Predicting Diabetes Patient Readmission

Sheng Weng edit by mahdi akbari zarkesh

Background

It was reported that in 2011 more than 3.3 million patients were readmitted in the US within 30 days of being
associated with about $41 billion in hospital costs. The need for readmission indicates that inadequate care
time of first admission. The readmission rate has become an important metric measuring the overall quality

Diabetes is the 7th leading cause of death and affects about 23.6 million people in the US. 1.4 million Americ
every year. Hospital readmission being a major concern in diabetes care, over 250 million dollars was spent
patients in 2011. Early identification of patients facing a high risk of readmission can enable healthcare provi
investigations and possibly prevent future readmissions.

In this project, I build a machine learning classifier model to predict diabetes patients with high risk of readm
(recall) is more desirable for hospitals because it is more crucial to correctly identify "high risk" patients who
identifying "low risk" patients.

Dataset Description

The dataset represents 10 years (1999-2008) of clinical care at 130 US hospitals and integrated delivery netw
representing 101766 diabetes patients and hospital outcomes. Information was extracted from the database
following criteria:

- It is an inpatient encounter (a hospital admission).
- It is a diabetic encounter, that is, one during which any kind of diabetes was entered to the system as a
- The length of stay was at least 1 day and at most 14 days.
- Laboratory tests were performed during the encounter.
- Medications were administered during the encounter.

The data contains such attributes as patient number, race, gender, age, admission type, time in hospital, med
physician, number of lab test performed, HbA1c test result, diagnosis, number of medication, diabetic medica
inpatient, and emergency visits in the year before the hospitalization, etc.

Source: UCI Machine Learning Repository, https://archive.ics.uci.edu/ml/datasets/Diabetes+130-US+hospita

VARIABLE : DESCRIPTION

- **Encounter ID** : Unique identifier of an encounter
- **Patient number** : Unique identifier of a patient
- **Race Values** : Caucasian, Asian, African American, Hispanic, and other
- **Gender** Values: male, female, and unknown/invalid
- **Age** : Grouped in 10-year intervals: 0, 10), 10, 20), …, 90, 100)
- **Weight** : Weight in pounds

- **Admission type** : Integer identifier corresponding to 9 distinct values, for example, emergency, urgent, e
- **Discharge disposition** : Integer identifier corresponding to 29 distinct values, for example, discharged to
- **Admission source** : Integer identifier corresponding to 21 distinct values, for example, physician referra from a hospital
- **Time in hospital** : Integer number of days between admission and discharge
- **Payer code** : Integer identifier corresponding to 23 distinct values, for example, Blue Cross/Blue Shield,
- **Medical specialty** : Integer identifier of a specialty of the admitting physician, corresponding to 84 distin internal medicine, family/general practice, and surgeon
- **Number of lab procedures** : Number of lab tests performed during the encounter
- **Number of procedures** : Numeric Number of procedures (other than lab tests) performed during the en
- **Number of medications** : Number of distinct generic names administered during the encounter
- **Number of outpatient visits** : Number of outpatient visits of the patient in the year preceding the encou
- **Number of emergency visits** : Number of emergency visits of the patient in the year preceding the enco
- **Number of inpatient visits** : Number of inpatient visits of the patient in the year preceding the encounte
- **Diagnosis 1** : The primary diagnosis (coded as first three digits of ICD9); 848 distinct values
- **Diagnosis 2** : Secondary diagnosis (coded as first three digits of ICD9); 923 distinct values
- **Diagnosis 3** : Additional secondary diagnosis (coded as first three digits of ICD9); 954 distinct values
- **Number of diagnoses** : Number of diagnoses entered to the system 0%
- **Glucose serum test result** : Indicates the range of the result or if the test was not taken. Values: ">200," measured
- **A1c test result** : Indicates the range of the result or if the test was not taken. Values: ">8" if the result w result was greater than 7% but less than 8%, "normal" if the result was less than 7%, and "none" if not m
- **Change of medications** : Indicates if there was a change in diabetic medications (either dosage or gene "no change"
- **Diabetes medications** : Indicates if there was any diabetic medication prescribed. Values: "yes" and "no
- 24 features for medications For the generic names: **metformin, repaglinide, nateglinide, chlorpropamic glipizide, glyburide, tolbutamide, pioglitazone, rosiglitazone, acarbose, miglitol, troglitazone, tolazami glyburide-metformin, glipizide-metformin, glimepiride- pioglitazone, metformin-rosiglitazone, and me** indicates whether the drug was prescribed or there was a change in the dosage. Values: "up" if the dosa encounter, "down" if the dosage was decreased, "steady" if the dosage did not change, and "no" if the dr
- **Readmitted** : Days to inpatient readmission. Values: "<30" if the patient was readmitted in less than 30 readmitted in more than 30 days, and "No" for no record of readmission

