Predicting Readmission for Patients with Diabetes Mellitus

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Problem Statement

Rehospitalizations impose a significant financial burden on the healthcare system. According to the Center for Health Information and Analysis, hospital readmissions cost Medicare $26 billion annually, with $17 billion considered avoidable (Reardon, 2015). These avoidable readmissions contribute to the rising healthcare costs and strain resources for both patients and healthcare providers. To incentivize hospitals to reduce their readmission rates, the Centers for Medicare and Medicaid Services (CMS) established the Hospital Readmission Reduction Program (HRRP). Under the program, hospitals are evaluated based on their ability to manage excess readmission and can face payment deductions as a consequence for poor performance (CMS.gov, 2023).

This data science project serves to contribute to the ongoing efforts to reduce hospital readmissions. We focus specifically on diabetes mellitus encounters and hope to gain valuable insights into the risk factors associated with readmission in diabetic patients. This targeted approach serves as a stepping stone towards a broader goal of predicting readmissions for other chronic diseases. Accurately predicting hospital readmission for diabetic patients has two major benefits. First, healthcare providers can identify patients who are most at risk and intervene in a timely manner. Secondly, there are financial incentives for hospitals to reduce admissions as this would keep costs down and prevent financial penalties. These advantages emphasize the importance of developing an accurate predictive model for diabetes with the potential for wider application in other chronic diseases.

Data Source

The original data comes from the Health Facts database and represents 10 years (1999-2008) of clinical patient records at 130 hospitals and integrated delivery systems across the United States. The dataset used for this project contains a subset of this database as extracted by Strack et al. (2013) in their journal article "Impact of HbA1c Measurement on Hospital Readmission Rates: Analysis of 70,000 Clinical Database Patient Records". The extracted dataset, accessed through the UCI Machine Learning Repository, contains 101766 patient encounters and 50 features that satisfy the following criteria:

1) It is an inpatient encounter (a hospital admission)
2) It is a "diabetic" encounter (i.e "diabetes" was entered into the system as either a primary/secondary diagnosis)
3) The length of stay was between 1-14 days
4) Laboratory tests were performed during the encounter
5) Medications were administered during the encounter (Clore et al., 2014).

The 50 features can be divided into three subcategories: (1) patient demographics including race, gender, weight, payer code, (2) admission information including discharge type, admission source, admission type, whether the patient was readmitted, and (3) laboratory and medical interventions during the encounter including number of medications administered, procedures performed, blood glucose test (A1c) result, and the change in dosage for a number of drugs (Clore et al., 2014).

Data Wrangling

Feature Deletion

The initial data preparation includes the removal of biased observations and irrelevant or missing features. For example, patient encounters who were discharged to hospice or resulted in death were removed to limit bias during modeling. Other categorical variables, such as 'admission_source_id' (25 IDs), 'admission_type_id' (8 IDs), and 'discharge_disposition_id' (30 IDs) contained IDs associated with null values (e.g "Not Available", "NULL", and "Not Mapped"). These levels in their original form would be misleading for modeling and were encoded as NA to reflect the absence of information. Features representing a patient's weight ('weight') and the medical speciality of the admitting physician ('medical_specialty') were removed due to a high percentage of null values, with 96.85% and 48.94% missing, respectively. Other attributes had less than 2% of null values, and the observations containing these nulls were removed. Degenerated variables and other irrelevant features (e.g payer code, patient ID, encounter ID) were also removed prior to modeling.

Feature Extraction

Primary and secondary diagnoses are encoded using the first three digits of ICD-9-CM, the official system for encoding diagnoses and procedures in hospitals in the United States (National Center for Health Statistics*,* 2021). The dataset contains three attributes for the primary diagnosis ('diag_1') and secondary diagnoses ('diag_2', 'diag_3), with over 800 levels for each attribute. These codes were grouped according to the 2016 edition of ICD-9-CM chapters as follows: 140-239 "Neoplasms", 250 "Diabetes", 320-459 "Circulatory", 460-519 "Respiratory", 520-579 "Digestive", 580-629 "Genitourinary System", 710-739 "Musculoskeletal", 760-779 "Perinatal", and 800-999 " Injury and Poisoning" (ICD.Codes, n.d.). All other chapters with less than 2500 instances in the primary diagnosis were grouped into "Other". These same levels were used to define the secondary diagnoses.

Target variable

The target variable, 'readmitted', defines the number of days until the patient is readmitted. It contains three values: "<30" if the patient was readmitted within 30 days, ">30" if the patient was readmitted after 30 days, and "NO" if the patient was not readmitted. For the purpose of this project, we consider all admissions as true regardless of the length of time between encounters. We redefined the target variable as "YES" if the patient was readmitted at any time and “NO” if the patient was not readmitted. After, there are 41094 (47%) readmissions and 45472 (53%) 1-chance encounters (or there is no record of readmission).

Final Dataset

The prepared dataset contains 18 predictors and 86566 patient encounters. The target variable is binary with levels of “YES” and “NO”.

Modeling Preparation

The dataset was split with stratification of the target variable into a training set containing 70% (59529) and a test set with 30% (25512) observations. Other preprocessing steps included standardization using centering and scaling, removal of outliers, and conversion of categorical variables into *n-1* dummy variables.

Exploratory Data Analysis

The distributions of the number of medications administered during the encounter (‘num_medications’) and number of lab procedures (‘num_lab_procedures’) are approximately normal and centered around 16.06 and 43.42, respectively. All other numeric variables are heavily right skewed, with the majority of values falling close to 0. There is moderate correlation between the time spent in the hospital and the number of procedures performed (*r*=0.33), time spent in the hospital and the number of medications administered (*r*=0.46), as well as the number of medications administered and lab procedures performed (*r*=0.38).

Figure 1

Boxplots for Readmitted vs. Time in Hospital and Number of Diagnoses

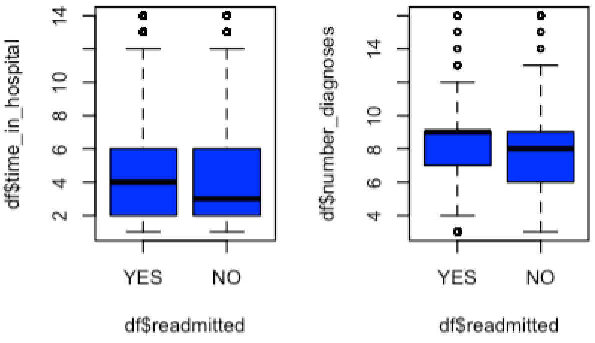


Figure 1 shows boxplots for readmitted vs. time in hospital and number of diagnoses entered into a patient's charts. In general, patients who are readmitted spend more time in the hospital and have more diagnoses entered into the system.

Figure 2

Stacked Bar Charts for Categorical Variables vs. Readmitted

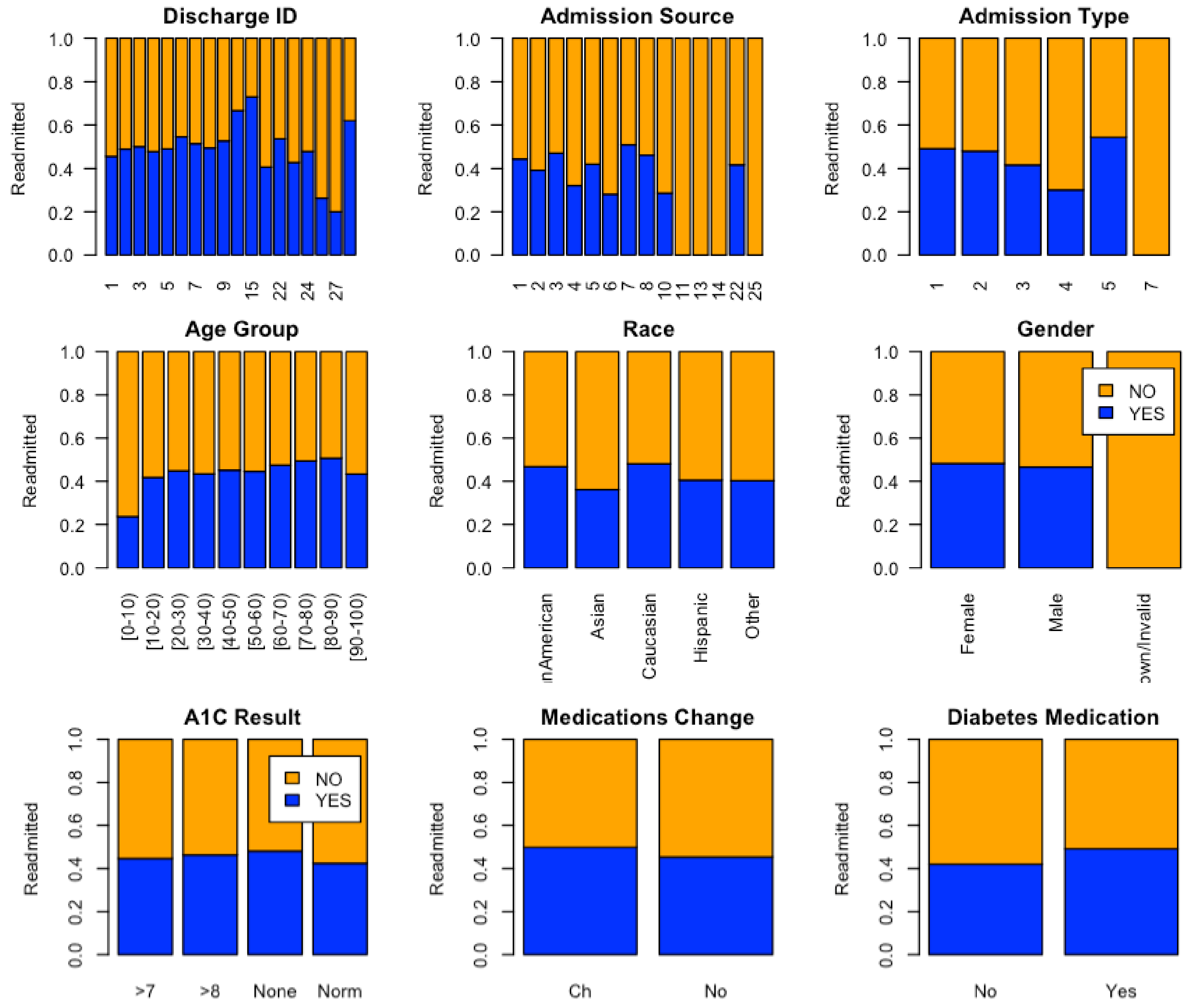
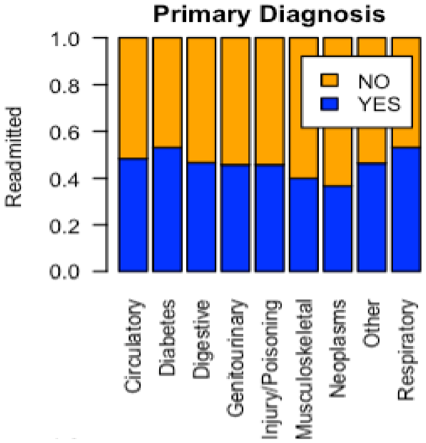


Figure 2 shows the normalized proportions of all categorical variables and the target variable. Patients who were discharged or transferred to a federal health facility (discharge disposition ID 27) were least likely to be readmitted (IDs 25 and 18 represent null values) while discharges to a Medicare approved swing bed (ID 15), outpatient services (ID 12) and psychiatric unit (ID 28) were most likely to be readmitted. Patients admitted through normal delivery (admission source ID 11), a sick baby (ID 13), extramural birth (ID 14), and transferred from ambulatory surgery center (ID 25) had no readmissions. Trauma center admission type patients (admission type ID 7) also had no readmissions. Looking at patient demographics, the risk of readmission was seen to increase with age and if the patient was African-American or Caucasian.

The most common primary diagnoses were circulatory (27207, 31.43%), other (18242, 21.07%), respiratory (8618, 9.96%), and digestive (7873, 9.09%). 7185 (8.30%) patients had a primary diagnosis of diabetes. This suggests that most patients are hospitalized for other root causes, and later developed diabetes or are dealing with chronic diabetes concurrently. Patients with a primary diagnosis of diabetes and respiratory diseases were more likely to be readmitted compared to other diseases (Figure 3).

Figure 3

Stacked Barchart for Primary Diagnosis vs Readmitted



Modeling

Using the preprocessed data, we next built different classification models to predict the target variable “readmitted”. We used the train dataset for training the models and used the test dataset for testing the models. A 10-fold cross-validation method is applied to optimize the training process.

When selecting the models, we considered if the model is suitable for solving binary classification problems, if it is capable of computing large dimensional data, and if it works with both numerical and categorical features. We explored linear classification models such as logistic regression, penalized logistic regression, and nearest shrunken centroids model. We also explored non-linear models including bagged tree, gradient boosted tree, random forest tree, and K-nearest neighbor models.

Logistic Regression

Logistic regression is a linear machine learning algorithm used for binary classification. It requires that each observation is independent of the other and assumes a linear relationship between the independent variables and the log-odds of the dependent variable. It predicts the probability of an instance belonging to a class which is then mapped to a binary value of 0 and 1 corresponding to the binary labels. The cross-validation resampling produced an accuracy of 0.59 and a sensitivity of 0.52.

Penalized Logistic Regression Model

Penalized logistic regression models apply regularization methods to the regular logistic regression model. We implemented the glmnet penalized model that adopts ridge and lasso penalties simultaneously, which means a squared penalty and an absolute value penalty are added on the binomial likelihood function. A tuning parameter alpha controls the mixing proportion between pure lasso penalty (alpha =1) and a pure ridge penalty (alpha=0). Another parameter lambda controls the amount of penalization.

We tuned the model with 4 alpha values (0, 0, 0.1, 0.2, 0.4) and 5 lambda values between 0.01 and 0.1. The optimal model is reached when alpha is 0 and lambda is 0.01. The resampling produced an accuracy of 0.59 and a sensitivity of 0.52.

Nearest Shrunken Centroids Model

The nearest shrunken centroids model is a linear classification model that assumes the centroids in the feature space are different for each target label. By taking the average of each feature in the training set, the algorithm first summarizes a set of centroids for each class. When predicting on new data, the distance between a given data instance and each centroid is calculated and the closest centroid is used to assign a class label to the query (Brownlee, 2020).

