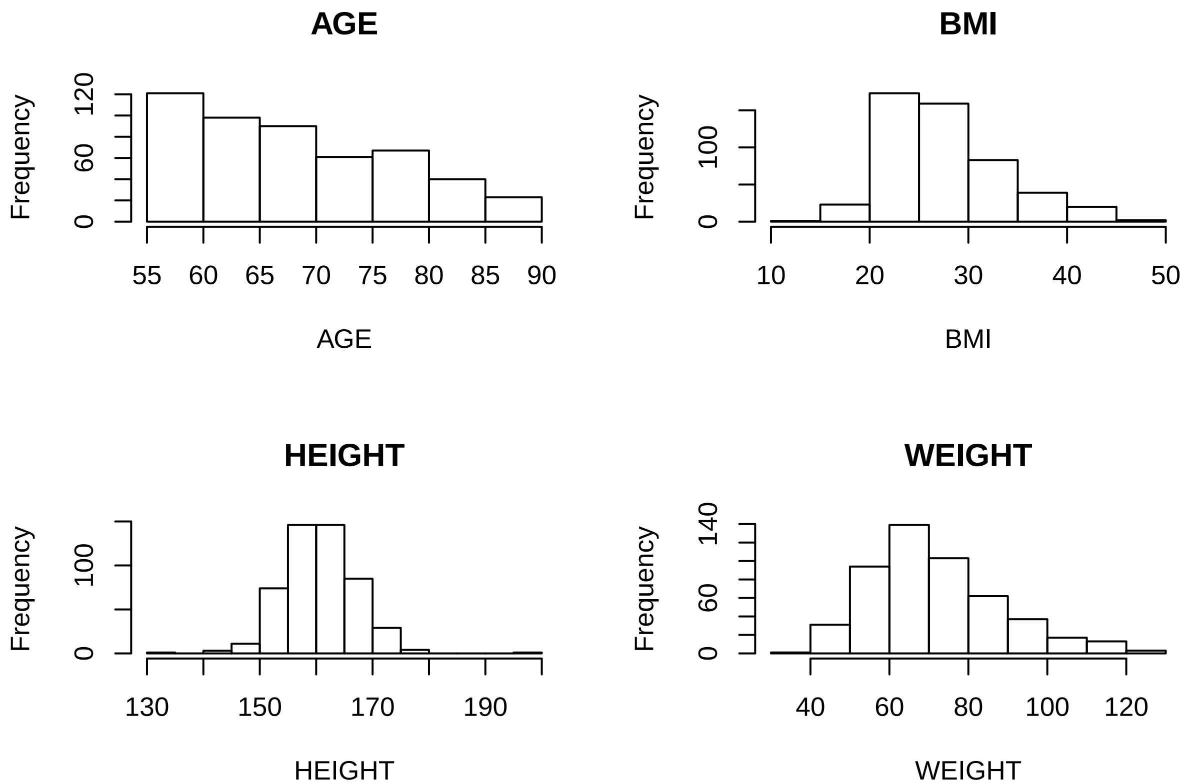
```r
#Training dataset without ID columns, convert PRIORFRAC to numeric for corrplot
train_df <- trainingData[2:5]
train_df$PRIORFRAC <- as.numeric(train_df$PRIORFRAC)
corrplot(cor(train_df), method = "number", type = "upper", order = "hclust",
         tl.col = "black", tl.srt = 45)
```



Visualization of Continuous Variables For the categorical variables, we show an unbalanced dataset of subjects with majority false PRIORFRAC, PREMENO, MOMFRAC, ARMASSIST, and SMOKE. There was a good balance of subjects in the 3 levels of RATERISK. An unblanced dataset will cause a model to favor the skewed numbers.

For the continous variables, we can see that BMI and Weight are highly correlated and weight and height are also correlated. When building the model, we will remove Weight as to meet the assumptions of logistic regression.

```
# Data visualizations
dataset_numeric = numericVar

#Histograms
par(mfrow=c(2,2))
for (i in 1:4) {
  hist(dataset_numeric[,i],xlab=names(dataset_numeric)[i],main=names(dataset_numeric)[i])
}
```



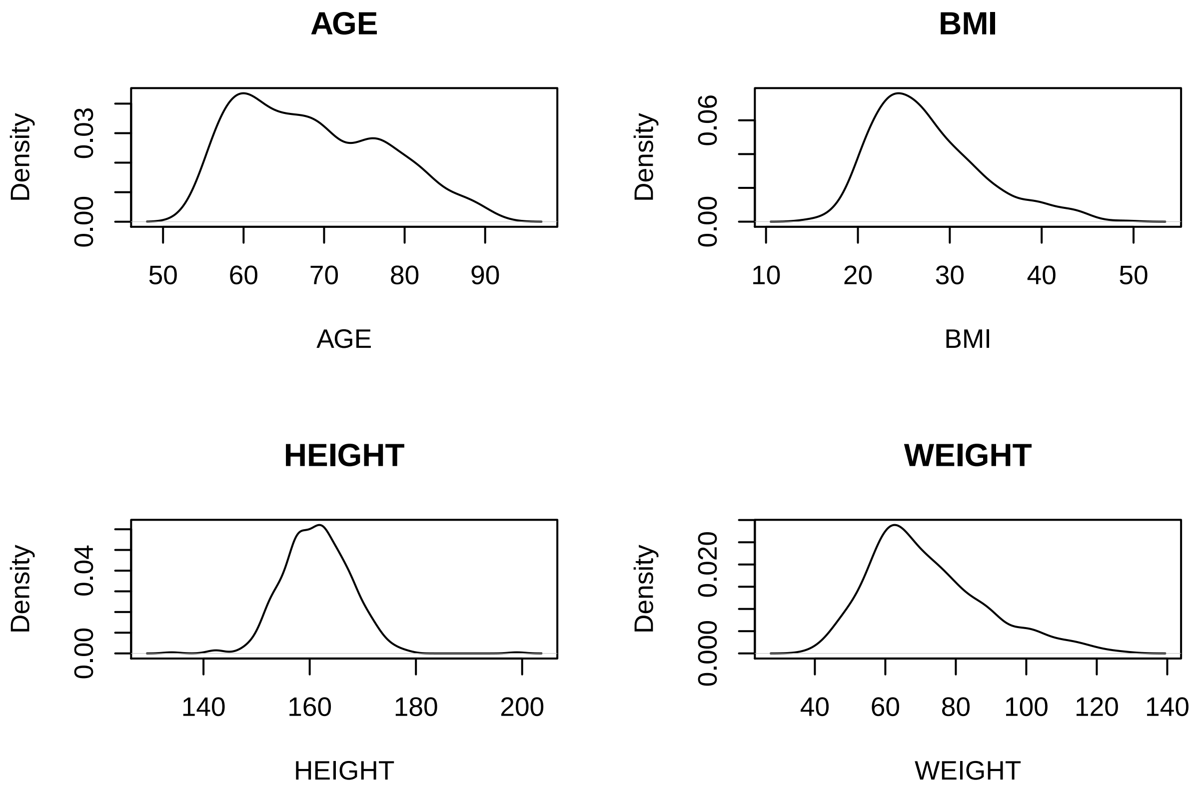
In the full dataset we have a majority of subjects are younger. The range of ages is between 55-90.

About 300 out of 500 subjects are in the 20-30 BMI score range.

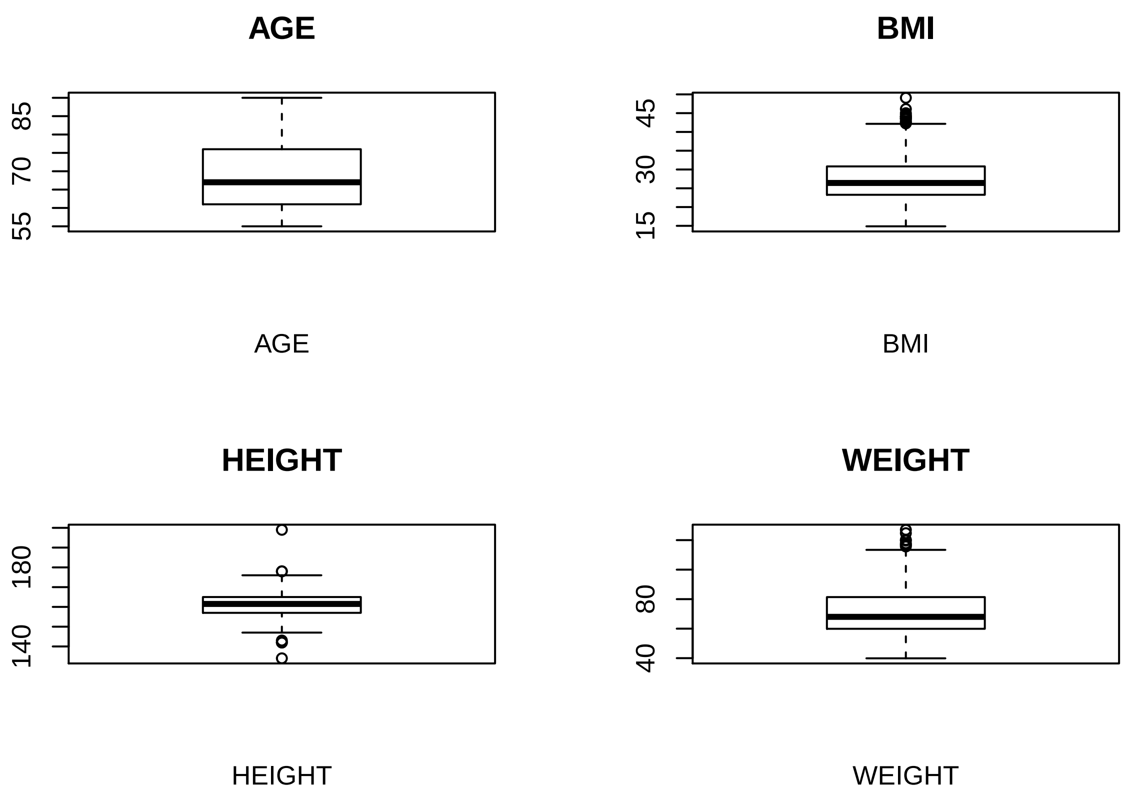
Majority of subjects landed between 150 and 180 inches in height.

We show a majority of subjects are in the weight range of 60-80.

```
#Density Plots
par(mfrow=c(2,2))
for(i in 1:4) {
  plot(density(dataset_numeric[,i]), xlab=names(dataset_numeric)[i], main=names(dataset_numeric)[i])
}
```

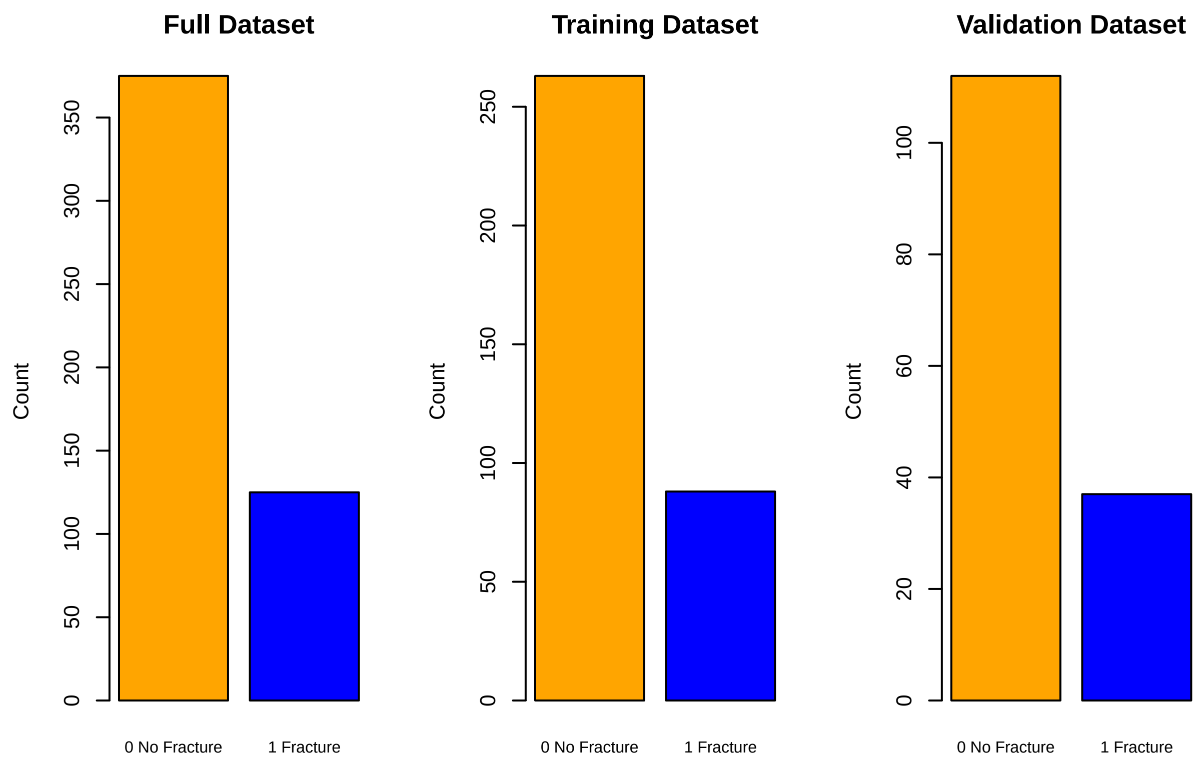



```r
#Box And Whisker Plots
par(mfrow=c(2,2))
for(i in 1:4) {
  boxplot(dataset_numeric[,i], xlab=names(dataset_numeric)[i], main=names(dataset_numeric)[i])
}
```



Frequency counts of subjects with Fracture. Compare Full, Train and Validation

```
par(mfrow=c(1,3))
#par(mar=c(5,8,4,2)) # increase y-axis margin.
count_full <- table(dataset$FRACTURE)
count_trn <- table(trainingData$FRACTURE)
count_test <- table(validationData$FRACTURE)


barplot(count_full,main="Full Dataset", ylab="Count", col=c("orange","blue"),names.arg=c("0 No Fracture

barplot(count_trn,main="Training Dataset", ylab="Count", col=c("orange","blue"),names.arg=c("0 No Fractu

barplot(count_test,main="Validation Dataset", ylab="Count", col=c("orange","blue"),names.arg=c("0 No Fra
```




```
#Multivariate Visualization
correlations1=cor(dataset_numeric)
print(correlations1)
```

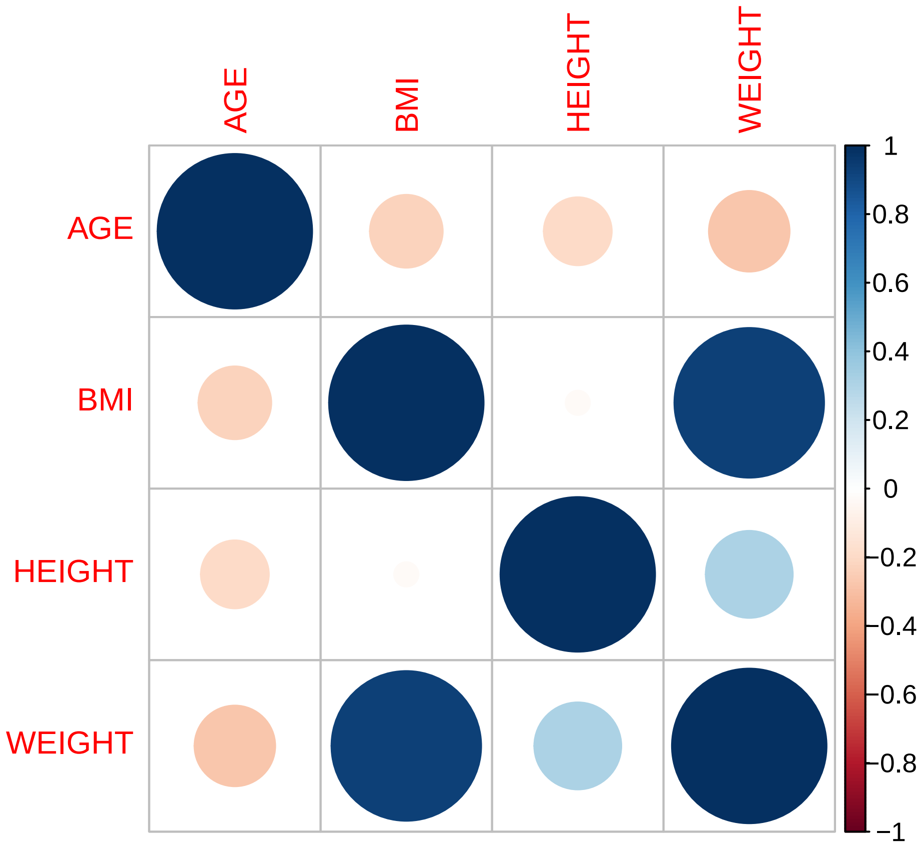
```
##               AGE         BMI      HEIGHT     WEIGHT
## AGE     1.0000000 -0.22125651 -0.19264861 -0.2715964
## BMI    -0.2212565  1.00000000 -0.02437689  0.9373360
## HEIGHT -0.1926486 -0.02437689  1.00000000  0.3159691
## WEIGHT -0.2715964  0.93733603  0.31596915  1.0000000
```

```
par(mfrow=c(1,1))
corrplot(correlations1, methods="circle")
```

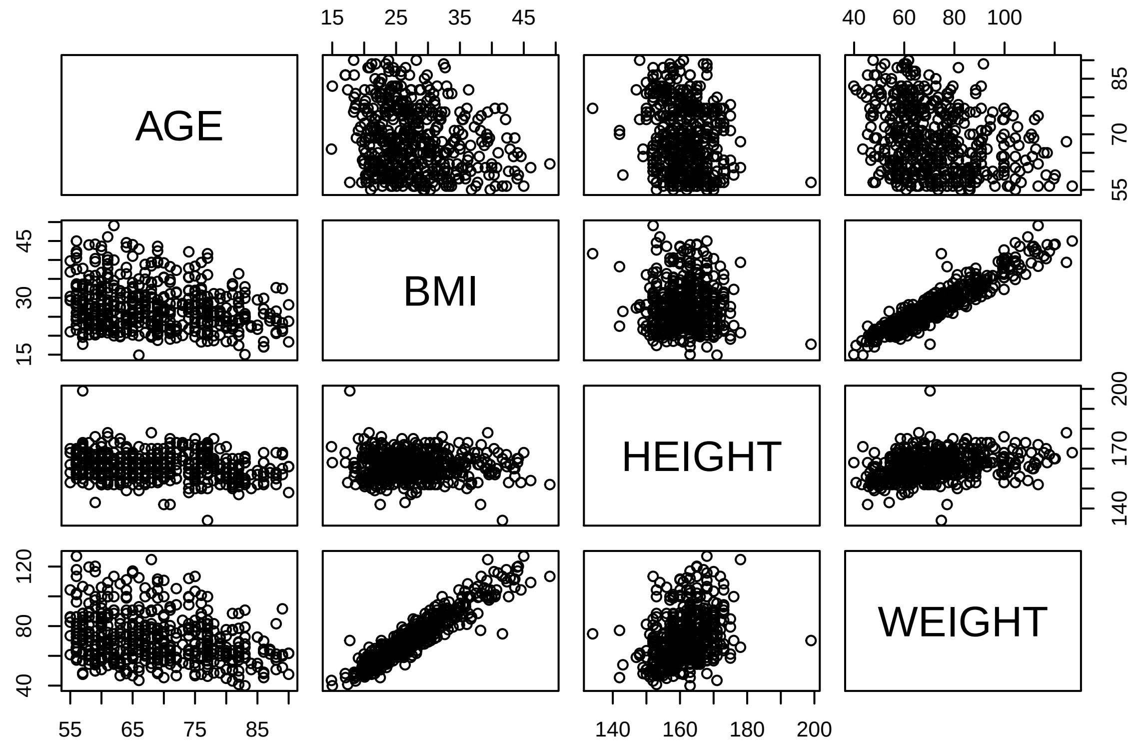
```
## Warning in text.default(pos.xlabel[, 1], pos.xlabel[, 2], newcolnames, srt
## = tl.srt, : "methods" is not a graphical parameter
```

```
## Warning in text.default(pos.ylabel[, 1], pos.ylabel[, 2], newrownames, col
## = tl.col, : "methods" is not a graphical parameter
```

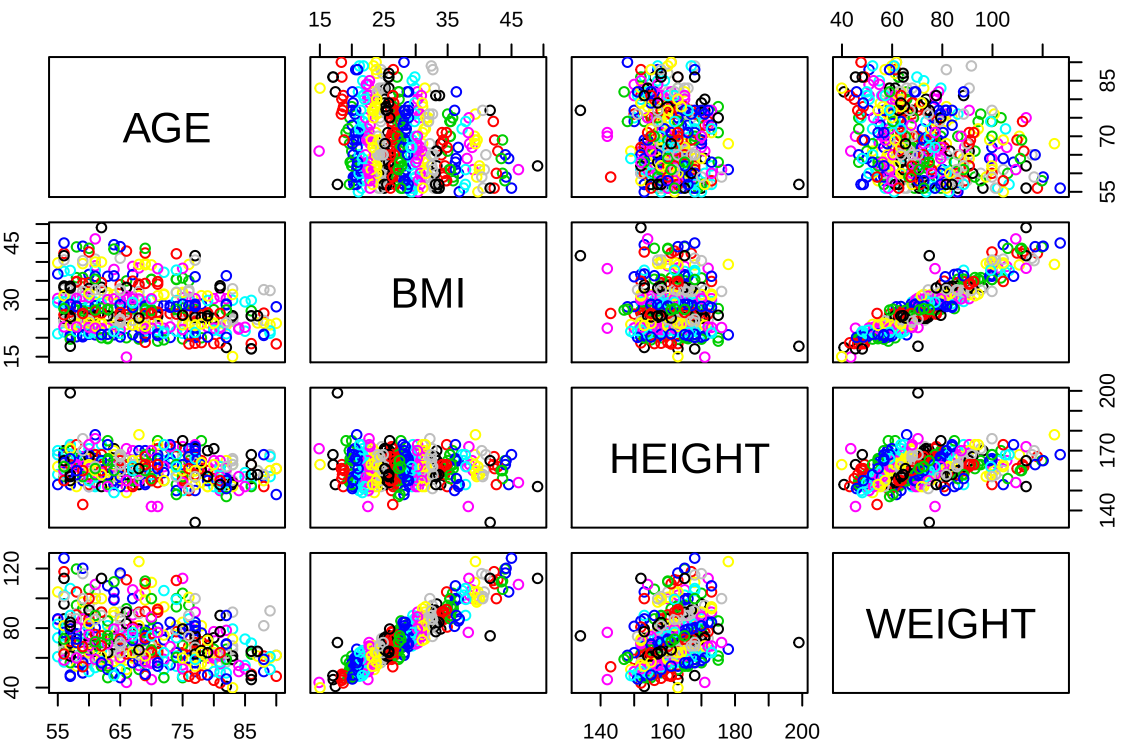
```
## Warning in title(title, ...): "methods" is not a graphical parameter
```



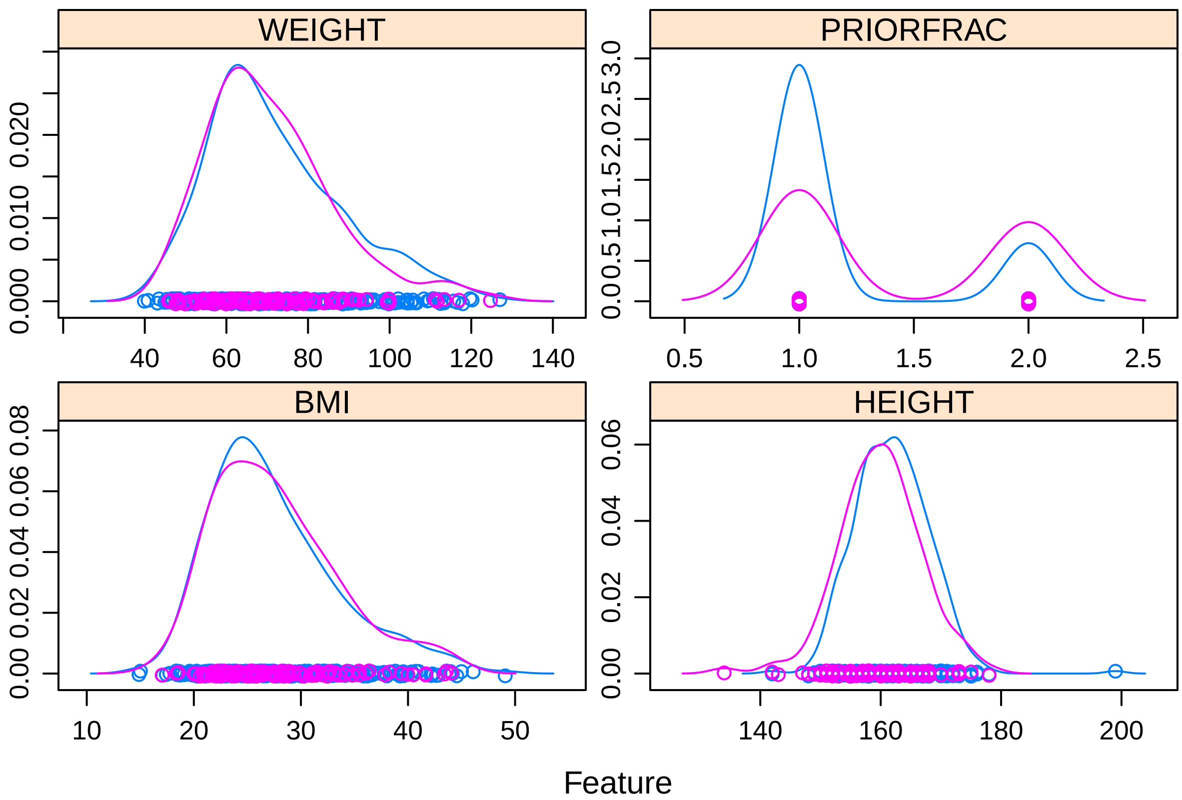

```r
# pair-wise scatterplots of the numeric attributes
par(mfrow=c(1,1))
pairs(dataset_numeric)
```



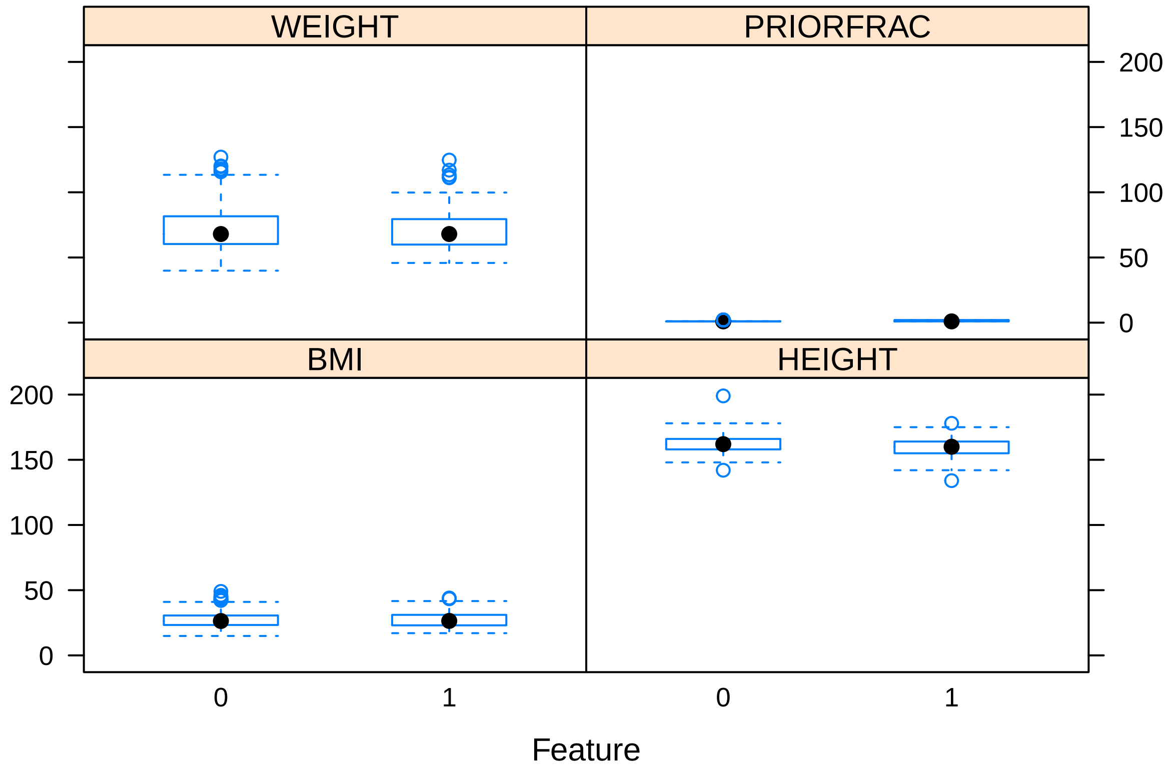

```
#Scatterplot Matrix By Class (use different color to distinguish different class)
par(mfrow=c(1,1))
pairs(dataset_numeric, col=dataset[,5])
```




```r
# density plots for each attribute by class value
X <- set_noID[2:5]
Y <- set_noID$FRACTURE
X$PRIORFRAC <- as.numeric(X$PRIORFRAC)
scales <- list(x=list(relation="free"), y=list(relation="free"))
par(mfrow=c(1,1))
featurePlot(x=X, y=set_noID$FRACTURE, plot="density", scales=scales)
```




```r
#Box And Whisker Plots By Class
par(mfrow=c(1,1))
featurePlot(x=X, y=set_noID$FRACTURE, plot="box")
```



Checking the Balance of the Full dataset

The current sample dataset containes a larger propotion of subjects that did not develop fracture. Building a model against this dataset could produce bias towards the majority class. Below you will see how many subjects with(1)/without(0) Fractures as well as the proportion percentage for each. After splitting the dataset into training and validation(test) sets, we noticed the proportion of the training and test was not any better.