Overview of Dataset

```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline

import matplotlib.pyplot as plt
plt.style.use('ggplot')
```

```
# read the file and create a pandas dataframe
```

```
data = pd.read_csv('diabetic_data.csv')
```

```
# check the dimensions of the data
data.shape
```

```
(101766, 50)
```

```
# take a first look at the dataset
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 101766 entries, 0 to 101765
Data columns (total 50 columns):
 #   Column                    Non-Null Count   Dtype 
---  ------                    --------------   ----- 
 0   encounter_id              101766 non-null  int64 
 1   patient_nbr               101766 non-null  int64 
 2   race                      101766 non-null  object
 3   gender                    101766 non-null  object
 4   age                       101766 non-null  object
 5   weight                    101766 non-null  object
 6   admission_type_id         101766 non-null  int64 
 7   discharge_disposition_id  101766 non-null  int64 
 8   admission_source_id       101766 non-null  int64 
 9   time_in_hospital          101766 non-null  int64 
 10  payer_code                101766 non-null  object
 11  medical_specialty         101766 non-null  object
 12  num_lab_procedures        101766 non-null  int64 
 13  num_procedures            101766 non-null  int64 
 14  num_medications           101766 non-null  int64 
 15  number_outpatient         101766 non-null  int64 
 16  number_emergency          101766 non-null  int64 
 17  number_inpatient          101766 non-null  int64 
 18  diag_1                    101766 non-null  object
 19  diag_2                    101766 non-null  object
 20  diag_3                    101766 non-null  object
 21  number_diagnoses          101766 non-null  int64 
 22  max_glu_serum             101766 non-null  object
 23  A1Cresult                 101766 non-null  object
 24  metformin                 101766 non-null  object
 25  repaglinide               101766 non-null  object
 26  nateglinide               101766 non-null  object
 27  chlorpropamide            101766 non-null  object
 28  glimepiride               101766 non-null  object
 29  acetohexamide             101766 non-null  object
 30  glipizide                 101766 non-null  object
 31  glyburide                 101766 non-null  object
 32  tolbutamide               101766 non-null  object
 33  pioglitazone              101766 non-null  object
 34  rosiglitazone             101766 non-null  object
 35  acarbose                  101766 non-null  object
 36  miglitol                  101766 non-null  object
 37  troglitazone              101766 non-null  object
 38  tolazamide                101766 non-null  object
 39  examide                   101766 non-null  object
 40  citoglipton               101766 non-null  object
 41  insulin                   101766 non-null  object
 42  glyburide-metformin       101766 non-null  object
 43  glipizide-metformin       101766 non-null  object
 44  glimepiride-pioglitazone  101766 non-null  object
 45  metformin-rosiglitazone   101766 non-null  object
 46  metformin-pioglitazone    101766 non-null  object
 47  change                    101766 non-null  object
 48  diabetesMed               101766 non-null  object
 49  readmitted                101766 non-null  object
dtypes: int64(13), object(37)
memory usage: 38.8+ MB
```

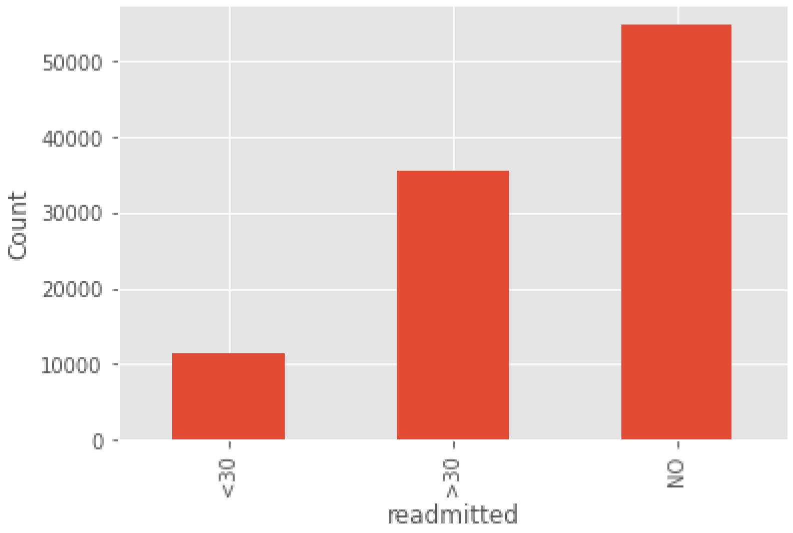
```
# first 5 rows of data
data.head()
```

	encounter_id	patient_nbr	race	gender	age	weight	admission_type_id	discharge
0	2278392	8222157	Caucasian	Female	[0-10)	?	6	
1	149190	55629189	Caucasian	Female	[10-20)	?	1	
2	64410	86047875	AfricanAmerican	Female	[20-30)	?	1	
3	500364	82442376	Caucasian	Male	[30-40)	?	1	
4	16680	42519267	Caucasian	Male	[40-50)	?	1	

The Response Variable: 'readmitted'

```
# the response variable 'readmitted' in the original dataset contains three categories.
# 11% of patients were readmitted within 30 days (<30)
# 35% of patients were readmitted after 30 days (>30)
# 54% of patients were never readmitted (NO)
data.groupby('readmitted').size().plot(kind='bar')
plt.ylabel('Count')
```