To extend the method for optimal classification, the centroids of each input variable are shrunk towards the centroid of the entire training dataset as means to select features. The amount of shrinkage is a tuning hyperparameter. In training our model, we tuned 20 shrinkage ranging between 0 and 15. The optimal model is reached when the shrinkage threshold is 0. The resampling produced an accuracy of 0.57 and a sensitivity of 0.50.

Bagged Trees

Bagged tree is an ensemble machine learning method used to strengthen the single decision tree model. The main purpose is to group a set of weak learners and form a strong learner. Weak learners learn from each other independently in parallel and then are combined to produce a powerful model. Bagging decreases variance, and solves over-fitting issues in a decision tree model (Vadapalli, 2022). With a number of bags parameter 30, the model produced an accuracy of 0.57, and a sensitivity of 0.54.

Gradient Boosted Trees

Boosted tree is another ensemble method to enhance the basic decision tree model. It starts with a base/weak learner tree, then constructs multiple tree models in sequence. Each of the trees corrects the previous one’s errors. The final tree model works as a strong learner that shows the weighted mean of all the tree models. Boosted tree algorithm decreases the bias error.

In tuning the model, we created a tuning grid with the following perimeters: interaction depth (5, 7), number of trees (500), and shrinkage (0.01, 0.1). The optimal model is achieved when shrinkage is 0.1 and depth is 5. The optimal model produced a resampling performance of accuracy of 0.60 and sensitivity, 0.56.

Random Forest

Random forest builds a series of decision trees with a random sample of the training dataset and combines them to decide the final classification. For each decision tree, a subset of features are selected and trained on a different set of sample data. All these decision trees then form a forest. When predicting a new data record, random forest takes the prediction from each tree and decides the final output based on the majority votes.

The tuning parameters include the number of trees and the number of randomly selected predictors. We tuned the model with 100 trees and the number of predictors of 1, 3, 5, and 7. The optimal model is reached with the number of predictors 3. The optimal resampling performance gave an accuracy of 0.59 and sensitivity of 0.53.

K-Nearest Neighbor (KNN)

The KNN model is called a lazy learner algorithm because it does not learn from the training set immediately. It stores the available data without training them. It classifies a new data sample into a category based on its similarity to its K nearest neighbors. KNN has one tuning parameter, K, the number of neighbors. When K is too low, the model will form a very complex decision boundary resulting in poor predictions. Therefore, it’s important to find the right value of K for the optimal classification result (Aggarwal, 2020). We tuned K with values of 5, 7, and 9 with 9 as the optimal value for K. The training performance produced an accuracy of 0.56 and a sensitivity of 0.53.

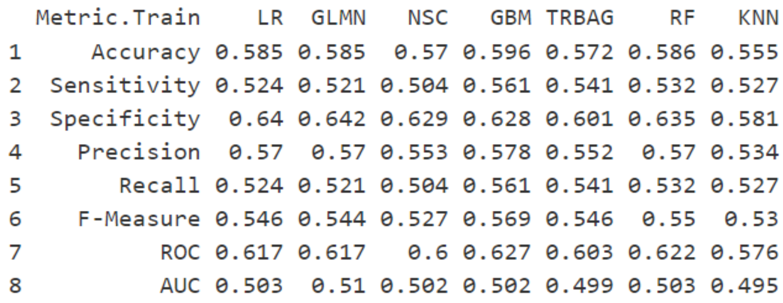
Results

For this data analysis problem, a model's ability to predict the positive (readmitted-Yes) accurately is most important. Therefore, we choose the all positive model as the baseline model. Analyzing the ratio of readmission yes and no in the training dataset, 48% of cases have readmitted label 'Yes'. It indicates that if we assign all predictions as positive, the accuracy for this baseline model to predict the positive is 0.48.

The resampling performance and testing performance are evaluated using various metrics based on the confusion matrix. They include accuracy, sensitivity, specificity, precision, recall, and F score. The comparison of the models on cross-validation performance is seen in Table 1. The comparison on testing performance is seen in Table 2.

Table 1

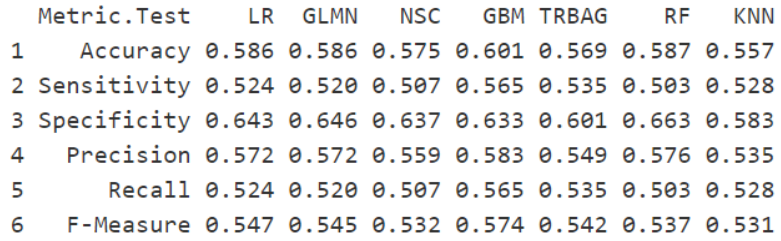
Metrics for Cross-Validation



```
  Metric.Train    LR  GLMN   NSC   GBM TRBAG    RF   KNN
1     Accuracy 0.585 0.585  0.57 0.596 0.572 0.586 0.555
2  Sensitivity 0.524 0.521 0.504 0.561 0.541 0.532 0.527
3  Specificity  0.64 0.642 0.629 0.628 0.601 0.635 0.581
4    Precision  0.57  0.57 0.553 0.578 0.552  0.57 0.534
5       Recall 0.524 0.521 0.504 0.561 0.541 0.532 0.527
6    F-Measure 0.546 0.544 0.527 0.569 0.546  0.55  0.53
7          ROC 0.617 0.617   0.6 0.627 0.603 0.622 0.576
8          AUC 0.503  0.51 0.502 0.502 0.499 0.503 0.495
```

Table 2

Metrics for Testing



```
  Metric.Test    LR  GLMN   NSC   GBM TRBAG    RF   KNN
1    Accuracy 0.586 0.586 0.575 0.601 0.569 0.587 0.557
2 Sensitivity 0.524 0.520 0.507 0.565 0.535 0.503 0.528
3 Specificity 0.643 0.646 0.637 0.633 0.601 0.663 0.583
4   Precision 0.572 0.572 0.559 0.583 0.549 0.576 0.535
5      Recall 0.524 0.520 0.507 0.565 0.535 0.503 0.528
6   F-Measure 0.547 0.545 0.532 0.574 0.542 0.537 0.531
```

From Tables 1 and 2, we see all models produced similar performance metrics. The accuracy ranges from 0.56 to 0.6. The sensitivity ranges from 0.52 to 0.56. The ROC ranges from 0.58 to 0.63. And it shows consistent performance output between cross-validation and testing. Gradient boosted tree model is selected to be the final model with the best performance on all metrics except specificity. It produced an accuracy of 0.60, a sensitivity of 0.57, a specificity of 0.63, a precision of 0.58, and a F1 of 0.57 from testing.

To analyze the importance of features, we checked the first 15 important features from logistic regression, random forest, and KNN model. Though each model displays the important features in different order, some features appeared to be important for all three models, including: number_diagnoses, num_procedures, num_lab_procedures, num_medication, time_in_hospital. etc.

Conclusion & Discussion

We created this predictive data analysis project with a goal to help hospitals reduce readmissions for diabetic patients and understand risk factors associated with readmissions. A dataset consisting of 101766 data records with 50 features of patients with diabetic encounters was analyzed to predict patients' possible future readmissions. After wrangling the data, 18 more relevant features were extracted for creating binary classification machine learning models that predict the readmission status of yes or no. Gradient boosted tree model was selected as the final model with its computational efficiency and the best performance in both training and testing. It can improve the baseline model's ability to predict the positive (readmission yes) by 10%.

The advantage of the project is that we have an ample amount of data so that we could remove the missing values and outliers without approximating the data. Another strength is that we were able to build and compare multiple linear and non-linear classification models. All the seven models we built produced very consistent training and testing outcomes indicating that we have reached the limits that the features might be able to predict the target of readmissions.

The weakness that refrains the models' performance lies in the fact that the dataset we used is not the original data, but extracted. Quite some useful information was lost during the extraction. For example, age, originally a numerical variable was binned into categorical, making it less useful. Some other variables lost their predictive ability likewise. Another challenge we have encountered is the lack of computing power to run more complicated and resource demanding classification models and to tune models with a larger range of tuning parameters. It turned out that when the data is highly dimensional, to train non-linear models with a bigger tuning grid requires a significant amount of running time that we could not afford. As a result, we were not able to examine more non-linear models or tune the built models with larger scale of parameters to discover the ideal model or optimal model results for this project.

To improve the project's outcome further, we should use the original dataset instead of the extracted one to retain informative features. Also, to conquer the computing power limitation, we should try to run the models on a cloud computing system, like AWS.

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Diabetes Readmission Prediction

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1. Initial Data Preparation

1.1 Import and check the Data

```
#Read in data, replace "?" with NA values
df <- read.csv(file = "diabetic_data.csv", na.strings=c("?"))
dim(df)
```

```
## [1] 101766     50
```

```
str(df)
```

```
## 'data.frame':    101766 obs. of  50 variables:
##  $ encounter_id            : int  2278392 149190 64410 500364 16680 35754 55842 63768 1252
2 15738 ...
##  $ patient_nbr             : int  8222157 55629189 86047875 82442376 42519267 82637451 842
59809 114882984 48330783 63555939 ...
##  $ race                    : chr  "Caucasian" "Caucasian" "AfricanAmerican" "Caucasian"
...
##  $ gender                  : chr  "Female" "Female" "Female" "Male" ...
##  $ age                     : chr  "[0-10)" "[10-20)" "[20-30)" "[30-40)" ...
##  $ weight                  : chr  NA NA NA NA ...
##  $ admission_type_id       : int  6 1 1 1 1 2 3 1 2 3 ...
##  $ discharge_disposition_id: int  25 1 1 1 1 1 1 1 1 3 ...
##  $ admission_source_id     : int  1 7 7 7 7 2 2 7 4 4 ...
##  $ time_in_hospital        : int  1 3 2 2 1 3 4 5 13 12 ...
##  $ payer_code              : chr  NA NA NA NA ...
##  $ medical_specialty       : chr  "Pediatrics-Endocrinology" NA NA NA ...
##  $ num_lab_procedures      : int  41 59 11 44 51 31 70 73 68 33 ...
##  $ num_procedures          : int  0 0 5 1 0 6 1 0 2 3 ...
##  $ num_medications         : int  1 18 13 16 8 16 21 12 28 18 ...
##  $ number_outpatient       : int  0 0 2 0 0 0 0 0 0 0 ...
##  $ number_emergency        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ number_inpatient        : int  0 0 1 0 0 0 0 0 0 0 ...
##  $ diag_1                  : chr  "250.83" "276" "648" "8" ...
##  $ diag_2                  : chr  NA "250.01" "250" "250.43" ...
##  $ diag_3                  : chr  NA "255" "V27" "403" ...
##  $ number_diagnoses        : int  1 9 6 7 5 9 7 8 8 8 ...
##  $ max_glu_serum           : chr  "None" "None" "None" "None" ...
##  $ A1Cresult               : chr  "None" "None" "None" "None" ...
##  $ metformin               : chr  "No" "No" "No" "No" ...
##  $ repaglinide             : chr  "No" "No" "No" "No" ...
##  $ nateglinide             : chr  "No" "No" "No" "No" ...
##  $ chlorpropamide          : chr  "No" "No" "No" "No" ...
##  $ glimepiride             : chr  "No" "No" "No" "No" ...
##  $ acetohexamide           : chr  "No" "No" "No" "No" ...
##  $ glipizide               : chr  "No" "No" "Steady" "No" ...
##  $ glyburide               : chr  "No" "No" "No" "No" ...
##  $ tolbutamide             : chr  "No" "No" "No" "No" ...
##  $ pioglitazone            : chr  "No" "No" "No" "No" ...
##  $ rosiglitazone           : chr  "No" "No" "No" "No" ...
##  $ acarbose                : chr  "No" "No" "No" "No" ...
##  $ miglitol                : chr  "No" "No" "No" "No" ...
##  $ troglitazone            : chr  "No" "No" "No" "No" ...
##  $ tolazamide              : chr  "No" "No" "No" "No" ...
##  $ examide                 : chr  "No" "No" "No" "No" ...
##  $ citoglipton             : chr  "No" "No" "No" "No" ...
##  $ insulin                 : chr  "No" "Up" "No" "Up" ...
##  $ glyburide.metformin     : chr  "No" "No" "No" "No" ...
##  $ glipizide.metformin     : chr  "No" "No" "No" "No" ...
##  $ glimepiride.pioglitazone: chr  "No" "No" "No" "No" ...
##  $ metformin.rosiglitazone : chr  "No" "No" "No" "No" ...
##  $ metformin.pioglitazone  : chr  "No" "No" "No" "No" ...
##  $ change                  : chr  "No" "Ch" "No" "Ch" ...
##  $ diabetesMed             : chr  "No" "Yes" "Yes" "Yes" ...
##  $ readmitted              : chr  "NO" ">30" "NO" "NO" ...
```

- There are 101766 data records with 50 features

1.2 Filter out Irrelevant Observations

- All patient encounters associated with a discharge to hospice or death will be removed, as the chance of readmission is low-impossible.

```
dischargedRemoved <- c(11,13,14,19,20,21)
df <- subset(df, !(discharge_disposition_id %in% dischargedRemoved))
```

- encounter_id and patient_nbr are identifiers, not useful features. Payer_code is irrelevant feature too. They will be removed.

```
df <- subset(df, select = -c(encounter_id, patient_nbr, payer_code))
dim(df)
```

```
## [1] 99343    47
```

1.3 Filter out degenerated features

```
library(caret)

# Use nearZeroVar function to filter out low variance features
degenerateCols <- nearZeroVar(df)
length(degenerateCols)
```

```
## [1] 18
```

```
degenerateColNames <- colnames(df[degenerateCols])
degenerateColNum <- length(degenerateColNames)

cat("These are ", degenerateColNum, " degenerated predictors:\n", degenerateColNames, "\n\n")
```

```
## These are  18  degenerated predictors:
##  max_glu_serum repaglinide nateglinide chlorpropamide glimepiride acetohexamide tolbutamid
e acarbose miglitol troglitazone tolazamide examide citoglipton glyburide.metformin glipizid
e.metformin glimepiride.pioglitazone metformin.rosiglitazone metformin.pioglitazone
```

```
df<- df[, -degenerateCols]
dim(df)
```

```
## [1] 99343    29
```

```
colnames(df)
```

```
##  [1] "race"                     "gender"
##  [3] "age"                      "weight"
##  [5] "admission_type_id"        "discharge_disposition_id"
##  [7] "admission_source_id"      "time_in_hospital"
##  [9] "medical_specialty"        "num_lab_procedures"
## [11] "num_procedures"           "num_medications"
## [13] "number_outpatient"        "number_emergency"
## [15] "number_inpatient"         "diag_1"
## [17] "diag_2"                   "diag_3"
## [19] "number_diagnoses"         "A1Cresult"
## [21] "metformin"                "glipizide"
## [23] "glyburide"                "pioglitazone"
## [25] "rosiglitazone"            "insulin"
## [27] "change"                   "diabetesMed"
## [29] "readmitted"
```

- 18 degenerated predictors that show near-zero variance have been removed. 29 columns are left in the dataset.