We fit a logistic model on the unbalanced training dataset with a threshold of .05. It shows a Precision of 1 which says there are no false positives. Recall equals 0.20 is low and indicates that we have higher number of false negatives. The F equals 0.20 is also low and suggests weak accuracy of this model.

We also plotted a ROC curve to visualize the model. The AUC equals 0.764 which is low and shows the data is not balanced.

We will attempt to balance the dataset in order to create a more balanced distribution of and a better prediction.

```
table(dataset$FRACTURE)
```

```
##
##   0   1
## 375 125
```

```
prop.table(table(dataset$FRACTURE))
```

```
##
##    0    1
## 0.75 0.25
```

```r
# split the data into training and validation sets
set.seed(84)
validation_index = createDataPartition(dataset$FRACTURE, p=0.75, list=FALSE)
validationData = dataset[-validation_index,c(4:14)]
trainingData = dataset[validation_index,c(4:14)]
prop.table(table(validationData$FRACTURE))
```

```
##
##    0    1
## 0.75 0.25
```

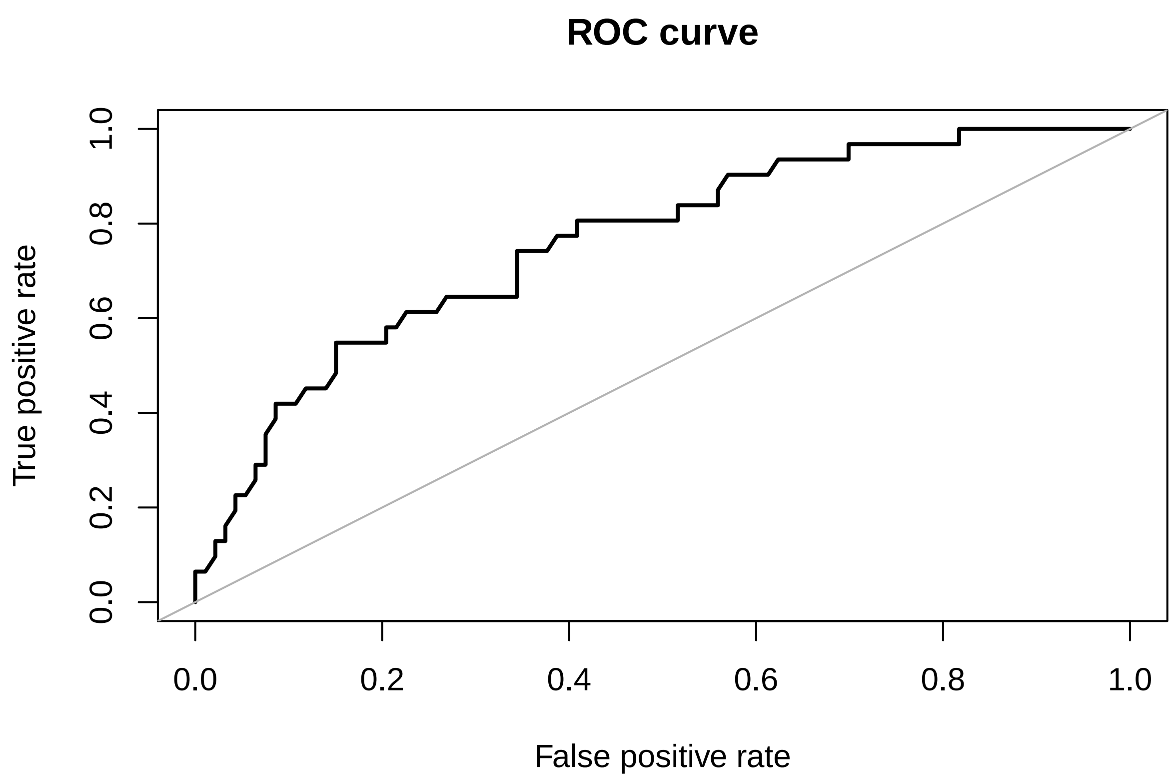
```r
prop.table(table(trainingData$FRACTURE))
```

```
##
##    0    1
## 0.75 0.25
```

```r
#fit a logistic regressio to unblanced training set
fit.dataset <- glm(formula=FRACTURE~ ., data = trainingData, family="binomial")
pred.fit.dataset <- predict(fit.dataset, newdata = validationData, type="response")
#Check Accuracy of fitted model.
accuracy.meas(validationData$FRACTURE,pred.fit.dataset, threshold=.05)
```

```
##
## Call:
## accuracy.meas(response = validationData$FRACTURE, predicted = pred.fit.dataset,
##     threshold = 0.05)
##
## Examples are labelled as positive when predicted is greater than 0.05
##
## precision: 0.250
## recall: 1.000
## F: 0.200
```

```r
#Check Accuracy of Test dataset using ROC curve
roc.curve(validationData$FRACTURE, pred.fit.dataset, plotit = TRUE)
```




```
## Area under the curve (AUC): 0.760
```

##Create a vector of all categorical variables and run frequency 2X2s with Mosaic plots.

Chi-Square Test For the 2-way tables the chisq test independence will show if 2 categorical variables are related in some population. Null Hypothesis: The two categorical variables are independent. Alternative Hypothesis: The two categorical variables are dependent

Variable: PRIORFRAC 41% of subjects with Prior Franctures also had current Fractures but only make up 25% of the overall subjects in the sample that had prior fractures. The Chi-squared p-value favors overwhemingly the alternative hypothesis that the PRIORFRAC variable is dependent on Fracture variable.

Variable: PREMENO 80% of the sample subjects are not in Pre-Menopausehad of which 24% had fractures. The same frequency of 25% Premenopausal women had fractures. The Chi-squared p-value favors the null hypothesis that the PREMENO variable is independent on Fracture variable.

Variable: MOMFRAC 13% of subjects have Mothers with a history of fractures. Out of those 13%, 36% of subjects also had fractures. The Chi-squared p-value favors the alternative hypothesis that the MOMFRAC variable is probably dependent on Fracture variable.

Variable: ARMASSIST 62% (312/500) subjects do not have Armassist of which 20% had fractures. Of those with Armassist, 33% had fractures. The Chi-squared p-value favors the alternative hypothesis that the ARMASSIST variable is most likely dependent on Fracture variable.

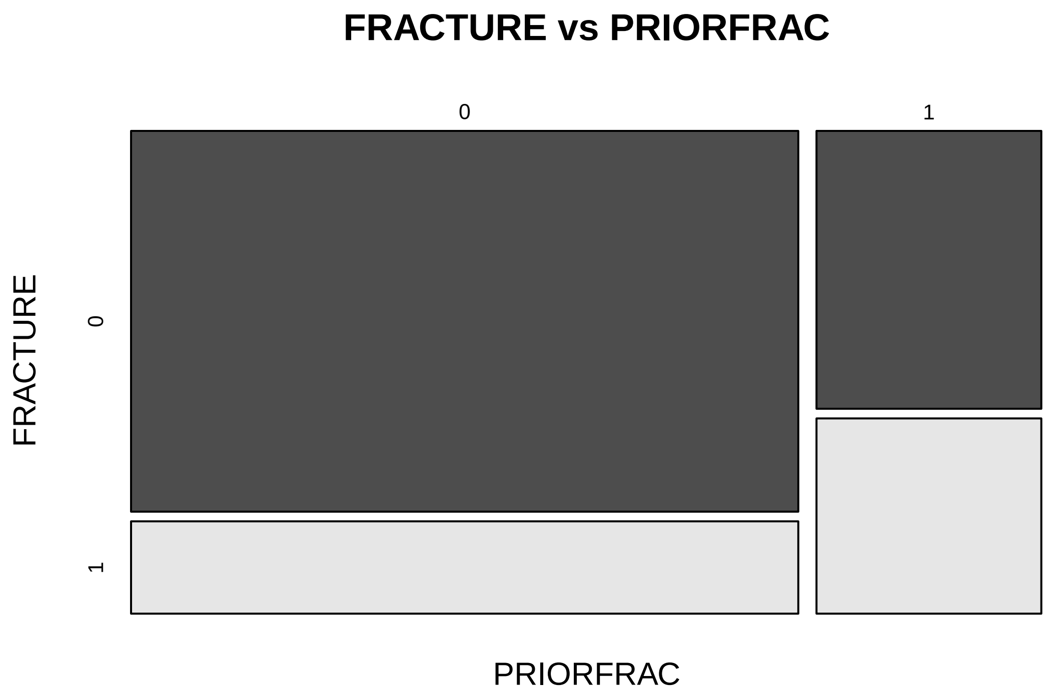
Variable: SMOKE In the dataset, 93% of subjects are non-smokers of which 26% had fractures. 7% of the subjects who were smokers of which 26% had no fractures. Although the subjects are not balance in smoker vs non-smoker category, the p-value for Chi-squared test shows .47 we favor the alternative hypothesis that the Smoke variable is dependent on the Fracture.

Variable: RATERISK Raterisk shows the frequency of subjects in each Raterisk level is between 29%-33%. This is pretty even in terms of how many subjects are within each Raterisk. For those that did have Fractures, their probability of a fracture increased with the level of Raterisk. This makes sense.

```
categoricalVarVec  <- c("PRIORFRAC","PREMENO","MOMFRAC","ARMASSIST","SMOKE","RATERISK")
for(categoricalVar in categoricalVarVec){
  CrossTable(dataset[,categoricalVar], dataset$FRACTURE, chisq = TRUE , expected = TRUE, dnn=c(categori
  mosaicplot(CrossTable(dataset[ ,categoricalVar], dataset$FRACTURE)$t, main=paste("FRACTURE vs",categor
}
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##              | FRACTURE
##    PRIORFRAC |         0 |         1 | Row Total |
## -------------|-----------|-----------|-----------|
##            0 |       301 |        73 |       374 |
##              |   280.500 |    93.500 |           |
##              |     1.498 |     4.495 |           |
##              |     0.805 |     0.195 |     0.748 |
##              |     0.803 |     0.584 |           |
##              |     0.602 |     0.146 |           |
## -------------|-----------|-----------|-----------|
##            1 |        74 |        52 |       126 |
##              |    94.500 |    31.500 |           |
##              |     4.447 |    13.341 |           |
##              |     0.587 |     0.413 |     0.252 |
##              |     0.197 |     0.416 |           |
##              |     0.148 |     0.104 |           |
## -------------|-----------|-----------|-----------|
## Column Total |       375 |       125 |       500 |
##              |     0.750 |     0.250 |           |
## -------------|-----------|-----------|-----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  23.78123     d.f. =  1     p =  1.079299e-06
```

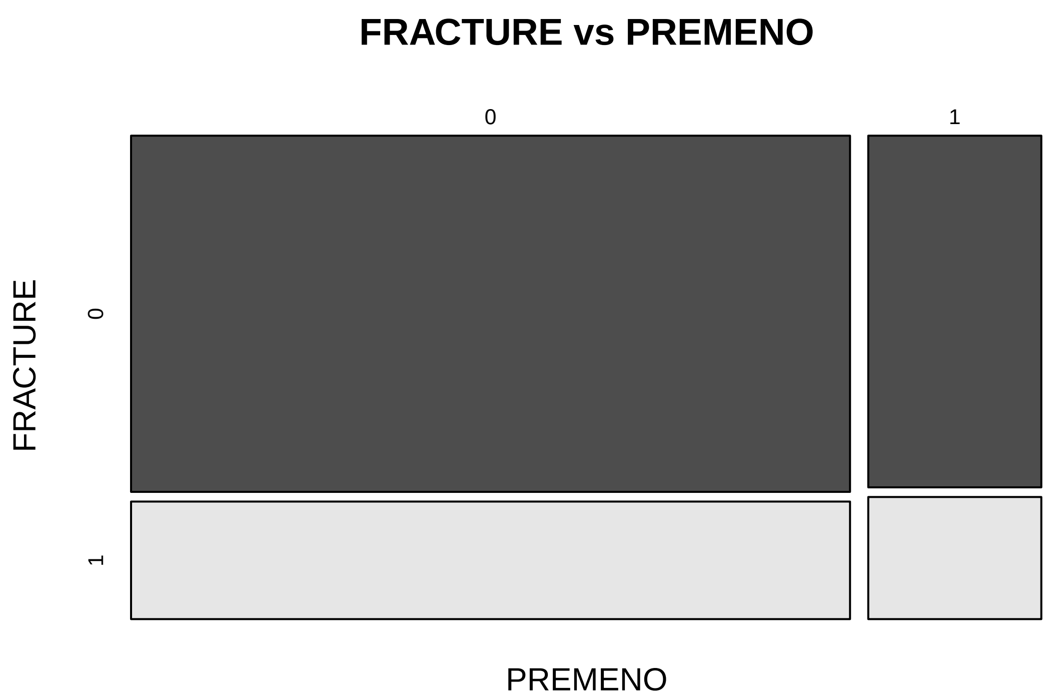
```
##
## Pearson's Chi-squared test with Yates' continuity correction
## ------------------------------------------------------------
## Chi^2 =  22.63532     d.f. =  1     p =  1.958512e-06
##
##
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##                          | dataset$FRACTURE
## dataset[, categoricalVar] |         0 |         1 | Row Total |
## --------------------------|-----------|-----------|-----------|
##                         0 |       301 |        73 |       374 |
##                           |     1.498 |     4.495 |           |
##                           |     0.805 |     0.195 |     0.748 |
##                           |     0.803 |     0.584 |           |
##                           |     0.602 |     0.146 |           |
## --------------------------|-----------|-----------|-----------|
##                         1 |        74 |        52 |       126 |
##                           |     4.447 |    13.341 |           |
##                           |     0.587 |     0.413 |     0.252 |
##                           |     0.197 |     0.416 |           |
##                           |     0.148 |     0.104 |           |
## --------------------------|-----------|-----------|-----------|
##              Column Total |       375 |       125 |       500 |
##                           |     0.750 |     0.250 |           |
## --------------------------|-----------|-----------|-----------|
##
##
```




```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##              | FRACTURE
##      PREMENO |         0 |         1 | Row Total |
## -------------|-----------|-----------|-----------|
##            0 |       303 |       100 |       403 |
##              |   302.250 |   100.750 |           |
##              |     0.002 |     0.006 |           |
##              |     0.752 |     0.248 |     0.806 |
##              |     0.808 |     0.800 |           |
##              |     0.606 |     0.200 |           |
## -------------|-----------|-----------|-----------|
```

```
##            1 |        72 |        25 |        97 |
##              |    72.750 |    24.250 |           |
##              |     0.008 |     0.023 |           |
##              |     0.742 |     0.258 |     0.194 |
##              |     0.192 |     0.200 |           |
##              |     0.144 |     0.050 |           |
## -------------|-----------|-----------|-----------|
## Column Total |       375 |       125 |       500 |
##              |     0.750 |     0.250 |           |
## -------------|-----------|-----------|-----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  0.038372     d.f. =  1     p =  0.844698
##
## Pearson's Chi-squared test with Yates' continuity correction
## ------------------------------------------------------------
## Chi^2 =  0.004263556     d.f. =  1     p =  0.9479384
##
##
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##                          | dataset$FRACTURE
## dataset[, categoricalVar] |         0 |         1 | Row Total |
## --------------------------|-----------|-----------|-----------|
##                         0 |       303 |       100 |       403 |
##                           |     0.002 |     0.006 |           |
##                           |     0.752 |     0.248 |     0.806 |
##                           |     0.808 |     0.800 |           |
##                           |     0.606 |     0.200 |           |
## --------------------------|-----------|-----------|-----------|
##                         1 |        72 |        25 |        97 |
##                           |     0.008 |     0.023 |           |
##                           |     0.742 |     0.258 |     0.194 |
##                           |     0.192 |     0.200 |           |
##                           |     0.144 |     0.050 |           |
## --------------------------|-----------|-----------|-----------|
```

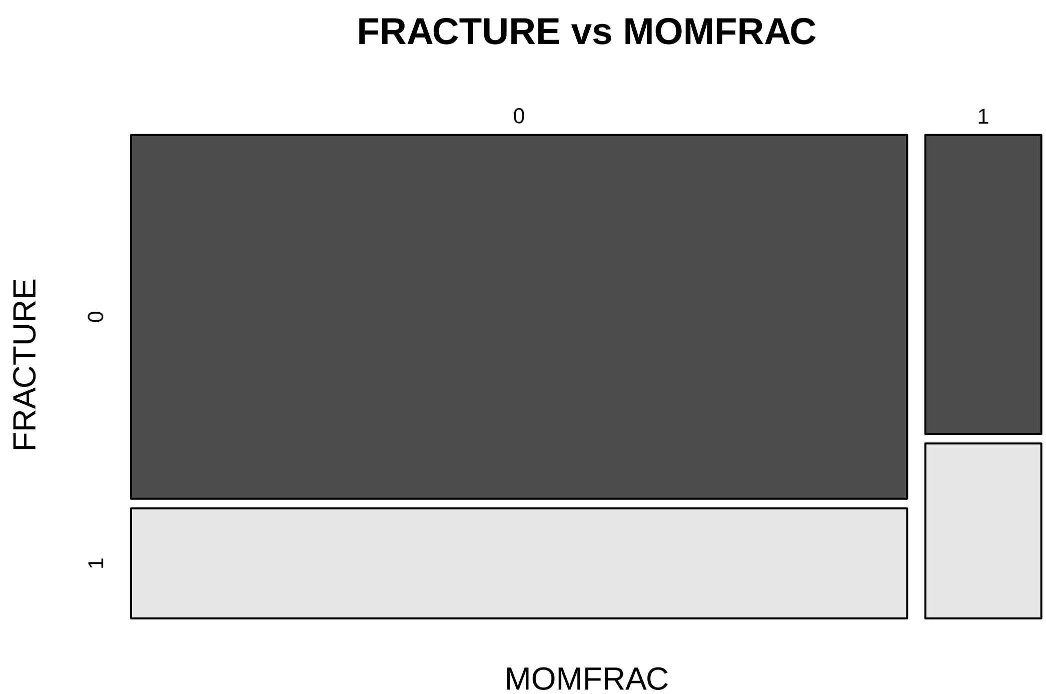
```
##              Column Total |       375 |       125 |       500 |
##                           |     0.750 |     0.250 |           |
## --------------------------|-----------|-----------|-----------|
##
##
```




```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##              | FRACTURE
##      MOMFRAC |         0 |         1 | Row Total |
## -------------|-----------|-----------|-----------|
##            0 |       334 |       101 |       435 |
```

```
##              |   326.250 |   108.750 |           |
##              |     0.184 |     0.552 |           |
##              |     0.768 |     0.232 |     0.870 |
##              |     0.891 |     0.808 |           |
##              |     0.668 |     0.202 |           |
## -------------|-----------|-----------|-----------|
##            1 |        41 |        24 |        65 |
##              |    48.750 |    16.250 |           |
##              |     1.232 |     3.696 |           |
##              |     0.631 |     0.369 |     0.130 |
##              |     0.109 |     0.192 |           |
##              |     0.082 |     0.048 |           |
## -------------|-----------|-----------|-----------|
## Column Total |       375 |       125 |       500 |
##              |     0.750 |     0.250 |           |
## -------------|-----------|-----------|-----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  5.664604     d.f. =  1     p =  0.01731063
##
## Pearson's Chi-squared test with Yates' continuity correction
## ------------------------------------------------------------
## Chi^2 =  4.957265     d.f. =  1     p =  0.02598127
##
##
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##                          | dataset$FRACTURE
## dataset[, categoricalVar] |         0 |         1 | Row Total |
## -------------------------|-----------|-----------|-----------|
##                         0 |       334 |       101 |       435 |
##                          |     0.184 |     0.552 |           |
##                          |     0.768 |     0.232 |     0.870 |
##                          |     0.891 |     0.808 |           |
##                          |     0.668 |     0.202 |           |
## -------------------------|-----------|-----------|-----------|
```

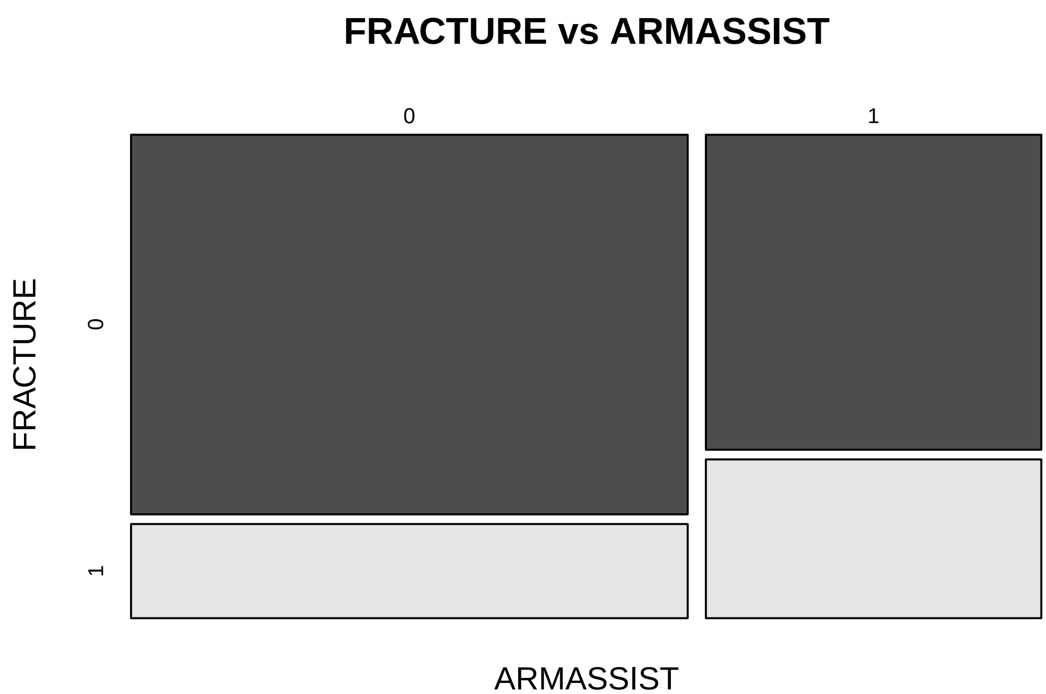
```
##                          1 |        41 |        24 |        65 |
##                            |     1.232 |     3.696 |           |
##                            |     0.631 |     0.369 |     0.130 |
##                            |     0.109 |     0.192 |           |
##                            |     0.082 |     0.048 |           |
## -------------------------|-----------|-----------|-----------|
##               Column Total |       375 |       125 |       500 |
##                            |     0.750 |     0.250 |           |
## -------------------------|-----------|-----------|-----------|
##
##
```




```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
```

```
## 
## 
##              | FRACTURE 
##    ARMASSIST |         0 |         1 | Row Total | 
## -------------|-----------|-----------|-----------|
##            0 |       250 |        62 |       312 | 
##              |   234.000 |    78.000 |           | 
##              |     1.094 |     3.282 |           | 
##              |     0.801 |     0.199 |     0.624 | 
##              |     0.667 |     0.496 |           | 
##              |     0.500 |     0.124 |           | 
## -------------|-----------|-----------|-----------|
##            1 |       125 |        63 |       188 | 
##              |   141.000 |    47.000 |           | 
##              |     1.816 |     5.447 |           | 
##              |     0.665 |     0.335 |     0.376 | 
##              |     0.333 |     0.504 |           | 
##              |     0.250 |     0.126 |           | 
## -------------|-----------|-----------|-----------|
## Column Total |       375 |       125 |       500 | 
##              |     0.750 |     0.250 |           | 
## -------------|-----------|-----------|-----------|
## 
## 
## Statistics for All Table Factors
## 
## 
## Pearson's Chi-squared test 
## ------------------------------------------------------------
## Chi^2 =  11.63848     d.f. =  1     p =  0.0006460138 
## 
## Pearson's Chi-squared test with Yates' continuity correction 
## ------------------------------------------------------------
## Chi^2 =  10.92244     d.f. =  1     p =  0.0009500637 
## 
## 
## 
## 
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
## 
## 
## Total Observations in Table:  500 
## 
## 
##                          | dataset$FRACTURE 
## dataset[, categoricalVar] |         0 |         1 | Row Total | 
## -------------------------|-----------|-----------|-----------|
```

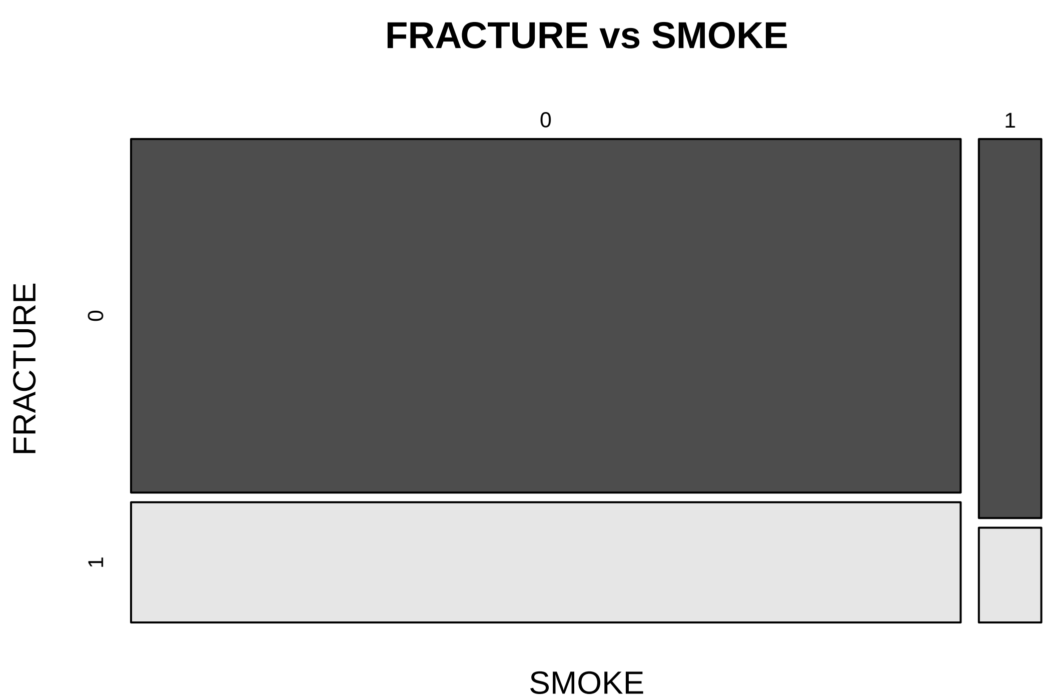
```
##                          0 |       250 |        62 |       312 |
##                            |     1.094 |     3.282 |           |
##                            |     0.801 |     0.199 |     0.624 |
##                            |     0.667 |     0.496 |           |
##                            |     0.500 |     0.124 |           |
## ---------------------------|-----------|-----------|-----------|
##                          1 |       125 |        63 |       188 |
##                            |     1.816 |     5.447 |           |
##                            |     0.665 |     0.335 |     0.376 |
##                            |     0.333 |     0.504 |           |
##                            |     0.250 |     0.126 |           |
## ---------------------------|-----------|-----------|-----------|
##               Column Total |       375 |       125 |       500 |
##                            |     0.750 |     0.250 |           |
## ---------------------------|-----------|-----------|-----------|
##
##
```




```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
```

```
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##              | FRACTURE
##        SMOKE |         0 |         1 | Row Total |
## -------------|-----------|-----------|-----------|
##            0 |       347 |       118 |       465 |
##              |   348.750 |   116.250 |           |
##              |     0.009 |     0.026 |           |
##              |     0.746 |     0.254 |     0.930 |
##              |     0.925 |     0.944 |           |
##              |     0.694 |     0.236 |           |
## -------------|-----------|-----------|-----------|
##            1 |        28 |         7 |        35 |
##              |    26.250 |     8.750 |           |
##              |     0.117 |     0.350 |           |
##              |     0.800 |     0.200 |     0.070 |
##              |     0.075 |     0.056 |           |
##              |     0.056 |     0.014 |           |
## -------------|-----------|-----------|-----------|
## Column Total |       375 |       125 |       500 |
##              |     0.750 |     0.250 |           |
## -------------|-----------|-----------|-----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  0.5017921     d.f. =  1     p =  0.4787137
##
## Pearson's Chi-squared test with Yates' continuity correction
## ------------------------------------------------------------
## Chi^2 =  0.2560164     d.f. =  1     p =  0.6128703
##
##
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
```

