Project

B203349

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Contents

Click here to link to my gpresentation

Loading the required packages required for this script

```
library(sparklyr)
library(dplyr)
library(ggplot2)
library(cowplot)
library(knitr)
library(kableExtra)
library(tidyverse)
library(lubridate)
library(ggplot2)
library(dbplot)
library(janitor)
library(broom)
library(formatR)
```

Connecting to Spark in local mode

```
sc = spark_connect(master = 'local')
```

Loading datasets

Data

The **Diabetes 130-US hospitals for years 1999-2008 Data Set** is an extract representing 10 years (1999–2008) of clinical care at 130 hospitals and integrated delivery networks throughout the United States. The dataset was compiled Strack et al[1] and is in .csv format.

Read .csv downloaded from and create dataframe

```
# diabetic_data = spark_read_csv(sc,
# '/Users/matt/Desktop/Dropbox/Home/College/Edinburgh - MSc Data Science/Big
# Data Analytics/diabetes_readmissions/RawData/diabetic_data.csv')
diabetic_data = spark_read_csv(sc, "/home/jovyan/Matt/diabetes_readmissions/RawData/diabetic_data.csv")
```

Exploratory analysis

Summary of data

The dataset contains over 50 variables, broadly these describe: patient demographics, patient diagnoses, admission and discharge dispositions, length of stay, blood glucose levels, medication types and changes, and readmission data. Furthermore, procedures, medications, and outpatient / inpatient / ED visits are all also quantified. The full list of variables is outlined below:

```
glimpse(diabetic_data)
```

```
## Rows: ??
## Columns: 50
## Database: spark_connection
## $ encounter_id             <int> 2278392, 149190, 64410, 500364, 16680, 35754,~
## $ patient_nbr              <int> 8222157, 55629189, 86047875, 82442376, 425192~
## $ race                     <chr> "Caucasian", "Caucasian", "AfricanAmerican", ~
## $ gender                   <chr> "Female", "Female", "Female", "Male", "Male",~
## $ age                      <chr> "[0-10)", "[10-20)", "[20-30)", "[30-40)", "[~
## $ weight                   <chr> "?", "?", "?", "?", "?", "?", "?", "?", "?", ~
## $ admission_type_id        <int> 6, 1, 1, 1, 1, 2, 3, 1, 2, 3, 1, 2, 1, 1, 3, ~
## $ discharge_disposition_id <int> 25, 1, 1, 1, 1, 1, 1, 1, 1, 3, 1, 1, 3, 6, 1,~
## $ admission_source_id      <int> 1, 7, 7, 7, 7, 2, 2, 7, 4, 4, 7, 4, 7, 7, 2, ~
## $ time_in_hospital         <int> 1, 3, 2, 2, 1, 3, 4, 5, 13, 12, 9, 7, 7, 10, ~
## $ payer_code               <chr> "?", "?", "?", "?", "?", "?", "?", "?", "?", ~
## $ medical_specialty        <chr> "Pediatrics-Endocrinology", "?", "?", "?", "?~
## $ num_lab_procedures       <int> 41, 59, 11, 44, 51, 31, 70, 73, 68, 33, 47, 6~
## $ num_procedures           <int> 0, 0, 5, 1, 0, 6, 1, 0, 2, 3, 2, 0, 0, 1, 5, ~
## $ num_medications          <int> 1, 18, 13, 16, 8, 16, 21, 12, 28, 18, 17, 11,~
## $ number_outpatient        <int> 0, 0, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
## $ number_emergency         <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, ~
## $ number_inpatient         <int> 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
## $ diag_1                   <chr> "250.83", "276", "648", "8", "197", "414", "4~
## $ diag_2                   <chr> "?", "250.01", "250", "250.43", "157", "411",~
## $ diag_3                   <chr> "?", "255", "V27", "403", "250", "250", "V45"~
## $ number_diagnoses         <int> 1, 9, 6, 7, 5, 9, 7, 8, 8, 8, 9, 7, 8, 8, 8, ~
## $ max_glu_serum            <chr> "None", "None", "None", "None", "None", "None~
## $ A1Cresult                <chr> "None", "None", "None", "None", "None", "None~
## $ metformin                <chr> "No", "No", "No", "No", "No", "No", "Steady",~
## $ repaglinide              <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ nateglinide              <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ chlorpropamide           <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ glimepiride              <chr> "No", "No", "No", "No", "No", "No", "Steady",~
## $ acetohexamide            <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ glipizide                <chr> "No", "No", "Steady", "No", "Steady", "No", "~
## $ glyburide                <chr> "No", "No", "No", "No", "No", "No", "No", "St~
## $ tolbutamide              <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ pioglitazone             <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ rosiglitazone            <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ acarbose                 <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ miglitol                 <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ troglitazone             <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ tolazamide               <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ examide                  <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ citoglipton              <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ insulin                  <chr> "No", "Up", "No", "Up", "Steady", "Steady", "~
## $ glyburidemetformin       <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ glipizidemetformin       <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ glimepiridepioglitazone  <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ metforminrosiglitazone   <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ metforminpioglitazone    <chr> "No", "No", "No", "No", "No", "No", "No", "No~
## $ change                   <chr> "No", "Ch", "No", "Ch", "Ch", "No", "Ch", "No~
## $ diabetesMed              <chr> "No", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes~
## $ readmitted               <chr> "NO", ">30", "NO", "NO", "NO", ">30", "NO", "~
```

Table 1: Summary of patient encounters

	n
Total number of patient encounters:	101,766
Number of patient encounters that can be classified as 'repeat':	47,021
Number of patients with repeat encounters:	16,773

Data cleaning, exploration, and feature engineering

Conversion of '?' to NA

From review of the dataframe is a apparent that '?' is used instead of NA. To faciliate data cleaning and wrangling '?' is switched to NA.

```
#replace '?' with NA
diabetic_data <- diabetic_data %>%
  mutate(across(where(is.character), ~na_if(., "?")))
```

Duplicate patients

```
#total number of patient encounters
total_number_of_patient_encounters <-pull(diabetic_data, patient_nbr)%>%
  length()

#number of patients with repeat encounters
number_of_patient_with_repeat_encounters <- diabetic_data %>%
  group_by(patient_nbr) %>%
  filter(n()>1) %>%
  tally() %>%
  sdf_nrow()

#number of patient encounters that can be classified as 'repeat'
number_of_patient_classed_as_repeat <- diabetic_data %>%
  group_by(patient_nbr) %>%
  filter(n()>1) %>%
  sdf_nrow()

patient_encounters_table <- data.frame( n = c(total_number_of_patient_encounters, number_of_patient_clas
row.names(patient_encounters_table) <- c("Total number of patient encounters:", "Number of patient encou
kable(patient_encounters_table, caption = "Summary of patient encounters", digits = 3, format.args = lis
  scientific = FALSE))
```

As outlined above. The dataset contains 16,773 patients with multiple admissions (accounting for 47,021 observed admissions).

Removing duplicate patients

It cannot be assumed that the reason for these repeat admissions are independent. Statistical independence between observations is an assumption in some predictive models e.g. logistic regression. Therefore the dataset was cleaned to include only the **initial encounter** of repeat patients using the following code:

```
#group by patient number then select only the earliest patient encounter
diabetic_data <- diabetic_data %>%
  group_by(patient_nbr) %>%
  slice_min(encounter_id) %>% #slice_min selects the rows with lowest values
  ungroup()
```

Once this is done `patient_nbr` and `ecnounter_id` are redundant so these columns are removed

```
diabetic_data <- select(diabetic_data, -c(patient_nbr, encounter_id))
```

Missing variables

```
#count the number of  NAs per column
NA_count <- diabetic_data %>%
  summarise_all(~sum(as.integer(is.na(.)))) %>%
  collect()
```

```
## Warning: Missing values are always removed in SQL aggregation functions.
## Use `na.rm = TRUE` to silence this warning
## This warning is displayed once every 8 hours.
```

```
#transpose dataframe (convert from wide to long)
NA_count <- t(NA_count)

#rename column 1 to missing_values
colnames(NA_count)[1] ="missing_values"

kable(NA_count)
```

	missing_values
race	1948
gender	0
age	0
weight	68665
admission_type_id	0
discharge_disposition_id	0
admission_source_id	0
time_in_hospital	0
payer_code	31043
medical_specialty	34477
num_lab_procedures	0
num_procedures	0
num_medications	0
number_outpatient	0
number_emergency	0
number_inpatient	0
diag_1	11
diag_2	294
diag_3	1225
number_diagnoses	0
max_glu_serum	0
A1Cresult	0
metformin	0
repaglinide	0
nateglinide	0
chlorpropamide	0
glimepiride	0
acetohexamide	0
glipizide	0
glyburide	0
tolbutamide	0
pioglitazone	0
rosiglitazone	0
acarbose	0
miglitol	0
troglitazone	0
tolazamide	0
examide	0
citoglipton	0
insulin	0
glyburidemetformin	0
glipizidemetformin	0
glimepiridepioglitazone	0
metforminrosiglitazone	0
metforminpioglitazone	0
change	0
diabetesMed	0
readmitted	0

From the table above it is clear that `weight`, `payer_code` and `medical_speciality` have a significant number of missing variables. The exact percentage of missing variables is further explored below:

Table 2: Variables with a high proportion of missing values

	percent
medical_specialty	48.21
payer_code:	43.41
weight	96.01

```
missing_medical_specialty <- diabetic_data %>%
  count(medical_specialty) %>%
  mutate(percent_missing = ((n / sum(n))*100)) %>%
  mutate(percent_missing = round(percent_missing, 2)) %>%
  filter(is.na(medical_specialty))%>%
  pull(percent_missing)

missing_payer_code <- diabetic_data %>%
  count(payer_code) %>%
  mutate(percent_missing = ((n / sum(n))*100)) %>%
  mutate(percent_missing = round(percent_missing, 2)) %>%
  filter(is.na(payer_code))%>%
  pull(percent_missing)

missing_weight <- diabetic_data %>%
  count(weight) %>%
  mutate(percent_missing = ((n / sum(n))*100)) %>%
  mutate(percent_missing = round(percent_missing, 2)) %>%
  filter(is.na(weight)) %>%
  pull(percent_missing)

missing_variables_table <- data.frame( percent = c(missing_medical_specialty, missing_payer_code, missi
row.names(missing_variables_table) <- c("medical_specialty", "payer_code:", "weight" )
kable(missing_variables_table, caption = "Variables with a high proportion of missing values", digits =
  scientific = FALSE))
```

Given the amount of missing values, `weight` and `payer_code` are removed from inclusion in further analysis. Although `medical_speciality` also has a high rate of missing values, this variable was retained as it was postulated that it may be very relevant to the further analysis.

```
diabetic_data <- select(diabetic_data, -c(weight, payer_code))
```

Exploration of numericcal variables

Summary stats numerical variables

```
summary_stats_num_var <- sdf_describe(diabetic_data, cols =
               c('time_in_hospital',
                 'num_medications',
                 'number_inpatient',
                 'num_lab_procedures',
                 'number_outpatient',
                 'number_diagnoses',
                 'num_procedures',
                 'number_emergency'))
```

summary	time_in_hospital	num_medications	number_inpatient	num_lab_procedures	number_outpatient	number_diagnoses	num_procedures	number_emergency
count	71518	71518	71518	71518	71518	71518	71518	71518
mean	4.289130009228446	15.70502530831399	0.1778293576442294	43.07547750216729	0.2800693531698314	7.245700383120333	1.4305769176990408	0.10354036745994015
stddev	2.949209936640064	8.311162711543068	0.6037895326226642	19.952337943882533	1.0689566542163038	1.9946744288895086	1.759863962227284	0.5091865990151034
min	1	1	0	1	0	1	0	0
max	14	81	12	132	42	16	6	42

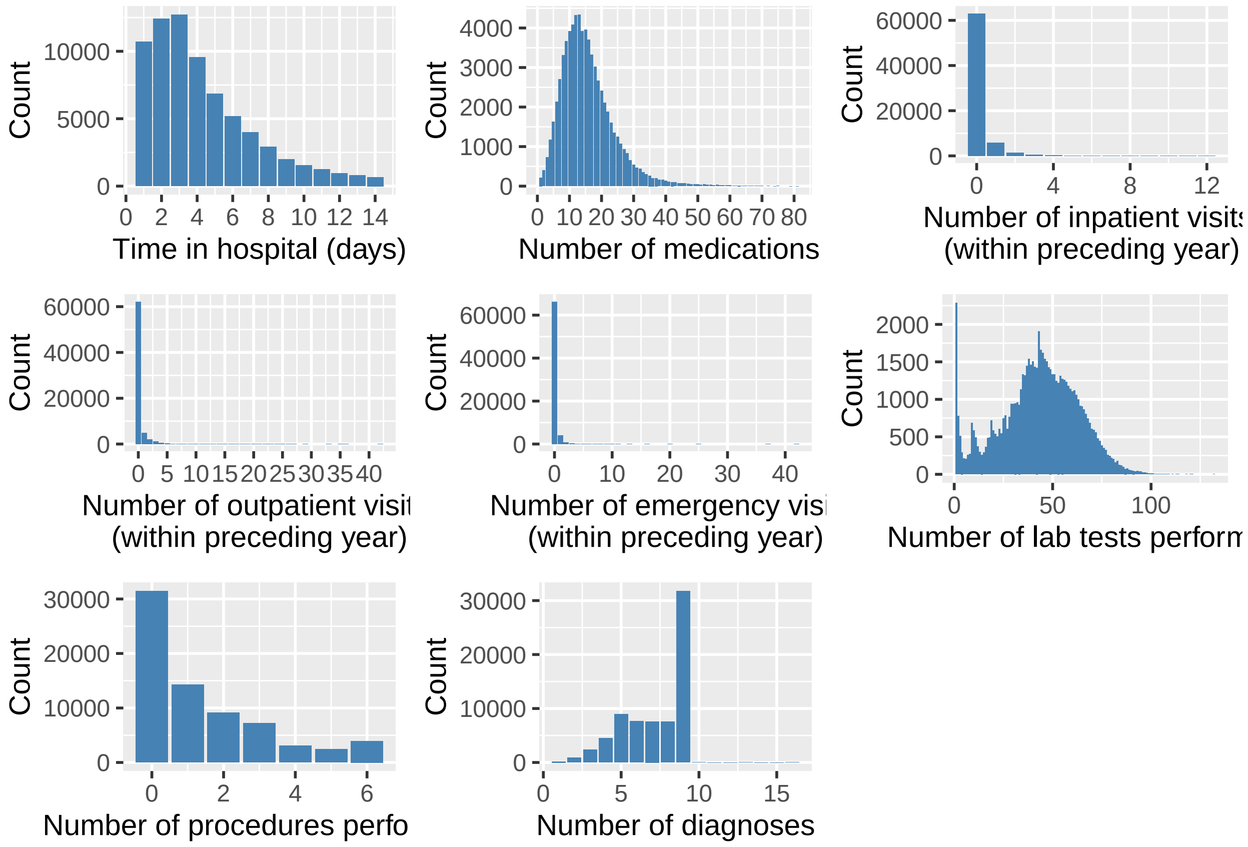
```
kable(summary_stats_num_var) %>%
  kable_styling(latex_options = "scale_down")
```

Visualisation of numerical variables

```
#create summary groups of numerical variable to collect and use in ggplot
time_in_hospital_group = diabetic_data %>%
  count(time_in_hospital) %>%
  arrange(time_in_hospital) %>%
  collect()

num_medications_group = diabetic_data %>%
  count(num_medications) %>%
  arrange(num_medications) %>%
  collect()

number_inpatient_group = diabetic_data %>%
  count(number_inpatient) %>%
  arrange(number_inpatient) %>%
  collect()

num_lab_procedures_group = diabetic_data %>%
  count(num_lab_procedures) %>%
  arrange(num_lab_procedures) %>%
  collect()

number_outpatient_group = diabetic_data %>%
  count(number_outpatient) %>%
  arrange(number_outpatient) %>%
  collect()

number_diagnoses_group = diabetic_data %>%
  count(number_diagnoses) %>%
  arrange(number_diagnoses) %>%
  collect()

num_procedures_group = diabetic_data %>%
  count(num_procedures) %>%
  arrange(num_procedures) %>%
  collect()

number_emergency_group = diabetic_data %>%
  count(number_emergency) %>%
  arrange(number_emergency) %>%
  collect()

#create plots
```

```r
time_in_hospital_plot <-
  ggplot(aes(as.numeric(time_in_hospital), n), data = time_in_hospital_group) +
  geom_col(fill = 'SteelBlue') +
  scale_x_continuous(breaks=seq(0, 20, 2))  +
  xlab('Time in hospital (days)') +
  ylab('Count')

num_medications_plot <-
  ggplot(aes(as.numeric(num_medications), n), data = num_medications_group) +
  geom_col(fill = 'SteelBlue') +
  scale_x_continuous(breaks=seq(0, 80, 10))  +
  xlab('Number of medications') +
  ylab('Count')

number_inpatient_plot <-
  ggplot(aes(as.numeric(number_inpatient), n), data = number_inpatient_group) +
  geom_col(fill = 'SteelBlue') +
  #scale_x_continuous(breaks=seq(0, 15, 5))  +
  xlab('Number of inpatient visits \n(within preceding year)') +
  ylab('Count')

number_outpatient_plot <-
  ggplot(aes(as.numeric(number_outpatient), n), data = number_outpatient_group) +
  geom_col(fill = 'SteelBlue') +
  scale_x_continuous(breaks=seq(0, 40, 5))  +
  xlab('Number of outpatient visits \n(within preceding year)') +
  ylab('Count')

number_emergency_plot <-
  ggplot(aes(as.numeric(number_emergency), n), data = number_emergency_group) +
  geom_col(fill = 'SteelBlue') +
  xlab('Number of emergency visits \n(within preceding year)') +
  ylab('Count')

num_lab_procedures_plot <-
  ggplot(aes(as.numeric(num_lab_procedures), n), data = num_lab_procedures_group) +
  geom_col(fill = 'SteelBlue') +
  xlab('Number of lab tests performed') +
  ylab('Count')

num_procedures_plot <-
  ggplot(aes(as.numeric(num_procedures), n), data = num_procedures_group) +
  geom_col(fill = 'SteelBlue') +
  xlab('Number of procedures performed') +
  ylab('Count')

number_diagnoses_plot <-
  ggplot(aes(as.numeric(number_diagnoses), n), data = number_diagnoses_group) +
  geom_col(fill = 'SteelBlue') +
  xlab('Number of diagnoses') +
  ylab('Count')

#combine plots into one grid
```

```
plot_grid(time_in_hospital_plot,
          num_medications_plot,
          number_inpatient_plot,
          number_outpatient_plot,
          number_emergency_plot,
          num_lab_procedures_plot,
          num_procedures_plot,
          number_diagnoses_plot)
```