1.4 Filter out categorical levels indicating nulls

‘discharge_disposition_id’ (discharge ID), ‘admission_type_id’ (admission type ID), and ‘admission_source_id’ (admission source ID) are categorical variables with levels identified by their ID number. For example, ‘admission_type_id’ 1 refers to ‘Emergency’.

For admission source and type, the following ID levels associated with null values will be replaced as NA:

- Admission source ID 9 (Not Available), 17 (NULL), and 20 (Not Mapped)
- Admission type ID 6 (NULL) and 8 (Not Mapped)

```
admissionsourceRemoved <- c(9,17,20)
df$admission_source_id[df$admission_source_id %in% admissionsourceRemoved] <- NA

admissiontypeRemoved <- c(6,8)
df$admission_type_id[df$admission_type_id %in% admissiontypeRemoved] <- NA
table(df$admission_source_id)
```

```
##
##     1     2     3     4     5     6     7     8    10    11    13    14    22
## 29168  1081   185  3118   806  2239 55850    15     8     2     1     2    12
##    25
##     2
```

```
sum(is.na(df$admission_source_id))
```

```
## [1] 6854
```

1.5 Handle missing values

- Check missing values

```
# Check null values
#Show null counts
null_counts <- sort(colSums(is.na(df)), decreasing=TRUE)
head(null_counts,10)
```

```
##              weight   medical_specialty admission_source_id   admission_type_id
##               96218               48616                6854                5527
##                race              diag_3              diag_2              diag_1
##                2234                1419                 356                  20
##              gender                 age
##                   0                   0
```

```
#Show proportion of null counts
nullProp <- sort(round(colMeans(is.na(df)),3), decreasing=TRUE)
head(nullProp,10)
```

```
##                   weight        medical_specialty      admission_source_id
##                    0.969                    0.489                    0.069
##        admission_type_id                     race                   diag_3
##                    0.056                    0.022                    0.014
##                   diag_2                   gender                      age
##                    0.004                    0.000                    0.000
## discharge_disposition_id
##                    0.000
```

- The following predictors contain a significant number of null values: ‘weight’ (96.9%), medical_specialty (48.9%). These two predictors will be removed.
- The following predictors contain less than 2% null values: ‘race’ (2.2%), ‘diag_3’ (1.4%), ‘diag_2’ (0.4%), and ‘diag_1’ (0.02%). Because the null percentages are very low, we will simply remove the rows with null values.

```
# remove weight and medical_specialty
df<- subset(df, select = -c(weight, medical_specialty))

# Remove other null values
df <- na.omit(df)

null_counts <- sort(colSums(is.na(df)), decreasing=TRUE)
head(null_counts,10)
```

```
##                     race                   gender                      age
##                        0                        0                        0
##        admission_type_id discharge_disposition_id      admission_source_id
##                        0                        0                        0
##         time_in_hospital       num_lab_procedures           num_procedures
##                        0                        0                        0
##          num_medications
##                        0
```

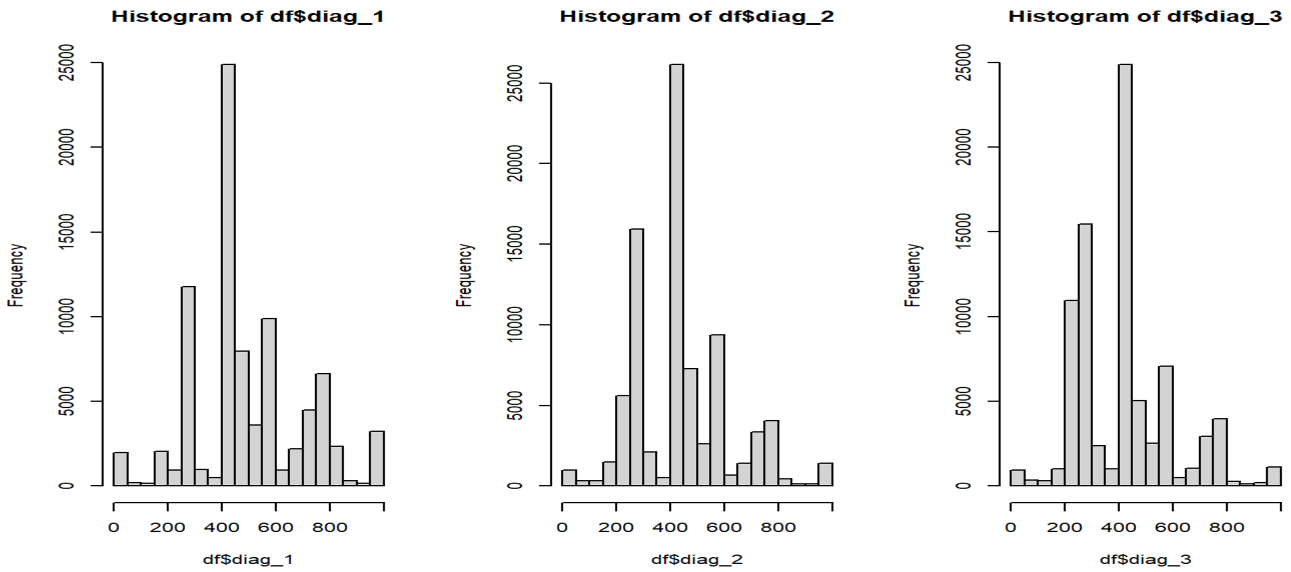
```
dim(df)
```

```
## [1] 86566    27
```

1.6 Feature Creation

- Explore primary diagnoses (‘diag_1’) and secondary diagnoses (‘diag_2’, ‘diag_3’)

```
# Convert to numeric
df$diag_1 <- as.numeric(df$diag_1)
df$diag_2 <- as.numeric(df$diag_2)
df$diag_3 <- as.numeric(df$diag_3)

# Show distributions of diagnoses
par(mfrow=c(1,3))
hist(df$diag_1)
hist(df$diag_2)
hist(df$diag_3)
```



```
#summary(df$diag_1)
```

- Extract primary/secondary diagnoses

```r
library(dplyr)

df <- df %>%
  mutate(primary_diagnosis = case_when(
    substr(diag_1, 1, 3) == "250" ~ "Diabetes",
    #between(as.numeric(diag_1), 001, 139) ~ "Infectious and Parasitic Diseases",
    between(as.numeric(diag_1), 140, 239) ~ "Neoplasms",
    between(as.numeric(diag_1), 320, 459) ~ "Circulatory",
    between(as.numeric(diag_1), 460, 519) ~ "Respiratory",
    between(as.numeric(diag_1), 520, 579) ~ "Digestive",
    between(as.numeric(diag_1), 580, 629) ~ "Genitourinary System",
    #between(as.numeric(diag_1), 680, 709) ~ "Skin/Subcutaneous Tissue",
    between(as.numeric(diag_1), 710, 739) ~ "Musculoskeletal",
    between(as.numeric(diag_1), 760, 779) ~ "Perinatal",
    between(as.numeric(diag_1), 800, 999) ~ "Injury and Poisoning",
    TRUE ~ "Other"
  ))

# Secondary Diagnosis
df <- df %>%
  mutate(secondary_diagnosis = case_when(
    substr(diag_2, 1, 3) == "250" ~ "Diabetes",
    #between(as.numeric(diag_2), 001, 139) ~ "Infectious and Parasitic Diseases",
    between(as.numeric(diag_2), 140, 239) ~ "Neoplasms",
    between(as.numeric(diag_2), 320, 459) ~ "Circulatory",
    between(as.numeric(diag_2), 460, 519) ~ "Respiratory",
    between(as.numeric(diag_2), 520, 579) ~ "Digestive",
    between(as.numeric(diag_2), 580, 629) ~ "Genitourinary System",
    #between(as.numeric(diag_2), 680, 709) ~ "Skin/Subcutaneous Tissue",
    between(as.numeric(diag_2), 710, 739) ~ "Musculoskeletal",
    between(as.numeric(diag_2), 760, 779) ~ "Perinatal",
    between(as.numeric(diag_2), 800, 999) ~ "Injury and Poisoning",
    TRUE ~ "Other"
  ))

# Secondary Diagnosis
df <- df %>%
  mutate(secondary_diagnosis2 = case_when(
    substr(diag_3, 1, 3) == "250" ~ "Diabetes",
    #between(as.numeric(diag_3), 001, 139) ~ "Infectious and Parasitic Diseases",
    between(as.numeric(diag_3), 140, 239) ~ "Neoplasms",
    between(as.numeric(diag_3), 320, 459) ~ "Circulatory",
    between(as.numeric(diag_3), 460, 519) ~ "Respiratory",
    between(as.numeric(diag_3), 520, 579) ~ "Digestive",
    between(as.numeric(diag_3), 580, 629) ~ "Genitourinary System",
    #between(as.numeric(diag_3), 680, 709) ~ "Skin/Subcutaneous Tissue",
    between(as.numeric(diag_3), 710, 739) ~ "Musculoskeletal",
    between(as.numeric(diag_3), 760, 779) ~ "Perinatal",
    between(as.numeric(diag_3), 800, 999) ~ "Injury and Poisoning",
    TRUE ~ "Other"
  ))
df$primary_diagnosis <- as.factor(df$primary_diagnosis)
df$secondary_diagnosis <- as.factor(df$secondary_diagnosis)
df$secondary_diagnosis2 <- as.factor(df$secondary_diagnosis2)
```

- Show counts of diseases for the primary and secondary diagnosis:

```
table(df$primary_diagnosis)
```

```
## 
##          Circulatory             Diabetes            Digestive 
##                27207                 7185                 7873 
## Genitourinary System Injury and Poisoning      Musculoskeletal 
##                 4445                 6017                 4217 
##            Neoplasms                Other          Respiratory 
##                 2762                18242                 8618
```

```
# table(df$secondary_diagnosis)
# table(df$secondary_diagnosis2)
```

- All levels w/ less than 2500 instances are combined into 'Other'

- Most common primary/secondary diagnosis were circulatory.

- 7185 patients had diabetes as their primary diagnosis

- diag_1, diag_2, and diag_3 are turned to new variables. They are not needed anymore and will be removed.

```
df <- subset(df, select = -c(diag_1, diag_2,diag_3))
dim(df)
```

```
## [1] 86566    27
```

1.7 Convert categorical variables into factors

- All feature that are recorded as chr type are categorical variables
- admission_type_id, discharge_disposition_id, admission_source_id are recorded as int, but should be taken as categorical variables.

```
#Convert categorical variables into factors (according to Table 1 https://www.hindawi.com/jou
rnals/bmri/2014/781670/tab1/)
df[sapply(df, is.character)] <- lapply(df[sapply(df, is.character)],
                                       as.factor)

df$admission_type_id <- as.factor(df$admission_type_id)
df$discharge_disposition_id <- as.factor(df$discharge_disposition_id)
df$admission_source_id <- as.factor(df$admission_source_id)
```

- All categorical variables have been converted into factors

1.8 Classify features

- 27 variables are left for further analysis.
- Subset numerical and categorical features

```
# Subset numerical and categorical features into new data frames
library(dplyr)
df_num <- df %>%  select_if(is.integer)
df_cat <- df %>% select_if(is.factor)

# Show numerical variables
cat("These are the numerical features:\n", colnames(df_num), "\n\n")
```

```
## These are the numerical features:
##  time_in_hospital num_lab_procedures num_procedures num_medications number_outpatient numb
er_emergency number_inpatient number_diagnoses
```

```
# Show categorical variables
cat("These are the categorical features:\n", colnames(df_cat), "\n\n")
```

```
## These are the categorical features:
##  race gender age admission_type_id discharge_disposition_id admission_source_id A1Cresult
metformin glipizide glyburide pioglitazone rosiglitazone insulin change diabetesMed readmitte
d primary_diagnosis secondary_diagnosis secondary_diagnosis2
```

1.9 Explore and revalue the response variable

- We use “readmitted” as our response variable

```
# Show readmission counts
table(df$readmitted)
```

```
## 
##   <30   >30    NO 
##  9985 31109 45472
```

We will combine all patients who were admitted into one level. Thus, our response variable will be binary:

- YES if the patient was readmitted at any time
- NO if the patient was not readmitted

```
library(plyr)

revalue(df$readmitted, c("<30" = "YES")) -> df$readmitted
revalue(df$readmitted, c(">30" = "YES")) -> df$readmitted

# Show readmission counts using binary levels
table(df$readmitted)
```

```
## 
##   YES    NO 
## 41094 45472
```

```
# Show readmission ratio using binary levels
round(table(df$readmitted) / length(df$readmitted),2)
```

```
##
##  YES   NO
## 0.47 0.53
```

- The response variable now contains 47% of “YES” and 53% of “NO”.