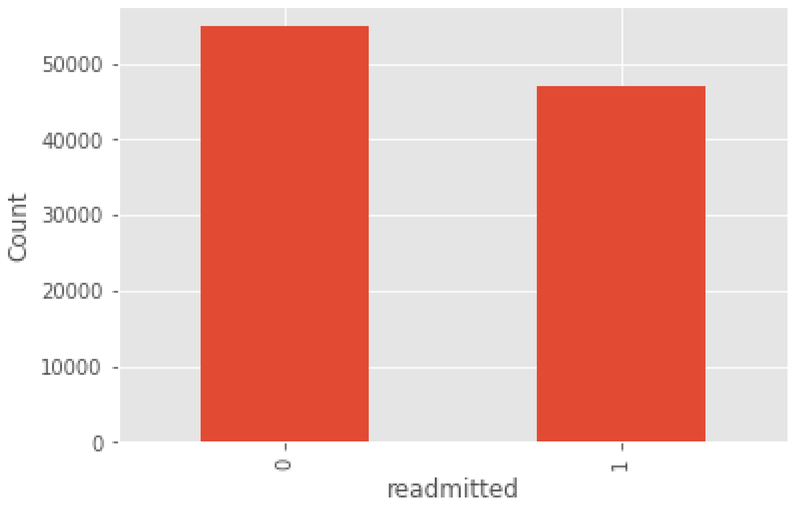
```
Text(0, 0.5, 'Count')
```



```
# recode the response variable so that it becomes a binary classification task.
# '0' means no readmission
# '1' means readmission no matter how many days after being discharged
data['readmitted'] = pd.Series([0 if val == 'NO' else 1 for val in data['readmitted']])
data_origin = data
```

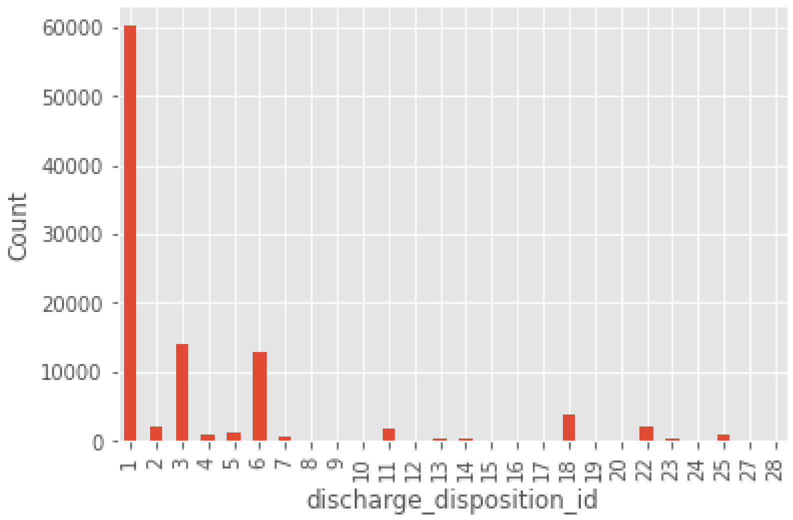
```
# plot 'readmitted' again to see the change
data.groupby('readmitted').size().plot(kind='bar')
plt.ylabel('Count')
```

```
Text(0, 0.5, 'Count')
```



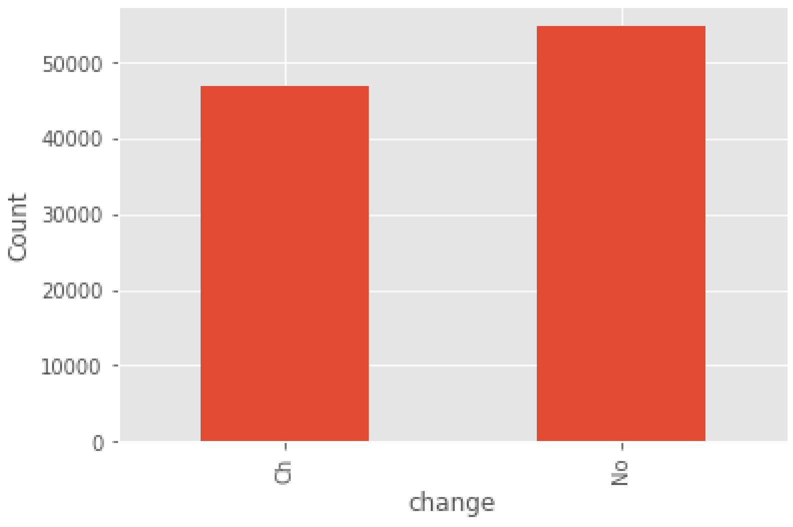
```
# the response variable 'discharge_disposition_id' in the original dataset contains 29 categories.
# now show resualt
data.groupby('discharge_disposition_id').size().plot(kind='bar')
plt.ylabel('Count')
```

```
Text(0, 0.5, 'Count')
```



```
# the response variable 'discharge_disposition_id' in the original dataset contains 29 categories.
# now show resualt
data.groupby('change').size().plot(kind='bar')
plt.ylabel('Count')
```

```
Text(0, 0.5, 'Count')
```



Feature Engineering and EDA

Explore data analysis on each feature and decide how to deal with them.

```
# remove irrelevant features
data.drop(['encounter_id','patient_nbr', 'payer_code'], axis=1, inplace=True)
```

```
# check NA in 'weight'
data[data['weight'] == '?'].shape[0] * 1.0 / data.shape[0]
```

```
0.9685847925633315
```

```
# check NA in 'medical_specialty'
data[data['medical_specialty'] == '?'].shape[0] * 1.0 / data.shape[0]
```