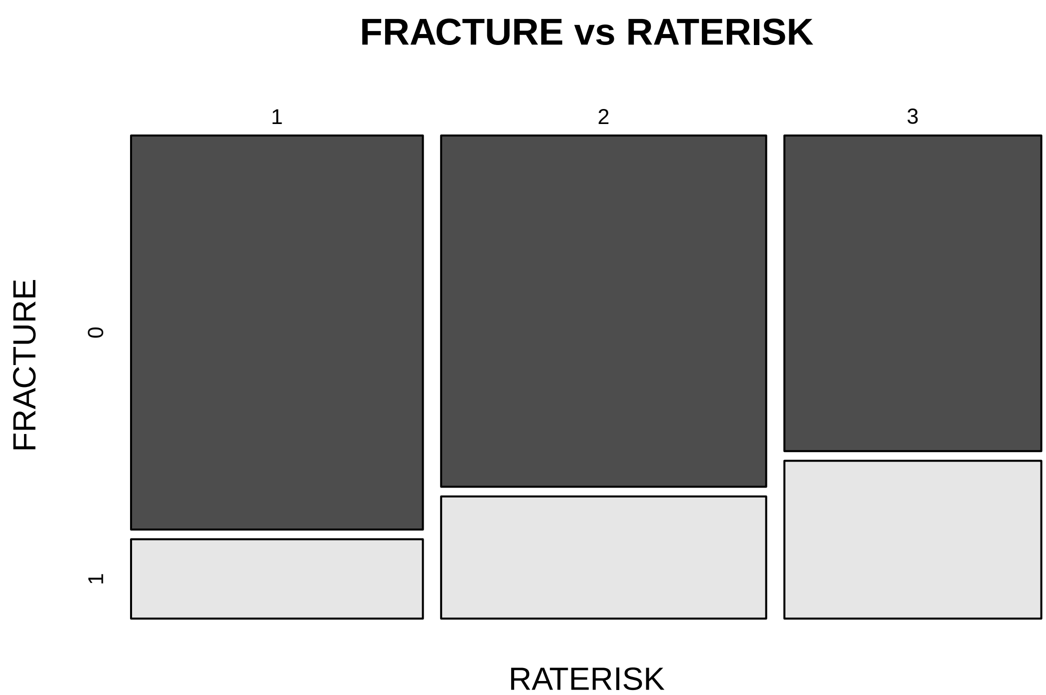
```
## Total Observations in Table:  500
##
##
##                           | dataset$FRACTURE
## dataset[, categoricalVar] |         0 |         1 | Row Total |
## --------------------------|-----------|-----------|-----------|
##                         0 |       347 |       118 |       465 |
##                           |     0.009 |     0.026 |           |
##                           |     0.746 |     0.254 |     0.930 |
##                           |     0.925 |     0.944 |           |
##                           |     0.694 |     0.236 |           |
## --------------------------|-----------|-----------|-----------|
##                         1 |        28 |         7 |        35 |
##                           |     0.117 |     0.350 |           |
##                           |     0.800 |     0.200 |     0.070 |
##                           |     0.075 |     0.056 |           |
##                           |     0.056 |     0.014 |           |
## --------------------------|-----------|-----------|-----------|
##              Column Total |       375 |       125 |       500 |
##                           |     0.750 |     0.250 |           |
## --------------------------|-----------|-----------|-----------|
##
##
```




```
##
##
```

```
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##              | FRACTURE
##     RATERISK |         0 |         1 | Row Total |
## -------------|-----------|-----------|-----------|
##            1 |       139 |        28 |       167 |
##              |   125.250 |    41.750 |           |
##              |     1.509 |     4.528 |           |
##              |     0.832 |     0.168 |     0.334 |
##              |     0.371 |     0.224 |           |
##              |     0.278 |     0.056 |           |
## -------------|-----------|-----------|-----------|
##            2 |       138 |        48 |       186 |
##              |   139.500 |    46.500 |           |
##              |     0.016 |     0.048 |           |
##              |     0.742 |     0.258 |     0.372 |
##              |     0.368 |     0.384 |           |
##              |     0.276 |     0.096 |           |
## -------------|-----------|-----------|-----------|
##            3 |        98 |        49 |       147 |
##              |   110.250 |    36.750 |           |
##              |     1.361 |     4.083 |           |
##              |     0.667 |     0.333 |     0.294 |
##              |     0.261 |     0.392 |           |
##              |     0.196 |     0.098 |           |
## -------------|-----------|-----------|-----------|
## Column Total |       375 |       125 |       500 |
##              |     0.750 |     0.250 |           |
## -------------|-----------|-----------|-----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  11.54688     d.f. =  2     p =  0.003109037
##
##
##
##
##
```

```
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  500
##
##
##                            | dataset$FRACTURE
## dataset[, categoricalVar] |         0 |         1 | Row Total |
## --------------------------|-----------|-----------|-----------|
##                         1 |       139 |        28 |       167 |
##                           |     1.509 |     4.528 |           |
##                           |     0.832 |     0.168 |     0.334 |
##                           |     0.371 |     0.224 |           |
##                           |     0.278 |     0.056 |           |
## --------------------------|-----------|-----------|-----------|
##                         2 |       138 |        48 |       186 |
##                           |     0.016 |     0.048 |           |
##                           |     0.742 |     0.258 |     0.372 |
##                           |     0.368 |     0.384 |           |
##                           |     0.276 |     0.096 |           |
## --------------------------|-----------|-----------|-----------|
##                         3 |        98 |        49 |       147 |
##                           |     1.361 |     4.083 |           |
##                           |     0.667 |     0.333 |     0.294 |
##                           |     0.261 |     0.392 |           |
##                           |     0.196 |     0.098 |           |
## --------------------------|-----------|-----------|-----------|
##              Column Total |       375 |       125 |       500 |
##                           |     0.750 |     0.250 |           |
## --------------------------|-----------|-----------|-----------|
##
##
```



#Logistic Regression

Training set will be 70% of dataset and Test set will be remaining 30%

Build Model using Training Data

Question of Interest? What are the odds of getting a fracture, given certain conditions?

```
set.seed(84)
model <- glm(FRACTURE ~ AGE + WEIGHT + HEIGHT + BMI + PRIORFRAC + PREMENO + MOMFRAC + ARMASSIST + SMOKE
model
```

```
##
## Call:  glm(formula = FRACTURE ~ AGE + WEIGHT + HEIGHT + BMI + PRIORFRAC +
##     PREMENO + MOMFRAC + ARMASSIST + SMOKE + RATERISK, family = "binomial",
##     data = trainingData)
##
## Coefficients:
## (Intercept)          AGE       WEIGHT       HEIGHT          BMI
##   -12.04673      0.03168     -0.10711      0.04735      0.29193
##  PRIORFRAC1     PREMENO1     MOMFRAC1   ARMASSIST1       SMOKE1
##     0.73265      0.04114      0.35482      0.30067     -0.08005
##   RATERISK2    RATERISK3
##     0.38692      0.57786
##
## Degrees of Freedom: 375 Total (i.e. Null);  364 Residual
```

```
## Null Deviance:       422.9
## Residual Deviance: 385.4     AIC: 409.4
```

```r
summary(model)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + WEIGHT + HEIGHT + BMI + PRIORFRAC +
##     PREMENO + MOMFRAC + ARMASSIST + SMOKE + RATERISK, family = "binomial",
##     data = trainingData)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4739  -0.7388  -0.5757  -0.1189   2.1597
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -12.04673   13.81668  -0.872  0.38326
## AGE           0.03168    0.01715   1.847  0.06472 .
## WEIGHT       -0.10711    0.09271  -1.155  0.24793
## HEIGHT        0.04735    0.08516   0.556  0.57823
## BMI           0.29193    0.23882   1.222  0.22157
## PRIORFRAC1    0.73265    0.28371   2.582  0.00981 **
## PREMENO1      0.04114    0.32545   0.126  0.89940
## MOMFRAC1      0.35482    0.36197   0.980  0.32697
## ARMASSIST1    0.30067    0.29666   1.014  0.31080
## SMOKE1       -0.08005    0.50041  -0.160  0.87290
## RATERISK2     0.38692    0.32506   1.190  0.23393
## RATERISK3     0.57786    0.34936   1.654  0.09812 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 422.88  on 375  degrees of freedom
## Residual deviance: 385.45  on 364  degrees of freedom
## AIC: 409.45
##
## Number of Fisher Scoring iterations: 4
```

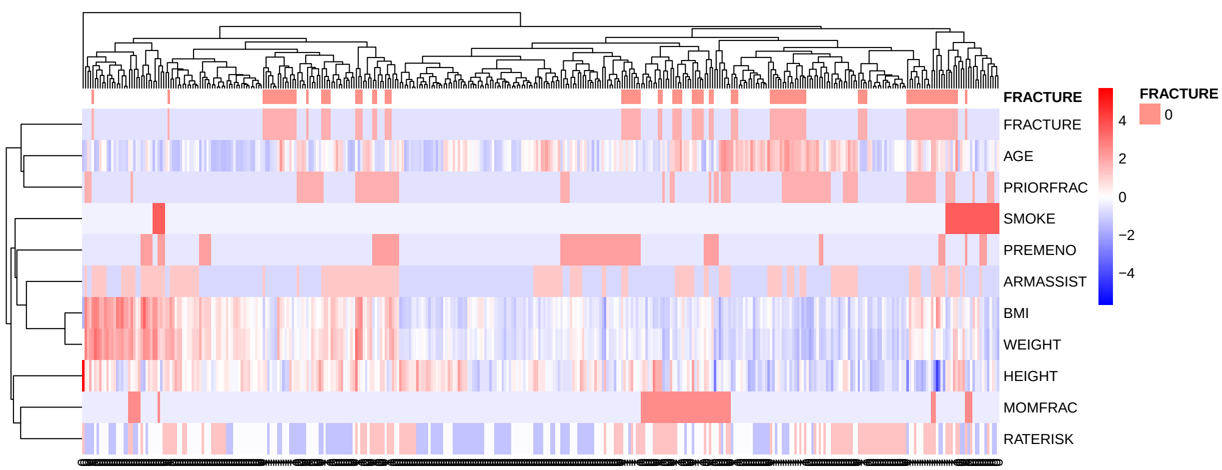
```r
h1 <- hoslem.test(model$y, fitted(model), g = 10) #number of groups to divide dataset into is 10
h1
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  model$y, fitted(model)
## X-squared = 7.8006, df = 8, p-value = 0.4532
```

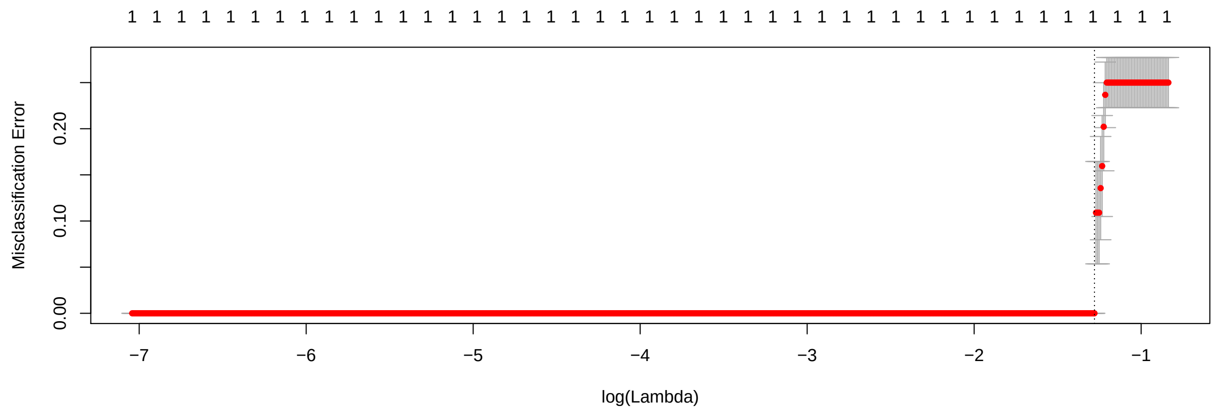
Interpretation of logistic regression model: Weight, height, BMI, Premeno, Armassist, and Smoke are not statistically significant variables. Priorfrac and Age are statistically significant variables and have the lowest p-value indicating a strong association with having a Fracture.

Clustering

```r
#Lets look at a heatmap using hierarchical clustering to see if the
#response naturally clusters out using the predictors

#Transposting the predictor matrix and giving the response categories its
#row names.
#Get Training Set

# convert factors to numeric for pheatmap
temp <- trainingData
indx <- sapply(temp, is.factor)
temp[indx] <- lapply(temp[indx], function(x) as.numeric(as.character(x)))

dat.train <- temp

dat.train.x <- dat.train[,1:ncol(dat.train)]
dat.train.y <- dat.train$FRACTURE

dat.train.y <- as.factor(as.character(dat.train.y))

#Heatmap
x<-t(dat.train.x)
colnames(x)<-dat.train.y
pheatmap(x,annotation_col=data.frame(FRACTURE=dat.train.y),scale="row",legend=T,color=colorRampPalette(c
```




```r
##logistic regression
dat.train.x <- as.matrix(dat.train.x)

cvfit <- cv.glmnet(dat.train.x, dat.train.y, family = "binomial", type.measure = "class", nlambda = 100
plot(cvfit)
```




```r
coef(cvfit, s = "lambda.min")
```

```
## 12 x 1 sparse Matrix of class "dgCMatrix"
##                     1
## (Intercept) -1.653758
## AGE          .
## BMI          .
## HEIGHT       .
## WEIGHT       .
## PRIORFRAC    .
## PREMENO      .
## MOMFRAC      .
## ARMASSIST    .
## SMOKE        .
## RATERISK     .
## FRACTURE     1.726571
```

*** *Appendix B:* Model Comparison - Analysis ==========

```
## 'data.frame':    500 obs. of  14 variables:
##  $ SUB_ID   : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ SITE_ID  : int  1 4 6 6 1 5 5 1 1 4 ...
##  $ PHY_ID   : int  14 284 305 309 37 299 302 36 8 282 ...
##  $ PRIORFRAC: Factor w/ 2 levels "0","1": 1 1 2 1 1 2 1 2 2 1 ...
##  $ AGE      : int  62 65 88 82 61 67 84 82 86 58 ...
##  $ WEIGHT   : num  70.3 87.1 50.8 62.1 68 68 50.8 40.8 62.6 63.5 ...
##  $ HEIGHT   : int  158 160 157 160 152 161 150 153 156 166 ...
##  $ BMI      : num  28.2 34 20.6 24.3 29.4 ...
##  $ PREMENO  : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ MOMFRAC  : Factor w/ 2 levels "0","1": 1 1 2 1 1 1 1 1 1 1 ...
##  $ ARMASSIST: Factor w/ 2 levels "0","1": 1 1 2 1 1 1 1 1 1 1 ...
##  $ SMOKE    : Factor w/ 2 levels "0","1": 1 1 1 1 1 2 1 1 1 1 ...
##  $ RATERISK : Factor w/ 3 levels "1","2","3": 2 2 1 1 2 2 1 2 2 1 ...
##  $ FRACTURE : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
```

Create Train and Validation Datasets

```
set.seed(999)
validation_index = createDataPartition(dataset$FRACTURE, p=0.70, list=FALSE)
validationData = dataset[-validation_index,c(4:14)]
trainingData = dataset[validation_index,c(4:14)]

table(dataset$FRACTURE)
```

```
##
##   0   1
## 375 125
```

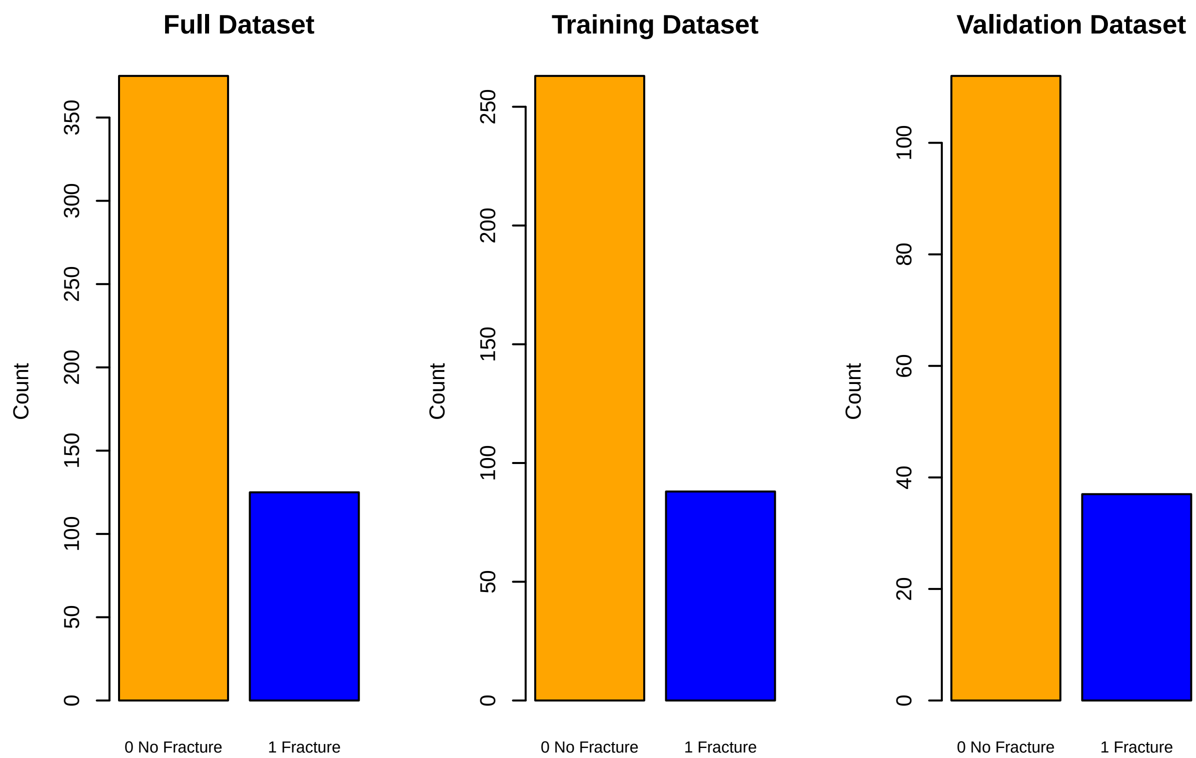
```
table(trainingData$FRACTURE)
```

```
##
##   0   1
## 263  88
```

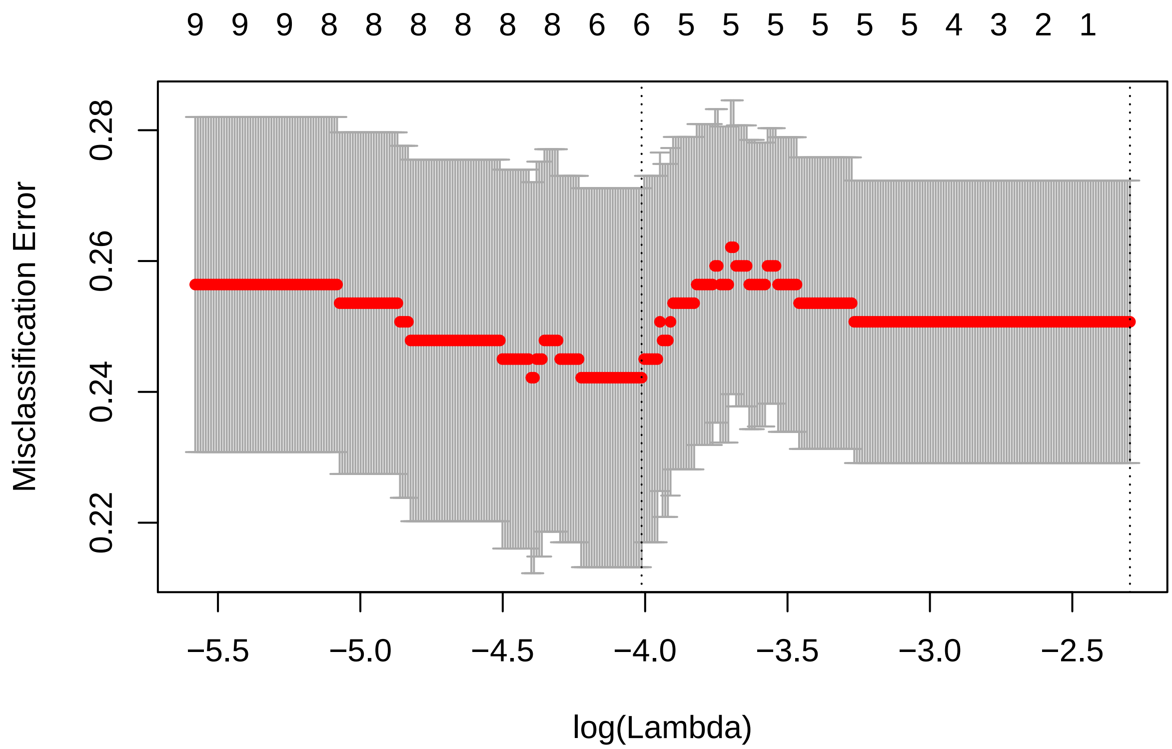
```
table(validationData$FRACTURE)
```

```
##
##   0   1
## 112  37
```

```
#BarPlots of Fracture counts between full, training and validation datasets.
par(mfrow=c(1,3))
#par(mar=c(5,8,4,2)) # increase y-axis margin.
count_full <- table(dataset$FRACTURE)
count_trn <- table(trainingData$FRACTURE)
count_test <- table(validationData$FRACTURE)


barplot(count_full,main="Full Dataset", ylab="Count", col=c("orange","blue"),names.arg=c("0 No Fracture

barplot(count_trn,main="Training Dataset", ylab="Count", col=c("orange","blue"),names.arg=c("0 No Fractu

barplot(count_test,main="Validation Dataset", ylab="Count", col=c("orange","blue"),names.arg=c("0 No Fra
```




```
set.seed(999)

## Formatting Test Data Set
# Recode Rate Risk Variable since its ordinal and we donot want to loose its info if it gets
# coded as nominal variable before running the Model
validationData$RATERISK <- factor(validationData$RATERISK, levels = c(1,2,3), ordered = T)

xfactors_test <- model.matrix(validationData$FRACTURE ~ validationData$PRIORFRAC + validationData$PREMEI
x_test <- as.matrix(data.frame(validationData$AGE, validationData$WEIGHT, validationData$HEIGHT, valida

## Formatting Training Data Set
trainingData$RATERISK <- factor(trainingData$RATERISK, levels = c(1,2,3), ordered = T)
xfactors_train <- model.matrix(trainingData$FRACTURE ~ trainingData$PRIORFRAC + trainingData$PREMENO + t
x_train <- as.matrix(data.frame(trainingData$AGE, trainingData$WEIGHT, trainingData$HEIGHT, trainingData

# Doing Cross validation to find the best fitting model based upon Lasso
cvfit <- cv.glmnet(x_train, y=trainingData$FRACTURE, family = "binomial", type.measure = "class", nlambd
plot(cvfit)
```

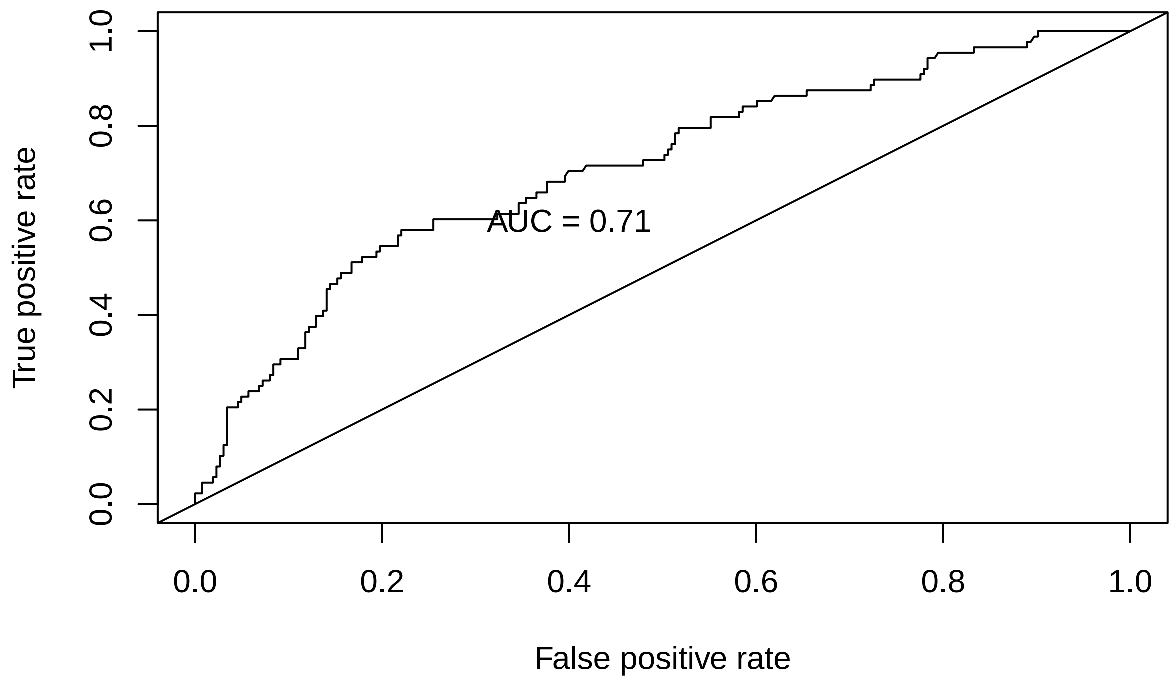



```r
# Model with Lowest Lambda is shrinking all the coefficients, hence selecting lambda based upon
# Test Set AUC and EDA Results
#cvfit$glmnet.fit
coef(cvfit, s="lambda.min")
```

