# CISC 6930 Course Project

December 7, 2018

## 1 UCI Diabetes - Readmission in 3 months or not?

In this project, several models will be created from the UCI diabetes dataset that will predict whether a patient is likely to be readmitted to the hospital for diabetes in 30 days or not.

### 1.1 Import packages

```
In [1]: # Import packages
        import pandas as pd
        import numpy as np
        import scipy.stats as ss
        import seaborn as sns
        import matplotlib.pyplot as plt
        import time

        from sklearn.preprocessing import Normalizer

        from sklearn.feature_selection import chi2, SelectPercentile
        from imblearn.over_sampling import SMOTE

        from sklearn.model_selection import train_test_split
        from sklearn.model_selection import KFold, cross_val_predict

        from sklearn.neighbors import KNeighborsClassifier
        from sklearn.tree import DecisionTreeClassifier, ExtraTreeClassifier
        from sklearn.naive_bayes import GaussianNB
        from sklearn.svm import LinearSVC
        from sklearn.linear_model import Perceptron

        from sklearn.ensemble import RandomForestClassifier, VotingClassifier

        from sklearn.metrics import accuracy_score
        from sklearn.metrics import confusion_matrix, classification_report

        import warnings
        warnings.simplefilter(action='ignore', category=FutureWarning)
```

## 2 Data Analysis

Start by reading in the data and removing extraneous information of individual patients.

```
In [2]: # Read in dataset
        df = pd.read_csv("diabetic_data.csv", na_values = "?", low_memory = False)

        # Drop observation specific features
        df = df.drop(["encounter_id", "patient_nbr"], axis = 1)

        # Display class label counts
        df.readmitted.value_counts()
```

```
Out[2]: NO     54864
        >30    35545
        <30    11357
        Name: readmitted, dtype: int64
```

```
In [3]: # Adjust to binary classification problem
        df.readmitted = df.readmitted.apply(lambda x: 1 if x == '<30' else 0)
```

```
In [4]: # Check class labels
        print("After adjusting the class labels, \n",
              'total number of class 0 (NO and >30) instances:',
              len(df.loc[df['readmitted'] == 0, 'readmitted']), "\n",
              "total number of class 1 (< 30) instances:",
              len(df.loc[df['readmitted'] == 1, 'readmitted']))
```

```
After adjusting the class labels,
 total number of class 0 (NO and >30) instances: 90409
 total number of class 1 (< 30) instances: 11357
```

Note which columns have continuous data and which have categorical data. If a certain column is of a wrong type, change it to the other type.

```
In [5]: # List the type of feature each column is
        df.columns.groupby(df.dtypes)
```

```
Out[5]: {dtype('int64'): Index(['admission_type_id', 'discharge_disposition_id', 'admission_sour
                'time_in_hospital', 'num_lab_procedures', 'num_procedures',
                'num_medications', 'number_outpatient', 'number_emergency',
                'number_inpatient', 'number_diagnoses', 'readmitted'],
               dtype='object'),
         dtype('O'): Index(['race', 'gender', 'age', 'weight', 'payer_code', 'medical_specialty'
                'diag_1', 'diag_2', 'diag_3', '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'],
               dtype='object')}
```

IDs are to be treated as categorical data rather than as numbers. The 3 ID columns are mistaken for numerical columns. Therefore change those to string types.

```
In [6]: # Change ID columns from numerical to string type
        df.admission_type_id = df.admission_type_id.astype('str')
        df.discharge_disposition_id = df.discharge_disposition_id.astype('str')
        df.admission_source_id = df.admission_source_id.astype('str')
```

## 2.1 Exploratory Data Analysis

```
In [7]: # What is the size of the dataset
        df.shape

Out[7]: (101766, 48)
```

There are 101,766 records in the dataset. Explore the dataset. If a certain column is overly populated by a frequent value, over 98%, remove the column from the dataset.

To find heavy tailed distributions, first find a cutoff point.

```
In [8]: # Find cut off point
        0.98 * df.shape[0]

Out[8]: 99730.68
```