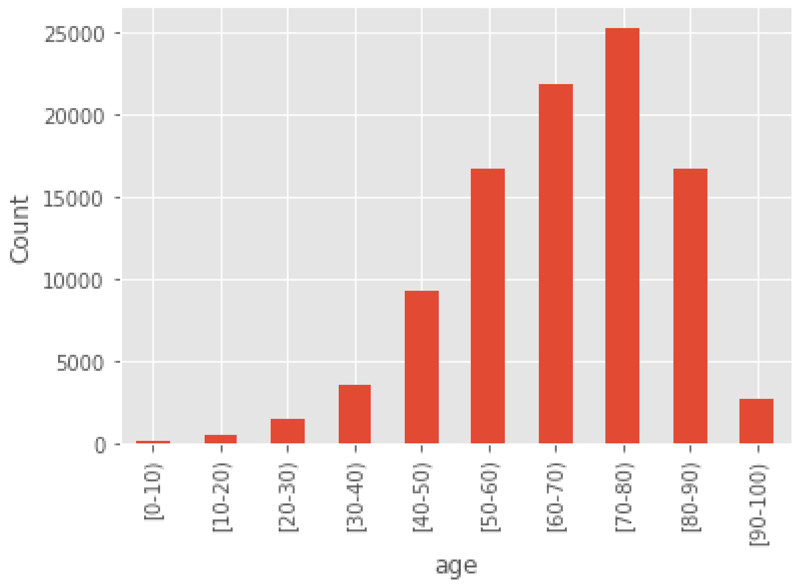
```
0.49082208203132677
```

```
# remove 'weight' and 'medical_specialty' because it's hard to do imputation on them
data.drop(['weight', 'medical_specialty'], axis=1, inplace=True)
```

```
# remove rows that have NA in 'race', 'diag_1', 'diag_2', or 'diag_3'
# remove rows that have invalid values in 'gender'
data = data[data['race'] != '?']
data = data[data['diag_1'] != '?']
data = data[data['diag_2'] != '?']
data = data[data['diag_3'] != '?']
data = data[data['gender'] != 'Unknown/Invalid']
```

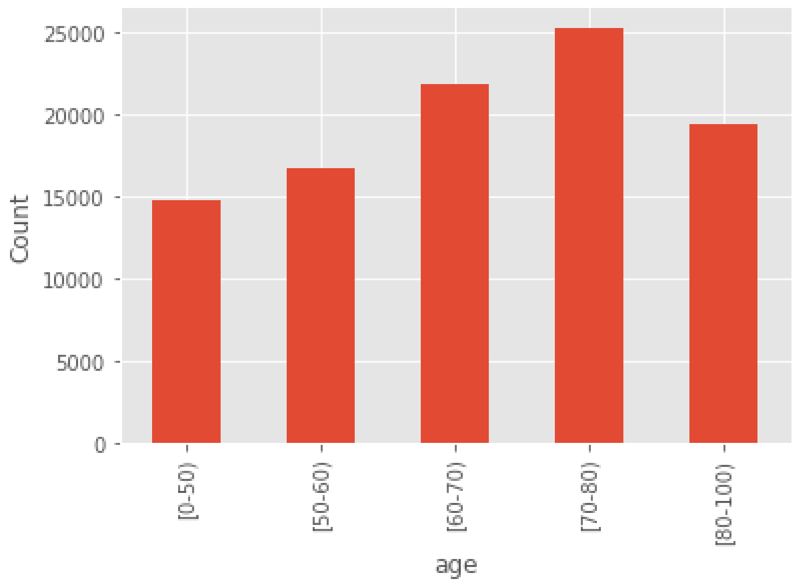
```
# check 'age' feature
data.groupby('age').size().plot(kind='bar')
plt.ylabel('Count')
```

```
Text(0, 0.5, 'Count')
```



```
# Recategorize 'age' so that the population is more evenly distributed
data['age'] = pd.Series(['[0-50)' if val in ['[0-10)', '[10-20)', '[20-30)', '[30-40)', '[40-50)'] e
                         for val in data['age']], index=data.index)
data['age'] = pd.Series(['[80-100)' if val in ['[80-90)', '[90-100)'] else val
                         for val in data['age']], index=data.index)

data.groupby('age').size().plot(kind='bar')
plt.ylabel('Count')
```

```
Text(0, 0.5, 'Count')
```



```
# original 'discharge_disposition_id' contains 28 levels
# reduce 'discharge_disposition_id' levels into 2 categories
# discharge_disposition_id = 1 corresponds to 'Discharge Home'
data['discharge_disposition_id'] = pd.Series(['Home' if val == 1 else 'Other discharge'
                                              for val in data['discharge_disposition_id']], index=da
```

```
# original 'admission_source_id' contains 25 levels
# reduce 'admission_source_id' into 3 categories
data['admission_source_id'] = pd.Series(['Emergency Room' if val == 7 else 'Referral' if val == 1 el
                                         for val in data['admission_source_id']], index=data.in
```

```
# original 'admission_type_id' contains 8 levels
# reduce 'admission_type_id' into 2 categories
data['admission_type_id'] = pd.Series(['Emergency' if val == 1 else 'Other type'
                                              for val in data['admission_type_id']], index=data.inde
```

23 features represent different medications, should we use them all in the model?