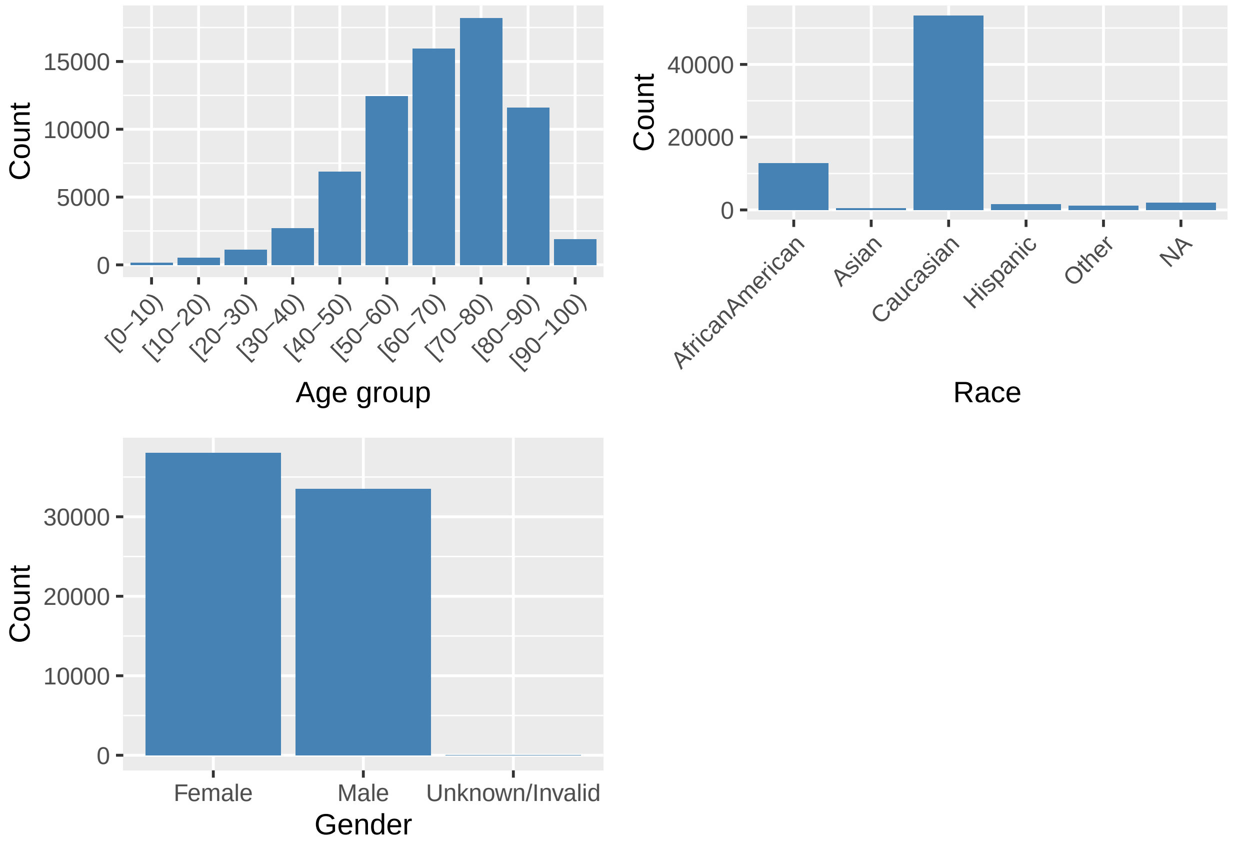
Exploration and feature engineering of categorical variables

Age, Race, and gender

Visualisation of Age, Race, and gender

```
# Data manipulations are done first using spark and collected
age_group = diabetic_data %>%
  count(age) %>%
  arrange(age) %>%
  collect()

race_group = diabetic_data %>%
  count(race) %>%
  arrange(race) %>%
  collect()
```

```
gender_group = diabetic_data %>%
  count(gender) %>%
  arrange(gender) %>%
  collect()


#plots created with ggplot
age_plot <-
  ggplot(aes(as.factor(age), n), data = age_group) +
  geom_col(fill = 'SteelBlue') +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  xlab('Age group') +
  ylab('Count')

race_plot <-
  ggplot(aes(as.factor(race), n), data = race_group) +
  geom_col(fill = 'SteelBlue') +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  xlab('Race') +
  ylab('Count')

gender_plot <-
  ggplot(aes(as.factor(gender), n), data = gender_group) +
  geom_col(fill = 'SteelBlue') +
  xlab('Gender') +
  ylab('Count')


plot_grid(age_plot, race_plot, gender_plot)
```



Feature engineering of 'Age'

Age is converted to an ordinal scale, using the central age from each category. i.e. patients classed as age '[10-20)' are given the value.

```
diabetic_data <- diabetic_data %>%
  mutate(
    age_contin = case_when(
      age == '[0-10)'    ~ 5,
      age == '[10-20)'   ~ 15,
      age == '[20-30)'   ~ 25,
      age == '[30-40)'   ~ 35,
      age == '[40-50)'   ~ 45,
      age == '[50-60)'   ~ 55,
      age == '[60-70)'   ~ 65,
      age == '[70-80)'   ~ 75,
      age == '[80-90)'   ~ 85,
      age == '[90-100)'  ~ 95
    ))
```

Feature engineering of 'Race'

Race is one hot encoded

```
diabetic_data <- diabetic_data %>%
  mutate(
    unknown_race = ifelse(is.na(race), 1,0),
    asian = ifelse(race == 'Asian' & !is.na(race), 1,0),
    african_american = ifelse(race == 'AfricanAmerican' & !is.na(race), 1,0),
    caucasian = ifelse(race == 'Caucasian' & !is.na(race), 1,0),
    hispanic = ifelse(race == 'Hispanic' & !is.na(race), 1,0),
    other = ifelse(race == 'Other' & !is.na(race), 1,0),
  )
```

Feature engineering of 'Gender'

Gender is on hot encoded

```
diabetic_data <- diabetic_data %>%
  mutate(
    female = ifelse(gender == 'Female', 1,0),
    gender_unknown_invalid = ifelse(gender == 'Unknown/Invalid', 1,0),
    male = ifelse(gender == 'Male', 1,0)
  )
```

Readmissions

View the breakdown of readmissions

```
diabetic_data %>%
  count(readmitted) %>%
  kable()
```

readmitted	n
<30	6293
NO	42985
>30	22240

Feature engineering of readmission data

A variable (`early_readmission`) is created that classifies those readmitted within 30 days and those not, as this is the specific question posed by the challenge.

```
## create a new column with readmission <30
diabetic_data = mutate(diabetic_data, early_readmission = ifelse(readmitted == '<30', 1, 0))

diabetic_data %>%
  group_by(early_readmission) %>%
  tally() %>%
  kable()
```

early_readmission	n
1	6293
0	65225

Diagnoses

With regard to the diagnosis variables (`diag_1`, `diag_2`, and `diag_3`) initial exploration determines the exact number of different diagnosis categories.

```
#count of the number of unique primary Dx (698)
n_primary_dx <- diabetic_data %>%
  summarise(count = n_distinct(diag_1)) %>%
  pull()
```

Table 3: Total number of different diagnosis categories

	n
Primary Dx	697
Secondary Dx:	726
Tertiary Dx	759

```
#count of the number of unique secondary Dx (749)
n_secondary_dx <- diabetic_data %>%
  summarise(count = n_distinct(diag_2)) %>%
  pull()

#count of the number of unique tertiary Dx (759)
n_tertiary_dx <- diabetic_data %>%
  summarise(count = n_distinct(diag_3)) %>%
  pull()

diagnosis_n <- data.frame( n = c(n_primary_dx, n_secondary_dx, n_tertiary_dx))
row.names(diagnosis_n) <- c("Primary Dx", "Secondary Dx:", "Tertiary Dx" )
kable(diagnosis_n, caption = "Total number of different diagnosis categories", digits = 3, format.args =
  scientific = FALSE))
```