Find the columns where at least 99,731 rows have the same value.

```
In [9]: # Get list of features ordered by top most frequent values
        df.describe(exclude = ['int64']).T.sort_values(by = ['freq'], ascending = False)

Out[9]:                            count unique              top    freq
        examide                   101766      1               No  101766
        citoglipton               101766      1               No  101766
        glimepiride-pioglitazone  101766      2               No  101765
        acetohexamide             101766      2               No  101765
        metformin-pioglitazone    101766      2               No  101765
        metformin-rosiglitazone   101766      2               No  101764
        troglitazone              101766      2               No  101763
        glipizide-metformin       101766      2               No  101753
        tolbutamide               101766      2               No  101743
        miglitol                  101766      4               No  101728
        tolazamide                101766      3               No  101727
        chlorpropamide            101766      4               No  101680
        acarbose                  101766      4               No  101458
```

```
nateglinide               101766     4              No  101063
glyburide-metformin       101766     4              No  101060
repaglinide               101766     4              No  100227
glimepiride               101766     4              No   96575
max_glu_serum             101766     4            None   96420
rosiglitazone             101766     4              No   95401
pioglitazone              101766     4              No   94438
glyburide                 101766     4              No   91116
glipizide                 101766     4              No   89080
A1Cresult                 101766     4            None   84748
metformin                 101766     4              No   81778
diabetesMed               101766     2             Yes   78363
race                       99493     5       Caucasian   76099
discharge_disposition_id  101766    26               1   60234
admission_source_id       101766    17               7   57494
change                    101766     2              No   54755
gender                    101766     3          Female   54708
admission_type_id         101766     8               1   53990
insulin                   101766     4              No   47383
payer_code                 61510    17              MC   32439
age                       101766    10         [70-80)   26068
medical_specialty          51817    72  InternalMedicine   14635
diag_3                    100343   789             250   11555
diag_1                    101745   716             428    6862
diag_2                    101408   748             276    6752
weight                      3197     9        [75-100)    1336
```

The 16 columns that are over 98% saturated with one value are: *examide*, *citoglipton*, *glimepiride-pioglitazone*, *acetohexamide*, *metformin-pioglitazone*, *metformin-rosiglitazone*, *troglitazone*, *glipizide-metformin*, *tolbutamide*, *miglitol*, *tolazamide*, *chlorpropamide*, *acarbose*, *nateglinide*, *glyburide-metformin* and *repaglinide*. Remove those from the dataframe.

```
In [10]: # Drop the overly saturated features
         df = df.drop(['examide', 'citoglipton', 'glimepiride-pioglitazone',
                       'acetohexamide', 'metformin-pioglitazone',
                       'metformin-rosiglitazone', 'troglitazone',
                       'glipizide-metformin',
                       'tolbutamide', 'miglitol', 'tolazamide',
                       'chlorpropamide',
                       'acarbose', 'nateglinide', 'glyburide-metformin',
                       'repaglinide'], axis = 1)
```

```
In [11]: # What is the new length of the dataset?
         df.shape
```

```
Out[11]: (101766, 32)
```

An important note about this dataset is that there are 3 columns designated for diagnoses. These columns give the icd9 code for what the patient was diagnosed with on the primary and two secondary diagnoses. According to the research article that was published alongside with the dataset, these diagnoses can be coded into a larger group for our use. These groups are circulatory, respiratory, digestive, diabetes, injury, musculoskeletal, genitourinary, neoplasms, symptoms, skin/tissue, parasitic and others. The others group makes up 17.3% of the dataset and is broken down into 7 smaller groups each of having 2.2% or less occurrence in the dataset.

Source: https://www.hindawi.com/journals/bmri/2014/781670/

Thus code the diagnoses columns into these groups.

```
In [12]: # A function to categorize diagnosis icd9 codes
         def diag_group(df, col):
             new_diags = []
             for i in df[col]:
                 if pd.isnull(i): new_diags.append(np.nan)
                 else:
                     try:
                         val = float(i)
                         if (val >= 390 and val <= 460) or val == 785:
                             new_diags.append("circulatory")
                         elif (val >= 460 and val <= 520) or val == 786:
                             new_diags.append("respiratory")
                         elif (val >= 520 and val <= 580) or val == 787:
                             new_diags.append("digestive")
                         elif (val >= 250 and val < 251):
                             new_diags.append("injury")
                         elif (val >= 710 and val <= 740):
                             new_diags.append("musculoskeletal")
                         elif (val >= 580 and val <= 630) or val == 788:
                             new_diags.append("genitourinary")
                         elif (val >= 140 and val <= 240):
                             new_diags.append("neoplasms")
                         elif (val in [780, 781, 784]) or (val >= 790 and val <= 799):
                             new_diags.append("other symptoms")
                         elif (val >= 240 and val <= 280):
                             new_diags.append("endocrine/nutritional")
                         elif (val >= 680 and val <= 709) or val == 782:
                             new_diags.append("skin/tissue")
                         elif (val >= 1 and val <= 139):
                             new_diags.append("infection/parasitic")
                         else: new_diags.append("other")
                     except:
                         new_diags.append("other")
             return new_diags
```

```
In [13]: # Fill in diagnosis category for all 3 diagnosis features
         df["diag_1"] = diag_group(df, "diag_1")
         df["diag_2"] = diag_group(df, "diag_2")
         df["diag_3"] = diag_group(df, "diag_3")
```

There are 72 different medical specialties with the most common one being present in only

14.3% of the dataset. To simplify this feature, if any specialty appears in the dataset with an occurence of less than 0.5%, change it to *other*.

```
In [14]: # Get list of top frequent appearing medical specialties
         med_spec = np.where(100 * df.medical_specialty.value_counts() / df.shape[0] > 0.5)[0]
         med_spec = list(df.medical_specialty.value_counts()[med_spec].index)

         # For each attribute, if it is common, keep it
         # Otherwise change it to other
         new_med_spec = []
         for i in df.medical_specialty:
             if i in med_spec or pd.isnull(i): new_med_spec.append(i)
             else: new_med_spec.append("other")
         df['medical_specialty'] = new_med_spec
```

```
In [15]: # Get number of different medical specialties
         df.medical_specialty.value_counts().count()
```

```
Out[15]: 17
```