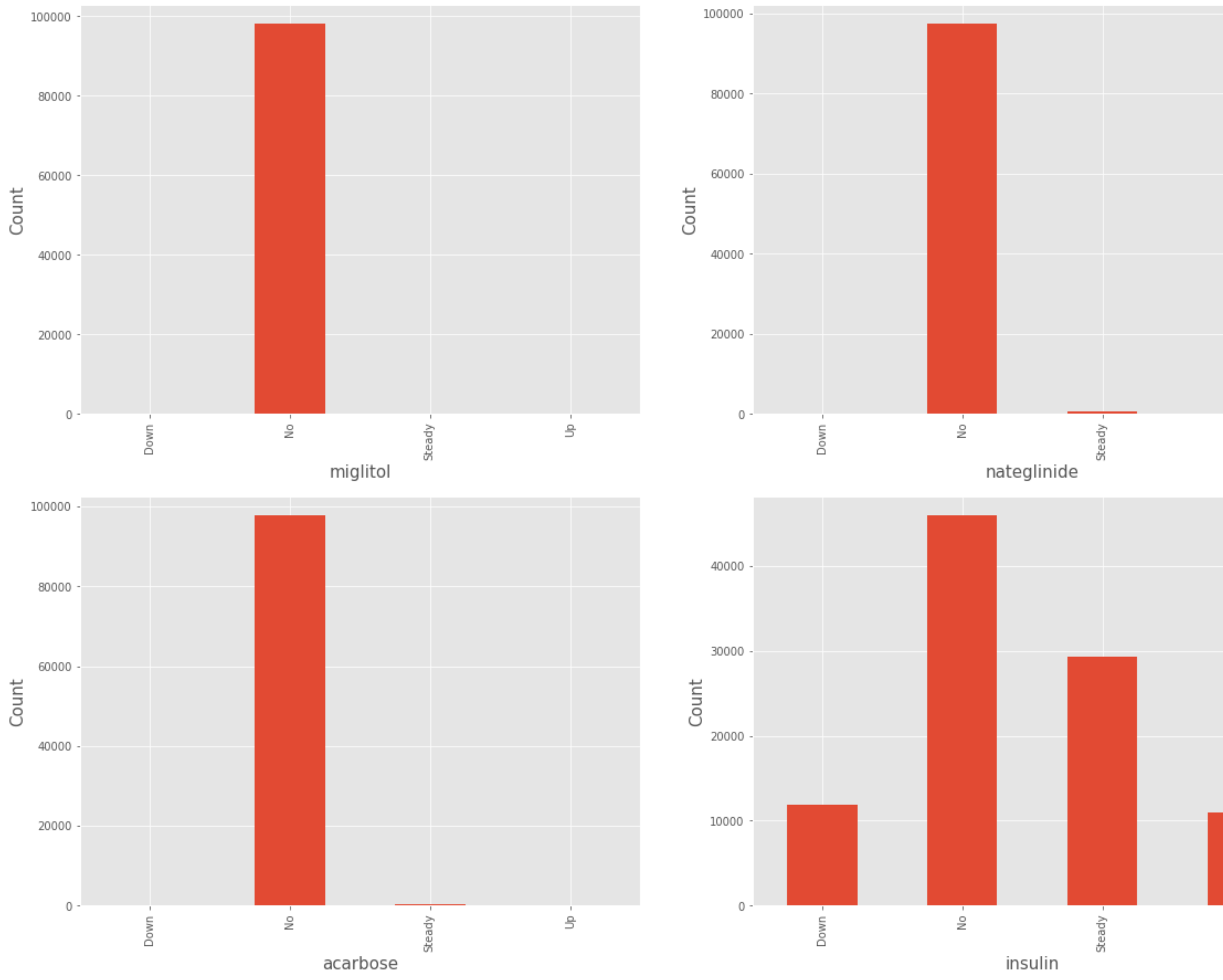
How to deal with 'diag_1', 'diag_2', and 'diag_3'?

Based on the results found in Reference[1], we know that:

- The statistical model suggests that the relationship between the probability of readmission and the Hb/ **primary diagnosis**.
- The only medication that varied significantly across the patients was the delivery of **insulin**, while other among all the patients.
- It may not be surprising that the attention given to diabetes care in individuals with admitting diagnoses diseases may have been less than those with a **primary diagnosis of diabetes mellitus**.
- Greater attention to diabetes care during the hospitalization for these high-risk individuals may have a s
- The primary, secondary, and third medical diagnoses are marked by the ICD9 codes.
- ICD9 code for diabetes: 250.xx

```
# compare diabetes medications 'miglitol', 'nateglinide' and 'acarbose' with 'insulin', as an exampl
fig = plt.figure(figsize=(20,15))

ax1 = fig.add_subplot(221)
ax1 = data.groupby('miglitol').size().plot(kind='bar')
plt.xlabel('miglitol', fontsize=15)
plt.ylabel('Count', fontsize=15)

ax2 = fig.add_subplot(222)
ax2 = data.groupby('nateglinide').size().plot(kind='bar')
plt.xlabel('nateglinide', fontsize=15)
plt.ylabel('Count', fontsize=15)

ax3 = fig.add_subplot(223)
ax3 = data.groupby('acarbose').size().plot(kind='bar')
plt.xlabel('acarbose', fontsize=15)
plt.ylabel('Count', fontsize=15)

ax4 = fig.add_subplot(224)
ax4 = data.groupby('insulin').size().plot(kind='bar')
plt.xlabel('insulin', fontsize=15)
plt.ylabel('Count', fontsize=15)
```

```
Text(0, 0.5, 'Count')
```



```python
# keep only 'insulin' and remove the other 22 diabetes medications
data.drop(['metformin', 'repaglinide', 'nateglinide', 'chlorpropamide', 'glimepiride',
           'acetohexamide', 'glipizide', 'glyburide', 'tolbutamide', 'pioglitazone',
           'rosiglitazone', 'acarbose', 'miglitol', 'troglitazone', 'tolazamide', 'examide',
           'citoglipton', 'glyburide-metformin', 'glipizide-metformin', 'glimepiride-pioglitazone',
           'metformin-rosiglitazone', 'metformin-pioglitazone'], axis=1, inplace=True)
```

```
# denote 'diag_1' as '1' if it relates to diabetes and '0' if it's not
# remove 'diag_2' and 'diag_3'
data['diag_1'] = pd.Series([1 if val.startswith('250') else 0 for val in data['diag_1']], index=data
data.drop(['diag_2', 'diag_3'], axis=1, inplace=True)
```

```
data.shape
```

```
(98052, 21)
```

```
# we end up with 98052 rows, 20 features, and one response variable 'readmitted'
list(data.columns.values)
```

```
['race',
 'gender',
 'age',
 'admission_type_id',
 'discharge_disposition_id',
 'admission_source_id',
 'time_in_hospital',
 'num_lab_procedures',
 'num_procedures',
 'num_medications',
 'number_outpatient',
 'number_emergency',
 'number_inpatient',
 'diag_1',
 'number_diagnoses',
 'max_glu_serum',
 'A1Cresult',
 'insulin',
 'change',
 'diabetesMed',
 'readmitted']
```