2. Exploratory Data Analysis

2.1 Statistics of the numerical variables

```
summary(df_num)
```

```
##  time_in_hospital num_lab_procedures num_procedures  num_medications
##  Min.   : 1.000   Min.   :  1.00     Min.   :0.000   Min.   : 1.00
##  1st Qu.: 2.000   1st Qu.: 33.00     1st Qu.:0.000   1st Qu.:10.00
##  Median : 4.000   Median : 44.00     Median :1.000   Median :15.00
##  Mean   : 4.413   Mean   : 43.42     Mean   :1.348   Mean   :16.06
##  3rd Qu.: 6.000   3rd Qu.: 57.00     3rd Qu.:2.000   3rd Qu.:20.00
##  Max.   :14.000   Max.   :132.00     Max.   :6.000   Max.   :81.00
##  number_outpatient number_emergency  number_inpatient  number_diagnoses
##  Min.   : 0.0000   Min.   : 0.0000   Min.   : 0.0000   Min.   : 3.000
##  1st Qu.: 0.0000   1st Qu.: 0.0000   1st Qu.: 0.0000   1st Qu.: 6.000
##  Median : 0.0000   Median : 0.0000   Median : 0.0000   Median : 9.000
##  Mean   : 0.3664   Mean   : 0.2017   Mean   : 0.6462   Mean   : 7.543
##  3rd Qu.: 0.0000   3rd Qu.: 0.0000   3rd Qu.: 1.0000   3rd Qu.: 9.000
##  Max.   :42.0000   Max.   :76.0000   Max.   :21.0000   Max.   :16.000
```

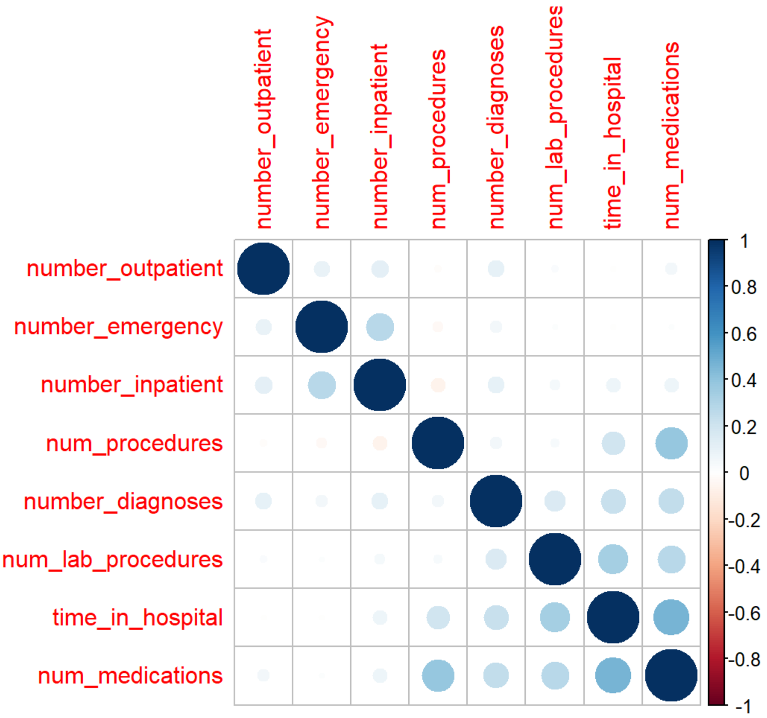
2.2 Correlations of the numerical variables

- Find Correlations of numerical features

```
library(corrplot)
correlations <- round(cor(df_num), 2)
correlations
```

```
##                    time_in_hospital num_lab_procedures num_procedures
## time_in_hospital               1.00               0.33           0.19
## num_lab_procedures             0.33               1.00           0.03
## num_procedures                 0.19               0.03           1.00
## num_medications                0.46               0.27           0.38
## number_outpatient             -0.01               0.02          -0.02
## number_emergency              -0.01               0.01          -0.04
## number_inpatient               0.07               0.04          -0.07
## number_diagnoses               0.22               0.16           0.05
##                    num_medications number_outpatient number_emergency
## time_in_hospital              0.46             -0.01            -0.01
## num_lab_procedures            0.27              0.02             0.01
## num_procedures                0.38             -0.02            -0.04
## num_medications               1.00              0.05             0.01
## number_outpatient             0.05              1.00             0.09
## number_emergency              0.01              0.09             1.00
## number_inpatient              0.07              0.11             0.27
## number_diagnoses              0.24              0.10             0.05
##                    number_inpatient number_diagnoses
## time_in_hospital               0.07             0.22
## num_lab_procedures             0.04             0.16
## num_procedures                -0.07             0.05
## num_medications                0.07             0.24
## number_outpatient              0.11             0.10
## number_emergency               0.27             0.05
## number_inpatient               1.00             0.10
## number_diagnoses               0.10             1.00
```

```
# Correlation plot
corrplot(correlations, order = "hclust")
```



Observing the correlation table and heatmap, there is modest correlations between:

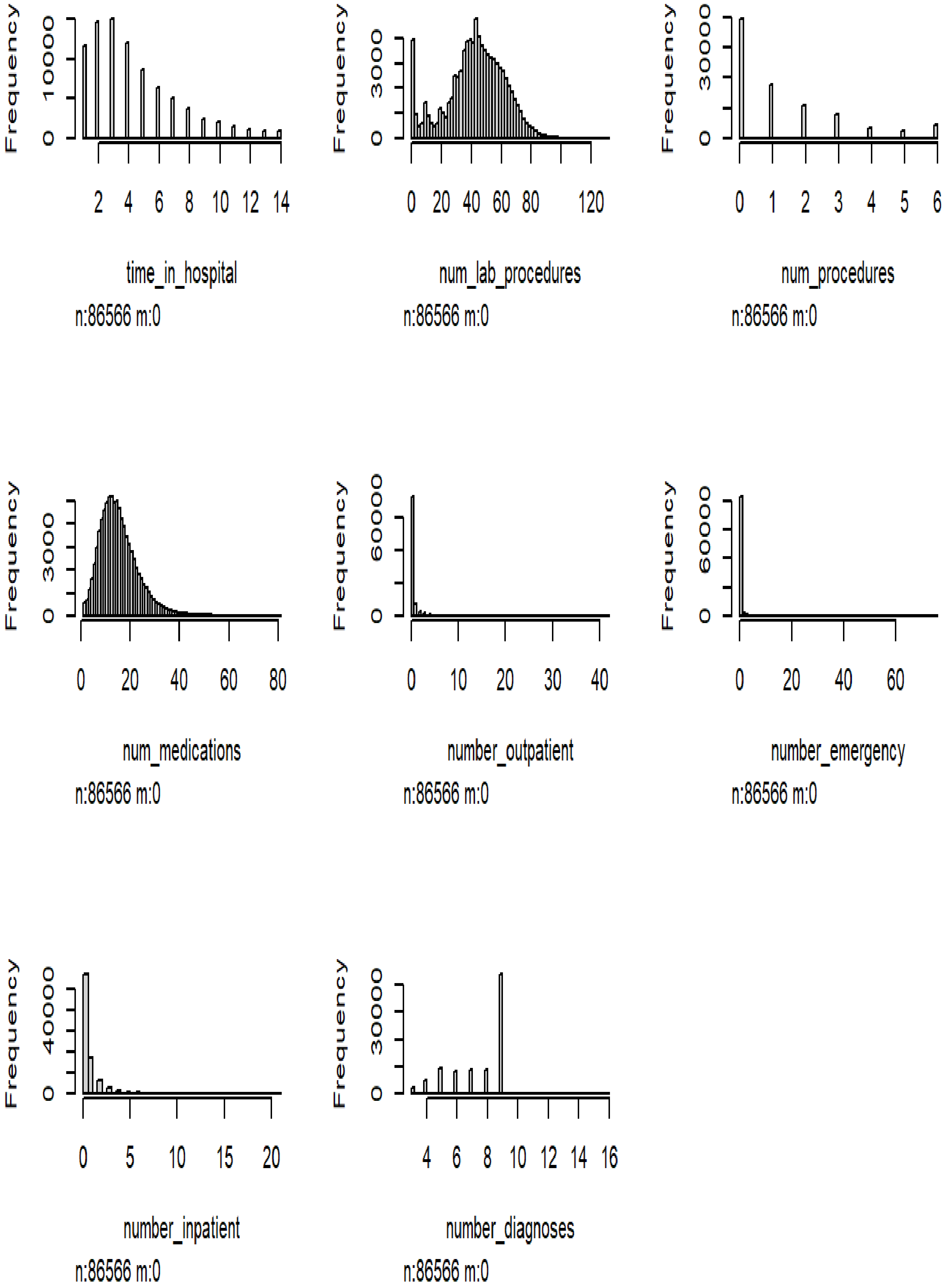
- num_lab_procedures and time_in_hospital (0.33)
- num_medications and and time_in_hospital (0.46)

- num_lab_procedures and num_medications (0.38)

Other than that, there is no much correlations between other variables.

2.3 Distribution of the numerical variables

```
library(Hmisc)
hist.data.frame(df_num)
```

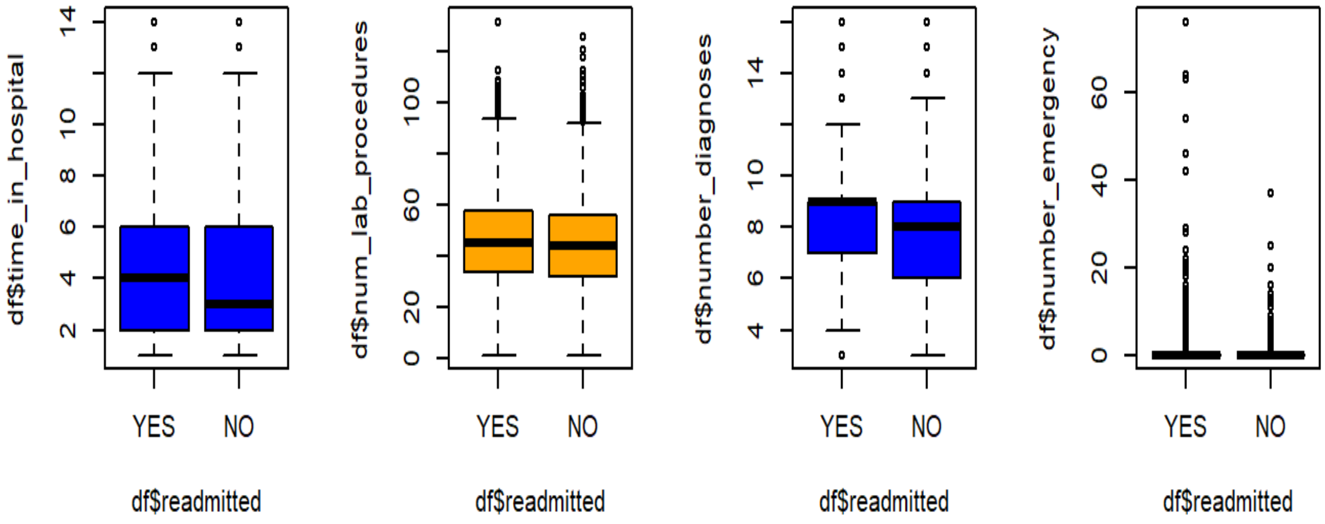


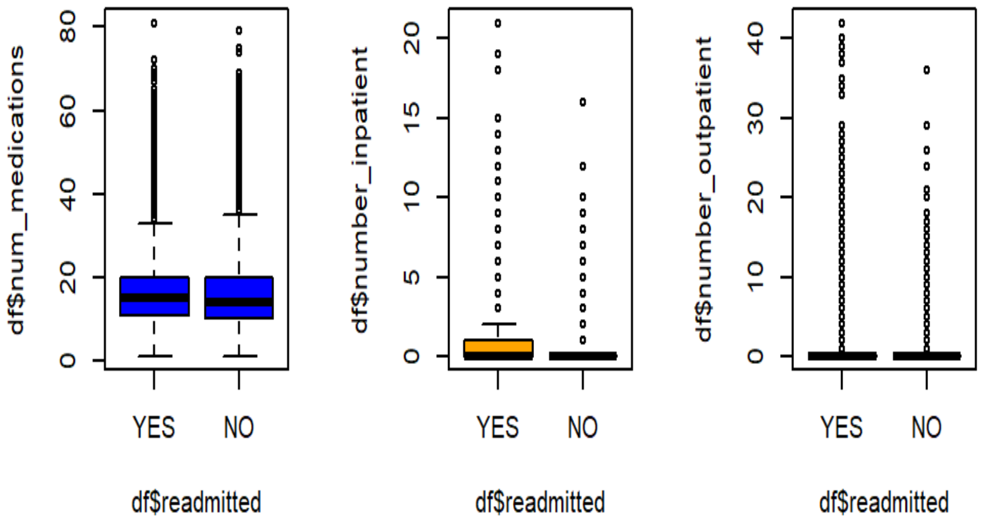
Frequency
0
10000
2
4
6
8
10
12
14
time_in_hospital
n:86566 m:0
Frequency
0
3000
0
20
40
60
80
120
num_lab_procedures
n:86566 m:0
Frequency
0
30000
0
1
2
3
4
5
6
num_procedures
n:86566 m:0
Frequency
0
3000
0
20
40
60
80
num_medications
n:86566 m:0
Frequency
0
60000
0
10
20
30
40
number_outpatient
n:86566 m:0
Frequency
0
60000
0
20
40
60
number_emergency
n:86566 m:0
Frequency
0
40000
0
5
10
15
20
number_inpatient
n:86566 m:0
Frequency
0
30000
4
6
8
10
12
14
16
number_diagnoses
n:86566 m:0

- number_medications and number_lab_procedures have a distribution that is close to normal distribution. The distribution for other variables are all skewed.