Feature engineering of Diagnosis variables

As illustrated above there are 698 unique primary diagnoses, 749 unique secondary diagnoses, and 759 tertiary diagnoses. Maintaining categorical variables with such high levels will be computationally expensive, diagnoses will be consolidated into more manageable levels. This is performed below using the ICD-9 code. Diagnoses have been consolidated according to the ICD-9 chapters, with each chapter essentially representing a different bodily system. A seperate category for diabetes has also been created. It should be noted that this still results in 19 categories.

```
#consolidate according to ICD9 code
diabetic_data <- diabetic_data %>%
  mutate(
    diag_1_cat = case_when(
      rlike(diag_1, "250") ~ 'diabetes', #case_when works in order therefore 'diabetes' will be classed
      diag_1 >= 000 & diag_1 < 140 ~ 'infection',
      diag_1 >= 140 & diag_1 < 240 ~ 'neoplasms',
      diag_1 >= 240 & diag_1 < 280 ~ 'endo_metabolic_immunity',
      diag_1 >= 280 & diag_1 < 290 ~ 'haematology',
      diag_1 >= 290 & diag_1 < 320 ~ 'mental',
      diag_1 >= 320 & diag_1 < 390 ~ 'neurology',
      diag_1 >= 390 & diag_1 < 460 ~ 'circulatory',
      diag_1 >= 460 & diag_1 < 520 ~ 'respiratory',
      diag_1 >= 520 & diag_1 < 580 ~ 'digestive',
      diag_1 >= 580 & diag_1 < 630 ~ 'genitourinary',
      diag_1 >= 630 & diag_1 < 680 ~ 'preg_birth_puerperium',
      diag_1 >= 680 & diag_1 < 710 ~ 'dermatology',
      diag_1 >= 710 & diag_1 < 740 ~ 'musculoskeletal',
      diag_1 >= 740 & diag_1 < 760 ~ 'congenital',
      diag_1 >= 760 & diag_1 < 780 ~ 'perinatal',
```

```r
      diag_1 >= 780 & diag_1 < 800 ~ 'ill_defined',
      diag_1 >= 800 & diag_1 < 1000 ~ 'injury_poisoning',
      rlike(diag_1, "V") | rlike(diag_1, "E") ~ 'supplementary',
      is.na(diag_1) ~ 'unknown_diag_1', #NA variables do not get special treatment
      TRUE ~ diag_1),
    diag_2_cat = case_when(
      rlike(diag_2, "250") ~ 'diabetes', #case_when work in order
      diag_2 >= 000 & diag_2 < 140 ~ 'infection',
      diag_2 >= 140 & diag_2 < 240 ~ 'neoplasms',
      diag_2 >= 240 & diag_2 < 280 ~ 'endo_metabolic_immunity',
      diag_2 >= 280 & diag_2 < 290 ~ 'haematology',
      diag_2 >= 290 & diag_2 < 320 ~ 'mental',
      diag_2 >= 320 & diag_2 < 390 ~ 'neurology',
      diag_2 >= 390 & diag_2 < 460 ~ 'circulatory',
      diag_2 >= 460 & diag_2 < 520 ~ 'respiratory',
      diag_2 >= 520 & diag_2 < 580 ~ 'digestive',
      diag_2 >= 580 & diag_2 < 630 ~ 'genitourinary',
      diag_2 >= 630 & diag_2 < 680 ~ 'preg_birth_puerperium',
      diag_2 >= 680 & diag_2 < 710 ~ 'dermatology',
      diag_2 >= 710 & diag_2 < 740 ~ 'musculoskeletal',
      diag_2 >= 740 & diag_2 < 760 ~ 'congenital',
      diag_2 >= 760 & diag_2 < 780 ~ 'perinatal',
      diag_2 >= 780 & diag_2 < 800 ~ 'ill_defined',
      diag_2 >= 800 & diag_2 < 1000 ~ 'injury_poisoning',
      rlike(diag_2, "V") | rlike(diag_2, "E") ~ 'supplementary',
      is.na(diag_2) ~ 'unknown_diag_2', #NA variable do not get special treatment
      TRUE ~ diag_2),
    diag_3_cat = case_when(
      rlike(diag_3, "250") ~ 'diabetes', #case_when work in order
      diag_3 >= 000 & diag_3 < 140 ~ 'infection',
      diag_3 >= 140 & diag_3 < 240 ~ 'neoplasms',
      diag_3 >= 240 & diag_3 < 280 ~ 'endo_metabolic_immunity',
      diag_3 >= 280 & diag_3 < 290 ~ 'haematology',
      diag_3 >= 290 & diag_3 < 320 ~ 'mental',
      diag_3 >= 320 & diag_3 < 390 ~ 'neurology',
      diag_3 >= 390 & diag_3 < 460 ~ 'circulatory',
      diag_3 >= 460 & diag_3 < 520 ~ 'respiratory',
      diag_3 >= 520 & diag_3 < 580 ~ 'digestive',
      diag_3 >= 580 & diag_3 < 630 ~ 'genitourinary',
      diag_3 >= 630 & diag_3 < 680 ~ 'preg_birth_puerperium',
      diag_3 >= 680 & diag_3 < 710 ~ 'dermatology',
      diag_3 >= 710 & diag_3 < 740 ~ 'musculoskeletal',
      diag_3 >= 740 & diag_3 < 760 ~ 'congenital',
      diag_3 >= 760 & diag_3 < 780 ~ 'perinatal',
      diag_3 >= 780 & diag_3 < 800 ~ 'ill_defined',
      diag_3 >= 800 & diag_3 < 1000 ~ 'injury_poisoning',
      rlike(diag_3, "V") | rlike(diag_3, "E") ~ 'supplementary',
      is.na(diag_3) ~ 'unknown_diag_3', #NA variable do not get special treatment
      TRUE ~ diag_3)
  )
```

Consolidation of `diag_1`, `diag_2`, and `diag_3` variables

One hot encoding of diagnnsis categories The diagnosis categories are then one hot encoded

```
#one_hot_encode diagnosis
diabetic_data <- diabetic_data %>%
  mutate(
    diag_1_infection = ifelse(diag_1_cat == 'infection' & !is.na(diag_1_cat), 1,0),
    diag_1_neoplasms = ifelse(diag_1_cat == 'neoplasms' & !is.na(diag_1_cat) , 1,0),
    diag_1_endo_metabolic_immunity = ifelse(diag_1_cat == 'endo_metabolic_immunity' & !is.na(diag_1_cat
    diag_1_haematology = ifelse(diag_1_cat == 'haematology' & !is.na(diag_1_cat), 1,0),
    diag_1_mental = ifelse(diag_1_cat == 'mental' & !is.na(diag_1_cat), 1,0),
    diag_1_neurology = ifelse(diag_1_cat == 'neurology' & !is.na(diag_1_cat), 1,0),
    diag_1_circulatory = ifelse(diag_1_cat == 'circulatory' & !is.na(diag_1_cat), 1,0),
    diag_1_respiratory = ifelse(diag_1_cat == 'respiratory' & !is.na(diag_1_cat), 1,0),
    diag_1_digestive = ifelse(diag_1_cat == 'digestive' & !is.na(diag_1_cat), 1,0),
    diag_1_genitourinary = ifelse(diag_1_cat == 'genitourinary' & !is.na(diag_1_cat), 1,0),
    diag_1_preg_birth_puerperium = ifelse(diag_1_cat == 'preg_birth_puerperium' & !is.na(diag_1_cat), 1
    diag_1_dermatology = ifelse(diag_1_cat == 'dermatology' & !is.na(diag_1_cat), 1,0),
    diag_1_musculoskeletal = ifelse(diag_1_cat == 'musculoskeletal'& !is.na(diag_1_cat), 1,0),
    diag_1_congenital = ifelse(diag_1_cat == 'congenital'& !is.na(diag_1_cat), 1,0),
    diag_1_perinatal = ifelse(diag_1_cat == 'perinatal'& !is.na(diag_1_cat), 1,0),
    diag_1_ill_defined = ifelse(diag_1_cat == 'ill_defined'& !is.na(diag_1_cat), 1,0),
    diag_1_injury_poisoning = ifelse(diag_1_cat == 'injury_poisoning'& !is.na(diag_1_cat), 1,0),
    diag_1_supplementary = ifelse(diag_1_cat == 'supplementary'& !is.na(diag_1_cat), 1,0),
    diag_1_diabetes = ifelse(diag_1_cat == 'diabetes'& !is.na(diag_1_cat), 1,0),
    diag_1_unknown = ifelse(diag_1_cat == 'unknown_diag_1'& !is.na(diag_1_cat), 1,0),
    diag_2_infection = ifelse(diag_2_cat == 'infection'& !is.na(diag_2_cat), 1,0),
    diag_2_neoplasms = ifelse(diag_2_cat == 'neoplasms'& !is.na(diag_2_cat), 1,0),
    diag_2_endo_metabolic_immunity = ifelse(diag_2_cat == 'endo_metabolic_immunity'& !is.na(diag_2_cat)
    diag_2_haematology = ifelse(diag_2_cat == 'haematology'& !is.na(diag_2_cat), 1,0),
    diag_2_mental = ifelse(diag_2_cat == 'mental'& !is.na(diag_2_cat), 1,0),
    diag_2_neurology = ifelse(diag_2_cat == 'neurology'& !is.na(diag_2_cat), 1,0),
    diag_2_circulatory = ifelse(diag_2_cat == 'circulatory'& !is.na(diag_2_cat), 1,0),
    diag_2_respiratory = ifelse(diag_2_cat == 'respiratory'& !is.na(diag_2_cat), 1,0),
    diag_2_digestive = ifelse(diag_2_cat == 'digestive'& !is.na(diag_2_cat), 1,0),
    diag_2_genitourinary = ifelse(diag_2_cat == 'genitourinary'& !is.na(diag_2_cat), 1,0),
    diag_2_preg_birth_puerperium = ifelse(diag_2_cat == 'preg_birth_puerperium'& !is.na(diag_2_cat), 1,
    diag_2_dermatology = ifelse(diag_2_cat == 'dermatology'& !is.na(diag_2_cat), 1,0),
    diag_2_musculoskeletal = ifelse(diag_2_cat == 'musculoskeletal'& !is.na(diag_2_cat), 1,0),
    diag_2_congenital = ifelse(diag_2_cat == 'congenital'& !is.na(diag_2_cat), 1,0),
    diag_2_perinatal = ifelse(diag_2_cat == 'perinatal'& !is.na(diag_2_cat), 1,0),
    diag_2_ill_defined = ifelse(diag_2_cat == 'ill_defined'& !is.na(diag_2_cat), 1,0),
    diag_2_injury_poisoning = ifelse(diag_2_cat == 'injury_poisoning'& !is.na(diag_2_cat), 1,0),
    diag_2_supplementary = ifelse(diag_2_cat == 'supplementary'& !is.na(diag_2_cat), 1,0),
    diag_2_diabetes = ifelse(diag_2_cat == 'diabetes'& !is.na(diag_2_cat), 1,0),
    diag_2_unknown = ifelse(diag_2_cat == 'unknown_diag_2'& !is.na(diag_2_cat), 1,0),
    diag_3_infection = ifelse(diag_3_cat == 'infection'& !is.na(diag_3_cat), 1,0),
    diag_3_neoplasms = ifelse(diag_3_cat == 'neoplasms'& !is.na(diag_3_cat), 1,0),
    diag_3_endo_metabolic_immunity = ifelse(diag_3_cat == 'endo_metabolic_immunity'& !is.na(diag_3_cat)
    diag_3_haematology = ifelse(diag_3_cat == 'haematology'& !is.na(diag_3_cat), 1,0),
    diag_3_mental = ifelse(diag_3_cat == 'mental'& !is.na(diag_3_cat), 1,0),
    diag_3_neurology = ifelse(diag_3_cat == 'neurology'& !is.na(diag_3_cat), 1,0),
    diag_3_circulatory = ifelse(diag_3_cat == 'circulatory'& !is.na(diag_3_cat), 1,0),
    diag_3_respiratory = ifelse(diag_3_cat == 'respiratory'& !is.na(diag_3_cat), 1,0),
    diag_3_digestive = ifelse(diag_3_cat == 'digestive'& !is.na(diag_3_cat), 1,0),
    diag_3_genitourinary = ifelse(diag_3_cat == 'genitourinary'& !is.na(diag_3_cat), 1,0),
    diag_3_preg_birth_puerperium = ifelse(diag_3_cat == 'preg_birth_puerperium'& !is.na(diag_3_cat), 1,
    diag_3_dermatology = ifelse(diag_3_cat == 'dermatology'& !is.na(diag_3_cat), 1,0),
    diag_3_musculoskeletal = ifelse(diag_3_cat == 'musculoskeletal'& !is.na(diag_3_cat), 1,0),
    diag_3_congenital = ifelse(diag_3_cat == 'congenital'& !is.na(diag_3_cat), 1,0),
    diag_3_perinatal = ifelse(diag_3_cat == 'perinatal'& !is.na(diag_3_cat), 1,0),
    diag_3_ill_defined = ifelse(diag_3_cat == 'ill_defined'& !is.na(diag_3_cat), 1,0),
    diag_3_injury_poisoning = ifelse(diag_3_cat == 'injury_poisoning'& !is.na(diag_3_cat), 1,0),
    diag_3_supplementary = ifelse(diag_3_cat == 'supplementary'& !is.na(diag_3_cat), 1,0),
    diag_3_diabetes = ifelse(diag_3_cat == 'diabetes'& !is.na(diag_3_cat), 1,0),
    diag_3_unknown = ifelse(diag_1_cat == 'unknown_diag_3'& !is.na(diag_3_cat), 1,0),
  )
```