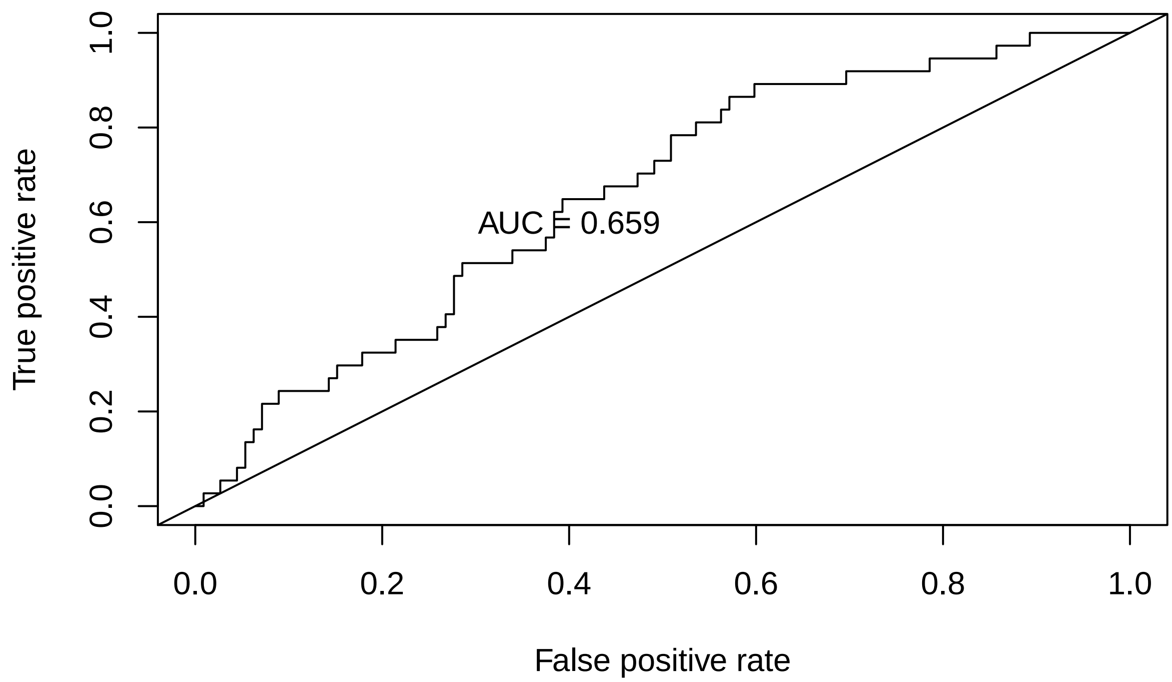
```
## 12 x 1 sparse Matrix of class "dgCMatrix"
##                                  1
## (Intercept)             1.52902669
## trainingData.AGE        0.03598544
## trainingData.WEIGHT     .
## trainingData.HEIGHT    -0.03340871
## trainingData.BMI        .
## trainingData.PRIORFRAC1  0.15180349
## trainingData.PREMENO1   .
## trainingData.MOMFRAC1   0.04035537
## trainingData.ARMASSIST1  0.52512963
## trainingData.SMOKE1     .
## trainingData.RATERISK.L  0.33991586
## trainingData.RATERISK.Q  .
```

```r
# Fitting the best model based upon selected lambda
fit <- glmnet(x_train, y=trainingData$FRACTURE, family="binomial", alpha = 1, lambda = cvfit$lambda.min)

# First Predicting the responses on training data set itself
fit.pred <- predict(fit, newx = x_train, type = "response")
```

```
#Create ROC curves for training Data Set
pred <- prediction(fit.pred[,1], trainingData$FRACTURE)
roc.perf = performance(pred, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred, measure = "auc")
auc.train <- auc.train@y.values

##Plot ROC for training Set
plot(roc.perf)
abline(a=0, b= 1) #Ref line indicating poor performance
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```




```
#Run model from training set on validation Set
fit.pred1 <- predict(fit, newx = x_test, type = "response")

#ROC curves
pred1 <- prediction(fit.pred1[,1], validationData$FRACTURE)
roc.perf1 = performance(pred1, measure = "tpr", x.measure = "fpr")
auc.val1 <- performance(pred1, measure = "auc")
auc.val1 <- auc.val1@y.values
plot(roc.perf1)
abline(a=0, b= 1)
text(x = .40, y = .6,paste("AUC = ", round(auc.val1[[1]],3), sep = ""))
```




```r
#confusion matrix
pdata <- predict(fit, newx = x_test, type = "response")
pdata_logical <- pdata[, 1] > 0.5
confusionMatrix(data = as.factor(as.numeric(pdata_logical)), reference = as.factor(as.numeric(validatio
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 108  35
##          1   4   2
##
##                Accuracy : 0.7383
##                  95% CI : (0.66, 0.8068)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.6866
##
##                   Kappa : 0.0255
##  Mcnemar's Test P-Value : 1.556e-06
##
##             Sensitivity : 0.96429
##             Specificity : 0.05405
##          Pos Pred Value : 0.75524
##          Neg Pred Value : 0.33333
##              Prevalence : 0.75168
##          Detection Rate : 0.72483
```

```
##    Detection Prevalence : 0.95973
##       Balanced Accuracy : 0.50917
##
##        'Positive' Class : 0
##
```

```r
#mydata <- dataset[, c(4:14)] %>% dplyr::select_if(is.numeric)
#predictors <- colnames(mydata)
#mydata <- mydata %>%
#  mutate(logit = log(probabilities/(1-probabilities))) %>%
#  gather(key = "predictors", value = "predictor.value", -logit)
```

Run Normal Logit Model with Identified Predictors

```r
set.seed(999)

logit.fit <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK , data = training
summary(logit.fit)
```

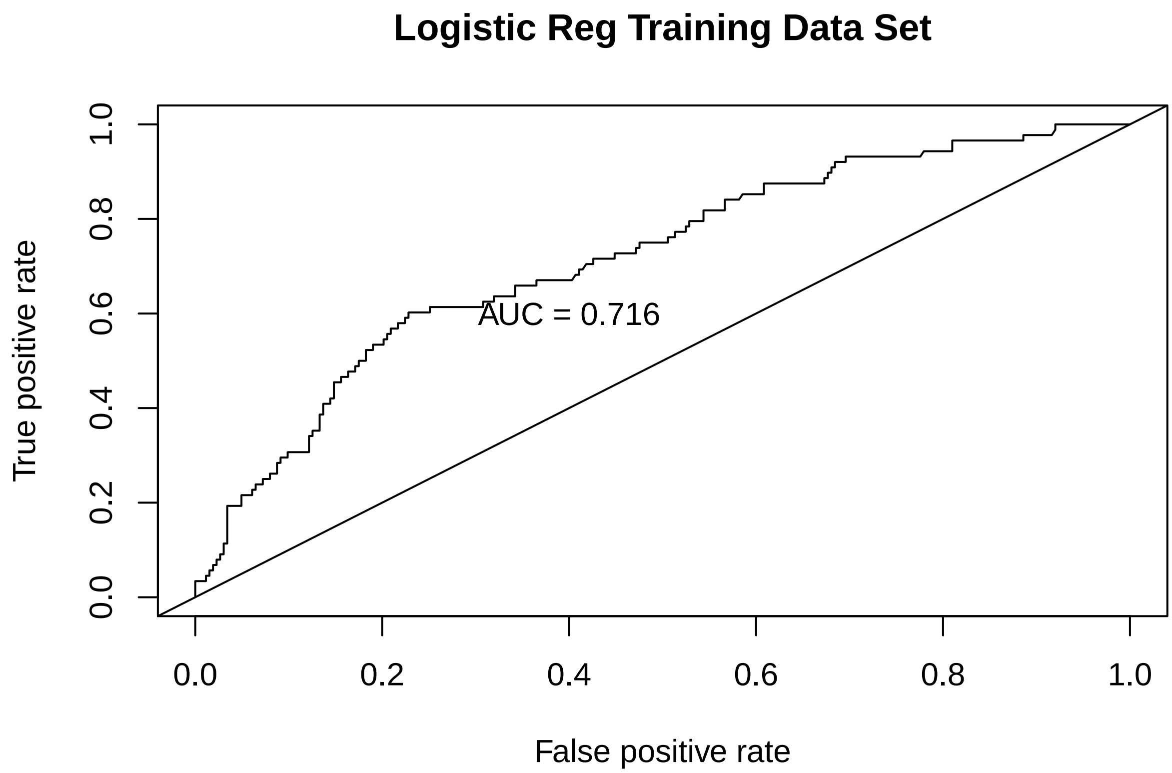
```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK, family = binomial(link = "logit"),
##     data = trainingData)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5491  -0.7377  -0.5763   0.2298   2.2214
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.33365    3.80104   0.877  0.38047
## AGE          0.04347    0.01578   2.755  0.00587 **
## HEIGHT      -0.04881    0.02165  -2.254  0.02418 *
## PRIORFRAC1   0.22281    0.30097   0.740  0.45912
## MOMFRAC1     0.33522    0.38263   0.876  0.38097
## ARMASSIST1   0.68418    0.27861   2.456  0.01406 *
## RATERISK.L   0.50762    0.24656   2.059  0.03951 *
## RATERISK.Q  -0.06727    0.22219  -0.303  0.76209
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 395.31  on 350  degrees of freedom
## Residual deviance: 355.55  on 343  degrees of freedom
## AIC: 371.55
##
## Number of Fisher Scoring iterations: 4
```

```r
# To exponentiate the log ODDS to make it ODDS Ratio and also get corresponding 95% CIs
exp(cbind(ODDs_Ratio = coef(logit.fit), confint(logit.fit)))
```

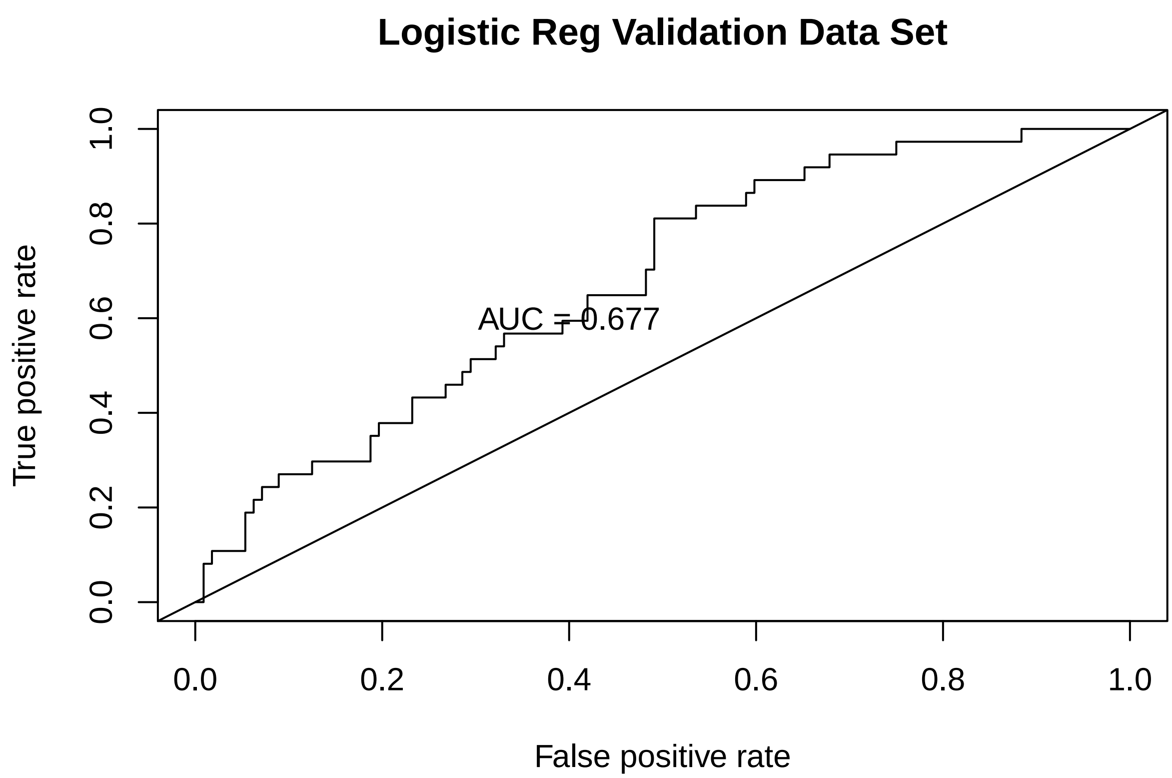
```
## Waiting for profiling to be done...
```

```
##              ODDs_Ratio     2.5 %       97.5 %
## (Intercept) 28.0403767 0.0172620 5.378401e+04
## AGE          1.0444253 1.0128322 1.077662e+00
## HEIGHT       0.9523628 0.9118527 9.929059e-01
## PRIORFRAC1   1.2495774 0.6857875 2.237992e+00
## MOMFRAC1     1.3982464 0.6449924 2.917750e+00
## ARMASSIST1   1.9821443 1.1469582 3.428352e+00
## RATERISK.L   1.6613370 1.0283916 2.713240e+00
## RATERISK.Q   0.9349462 0.6060378 1.451499e+00
```

```r
# First Predicting the responses on training data set itself
logistic.fit.pred.train <- predict(logit.fit, newdata=trainingData, type = "response")

#Create ROC curves for training Data Set
pred.train <- prediction(logistic.fit.pred.train, trainingData$FRACTURE)
roc.perf = performance(pred.train, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.train, measure = "auc")
auc.train <- auc.train@y.values

##Plot ROC for training Set
plot(roc.perf, main="Logistic Reg Training Data Set")
abline(a=0, b= 1) #Ref line indicating poor performance
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```




```r
#Run model from training set on validation Set
logistic.fit.pred.test <- predict(logit.fit, newdata=validationData, type = "response")

#ROC curves
pred.test <- prediction(logistic.fit.pred.test, validationData$FRACTURE)
roc.perf1 = performance(pred.test, measure = "tpr", x.measure = "fpr")
auc.val1 <- performance(pred.test, measure = "auc")
auc.val1 <- auc.val1@y.values
plot(roc.perf1, main="Logistic Reg Validation Data Set")
abline(a=0, b= 1)
text(x = .40, y = .6,paste("AUC = ", round(auc.val1[[1]],3), sep = ""))
```




```
#confusion matrix
pdata_logical <-  logistic.fit.pred.test > 0.5
confusionMatrix(data = as.factor(as.numeric(pdata_logical)), reference = as.factor(as.numeric(validatio
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 106  32
##          1   6   5
##
##                Accuracy : 0.745
##                  95% CI : (0.6672, 0.8128)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.6175
##
##                   Kappa : 0.1067
##  Mcnemar's Test P-Value : 5.002e-05
##
##             Sensitivity : 0.9464
##             Specificity : 0.1351
##          Pos Pred Value : 0.7681
##          Neg Pred Value : 0.4545
##              Prevalence : 0.7517
##          Detection Rate : 0.7114
##    Detection Prevalence : 0.9262
```

```
##       Balanced Accuracy : 0.5408
##
##        'Positive' Class : 0
##
```

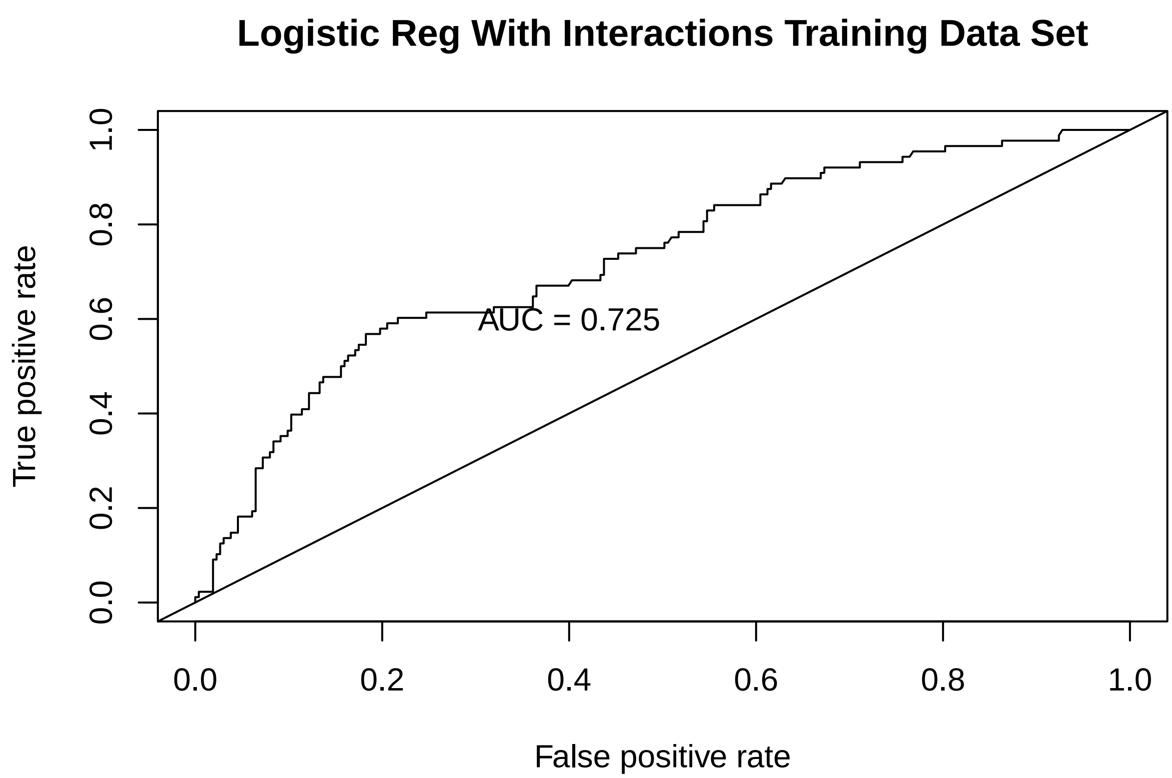
Add Interactions to Normal logit

```r
set.seed(999)
# Since top 3 predictors are Age, PriorFrac and RISK, adding model complexity
# via interactions
logit.fit.interactions <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK + AGE
summary(logit.fit.interactions)
```

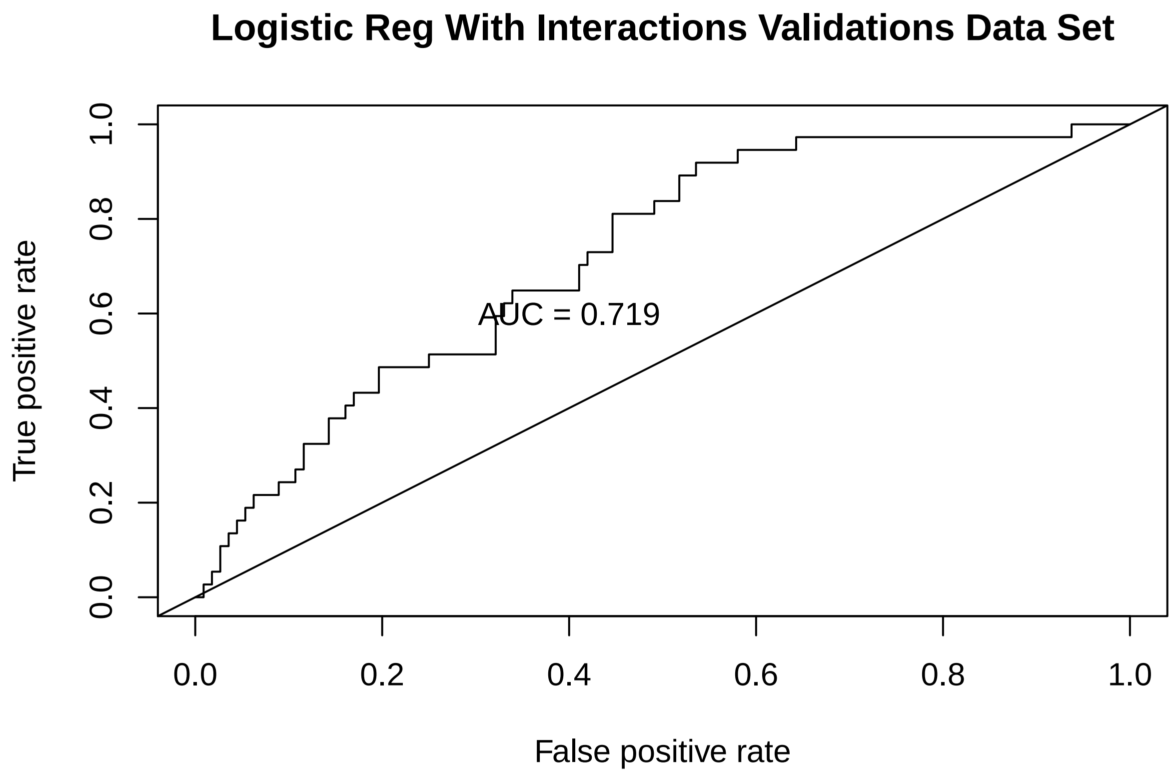
```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:PRIORFRAC + RATERISK:AGE + MOMFRAC:ARMASSIST,
##     family = binomial(link = "logit"), data = trainingData)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5521  -0.7592  -0.5543   0.2845   2.3802
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          1.65488    3.98301   0.415  0.67779
## AGE                  0.06735    0.02058   3.273  0.00107 **
## HEIGHT              -0.04913    0.02191  -2.242  0.02495 *
## PRIORFRAC1           3.83397    2.26015   1.696  0.08982 .
## MOMFRAC1             0.74167    0.50795   1.460  0.14426
## ARMASSIST1           0.80585    0.29990   2.687  0.00721 **
## RATERISK.L           1.64141    2.00121   0.820  0.41210
## RATERISK.Q          -1.25322    1.78216  -0.703  0.48193
## AGE:PRIORFRAC1      -0.05038    0.03124  -1.612  0.10688
## AGE:RATERISK.L      -0.01548    0.02788  -0.555  0.57869
## AGE:RATERISK.Q       0.01632    0.02498   0.653  0.51355
## MOMFRAC1:ARMASSIST1 -0.74229    0.76220  -0.974  0.33011
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 395.31  on 350  degrees of freedom
## Residual deviance: 351.13  on 339  degrees of freedom
## AIC: 375.13
##
## Number of Fisher Scoring iterations: 5
```

```r
# First Predicting the responses on training data set itself
logistic.fit.pred.train.interaction <- predict(logit.fit.interactions, newdata=trainingData, type = "re
```

```
#Create ROC curves for training Data Set
pred.train.interaction <- prediction(logistic.fit.pred.train.interaction, trainingData$FRACTURE)
roc.perf = performance(pred.train.interaction, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.train.interaction, measure = "auc")
auc.train <- auc.train@y.values

##Plot ROC for training Set
plot(roc.perf, main="Logistic Reg With Interactions Training Data Set")
abline(a=0, b= 1) #Ref line indicating poor performance
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```




```
#Run model from training set on validation Set
logistic.fit.pred.test.interaction <- predict(logit.fit.interactions, newdata=validationData, type = "r

#ROC curves
pred.test.interaction <- prediction(logistic.fit.pred.test.interaction, validationData$FRACTURE)
roc.perf1 = performance(pred.test.interaction, measure = "tpr", x.measure = "fpr")
auc.val1 <- performance(pred.test.interaction, measure = "auc")
auc.val1 <- auc.val1@y.values
plot(roc.perf1, main="Logistic Reg With Interactions Validations Data Set")
abline(a=0, b= 1)
text(x = .40, y = .6,paste("AUC = ", round(auc.val1[[1]],3), sep = ""))
```




```
#confusion matrix
pdata_logical <-  logistic.fit.pred.test.interaction > 0.5
confusionMatrix(data = as.factor(as.numeric(pdata_logical)), reference = as.factor(as.numeric(validatio
```

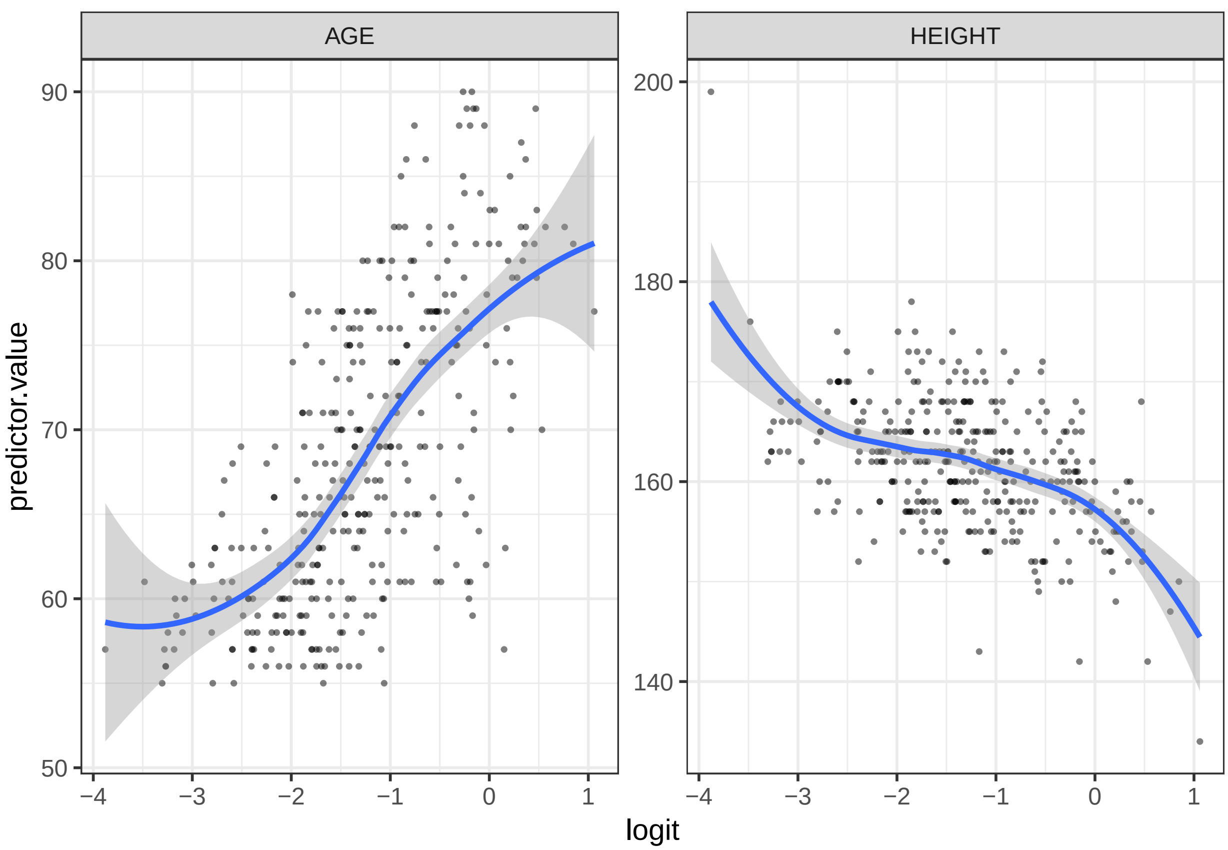
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 105  30
##          1   7   7
##
##                Accuracy : 0.7517
##                  95% CI : (0.6743, 0.8187)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.5440183
##
##                   Kappa : 0.16
##  Mcnemar's Test P-Value : 0.0002983
##
##             Sensitivity : 0.9375
##             Specificity : 0.1892
##          Pos Pred Value : 0.7778
##          Neg Pred Value : 0.5000
##              Prevalence : 0.7517
##          Detection Rate : 0.7047
##    Detection Prevalence : 0.9060
```

```
##        Balanced Accuracy : 0.5633
##
##         'Positive' Class : 0
##
```