2.4 Explore the relationship between the numerical predictors and the predicted variable

```
par(mfrow = c(2,4))

boxplot(df$time_in_hospital ~ df$readmitted, col="blue")
boxplot(df$num_lab_procedures ~ df$readmitted, col="orange")
boxplot(df$number_diagnoses ~ df$readmitted, col="blue")

boxplot(df$number_emergency ~ df$readmitted, col="orange")
boxplot(df$num_medications ~ df$readmitted, col="blue")
boxplot(df$number_inpatient ~ df$readmitted, col="orange")
boxplot(df$number_outpatient ~ df$readmitted, col="blue")
```



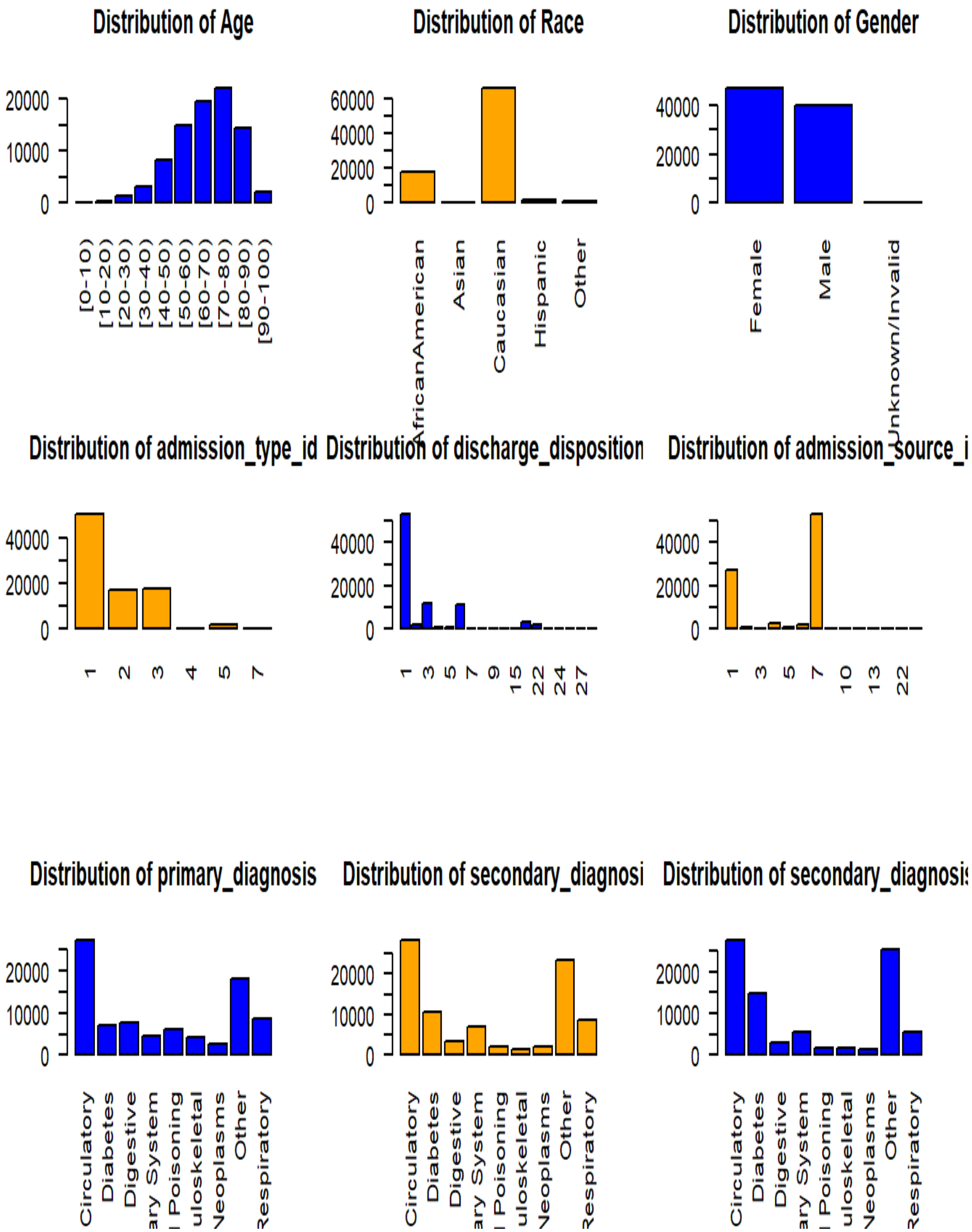


Patients who are readmitted, in general:

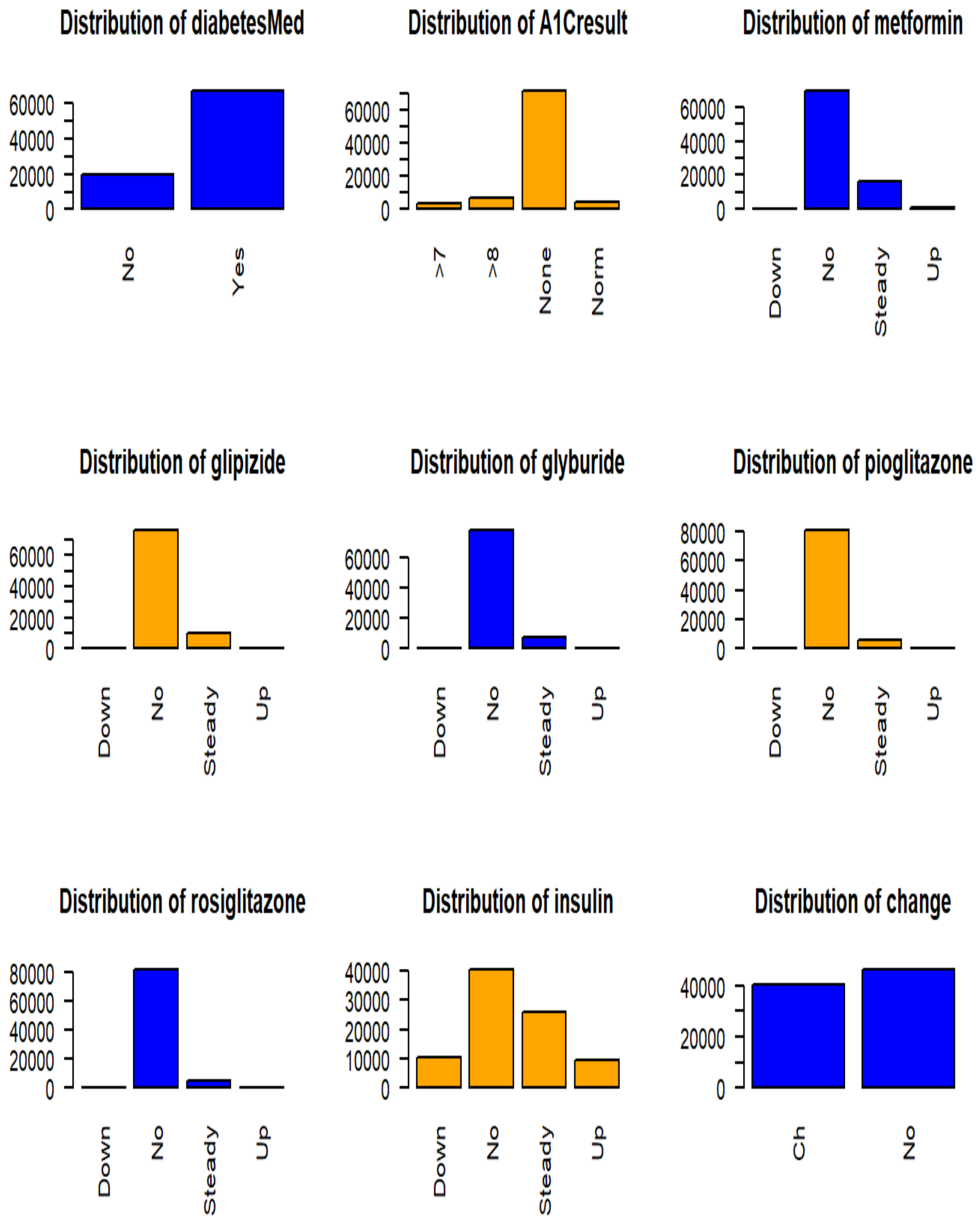
- Spend more time in the hospital
- Have more lab procedures done

2.5 Distribution of the categorical variables

```
par(mfrow = c(3,3))

barplot(table(df$age), main="Distribution of Age", col="blue", las=2)
barplot(table(df$race), main="Distribution of Race", col="orange", las=2)
barplot(table(df$gender), main="Distribution of Gender", col="blue", las=2)

barplot(table(df$admission_type_id), main="Distribution of admission_type_id",
        col="orange", las=2)
barplot(table(df$discharge_disposition_id), main="Distribution of discharge_disposition_id",
        col="blue", las=2)
barplot(table(df$admission_source_id), main="Distribution of admission_source_id",
        col="orange",las=2)


barplot(table(df$primary_diagnosis), main="Distribution of primary_diagnosis",
        col="blue", las=2)
barplot(table(df$secondary_diagnosis), main="Distribution of secondary_diagnosis",
        col="orange", las=2)
barplot(table(df$secondary_diagnosis2), main="Distribution of secondary_diagnosis2",
        col="blue", las=2)
```


Distribution of Age
20000
10000
0
[0-10)
[10-20)
[20-30)
[30-40)
[40-50)
[50-60)
[60-70)
[70-80)
[80-90)
[90-100)
Distribution of Race
60000
40000
20000
0
AfricanAmerican
Asian
Caucasian
Hispanic
Other
Distribution of Gender
40000
20000
0
Female
Male
Unknown/Invalid
Distribution of admission_type_id
40000
20000
0
1
2
3
4
5
7
Distribution of discharge_disposition
40000
20000
0
1
3
5
7
9
15
22
24
27
Distribution of admission_source_i
40000
20000
0
1
3
5
7
10
13
22
Distribution of primary_diagnosis
20000
10000
0
Circulatory
Diabetes
Digestive
ary System
l Poisoning
uloskeletal
Neoplasms
Other
Respiratory
Distribution of secondary_diagnosi
20000
10000
0
Circulatory
Diabetes
Digestive
ary System
l Poisoning
uloskeletal
Neoplasms
Other
Respiratory
Distribution of secondary_diagnosis
20000
10000
0
Circulatory
Diabetes
Digestive
ary System
l Poisoning
uloskeletal
Neoplasms
Other
Respiratory

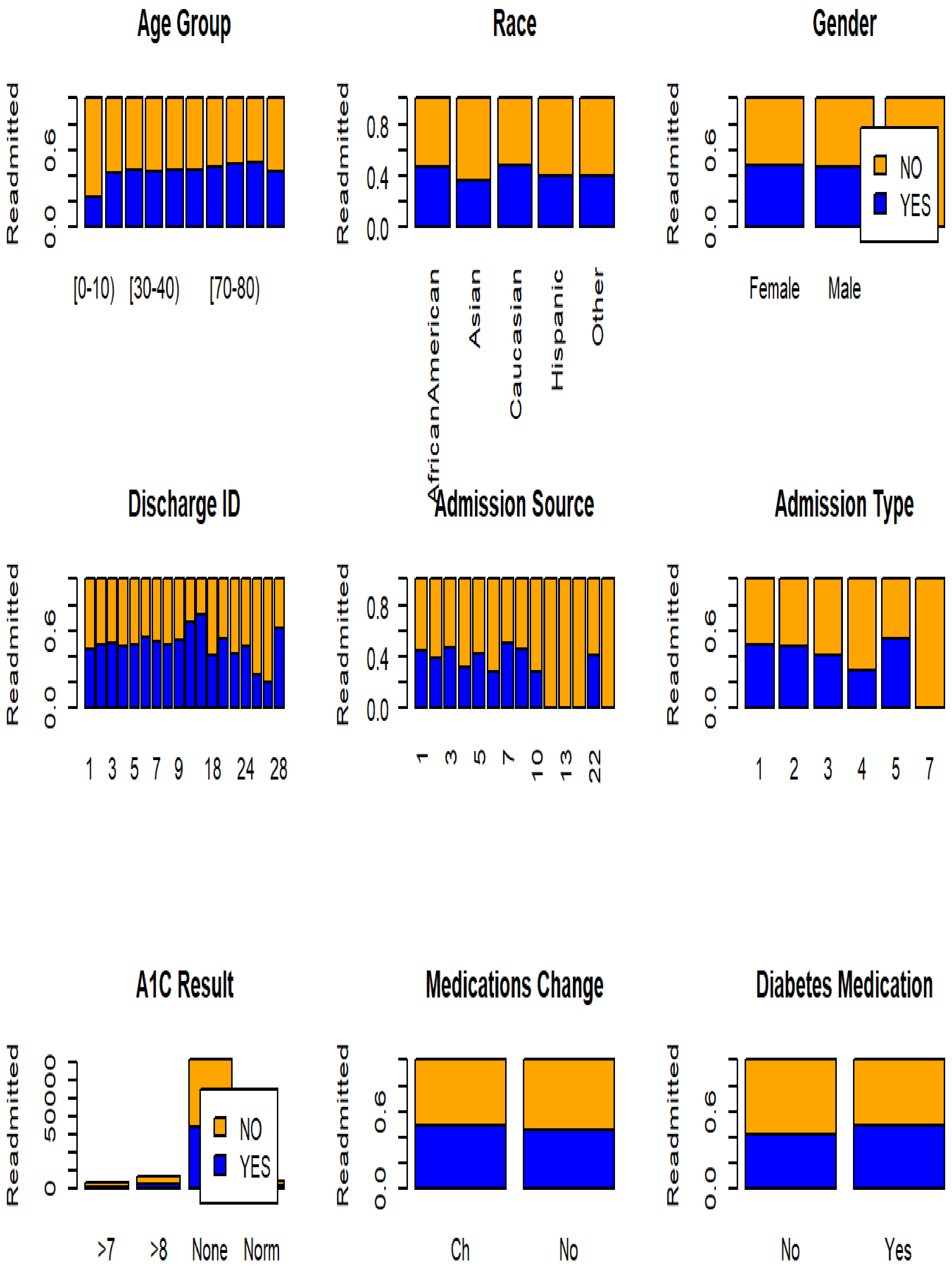
```r
par(mfrow = c(3,3))

barplot(table(df$diabetesMed), main="Distribution of diabetesMed", col="blue", las=2)
barplot(table(df$A1Cresult), main="Distribution of A1Cresult", col="orange", las=2)
barplot(table(df$metformin), main="Distribution of metformin", col="blue", las=2)


barplot(table(df$glipizide), main="Distribution of glipizide", col="orange", las=2)
barplot(table(df$glyburide), main="Distribution of glyburide", col="blue", las=2)
barplot(table(df$pioglitazone), main="Distribution of pioglitazone", col="orange", las=2)


barplot(table(df$rosiglitazone), main="Distribution of rosiglitazone", col="blue", las=2)
barplot(table(df$insulin), main="Distribution of insulin", col="orange", las=2)
barplot(table(df$change), main="Distribution of change", col="blue", las=2)
```



