Diabetes Patient Readmitted Prediction

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1 Diabetes Patient Readmitted Prediction

1.0.1 Introduction

The goal of this project is to develop a pattern recognition system that operates on a given real-world dataset.

1.0.2 Dataset

Our dataset is: Diabetes 130-US hospitals for years 1999-2008 Data Set.

Source: https://archive.ics.uci.edu/ml/datasets/Diabetes+130-US+hospitals+for+years+1999-2008

The dataset represents 10 years (1999-2008) of clinical care at 130 US hospitals and integrated delivery networks. It includes over 50 features representing patient and hospital outcomes. Information was extracted from the database for encounters that satisfied the following criteria. 1. It is an inpatient encounter (a hospital admission). 2. It is a diabetic encounter, that is, one during which any kind of diabetes was entered to the system as a diagnosis. 3. The length of stay was at least 1 day and at most 14 days. 4. Laboratory tests were performed during the encounter. 5. Medications were administered during the encounter.

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

The last attribute is our target, indicating the days to inpatient readmission: * "<30" if the patient was readmitted in less than 30 days * ">30" if the patient was readmitted in more than 30 days * "No" for no record of readmission.

This problem is then a 3-class classification problem.

1.0.3 Libraries Import

[234]:
```
import numpy as np
import pandas as pd

import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
```

```
plt.style.use('ggplot')

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn import metrics
from sklearn.model_selection import GridSearchCV
from sklearn.model_selection import RandomizedSearchCV
from sklearn.model_selection import cross_val_score
from sklearn.metrics import confusion_matrix
from sklearn.metrics import roc_curve, auc
from sklearn.metrics import classification_report

from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier
```

1.0.4 Data Import

[143]:
```
df = pd.read_csv("diabetic_data.csv")
```

1.0.5 Data Description

Data Header

[115]:
```
df.head()
```

[115]:
```
   encounter_id  patient_nbr             race  gender      age weight  \
0       2278392      8222157        Caucasian  Female   [0-10)      ?
1        149190     55629189        Caucasian  Female  [10-20)      ?
2         64410     86047875  AfricanAmerican  Female  [20-30)      ?
3        500364     82442376        Caucasian    Male  [30-40)      ?
4         16680     42519267        Caucasian    Male  [40-50)      ?

   admission_type_id  discharge_disposition_id  admission_source_id  \
0                  6                        25                    1
1                  1                         1                    7
2                  1                         1                    7
3                  1                         1                    7
4                  1                         1                    7

   time_in_hospital  … citoglipton insulin  glyburide-metformin  \
0                 1  …          No      No                   No
1                 3  …          No      Up                   No
2                 2  …          No      No                   No
3                 2  …          No      Up                   No
```

```
4                  1  …          No  Steady                 No

   glipizide-metformin  glimepiride-pioglitazone  metformin-rosiglitazone  \
0                   No                        No                       No
1                   No                        No                       No
2                   No                        No                       No
3                   No                        No                       No
4                   No                        No                       No

   metformin-pioglitazone  change diabetesMed readmitted
0                      No      No          No         NO
1                      No      Ch         Yes        >30
2                      No      No         Yes         NO
3                      No      Ch         Yes         NO
4                      No      Ch         Yes         NO

[5 rows x 50 columns]
```

Data Types

[116]:
```
df.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
```

- 101766 data points (examples)
- 50 features, the last one `readmitted` is our target
- There are some missing data, but `df.info()` does not show them
- The features are either integer ot object (string) type.

Statistical Analysis

[117]:
```
df.describe()
```

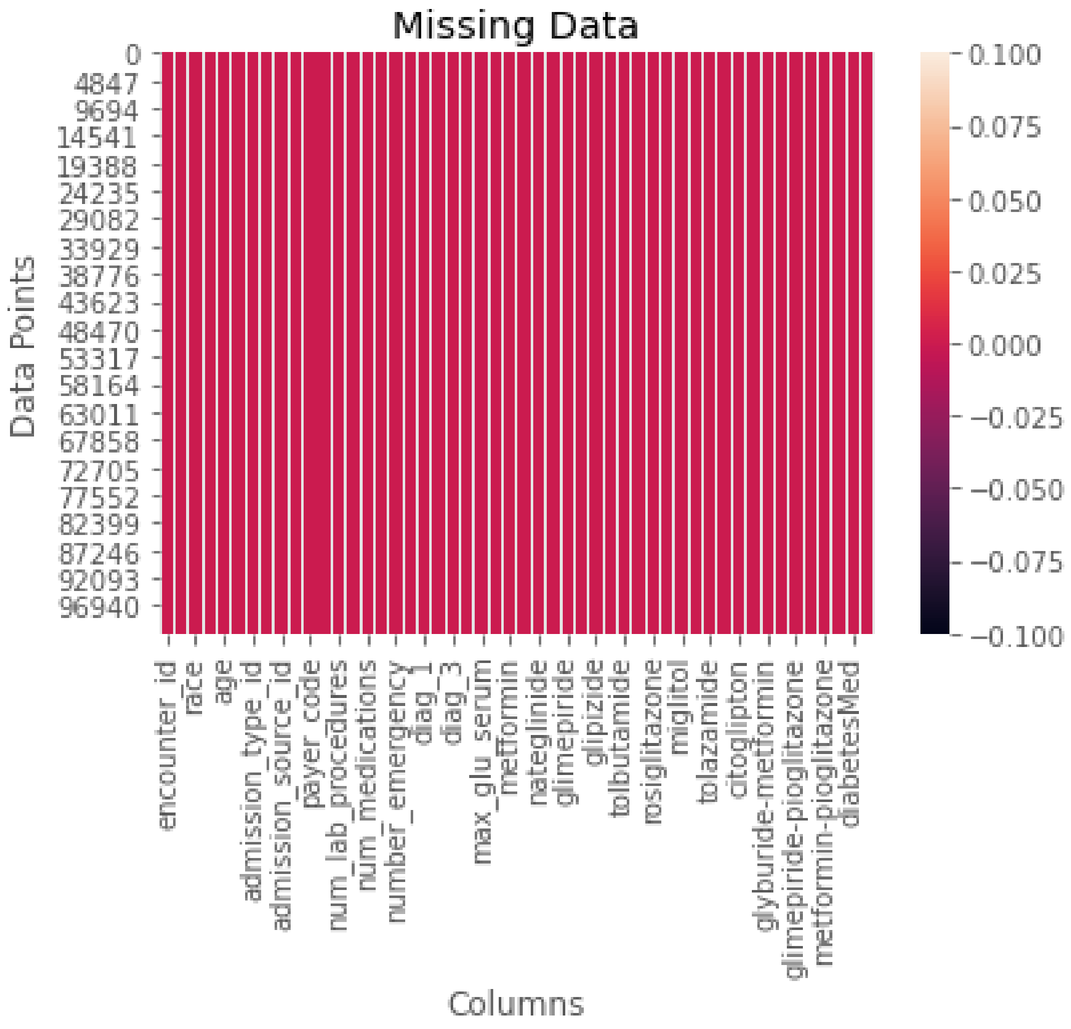
[117]:
```
       encounter_id   patient_nbr  admission_type_id  \
count  1.017660e+05  1.017660e+05      101766.000000
mean   1.652016e+08  5.433040e+07           2.024006
std    1.026403e+08  3.869636e+07           1.445403
min    1.252200e+04  1.350000e+02           1.000000
25%    8.496119e+07  2.341322e+07           1.000000
50%    1.523890e+08  4.550514e+07           1.000000
```

```
75%    2.302709e+08  8.754595e+07           3.000000
max    4.438672e+08  1.895026e+08           8.000000

       discharge_disposition_id  admission_source_id  time_in_hospital  \
count             101766.000000        101766.000000     101766.000000
mean                   3.715642             5.754437          4.395987
std                    5.280166             4.064081          2.985108
min                    1.000000             1.000000          1.000000
25%                    1.000000             1.000000          2.000000
50%                    1.000000             7.000000          4.000000
75%                    4.000000             7.000000          6.000000
max                   28.000000            25.000000         14.000000

       num_lab_procedures  num_procedures  num_medications  number_outpatient  \
count       101766.000000   101766.000000    101766.000000      101766.000000
mean            43.095641        1.339730        16.021844           0.369357
std             19.674362        1.705807         8.127566           1.267265
min              1.000000        0.000000         1.000000           0.000000
25%             31.000000        0.000000        10.000000           0.000000
50%             44.000000        1.000000        15.000000           0.000000
75%             57.000000        2.000000        20.000000           0.000000
max            132.000000        6.000000        81.000000          42.000000

       number_emergency  number_inpatient  number_diagnoses
count     101766.000000     101766.000000     101766.000000
mean           0.197836          0.635566          7.422607
std            0.930472          1.262863          1.933600
min            0.000000          0.000000          1.000000
25%            0.000000          0.000000          6.000000
50%            0.000000          0.000000          8.000000
75%            0.000000          1.000000          9.000000
max           76.000000         21.000000         16.000000
```

Missing Data Points

[118]:
```
sns.heatmap(df.isnull()).set(title = 'Missing Data', xlabel = 'Columns', ylabel␣
 ↪= 'Data Points')
```

[118]:
```
[Text(33.0, 0.5, 'Data Points'),
 Text(0.5, 14.09375, 'Columns'),
 Text(0.5, 1.0, 'Missing Data')]
```



[119]:
```
#names of all features
print(list(df))
```

```
['encounter_id', 'patient_nbr', 'race', 'gender', 'age', 'weight',
'admission_type_id', 'discharge_disposition_id', 'admission_source_id',
'time_in_hospital', 'payer_code', 'medical_specialty', 'num_lab_procedures',
'num_procedures', 'num_medications', 'number_outpatient', 'number_emergency',
'number_inpatient', 'diag_1', 'diag_2', 'diag_3', 'number_diagnoses',
'max_glu_serum', 'A1Cresult', 'metformin', 'repaglinide', 'nateglinide',
'chlorpropamide', 'glimepiride', 'acetohexamide', 'glipizide', 'glyburide',
'tolbutamide', 'pioglitazone', 'rosiglitazone', 'acarbose', 'miglitol',
'troglitazone', 'tolazamide', 'examide', 'citoglipton', 'insulin', 'glyburide-
metformin', 'glipizide-metformin', 'glimepiride-pioglitazone', 'metformin-
rosiglitazone', 'metformin-pioglitazone', 'change', 'diabetesMed', 'readmitted']
```

It looks like our dataset does not store null values as `Nan`, and uses some other characters to refere to different missing values. A full description of each feature in the dataset, and the percentage of missing values can be found on the following links: * Features description & missing data percentages: https://www.hindawi.com/journals/bmri/2014/781670/tab1/ * Values of the primary diagnosis: https://www.hindawi.com/journals/bmri/2014/781670/tab2/ * Distribution of variable values: https://www.hindawi.com/journals/bmri/2014/781670/tab3/

Later, we will use `df.feature_name.unique()` & `df.groupby(['feature_name']).count()` to further examine the features which have missing datapoints.

Notice that in the data secription it is mentioned that there are ~70,000 data points, while there is ~100,000 in our dataset, which means there are some duplicate records that need to be fixed.

1.0.6 Data Cleaning

Remove Duplicate Data Points There are 101,766 data points in the dataset, some of them are doublicates. We will use `patient_nbr` column as a reference, since it is a unique number given to each unique patient.

[144]:
```
#df.groupby(['patient_nbr']).count()
df['patient_nbr'].value_counts()
```

[144]:
```
88785891     40
43140906     28
23199021     23
1660293      23
88227540     23
             ..
71081460      1
30060018      1
67443444      1
141344240     1
93251151      1
Name: patient_nbr, Length: 71518, dtype: int64
```

There is only 71,518 unique patient records out of 101,766 in the dataset.