Now look at the continuous columns.

```
In [16]: # Display the continuous features and their statistics
         df.describe(exclude = ['object']).T
```

```
Out[16]:                        count       mean        std  min   25%   50%   75%  \
         time_in_hospital    101766.0   4.395987   2.985108  1.0   2.0   4.0   6.0
         num_lab_procedures  101766.0  43.095641  19.674362  1.0  31.0  44.0  57.0
         num_procedures      101766.0   1.339730   1.705807  0.0   0.0   1.0   2.0
         num_medications     101766.0  16.021844   8.127566  1.0  10.0  15.0  20.0
         number_outpatient   101766.0   0.369357   1.267265  0.0   0.0   0.0   0.0
         number_emergency    101766.0   0.197836   0.930472  0.0   0.0   0.0   0.0
         number_inpatient    101766.0   0.635566   1.262863  0.0   0.0   0.0   1.0
         number_diagnoses    101766.0   7.422607   1.933600  1.0   6.0   8.0   9.0
         readmitted          101766.0   0.111599   0.314874  0.0   0.0   0.0   0.0

                               max
         time_in_hospital     14.0
         num_lab_procedures  132.0
         num_procedures        6.0
         num_medications      81.0
         number_outpatient    42.0
         number_emergency     76.0
         number_inpatient     21.0
         number_diagnoses     16.0
         readmitted            1.0
```

Create two lists, one for categorical features and one for continous features

```
In [17]: # Group the features by their type
         df.columns.groupby(df.dtypes)

Out[17]: {dtype('int64'): Index(['time_in_hospital', 'num_lab_procedures', 'num_procedures',
                 'num_medications', 'number_outpatient', 'number_emergency',
                 'number_inpatient', 'number_diagnoses', 'readmitted'],
                dtype='object'),
          dtype('O'): Index(['race', 'gender', 'age', 'weight', 'admission_type_id',
                 'discharge_disposition_id', 'admission_source_id', 'payer_code',
                 'medical_specialty', 'diag_1', 'diag_2', 'diag_3', 'max_glu_serum',
                 'A1Cresult', 'metformin', 'glimepiride', 'glipizide', 'glyburide',
                 'pioglitazone', 'rosiglitazone', 'insulin', 'change', 'diabetesMed'],
                dtype='object')}
```

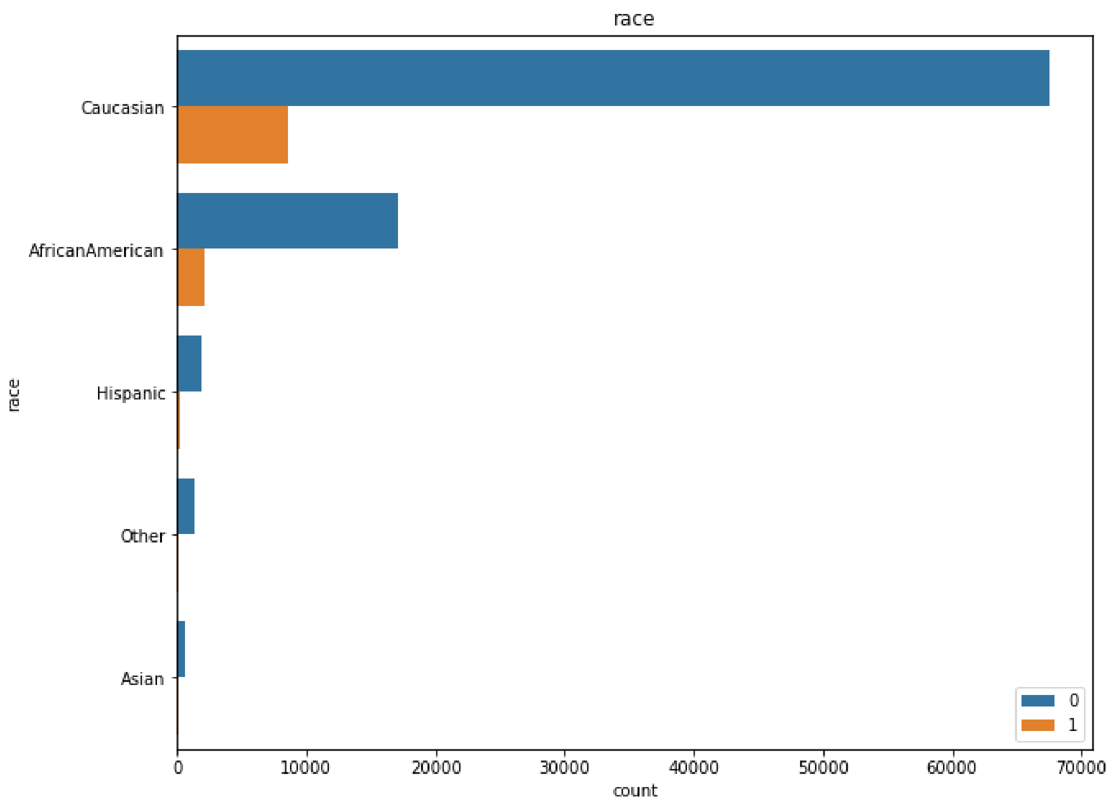
```
In [18]: # Create 2 lists, one for continuous features
         # and one for categorical features
         num_feats = ['time_in_hospital', 'num_lab_procedures', 'num_procedures',
                 'num_medications', 'number_outpatient', 'number_emergency',
                 'number_inpatient', 'number_diagnoses']

         cat_feats = ['race', 'gender', 'age', 'weight', 'admission_type_id',
                 'discharge_disposition_id', 'admission_source_id', 'payer_code',
                 'medical_specialty', 'diag_1', 'diag_2', 'diag_3', 'max_glu_serum',
                 'A1Cresult', 'metformin', 'glimepiride', 'glipizide', 'glyburide',
                 'pioglitazone', 'rosiglitazone', 'insulin', 'change']
```