Data Preprocessing

```
# one-hot-encoding on categorical features
# convert nominal values to dummy values
# make age group
data['age'] = pd.Series([25 if val == '[0-50)' else 55 if val == '[50-60)' else 65 if val == '[60-70

df_race = pd.get_dummies(data['race'])
df_gender = pd.get_dummies(data['gender'])
df_max_glu_serum = pd.get_dummies(data['max_glu_serum'])
df_A1Cresult = pd.get_dummies(data['A1Cresult'])
df_insulin = pd.get_dummies(data['insulin'])
df_change = pd.get_dummies(data['change'])
df_diabetesMed = pd.get_dummies(data['diabetesMed'])
df_discharge_disposition_id = pd.get_dummies(data['discharge_disposition_id'])
df_admission_source_id = pd.get_dummies(data['admission_source_id'])
df_admission_type_id = pd.get_dummies(data['admission_type_id'])

data = pd.concat([data, df_race, df_gender, df_max_glu_serum, df_A1Cresult,
                  df_insulin, df_change, df_diabetesMed, df_discharge_disposition_id,
                  df_admission_source_id, df_admission_type_id], axis=1)
data.drop(['race', 'gender', 'max_glu_serum', 'A1Cresult', 'insulin', 'change',
                  'diabetesMed', 'discharge_disposition_id', 'admission_source_id',
                  'admission_type_id'], axis=1, inplace=True)
```

```
data.head()
```

	age	time_in_hospital	num_lab_procedures	num_procedures	num_medications	number_outpatier
1	25	3	59	0	18	
2	25	2	11	5	13	
3	25	2	44	1	16	
4	25	1	51	0	8	
5	55	3	31	6	16	

```
# feature scaling, features are standardized to have zero mean and unit variance
feature_scale_cols = ['time_in_hospital', 'num_lab_procedures', 'num_procedures', 'num_medications',
                      'number_diagnoses', 'number_inpatient', 'number_emergency', 'number_outpatient

from sklearn import preprocessing
scaler = preprocessing.StandardScaler().fit(data[feature_scale_cols])
data_scaler = scaler.transform(data[feature_scale_cols])

data_scaler_df = pd.DataFrame(data=data_scaler, columns=feature_scale_cols, index=data.index)
data.drop(feature_scale_cols, axis=1, inplace=True)
data = pd.concat([data, data_scaler_df], axis=1)
```

Data Preparation Summary

1. Remove NA in 'race', 'gender', 'diag_1', 'diag_2', and 'diag_3'
2. Remove 29 features in total: 'encounter_id', 'patient_nbr', 'payer_code', 'weight', 'medical_specialty', 'diag_2', 'diag_3', anc 'metformin', 'repaglinide', 'nateglinide', 'chlorpropamide', 'glimepiride', 'acetohexamide', 'glipizide', 'glyburide', 'tolbutamid 'acarbose', 'miglitol', 'troglitazone', 'tolazamide', 'examide', 'citoglipton', 'glyburide-metformin', 'glipizide-metformin', 'glim rosiglitazone', and 'metformin-pioglitazone'
3. Recategorize 'age' feature
4. Reduce levels in 'discharge_disposition_id', 'admission_source_id', and 'admission_type_id'
5. One-hot-encode on categorical data
6. Square root transform on right skewed count data
7. Apply feature standardizing on numerical data

Feature Importance

Evaluate the importance of different features by using emsemble method.