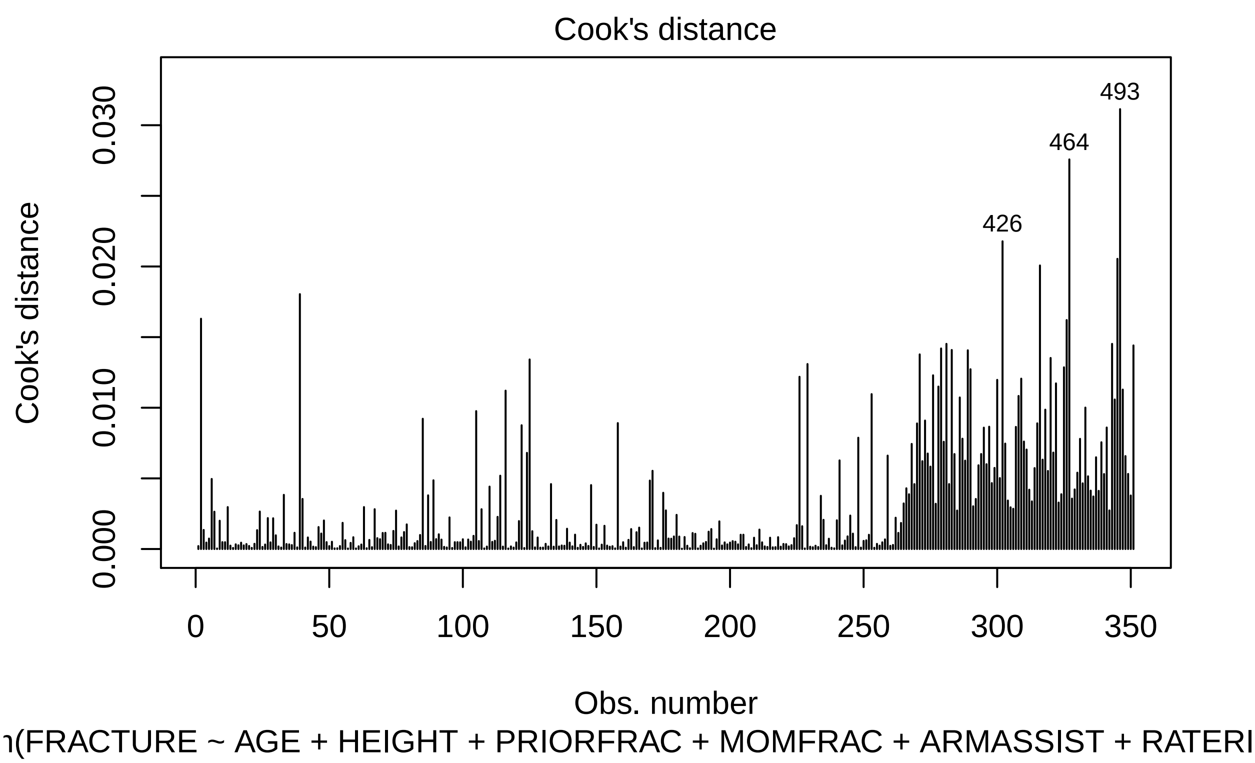
```r
# Checking the assumptions
probabilities <- predict(logit.fit.interactions, type = "response")
predicted.classes <- ifelse(probabilities > 0.5, "pos", "neg")
head(predicted.classes)
```

```
##     1     3     4     5     6     7
## "neg" "neg" "neg" "neg" "neg" "neg"
```

```r
# Linearity assumption
subNumericPred <- trainingData %>% dplyr::select(AGE, HEIGHT)
predictors <- colnames(subNumericPred)
subNumericPred <- subNumericPred %>%
                  mutate(logit = log(probabilities/(1-probabilities))) %>%
                  gather(key = "predictors", value = "predictor.value", -logit)

ggplot(subNumericPred, aes(logit, predictor.value)) +
                geom_point(size = 0.5, alpha = 0.5) +
                geom_smooth(method = "loess") +
                theme_bw() +
                facet_wrap(~predictors, scales = "free_y")
```



```r
plot(logit.fit.interactions, which = 4, id.n =3)
```



Running Random Forest Fit

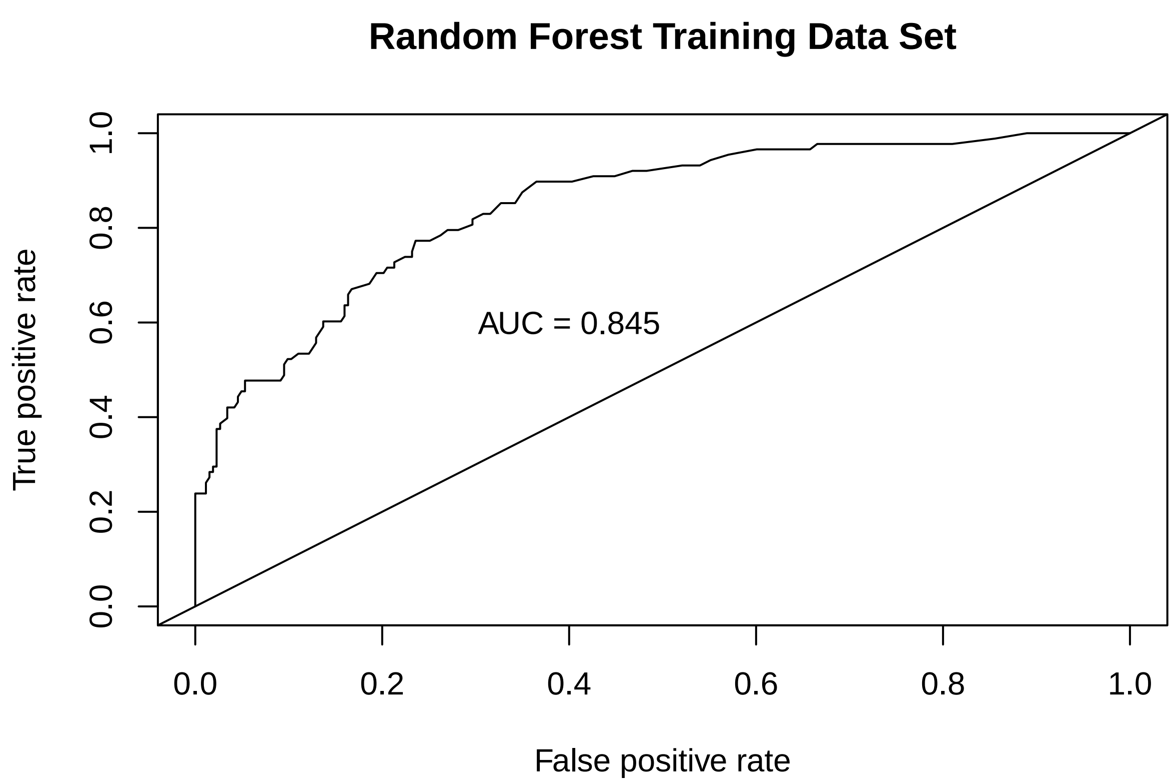
```r
set.seed(999)

str(trainingData)
```

```
## 'data.frame':    351 obs. of  11 variables:
##  $ PRIORFRAC: Factor w/ 2 levels "0","1": 1 2 1 1 2 1 2 1 1 1 ...
##  $ AGE      : int  62 88 82 61 67 84 86 58 67 56 ...
##  $ WEIGHT   : num  70.3 50.8 62.1 68 68 ...
##  $ HEIGHT   : int  158 157 160 152 161 150 156 166 153 167 ...
##  $ BMI      : num  28.2 20.6 24.3 29.4 26.2 ...
##  $ PREMENO  : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ MOMFRAC  : Factor w/ 2 levels "0","1": 1 2 1 1 1 1 1 1 2 1 ...
##  $ ARMASSIST: Factor w/ 2 levels "0","1": 1 2 1 1 1 1 1 1 1 2 ...
##  $ SMOKE    : Factor w/ 2 levels "0","1": 1 1 1 1 2 1 1 1 2 2 ...
##  $ RATERISK : Ord.factor w/ 3 levels "1"<"2"<"3": 2 1 1 2 2 1 2 1 1 2 ...
##  $ FRACTURE : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
```

```r
rf.fit <- randomForest(FRACTURE ~ ., data=trainingData, mtry=4, ntree=500, maxnodes = 12, importance=T)
rf.fit
```

```
##
## Call:
##  randomForest(formula = FRACTURE ~ ., data = trainingData, mtry = 4,      ntree = 500, maxnodes = 12
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 4
##
##         OOB estimate of  error rate: 24.79%
## Confusion matrix:
##     0 1 class.error
## 0 260 3  0.01140684
## 1  84 4  0.95454545
```

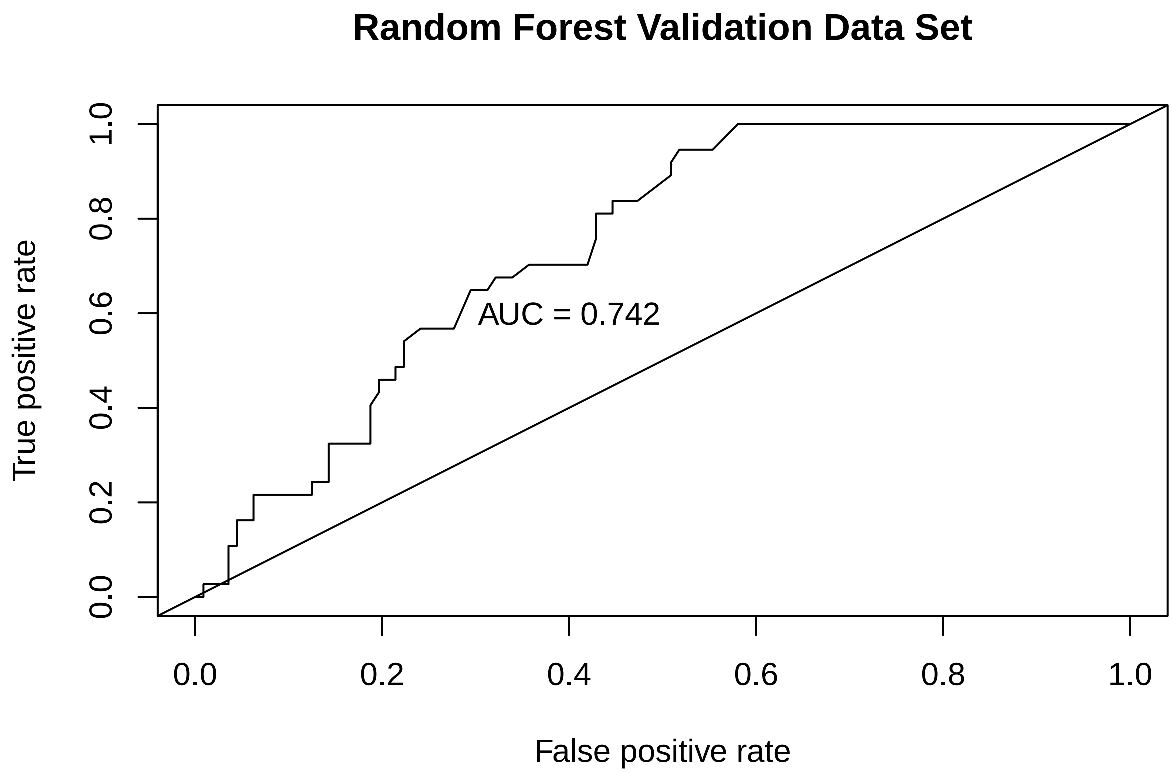
```r
rf.fit.pred.train <- predict(rf.fit, newdata=trainingData, type="prob")
pred.train.rf <- prediction(rf.fit.pred.train[,2], trainingData$FRACTURE)
roc.perf = performance(pred.train.rf, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.train.rf, measure = "auc")
auc.train <- auc.train@y.values
plot(roc.perf, main="Random Forest Training Data Set")
abline(a=0, b= 1)
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```



```r
#confusion matrix Training
pdata_logical_train <-  (rf.fit.pred.train[,2] >= 0.5)
confusionMatrix(data = as.factor(as.numeric(pdata_logical_train)), reference = as.factor(as.numeric(tra
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 263  76
##          1   0  12
##
##                Accuracy : 0.7835
##                  95% CI : (0.7367, 0.8254)
##     No Information Rate : 0.7493
##     P-Value [Acc > NIR] : 0.07672
##
##                   Kappa : 0.1913
##  Mcnemar's Test P-Value : < 2e-16
##
##             Sensitivity : 1.0000
##             Specificity : 0.1364
##          Pos Pred Value : 0.7758
##          Neg Pred Value : 1.0000
##              Prevalence : 0.7493
##          Detection Rate : 0.7493
##    Detection Prevalence : 0.9658
##       Balanced Accuracy : 0.5682
##
##        'Positive' Class : 0
##
```

```r
rf.fit.pred.test <- predict(rf.fit, newdata=validationData, type="prob")
pred.test.rf <- prediction(rf.fit.pred.test[,2], validationData$FRACTURE)
roc.perf = performance(pred.test.rf, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.test.rf, measure = "auc")
auc.train <- auc.train@y.values
plot(roc.perf, main="Random Forest Validation Data Set")
abline(a=0, b= 1)
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```




```r
#confusion matrix Test
pdata_logical <-  rf.fit.pred.test[,2] > 0.5
confusionMatrix(data = as.factor(as.numeric(pdata_logical)), reference = as.factor(as.numeric(validatio
```

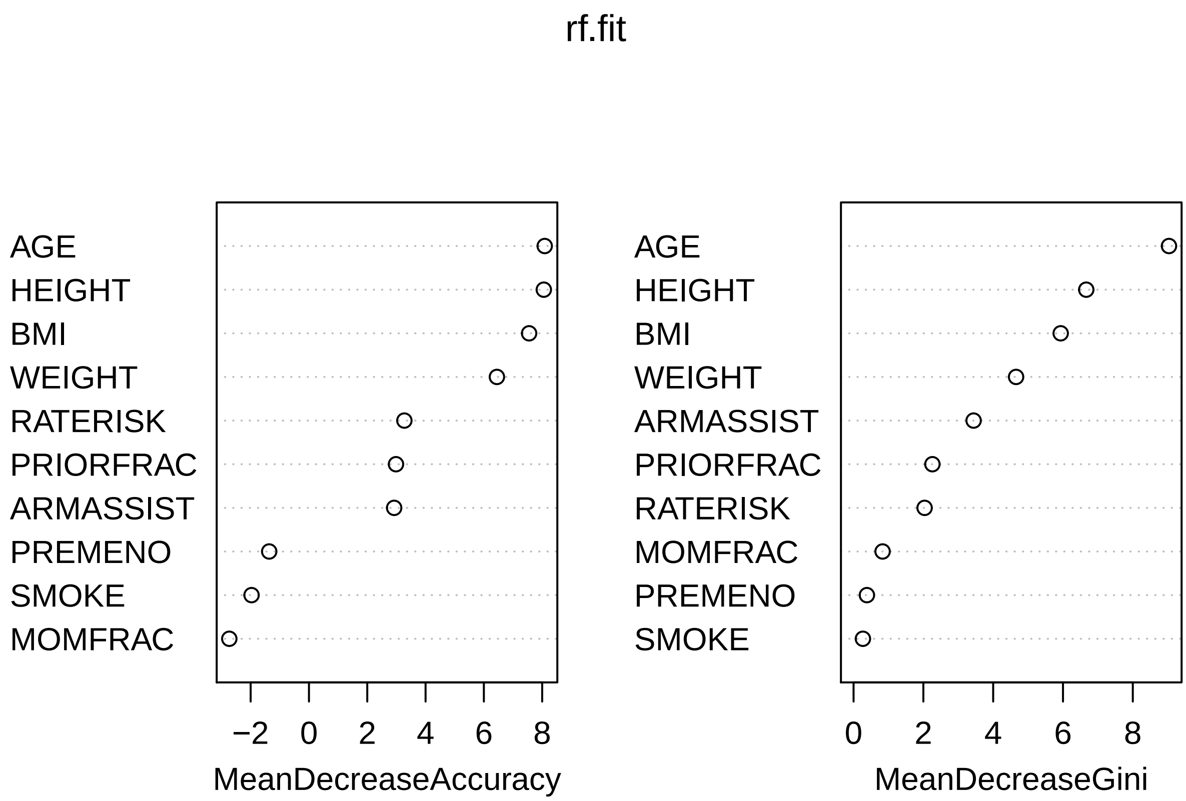
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 111  37
##          1   1   0
##
##                Accuracy : 0.745
##                  95% CI : (0.6672, 0.8128)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.6175
##
##                   Kappa : -0.0132
##  Mcnemar's Test P-Value : 1.365e-08
##
##             Sensitivity : 0.9911
##             Specificity : 0.0000
##          Pos Pred Value : 0.7500
##          Neg Pred Value : 0.0000
##              Prevalence : 0.7517
##          Detection Rate : 0.7450
##    Detection Prevalence : 0.9933
```

```
##       Balanced Accuracy : 0.4955
##
##        'Positive' Class : 0
##
```

```r
#confusion matrix Test Lower Cutoff
pdata_logical_lowercf <-  rf.fit.pred.test[,2] >= 0.3
confusionMatrix(data = as.factor(as.numeric(pdata_logical_lowercf)), reference = as.factor(as.numeric(va
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 102  29
##          1  10   8
##
##                Accuracy : 0.7383
##                  95% CI : (0.66, 0.8068)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.686582
##
##                   Kappa : 0.1533
##  Mcnemar's Test P-Value : 0.003948
##
##             Sensitivity : 0.9107
##             Specificity : 0.2162
##          Pos Pred Value : 0.7786
##          Neg Pred Value : 0.4444
##              Prevalence : 0.7517
##          Detection Rate : 0.6846
##    Detection Prevalence : 0.8792
##       Balanced Accuracy : 0.5635
##
##        'Positive' Class : 0
##
```

```r
varImpPlot(rf.fit)
```



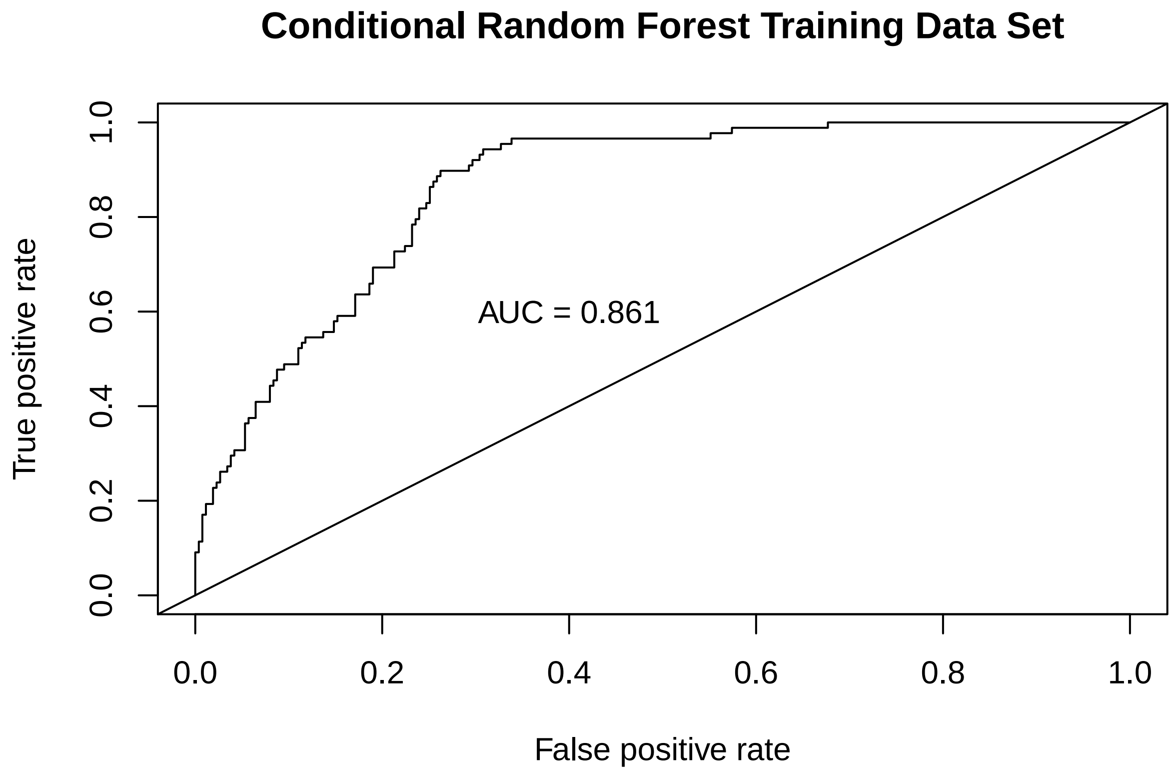
Running Conditional Random Forest Fit

```r
set.seed(999)

crf.fit <- cforest(FRACTURE ~ ., data=trainingData, control=cforest_unbiased(ntree=500))
crf.fit
```

```
##
##   Random Forest using Conditional Inference Trees
##
## Number of trees:  500
##
## Response:  FRACTURE
## Inputs:  PRIORFRAC, AGE, WEIGHT, HEIGHT, BMI, PREMENO, MOMFRAC, ARMASSIST, SMOKE, RATERISK
## Number of observations:  351
```

```r
crf.fit.pred.train <- predict(crf.fit, newdata=trainingData, OOB = TRUE, type="prob")
unlist.Pred.train <- matrix(unlist(crf.fit.pred.train), ncol=2,  byrow = TRUE)
pred.train.crf <- prediction(unlist.Pred.train[,2], trainingData$FRACTURE)
roc.perf = performance(pred.train.crf, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.train.crf, measure = "auc")
auc.train <- auc.train@y.values
plot(roc.perf, main="Conditional Random Forest Training Data Set")
```

```r
abline(a=0, b= 1)
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```

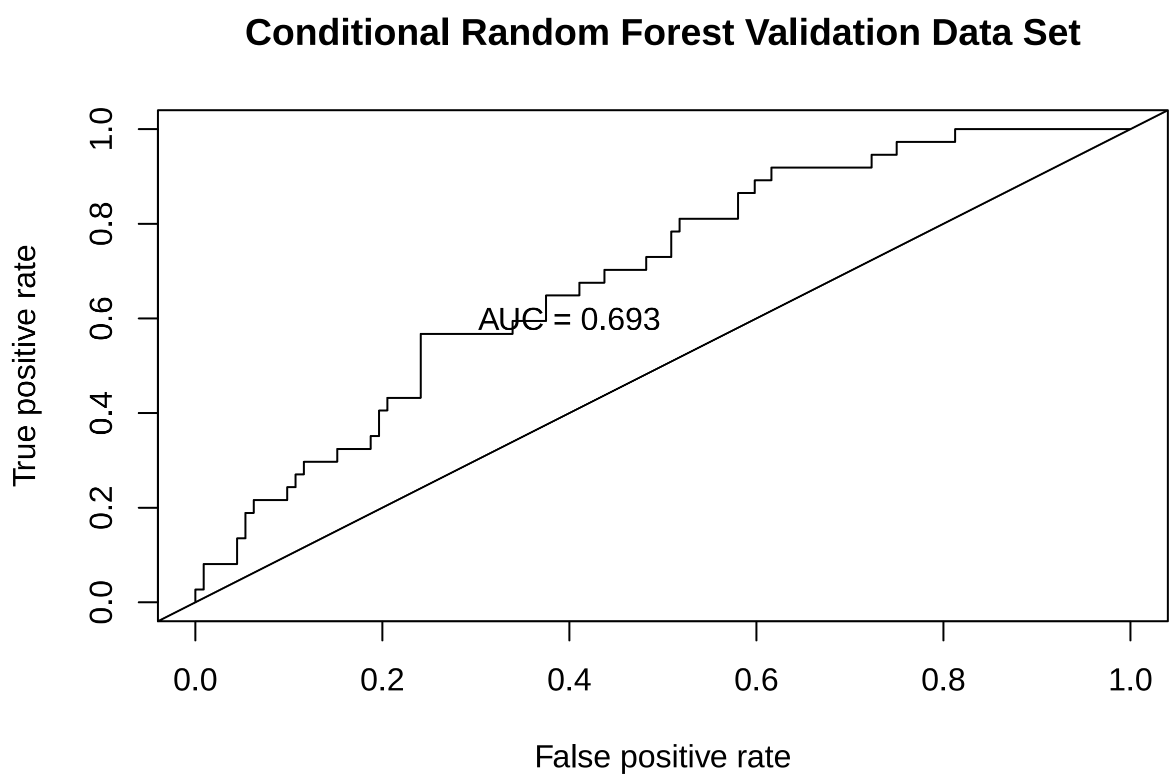



```r
#confusion matrix Training
pdata_logical_train <-  (unlist.Pred.train[,2] >= 0.5)
confusionMatrix(data = as.factor(as.numeric(pdata_logical_train)), reference = as.factor(as.numeric(tra
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 258  70
##          1   5  18
##
##                Accuracy : 0.7863
##                  95% CI : (0.7397, 0.8281)
##     No Information Rate : 0.7493
##     P-Value [Acc > NIR] : 0.06
##
##                   Kappa : 0.246
##  Mcnemar's Test P-Value : 1.467e-13
##
##             Sensitivity : 0.9810
##             Specificity : 0.2045
##          Pos Pred Value : 0.7866
```

```
##          Neg Pred Value : 0.7826
##              Prevalence : 0.7493
##          Detection Rate : 0.7350
##    Detection Prevalence : 0.9345
##       Balanced Accuracy : 0.5928
##
##        'Positive' Class : 0
##
```

```
crf.fit.pred.test <- predict(crf.fit, newdata=validationData, OOB = T, type="prob")
unlist.Pred.test <- matrix(unlist(crf.fit.pred.test), ncol=2,  byrow = TRUE)
pred.test.crf <- prediction(unlist.Pred.test[,2], validationData$FRACTURE)
roc.perf = performance(pred.test.crf, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.test.crf, measure = "auc")
auc.train <- auc.train@y.values
plot(roc.perf, main="Conditional Random Forest Validation Data Set")
abline(a=0, b= 1)
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```




```
#confusion matrix
pdata_logical <-   unlist.Pred.test[,2] > 0.5
confusionMatrix(data = as.factor(as.numeric(pdata_logical)), reference = as.factor(as.numeric(validation
```

```
## Confusion Matrix and Statistics
##
```

```
##           Reference
## Prediction   0   1
##          0 106  31
##          1   6   6
##
##                Accuracy : 0.7517
##                  95% CI : (0.6743, 0.8187)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.544
##
##                   Kappa : 0.1403
##  Mcnemar's Test P-Value : 7.961e-05
##
##             Sensitivity : 0.9464
##             Specificity : 0.1622
##          Pos Pred Value : 0.7737
##          Neg Pred Value : 0.5000
##              Prevalence : 0.7517
##          Detection Rate : 0.7114
##    Detection Prevalence : 0.9195
##       Balanced Accuracy : 0.5543
##
##        'Positive' Class : 0
##
```

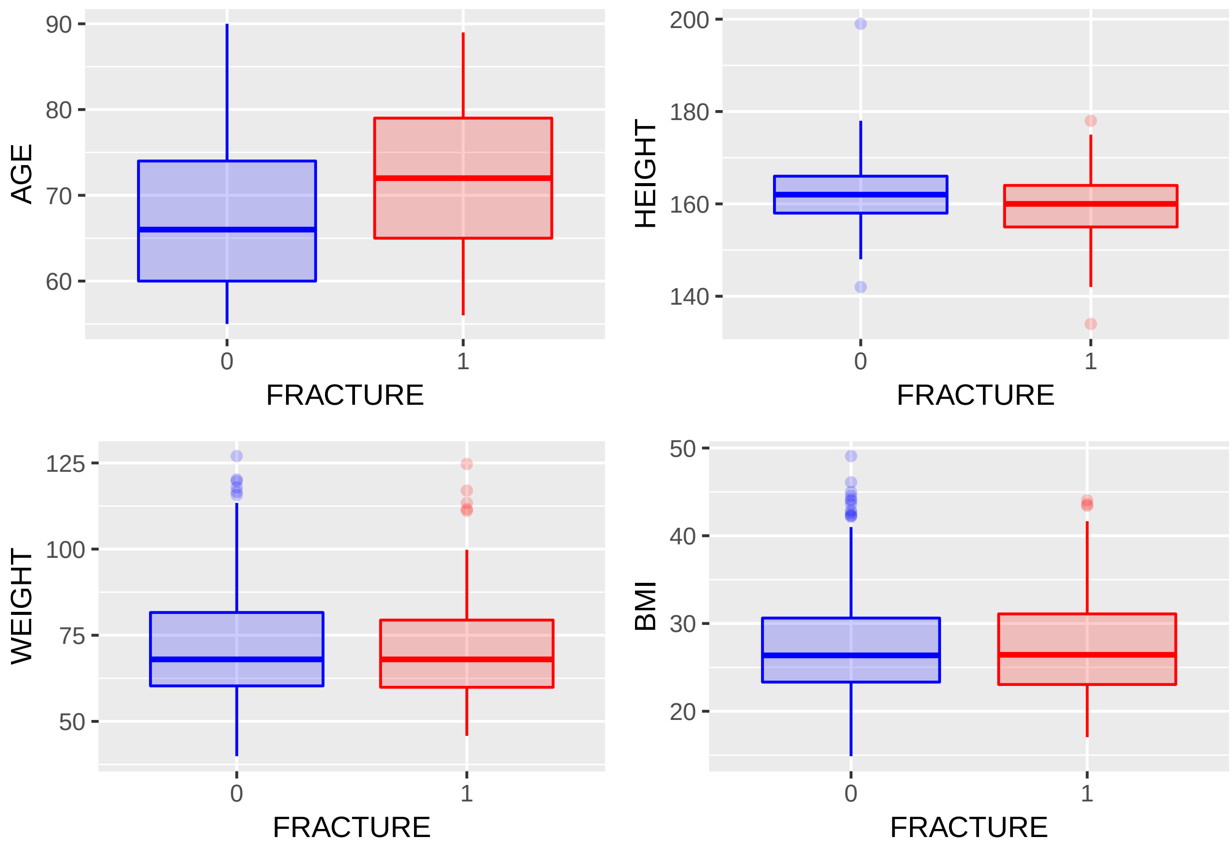
```r
relativeImp <- varimp(crf.fit)
sort(relativeImp, decreasing = T)
```