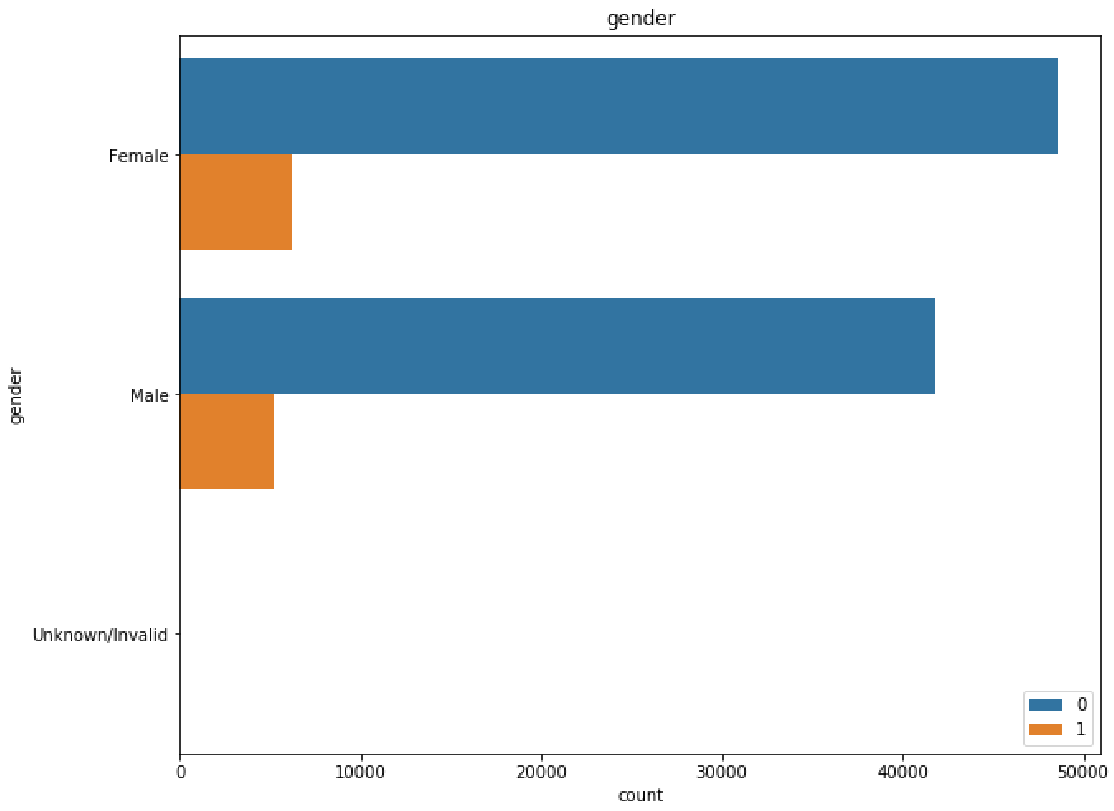
The continous columns will be normalized as part of preprocessing so there are no extremities.