2.6 Explore the relationship between the categorical predictors and the predicted variable

```
# Frequency counts
ct_race <- table(df$readmitted, df$race)
ct_gender <- table(df$readmitted, df$gender)
ct_age <- table(df$readmitted, df$age)
ct_admissionType <- table(df$readmitted, df$admission_type_id)
ct_dischargeID <- table(df$readmitted, df$discharge_disposition_id)
ct_admissionSource <- table(df$readmitted, df$admission_source_id)
ct_A1C <- table(df$readmitted, df$A1Cresult)
ct_metf <- table(df$readmitted, df$metformin)
ct_glipz <- table(df$readmitted, df$glipizide)
ct_glyb <- table(df$readmitted, df$glyburide)
ct_piog <- table(df$readmitted, df$pioglitazone)
ct_rosig <- table(df$readmitted, df$rosiglitazone)
ct_insulin <- table(df$readmitted, df$insulin)
ct_change <- table(df$readmitted, df$change)
ct_diabMeds <- table(df$readmitted, df$diabetesMed)

# Create contingency tables showing proportions
ct_race1 <- prop.table(table(df$readmitted, df$race),2)
ct_gender1 <- prop.table(table(df$readmitted, df$gender),2)
ct_age1 <- prop.table(table(df$readmitted, df$age),2)
ct_admissionType1 <- prop.table(table(df$readmitted, df$admission_type_id),2)
ct_dischargeID1 <- prop.table(table(df$readmitted, df$discharge_disposition_id),2)
ct_admissionSource1 <- prop.table(table(df$readmitted, df$admission_source_id),2)
ct_A1C1 <- prop.table(table(df$readmitted, df$A1Cresult),2)
ct_metf1 <- prop.table(table(df$readmitted, df$metformin),2)
ct_glipz1 <- prop.table(table(df$readmitted, df$glipizide),2)
ct_glyb1 <- prop.table(table(df$readmitted, df$glyburide),2)
ct_piog1 <- prop.table(table(df$readmitted, df$pioglitazone),2)
ct_rosig1 <- prop.table(table(df$readmitted, df$rosiglitazone),2)
ct_insulin1 <- prop.table(table(df$readmitted, df$insulin),2)
ct_change1 <- prop.table(table(df$readmitted, df$change),2)
ct_diabMeds1 <- prop.table(table(df$readmitted, df$diabetesMed),2)
```

```
## Create barplots ##
# Patient Demographics (Legend removed for individual graphs where bars would be blocked)
par(mfrow=c(3,3))
barplot(ct_age1,main="Age Group", ylab="Readmitted",col=c("blue", "orange"))
barplot(ct_race1,main="Race", ylab="Readmitted",col=c("blue", "orange"),las=2)
barplot(ct_gender1,main="Gender", ylab="Readmitted",col=c("blue", "orange"),
        legend=rownames(ct_gender1))

barplot(ct_dischargeID1,main="Discharge ID", ylab="Readmitted",col=c("blue", "orange"))
barplot(ct_admissionSource1,main="Admission Source",
        ylab="Readmitted",col=c("blue", "orange"),las=2)
barplot(ct_admissionType1,main="Admission Type", ylab="Readmitted",col=c("blue", "orange"))


barplot(ct_A1C,main="A1C Result", ylab="Readmitted",col=c("blue", "orange"),legend=rownames(c
t_A1C))
barplot(ct_change1,main="Medications Change", ylab="Readmitted",col=c("blue", "orange"))
barplot(ct_diabMeds1,main="Diabetes Medication",ylab="Readmitted",col=c("blue", "orange"))
```



- Race: Asians were disproportionately less likely to be readmitted.

- Discharge ID: Discharge IDs 11, 19, and 20 were disproportionately less likely to be readmitted. Patients with discharge IDs 10,12,15 were disproportionately more likely to be readmitted.
- Admission sources 10, 11, 13, 14, 22, and 25 were less likely to be readmitted (0% readmission rates)
- Admission type 7 proportionately less likely to be readmitted
- No significant differences for the change in/prescription of drugs were observed.

3. Data Preprocessing

3.1 Select features

- From EDA, we observe that variables number_emergency, number_outpatient, number_inpatient, A1Cresult, glyburide, pioglitazone, pioglitazone, rosiglitazone, glipizide show low variance or are extremely skewed. They will be excluded from modeling.

```
df <- subset(df, select = -c(number_emergency, number_outpatient, number_inpatient, A1Cresul
t, glyburide, pioglitazone, pioglitazone, rosiglitazone, glipizide))

dim(df)
```

```
## [1] 86566    19
```

- After this step, 19 variables are left for modeling.

3.2 Remove outliers

- From visualizations in the EDA section, we observe some NUmerical variables including num_lab_procedures, number_diagnoses, and num_medications have outliers. We use 1.5 IQR to remove them.

```
# Remove outlier from column 'num_lab_procedures'
quartiles <- quantile(df$num_lab_procedures, probs=c(.25, .75), na.rm = FALSE)
IQR <- IQR(df$num_lab_procedures)
Lower <- quartiles[1] - 1.5*IQR
Upper <- quartiles[2] + 1.5*IQR

count_before <-dim(df)[1]
df<- subset(df, df$num_lab_procedures > Lower & df$num_lab_procedures < Upper)
count_after <-dim(df)[1]
cat(count_before-count_after, " outliers in num_lab_procedures have been removed. \n")
```

```
## 186  outliers in num_lab_procedures have been removed.
```

```
# Remove outliers from column 'number_diagnoses'
quartiles <- quantile(df$number_diagnoses, probs=c(.25, .75), na.rm = FALSE)
IQR <- IQR(df$number_diagnoses)
Lower <- quartiles[1] - 1.5*IQR
Upper <- quartiles[2] + 1.5*IQR

count_before <-dim(df)[1]
df <- subset(df, df$number_diagnoses > Lower & df$number_diagnoses < Upper)
count_after <-dim(df)[1]
cat(count_before-count_after, " outliers in number_diagnoses have been removed. \n")
```

```
## 52  outliers in number_diagnoses have been removed.
```

```
# Remove outliers from column 'num_medications'
quartiles <- quantile(df$num_medications, probs=c(.25, .75), na.rm = FALSE)
IQR <- IQR(df$num_medications)
Lower <- quartiles[1] - 2*IQR
Upper <- quartiles[2] + 2*IQR

count_before <-dim(df)[1]
df <- subset(df, df$num_medications > Lower & df$num_medications < Upper)
count_after <-dim(df)[1]
cat(count_before-count_after, " outliers in num_medications have been removed. \n")
```

```
## 1287  outliers in num_medications have been removed.
```

3.3 Partition data into training and test datasets using a 70% ratio

- readmitted is the predicted variable. It will be separated from the predictors.

```
#Separate X and Y using readmitted as predicted variable
dfX <- subset(df, select = -c(readmitted))
dfY <- subset(df, select = c(readmitted))

set.seed(123)
# Partition the dataset
trainRows <- createDataPartition(dfY$readmitted, p = .70, list = FALSE)

trainX <- dfX[trainRows,]
testX <-  dfX[-trainRows,]

trainY <- dfY[trainRows,]
testY <- dfY[-trainRows,]

dim(trainX)
```

```
## [1] 59529    18
```

```
dim(testX)
```

```
## [1] 25512    18
```

- After the partition, there are 59529 instances in the training set and 25512 instances in the test set.

3.4 Trandform and standardize features: center and scale

```
# center and scale the training set
train_tran <- preProcess(trainX, method=c("center", "scale"))
trainX <- predict(train_tran, trainX)

# center and scale the test set
testX <- predict(train_tran, testX)
```

3.5 Convert categorical variables to dummy variables

- Backup the training and testing sets before adding dummy variables for training different models

```
library(fastDummies)

# Some models do not require dummy variable, like the trees
# Will use the sets without dummies for models
trainX_noDummy <- trainX
testX_noDummy <- testX

colnames(trainX_noDummy)
```

```
##  [1] "race"                     "gender"
##  [3] "age"                      "admission_type_id"
##  [5] "discharge_disposition_id" "admission_source_id"
##  [7] "time_in_hospital"         "num_lab_procedures"
##  [9] "num_procedures"           "num_medications"
## [11] "number_diagnoses"         "metformin"
## [13] "insulin"                  "change"
## [15] "diabetesMed"              "primary_diagnosis"
## [17] "secondary_diagnosis"      "secondary_diagnosis2"
```

- Categorical variables will now be converted into n-1 dummy variables.

```
# Add dummy variables
trainX <- dummy_cols(trainX,
                     select_columns=c("race", "gender","age",
                                      "admission_type_id", "discharge_disposition_id","metfor
min",
                                      "insulin", "change","diabetesMed",
                                      "admission_source_id","primary_diagnosis",
                                      "secondary_diagnosis", "secondary_diagnosis2"),
                     remove_first_dummy=TRUE,
                     remove_selected_columns=TRUE)

testX <- dummy_cols(testX,
                     select_columns=c("race", "gender","age",
                                      "admission_type_id", "discharge_disposition_id","metfor
min",
                                      "insulin", "change","diabetesMed",
                                      "admission_source_id","primary_diagnosis",
                                      "secondary_diagnosis", "secondary_diagnosis2"),
                     remove_first_dummy=TRUE,
                     remove_selected_columns=TRUE)
```

3.6 PCA Analysis

- This is a high-dimensional dataset, we want to see if PCA can be applied to reduce feature dimension.

```
# Find the PCA from the training set
pca <- prcomp(trainX)
pca_var <- pca$sdev^2

# Find the percentage of each PCA component
pca_percents <- pca_var / sum(pca_var)
cat("Percentage of the first 15 PCAs: ", pca_percents[1:15], "\n")
```

```
## Percentage of the first 15 PCAs:  0.1910663 0.1092462 0.08477103 0.06680895 0.06017332 0.0
4253663 0.03169632 0.02533176 0.02446798 0.02444144 0.02292527 0.02127575 0.02083785 0.019348
05 0.01887004
```

```
# The total percentage of the first 35 PCAs
cat("The total percentage of the first 35 PCAs: ", sum(pca_percents[1:35]), "\n")
```

```
## The total percentage of the first 35 PCAs:  0.9428998
```

- We see there are no dominant PCA components. The first 35 components represent 94% of the features.

4. Modeling

4.0 Define functions

First we will define a function to calculate the metrics of a trained model

- The function will take one parameters: a trained model
- The function will calculate these metrics including accuracy, sensitivity, specificity, precision
- It will return a vector containing those metrics

```
# Define a function to calculate the metrics of a trained model
get_training_metrics <- function(model, roc) {

  # Total number of training objects
  total <- dim(trainX)[1]

 # Construct model's confusion matrix
  cm <- confusionMatrix(model, norm = "none")

  # Calculate metrics
  accuracy <- round((cm$table[1,1] + cm$table[2,2]) / total, 3)
  sensitivity <- round(cm$table[1,1] / (cm$table[1,1] + cm$table[2,1]), 3)
  specificity <- round(cm$table[2,2] / (cm$table[2,2] + cm$table[1,2]), 3)
  precision <- round(cm$table[1,1] / (cm$table[1,1] + cm$table[1,2]), 3)
  recall <- sensitivity
  F1 <- round(2 * recall * precision / (recall + precision ), 3)

  # Return a vector of metrics
  c(accuracy, sensitivity, specificity, precision, recall, F1, round(roc,3))
}
```

Next we will define a function to calculate the metrics of prediction result on test dataset

- The function will take one parameters: predicted results of the test set
- The function will calculate these metrics including ROC, accuracy, sensitivity, specificity, precision
- It will return a vector containing those metrics

```
# Define a function to calculate the metrics of a trained model
get_test_metrics <- function(test_results) {
  total <- dim(testX)[1]

  # Construct prediction's confusion matrix
  cm <- confusionMatrix(test_results, testY, positive = "YES")

  # Calculate metrics
  accuracy <- round((cm$table[1,1] + cm$table[2,2]) / total, 3)
  sensitivity <- round(cm$table[1,1] / (cm$table[1,1] + cm$table[2,1]), 3)
  specificity <- round(cm$table[2,2] / (cm$table[2,2] + cm$table[1,2]), 3)
  precision <- round(cm$table[1,1] / (cm$table[1,1] + cm$table[1,2]), 3)
  recall <- sensitivity
  F1 <- round(2 * recall * precision / (recall + precision ), 3)
  # Return a vector of metrics
  c(accuracy, sensitivity, specificity, precision, recall, F1)
}
```

4.1 Logistic Regression Model

- First we will define a control variable that will be used to train all the models.
- We will use a 10 fold cross-validation method to optimize the training process.
- For each model, we will first train the model using training dataset, then use test dataset to test the model.
- We will generate a data frame to hold the training and testing performance metrics.

```
# Define train control
ctrl <- trainControl(method = "cv", summaryFunction = twoClassSummary,
                     classProbs = TRUE, savePredictions = "final")

# Logistic Regression
set.seed(123)
lrFit <- train(x = trainX, y = trainY,
               method = "glm", metric = "ROC", trControl = ctrl)

# Calculate training/resampling performance metrics
metrics_tr <- data.frame(Metric.Train = c("Accuracy", "Sensitivity", "Specificity", "Precisio
n", "Recall", "F-Measure", "ROC"))

metrics_tr$LR <- get_training_metrics(lrFit, lrFit$results$ROC)

#metrics_tr

# Predict on test data
lrTestResults <- predict(lrFit, testX)

# Calculate test performance metrics
metrics_test <- data.frame(Metric.Test = c("Accuracy", "Sensitivity", "Specificity", "Precisi
on", "Recall", "F-Measure"))
metrics_test$LR <- get_test_metrics(lrTestResults)

# Importance of the predictors
lrImp <- varImp(lrFit, scale = FALSE)

# Display model's performance
metrics_tr[, c("Metric.Train", "LR")]
```

```
##   Metric.Train    LR
## 1     Accuracy 0.585
## 2  Sensitivity 0.524
## 3  Specificity 0.640
## 4    Precision 0.570
## 5       Recall 0.524
## 6    F-Measure 0.546
## 7          ROC 0.617
```

```
metrics_test[, c("Metric.Test", "LR")]
```

```
##   Metric.Test    LR
## 1    Accuracy 0.586
## 2 Sensitivity 0.524
## 3 Specificity 0.643
## 4   Precision 0.572
## 5      Recall 0.524
## 6   F-Measure 0.547
```

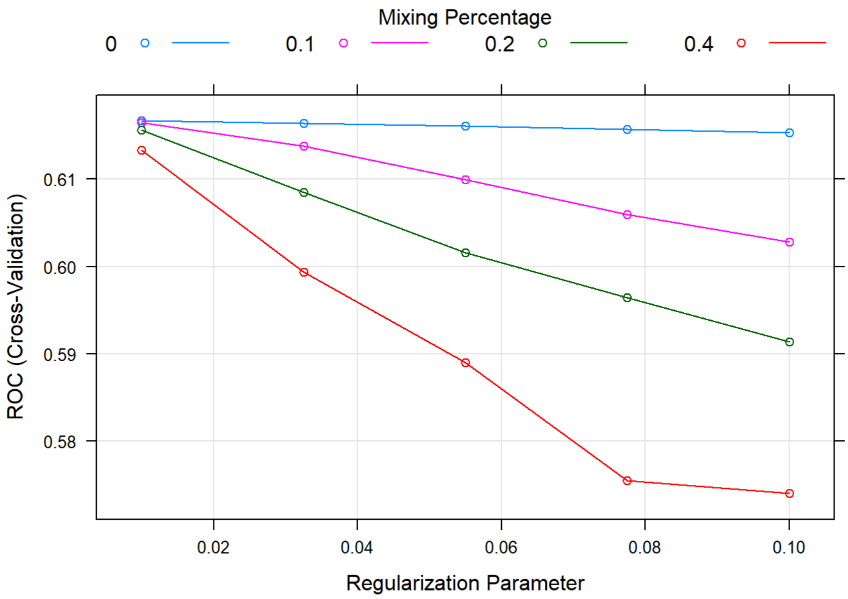
- The training (cross validation) performance and testing performance for logistic regression model is displayed in the above metrics.