```
##           AGE        HEIGHT     ARMASSIST           BMI     PRIORFRAC
##  8.372093e-03  7.581395e-03  6.124031e-03  1.674419e-03  4.496124e-04
##        WEIGHT      RATERISK         SMOKE       PREMENO       MOMFRAC
##  2.790698e-04 -7.751938e-05 -7.751938e-05 -3.255814e-04 -7.751938e-04
```

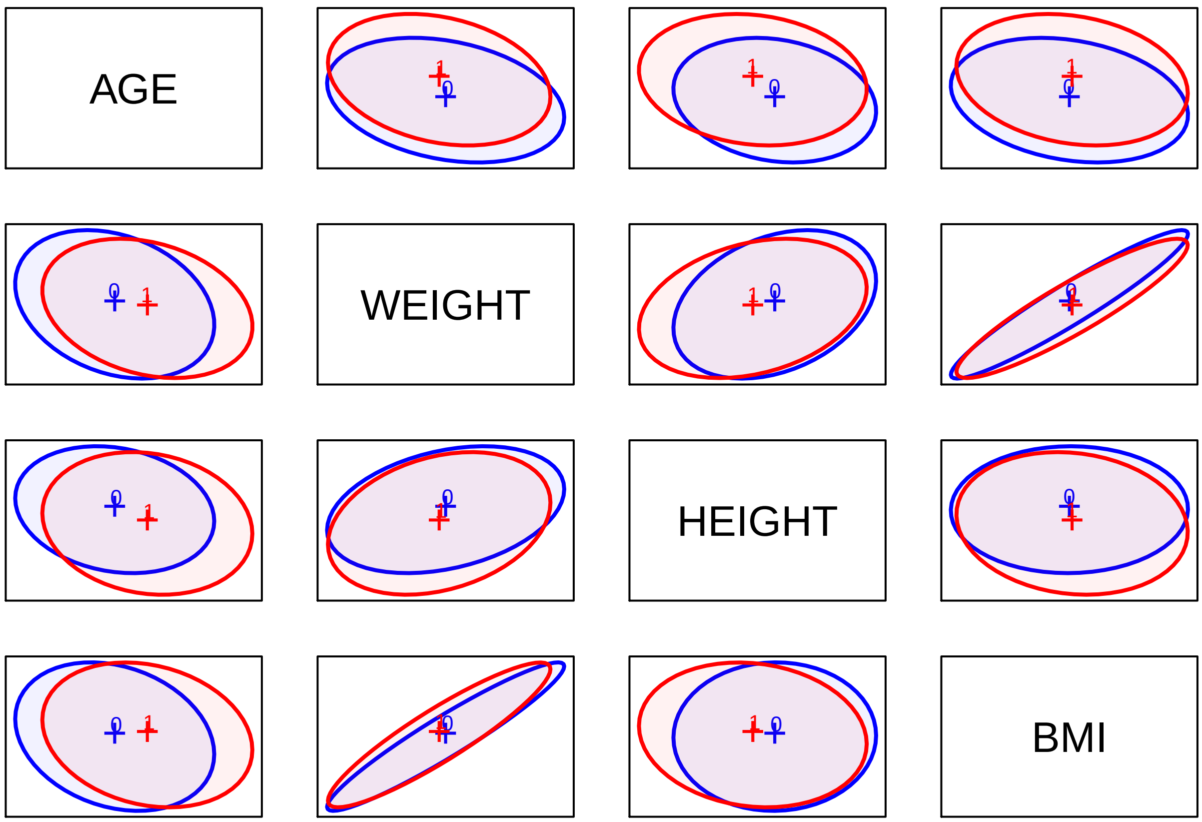
LDA AND QDA Model fit

```r
library(MASS)
library(gridExtra)

## Assumption of Eq Variance / CoVariance
box.AGE <- ggplot(dataset, aes(x = FRACTURE, y = AGE, col = FRACTURE, fill = FRACTURE)) +
  geom_boxplot(alpha = 0.2) +
  theme(legend.position = "none") +
  scale_color_manual(values = c("blue", "red")) +
  scale_fill_manual(values = c("blue", "red"))

box.HEIGHT <- ggplot(dataset, aes(x = FRACTURE, y = HEIGHT, col = FRACTURE, fill = FRACTURE)) +
  geom_boxplot(alpha = 0.2) +
  theme(legend.position = "none") +
  scale_color_manual(values = c("blue", "red")) +
  scale_fill_manual(values = c("blue", "red"))
```

```
box.WEIGHT <- ggplot(dataset, aes(x = FRACTURE, y = WEIGHT, col = FRACTURE, fill = FRACTURE)) +
  geom_boxplot(alpha = 0.2) +
  theme(legend.position = "none") +
  scale_color_manual(values = c("blue", "red")) +
  scale_fill_manual(values = c("blue", "red"))

box.BMI <- ggplot(dataset, aes(x = FRACTURE, y = BMI, col = FRACTURE, fill = FRACTURE)) +
  geom_boxplot(alpha = 0.2) +
  theme(legend.position = "none") +
  scale_color_manual(values = c("blue", "red")) +
  scale_fill_manual(values = c("blue", "red"))

grid.arrange(box.AGE, box.HEIGHT, box.WEIGHT, box.BMI, nrow = 2, ncol = 2)
```




```
covEllipses(dataset[,c(5:8)], dataset$FRACTURE, fill = TRUE, pooled = FALSE,  col = c("blue", "red"), va
```




```
#
# Conducting Levene Test
leveneTest(AGE ~ FRACTURE, dataset) # Came Back Not Significant
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1   1.522 0.2179
##       498
```

```
leveneTest(HEIGHT ~ FRACTURE, dataset)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.9566 0.3285
##       498
```

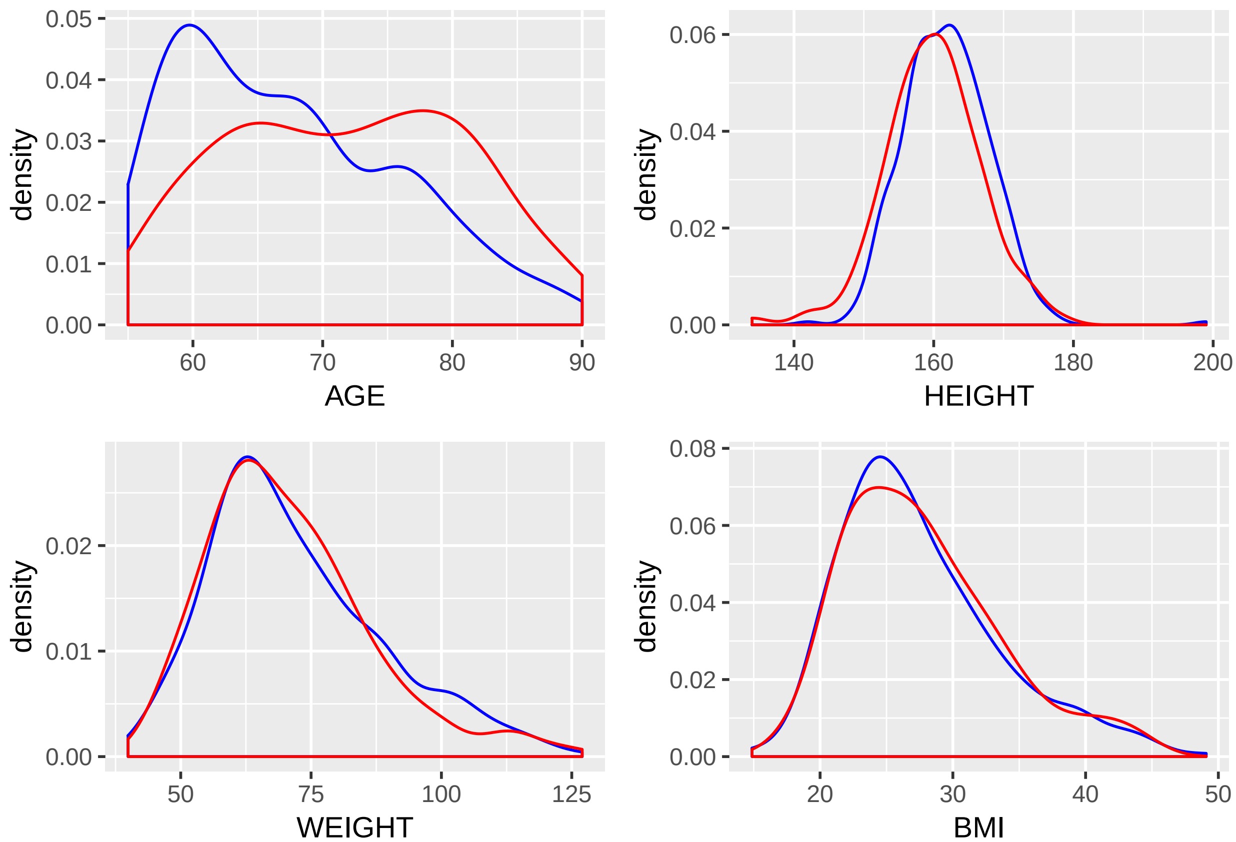
```
leveneTest(WEIGHT ~ FRACTURE, dataset)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.9475 0.3308
##       498
```

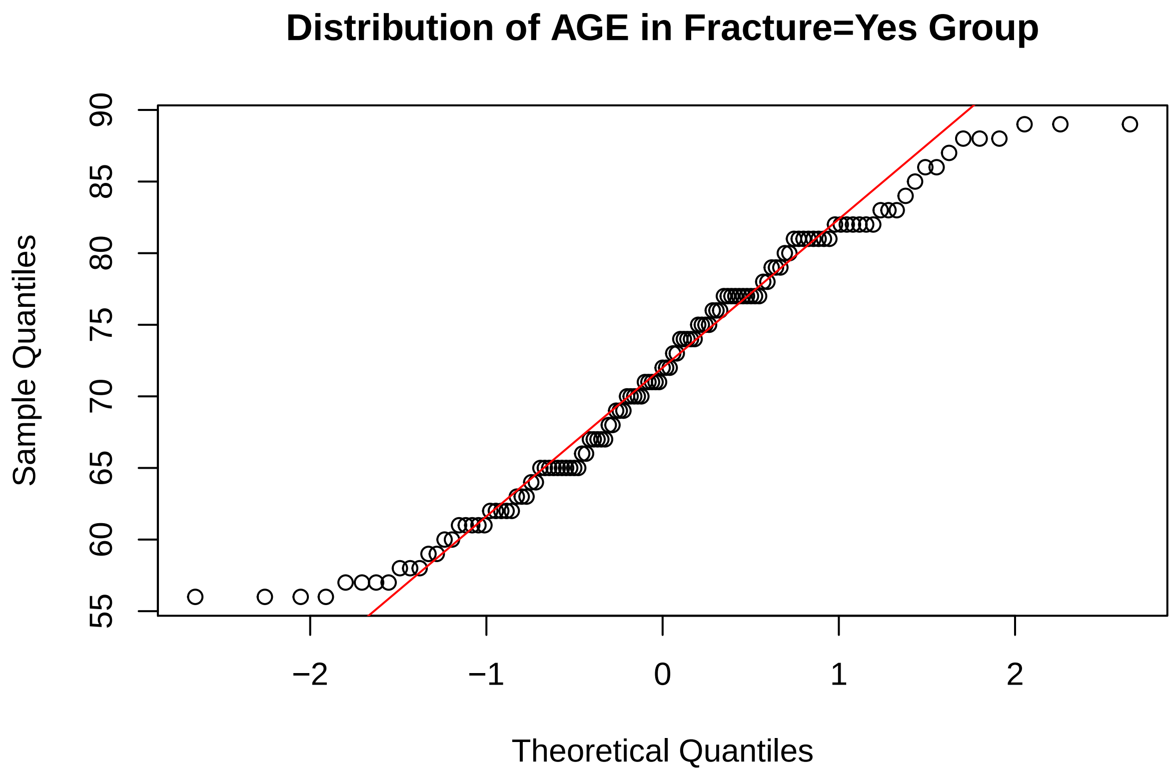
```r
leveneTest(BMI ~ FRACTURE, dataset)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  0.0188 0.8911
##       498
```

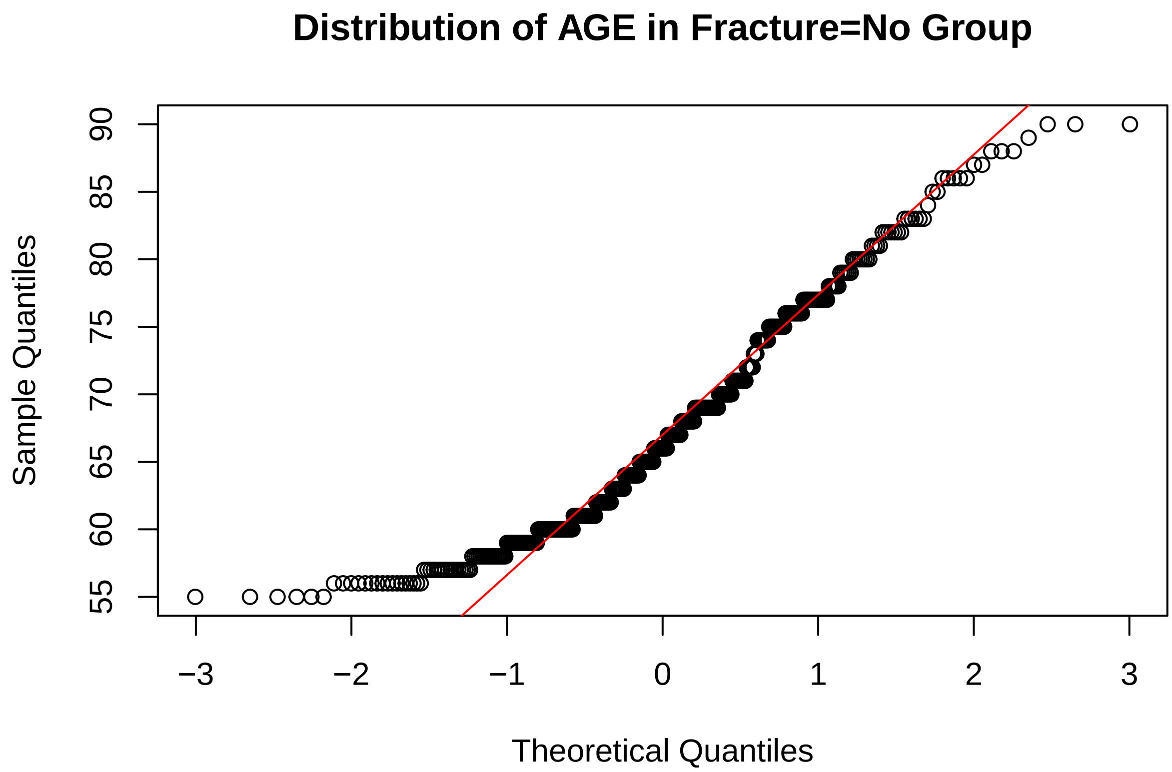
```r
# Came Back Not Significant, Confirms findings from previous plots

density.AGE <- ggplot(dataset, aes(x = AGE, y = ..density.., col = FRACTURE)) +
  geom_density(aes(y = ..density..)) +
  scale_color_manual(values = c("blue", "red")) +
  theme(legend.position = "none")

density.HEIGHT <- ggplot(dataset, aes(x = HEIGHT, y = ..density.., col = FRACTURE)) +
  geom_density(aes(y = ..density..)) +
  scale_color_manual(values = c("blue", "red")) +
  theme(legend.position = "none")

density.WEIGHT <- ggplot(dataset, aes(x = WEIGHT, y = ..density.., col = FRACTURE)) +
  geom_density(aes(y = ..density..)) +
  scale_color_manual(values = c("blue", "red")) +
  theme(legend.position = "none")

density.BMI <- ggplot(dataset, aes(x = BMI, y = ..density.., col = FRACTURE)) +
  geom_density(aes(y = ..density..)) +
  scale_color_manual(values = c("blue", "red")) +
  theme(legend.position = "none")

grid.arrange(density.AGE, density.HEIGHT, density.WEIGHT, density.BMI, nrow = 2, ncol = 2)
```




```
# Check QQ Plot for AGE to ascertain Normality in BOTH Groups
frac.yes <- subset(dataset, FRACTURE == 1)
frac.no <- subset(dataset, FRACTURE == 0)
# Plot
qqnorm(frac.yes$AGE, main = "Distribution of AGE in Fracture=Yes Group"); qqline(frac.yes$AGE, col = 2)
```



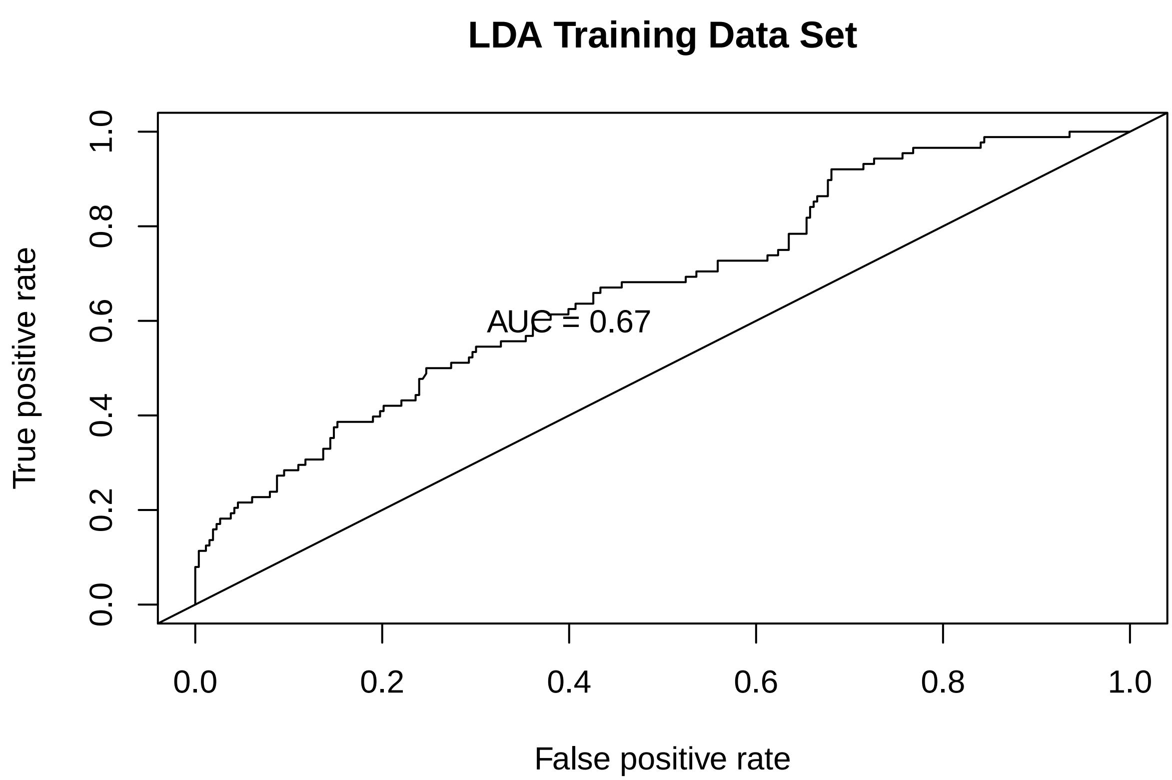

```
qqnorm(frac.no$AGE, main = "Distribution of AGE in Fracture=No Group"); qqline(frac.no$AGE, col = 2)
```




```
## Assumptions for Normality and of Equal Variance-Coavariance matrices Are Successfully Met.
## Run the LDA Now

set.seed(999)

lda.fit <- lda(FRACTURE ~ AGE + HEIGHT + WEIGHT + BMI, data = trainingData)
lda.fit
```

```
## Call:
## lda(FRACTURE ~ AGE + HEIGHT + WEIGHT + BMI, data = trainingData)
##
## Prior probabilities of groups:
##         0         1
## 0.7492877 0.2507123
##
## Group means:
##        AGE   HEIGHT   WEIGHT      BMI
## 0 67.16730 162.2129 72.01559 27.31879
## 1 71.95455 159.7614 70.53409 27.69421
##
## Coefficients of linear discriminants:
##                LD1
## AGE     0.08790497
## HEIGHT  0.20784982
## WEIGHT -0.31576637
## BMI     0.86125425
```

```r
#ROC on training data set
ldaprd <- predict(lda.fit, newdata = trainingData)$posterior
ldaprd <- ldaprd[,2]
pred.train <- prediction(ldaprd, trainingData$FRACTURE)
roc.perf = performance(pred.train, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.train, measure = "auc")
auc.train <- auc.train@y.values

#Plot ROC on Training Data
plot(roc.perf,main="LDA Training Data Set")
abline(a=0, b= 1) #Ref line indicating poor performance
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```

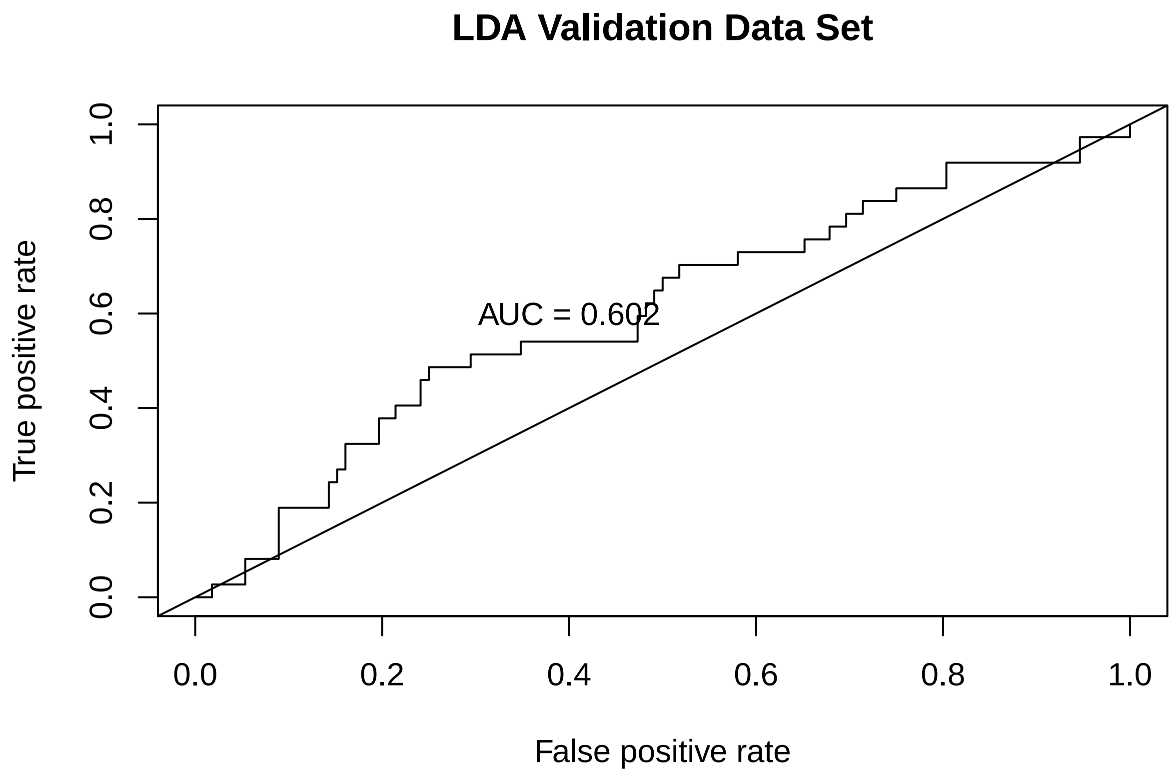



```r
prd <- predict(lda.fit, newdata = trainingData)$class
confusionMatrix(data = prd, reference = trainingData$FRACTURE)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 258  76
##          1   5  12
##
##                Accuracy : 0.7692
##                  95% CI : (0.7216, 0.8123)
```

```
##     No Information Rate : 0.7493
##     P-Value [Acc > NIR] : 0.2128
##
##                   Kappa : 0.1604
##  Mcnemar's Test P-Value : 7.381e-15
##
##             Sensitivity : 0.9810
##             Specificity : 0.1364
##          Pos Pred Value : 0.7725
##          Neg Pred Value : 0.7059
##              Prevalence : 0.7493
##          Detection Rate : 0.7350
##    Detection Prevalence : 0.9516
##       Balanced Accuracy : 0.5587
##
##        'Positive' Class : 0
##
```

```
#ROC on test data set
ldaprd.test <- predict(lda.fit, newdata = validationData)$posterior
ldaprd.test <- ldaprd.test[,2]
pred.test <- prediction(ldaprd.test, validationData$FRACTURE)
roc.perf = performance(pred.test, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.test, measure = "auc")
auc.train <- auc.train@y.values

#Plot ROC on Training Data
plot(roc.perf,main="LDA Validation Data Set")
abline(a=0, b= 1) #Ref line indicating poor performance
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```

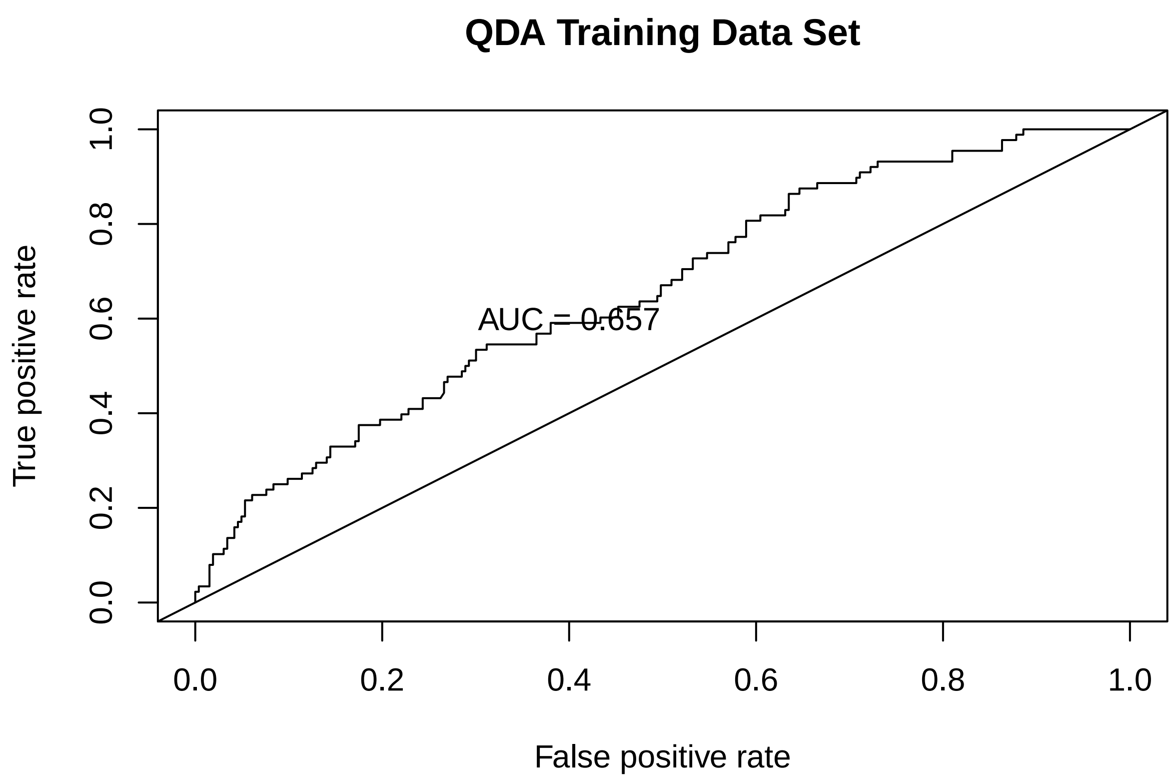



```r
prd.test <- predict(lda.fit, newdata = validationData)$class
confusionMatrix(data = prd.test, reference = validationData$FRACTURE)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 106  34
##          1   6   3
##
##                Accuracy : 0.7315
##                  95% CI : (0.6529, 0.8008)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.7493
##
##                   Kappa : 0.0368
##  Mcnemar's Test P-Value : 1.963e-05
##
##             Sensitivity : 0.94643
##             Specificity : 0.08108
##          Pos Pred Value : 0.75714
##          Neg Pred Value : 0.33333
##              Prevalence : 0.75168
##          Detection Rate : 0.71141
##    Detection Prevalence : 0.93960
```

```
##        Balanced Accuracy : 0.51375
##
##         'Positive' Class : 0
##
```