[145]:
```
df = df.drop_duplicates(subset=['patient_nbr'])
```

[122]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 71518 entries, 0 to 101765
Data columns (total 50 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   encounter_id              71518 non-null  int64
 1   patient_nbr               71518 non-null  int64
 2   race                      71518 non-null  object
 3   gender                    71518 non-null  object
 4   age                       71518 non-null  object
 5   weight                    71518 non-null  object
 6   admission_type_id         71518 non-null  int64
 7   discharge_disposition_id  71518 non-null  int64
 8   admission_source_id       71518 non-null  int64
 9   time_in_hospital          71518 non-null  int64
 10  payer_code                71518 non-null  object
 11  medical_specialty         71518 non-null  object
 12  num_lab_procedures        71518 non-null  int64
 13  num_procedures            71518 non-null  int64
 14  num_medications           71518 non-null  int64
 15  number_outpatient         71518 non-null  int64
 16  number_emergency          71518 non-null  int64
 17  number_inpatient          71518 non-null  int64
 18  diag_1                    71518 non-null  object
 19  diag_2                    71518 non-null  object
 20  diag_3                    71518 non-null  object
 21  number_diagnoses          71518 non-null  int64
 22  max_glu_serum             71518 non-null  object
 23  A1Cresult                 71518 non-null  object
 24  metformin                 71518 non-null  object
 25  repaglinide               71518 non-null  object
 26  nateglinide               71518 non-null  object
 27  chlorpropamide            71518 non-null  object
 28  glimepiride               71518 non-null  object
 29  acetohexamide             71518 non-null  object
 30  glipizide                 71518 non-null  object
 31  glyburide                 71518 non-null  object
 32  tolbutamide               71518 non-null  object
 33  pioglitazone              71518 non-null  object
 34  rosiglitazone             71518 non-null  object
 35  acarbose                  71518 non-null  object
 36  miglitol                  71518 non-null  object
 37  troglitazone              71518 non-null  object
 38  tolazamide                71518 non-null  object
 39  examide                   71518 non-null  object
 40  citoglipton               71518 non-null  object
 41  insulin                   71518 non-null  object
 42  glyburide-metformin       71518 non-null  object
 43  glipizide-metformin       71518 non-null  object
 44  glimepiride-pioglitazone  71518 non-null  object
 45  metformin-rosiglitazone   71518 non-null  object
 46  metformin-pioglitazone    71518 non-null  object
 47  change                    71518 non-null  object
 48  diabetesMed               71518 non-null  object
 49  readmitted                71518 non-null  object
dtypes: int64(13), object(37)
memory usage: 27.8+ MB
```

Now we only have 71518 rows in our dataset.

Remove Uninformative Features the uninformative features in the dataset (21 in total) were discarded as shown in the table below, due to either, a huge amount of missing sample values (>50%), or due to the fact that somefeatures are not relevant to classify the data towards our target (Like patient ID), or if the feature is compeletly unbalanced (>95% of data points have the same value for the feature).

Feature	Discarding Reasons
incounter_id	Irrelevant to our target (readmitted)
Patient_nbr	Irrelevant to our target (readmitted)
Weight	97% of samples are missing
Payer_code	Irrelevant to our target (readmitted)
Medical_speciality	53% of samples are missing
Repaglinide	>100K samples not using the drug
Nateglinide	>100K samples not using the drug
Chlorpropamide	>100K samples not using the drug
Acarbose	>100K samples not using the drug
Miglitol	>100K samples not using the drug
Troglitazone	Only 3 patients using the drug
Tolazamide	Only 39 patients using the drug
Examide	All patients not using the drug
Citoglipton	All patients not using the drug
Glyburide_metformin	>100K samples not using the drug
Glipizide_metfotmin	Only 13 patients using the drug
Glimepiride_pioglitazone	Only 1 patient using the drug
Metformin_rosiglitazone	Only 2 patients using the drug
Metformin_pioglitazone	Only 1 patient using the drug
Acetohexamide	Only 1 patient using the drug
tolbutamide	Only 23 patients using the drug

```
[146]: features_drop_list = ['encounter_id', 'patient_nbr', 'weight', 'payer_code',␣
        ↪'medical_specialty', 'repaglinide', 'nateglinide', 'chlorpropamide',␣
        ↪'acarbose', 'miglitol', 'troglitazone', 'tolazamide', 'examide',␣
        ↪'citoglipton', 'glyburide-metformin', 'glipizide-metformin',␣
        ↪'glimepiride-pioglitazone',␣
        ↪'metformin-rosiglitazone','metformin-pioglitazone', 'acetohexamide',␣
        ↪'tolbutamide']
```

```
[147]: df.drop(features_drop_list, axis=1,inplace=True)
```

```
[7]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 71518 entries, 0 to 101765
Data columns (total 29 columns):
 #   Column                    Non-Null Count  Dtype 
---  ------                    --------------  ----- 
 0   race                      71518 non-null  object
 1   gender                    71518 non-null  object
 2   age                       71518 non-null  object
 3   admission_type_id         71518 non-null  int64 
 4   discharge_disposition_id  71518 non-null  int64 
 5   admission_source_id       71518 non-null  int64 
 6   time_in_hospital          71518 non-null  int64 
 7   num_lab_procedures        71518 non-null  int64 
 8   num_procedures            71518 non-null  int64 
 9   num_medications           71518 non-null  int64 
 10  number_outpatient         71518 non-null  int64 
 11  number_emergency          71518 non-null  int64 
 12  number_inpatient          71518 non-null  int64 
 13  diag_1                    71518 non-null  object
 14  diag_2                    71518 non-null  object
 15  diag_3                    71518 non-null  object
 16  number_diagnoses          71518 non-null  int64 
 17  max_glu_serum             71518 non-null  object
 18  A1Cresult                 71518 non-null  object
 19  metformin                 71518 non-null  object
 20  glimepiride               71518 non-null  object
 21  glipizide                 71518 non-null  object
 22  glyburide                 71518 non-null  object
 23  pioglitazone              71518 non-null  object
 24  rosiglitazone             71518 non-null  object
 25  insulin                   71518 non-null  object
 26  change                    71518 non-null  object
 27  diabetesMed               71518 non-null  object
 28  readmitted                71518 non-null  object
dtypes: int64(11), object(18)
memory usage: 16.4+ MB
```

Diag Features Fix Diag features indicate the diagnoses of the cause of the patien's health problem.

- diag_1: First diagnose
- diag_2: Second diagnose
- diag_3: Third diagnose

They are coded in ICD-9 code (https://en.wikipedia.org/wiki/List_of_ICD-9_codes), resulting in hundreds of distinct categories. One way to simplify this, is by grouping every ICD-9 code value into one of 18 generic health problems, depending on the first 3 digits as following:

- List of ICD-9 codes 001–139: infectious and parasitic diseases
- List of ICD-9 codes 140–239: neoplasms
- List of ICD-9 codes 240–279: endocrine, nutritional and metabolic diseases, and immunity disorders

- List of ICD-9 codes 280–289: diseases of the blood and blood-forming organs
- List of ICD-9 codes 290–319: mental disorders
- List of ICD-9 codes 320–389: diseases of the nervous system and sense organs
- List of ICD-9 codes 390–459: diseases of the circulatory system
- List of ICD-9 codes 460–519: diseases of the respiratory system
- List of ICD-9 codes 520–579: diseases of the digestive system
- List of ICD-9 codes 580–629: diseases of the genitourinary system
- List of ICD-9 codes 630–679: complications of pregnancy, childbirth, and the puerperium
- List of ICD-9 codes 680–709: diseases of the skin and subcutaneous tissue
- List of ICD-9 codes 710–739: diseases of the musculoskeletal system and connective tissue
- List of ICD-9 codes 740–759: congenital anomalies
- List of ICD-9 codes 760–779: certain conditions originating in the perinatal period
- List of ICD-9 codes 780–799: symptoms, signs, and ill-defined conditions
- List of ICD-9 codes 800–999: injury and poisoning
- List of ICD-9 codes E and V codes: external causes of injury and supplemental classification

After that we will fill the missing values with E and V codes

[148]:
```
#start by setting all values containing E or V into 0 (as one category)
df.loc[df['diag_1'].str.contains('V',na=False,case=False), 'diag_1'] = 0
df.loc[df['diag_1'].str.contains('E',na=False,case=False), 'diag_1'] = 0
df.loc[df['diag_2'].str.contains('V',na=False,case=False), 'diag_2'] = 0
df.loc[df['diag_2'].str.contains('E',na=False,case=False), 'diag_2'] = 0
df.loc[df['diag_3'].str.contains('V',na=False,case=False), 'diag_3'] = 0
df.loc[df['diag_3'].str.contains('E',na=False,case=False), 'diag_3'] = 0

#setting all missing values into -1
df['diag_1'] = df['diag_1'].replace('?', -1)
df['diag_2'] = df['diag_2'].replace('?', -1)
df['diag_3'] = df['diag_3'].replace('?', -1)

#No all diag values can be converted into numeric values
df['diag_1'] = df['diag_1'].astype(float)
df['diag_2'] = df['diag_2'].astype(float)
df['diag_3'] = df['diag_3'].astype(float)
```

[154]:
```
#Now we will reduce the number of categories in diag features according to␣
 ↪ICD-9 code
#(Missing values will be grouped as E & V values)
df['diag_1'].loc[(df['diag_1']>=1) & (df['diag_1']< 140)] = 1
df['diag_1'].loc[(df['diag_1']>=140) & (df['diag_1']< 240)] = 2
df['diag_1'].loc[(df['diag_1']>=240) & (df['diag_1']< 280)] = 3
df['diag_1'].loc[(df['diag_1']>=280) & (df['diag_1']< 290)] = 4
df['diag_1'].loc[(df['diag_1']>=290) & (df['diag_1']< 320)] = 5
df['diag_1'].loc[(df['diag_1']>=320) & (df['diag_1']< 390)] = 6
df['diag_1'].loc[(df['diag_1']>=390) & (df['diag_1']< 460)] = 7
df['diag_1'].loc[(df['diag_1']>=460) & (df['diag_1']< 520)] = 8
df['diag_1'].loc[(df['diag_1']>=520) & (df['diag_1']< 580)] = 9
```

```
df['diag_1'].loc[(df['diag_1']>=580) & (df['diag_1']< 630)] = 10
df['diag_1'].loc[(df['diag_1']>=630) & (df['diag_1']< 680)] = 11
df['diag_1'].loc[(df['diag_1']>=680) & (df['diag_1']< 710)] = 12
df['diag_1'].loc[(df['diag_1']>=710) & (df['diag_1']< 740)] = 13
df['diag_1'].loc[(df['diag_1']>=740) & (df['diag_1']< 760)] = 14
df['diag_1'].loc[(df['diag_1']>=760) & (df['diag_1']< 780)] = 15
df['diag_1'].loc[(df['diag_1']>=780) & (df['diag_1']< 800)] = 16
df['diag_1'].loc[(df['diag_1']>=800) & (df['diag_1']< 1000)] = 17
df['diag_1'].loc[(df['diag_1']==-1)] = 0

df['diag_2'].loc[(df['diag_2']>=1) & (df['diag_2']< 140)] = 1
df['diag_2'].loc[(df['diag_2']>=140) & (df['diag_2']< 240)] = 2
df['diag_2'].loc[(df['diag_2']>=240) & (df['diag_2']< 280)] = 3
df['diag_2'].loc[(df['diag_2']>=280) & (df['diag_2']< 290)] = 4
df['diag_2'].loc[(df['diag_2']>=290) & (df['diag_2']< 320)] = 5
df['diag_2'].loc[(df['diag_2']>=320) & (df['diag_2']< 390)] = 6
df['diag_2'].loc[(df['diag_2']>=390) & (df['diag_2']< 460)] = 7
df['diag_2'].loc[(df['diag_2']>=460) & (df['diag_2']< 520)] = 8
df['diag_2'].loc[(df['diag_2']>=520) & (df['diag_2']< 580)] = 9
df['diag_2'].loc[(df['diag_2']>=580) & (df['diag_2']< 630)] = 10
df['diag_2'].loc[(df['diag_2']>=630) & (df['diag_2']< 680)] = 11
df['diag_2'].loc[(df['diag_2']>=680) & (df['diag_2']< 710)] = 12
df['diag_2'].loc[(df['diag_2']>=710) & (df['diag_2']< 740)] = 13
df['diag_2'].loc[(df['diag_2']>=740) & (df['diag_2']< 760)] = 14
df['diag_2'].loc[(df['diag_2']>=760) & (df['diag_2']< 780)] = 15
df['diag_2'].loc[(df['diag_2']>=780) & (df['diag_2']< 800)] = 16
df['diag_2'].loc[(df['diag_2']>=800) & (df['diag_2']< 1000)] = 17
df['diag_2'].loc[(df['diag_2']==-1)] = 0