Blood sugars

Feature engineering of blood sugar variables

The blood sugar variable (i.e. `max_glu_serum` and `A1Cresult`) are one hot encoded

```
diabetic_data <- diabetic_data %>%
  mutate(
    max_glu_serum_none = ifelse(max_glu_serum == 'None', 1,0),
    max_glu_serum_norm = ifelse(max_glu_serum == 'Norm', 1,0),
    max_glu_serum_300 = ifelse(max_glu_serum == '>300', 1,0),
    max_glu_serum_200 = ifelse(max_glu_serum == '>200', 1,0),
    A1Cresult_none = ifelse(A1Cresult == 'None', 1,0),
    A1Cresult_norm = ifelse(A1Cresult == 'Norm', 1,0),
    A1Cresult_7 = ifelse(A1Cresult == '>7', 1,0),
    A1Cresult_8 = ifelse(A1Cresult == '>8', 1,0))
```

Exploration and feature engineering of `medical_speciality`

First the list of unique medical specialites is compiled along with the frequency of each observation

```
list_of_medical_specialty <- diabetic_data %>%
  group_by(medical_specialty) %>%
  tally() %>%
  mutate(percent = ((n / sum(n))*100)) %>%
  mutate(percent = round(percent, 2)) %>%
  arrange(desc(n)) %>%
  collect()

kable(list_of_medical_specialty) %>%
  kable_styling(latex_options = "scale_down")
```

Feature engineering of `medical_specialty`

Each category of `medical_speciality` is one hot encoded. I did not consolidate this group as getting a granular understanding of the influence that each group has on the readmission rate is important. As this can be directly fed back to the respective group to affect change.

```
#one_hot_encode diagnosis 1
diabetic_data <- diabetic_data %>%
  mutate(
    Cardiology = ifelse(medical_specialty == 'Cardiology' & !is.na(medical_specialty), 1,0),
    ObstetricsandGynecology = ifelse(medical_specialty == 'ObstetricsandGynecology' & !is.na(medical_spe
```