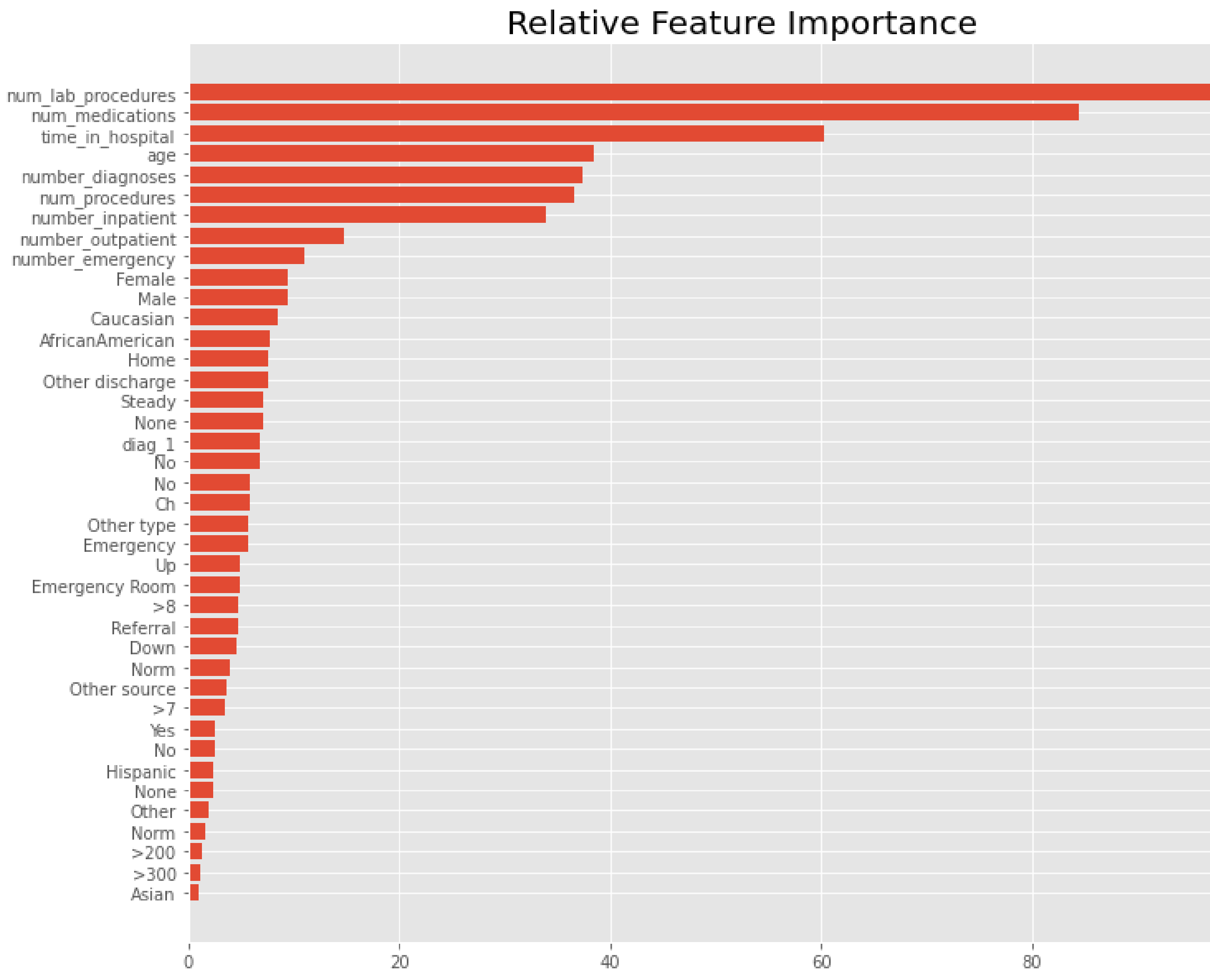
```
# create X (features) and y (response)
X = data.drop(['readmitted'], axis=1)
```

```
y = data['readmitted']
```

```
# split X and y into cross-validation (85%) and testing (15%) data sets
from sklearn.model_selection import train_test_split
X_cv, X_test, y_cv, y_test = train_test_split(X, y, test_size=0.15)
```

```
# fit Random Forest model to the cross-validation data
from sklearn.ensemble import RandomForestClassifier
forest = RandomForestClassifier()
forest.fit(X_cv, y_cv)
importances = forest.feature_importances_

# make importance relative to the max importance
feature_importance = 100.0 * (importances / importances.max())
sorted_idx = np.argsort(feature_importance)
feature_names = list(X_cv.columns.values)
feature_names_sort = [feature_names[indice] for indice in sorted_idx]
pos = np.arange(sorted_idx.shape[0]) + .5
print ('Top 10 features are: ')
for feature in feature_names_sort[::-1][:10]:
    print (feature)

# plot the result
plt.figure(figsize=(12, 10))
plt.barh(pos, feature_importance[sorted_idx], align='center')
plt.yticks(pos, feature_names_sort)
plt.title('Relative Feature Importance', fontsize=20)
plt.show()
```

```
Top 10 features are:
num_lab_procedures
num_medications
time_in_hospital
age
number_diagnoses
num_procedures
number_inpatient
number_outpatient
number_emergency
Female
```



```
# make a smaller feature set which only contains the top 10 features
X_cv_top10 = X_cv[['time_in_hospital', 'num_lab_procedures', 'num_procedures', 'num_medications', 'n
           'number_inpatient','number_outpatient','number_emergency','Female','age']]
X_test_top10 = X_test[['time_in_hospital', 'num_lab_procedures', 'num_procedures', 'num_medications'
           'number_inpatient','number_outpatient','number_emergency','Female','age']]
data.dtypes
```

```
age                        int64
diag_1                     int64
readmitted                 int64
AfricanAmerican            uint8
Asian                      uint8
Caucasian                  uint8
Hispanic                   uint8
Other                      uint8
Female                     uint8
Male                       uint8
>200                       uint8
>300                       uint8
None                       uint8
Norm                       uint8
>7                         uint8
>8                         uint8
None                       uint8
Norm                       uint8
Down                       uint8
No                         uint8
Steady                     uint8
Up                         uint8
Ch                         uint8
No                         uint8
No                         uint8
Yes                        uint8
Home                       uint8
Other discharge            uint8
Emergency Room             uint8
Other source               uint8
Referral                   uint8
Emergency                  uint8
Other type                 uint8
time_in_hospital         float64
num_lab_procedures       float64
num_procedures           float64
num_medications          float64
number_diagnoses         float64
number_inpatient         float64
number_emergency         float64
number_outpatient        float64
dtype: object
```