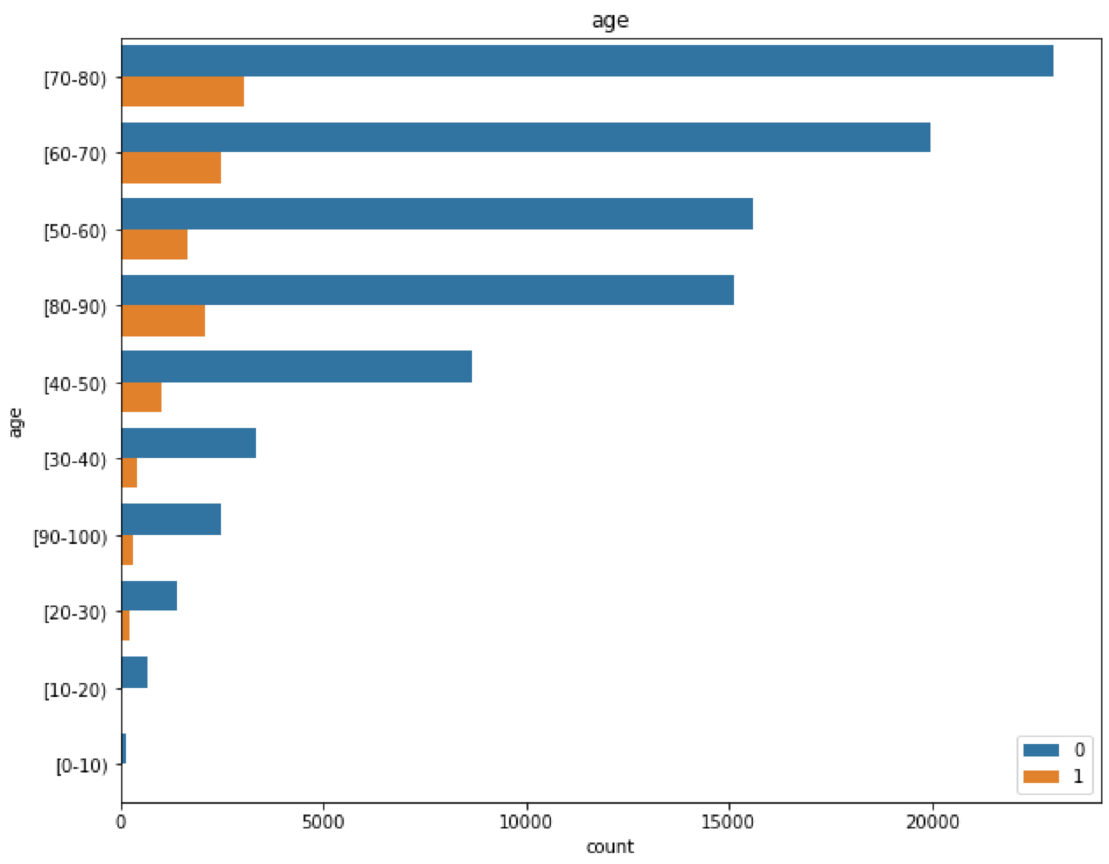
```
In [19]: # Normalize the continuous features so it becomes continuous
         df[num_feats] = Normalizer().fit_transform(df[num_feats])
```

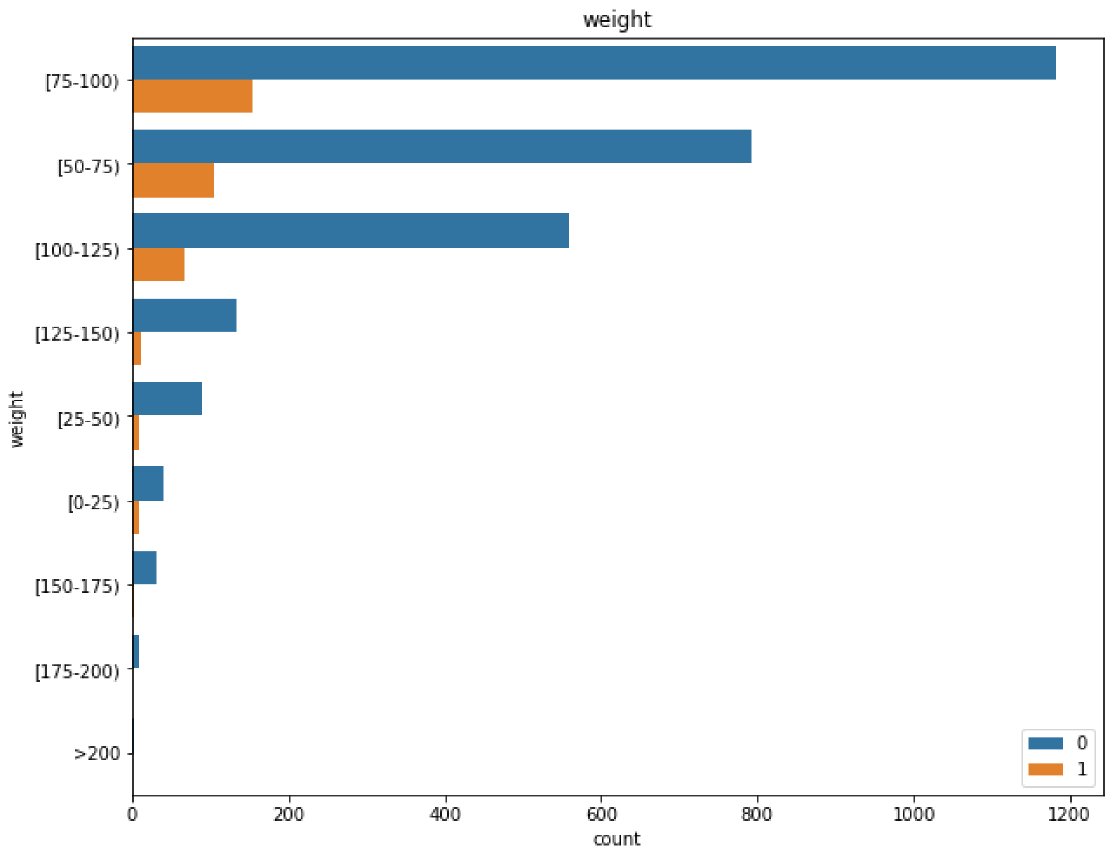
Plot the features filtered by readmission