medical_specialty	n	percent
NA	34477	48.21
InternalMedicine	10919	15.27
Family/GeneralPractice	5118	7.16
Emergency/Trauma	4465	6.24
Cardiology	4266	5.96
Surgery-General	2221	3.11
Orthopedics	1134	1.59
Orthopedics-Reconstructive	1043	1.46
Radiologist	831	1.16
Nephrology	828	1.16
Pulmonology	653	0.91
Psychiatry	614	0.86
ObstetricsandGynecology	595	0.83
Urology	530	0.74
Surgery-Cardiovascular/Thoracic	497	0.69
Surgery-Neuro	409	0.57
Gastroenterology	398	0.56
Surgery-Vascular	362	0.51
Oncology	218	0.30
Pediatrics	196	0.27
PhysicalMedicineandRehabilitation	194	0.27
Neurology	168	0.23
Pediatrics-Endocrinology	147	0.21
Hematology/Oncology	122	0.17
Otolaryngology	110	0.15
Endocrinology	98	0.14
Surgery-Thoracic	92	0.13
Surgery-Cardiovascular	85	0.12
Pediatrics-CriticalCare	73	0.10
Podiatry	63	0.09
Gynecology	54	0.08
Psychology	53	0.07
Surgeon	40	0.06

```
    Pediatrics = ifelse(medical_specialty == 'Pediatrics' & !is.na(medical_specialty), 1,0),
    SurgeryColonRectal = ifelse(medical_specialty == 'Surgery-Colon&Rectal' & !is.na(medical_specialty)
    PediatricsCriticalCare = ifelse(medical_specialty == 'Pediatrics-CriticalCare' & !is.na(medical_spe
    Anesthesiology_Pediatric = ifelse(medical_specialty == 'Anesthesiology-Pediatric' & !is.na(medical_
    Ophthalmology = ifelse(medical_specialty == 'Ophthalmology' & !is.na(medical_specialty), 1,0),
    InfectiousDiseases = ifelse(medical_specialty == 'InfectiousDiseases' & !is.na(medical_specialty),
    SurgeryMaxillofacial = ifelse(medical_specialty == 'Surgery-Maxillofacial' & !is.na(medical_special
    PsychiatryAddictive = ifelse(medical_specialty == 'Psychiatry-Addictive' & !is.na(medical_specialty
    SurgeryCardiovascular = ifelse(medical_specialty == 'Surgery-Cardiovascular' & !is.na(medical_specia
    Speech = ifelse(medical_specialty == 'Speech' & !is.na(medical_specialty), 1,0),
    Endocrinology_Metabolism = ifelse(medical_specialty == 'Endocrinology-Metabolism' & !is.na(medical_
    FamilyGeneralPractice = ifelse(medical_specialty == 'Family/GeneralPractice' & !is.na(medical_specia
    SurgeryGeneral = ifelse(medical_specialty == 'Surgery-General' & !is.na(medical_specialty), 1,0),
    Orthopedics = ifelse(medical_specialty == 'Orthopedics' & !is.na(medical_specialty), 1,0),
    EmergencyTrauma = ifelse(medical_specialty == 'Emergency/Trauma' & !is.na(medical_specialty), 1,0),
    HematologyOncology = ifelse(medical_specialty == 'Hematology/Oncology' & !is.na(medical_specialty),
    Otolaryngology = ifelse(medical_specialty == 'Otolaryngology' & !is.na(medical_specialty), 1,0),
    Oncology = ifelse(medical_specialty == 'Oncology' & !is.na(medical_specialty), 1,0),
    SurgeryPediatric = ifelse(medical_specialty == 'Surgery-Pediatric' & !is.na(medical_specialty), 1,0
    PediatricsEmergencyMedicine = ifelse(medical_specialty == 'Pediatrics-EmergencyMedicine' & !is.na(me
    AllergyandImmunology = ifelse(medical_specialty == 'AllergyandImmunology' & !is.na(medical_specialt
    PediatricsInfectiousDiseases = ifelse(medical_specialty == 'Pediatrics-InfectiousDiseases' & !is.na
    Osteopath = ifelse(medical_specialty == 'Osteopath' & !is.na(medical_specialty), 1,0),
    SurgicalSpecialty = ifelse(medical_specialty == 'SurgicalSpecialty' & !is.na(medical_specialty), 1,
    Dermatology = ifelse(medical_specialty == 'Dermatology' & !is.na(medical_specialty), 1,0),
    SportsMedicine = ifelse(medical_specialty == 'SportsMedicine' & !is.na(medical_specialty), 1,0),
    Resident = ifelse(medical_specialty == 'Resident' & !is.na(medical_specialty), 1,0),
    InternalMedicine = ifelse(medical_specialty == 'InternalMedicine' & !is.na(medical_specialty), 1,0)
    Gastroenterology = ifelse(medical_specialty == 'Gastroenterology' & !is.na(medical_specialty), 1,0)
    SurgeryCardiovascularThoracic = ifelse(medical_specialty == 'Surgery-Cardiovascular/Thoracic' & !is
    Nephrology = ifelse(medical_specialty == 'Nephrology' & !is.na(medical_specialty), 1,0),
    OrthopedicsReconstructive = ifelse(medical_specialty == 'Orthopedics-Reconstructive'& !is.na(medica
    ObstericsGynecologyGynecologicOnco = ifelse(medical_specialty == 'Obsterics&Gynecology-GynecologicO
    Endocrinology = ifelse(medical_specialty == 'Endocrinology' & !is.na(medical_specialty), 1,0),
    Pediatrics_Pulmonology = ifelse(medical_specialty == 'Pediatrics-Pulmonology' & !is.na(medical_spec
    Neurology = ifelse(medical_specialty == 'Neurology' & !is.na(medical_specialty), 1,0),
    Psychology = ifelse(medical_specialty == 'Psychology' & !is.na(medical_specialty), 1,0),
    Podiatry = ifelse(medical_specialty == 'Podiatry' & !is.na(medical_specialty), 1,0),
    Gynecology = ifelse(medical_specialty == 'Gynecology' & !is.na(medical_specialty), 1,0),
    SurgeryPlastic = ifelse(medical_specialty == 'Surgery-Plastic' & !is.na(medical_specialty), 1,0),
    SurgeryThoracic = ifelse(medical_specialty == 'Surgery-Thoracic' & !is.na(medical_specialty), 1,0),
    SurgeryPlasticwithinHeadandNeck = ifelse(medical_specialty == 'Surgery-PlasticwithinHeadandNeck' &
    PhysicalMedicineandRehabilitation = ifelse(medical_specialty == 'PhysicalMedicineandRehabilitation'
    Rheumatology = ifelse(medical_specialty == 'Rheumatology' & !is.na(medical_specialty), 1,0),
    PediatricsAllergyandImmunology = ifelse(medical_specialty == 'Pediatrics-AllergyandImmunology' & !i
    Surgeon = ifelse(medical_specialty == 'Surgeon' & !is.na(medical_specialty), 1,0),
    SurgeryVascular = ifelse(medical_specialty == 'Surgery-Vascular' & !is.na(medical_specialty), 1,0),
    Pathology = ifelse(medical_specialty == 'Pathology' & !is.na(medical_specialty), 1,0),
    Hospitalist = ifelse(medical_specialty == 'Hospitalist'& !is.na(medical_specialty), 1,0),
    OutreachServices = ifelse(medical_specialty == 'OutreachServices' & !is.na(medical_specialty), 1,0)
    CardiologyPediatric = ifelse(medical_specialty == 'Cardiology-Pediatric'& !is.na(medical_specialty)
    Neurophysiology = ifelse(medical_specialty == 'Neurophysiology' & !is.na(medical_specialty), 1,0),
    PediatricsEndocrinology = ifelse(medical_specialty == 'Pediatrics-Endocrinology'& !is.na(medical_sp
    Psychiatry = ifelse(medical_specialty == 'Psychiatry'& !is.na(medical_specialty), 1,0),
    Pulmonology = ifelse(medical_specialty == 'Pulmonology'& !is.na(medical_specialty), 1,0),
    SurgeryNeuro = ifelse(medical_specialty == 'Surgery-Neuro'& !is.na(medical_specialty), 1,0),
    Urology = ifelse(medical_specialty == 'Urology'& !is.na(medical_specialty), 1,0),
    PsychiatryChildAdolescent = ifelse(medical_specialty == 'Psychiatry-Child/Adolescent'& !is.na(medica
    Radiology = ifelse(medical_specialty == 'Radiology'& !is.na(medical_specialty), 1,0),
    PediatricsHematologyOncology = ifelse(medical_specialty == 'Pediatrics-Hematology-Oncology'& !is.na
    PediatricsNeurology = ifelse(medical_specialty == 'Pediatrics-Neurology'& !is.na(medical_specialty)
    Anesthesiology = ifelse(medical_specialty == 'Anesthesiology'& !is.na(medical_specialty), 1,0),
    Dentistry = ifelse(medical_specialty == 'Dentistry'& !is.na(medical_specialty), 1,0),
    PhysicianNotFound = ifelse(medical_specialty == 'PhysicianNotFound'& !is.na(medical_specialty), 1,0
    Hematology = ifelse(medical_specialty == 'Hematology'& !is.na(medical_specialty), 1,0),
    Proctology = ifelse(medical_specialty == 'Proctology'& !is.na(medical_specialty), 1,0),
    Obstetrics = ifelse(medical_specialty == 'Obstetrics'& !is.na(medical_specialty), 1,0),
    Radiologist = ifelse(medical_specialty == 'Radiologist'& !is.na(medical_specialty), 1,0),
    Perinatology = ifelse(medical_specialty == 'Perinatology'& !is.na(medical_specialty), 1,0),
    DCPTEAM = ifelse(medical_specialty == 'DCPTEAM' & !is.na(medical_specialty), 1,0),
    medical_specialty_unkown = ifelse(is.na(medical_specialty), 1,0))
```

Admission type

Consolidation of `admission_type_id`

`admission_type_id` in consolidated into 4 categories. Using the IDs_mapping.csv file the numerical value for `admission_type_id` is exchanged for character / descriptive value

```
diabetic_data <- diabetic_data %>%
  mutate(
    admission_type_consolidated = case_when(
      admission_type_id %in% c(1) ~ 'emergency',
      admission_type_id %in% c(2) ~ 'urgent',
      admission_type_id %in%c(3) ~ 'elective',
      admission_type_id %in% c(4,5,6,7,8) ~ 'admisison_type_other',
      is.na(admission_type_id) ~ 'admisison_type_other', #NA variables do not get special treatment
      TRUE ~ admission_type_id))
```

One hot encoding of `admission_type_consolidated`

The `admission_type_consolidated` variable is then one hot encoded

```
diabetic_data <- diabetic_data %>%
  mutate(
    emergency = ifelse(admission_type_consolidated == 'emergency', 1,0),
    urgent = ifelse(admission_type_consolidated == 'urgent', 1,0),
    elective = ifelse(admission_type_consolidated == 'elective', 1,0),
    admisison_type_other = ifelse(admission_type_consolidated == 'admisison_type_other', 1,0))
```

Discharge disposition

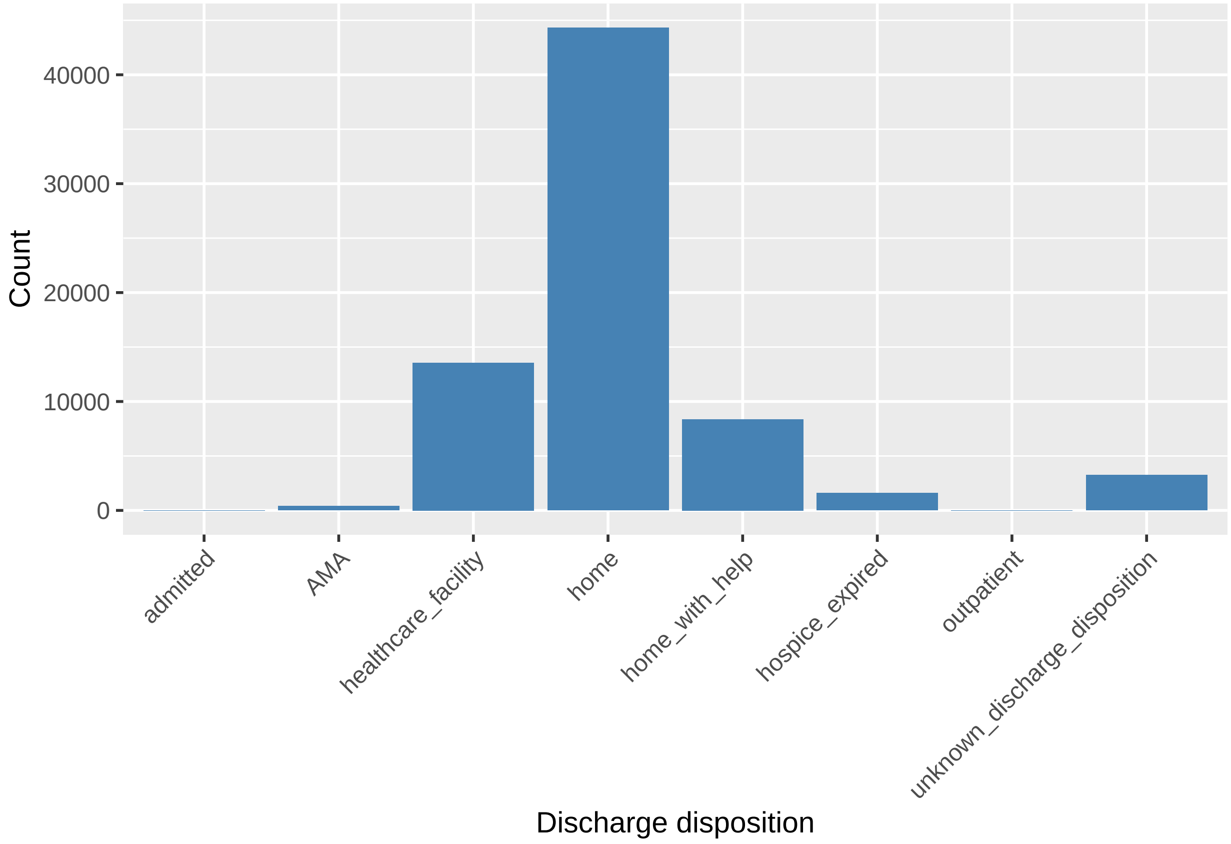
Consolidation of `discharge_disposition` variable