df['diag_3'].loc[(df['diag_3']>=1) & (df['diag_3']< 140)] = 1
df['diag_3'].loc[(df['diag_3']>=140) & (df['diag_3']< 240)] = 2
df['diag_3'].loc[(df['diag_3']>=240) & (df['diag_3']< 280)] = 3
df['diag_3'].loc[(df['diag_3']>=280) & (df['diag_3']< 290)] = 4
df['diag_3'].loc[(df['diag_3']>=290) & (df['diag_3']< 320)] = 5
df['diag_3'].loc[(df['diag_3']>=320) & (df['diag_3']< 390)] = 6
df['diag_3'].loc[(df['diag_3']>=390) & (df['diag_3']< 460)] = 7
df['diag_3'].loc[(df['diag_3']>=460) & (df['diag_3']< 520)] = 8
df['diag_3'].loc[(df['diag_3']>=520) & (df['diag_3']< 580)] = 9
df['diag_3'].loc[(df['diag_3']>=580) & (df['diag_3']< 630)] = 10
df['diag_3'].loc[(df['diag_3']>=630) & (df['diag_3']< 680)] = 11
df['diag_3'].loc[(df['diag_3']>=680) & (df['diag_3']< 710)] = 12
df['diag_3'].loc[(df['diag_3']>=710) & (df['diag_3']< 740)] = 13
df['diag_3'].loc[(df['diag_3']>=740) & (df['diag_3']< 760)] = 14
df['diag_3'].loc[(df['diag_3']>=760) & (df['diag_3']< 780)] = 15
df['diag_3'].loc[(df['diag_3']>=780) & (df['diag_3']< 800)] = 16
df['diag_3'].loc[(df['diag_3']>=800) & (df['diag_3']< 1000)] = 17
df['diag_3'].loc[(df['diag_3']==-1)] = 0
```

```
/home/trojan/miniconda3/envs/ds/lib/python3.8/site-
packages/pandas/core/indexing.py:671: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-
docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  self._setitem_with_indexer(indexer, value)
```

[161]:
```
#check the results
df.diag_1.unique()
```

[161]:
```
array([ 3., 11.,  1.,  2.,  7.,  8., 17., 12., 13.,  9.,  0., 16., 10.,
        5.,  6.,  4., 14.])
```

Race Feature Fix Here we will replace the missing data points values with ‘Other’ category, as most likely people who skip filling their race have done that because they couldn’t find their race listed within the options.

[163]:
```
df['race'] = df['race'].replace('?', 'Other')
```

[164]:
```
df.race.value_counts()
```

[164]:
```
Caucasian          53491
AfricanAmerican    12887
Other               3126
Hispanic            1517
Asian                497
Name: race, dtype: int64
```

Gender Feature Fix

[166]:
```
df.gender.value_counts()
```

[166]:
```
Female             38025
Male               33490
Unknown/Invalid        3
Name: gender, dtype: int64
```

Here we have just 3 values that are Invalid, as a result we will change them into `Female`, which is the mod for this feature.

[167]:
```
df['gender'] = df['gender'].replace('Unknown/Invalid', 'Female')
df.gender.value_counts()
```

[167]:
```
Female    38028
Male      33490
Name: gender, dtype: int64
```

Now we can easliy change Male/Female into 1/0

[170]:
```
df['gender'] = df['gender'].replace('Male', 1)
df['gender'] = df['gender'].replace('Female', 0)
df.gender.value_counts()
```

[170]:
```
0    38028
1    33490
Name: gender, dtype: int64
```

Age Feature Fix For age, we have 10 categories, each represents 10 years range from [0-10] to [90-100]. We will replace those with the middle age for each age range: for example (0,10] will be repleased with 5; (60, 70] will be replaces by 65; and so on.

[168]:
```
df.age.value_counts()
```

[168]:
```
[70-80)     18210
[60-70)     15960
[50-60)     12466
[80-90)     11589
[40-50)      6878
[30-40)      2699
[90-100)     1900
[20-30)      1127
[10-20)       535
[0-10)        154
Name: age, dtype: int64
```

[169]:
```
for i in range(0,10):
    df['age'] = df['age'].replace('['+str(10*i)+'-'+str(10*(i+1))+')', i*10+5)
df['age'].value_counts()
```

[169]:
```
75    18210
65    15960
55    12466
85    11589
45     6878
35     2699
95     1900
25     1127
15      535
5       154
Name: age, dtype: int64
```

max_glue_serum Feature Fix We want to make the following changes:

Raw Values	New Values
non	0
norm	1
>200	2
>300	3

[171]:
```
df.max_glu_serum.value_counts()
```

[171]:
```
None    68062
Norm     1731
>200      969
>300      756
Name: max_glu_serum, dtype: int64
```

[172]:
```
df['max_glu_serum']=df['max_glu_serum'].replace("None", 0)
df['max_glu_serum']=df['max_glu_serum'].replace("Norm", 1)
df['max_glu_serum']=df['max_glu_serum'].replace(">200", 2)
df['max_glu_serum']=df['max_glu_serum'].replace(">300", 3)
df.max_glu_serum.value_counts()
```

[172]:
```
0    68062
1     1731
2      969
3      756
Name: max_glu_serum, dtype: int64
```

A1Cresult Feature Fix We want to make the following changes:

Raw Values	New Values
None	0
Norm	1
>7	2
>8	3

[173]:
```
df.A1Cresult.value_counts()
```

[173]:
```
None    58532
>8       6304
Norm     3791
>7       2891
Name: A1Cresult, dtype: int64
```

[174]:
```
df['A1Cresult']=df['A1Cresult'].replace("None", 0)
df['A1Cresult']=df['A1Cresult'].replace("Norm", 1)
```

```
df['A1Cresult']=df['A1Cresult'].replace(">7", 2)
df['A1Cresult']=df['A1Cresult'].replace(">8", 3)
```

```
[174]: 0    68062
       1     1731
       2      969
       3      756
       Name: max_glu_serum, dtype: int64
```

```
[175]: df.A1Cresult.value_counts()
```

```
[175]: 0    58532
       3     6304
       1     3791
       2     2891
       Name: A1Cresult, dtype: int64
```

Drugs Features Fix We still have 7 features, each one represents the change in the patient's dusage of a specific drug, during hospital encounter. Those 7 drugs are the following: * metformin
* glimepiride
* glipizide
* glyburide
* pioglitazone
* rosiglitazone
* insulin

For all those drugs, we want to apply the following changes, since the values are ordinal categories:

Raw Values	New Values
No	0
Down	1
Steady	2
Up	3

```
[176]: #df.metformin.value_counts()
       #df.glimepiride.value_counts()
       #df.glipizide.value_counts()
       #df.glyburide.value_counts()
       #df.pioglitazone.value_counts()
       #df.rosiglitazone.value_counts()
       df.insulin.value_counts()
```

```
[176]: No        34921
       Steady    22129
       Down       7505
       Up         6963
```

```
Name: insulin, dtype: int64
```

```
[177]: drug_list = ['metformin', 'glimepiride', 'glipizide', 'glyburide',␣
        ↪'pioglitazone', 'rosiglitazone', 'insulin']
       for i in drug_list:
           df[i] = df[i].replace('No', 0)
           df[i] = df[i].replace('Steady', 2)
           df[i] = df[i].replace('Down', 1)
           df[i] = df[i].replace('Up', 3)
```

```
[178]: #df.metformin.value_counts()
       #df.glimepiride.value_counts()
       #df.glipizide.value_counts()
       #df.glyburide.value_counts()
       #df.pioglitazone.value_counts()
       #df.rosiglitazone.value_counts()
       df.insulin.value_counts()
```

```
[178]: 0    34921
       2    22129
       1     7505
       3     6963
       Name: insulin, dtype: int64
```

Change Feature Fix We want to change the values of the feature `change` from string into binary numeric.

```
[179]: df.change.value_counts()
```

```
[179]: No     39494
       Ch     32024
       Name: change, dtype: int64
```

```
[180]: df['change']=df['change'].replace('No', 0)
       df['change']=df['change'].replace('Ch', 1)
       df.change.value_counts()
```

```
[180]: 0    39494
       1    32024
       Name: change, dtype: int64
```

DiabetesMed Feature Fix We want to change the values of the feature `diabetesMed` from string into binary numeric.