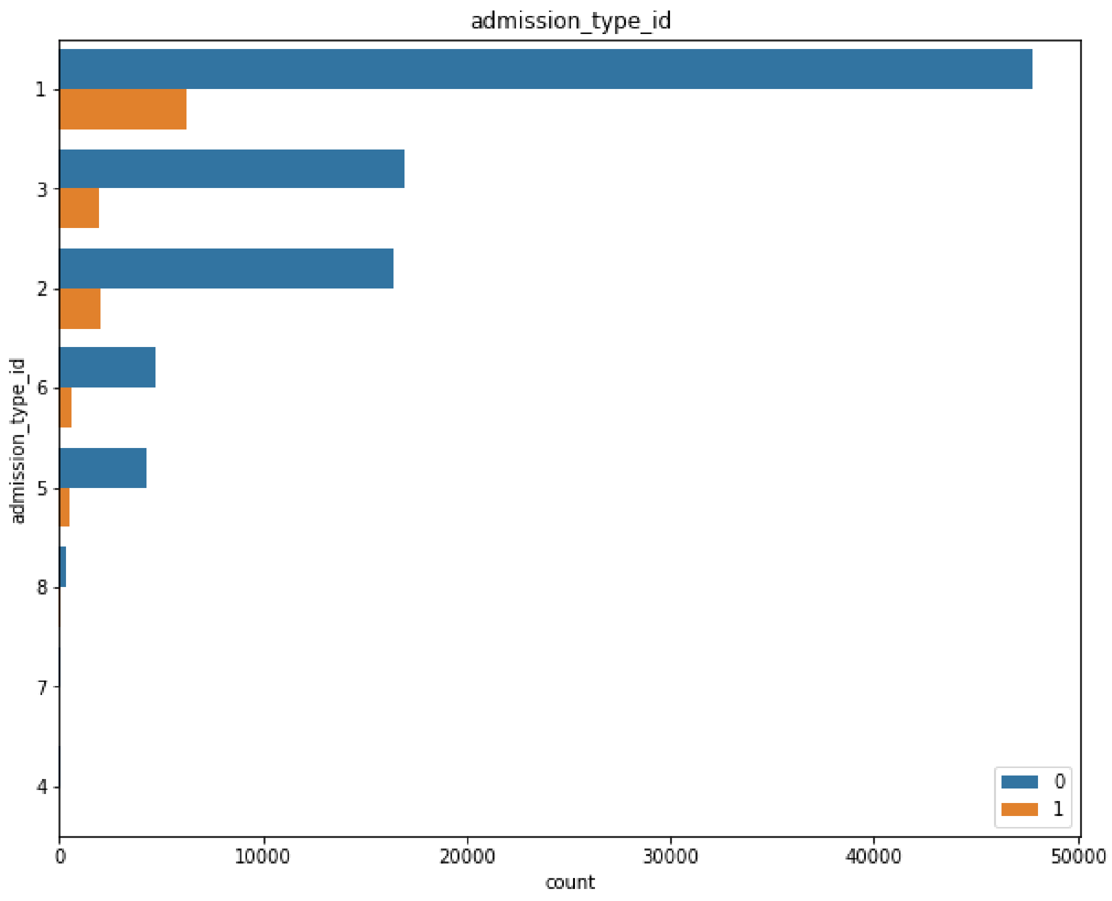
```
In [20]: # Plot categorical features by readmission label
         for i in cat_feats:
             fig = plt.figure(figsize = (10, 8))
             sns.countplot(y = df[i], hue = df.readmitted, order = df[i].value_counts().index)
             plt.title(i)
             plt.legend(loc = "lower right")
             plt.show()
```