Model Selection

Compare the performance of three machine learning algorithms: Random Forest, Naive Bayes, and Logistic R

Select the best model using 10-fold cross validation. The metric that will be using is the accuracy of predictio

```
from sklearn.model_selection import cross_val_score
```

```
# Random Forest
from sklearn.ensemble import RandomForestClassifier
clf1 = RandomForestClassifier()
RF_score = cross_val_score(clf1, X_cv_top10, y_cv, cv=10, scoring='accuracy').mean()
RF_score
```

```
0.5893984075709607
```

```
# Naive Bayes
from sklearn.naive_bayes import GaussianNB
clf2 = GaussianNB()
NB_score = cross_val_score(clf2, X_cv_top10, y_cv, cv=10, scoring='accuracy').mean()
NB_score
```

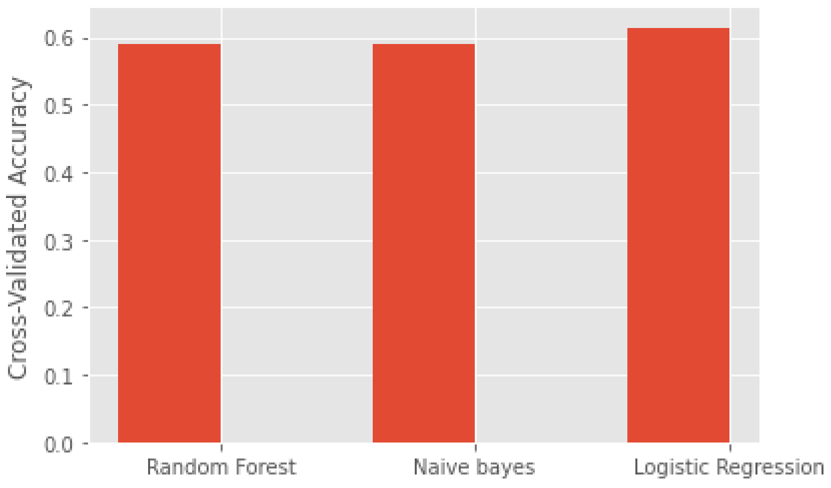
```
0.5892709345949001
```

```
# Logistic Regression
from sklearn.linear_model import LogisticRegression
clf3 = LogisticRegression()
LR_score = cross_val_score(clf3, X_cv_top10, y_cv, cv=10, scoring='accuracy').mean()
LR_score
```

```
0.614410889658734
```

```
# plot and compare the scores
# LR outperforms the other two a little bit
x_axis = np.arange(3)
y_axis = [RF_score, NB_score, LR_score]
plt.bar(x_axis, y_axis, width=0.4)
plt.xticks(x_axis + 0.4/2., ('Random Forest', 'Naive bayes', 'Logistic Regression'))
plt.ylabel('Cross-Validated Accuracy')
```

```
Text(0, 0.5, 'Cross-Validated Accuracy')
```



```
#  DecisionTree
from sklearn.tree import DecisionTreeClassifier
clf4 = DecisionTreeClassifier(random_state=0,max_depth=32, criterion = "entropy", min_samples_split=
De_score = cross_val_score(clf4, X_cv_top10, y_cv, cv=10, scoring='accuracy').mean()
De_score
```

```
0.553728205098204
```

```
# k means
from sklearn.neighbors import KNeighborsClassifier
clf5 =  KNeighborsClassifier(12)
Kn_score = cross_val_score(clf5, X_cv_top10, y_cv, cv=10, scoring='accuracy').mean()
Kn_score
```

```
0.5888757784444858
```

```
# neural network keras

import keras
from tensorflow.python.keras.layers import Dense
from tensorflow.python.keras import Sequential

classifier = Sequential()
classifier.add(Dense(input_shape=(10,), units=6, kernel_initializer='random_uniform', activation='re
classifier.add(Dense(units=10, kernel_initializer='random_uniform', activation='relu'))
classifier.add(Dense(units=15, kernel_initializer='random_uniform', activation='relu'))
classifier.add(Dense(units=1, kernel_initializer='random_uniform', activation='sigmoid'))
classifier.compile(optimizer='adam', loss='binary_crossentropy', metrics =['accuracy'])
classifier.fit(X_cv_top10, y_cv, batch_size=10 , epochs=3)

y_pred_nn = classifier.predict(X_test_top10)
y_pred_nn = [1 if y > 0.5 else 0 for y in y_pred_nn]


from sklearn.metrics import accuracy_score

acc1 = accuracy_score(y_test, y_pred_nn)

acc1
```

```
Epoch 1/3
8335/8335 [==============================] - 12s 1ms/step - loss: 0.6608 - accuracy: 0.6061
Epoch 2/3
8335/8335 [==============================] - 11s 1ms/step - loss: 0.6563 - accuracy: 0.6125
Epoch 3/3
8335/8335 [==============================] - 11s 1ms/step - loss: 0.6554 - accuracy: 0.6153
0.6231982594506391
```

other solution for classtering this dataset

https://www.kaggle.com/iabhishekofficial/prediction-on-hospital-readmission/notebook link

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