```
[181]: df.diabetesMed.value_counts()
```

[181]:
```
Yes    54319
No     17199
Name: diabetesMed, dtype: int64
```

[182]:
```
df['diabetesMed']=df['diabetesMed'].replace('Yes', 1)
df['diabetesMed']=df['diabetesMed'].replace('No', 0)
df.diabetesMed.value_counts()
```

[182]:
```
1    54319
0    17199
Name: diabetesMed, dtype: int64
```

Target Feature Fix The outcome we are looking at in the labels is whether the patient gets readmitted to the hospital within 30 days, after 30 days, or not readmitted again. The variable actually has <30, >30 and No Readmission categories.

[183]:
```
df.readmitted.value_counts()
```

[183]:
```
NO     42985
>30    22240
<30     6293
Name: readmitted, dtype: int64
```

Here we will use a simple encoding as following:

[185]:
```
df['readmitted']=df['readmitted'].replace('NO', 0)
df['readmitted']=df['readmitted'].replace('>30', 1)
df['readmitted']=df['readmitted'].replace('<30', 2)
df.readmitted.value_counts()
```

[185]:
```
0    42985
1    22240
2     6293
Name: readmitted, dtype: int64
```

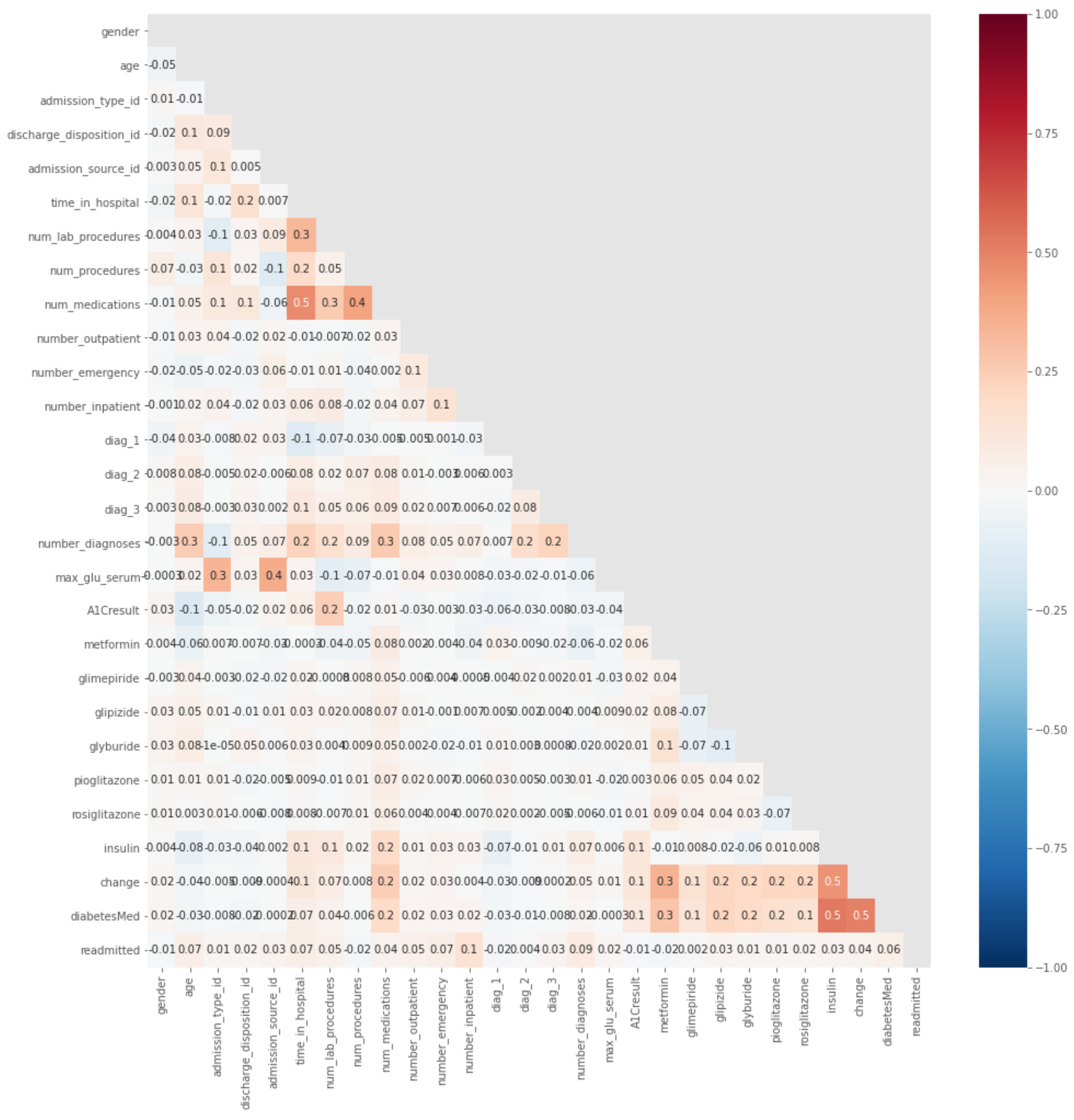
1.0.7 EDA

[186]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 71518 entries, 0 to 101765
Data columns (total 29 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   race                      71518 non-null  object
 1   gender                    71518 non-null  int64
 2   age                       71518 non-null  int64
 3   admission_type_id         71518 non-null  int64
 4   discharge_disposition_id  71518 non-null  int64
 5   admission_source_id       71518 non-null  int64
 6   time_in_hospital          71518 non-null  int64
 7   num_lab_procedures        71518 non-null  int64
 8   num_procedures            71518 non-null  int64
 9   num_medications           71518 non-null  int64
 10  number_outpatient         71518 non-null  int64
 11  number_emergency          71518 non-null  int64
 12  number_inpatient          71518 non-null  int64
 13  diag_1                    71518 non-null  float64
 14  diag_2                    71518 non-null  float64
 15  diag_3                    71518 non-null  float64
 16  number_diagnoses          71518 non-null  int64
 17  max_glu_serum             71518 non-null  int64
 18  A1Cresult                 71518 non-null  int64
 19  metformin                 71518 non-null  int64
 20  glimepiride               71518 non-null  int64
 21  glipizide                 71518 non-null  int64
 22  glyburide                 71518 non-null  int64
 23  pioglitazone              71518 non-null  int64
 24  rosiglitazone             71518 non-null  int64
 25  insulin                   71518 non-null  int64
 26  change                    71518 non-null  int64
 27  diabetesMed               71518 non-null  int64
 28  readmitted                71518 non-null  int64
dtypes: float64(3), int64(25), object(1)
memory usage: 16.4+ MB
```

Correlation Analysis Let's first check how correlated are our predectors

[188]:
```
matrix = np.triu(df.corr())
fig, ax = plt.subplots(figsize=(16,16))
sns.heatmap(df.corr(), annot=True, ax=ax, fmt='.1g', vmin=-1, vmax=1, center=␣
 ↪0, mask=matrix, cmap='RdBu_r')
plt.show()
```

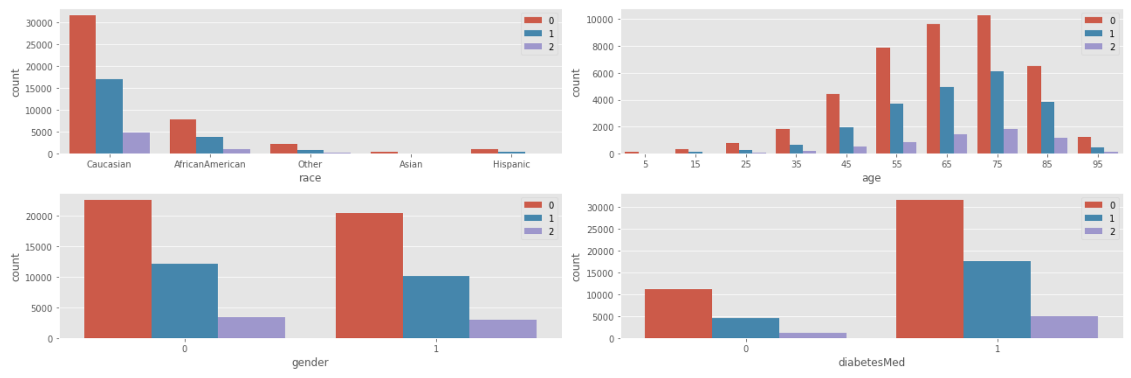


- The strongest correlations among the predectors are:
  - num_medications & time_in_hospital (corr = 0.5)
  - change & insulin (corr = 0.5)
  - change & diabetesMed (corr = 0.5)
  - diabetesMed & insulin (corr = 0.5)
- Also, our labels `readmitted` has in general week correlation with all predictors.

Patient Analysis

[189]:
```
fig = plt.figure(figsize=(18, 6))

ax1 = fig.add_subplot(2, 2, 1)
ax2 = fig.add_subplot(2, 2, 2)
```

```
ax3 = fig.add_subplot(2, 2, 3)
ax4 = fig.add_subplot(2, 2, 4)

sns.countplot(data=df, x='race', hue='readmitted', ax=ax1)
sns.countplot(data=df, x='age', hue='readmitted', ax=ax2)
sns.countplot(data=df, x='gender', hue='readmitted', ax=ax3)
sns.countplot(data=df, x='diabetesMed', hue='readmitted', ax=ax4)

ax1.legend(loc='upper right')
ax2.legend(loc='upper right')
ax3.legend(loc='upper right')
ax4.legend(loc='upper right')
plt.tight_layout()
plt.show()
# readmitted: 0 = No, 1 = >30, 2 = <30
```

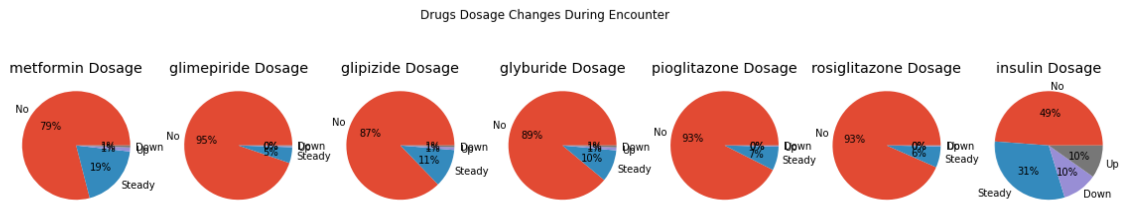


- readmittion has simmilar distripution across different races.
- Very few cases of readmition for youbnger patients (< 40).
- Females have slightly higher rate of no readmittion than males.
- readmittion has simmilar distripution for patients with and without prescribed diabetes medications prior to hospital encounter.

Drugs Analysis

[208]:
```
fig, ax = plt.subplots(1, 7,figsize=(20, 4), subplot_kw=dict(aspect="equal"))
ax[0].pie(df['metformin'].value_counts(), autopct='%1.0f%%', labels=['No',␣
↪'Steady', 'Up', 'Down'])
ax[0].set_title('metformin Dosage')
ax[1].pie(df['glimepiride'].value_counts(), autopct='%1.0f%%', labels=['No',␣
↪'Steady', 'Up', 'Down'])
ax[1].set_title('glimepiride Dosage')
ax[2].pie(df['glipizide'].value_counts(), autopct='%1.0f%%', labels=['No',␣
↪'Steady', 'Up', 'Down'])
ax[2].set_title('glipizide Dosage')
```

```
ax[3].pie(df['glyburide'].value_counts(), autopct='%1.0f%%', labels=['No',␣
↪'Steady', 'Up', 'Down'])
ax[3].set_title('glyburide Dosage')
ax[4].pie(df['pioglitazone'].value_counts(), autopct='%1.0f%%', labels=['No',␣
↪'Steady', 'Up', 'Down'])
ax[4].set_title('pioglitazone Dosage')
ax[5].pie(df['rosiglitazone'].value_counts(), autopct='%1.0f%%', labels=['No',␣
↪'Steady', 'Up', 'Down'])
ax[5].set_title('rosiglitazone Dosage')
ax[6].pie(df['insulin'].value_counts(), autopct='%1.0f%%', labels=['No',␣
↪'Steady', 'Down', 'Up'])
ax[6].set_title('insulin Dosage')

fig.suptitle('Drugs Dosage Changes During Encounter')
plt.show()
```

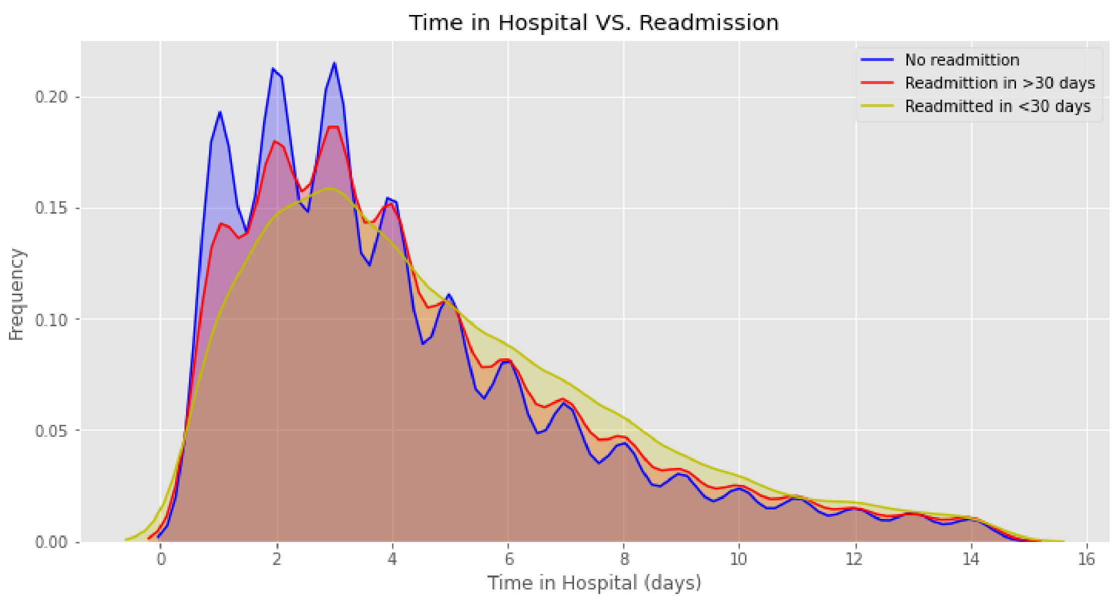


Except of insulin, the other drugs have very similar distripution.

Time in Hospital and Readmission

```
[212]: fig = plt.figure(figsize=(12,6))
ax=sns.kdeplot(df.loc[(df['readmitted'] == 0),'time_in_hospital'] ,␣
↪color='b',shade=True,label='No readmittion')
ax=sns.kdeplot(df.loc[(df['readmitted'] == 1),'time_in_hospital'] ,␣
↪color='r',shade=True, label='Readmittion in >30 days')
ax=sns.kdeplot(df.loc[(df['readmitted'] == 2),'time_in_hospital'] ,␣
↪color='y',shade=True, label='Readmitted in <30 days')
ax.set(xlabel='Time in Hospital (days)', ylabel='Frequency')
plt.title('Time in Hospital VS. Readmission')
```

```
[212]: Text(0.5, 1.0, 'Time in Hospital VS. Readmission')
```



The very similar distripution of time_in_hospital over the 3 classes reflects the very weak correlation between our targets (readmitted) and time_in_hospital predictor.