```
## Running QDA to see if it improves AUC

qda.fit <- qda(FRACTURE ~ AGE + HEIGHT + WEIGHT + BMI, data = trainingData)

#ROC on training data set
qdaprd <- predict(qda.fit, newdata = trainingData)$posterior
qdaprd <- qdaprd[,2]
pred.train <- prediction(qdaprd, trainingData$FRACTURE)
roc.perf = performance(pred.train, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.train, measure = "auc")
auc.train <- auc.train@y.values

#Plot ROC on Training Data
plot(roc.perf,main="QDA Training Data Set")
abline(a=0, b= 1) #Ref line indicating poor performance
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```

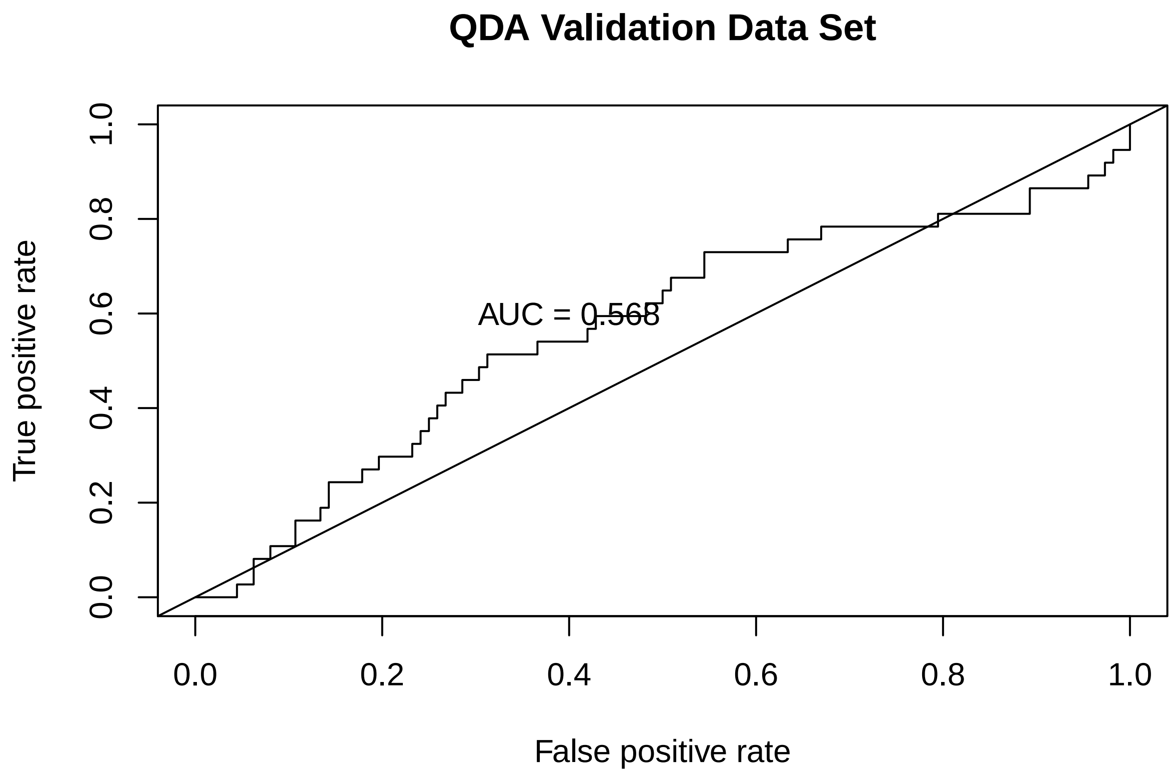



```
prd <- predict(qda.fit, newdata = trainingData)$class
confusionMatrix(data = prd, reference = trainingData$FRACTURE)
```

```
## Confusion Matrix and Statistics
```

```
##
##           Reference
## Prediction   0   1
##          0 249  71
##          1  14  17
##
##                Accuracy : 0.7578
##                  95% CI : (0.7095, 0.8017)
##     No Information Rate : 0.7493
##     P-Value [Acc > NIR] : 0.3827
##
##                   Kappa : 0.1784
##  Mcnemar's Test P-Value : 1.247e-09
##
##             Sensitivity : 0.9468
##             Specificity : 0.1932
##          Pos Pred Value : 0.7781
##          Neg Pred Value : 0.5484
##              Prevalence : 0.7493
##          Detection Rate : 0.7094
##    Detection Prevalence : 0.9117
##       Balanced Accuracy : 0.5700
##
##        'Positive' Class : 0
##
```

```
#ROC on test data set
qdaprd.test <- predict(qda.fit, newdata = validationData)$posterior
qdaprd.test <- qdaprd.test[,2]
pred.test <- prediction(qdaprd.test, validationData$FRACTURE)
roc.perf = performance(pred.test, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred.test, measure = "auc")
auc.train <- auc.train@y.values

#Plot ROC on Training Data
plot(roc.perf,main="QDA Validation Data Set")
abline(a=0, b= 1) #Ref line indicating poor performance
text(x = .40, y = .6,paste("AUC = ", round(auc.train[[1]],3), sep = ""))
```

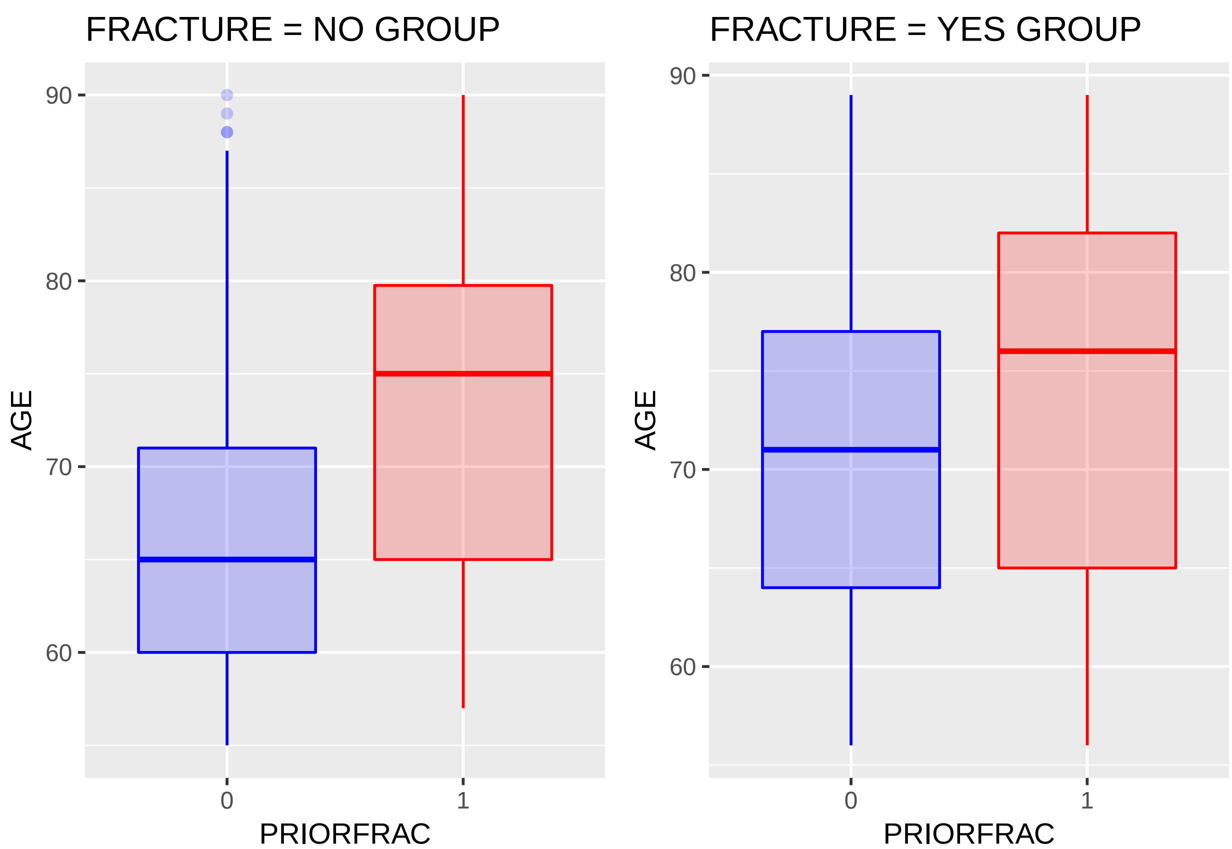



```r
prd.test <- predict(qda.fit, newdata = validationData)$class
confusionMatrix(data = prd.test, reference = validationData$FRACTURE)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 103  33
##          1   9   4
##
##                Accuracy : 0.7181
##                  95% CI : (0.6387, 0.7887)
##     No Information Rate : 0.7517
##     P-Value [Acc > NIR] : 0.8512971
##
##                   Kappa : 0.0355
##  Mcnemar's Test P-Value : 0.0003867
##
##             Sensitivity : 0.9196
##             Specificity : 0.1081
##          Pos Pred Value : 0.7574
##          Neg Pred Value : 0.3077
##              Prevalence : 0.7517
##          Detection Rate : 0.6913
##    Detection Prevalence : 0.9128
```

```
##        Balanced Accuracy : 0.5139
##
##         'Positive' Class : 0
##
```

```
frac.yes <- subset(dataset, FRACTURE == 1)
frac.no <- subset(dataset, FRACTURE == 0)

box.Prior.Age.Frac.Yes <- ggplot(frac.yes, aes(x = PRIORFRAC, y = AGE, col = PRIORFRAC, fill = PRIORFRAC
  geom_boxplot(alpha = 0.2) +
  theme(legend.position = "none") +
  scale_color_manual(values = c("blue", "red")) +
  scale_fill_manual(values = c("blue", "red")) +
  ggtitle("FRACTURE = YES GROUP")

box.Prior.Age.Frac.No <- ggplot(frac.no, aes(x = PRIORFRAC, y = AGE, col = PRIORFRAC, fill = PRIORFRAC )
  geom_boxplot(alpha = 0.2) +
  theme(legend.position = "none") +
  scale_color_manual(values = c("blue", "red")) +
  scale_fill_manual(values = c("blue", "red"))+
   ggtitle("FRACTURE = NO GROUP")

grid.arrange(box.Prior.Age.Frac.No, box.Prior.Age.Frac.Yes, nrow = 1, ncol = 2)
```



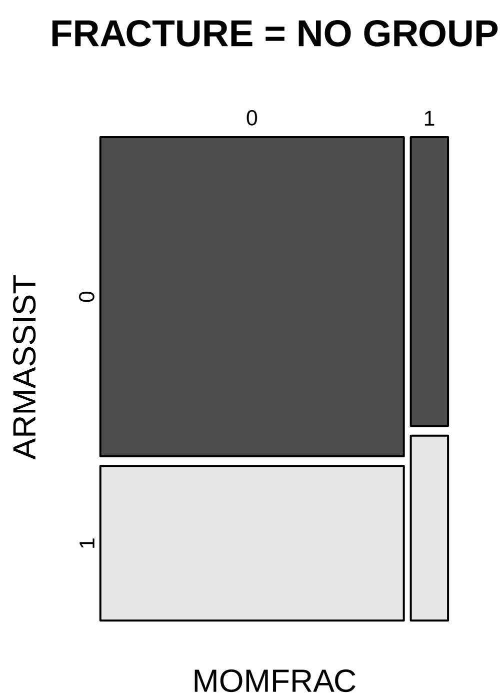
```r
#MOMFRAC:ARMASSIST

par(mfrow = c(1, 2))
mosplot.Frac.No <- mosaicplot(CrossTable(frac.no$MOMFRAC, frac.no$ARMASSIST)$t, main = "FRACTURE = NO GI
```

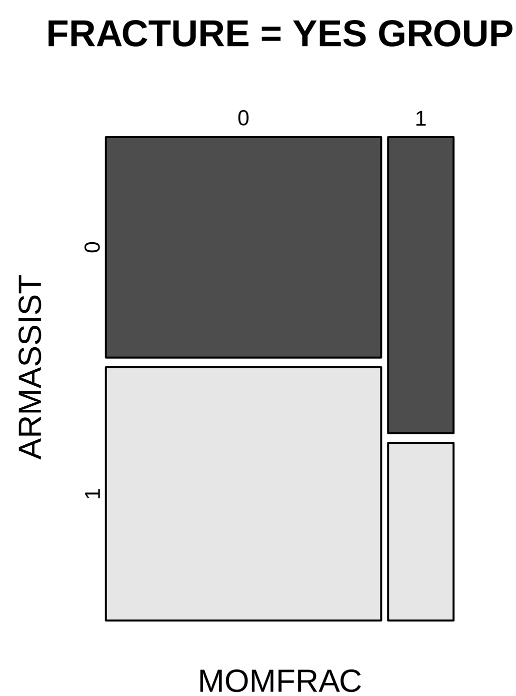
```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  375
##
##
##                  | frac.no$ARMASSIST
## frac.no$MOMFRAC |         0 |         1 | Row Total |
## ----------------|-----------|-----------|-----------|
##               0 |       225 |       109 |       334 |
##                 |     0.024 |     0.049 |           |
##                 |     0.674 |     0.326 |     0.891 |
##                 |     0.900 |     0.872 |           |
##                 |     0.600 |     0.291 |           |
## ----------------|-----------|-----------|-----------|
##               1 |        25 |        16 |        41 |
##                 |     0.199 |     0.398 |           |
##                 |     0.610 |     0.390 |     0.109 |
##                 |     0.100 |     0.128 |           |
##                 |     0.067 |     0.043 |           |
## ----------------|-----------|-----------|-----------|
##    Column Total |       250 |       125 |       375 |
##                 |     0.667 |     0.333 |           |
## ----------------|-----------|-----------|-----------|
##
##
```

```r
mosplot.Frac.Yes <- mosaicplot(CrossTable(frac.yes$MOMFRAC, frac.yes$ARMASSIST)$t, main = "FRACTURE = YI
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
```

```
## |-------------------------|
##
##
## Total Observations in Table:  125
##
##
##                  | frac.yes$ARMASSIST
## frac.yes$MOMFRAC |         0 |         1 | Row Total |
## -----------------|-----------|-----------|-----------|
##                0 |        47 |        54 |       101 |
##                  |     0.191 |     0.188 |           |
##                  |     0.465 |     0.535 |     0.808 |
##                  |     0.758 |     0.857 |           |
##                  |     0.376 |     0.432 |           |
## -----------------|-----------|-----------|-----------|
##                1 |        15 |         9 |        24 |
##                  |     0.805 |     0.792 |           |
##                  |     0.625 |     0.375 |     0.192 |
##                  |     0.242 |     0.143 |           |
##                  |     0.120 |     0.072 |           |
## -----------------|-----------|-----------|-----------|
##     Column Total |        62 |        63 |       125 |
##                  |     0.496 |     0.504 |           |
## -----------------|-----------|-----------|-----------|
##
##
```





*** *Appendix C:* Test interaction - LDA ================

Get Glow dataset

```r
glow <- read_glow_dataset()
```

model interactions - main effects

```
model_z1 <- glm(FRACTURE ~ AGE, family = binomial, data = glow)
model_z2 <- glm(FRACTURE ~ WEIGHT, family = binomial, data = glow)
model_z3 <- glm(FRACTURE ~ HEIGHT, family = binomial, data = glow)
model_z4 <- glm(FRACTURE ~ BMI, family = binomial, data = glow)
model_z5 <- glm(FRACTURE ~ PRIORFRAC, family = binomial, data = glow)
model_z6 <- glm(FRACTURE ~ PREMENO, family = binomial, data = glow)
model_z7 <- glm(FRACTURE ~ MOMFRAC, family = binomial, data = glow)
model_z8 <- glm(FRACTURE ~ ARMASSIST, family = binomial, data = glow)
model_z9 <- glm(FRACTURE ~ SMOKE, family = binomial, data = glow)
model_z10 <- glm(FRACTURE ~ RATERISK, family = binomial, data = glow)

## AGE          0.05289    0.01163   4.548 5.42e-06 ***
## WEIGHT      -0.005197   0.006415 -0.810    0.418
## HEIGHT      -0.05167    0.01709  -3.022  0.00251 **
## BMI          0.005758   0.017185  0.335  0.73760
## PRIORFRACYes 1.0638     0.2231    4.769 1.85e-06 ***
## PREMENOYes   0.05077    0.25921   0.196    0.845
## MOMFRACYes   0.6605     0.2810    2.351   0.0187 *
## ARMASSISTYes 0.7091     0.2098    3.381 0.000723 ***
## SMOKEYes    -0.3077     0.4358   -0.706     0.48
## RATERISKSame      0.5462     0.2664   2.050   0.0404 *
## RATERISKGreater   0.9091     0.2711   3.353   0.0008 ***

> code below:
```

This leads us to consider the covariates above that are significant in the univariate results above at the 25% level.

AGE, HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK {SAME, GREATER}

```r
# fit a univariate logistic regression model for each covariate
# continuous - AGE WEIGHT HEIGHT BMI
# categorical - PRIORFRAC PREMENO MOMFRAC ARMASSIST SMOKE RATERISK

# model0
#model_z1 <- glm(FRACTURE ~ AGE, family = binomial, data = glow)
#model_z2 <- glm(FRACTURE ~ WEIGHT, family = binomial, data = glow)
#model_z3 <- glm(FRACTURE ~ HEIGHT, family = binomial, data = glow)
#model_z4 <- glm(FRACTURE ~ BMI, family = binomial, data = glow)
#model_z5 <- glm(FRACTURE ~ PRIORFRAC, family = binomial, data = glow)
#model_z6 <- glm(FRACTURE ~ PREMENO, family = binomial, data = glow)
#model_z7 <- glm(FRACTURE ~ MOMFRAC, family = binomial, data = glow)
#model_z8 <- glm(FRACTURE ~ ARMASSIST, family = binomial, data = glow)
#model_z9 <- glm(FRACTURE ~ SMOKE, family = binomial, data = glow)
```

```r
#model_z10 <- glm(FRACTURE ~ RATERISK, family = binomial, data = glow)

#summary(model_z1)
#summary(model_z2)
#summary(model_z3)
#summary(model_z4)
#summary(model_z5)
#summary(model_z6)
#summary(model_z7)
#summary(model_z8)
#summary(model_z9)
#summary(model_z10)

# not interesting due to all variables (i.e. SUB_ID, SITE_ID, PHY_ID)
# model00 <- glm(FRACTURE ~ ., family = binomial, data = glow)
# summary(model00)

# full model, order by continuous, then factor
model0 <- glm(FRACTURE ~ AGE + WEIGHT + HEIGHT + BMI + PRIORFRAC + PREMENO + MOMFRAC + ARMASSIST + SMOKE
summary(model0)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + WEIGHT + HEIGHT + BMI + PRIORFRAC +
##     PREMENO + MOMFRAC + ARMASSIST + SMOKE + RATERISK, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6811  -0.7228  -0.5639  -0.1008   2.2182
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -15.74709   12.67053  -1.243  0.21394
## AGE               0.03895    0.01476   2.640  0.00829 **
## WEIGHT           -0.12189    0.08664  -1.407  0.15949
## HEIGHT            0.06620    0.07825   0.846  0.39755
## BMI               0.33181    0.22339   1.485  0.13745
## PRIORFRACYes      0.67577    0.25012   2.702  0.00690 **
## PREMENOYes        0.10080    0.28540   0.353  0.72395
## MOMFRACYes        0.63438    0.30784   2.061  0.03933 *
## ARMASSISTYes      0.36102    0.25647   1.408  0.15924
## SMOKEYes         -0.31228    0.46216  -0.676  0.49923
## RATERISKSame      0.42256    0.28144   1.501  0.13324
## RATERISKGreater   0.75645    0.29944   2.526  0.01153 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 503.84  on 488  degrees of freedom
## AIC: 527.84
```

```
##
## Number of Fisher Scoring iterations: 4
```

```r
# fit model # note - should remove below model1
model0_fitted <- update(model0, . ~ . - WEIGHT - BMI - PREMENO - SMOKE)
summary(model0_fitted)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK, family = binomial, data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.66692  -0.72502  -0.56338  -0.03841   2.22148
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.70935    3.22992   0.839  0.40157
## AGE              0.03434    0.01305   2.632  0.00848 **
## HEIGHT          -0.04383    0.01827  -2.400  0.01640 *
## PRIORFRACYes     0.64526    0.24606   2.622  0.00873 **
## MOMFRACYes       0.62122    0.30698   2.024  0.04300 *
## ARMASSISTYes     0.44579    0.23281   1.915  0.05551 .
## RATERISKSame     0.42202    0.27925   1.511  0.13071
## RATERISKGreater  0.70692    0.29342   2.409  0.01599 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.50  on 492  degrees of freedom
## AIC: 523.5
##
## Number of Fisher Scoring iterations: 4
```

```r
# build model with following covariates (drop WEIGHT, BMI, PREMENO, SMOKE)
# AGE, HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK {SAME, GREATER}

model1 <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK, family = binomial, 
summary(model1)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK, family = binomial, data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.66692  -0.72502  -0.56338  -0.03841   2.22148
##
## Coefficients:
```

```
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.70935    3.22992   0.839  0.40157
## AGE              0.03434    0.01305   2.632  0.00848 **
## HEIGHT          -0.04383    0.01827  -2.400  0.01640 *
## PRIORFRACYes     0.64526    0.24606   2.622  0.00873 **
## MOMFRACYes       0.62122    0.30698   2.024  0.04300 *
## ARMASSISTYes     0.44579    0.23281   1.915  0.05551 .
## RATERISKSame     0.42202    0.27925   1.511  0.13071
## RATERISKGreater  0.70692    0.29342   2.409  0.01599 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.50  on 492  degrees of freedom
## AIC: 523.5
##
## Number of Fisher Scoring iterations: 4
```

```
# from above result, adding back the removed covariates we see they are not needed to keep the remainin
# this becomes the model, adding back removed covariates WEIGHT, BMI, PREMENO, SMOKE the coefficients d
# this becomes the main effects model


# need to check scale of logit for remaining continous variables AGE HEIGHT
# assume HEIGHT is linearin logit
```

The main effects model

model1 <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK, family = binomial, data = glow)

use lrtest from package lmtest

test interactions for the following:

5. AGE: [HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]
6. HEIGHT: [PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]
7. PRIORFRAC: [MOMFRAC, ARMASSIST, RATERISK]
8. MOMFRAC: [ARMASSIST, RATERISK]
9. ARMASSIST: RATERISK

total 15 interactions

```
library(lmtest)

# model AGE* , HEIGHT* , PRIORFRAC*

model_effects <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK, family = bin
lrtest(model_effects)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -253.75
## 2   1 -281.17 -7 54.835  1.608e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# (5) AGE: [HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]

test <- model_effects
test <- update(test, . ~ . + AGE:HEIGHT)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:HEIGHT, family = binomial, data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.66848  -0.73323  -0.56252   0.02069   2.23640
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)     14.749125  23.931667   0.616   0.5377
## AGE             -0.135869   0.335087  -0.405   0.6851
## HEIGHT          -0.119095   0.149402  -0.797   0.4254
## PRIORFRACYes     0.634947   0.246751   2.573   0.0101 *
## MOMFRACYes       0.623682   0.307316   2.029   0.0424 *
## ARMASSISTYes     0.447271   0.232895   1.920   0.0548 .
## RATERISKSame     0.435127   0.280319   1.552   0.1206
## RATERISKGreater  0.707865   0.293394   2.413   0.0158 *
## AGE:HEIGHT       0.001065   0.002095   0.508   0.6113
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.24  on 491  degrees of freedom
## AIC: 525.24
##
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     AGE:HEIGHT
```

```
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -253.62
## 2   1 -281.17 -8 55.096   4.23e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
test <- model_effects
test <- update(test, . ~ . + AGE:PRIORFRAC)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:PRIORFRAC, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.48423  -0.74080  -0.53895  -0.00078   2.26588
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        0.63708    3.35881   0.190 0.849565
## AGE                0.05669    0.01649   3.437 0.000589 ***
## HEIGHT            -0.04058    0.01828  -2.220 0.026406 *
## PRIORFRACYes       4.85428    1.86766   2.599 0.009346 **
## MOMFRACYes         0.66973    0.30857   2.170 0.029972 *
## ARMASSISTYes       0.41887    0.23395   1.790 0.073391 .
## RATERISKSame       0.43496    0.28053   1.551 0.121014
## RATERISKGreater    0.72044    0.29561   2.437 0.014804 *
## AGE:PRIORFRACYes -0.05864    0.02583  -2.270 0.023188 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 502.34  on 491  degrees of freedom
## AIC: 520.34
##
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     AGE:PRIORFRAC
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -251.17
## 2   1 -281.17 -8 59.991  4.679e-10 ***
```