`discharge_disposition` in consolidated into 9 categories. Using the IDs_mapping.csv file the numerical value for `discharge_disposition` is exchanged for a character / descriptive value

```
diabetic_data <- diabetic_data %>%
  mutate(
    discharge_disposition_consolidated = case_when(
      discharge_disposition_id %in% c(1) ~ 'home',
      discharge_disposition_id %in% c(2,3,4,5,10,22,23,24,30,27,28,29) ~ 'healthcare_facility',
      discharge_disposition_id %in%c(6,8) ~ 'home_with_help',
      discharge_disposition_id %in% c(7) ~ 'AMA',
      discharge_disposition_id %in% c(9) ~ 'admitted',
      discharge_disposition_id %in% c(11,13,14,15,19,20,21) ~ 'hospice_expired',
      discharge_disposition_id %in% c(12,16,17) ~ 'outpatient',
      discharge_disposition_id %in% c(18,25,26) ~ 'unknown_discharge_disposition',
      is.na(discharge_disposition_id) ~ 'unknown_discharge_disposition', #NA variables do not get speci
      TRUE ~ discharge_disposition_id))
```

###Graphing of consolidated discharge dispositions

```
discharge_disposition_group = diabetic_data %>%
  count(discharge_disposition_consolidated) %>%
  arrange(discharge_disposition_consolidated) %>%
  collect()

discharge_disposition_plot <-
  ggplot(aes(as.factor(discharge_disposition_consolidated), n), data = discharge_disposition_group) +
  geom_col(fill = 'SteelBlue') +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  xlab('Discharge disposition') +
  ylab('Count')

discharge_disposition_plot
```



One hot encoding of `discharge_disposition_consolidated`

The consolidated discharge disposition variable (`discharge_disposition_consolidated`) is then one hot encoded

```
#one_hot_encode discharge_disposition_consolidated
diabetic_data <- diabetic_data %>%
  mutate(
    home = ifelse(discharge_disposition_consolidated == 'home', 1,0),
    healthcare_facility = ifelse(discharge_disposition_consolidated == 'healthcare_facility', 1,0),
    home_with_help = ifelse(discharge_disposition_consolidated == 'home_with_help', 1,0),
    AMA = ifelse(discharge_disposition_consolidated == 'AMA', 1,0),
    admitted = ifelse(discharge_disposition_consolidated == 'admitted', 1,0),
    hospice_expired = ifelse(discharge_disposition_consolidated == 'hospice_expired', 1,0),
    outpatient = ifelse(discharge_disposition_consolidated == 'outpatient', 1,0),
    unknown_discharge_disposition = ifelse(discharge_disposition_consolidated == 'unknown_discharge_disp
```

Change to diabetic medication

The `change` variable indicates if there was a change in diabetic medications (either dosage or generic name). Initial values are: “change” and “no change”. These are respectively encoded to 1 and 0.

```
diabetic_data <- diabetic_data %>%
  mutate(
    change = ifelse(change == 'Ch', 1,0)
  )
```

Diabetes medication

The diabetesMed variable indicates if there was any diabetic medication prescribed. Values are: “yes” and “no”. These are respectively encoded to 1 and 0.

```
diabetic_data <- diabetic_data %>%
  mutate(
    diabetesMed = ifelse(diabetesMed == 'Yes', 1,0)
  )
```

Partitioning of dataset

The diabetic_data dataset is partition into a **training** and **test** dataset. Importantly this is done before creating the z-scores for the respective numerical variables. Otherwise there would be cross over of data.

```
diabetic_data_partitions <- diabetic_data %>%
  sdf_random_split(diabetic_data_training = 0.3, diabetic_data_test = 0.7, seed = 1099)
```

Z-scoring numerical variables

The z-scores for the training and test dataset are calculated independently

```
#z-score partitioned training dataset
diabetic_data_partitions$diabetic_data_training <- diabetic_data_partitions$diabetic_data_training %>%
  mutate(
    z_age_contin = (age_contin - mean(age_contin, na.rm = TRUE)) / sd(age_contin, na.rm = TRUE),
    z_time_in_hospital = (time_in_hospital - mean(time_in_hospital, na.rm = TRUE)) / sd(time_in_hospital
    z_num_lab_procedures = (num_lab_procedures - mean(num_lab_procedures, na.rm = TRUE)) / sd(num_lab_pr
    z_num_procedures = (num_procedures - mean(num_procedures, na.rm = TRUE)) / sd(num_procedures, na.rm
    z_number_outpatient = (number_outpatient - mean(number_outpatient, na.rm = TRUE)) / sd(number_outpat
    z_number_emergency = (number_emergency - mean(number_emergency, na.rm = TRUE)) / sd(number_emergency
    z_number_inpatient = (number_inpatient - mean(number_inpatient, na.rm = TRUE)) / sd(number_inpatient
    z_number_diagnoses = (number_diagnoses - mean(number_diagnoses, na.rm = TRUE)) / sd(number_diagnoses
  )

#z-score partitioned test dataset
diabetic_data_partitions$diabetic_data_test <- diabetic_data_partitions$diabetic_data_test %>%
  mutate(
    z_age_contin = (age_contin - mean(age_contin, na.rm = TRUE)) / sd(age_contin, na.rm = TRUE),
    z_time_in_hospital = (time_in_hospital - mean(time_in_hospital, na.rm = TRUE)) / sd(time_in_hospital
    z_num_lab_procedures = (num_lab_procedures - mean(num_lab_procedures, na.rm = TRUE)) / sd(num_lab_pr
    z_num_procedures = (num_procedures - mean(num_procedures, na.rm = TRUE)) / sd(num_procedures, na.rm
    z_number_outpatient = (number_outpatient - mean(number_outpatient, na.rm = TRUE)) / sd(number_outpat
    z_number_emergency = (number_emergency - mean(number_emergency, na.rm = TRUE)) / sd(number_emergency
    z_number_inpatient = (number_inpatient - mean(number_inpatient, na.rm = TRUE)) / sd(number_inpatient
    z_number_diagnoses = (number_diagnoses - mean(number_diagnoses, na.rm = TRUE)) / sd(number_diagnoses
  )
```

Machine learning modelling

Gradient boosted trees

```
gbt_model = ml_gradient_boosted_trees(diabetic_data_partitions$diabetic_data_training, early_readmissio
                                        diag_1_infection +
                                        diag_1_neoplasms +
                                        diag_1_endo_metabolic_immunity +
                                        diag_1_haematology +
                                        diag_1_mental +
                                        diag_1_neurology +
                                        diag_1_circulatory +
                                        diag_1_respiratory +
                                        diag_1_digestive +
                                        diag_1_genitourinary +
                                        diag_1_preg_birth_puerperium +
                                        diag_1_dermatology +
                                        diag_1_musculoskeletal +
                                        diag_1_congenital +
                                        diag_1_perinatal +
                                        diag_1_ill_defined +
                                        diag_1_injury_poisoning +
                                        diag_1_supplementary +
                                        diag_1_diabetes +
                                        diag_2_unknown +
                                        diag_2_infection +
                                        diag_2_neoplasms +
                                        diag_2_endo_metabolic_immunity +
                                        diag_2_haematology +
                                        diag_2_mental +
                                        diag_2_neurology +
                                        diag_2_circulatory +
                                        diag_2_respiratory +
                                        diag_2_digestive +
                                        diag_2_genitourinary +
                                        diag_2_preg_birth_puerperium +
                                        diag_2_dermatology +
                                        diag_2_musculoskeletal +
                                        diag_2_congenital +
                                        diag_2_perinatal +
                                        diag_2_ill_defined +
                                        diag_2_injury_poisoning +
                                        diag_2_supplementary +
                                        diag_2_diabetes +
                                        diag_2_unknown +
                                        diag_3_infection +
                                        diag_3_neoplasms +
                                        diag_3_endo_metabolic_immunity +
                                        diag_3_haematology +
                                        diag_3_mental +
                                        diag_3_neurology +
                                        diag_3_circulatory +
                                        diag_3_respiratory +
                                        diag_3_digestive +
                                        diag_3_genitourinary +
                                        diag_3_preg_birth_puerperium +
                                        diag_3_dermatology +
                                        diag_3_musculoskeletal +
                                        diag_3_congenital +
                                        diag_3_perinatal +
                                        diag_3_ill_defined +
                                        diag_3_injury_poisoning +
                                        diag_3_supplementary +
                                        diag_3_diabetes +
                                        diag_3_unknown +
                                        home +
                                        healthcare_facility +
                                        home_with_help +
                                        AMA +
                                        admitted +
                                        hospice_expired +
                                        outpatient +
                                        unknown_discharge_disposition +
                                        asian +
                                        african_american +
                                        caucasian +
                                        hispanic +
                                        unknown_race +
                                        emergency +
                                        urgent +
                                        elective +
                                        admisison_type_other +
                                        max_glu_serum_none +
                                        max_glu_serum_norm +
                                        max_glu_serum_300 +
                                        max_glu_serum_200 +
                                        A1Cresult_none +
                                        A1Cresult_norm +
                                        A1Cresult_7 +
                                        A1Cresult_8 +
                                        z_age_contin +
                                        z_time_in_hospital +
                                        z_num_lab_procedures +
                                        z_num_procedures +
                                        z_number_outpatient +
                                        z_number_emergency +
                                        z_number_inpatient +
                                        z_number_diagnoses +
                                        Cardiology +
                                        ObstetricsandGynecology +
                                        Pediatrics +
                                        SurgeryColonRectal +
                                        PediatricsCriticalCare +
                                        Anesthesiology_Pediatric +
                                        Ophthalmology +
                                        InfectiousDiseases +
                                        SurgeryMaxillofacial +
                                        PsychiatryAddictive +
                                        SurgeryCardiovascular +
                                        Speech +
                                        Endocrinology_Metabolism +
                                        FamilyGeneralPractice +
                                        SurgeryGeneral +
                                        Orthopedics +
                                        EmergencyTrauma +
                                        HematologyOncology +
                                        Otolaryngology +
                                        Oncology +
                                        SurgeryPediatric +
                                        PediatricsEmergencyMedicine +
                                        AllergyandImmunology +
                                        PediatricsInfectiousDiseases +
                                        Osteopath +
                                        SurgicalSpecialty +
                                        Dermatology +
                                        SportsMedicine +
                                        Resident +
                                        InternalMedicine +
                                        Gastroenterology +
                                        SurgeryCardiovascularThoracic +
                                        Nephrology +
                                        OrthopedicsReconstructive +
                                        ObstericsGynecologyGynecologicOnco +
                                        Endocrinology +
                                        Pediatrics_Pulmonology +
                                        Neurology +
                                        Psychology +
                                        Podiatry +
                                        Gynecology +
                                        SurgeryPlastic +
                                        SurgeryThoracic +
                                        SurgeryPlasticwithinHeadandNeck +
                                        PhysicalMedicineandRehabilitation +
                                        Rheumatology +
                                        PediatricsAllergyandImmunology +
                                        Surgeon +
                                        SurgeryVascular +
                                        Pathology +
                                        Hospitalist +
                                        OutreachServices +
                                        CardiologyPediatric +
                                        Neurophysiology +
                                        PediatricsEndocrinology +
                                        Psychiatry +
                                        Pulmonology +
                                        SurgeryNeuro +
                                        Urology +
                                        PsychiatryChildAdolescent +
                                        Radiology +
                                        PediatricsHematologyOncology +
                                        PediatricsNeurology +
                                        Anesthesiology +
                                        Dentistry +
                                        PhysicianNotFound +
                                        Hematology +
                                        Proctology +
                                        Obstetrics +
                                        Radiologist +
                                        Perinatology +
                                        DCPTEAM +
                                        medical_specialty_unkown +
                                        change +
                                        diabetesMed,
                                    type = "classification")
```