1.0.8 Data Pre-processing

Race Feature Encoding Race feature has catagorical values stored as strings ('Asian', … etc). Dummy coding scheme is used to encode the race feature. This categorical data encoding method transforms the categorical variable into an N-1 set of binary variables (also known as dummy variables).

[214]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 71518 entries, 0 to 101765
Data columns (total 29 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   race                      71518 non-null  object
 1   gender                    71518 non-null  int64
 2   age                       71518 non-null  int64
 3   admission_type_id         71518 non-null  int64
 4   discharge_disposition_id  71518 non-null  int64
 5   admission_source_id       71518 non-null  int64
 6   time_in_hospital          71518 non-null  int64
 7   num_lab_procedures        71518 non-null  int64
 8   num_procedures            71518 non-null  int64
 9   num_medications           71518 non-null  int64
 10  number_outpatient         71518 non-null  int64
 11  number_emergency          71518 non-null  int64
 12  number_inpatient          71518 non-null  int64
 13  diag_1                    71518 non-null  float64
 14  diag_2                    71518 non-null  float64
 15  diag_3                    71518 non-null  float64
 16  number_diagnoses          71518 non-null  int64
 17  max_glu_serum             71518 non-null  int64
 18  A1Cresult                 71518 non-null  int64
 19  metformin                 71518 non-null  int64
 20  glimepiride               71518 non-null  int64
 21  glipizide                 71518 non-null  int64
 22  glyburide                 71518 non-null  int64
 23  pioglitazone              71518 non-null  int64
 24  rosiglitazone             71518 non-null  int64
 25  insulin                   71518 non-null  int64
 26  change                    71518 non-null  int64
 27  diabetesMed               71518 non-null  int64
 28  readmitted                71518 non-null  int64
dtypes: float64(3), int64(25), object(1)
memory usage: 18.9+ MB
```

[215]:
```
df = pd.concat([df,pd.get_dummies(df['race'], prefix='race')], axis=1).
 ↪drop(['race'],axis=1)
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 71518 entries, 0 to 101765
Data columns (total 33 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   gender                    71518 non-null  int64
 1   age                       71518 non-null  int64
 2   admission_type_id         71518 non-null  int64
 3   discharge_disposition_id  71518 non-null  int64
 4   admission_source_id       71518 non-null  int64
 5   time_in_hospital          71518 non-null  int64
 6   num_lab_procedures        71518 non-null  int64
 7   num_procedures            71518 non-null  int64
 8   num_medications           71518 non-null  int64
 9   number_outpatient         71518 non-null  int64
 10  number_emergency          71518 non-null  int64
 11  number_inpatient          71518 non-null  int64
 12  diag_1                    71518 non-null  float64
 13  diag_2                    71518 non-null  float64
 14  diag_3                    71518 non-null  float64
 15  number_diagnoses          71518 non-null  int64
 16  max_glu_serum             71518 non-null  int64
 17  A1Cresult                 71518 non-null  int64
 18  metformin                 71518 non-null  int64
 19  glimepiride               71518 non-null  int64
 20  glipizide                 71518 non-null  int64
 21  glyburide                 71518 non-null  int64
 22  pioglitazone              71518 non-null  int64
 23  rosiglitazone             71518 non-null  int64
 24  insulin                   71518 non-null  int64
 25  change                    71518 non-null  int64
 26  diabetesMed               71518 non-null  int64
 27  readmitted                71518 non-null  int64
 28  race_AfricanAmerican      71518 non-null  uint8
 29  race_Asian                71518 non-null  uint8
 30  race_Caucasian            71518 non-null  uint8
 31  race_Hispanic             71518 non-null  uint8
 32  race_Other                71518 non-null  uint8
dtypes: float64(3), int64(25), uint8(5)
memory usage: 18.7 MB
```

Data Split

[216]:
```
y = df['readmitted']
X = df.drop(['readmitted'], axis=1)
```

[217]:
```
X_train, X_valtest, y_train, y_valtest = train_test_split(X, y, test_size=0.3,␣
 ↪random_state=101)
X_val, X_test, y_val, y_test = train_test_split(X_valtest, y_valtest,␣
 ↪test_size=0.5, random_state=101)
```

Now we have the following data subsets:

- Train data (X_train) and train labels (y_train) ==> 70%
- Validation data (X_val) and validation labels (y_val) ==> 15%
- Test data (X_test) and test labels (y)test) ==> 15%

Data Scaling We will scale the features in our subsets, in order to use them to train models that will benefit from feature scaling.

[218]:
```
sc_X = StandardScaler()

Xsc_train = sc_X.fit_transform(X_train)
Xsc_val = sc_X.fit_transform(X_val)
Xsc_test = sc_X.fit_transform(X_test)
```

1.0.9 Model Building

We will be testing a set of different classifiers, then we will pick the one with best performance, and apply hyperparameter tuning to improve its performance. The following classifiers are used: * Naive Bayes * KNN * SVM * Random Forest * Gradient Boosting

1.0.10 Initial Build

[220]:
```
#Naive Bayes
nbm = GaussianNB()
nbm.fit(X_train,y_train)
nbm_pred = nbm.predict(X_val)

#KNN
knn = KNeighborsClassifier()
knn.fit(Xsc_train,y_train)
knn_pred = knn.predict(Xsc_val)

#SVM
svm = SVC()
svm.fit(Xsc_train,y_train)
svm_pred = svm.predict(Xsc_val)

#Randon Forest
rfm = RandomForestClassifier()
rfm.fit(X_train,y_train)
rfm_pred = rfm.predict(X_val)

#Gradient Boosting
gbm = GradientBoostingClassifier()
gbm.fit(X_train,y_train)
gbm_pred = gbm.predict(X_val)
```

[225]:
```
#Results
print('\nGaussian Naive Bayes Performance:')
print('---------------------------------')
print('F1 Score        : ', metrics.f1_score(y_val, nbm_pred,average='micro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, nbm_pred))

print('\nK-Nearest Neighbor Initial Performance:')
print('---------------------------------------')
print('F1 Score        : ', metrics.f1_score(y_val, knn_pred,average='micro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, knn_pred))

print('\nSVM Initial Performance:')
print('------------------------')
print('F1 Score        : ', metrics.f1_score(y_val, svm_pred,average='micro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, svm_pred))

print('\nRandom Forest initial Performance:')
print('----------------------------------')
print('F1 Score        : ', metrics.f1_score(y_val, rfm_pred,average='micro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, rfm_pred))
```

```python
print('\nGradient Boost initial Performance:')
print('-----------------------------------')
print('F1 Score        : ', metrics.f1_score(y_val, gbm_pred,average='micro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, gbm_pred))
```

```
Gaussian Naive Bayes Performance:
---------------------------------
F1 Score        :  0.5798844146159582
Confusion Matrix:
  [[5296  927  178]
 [2404  834  152]
 [ 623  223   91]]

K-Nearest Neighbor Initial Performance:
---------------------------------------
F1 Score        :  0.5594705443698732
Confusion Matrix:
  [[5186 1176   39]
 [2552  798   40]
 [ 701  218   18]]

SVM Initial Performance:
------------------------
F1 Score        :  0.6068232662192393
Confusion Matrix:
  [[6156  243    2]
 [3035  353    2]
 [ 823  113    1]]

Random Forest initial Performance:
----------------------------------
F1 Score        :  0.6061707680835198
Confusion Matrix:
  [[5841  558    2]
 [2731  657    2]
 [ 755  177    5]]

Gradient Boost initial Performance:
-----------------------------------
F1 Score        :  0.610178970917226
Confusion Matrix:
  [[6043  349    9]
 [2888  493    9]
 [ 761  166   10]]
```

All models resulted in very close F1-Score, and similar confusion matrix, yet the best performant is gradient Boosting model, which is the one we pick to apply hyperparameter tuning next.

1.0.11 Gradiant Boosting Model Tuning

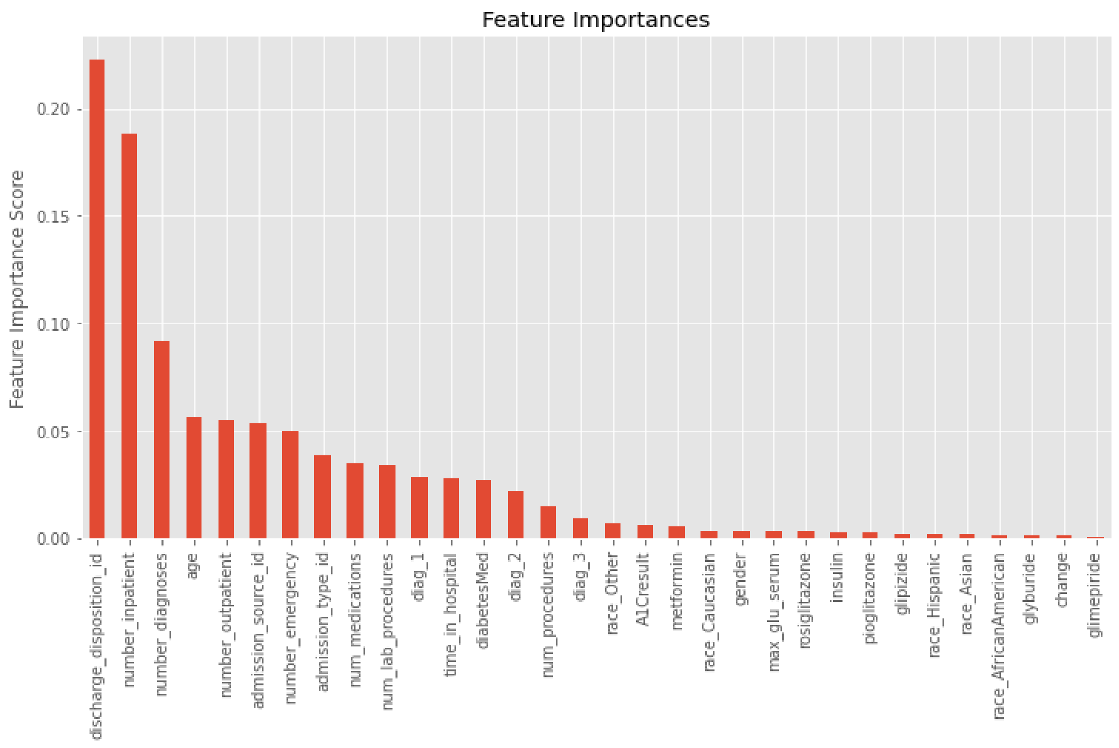
[241]:
```
#define a list that has all feature names
predictors = [x for x in X_train.columns]
```

Now, let's evaluate Baseline (default) GBM

[269]:
```
gbm0 = GradientBoostingClassifier()
gbm0.fit(X_train,y_train)
gbm0_pred = gbm0.predict(X_val)

print('\nGradient Boost [0] Performance:')
print('------------------------------------')
print('F1 Score micro        : ', metrics.f1_score(y_val,␣
 ↪gbm0_pred,average='micro'))
print('F1 Score macro        : ', metrics.f1_score(y_val,␣
 ↪gbm0_pred,average='macro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, gbm0_pred))

feat_imp = pd.Series(gbm0.feature_importances_, predictors).
 ↪sort_values(ascending=False)
fig = plt.figure(figsize=(12, 6))
feat_imp.plot(kind='bar', title='Feature Importances')
plt.ylabel('Feature Importance Score')
```