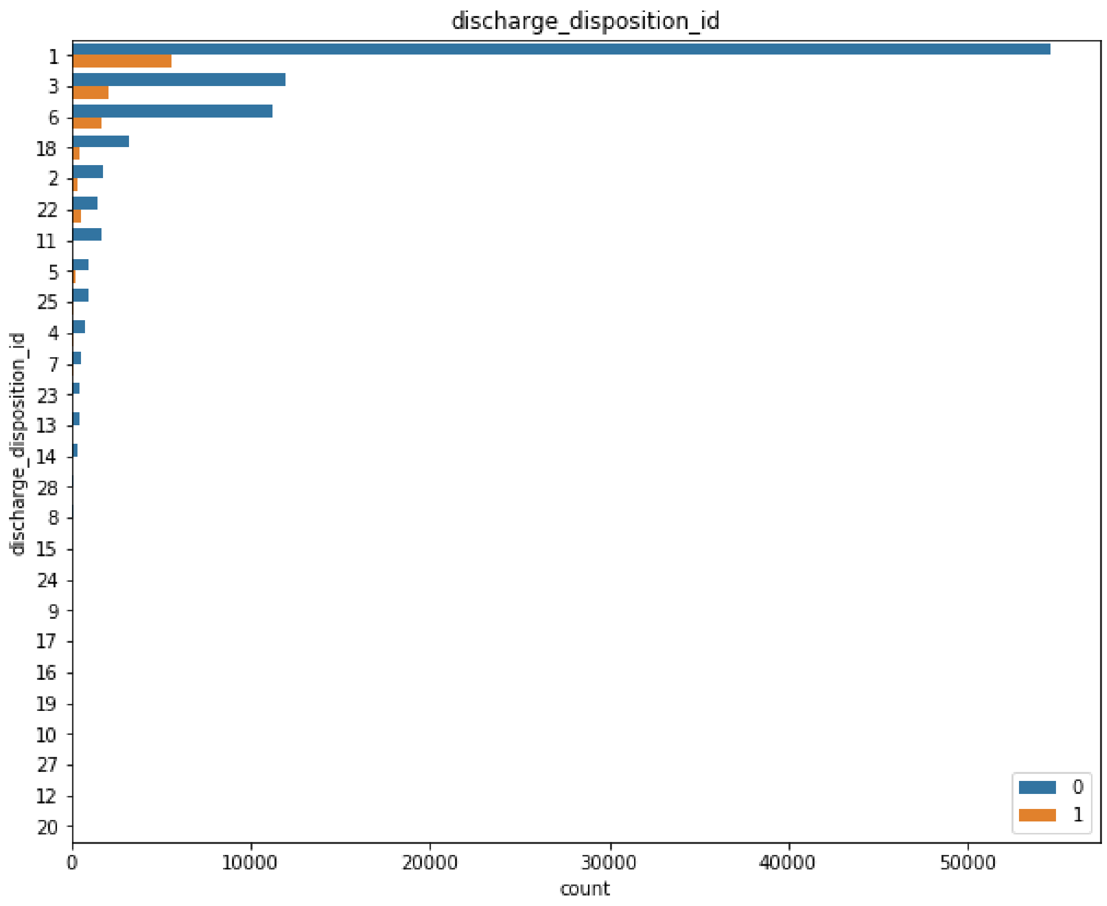

race
Caucasian
AfricanAmerican
Hispanic
Other
Asian
race
0
1
0
10000
20000
30000
40000
50000
60000
70000
count