4.2 Penalized Logistic Regression Model

For penalized logistic regression model, we use the following perimeters to build the tuning grid:

- alpha values: 0, 0,0.1,0.2,0.4
- regularization perimeter lambda takes 5 values evenly between 0.01 and 0.1
- length: 5

```
# Penalized Logistic Regression
set.seed(123)
glmnGrid <- expand.grid(alpha=c(0,0.1,0.2,0.4),
                        lambda=seq(.01, .1, length=5))
glmnFit <- train(x = trainX, y = trainY,
                 method="glmnet", tuneGrid=glmnGrid,
                 metric="ROC", trControl=ctrl)
#glmnFit

# Calculate training/resampling performance metrics
metrics_tr$GLMN <- get_training_metrics(glmnFit, glmnFit$results$ROC[1])
#metrics_tr

# Predict on test data
glmnTestResults <- predict(glmnFit, testX)

# Calculate test performance metrics
metrics_test$GLMN <- get_test_metrics(glmnTestResults)

# Importance of the predictors
glmnImp <- varImp(glmnFit, scale = FALSE)


# Plot the tuning results
plot(glmnFit)
```



```
# Display model's performance
metrics_tr[, c("Metric.Train", "GLMN")]
```

```
##   Metric.Train  GLMN
## 1     Accuracy 0.585
## 2  Sensitivity 0.521
## 3  Specificity 0.642
## 4    Precision 0.570
## 5       Recall 0.521
## 6    F-Measure 0.544
## 7          ROC 0.617
```

```
metrics_test[, c("Metric.Test", "GLMN")]
```

```
##   Metric.Test  GLMN
## 1    Accuracy 0.586
## 2 Sensitivity 0.520
## 3 Specificity 0.646
## 4   Precision 0.572
## 5      Recall 0.520
## 6   F-Measure 0.545
```

- The cross validation result shows the optimal model comes when alpha=0, lambda=0.01
- The training (cross validation) performance and testing performance is displayed in the above metrics.

4.3 Nearest Shrunken Centroids Model

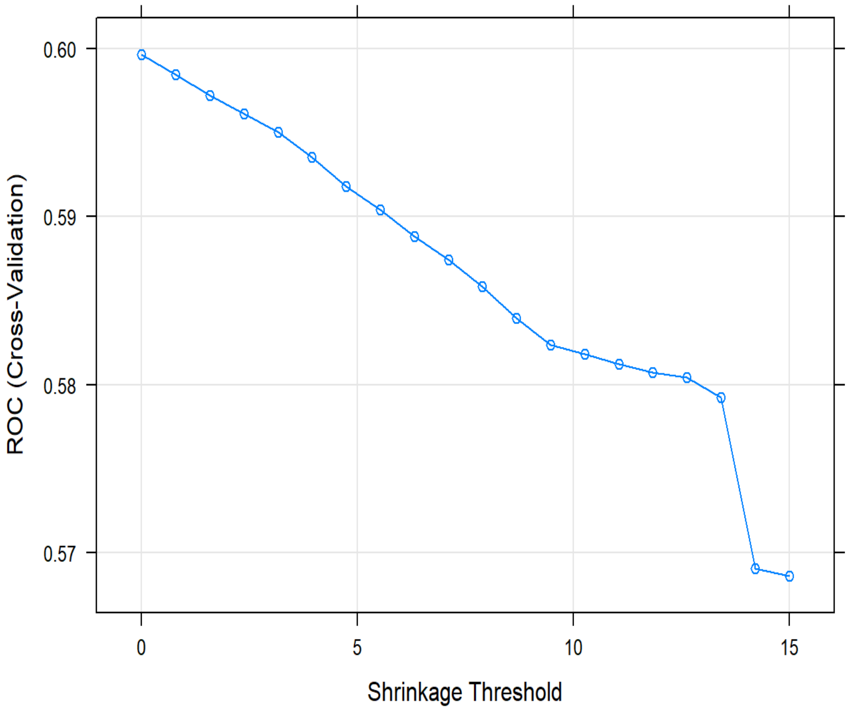
For Nearest Shrunken Centroids model, we use the following perimeter to build the tuning grid:

- threshold takes 20 values evenly spaced between 0 and 15

```
# Nearest Shrunken Centroids
set.seed(123)
nscFit <- train(x=trainX,y=trainY,
                method="pam", tuneGrid=data.frame(threshold=seq(0,15, length=20)),
                metric="ROC", trControl=ctrl)
```

```
## 11111111111
```

```
#nscFit

# Calculate training/resampling performance metrics
metrics_tr$NSC <- get_training_metrics(nscFit, nscFit$results$ROC[1])

# Predict on test data
nscTestResults <- predict(nscFit, testX)

# Calculate test performance metrics
metrics_test$NSC <- get_test_metrics(nscTestResults)

# Importance of the predictors
nscImp <- varImp(nscFit, scale = FALSE)

# Plot the tuning result
plot(nscFit)
```



```
# Display model's performance
metrics_tr[, c("Metric.Train", "NSC")]
```

```
##   Metric.Train   NSC
## 1     Accuracy 0.570
## 2  Sensitivity 0.504
## 3  Specificity 0.629
## 4    Precision 0.553
## 5       Recall 0.504
## 6    F-Measure 0.527
## 7          ROC 0.600
```

```
metrics_test[, c("Metric.Test", "NSC")]
```

```
##   Metric.Test   NSC
## 1    Accuracy 0.575
## 2 Sensitivity 0.507
## 3 Specificity 0.637
## 4   Precision 0.559
## 5      Recall 0.507
## 6   F-Measure 0.532
```

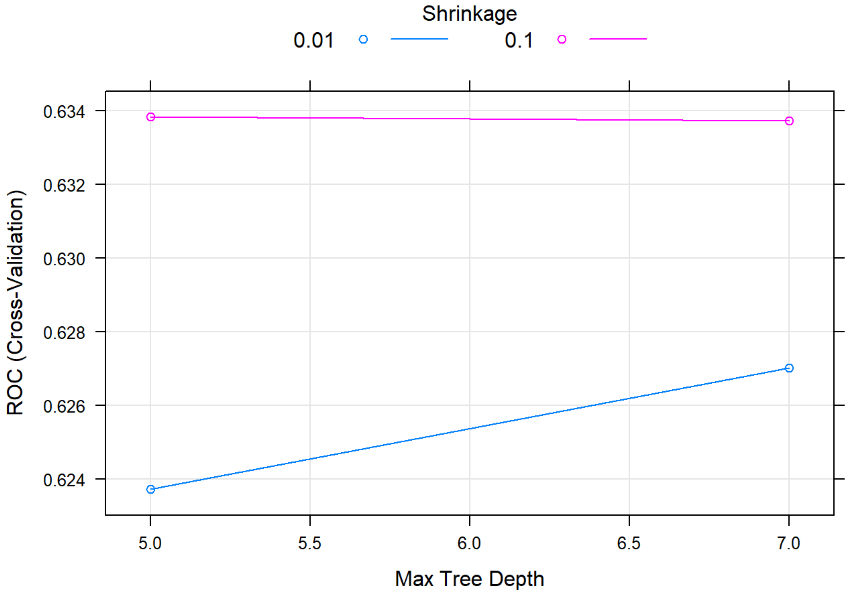
- The cross validation result shows the optimal model comes when shrinkage threshhold is 0.
- The training (cross validation) performance and testing performance is displayed in the above metrics.

4.4 Boosted Trees

For the boosted trees model, we use the following perimeter to build the tuning grid:

- interaction depth: 5, 7
- number of trees: 500
- shrinkage: 0.01, 0.1

```
gbmGrid <- expand.grid(interaction.depth = c(5, 7),
                       n.trees = 500,
                       shrinkage = c(.01, .1),
                       n.minobsinnode = 5)

set.seed(123)

gbmFit <- train(x = trainX_noDummy, y = trainY,
                method = "gbm", tuneGrid = gbmGrid,
                verbose = FALSE, metric = "ROC", trControl = ctrl)

# Calculate training/resampling performance metrics
metrics_tr$GBM <- get_training_metrics(gbmFit, gbmFit$results$ROC[3])
#metrics_tr

# Predict on test data
gbmTestResults <- predict(gbmFit, testX_noDummy)

# Calculate test performance metrics
metrics_test$GBM <- get_test_metrics(gbmTestResults)

#The tunning result
#gbmFit
plot(gbmFit)
```



```
# Display model's performance
metrics_tr[, c("Metric.Train", "GBM")]
```

```
##   Metric.Train   GBM
## 1     Accuracy 0.596
## 2  Sensitivity 0.561
## 3  Specificity 0.628
## 4    Precision 0.578
## 5       Recall 0.561
## 6    F-Measure 0.569
## 7          ROC 0.627
```

```
metrics_test[, c("Metric.Test", "GBM")]
```

```
##   Metric.Test   GBM
## 1    Accuracy 0.601
## 2 Sensitivity 0.565
## 3 Specificity 0.633
## 4   Precision 0.583
## 5      Recall 0.565
## 6   F-Measure 0.574
```

- The cross validation result shows the optimal model comes when shrinkage is 0.1 and depth is 5..
- The training (cross validation) performance and testing performance is displayed in the above metrics.

4.5 Bagged Tree

For bagged tree model, we use the following perimeter to train:

- number of bag(nbagg) = 30

```
set.seed(123)

trbagFit <- train(x = trainX_noDummy, y = trainY,
                method = "treebag",
                nbagg = 30,
                metric = "ROC",
                trControl = ctrl)

#trbagFit

# Calculate training/resampling performance metrics
metrics_tr$TRBAG <- get_training_metrics(trbagFit, trbagFit$results$ROC)

# Predict on test data
trbagTestResults <- predict(trbagFit, testX_noDummy)

# Calculate test performance metrics
metrics_test$TRBAG <- get_test_metrics(trbagTestResults)

# Display model's performance
metrics_tr[, c("Metric.Train", "TRBAG")]
```

```
##   Metric.Train TRBAG
## 1     Accuracy 0.572
## 2  Sensitivity 0.541
## 3  Specificity 0.601
## 4    Precision 0.552
## 5       Recall 0.541
## 6    F-Measure 0.546
## 7          ROC 0.603
```

```
metrics_test[, c("Metric.Test", "TRBAG")]
```

```
##   Metric.Test TRBAG
## 1    Accuracy 0.569
## 2 Sensitivity 0.535
## 3 Specificity 0.601
## 4   Precision 0.549
## 5      Recall 0.535
## 6   F-Measure 0.542
```

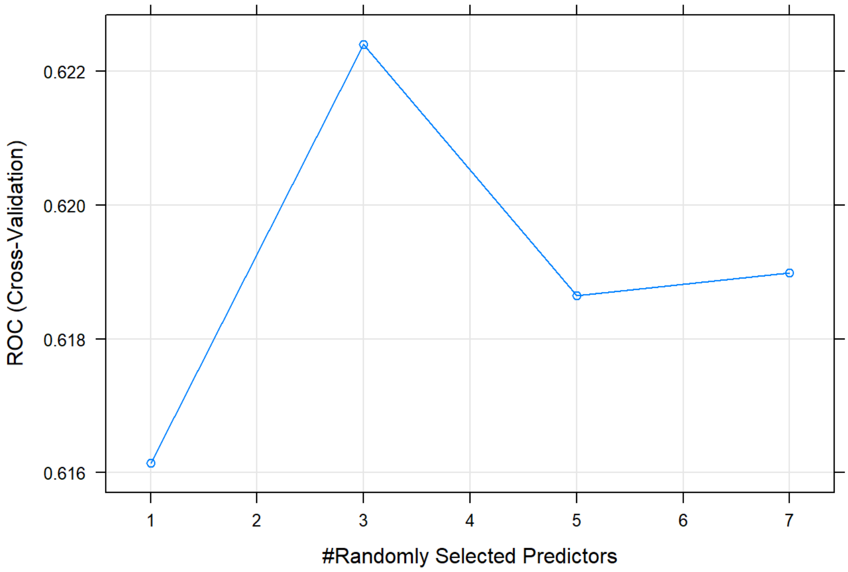
- The training (cross validation) performance and testing performance is displayed in the above metrics.

4.6 Random Forest Tree

For random forest tree model, we use the following perimeter to build the tuning grid:

- number of randomly selected predictors: 1, 3, 5, 7
- number of trees: 100

```
mtryValues <- seq(1,8,2)

set.seed(123)
rfFit <- train(x = trainX_noDummy, y = trainY,
                method = "rf",
                ntree = 100,
                tuneGrid = data.frame(mtry = mtryValues),
                metric = "ROC",
                trControl = ctrl)


# Calculate training/resampling performance metrics
metrics_tr$RF <- get_training_metrics(rfFit, rfFit$results$ROC[2])

# Predict on test data
rfTestResults <- predict(rfFit, testX_noDummy)

# Calculate test performance metrics
metrics_test$RF <- get_test_metrics(rfTestResults)

# Importance of the predictors
rfImp <- varImp(rfFit, scale = FALSE)

# Plot tuning result
#rfFit
plot(rfFit)
```



```
# Display model's performance
metrics_tr[, c("Metric.Train", "RF")]
```

```
##   Metric.Train    RF
## 1     Accuracy 0.586
## 2  Sensitivity 0.532
## 3  Specificity 0.635
## 4    Precision 0.570
## 5       Recall 0.532
## 6    F-Measure 0.550
## 7          ROC 0.622
```

```
metrics_test[, c("Metric.Test", "RF")]
```

```
##   Metric.Test    RF
## 1    Accuracy 0.587
## 2 Sensitivity 0.503
## 3 Specificity 0.663
## 4   Precision 0.576
## 5      Recall 0.503
## 6   F-Measure 0.537
```

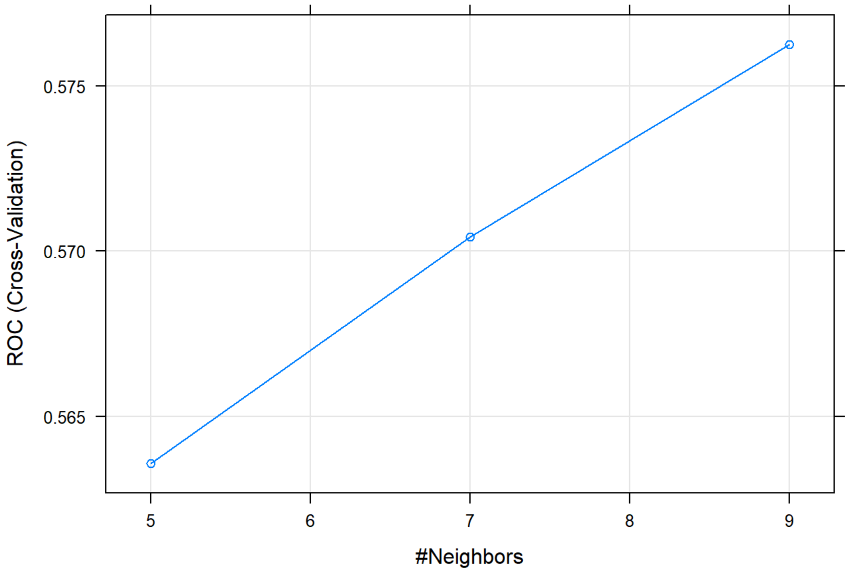
- The cross validation result shows the optimal model comes when the number of randomly selected predictors is 3
- The training (cross validation) performance and testing performance is displayed in the above metrics.