```
Gradient Boost [0] Performance:
-----------------------------------
F1 Score micro        :  0.6102721849366145
F1 Score macro        :  0.33267596183642495
Confusion Matrix:
  [[6043  349    9]
 [2888  493    9]
 [ 761  165   11]]
```

[269]:
```
Text(0, 0.5, 'Feature Importance Score')
```



HyperParameter tuning roadmap:

1. Decide a relatively higher value for learning rate and tune the number of estimators requried for that.
2. Tune the tree specific parameters (min_samples_split, min_samples_leaf, max_depth, max_features) for that learning rate
3. Tune subsample, and lower learning rate as much as possible computationally and increase the number of estimators accordingly.

Step 1 - Find the number of estimators for a high learning rate In order to decide on boosting parameters, we need to set some initial values of other parameters. Lets take the following values:

1. min_samples_split = 400 : This should be ~0.5-1% of total values. Since this is imbalanced multi-class problem, we'll take a small value from the range (our total sample points ~71k).
2. min_samples_leaf = 50 : Can be selected based on intuition. This is just used for preventing overfitting and again a small value because of imbalanced classes.
3. max_depth = 8 : Should be chosen (5-8) based on the number of observations and predictors. This has ~71K rows and 32 columns so lets take 8 here.
4. max_features = 'sqrt' : Its a general rule of thumb to start with square root.
5. subsample = 0.8 : This is a commonly used used start value

Please note that all the above are just initial estimates and will be tuned later. Lets take the default learning rate of 0.1 here and check the optimum number of trees for that. For this purpose, we can do a grid search and test out values from 20 to 80 in steps of 10.

[250]:
```
#1.0 - Grid seach on n_estimators
param_test1 = {'n_estimators':range(20,81,10)}
gsearch1 = GridSearchCV(estimator = GradientBoostingClassifier(learning_rate=0.
 ↪1,
                                                                                ␣
 ↪min_samples_split=400,
                                                                                ␣
 ↪min_samples_leaf=50,
                                                                                 max_depth=8,
                                                                                ␣
 ↪max_features='sqrt',
                                                                                 subsample=0.8,
                                                                                ␣
 ↪random_state=101), param_grid = param_test1,␣
 ↪scoring='f1_micro',n_jobs=4,iid=False, cv=5)
gsearch1.fit(X_train,y_train)
```

```
/home/trojan/miniconda3/envs/ds/lib/python3.8/site-
packages/sklearn/model_selection/_search.py:847: FutureWarning: The parameter
'iid' is deprecated in 0.22 and will be removed in 0.24.
  warnings.warn(
```

[250]:
```
GridSearchCV(cv=5,
             estimator=GradientBoostingClassifier(max_depth=8,
                                                  max_features='sqrt',
                                                  min_samples_leaf=50,
                                                  min_samples_split=400,
                                                  random_state=101,
                                                  subsample=0.8),
             iid=False, n_jobs=4,
             param_grid={'n_estimators': range(20, 81, 10)},
             scoring='f1_micro')
```

[254]:
```
gsearch1.best_params_, gsearch1.best_score_
```

[254]:
```
({'n_estimators': 70}, 0.6198314803619858)
```

So we got 70 as the optimal estimators for the 0.1 learning rate. Note that 70 is a reasonable value and can be used as it is. But it might not be the same in all cases. Other situations:

1. If the value is around 20, you might want to try lowering the learning rate to 0.05 and re-run grid search.
2. If the values are too high ~100, tuning the other parameters will take long time and you can try a higher learning rate.

Step 2 - Tune tree-specific parameters Now, lets move onto tuning the tree parameters. We will do this in 3 stages:

1. Tune max_depth and min_samples_split
2. Tune min_samples_leaf
3. Tune max_features

[255]:
```
#2.1 - Grid seach on max_depth and min_samples_split
param_test2 = {'max_depth':range(3,16,3), 'min_samples_split':
↪range(200,1001,200)}
gsearch2 = GridSearchCV(estimator = GradientBoostingClassifier(learning_rate=0.
↪1, n_estimators=70,
                                                    max_features='sqrt',␣
↪subsample=0.8, random_state=101),
                        param_grid = param_test2,␣
↪scoring='f1_micro',n_jobs=4,iid=False, cv=5)
gsearch2.fit(X_train,y_train)
```

```
/home/trojan/miniconda3/envs/ds/lib/python3.8/site-
packages/sklearn/model_selection/_search.py:847: FutureWarning: The parameter
'iid' is deprecated in 0.22 and will be removed in 0.24.
  warnings.warn(
```

[255]:
```
GridSearchCV(cv=5,
             estimator=GradientBoostingClassifier(max_features='sqrt',
                                                  n_estimators=70,
                                                  random_state=101,
                                                  subsample=0.8),
             iid=False, n_jobs=4,
             param_grid={'max_depth': range(3, 16, 3),
                         'min_samples_split': range(200, 1001, 200)},
             scoring='f1_micro')
```

[258]:
```
gsearch2.best_params_, gsearch2.best_score_
```

[258]:
```
({'max_depth': 12, 'min_samples_split': 800}, 0.6206105275287552)
```

[259]:
```
#2.2 - Grid seach on min_samples_leaf
param_test3 = {'min_samples_leaf':range(30,71,10)}
gsearch3 = GridSearchCV(estimator = GradientBoostingClassifier(learning_rate=0.
↪1, n_estimators=70,min_samples_split=800,
                                                            max_depth=12,␣
↪max_features='sqrt', subsample=0.8, random_state=101),
                        param_grid = param_test3,␣
↪scoring='f1_micro',n_jobs=4,iid=False, cv=5)
gsearch3.fit(X_train,y_train)
```

```
/home/trojan/miniconda3/envs/ds/lib/python3.8/site-
packages/sklearn/model_selection/_search.py:847: FutureWarning: The parameter
'iid' is deprecated in 0.22 and will be removed in 0.24.
  warnings.warn(
[259]: GridSearchCV(cv=5,
                    estimator=GradientBoostingClassifier(max_depth=12,
                                                         max_features='sqrt',
                                                         min_samples_split=800,
                                                         n_estimators=70,
                                                         random_state=101,
                                                         subsample=0.8),
                    iid=False, n_jobs=4,
                    param_grid={'min_samples_leaf': range(30, 71, 10)},
                    scoring='f1_micro')
```

```
[260]: gsearch3.best_params_, gsearch3.best_score_
```

```
[260]: ({'min_samples_leaf': 70}, 0.6203308750960945)
```

```
[261]: # 2.3 Grid seach on max_features
param_test4 = {'max_features':range(4,20,2)}
gsearch4 = GridSearchCV(estimator = GradientBoostingClassifier(learning_rate=0.
 ↪1, n_estimators=70,max_depth=12,
                            min_samples_split=800, min_samples_leaf=70,␣
 ↪subsample=0.8, random_state=101),
                       param_grid = param_test4,␣
 ↪scoring='f1_micro',n_jobs=4,iid=False, cv=5)
gsearch4.fit(X_train,y_train)
```

```
/home/trojan/miniconda3/envs/ds/lib/python3.8/site-
packages/sklearn/model_selection/_search.py:847: FutureWarning: The parameter
'iid' is deprecated in 0.22 and will be removed in 0.24.
  warnings.warn(
```

```
[261]: GridSearchCV(cv=5,
                    estimator=GradientBoostingClassifier(max_depth=12,
                                                         min_samples_leaf=70,
                                                         min_samples_split=800,
                                                         n_estimators=70,
                                                         random_state=101,
                                                         subsample=0.8),
                    iid=False, n_jobs=4, param_grid={'max_features': range(4, 20, 2)},
                    scoring='f1_micro')
```

```
[262]: gsearch4.best_params_, gsearch4.best_score_
```

```
[262]: ({'max_features': 18}, 0.6204906194859189)
```

```
[263]: #The best parameter values so far:
gsearch4.best_estimator_
```

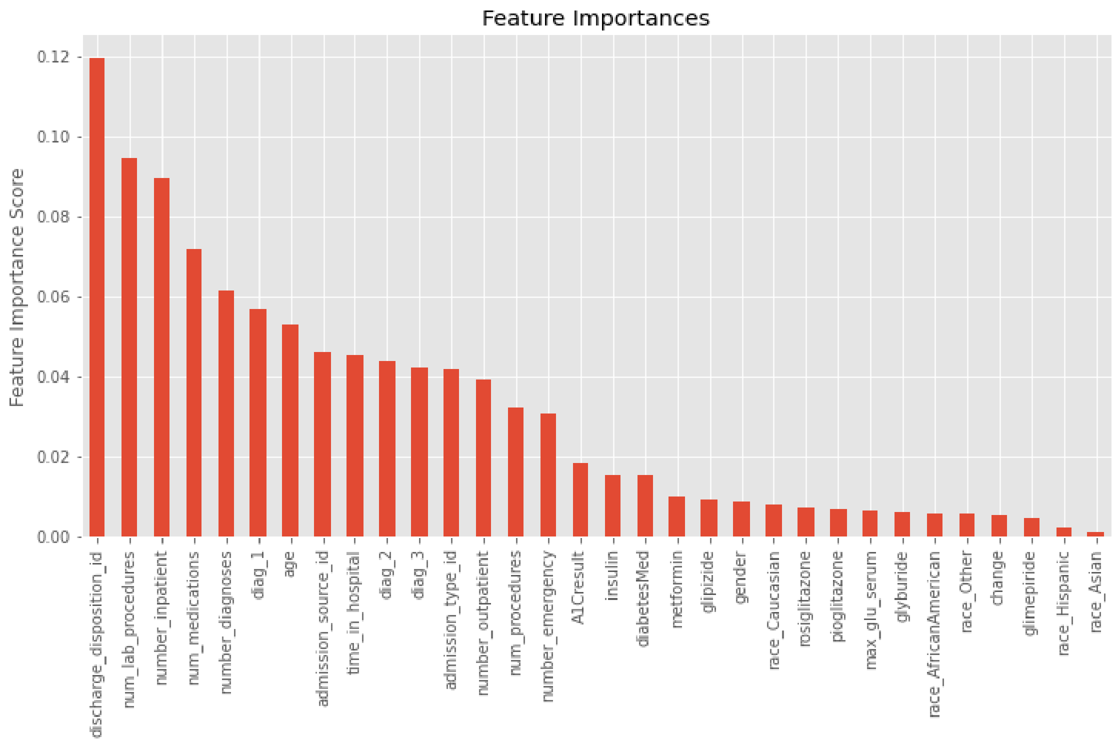
```
[263]: GradientBoostingClassifier(max_depth=12, max_features=18, min_samples_leaf=70,
                                  min_samples_split=800, n_estimators=70,
                                  random_state=101, subsample=0.8)
```

Let’s see the GBM performance on our validation set with hyperparameters choosen so far

```
[271]: gbm1 = GradientBoostingClassifier(max_depth=12, max_features=18,␣
        ↪min_samples_leaf=70,
                                         min_samples_split=800, n_estimators=70,
                                         random_state=101, subsample=0.8)
       gbm1.fit(X_train,y_train)
       gbm1_pred = gbm1.predict(X_val)

       print('\nGradient Boost [1] Performance:')
       print('------------------------------------')
       print('F1 Score micro        : ', metrics.f1_score(y_val,␣
        ↪gbm1_pred,average='micro'))
       print('F1 Score macro        : ', metrics.f1_score(y_val,␣
        ↪gbm1_pred,average='macro'))
       print('Confusion Matrix:\n ', confusion_matrix(y_val, gbm1_pred))

       feat_imp = pd.Series(gbm1.feature_importances_, predictors).
        ↪sort_values(ascending=False)
       fig = plt.figure(figsize=(12, 6))
       feat_imp.plot(kind='bar', title='Feature Importances')
       plt.ylabel('Feature Importance Score')
```

```
Gradient Boost [1] Performance:
------------------------------------
F1 Score micro        :  0.6152125279642058
F1 Score macro        :  0.36337173599046196
Confusion Matrix:
  [[5824  571    6]
 [2622  760    8]
 [ 717  204   16]]
```