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

```r
test <- model_effects
test <- update(test, . ~ . + AGE:MOMFRAC)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:MOMFRAC, family = binomial, data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.58376  -0.72859  -0.56182  -0.02562   2.22962
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)       2.59055    3.24368   0.799  0.42450
## AGE               0.03633    0.01393   2.609  0.00908 **
## HEIGHT           -0.04402    0.01827  -2.409  0.01601 *
## PRIORFRACYes      0.65010    0.24630   2.639  0.00830 **
## MOMFRACYes        1.57119    2.31121   0.680  0.49662
## ARMASSISTYes      0.45447    0.23374   1.944  0.05185 .
## RATERISKSame      0.42505    0.27940   1.521  0.12819
## RATERISKGreater   0.71044    0.29363   2.420  0.01554 *
## AGE:MOMFRACYes   -0.01353    0.03264  -0.414  0.67854
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.33  on 491  degrees of freedom
## AIC: 525.33
##
## Number of Fisher Scoring iterations: 4
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     AGE:MOMFRAC
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -253.66
## 2   1 -281.17 -8 55.005  4.406e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
test <- model_effects
test <- update(test, . ~ . + AGE:ARMASSIST)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:ARMASSIST, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6352  -0.7272  -0.5646  -0.0295   2.2329
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)       2.33972    3.33003   0.703  0.48230
## AGE               0.03990    0.01785   2.235  0.02542 *
## HEIGHT           -0.04395    0.01827  -2.406  0.01614 *
## PRIORFRACYes      0.64031    0.24609   2.602  0.00927 **
## MOMFRACYes        0.63376    0.30795   2.058  0.03959 *
## ARMASSISTYes      1.24419    1.76410   0.705  0.48063
## RATERISKSame      0.42815    0.27964   1.531  0.12575
## RATERISKGreater   0.71996    0.29494   2.441  0.01464 *
## AGE:ARMASSISTYes -0.01132    0.02479  -0.457  0.64802
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.29  on 491  degrees of freedom
## AIC: 525.29
##
## Number of Fisher Scoring iterations: 4
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     AGE:ARMASSIST
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -253.65
## 2   1 -281.17 -8 55.043  4.331e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
test <- model_effects
test <- update(test, . ~ . + AGE:RATERISK)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:RATERISK, family = binomial, data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.68668  -0.74463  -0.56590  -0.02638   2.34976
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           0.53632    3.53444   0.152  0.87939
## AGE                   0.06673    0.02473   2.698  0.00697 **
## HEIGHT               -0.04496    0.01840  -2.443  0.01456 *
## PRIORFRACYes          0.65827    0.24598   2.676  0.00745 **
## MOMFRACYes            0.65241    0.30765   2.121  0.03395 *
## ARMASSISTYes          0.48569    0.23443   2.072  0.03828 *
## RATERISKSame          3.28427    2.27575   1.443  0.14898
## RATERISKGreater       4.25804    2.28873   1.860  0.06282 .
## AGE:RATERISKSame     -0.03999    0.03151  -1.269  0.20438
## AGE:RATERISKGreater -0.05021    0.03202  -1.568  0.11690
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 504.79  on 490  degrees of freedom
## AIC: 524.79
##
## Number of Fisher Scoring iterations: 5
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     AGE:RATERISK
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1  10 -252.40
## 2   1 -281.17 -9 57.54  3.982e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# (4) HEIGHT: [PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]

test <- model_effects
test <- update(test, . ~ . + HEIGHT:PRIORFRAC)
summary(test)
```

```
##
## Call:
```

```
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + HEIGHT:PRIORFRAC, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6670  -0.7274  -0.5615  -0.0037   2.2377
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          3.79297    3.89138   0.975  0.32970
## AGE                  0.03395    0.01307   2.597  0.00941 **
## HEIGHT              -0.05041    0.02253  -2.238  0.02524 *
## PRIORFRACYes        -2.41864    6.03699  -0.401  0.68869
## MOMFRACYes           0.63692    0.30850   2.065  0.03896 *
## ARMASSISTYes         0.43526    0.23394   1.861  0.06281 .
## RATERISKSame         0.42634    0.27946   1.526  0.12711
## RATERISKGreater      0.70410    0.29356   2.399  0.01646 *
## HEIGHT:PRIORFRACYes  0.01915    0.03770   0.508  0.61146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.24  on 491  degrees of freedom
## AIC: 525.24
##
## Number of Fisher Scoring iterations: 4
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     HEIGHT:PRIORFRAC
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -253.62
## 2   1 -281.17 -8 55.092  4.236e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
test <- model_effects
test <- update(test, . ~ . + HEIGHT:MOMFRAC)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + HEIGHT:MOMFRAC, family = binomial,
##     data = glow)
##
```

```
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.62068  -0.74163  -0.55649   0.06604   2.26717
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           4.73834    3.51132   1.349  0.17719
## AGE                   0.03385    0.01307   2.589  0.00961 **
## HEIGHT               -0.05646    0.02021  -2.794  0.00521 **
## PRIORFRACYes          0.68102    0.24763   2.750  0.00596 **
## MOMFRACYes          -11.35526    7.64959  -1.484  0.13770
## ARMASSISTYes          0.47848    0.23444   2.041  0.04126 *
## RATERISKSame          0.42455    0.28002   1.516  0.12949
## RATERISKGreater       0.70475    0.29372   2.399  0.01642 *
## HEIGHT:MOMFRACYes     0.07401    0.04718   1.569  0.11675
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 505.08  on 491  degrees of freedom
## AIC: 523.08
##
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     HEIGHT:MOMFRAC
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -252.54
## 2   1 -281.17 -8 57.258  1.603e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
test <- model_effects
test <- update(test, . ~ . + HEIGHT:ARMASSIST)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + HEIGHT:ARMASSIST, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6742  -0.7177  -0.5638  -0.1472   2.1734
##
```

```
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -0.57428    4.12234  -0.139  0.88920
## AGE                  0.03401    0.01308   2.601  0.00931 **
## HEIGHT              -0.02318    0.02432  -0.953  0.34051
## PRIORFRACYes         0.67913    0.24841   2.734  0.00626 **
## MOMFRACYes           0.58729    0.30807   1.906  0.05660 .
## ARMASSISTYes         7.53985    5.77628   1.305  0.19179
## RATERISKSame         0.41583    0.27981   1.486  0.13725
## RATERISKGreater      0.70729    0.29369   2.408  0.01603 *
## HEIGHT:ARMASSISTYes -0.04419    0.03594  -1.229  0.21890
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 505.98  on 491  degrees of freedom
## AIC: 523.98
##
## Number of Fisher Scoring iterations: 4
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     HEIGHT:ARMASSIST
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -252.99
## 2   1 -281.17 -8 56.352  2.409e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
test <- model_effects
test <- update(test, . ~ . + HEIGHT:RATERISK)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + HEIGHT:RATERISK, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.64936  -0.72375  -0.57251  -0.05841   2.22612
##
## Coefficients:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)             3.25641    5.81516   0.560  0.57549
## AGE                     0.03321    0.01310   2.536  0.01122 *
```

```
## HEIGHT                  -0.04674    0.03532  -1.323  0.18573
## PRIORFRACYes             0.64451    0.24655   2.614  0.00895 **
## MOMFRACYes               0.62504    0.30650   2.039  0.04142 *
## ARMASSISTYes             0.44610    0.23290   1.915  0.05544 .
## RATERISKSame             2.93823    7.29965   0.403  0.68730
## RATERISKGreater         -3.15056    7.29448  -0.432  0.66581
## HEIGHT:RATERISKSame     -0.01577    0.04550  -0.347  0.72890
## HEIGHT:RATERISKGreater   0.02394    0.04528   0.529  0.59695
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 506.55  on 490  degrees of freedom
## AIC: 526.55
##
## Number of Fisher Scoring iterations: 4
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     HEIGHT:RATERISK
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  10 -253.28
## 2   1 -281.17 -9 55.786  8.624e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# (3) PRIORFRAC: [MOMFRAC, ARMASSIST, RATERISK]

test <- model_effects
test <- update(test, . ~ . + PRIORFRAC:MOMFRAC)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + PRIORFRAC:MOMFRAC, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.52616  -0.73215  -0.54992   0.02399   2.25279
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)               2.97592    3.23781   0.919  0.35804
## AGE                       0.03598    0.01313   2.741  0.00612 **
## HEIGHT                   -0.04652    0.01837  -2.533  0.01130 *
```

```
## PRIORFRACYes             0.80102    0.26285   3.047  0.00231 **
## MOMFRACYes               0.95902    0.35985   2.665  0.00770 **
## ARMASSISTYes             0.43294    0.23384   1.851  0.06411 .
## RATERISKSame             0.41959    0.28027   1.497  0.13437
## RATERISKGreater          0.71282    0.29401   2.425  0.01533 *
## PRIORFRACYes:MOMFRACYes -1.07823    0.65021  -1.658  0.09726 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 504.75  on 491  degrees of freedom
## AIC: 522.75
##
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     PRIORFRAC:MOMFRAC
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   9 -252.37
## 2   1 -281.17 -8 57.59  1.382e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
test <- model_effects
test <- update(test, . ~ . + PRIORFRAC:ARMASSIST)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + PRIORFRAC:ARMASSIST, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.69860  -0.71874  -0.56691  -0.04199   2.21033
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 2.90711    3.25923   0.892  0.37241
## AGE                         0.03434    0.01306   2.630  0.00854 **
## HEIGHT                     -0.04486    0.01842  -2.436  0.01487 *
## PRIORFRACYes                0.52412    0.34418   1.523  0.12780
## MOMFRACYes                  0.63247    0.30798   2.054  0.04001 *
## ARMASSISTYes                0.36456    0.28322   1.287  0.19803
## RATERISKSame                0.42507    0.27929   1.522  0.12802
```

```
## RATERISKGreater            0.68837    0.29591   2.326  0.02000 *
## PRIORFRACYes:ARMASSISTYes  0.24587    0.48467   0.507  0.61194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.24  on 491  degrees of freedom
## AIC: 525.24
##
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     PRIORFRAC:ARMASSIST
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -253.62
## 2   1 -281.17 -8 55.093  4.235e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
test <- model_effects
test <- update(test, . ~ . + PRIORFRAC:RATERISK)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + PRIORFRAC:RATERISK, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.69776  -0.71989  -0.56384  -0.03822   2.21130
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  2.733523   3.235459   0.845  0.39819
## AGE                          0.034508   0.013060   2.642  0.00823 **
## HEIGHT                      -0.043896   0.018313  -2.397  0.01653 *
## PRIORFRACYes                 0.564292   0.497212   1.135  0.25641
## MOMFRACYes                   0.623104   0.307302   2.028  0.04260 *
## ARMASSISTYes                 0.429891   0.236033   1.821  0.06856 .
## RATERISKSame                 0.426181   0.324504   1.313  0.18907
## RATERISKGreater              0.632806   0.355571   1.780  0.07513 .
## PRIORFRACYes:RATERISKSame    0.001597   0.625563   0.003  0.99796
## PRIORFRACYes:RATERISKGreater 0.208811   0.624586   0.334  0.73814
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 507.32  on 490  degrees of freedom
## AIC: 527.32
##
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     PRIORFRAC:RATERISK
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  10 -253.66
## 2   1 -281.17 -9 55.015   1.21e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# (2) MOMFRAC: [ARMASSIST, RATERISK]

test <- model_effects
test <- update(test, . ~ . + MOMFRAC:ARMASSIST)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + MOMFRAC:ARMASSIST, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.65273  -0.72683  -0.55140   0.03367   2.27218
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)              2.96640    3.25148   0.912  0.36160
## AGE                      0.03760    0.01323   2.842  0.00448 **
## HEIGHT                  -0.04738    0.01846  -2.567  0.01025 *
## PRIORFRACYes             0.61633    0.24770   2.488  0.01284 *
## MOMFRACYes               1.17111    0.38940   3.007  0.00263 **
## ARMASSISTYes             0.65026    0.25220   2.578  0.00993 **
## RATERISKSame             0.41386    0.28032   1.476  0.13985
## RATERISKGreater          0.71051    0.29445   2.413  0.01582 *
## MOMFRACYes:ARMASSISTYes -1.33817    0.62405  -2.144  0.03201 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 502.83  on 491  degrees of freedom
## AIC: 520.83
##
## Number of Fisher Scoring iterations: 4
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     MOMFRAC:ARMASSIST
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   9 -251.41
## 2   1 -281.17 -8 59.509  5.818e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
test <- model_effects
test <- update(test, . ~ . + MOMFRAC:RATERISK)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + MOMFRAC:RATERISK, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.73530  -0.73156  -0.56262  -0.02886   2.20217
##
## Coefficients:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  2.76974    3.23715   0.856  0.39221
## AGE                          0.03436    0.01308   2.627  0.00861 **
## HEIGHT                      -0.04393    0.01832  -2.398  0.01649 *
## PRIORFRACYes                 0.64526    0.24663   2.616  0.00889 **
## MOMFRACYes                   0.02648    0.83795   0.032  0.97479
## ARMASSISTYes                 0.44890    0.23340   1.923  0.05444 .
## RATERISKSame                 0.29742    0.29700   1.001  0.31663
## RATERISKGreater              0.70206    0.31167   2.253  0.02428 *
## MOMFRACYes:RATERISKSame      1.04615    0.95957   1.090  0.27561
## MOMFRACYes:RATERISKGreater   0.36775    0.96207   0.382  0.70227
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
```

```
## Residual deviance: 505.79  on 490  degrees of freedom
## AIC: 525.79
##
## Number of Fisher Scoring iterations: 4
```

```r
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     MOMFRAC:RATERISK
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  10 -252.90
## 2   1 -281.17 -9 56.542  6.183e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# (1) ARMASSIST: RATERISK

test <- model_effects
test <- update(test, . ~ . + ARMASSIST:RATERISK)
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + ARMASSIST:RATERISK, family = binomial,
##     data = glow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6586  -0.7419  -0.5544  -0.0470   2.2531
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   2.38363    3.22529   0.739  0.45988
## AGE                           0.03534    0.01314   2.691  0.00713 **
## HEIGHT                       -0.04274    0.01819  -2.349  0.01883 *
## PRIORFRACYes                  0.70856    0.25028   2.831  0.00464 **
## MOMFRACYes                    0.61378    0.30782   1.994  0.04616 *
## ARMASSISTYes                  0.60776    0.44193   1.375  0.16906
## RATERISKSame                  0.36244    0.36906   0.982  0.32607
## RATERISKGreater               0.98400    0.38373   2.564  0.01034 *
## ARMASSISTYes:RATERISKSame     0.10760    0.56723   0.190  0.84956
## ARMASSISTYes:RATERISKGreater -0.60953    0.58200  -1.047  0.29496
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 505.42  on 490  degrees of freedom
```

```
## AIC: 525.42
##
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
```

```
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##     ARMASSIST:RATERISK
## Model 2: FRACTURE ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1  10 -252.71
## 2   1 -281.17 -9 56.912  5.253e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Results from interactions

```
## AGE:HEIGHT           0.001065   0.002095  0.508  0.6113
   AGE:PRIORFRACYes    -0.05864    0.02583  -2.270  0.023188 *
## AGE:MOMFRACYes      -0.01353    0.03264  -0.414  0.67854
## AGE:ARMASSISTYes    -0.01132    0.02479  -0.457  0.64802
## AGE:RATERISKSame    -0.03999    0.03151  -1.269  0.20438
## AGE:RATERISKGreater -0.05021    0.03202  -1.568  0.11690
## HEIGHT:PRIORFRACYes  0.01915    0.03770   0.508  0.61146
## HEIGHT:MOMFRACYes    0.07401    0.04718   1.569  0.11675
## HEIGHT:ARMASSISTYes -0.04419    0.03594  -1.229  0.21890
## HEIGHT:RATERISKSame      -0.01577    0.04550  -0.347  0.72890
## HEIGHT:RATERISKGreater    0.02394    0.04528   0.529  0.59695
   PRIORFRACYes:MOMFRACYes  -1.07823    0.65021  -1.658  0.09726 .
## PRIORFRACYes:ARMASSISTYes 0.24587    0.48467   0.507  0.61194
## PRIORFRACYes:RATERISKSame     0.001597   0.625563   0.003  0.99796
## PRIORFRACYes:RATERISKGreater  0.208811   0.624586   0.334  0.73814
   MOMFRACYes:ARMASSISTYes  -1.33817    0.62405  -2.144  0.03201 *
## MOMFRACYes:RATERISKSame     1.04615    0.95957   1.090  0.27561
## MOMFRACYes:RATERISKGreater  0.36775    0.96207   0.382  0.70227
## ARMASSISTYes:RATERISKSame     0.10760    0.56723   0.190  0.84956
## ARMASSISTYes:RATERISKGreater -0.60953    0.58200  -1.047  0.29496
```

Add to main effects model

we find three interactions, AGE:PRIORFRACYes, PRIORFRACYes:MOMFRACYes, MOMFRACYes:ARMASSISTYes

```
model_effects_new <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
                       AGE:PRIORFRAC + PRIORFRAC:MOMFRAC + MOMFRAC:ARMASSIST, family = binomial, data =
summary(model_effects_new)
```

```
##
```

```
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:PRIORFRAC + PRIORFRAC:MOMFRAC +
##     MOMFRAC:ARMASSIST, family = binomial, data = glow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.47664  -0.74929  -0.51571   0.07753   2.33224
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                1.20626    3.38765   0.356 0.721785
## AGE                        0.05949    0.01677   3.547 0.000389 ***
## HEIGHT                    -0.04610    0.01854  -2.487 0.012886 *
## PRIORFRACYes               4.63031    1.88158   2.461 0.013860 *
## MOMFRACYes                 1.42093    0.42468   3.346 0.000820 ***
## ARMASSISTYes               0.59571    0.25545   2.332 0.019701 *
## RATERISKSame               0.42125    0.28217   1.493 0.135462
## RATERISKGreater            0.72341    0.29695   2.436 0.014847 *
## AGE:PRIORFRACYes          -0.05408    0.02602  -2.079 0.037662 *
## PRIORFRACYes:MOMFRACYes   -0.83184    0.64852  -1.283 0.199606
## MOMFRACYes:ARMASSISTYes   -1.15254    0.61838  -1.864 0.062350 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 496.53  on 489  degrees of freedom
## AIC: 518.53
##
## Number of Fisher Scoring iterations: 4
```

```r
# create final model with interactions terms AGE:PRIORFRAC + MOMFRAC:ARMASSIST
model_effects_final <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
                       AGE:PRIORFRAC + MOMFRAC:ARMASSIST, family = binomial, data = glow)
summary(model_effects_final)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:PRIORFRAC + MOMFRAC:ARMASSIST,
##     family = binomial, data = glow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6995  -0.7459  -0.5238   0.0620   2.3123
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                0.96955    3.38252   0.287 0.774392
## AGE                        0.05890    0.01666   3.535 0.000408 ***
## HEIGHT                    -0.04413    0.01848  -2.388 0.016949 *
## PRIORFRACYes               4.65073    1.88342   2.469 0.013538 *
```

```
## MOMFRACYes               1.19902    0.39487   3.036 0.002393 **
## ARMASSISTYes             0.61423    0.25358   2.422 0.015426 *
## RATERISKSame             0.42626    0.28154   1.514 0.130012
## RATERISKGreater          0.72116    0.29660   2.431 0.015040 *
## AGE:PRIORFRACYes        -0.05610    0.02600  -2.158 0.030950 *
## MOMFRACYes:ARMASSISTYes -1.26534    0.62377  -2.029 0.042507 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 562.34  on 499  degrees of freedom
## Residual deviance: 498.17  on 490  degrees of freedom
## AIC: 518.17
##
## Number of Fisher Scoring iterations: 4
```

Final Interaction Model

```
(Intercept)
AGE                      0.05890    0.01666   3.535 0.000408 ***
HEIGHT                  -0.04413    0.01848  -2.388 0.016949 *
PRIORFRACYes             4.65073    1.88342   2.469 0.013538 *
MOMFRACYes               1.19902    0.39487   3.036 0.002393 **
ARMASSISTYes             0.61423    0.25358   2.422 0.015426 *
RATERISKGreater          0.72116    0.29660   2.431 0.015040 *
AGE:PRIORFRACYes        -0.05610    0.02600  -2.158 0.030950 *
MOMFRACYes:ARMASSISTYes -1.26534    0.62377  -2.029 0.042507 *

FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK + AGE:PRIORFRAC + MOMFRAC:ARMASSIS
```

```r
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

```
## The following object is masked from 'package:gmodels':
##
##     ci
```

```
## The following object is masked from 'package:glmnet':
##
##     auc
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```r
library(vcdExtra)
```

```
## Loading required package: gnm

##
## Attaching package: 'gnm'

## The following object is masked from 'package:modeltools':
##
##     parameters

## The following object is masked from 'package:lattice':
##
##     barley

##
## Attaching package: 'vcdExtra'

## The following object is masked from 'package:carData':
##
##     Burt

## The following object is masked from 'package:plyr':
##
##     summarise

## The following object is masked from 'package:dplyr':
##
##     summarise
```

```r
# vcov(model_effects_final)

HLtest(model_effects_final)
```

```
## Hosmer and Lemeshow Goodness-of-Fit Test
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##     ARMASSIST + RATERISK + AGE:PRIORFRAC + MOMFRAC:ARMASSIST,
##     family = binomial, data = glow)
##  ChiSquare df   P_value
##   7.268011  8 0.5080118
```

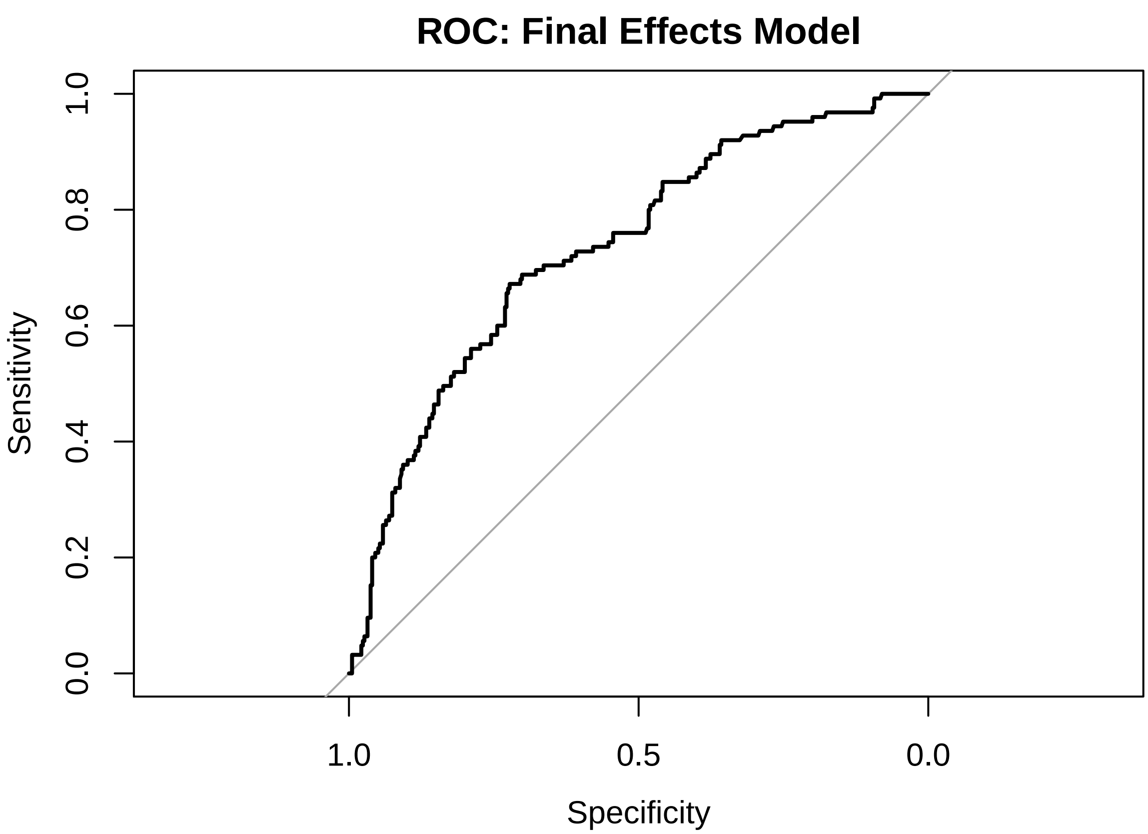
```r
glow$predict_mfinal <- predict(model_effects_final, type = "response")
with(glow, addmargins(table(glow$predict_mfinal > 0.5, glow$FRACTURE)))
```

```
##
##          No Yes Sum
##   FALSE 354  97 451
##   TRUE   21  28  49
##   Sum   375 125 500
```

```r
(roc_final_model <- roc(glow$FRACTURE ~ glow$predict_mfinal, data = glow))
```

```
##
## Call:
## roc.formula(formula = glow$FRACTURE ~ glow$predict_mfinal, data = glow)
##
## Data: glow$predict_mfinal in 375 controls (glow$FRACTURE No) < 125 cases (glow$FRACTURE Yes).
## Area under the curve: 0.7331
```

```r
plot(roc_final_model, main = "ROC: Final Effects Model")
```



misc

```r
## restart with clean data
glow <- read_glow_dataset()

model_last <- glm(FRACTURE ~ AGE:PRIORFRAC + HEIGHT + MOMFRAC:ARMASSIST + I(as.integer(RATERISK) == 3),
HLtest(model_last)
```

```
## Hosmer and Lemeshow Goodness-of-Fit Test
##
## Call:
## glm(formula = FRACTURE ~ AGE:PRIORFRAC + HEIGHT + MOMFRAC:ARMASSIST +
##     I(as.integer(RATERISK) == 3), family = binomial, data = glow)
##  ChiSquare df   P_value
##    3.10152  8 0.9278259
```

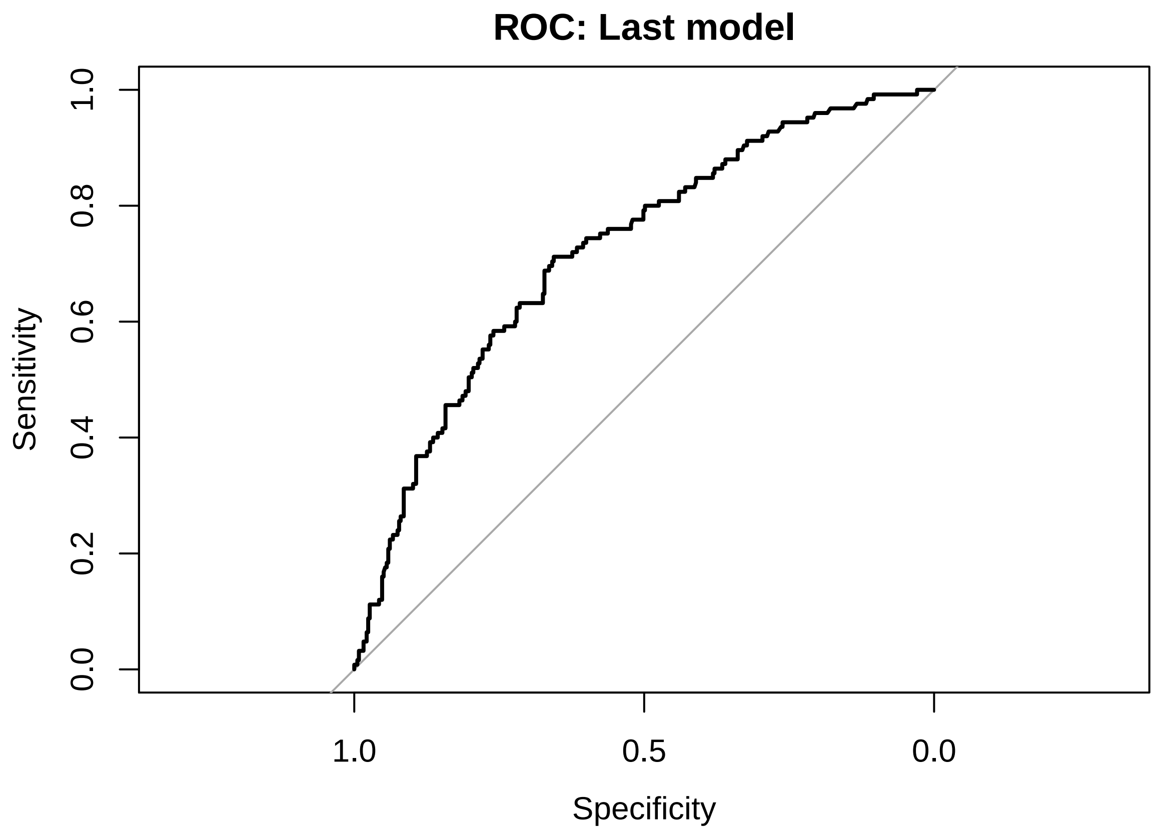
```r
summary(HLtest(model_last))
```

```
## Partition for Hosmer and Lemeshow Goodness-of-Fit Test
##
##                cut total obs      exp        chi
## 1  [0.0243,0.0967]    50  47 45.97075  0.1518032
## 2   (0.0967,0.123]    50  46 44.35914  0.2463653
## 3    (0.123,0.152]    50  42 43.19969 -0.1825284
## 4     (0.152,0.18]    50  41 41.81265 -0.1256745
## 5     (0.18,0.213]    50  42 40.34124  0.2611609
## 6    (0.213,0.251]    50  36 38.55936 -0.4121599
## 7    (0.251,0.292]    50  38 36.55362  0.2392312
## 8    (0.292,0.372]    50  32 33.67421 -0.2885110
## 9     (0.372,0.47]    50  28 29.25398 -0.2318447
## 10    (0.47,0.724]    50  23 21.27536  0.3739034
## Hosmer and Lemeshow Goodness-of-Fit Test
##
## Call:
## glm(formula = FRACTURE ~ AGE:PRIORFRAC + HEIGHT + MOMFRAC:ARMASSIST +
##     I(as.integer(RATERISK) == 3), family = binomial, data = glow)
##  ChiSquare df   P_value
##    3.10152  8 0.9278259
```

```r
# classification table
glow$predict_last <- predict(model_last, type = "response")
with(glow, addmargins(table(predict_last > 0.5, FRACTURE)))
```

```
##        FRACTURE
##          No Yes Sum
##   FALSE 355 103 458
##   TRUE   20  22  42
##   Sum   375 125 500
```

```r
# Sensitivy, specificity, ROC (using pROC)
roc_model_last <- roc(glow$FRACTURE ~ glow$predict_last, data = glow)
plot(roc_model_last, main = "ROC: Last model")
```




```r
# create table
vars <- c("thresholds","sensitivities","specificities")
model_table <- data.frame(roc_model_last[vars])

findIndex <- function(x, y) which.min( (x-y)^2 )
cutPoints <- seq(0.05, 0.75, by = 0.05)

tableIndex <- mapply(findIndex, y = cutPoints, MoreArgs = list(x = roc_model_last$thresholds))

model_table[tableIndex, ]
```

```
##     thresholds sensitivities specificities
## 3   0.05165803         1.000   0.005333333
## 43  0.09905744         0.976   0.128000000
## 120 0.15054070         0.880   0.349333333
## 202 0.20014367         0.760   0.549333333
## 259 0.25035362         0.640   0.674666667
## 316 0.29918726         0.520   0.789333333
## 349 0.34952747         0.416   0.842666667
## 379 0.40012793         0.320   0.893333333
## 401 0.44487716         0.240   0.925333333
## 416 0.49400138         0.176   0.944000000
## 426 0.55045683         0.120   0.954666667
## 443 0.59996390         0.056   0.978666667
## 452 0.65801860         0.024   0.992000000
## 455 0.69417409         0.008   0.994666667
```

```
## 457 0.71832154         0.008   1.000000000
```

```r
# plot
plot(specificities ~ thresholds, xlim = c(0, 1), type = "l",
xlab = "probability cutoff", ylab = "sensitivity / specificity",
ylim = c(0, 1), data = model_table, main = "probability sensitivity")
with(model_table, lines(thresholds, sensitivities, col = "red"))
legend(x = 0.75, y = 0.55, legend = c("Sensitivity", "Specificity"),
lty = 1, col = c("red","black"))
abline(h = c(0, 1), col = "grey80", lty = "dotted")
```