Testing model on training data

```
predictions = ml_predict(gbt_model, diabetic_data_partitions$diabetic_data_training)
ml_binary_classification_evaluator(predictions, label_col = "early_readmission")
```

```
## [1] 0.7063252
```

```
diabetic_data_partitions$diabetic_data_test
```

```
## # Source: spark<?> [?? x 223]
##    race  gender age     admiss~1 disch~2 admis~3 time_~4 medic~5 num_l~6 num_p~7
##    <chr> <chr>  <chr>      <int>   <int>   <int>   <int> <chr>     <int>   <int>
##  1 <NA>  Female [10-20)        1       1       7       1 <NA>           62       0
##  2 <NA>  Female [20-30)        2       1       1       3 Obstet~       43       2
##  3 <NA>  Female [20-30)        2       1       4       4 Intern~       34       0
##  4 <NA>  Female [20-30)        2      18       4       4 Family~       71       3
##  5 <NA>  Female [20-30)        3       1       4       5 <NA>           60       0
##  6 <NA>  Female [30-40)        1       1       6       4 Family~       49       3
##  7 <NA>  Female [30-40)        1       1       7       1 <NA>           34       0
##  8 <NA>  Female [30-40)        1       1       7       1 Intern~       59       0
##  9 <NA>  Female [30-40)        1       1       7       3 <NA>           47       0
## 10 <NA>  Female [30-40)        1       1       7       4 <NA>           60       0
## # ... with more rows, 213 more variables: num_medications <int>,
## #   number_outpatient <int>, number_emergency <int>, number_inpatient <int>,
## #   diag_1 <chr>, diag_2 <chr>, diag_3 <chr>, number_diagnoses <int>,
## #   max_glu_serum <chr>, A1Cresult <chr>, metformin <chr>, repaglinide <chr>,
## #   nateglinide <chr>, chlorpropamide <chr>, glimepiride <chr>,
## #   acetohexamide <chr>, glipizide <chr>, glyburide <chr>, tolbutamide <chr>,
## #   pioglitazone <chr>, rosiglitazone <chr>, acarbose <chr>, ...
## # i Use `print(n = ...)` to see more rows, and `colnames()` to see all variable names
```

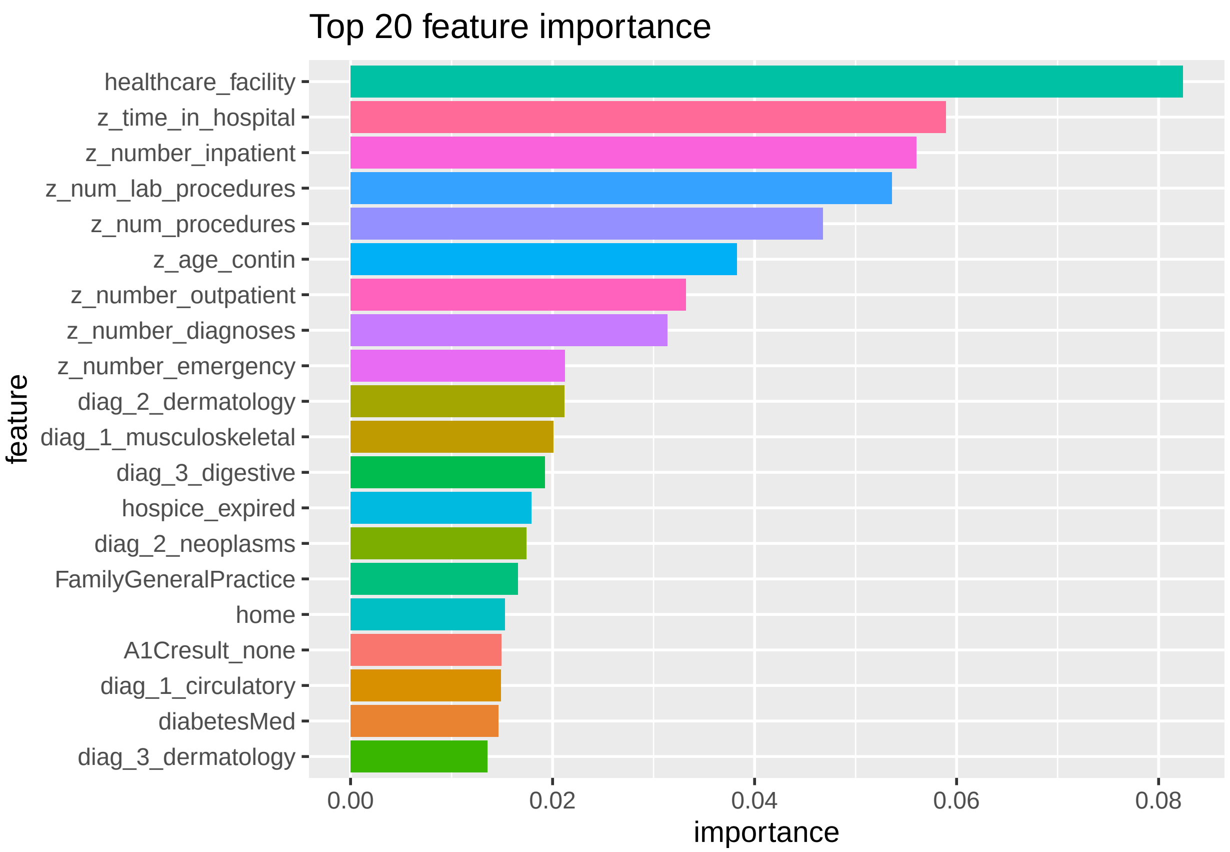
Testing model on test data

```
predictions = ml_predict(gbt_model, diabetic_data_partitions$diabetic_data_test)
ml_binary_classification_evaluator(predictions, label_col = "early_readmission")
```

```
## [1] 0.6417963
```

Graphing of feature importance

```
featureImport <- ml_tree_feature_importance(gbt_model)
featureImport[1:20,] %>% ggplot(aes(reorder(feature, importance),importance,fill=feature)) +
  geom_bar(stat = "identity") + coord_flip() + ggtitle("Top 20 feature importance") +
  theme(legend.position="none") + ylab("importance") + xlab("feature")
```


Top 20 feature importance
feature
healthcare_facility
z_time_in_hospital
z_number_inpatient
z_num_lab_procedures
z_num_procedures
z_age_contin
z_number_outpatient
z_number_diagnoses
z_number_emergency
diag_2_dermatology
diag_1_musculoskeletal
diag_3_digestive
hospice_expired
diag_2_neoplasms
FamilyGeneralPractice
home
A1Cresult_none
diag_1_circulatory
diabetesMed
diag_3_dermatology
0.00
0.02
0.04
0.06
0.08
importance