```
[271]: Text(0, 0.5, 'Feature Importance Score')
```



We can see some improvement in F1 score (macro & micro), and a change in feature importance ranking.

Step3 - Tune Subsample and Lower Learning Rate

[265]:
```
#3.1 Grid seach on subsample
param_test5 = {'subsample':[0.6,0.7,0.75,0.8,0.85,0.9, 1]}
gsearch5 = GridSearchCV(estimator = GradientBoostingClassifier(learning_rate=0.
↪1, n_estimators=70,max_depth=12,
                                min_samples_split=800, min_samples_leaf=70,␣
↪random_state=101, max_features=18),
                           param_grid = param_test5,␣
↪scoring='f1_micro',n_jobs=4,iid=False, cv=5)
gsearch5.fit(X_train,y_train)
```

```
/home/trojan/miniconda3/envs/ds/lib/python3.8/site-
packages/sklearn/model_selection/_search.py:847: FutureWarning: The parameter
'iid' is deprecated in 0.22 and will be removed in 0.24.
  warnings.warn(
```

[265]:
```
GridSearchCV(cv=5,
             estimator=GradientBoostingClassifier(max_depth=12, max_features=18,
                                                  min_samples_leaf=70,
                                                  min_samples_split=800,
                                                  n_estimators=70,
                                                  random_state=101),
             iid=False, n_jobs=4,
             param_grid={'subsample': [0.6, 0.7, 0.75, 0.8, 0.85, 0.9, 1]},
             scoring='f1_micro')
```

[266]:
```
gsearch5.best_params_, gsearch5.best_score_
```

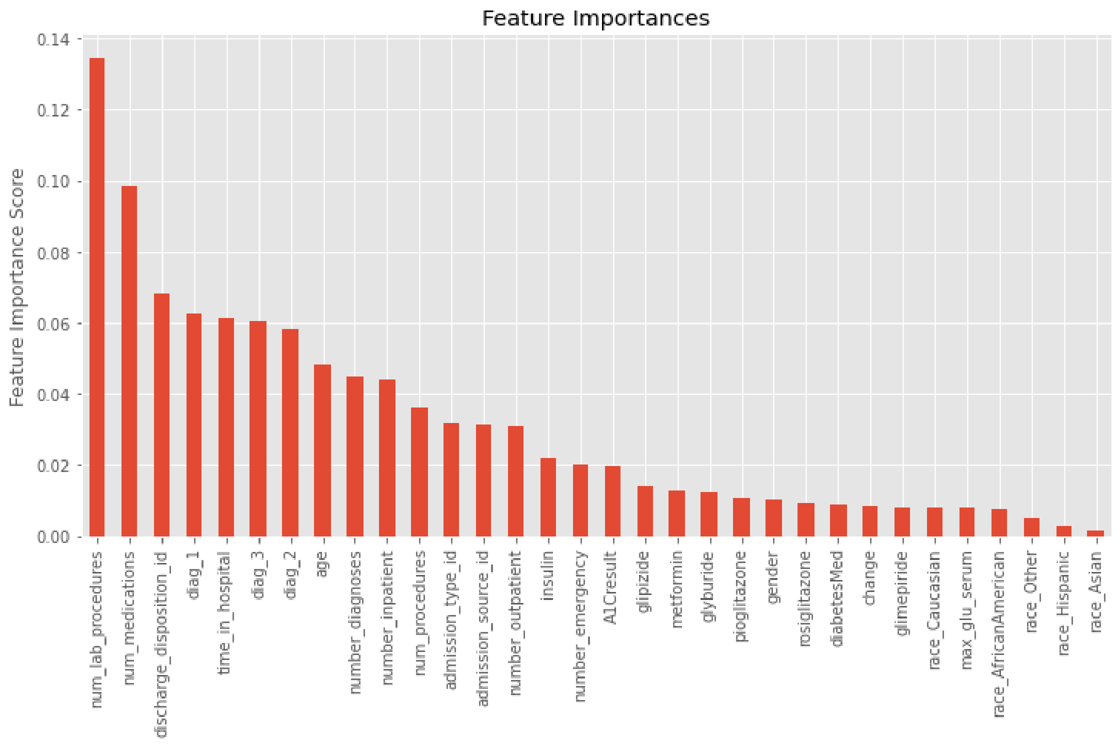
[266]:
```
({'subsample': 0.85}, 0.6208102239761104)
```

With all tuned lets get GBM performance on our validation set

[272]:
```
#3.2 reducing the learning rate and proportionally increasing the number of␣
 ↪estimators
gbm2 = GradientBoostingClassifier(max_depth=12, max_features=18,␣
 ↪min_samples_leaf=70,
                           min_samples_split=800, n_estimators=700,
                           random_state=101, subsample=0.85, learning_rate=0.1)
gbm2.fit(X_train,y_train)
gbm2_pred = gbm2.predict(X_val)

print('\nGradient Boost [2] Performance:')
print('-----------------------------------')
print('F1 Score micro        : ', metrics.f1_score(y_val,␣
 ↪gbm2_pred,average='micro'))
print('F1 Score macro        : ', metrics.f1_score(y_val,␣
 ↪gbm2_pred,average='macro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, gbm2_pred))

feat_imp = pd.Series(gbm2.feature_importances_, predictors).
 ↪sort_values(ascending=False)
fig = plt.figure(figsize=(12, 6))
feat_imp.plot(kind='bar', title='Feature Importances')
plt.ylabel('Feature Importance Score')
```

```

Gradient Boost [2] Performance:
-----------------------------------
F1 Score micro        :  0.5878076062639821
F1 Score macro        :  0.3846271851942651
Confusion Matrix:
  [[5248 1072   81]
 [2325 1012   53]
 [ 621  270   46]]
```

[272]:
```
Text(0, 0.5, 'Feature Importance Score')
```



Even though confusion matrix and F1 score macro became better, yet our F1 score micro has dropped to 0.5878.

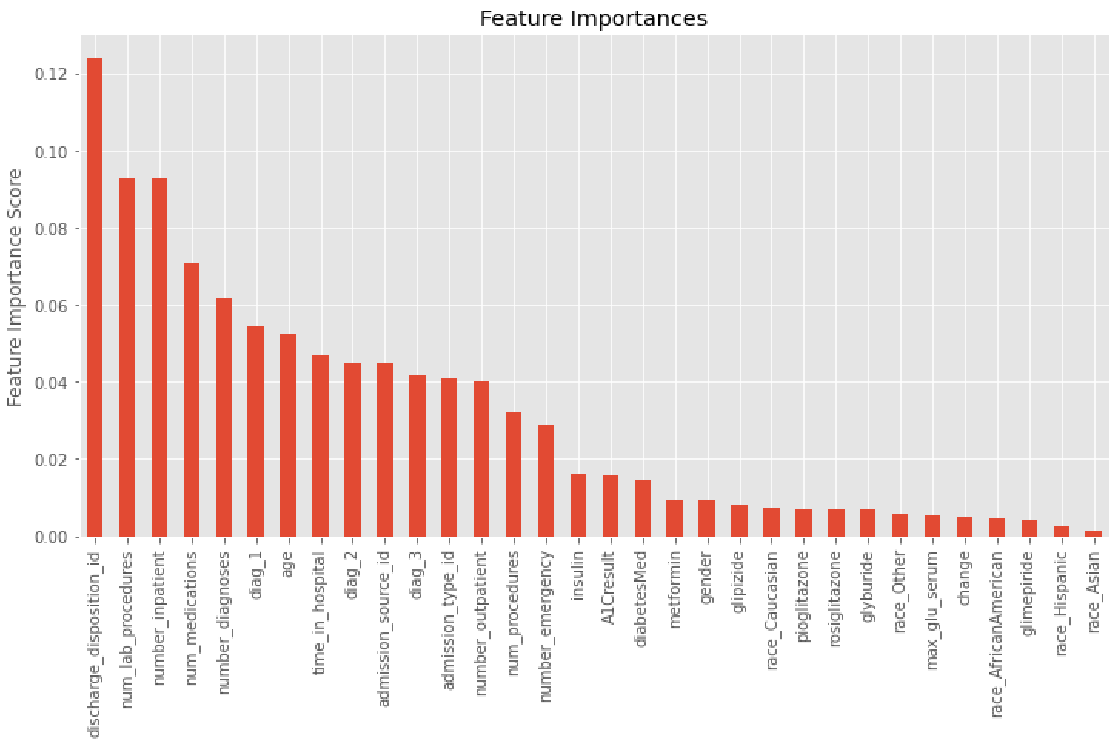
Now lets try reducing the learning rate and proportionally increasing the number of estimators to get more robust results:

```
[273]: #3.3 reducing the learning rate to 50% and proportionally increasing the number␣
        ↪of estimators
       gbm3 = GradientBoostingClassifier(max_depth=12, max_features=18,␣
        ↪min_samples_leaf=70,
                                      min_samples_split=800, n_estimators=140,
                                      random_state=101, subsample=0.85, learning_rate=0.05)
       gbm3.fit(X_train,y_train)
       gbm3_pred = gbm3.predict(X_val)

       print('\nGradient Boost [3] Performance:')
       print('-----------------------------------')
       print('F1 Score micro        : ', metrics.f1_score(y_val,␣
        ↪gbm3_pred,average='micro'))
       print('F1 Score macro        : ', metrics.f1_score(y_val,␣
        ↪gbm3_pred,average='macro'))
       print('Confusion Matrix:\n ', confusion_matrix(y_val, gbm3_pred))
```

```
feat_imp = pd.Series(gbm3.feature_importances_, predictors).
 ↪sort_values(ascending=False)
fig = plt.figure(figsize=(12, 6))
feat_imp.plot(kind='bar', title='Feature Importances')
plt.ylabel('Feature Importance Score')
```

```
Gradient Boost [3] Performance:
-----------------------------------
F1 Score micro        :  0.6141871737509321
F1 Score macro        :  0.362448377830546
Confusion Matrix:
  [[5838  555    8]
 [2649  732    9]
 [ 713  205   19]]
```

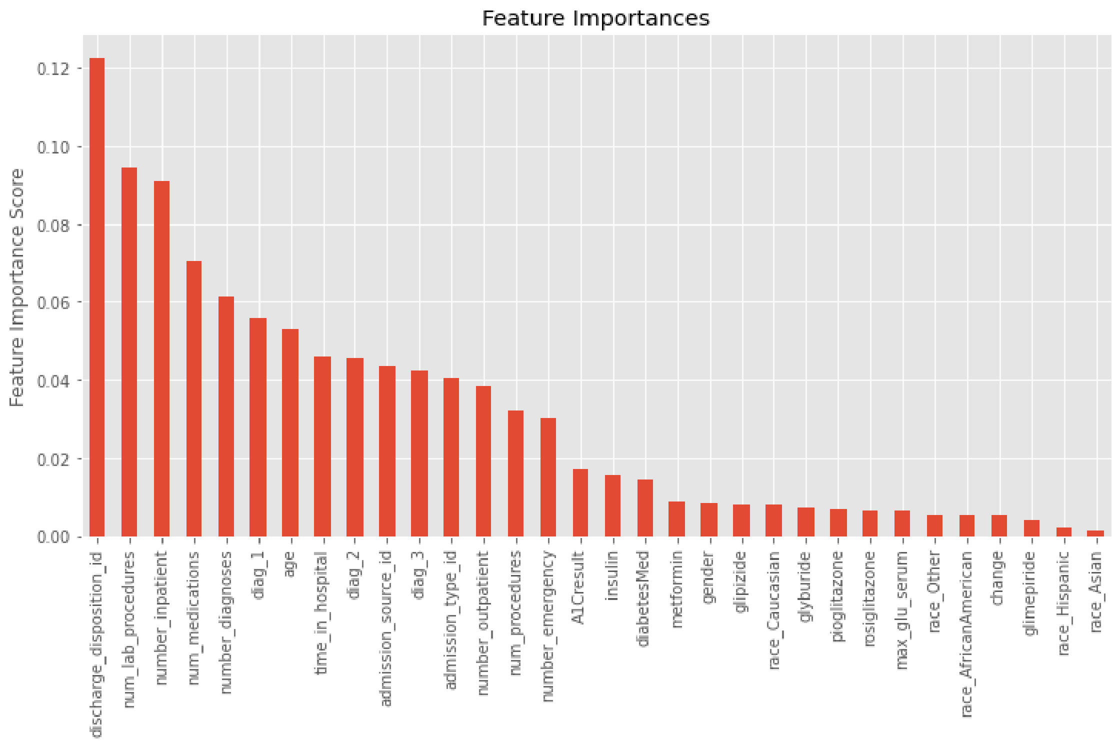
[273]:
```
Text(0, 0.5, 'Feature Importance Score')
```



[274]:
```
#3.4 reducing the learning rate to 10% and proportionally increasing the number␣
 ↪of estimators
gbm4 = GradientBoostingClassifier(max_depth=12, max_features=18,␣
 ↪min_samples_leaf=70,
                                  min_samples_split=800, n_estimators=700,
                                random_state=101, subsample=0.85, learning_rate=0.01)
gbm4.fit(X_train,y_train)
gbm4_pred = gbm4.predict(X_val)

print('\nGradient Boost [4] Performance:')
print('-----------------------------------')
print('F1 Score micro        : ', metrics.f1_score(y_val,␣
 ↪gbm4_pred,average='micro'))
print('F1 Score macro        : ', metrics.f1_score(y_val,␣
 ↪gbm4_pred,average='macro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, gbm4_pred))

feat_imp = pd.Series(gbm4.feature_importances_, predictors).
 ↪sort_values(ascending=False)
fig = plt.figure(figsize=(12, 6))
feat_imp.plot(kind='bar', title='Feature Importances')
plt.ylabel('Feature Importance Score')
```