4.7 K-Nearest Neighbor (KNN) Model

For KNN model, we use the following perimeter to build the tuning grid:

- tuneLength = 3
- number of neighbors: 5, 7, 9

```
set.seed(123)

knnFit <- train(x = trainX, y = trainY,
                 method = "knn",
                 tuneLength = 3,
                 metric = "ROC", trControl = ctrl)


# Calculate training/resampling performance metrics
metrics_tr$KNN <- get_training_metrics(knnFit, knnFit$results$ROC[3])

# Predict on test data
knnTestResults <- predict(knnFit, testX)

# Calculate test performance metrics
metrics_test$KNN <- get_test_metrics(knnTestResults)

# Importance of the predictors
knnImp <- varImp(knnFit, scale = FALSE)

# Plot the tuning results
#knnFit
plot(knnFit)
```



```
# Display model's performance
metrics_tr[, c("Metric.Train", "KNN")]
```

```
##   Metric.Train   KNN
## 1     Accuracy 0.555
## 2  Sensitivity 0.527
## 3  Specificity 0.581
## 4    Precision 0.534
## 5       Recall 0.527
## 6    F-Measure 0.530
## 7          ROC 0.576
```

```
metrics_test[, c("Metric.Test", "KNN")]
```

```
##   Metric.Test   KNN
## 1    Accuracy 0.557
## 2 Sensitivity 0.528
## 3 Specificity 0.583
## 4   Precision 0.535
## 5      Recall 0.528
## 6   F-Measure 0.531
```

- The cross validation result shows the optimal model comes when K is 9.
- The training (cross validation) performance and testing performance is displayed in the above metrics.

5. Model Evaluation and Conclusion

5.1 Baseline Model

- For this data analysis, a model's ability to predict the positive (readmitted-Yes) accurately is the most important metric. Therefore, we choose All Positive Model as the base model.

```
round(table(trainY) / length(trainY), 3)
```

```
## trainY
##   YES    NO
## 0.476 0.524
```

- From the above table, we see that when we assign all predictions as positive, the accuracy of this base model is 0.476

5.2 Calculate AUC (Area Under ROC Curve)

For each model, based on the trained models' result, we first generate ROC, then calculate the area under ROC curve (AUC)

```
#ROC Curve
library(pROC)
lrROC <- roc(response=trainY,predictor=lrFit$pred$YES,levels=rev(levels(lrFit$pred$obs)))
glmnROC <- roc(response=trainY,predictor=glmnFit$pred$YES,levels=rev(levels(glmnFit$pred$ob
s)))
nscROC <- roc(response=trainY,predictor=nscFit$pred$YES,levels=rev(levels(nscFit$pred$obs)))
gbmROC <- roc(response=trainY,predictor=gbmFit$pred$YES,levels=rev(levels(gbmFit$pred$obs)))
rfROC <- roc(response=trainY,predictor=rfFit$pred$YES,levels=rev(levels(rfFit$pred$obs)))
trbagROC <- roc(response=trainY,predictor=trbagFit$pred$YES,levels=rev(levels(trbagFit$pred$o
bs)))
knnROC <- roc(response=trainY,predictor=knnFit$pred$YES,levels=rev(levels(knnFit$pred$obs)))

lrAUC <-round(auc(lrROC), 3)
glmnAUC <-round(auc(glmnROC), 3)
nscAUC <-round(auc(nscROC), 3)
gbmAUC <-round(auc(gbmROC), 3)
rfAUC <-round(auc(rfROC), 3)
trbagAUC <-round(auc(trbagROC), 3)
knnAUC <-round(auc(knnROC), 3)

# Get Area under the ROC
metrics_tr <- rbind(metrics_tr, c("AUC", lrAUC, glmnAUC, nscAUC,
                                  gbmAUC, rfAUC, trbagAUC, knnAUC))
```

- The AUC values are added to the training model’s performance metrics data frame.

5.3 Compare models’ performance metrics

- Compare Models’ training (cross-validation) performance

```
metrics_tr
```

```
##   Metric.Train    LR  GLMN   NSC   GBM TRBAG    RF   KNN
## 1     Accuracy 0.585 0.585  0.57 0.596 0.572 0.586 0.555
## 2  Sensitivity 0.524 0.521 0.504 0.561 0.541 0.532 0.527
## 3  Specificity  0.64 0.642 0.629 0.628 0.601 0.635 0.581
## 4    Precision  0.57  0.57 0.553 0.578 0.552  0.57 0.534
## 5       Recall 0.524 0.521 0.504 0.561 0.541 0.532 0.527
## 6    F-Measure 0.546 0.544 0.527 0.569 0.546  0.55  0.53
## 7          ROC 0.617 0.617   0.6 0.627 0.603 0.622 0.576
## 8          AUC 0.503  0.51 0.502 0.502 0.499 0.503 0.495
```

- Compare Models’ test performance

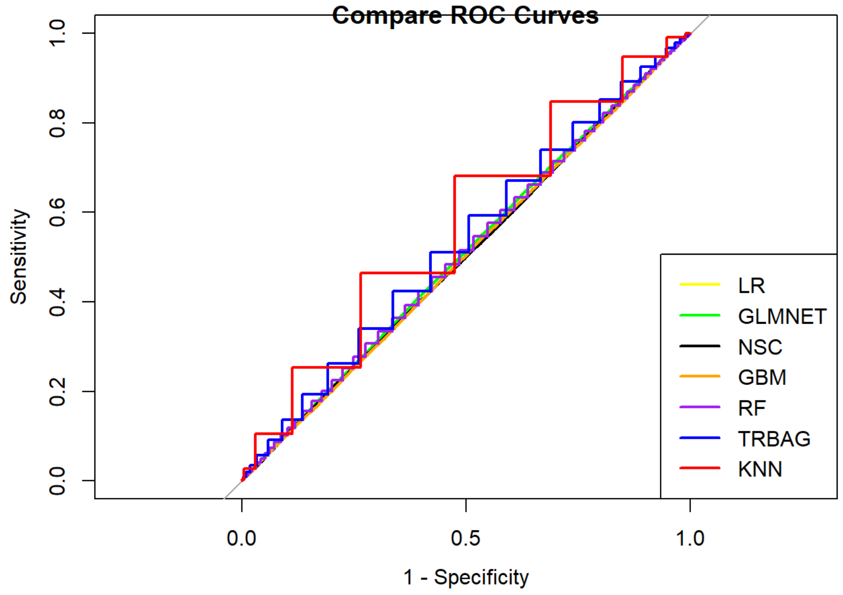
```
metrics_test
```

```
##   Metric.Test    LR  GLMN   NSC   GBM TRBAG    RF   KNN
## 1    Accuracy 0.586 0.586 0.575 0.601 0.569 0.587 0.557
## 2 Sensitivity 0.524 0.520 0.507 0.565 0.535 0.503 0.528
## 3 Specificity 0.643 0.646 0.637 0.633 0.601 0.663 0.583
## 4   Precision 0.572 0.572 0.559 0.583 0.549 0.576 0.535
## 5      Recall 0.524 0.520 0.507 0.565 0.535 0.503 0.528
## 6   F-Measure 0.547 0.545 0.532 0.574 0.542 0.537 0.531
```

5.4 Plot Roc Curves

- We plot the ROC curves for all trainings models in one graph. The comparison can be seen with different marking colors.

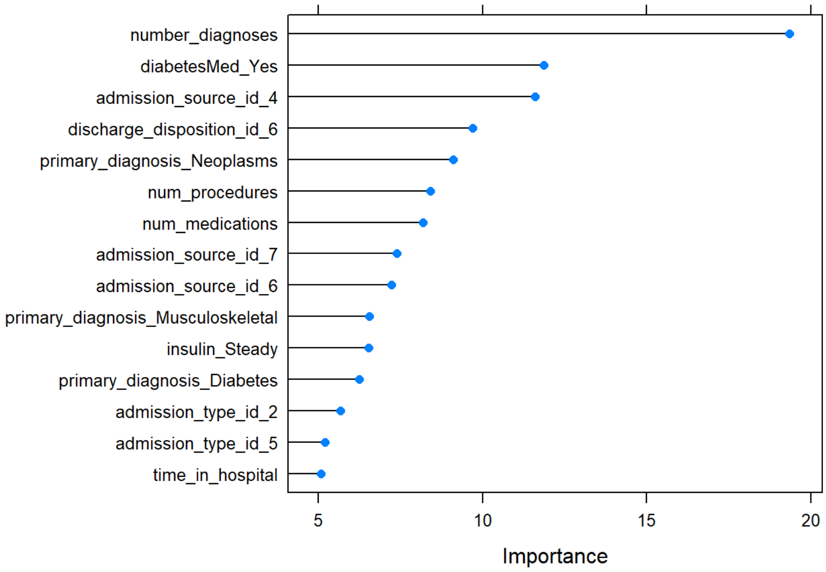
```
plot(lrROC, type="s", col='yellow', legacy.axes=TRUE)
plot(glmnROC, type="s", add=TRUE, col='green', legacy.axes=TRUE)
plot(nscROC, type="s", add=TRUE, col='black', legacy.axes=TRUE)
plot(gbmROC, type="s", add=TRUE, col='orange',legacy.axes=TRUE)
plot(rfROC, type="s", add=TRUE, col='purple', legacy.axes=TRUE)
plot(trbagROC, type="s", add=TRUE, col='blue',legacy.axes=TRUE)
plot(knnROC, type="s", add=TRUE, col='red', legacy.axes=TRUE)

legend("bottomright", legend=c("LR", "GLMNET", "NSC", "GBM", "RF", "TRBAG", "KNN"),
       col=c("yellow","green", "black",'orange', 'purple','blue', 'red'), lwd=2)


title(main="Compare ROC Curves")
```



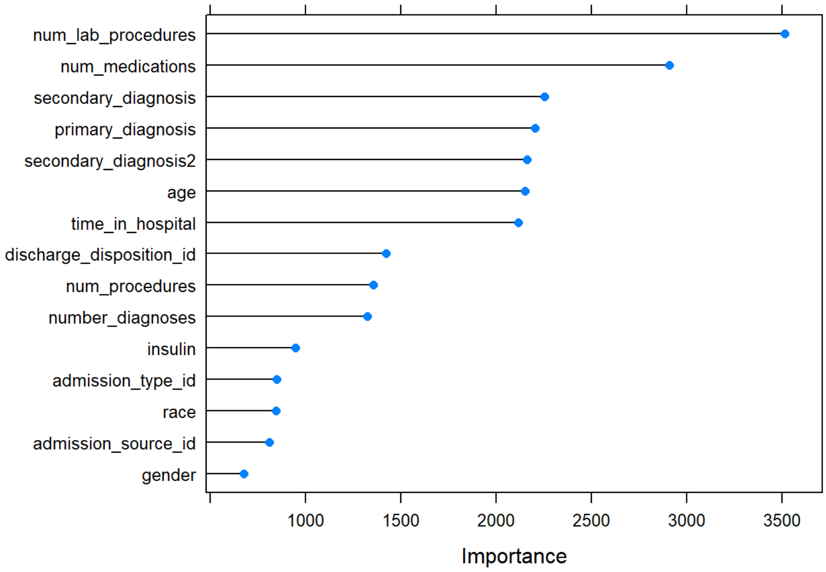
5.5 Check Feature’s Importance

- We displayed the first 15 important features from logistic regression model, random forest model, and KNN model respectively.

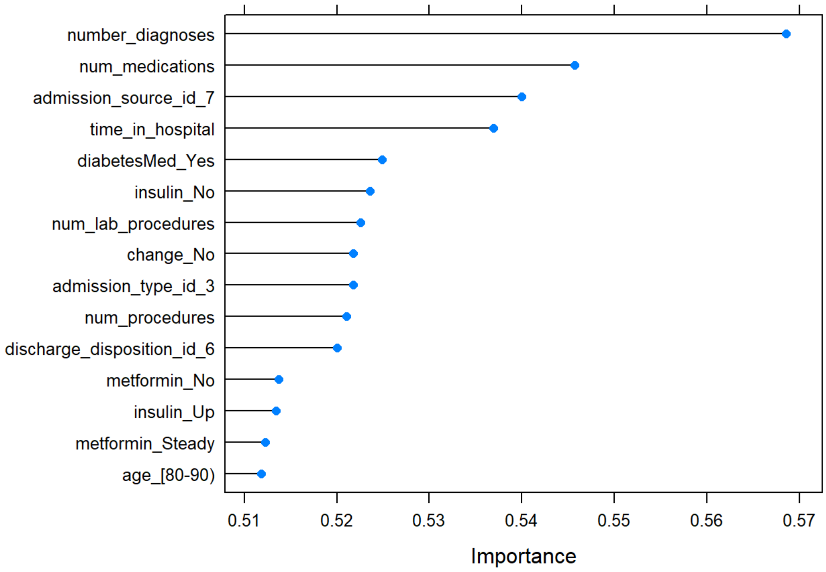
```
plot(lrImp, top = 15)
```



```
plot(rfImp, top = 15)
```



```
plot(knnImp, top = 15)
```



- Though each model displays the important features in different order, some features appear commonly in the top list.
- These important features include: number_diagnoses, num_procedures, num_lab_procedures, num_medication, time_in_hospital. etc.