```
Gradient Boost [4] Performance:
-----------------------------------
F1 Score micro        :  0.6147464578672632
F1 Score macro        :  0.363164182489389
Confusion Matrix:
  [[5832  564    5]
 [2639  745    6]
 [ 716  203   18]]
```

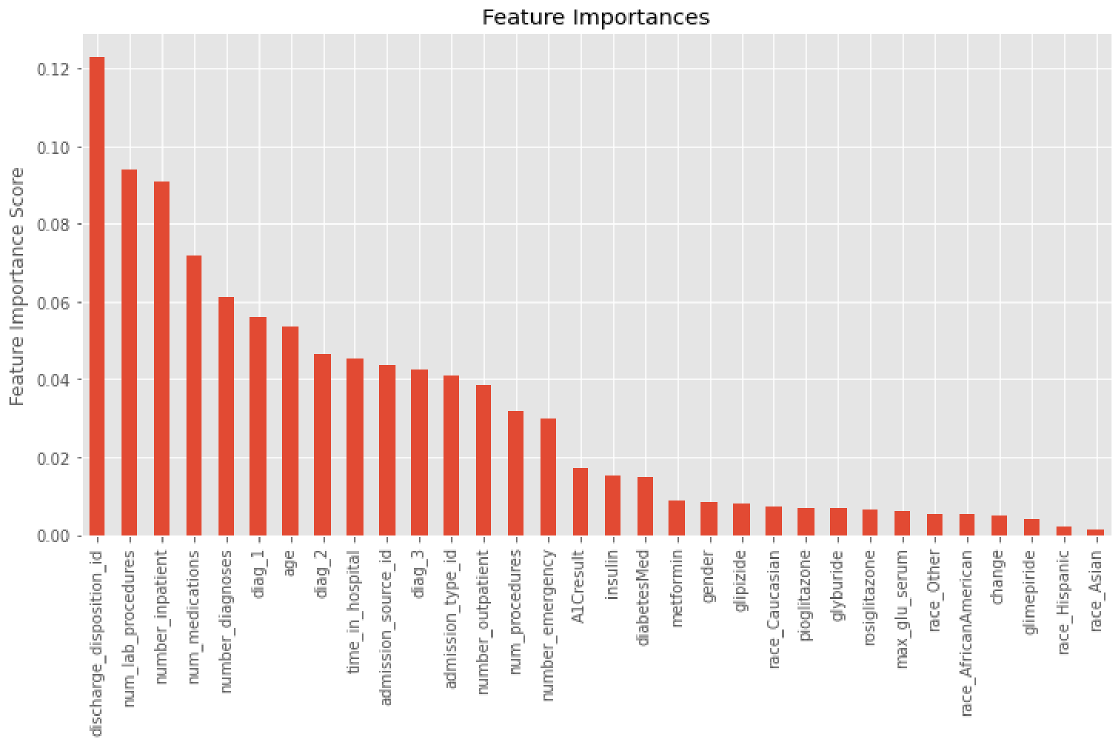
```
[274]: Text(0, 0.5, 'Feature Importance Score')
```



[275]:
```
#3.5 reducing the learning rate to 5% and proportionally increasing the number␣
↪of estimators
gbm5 = GradientBoostingClassifier(max_depth=12, max_features=18,␣
↪min_samples_leaf=70,
                                  min_samples_split=800, n_estimators=1400,
                                  random_state=101, subsample=0.85, learning_rate=0.
↪005)
gbm5.fit(X_train,y_train)
gbm5_pred = gbm5.predict(X_val)

print('\nGradient Boost [5] Performance:')
print('------------------------------------')
print('F1 Score micro        : ', metrics.f1_score(y_val,␣
↪gbm5_pred,average='micro'))
print('F1 Score macro        : ', metrics.f1_score(y_val,␣
↪gbm5_pred,average='macro'))
print('Confusion Matrix:\n ', confusion_matrix(y_val, gbm5_pred))

feat_imp = pd.Series(gbm5.feature_importances_, predictors).
↪sort_values(ascending=False)
fig = plt.figure(figsize=(12, 6))
feat_imp.plot(kind='bar', title='Feature Importances')
plt.ylabel('Feature Importance Score')
```

```
Gradient Boost [5] Performance:
-----------------------------------
F1 Score micro        :  0.6150260999254288
F1 Score macro        :  0.363352980542246
Confusion Matrix:
  [[5841  555    5]
 [2646  738    6]
 [ 713  205   19]]
```

```
[275]: Text(0, 0.5, 'Feature Importance Score')
```



With learning rate of 0.005 and number of estemators 1400, we have acheived the best balance between micro and macro F1 scores, and hence the best result.

Micro vs Macro F1 Score

When all the labels are more or less equally sized (have roughly the same number of instances), we use any f1 score averaging method.

If we think there are labels with more instances than others and if we want to bias your metric towards the most populated ones, use micro f1 score.

If we think there are labels with more instances than others and if we want to bias your metric toward the least populated ones (or at least you don't want to bias toward the most populated ones), use macro f1 score.

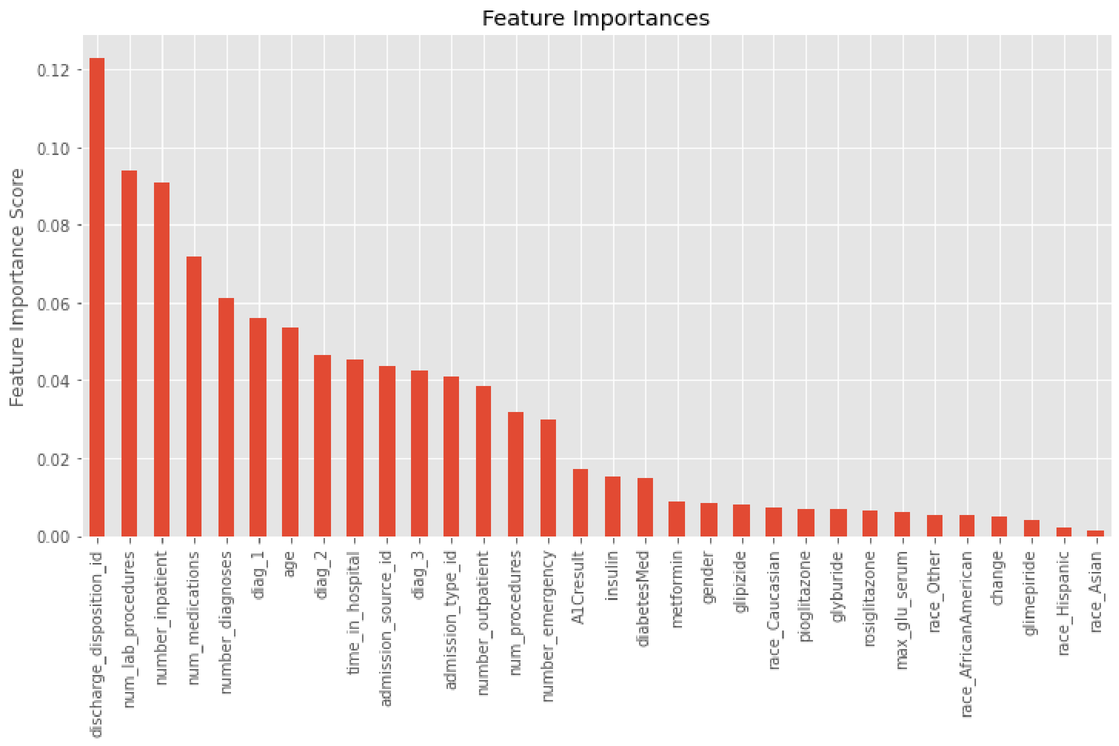
If the microf1 score result is significantly lower than the macro one, it means that we have some gross misclassification in the most populated labels, whereas our smaller labels are probably correctly classified. If the macro f1 score result is significantly lower than the micromedia one, it means your smaller labels are poorly classified, whereas your larger ones are probably correctly classified, and that is what is happening in our dataset.

1.0.12 Final Performance on Testing Data

[276]:
```
#Performance on test dataset
gbm5f_pred = gbm5.predict(X_test)

print('\nGradient Boost Final Performance:')
print('-----------------------------------')
print('F1 Score micro        : ', metrics.f1_score(y_test,␣
 ↪gbm5f_pred,average='micro'))
print('F1 Score macro        : ', metrics.f1_score(y_test,␣
 ↪gbm5f_pred,average='macro'))
print('Confusion Matrix:\n ', confusion_matrix(y_test, gbm5f_pred))

feat_imp = pd.Series(gbm5.feature_importances_, predictors).
 ↪sort_values(ascending=False)
fig = plt.figure(figsize=(12, 6))
feat_imp.plot(kind='bar', title='Feature Importances')
plt.ylabel('Feature Importance Score')
```

```
Gradient Boost Final Performance:
-----------------------------------
F1 Score micro        :  0.6214578672632364
F1 Score macro        :  0.3612444410496832
Confusion Matrix:
  [[5899  553    4]
 [2571  760    5]
 [ 716  212    8]]
```

[276]:
```
Text(0, 0.5, 'Feature Importance Score')
```



1.0.13 Conclusion

In this project, we used Diabetes Patient dataset to build a Readmitted Prediction, where we have acheived the best prediction performance using Gradient Boost classifier.

- F1 Score (micro): 0.6215
- F1 Score (macro): 0.3612

The main reasons for not high performance is the fact that our labels are not palnced thoughout the dataset, where 1 label (No readmittion) accounts for over 60% of the data points, while another label (Readmitted in $<$ 30 days) accounts for only ~8%. Another reason for low performance is that our target has very low correlation with all of our predectors.

Future Work In the future, we can try the following to improve the performance of our classifier: 1. combine (readmitted in $<$ 30 days) and (readmitted in $>$ 30 days) into one feature, and turn the problem in to binary classification problem (readmitted vs not readmmited) which is going to result in a better palanced label classes. 2. We can try selecting a subset of feature, with higher classification importance according to our classifier, and just using those in training.

References

- https://archive.ics.uci.edu/ml/datasets/Diabetes+130-US+hospitals+for+years+1999-2008
- https://www.hindawi.com/journals/bmri/2014/781670/
- https://www.analyticsvidhya.com/blog/2016/02/complete-guide-parameter-tuning-gradient-boosting-gbm-python/

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