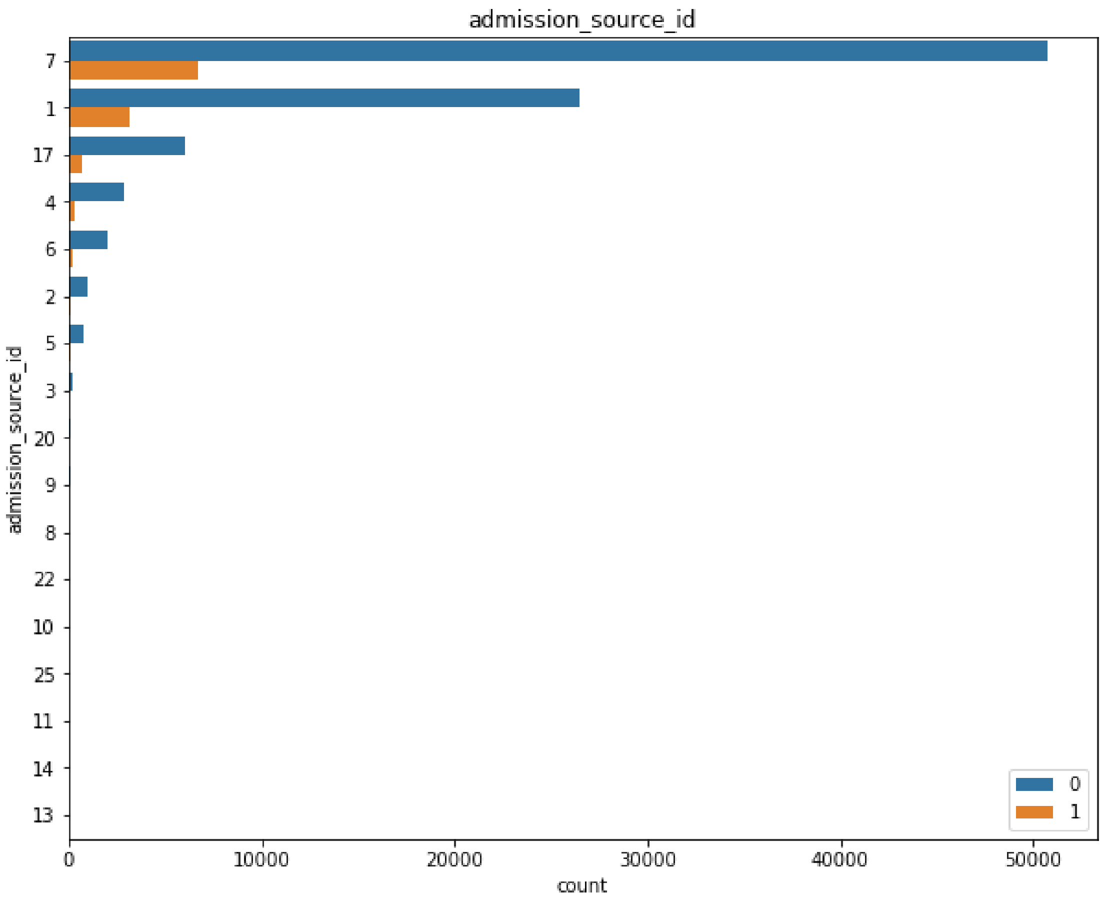

gender
Female
Male
Unknown/Invalid
gender
count
0
10000
20000
30000
40000
50000
0
1

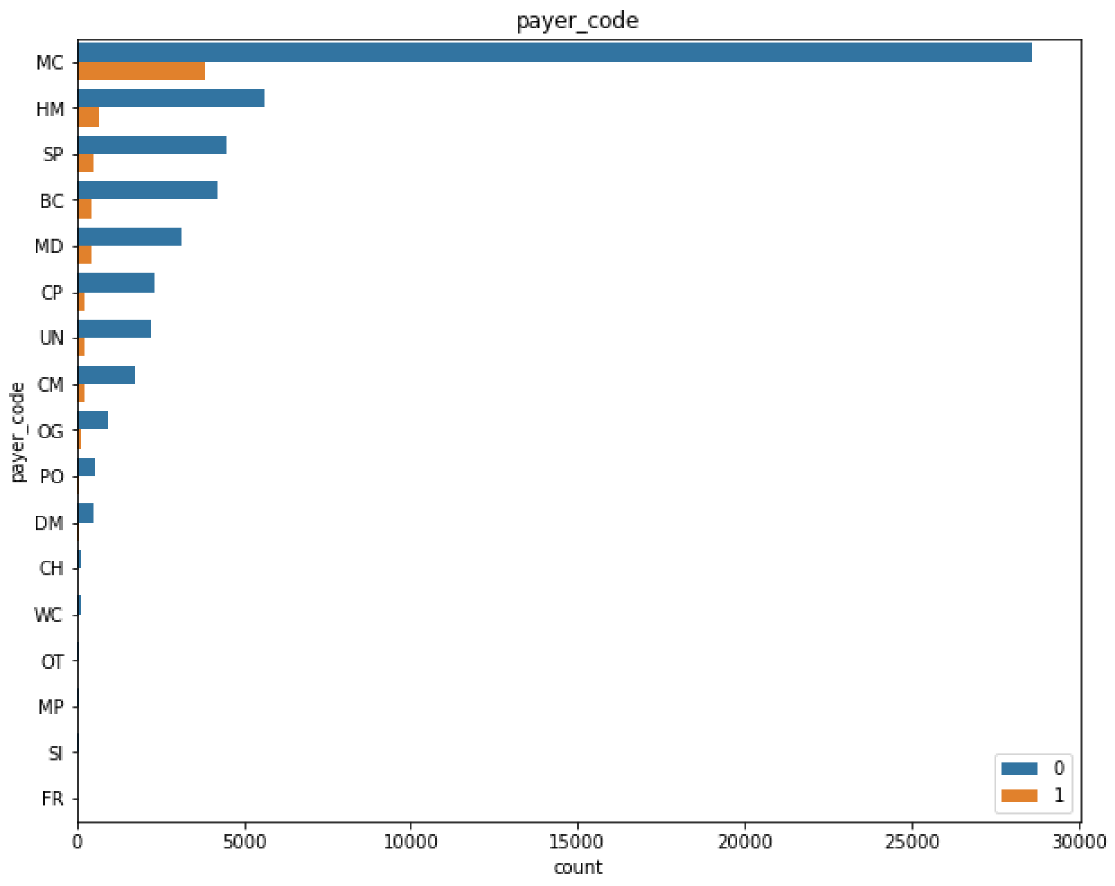

age
[70-80)
[60-70)
[50-60)
[80-90)
[40-50)
[30-40)
[90-100)
[20-30)
[10-20)
[0-10)
age
0
5000
10000
15000
20000
count
0
1

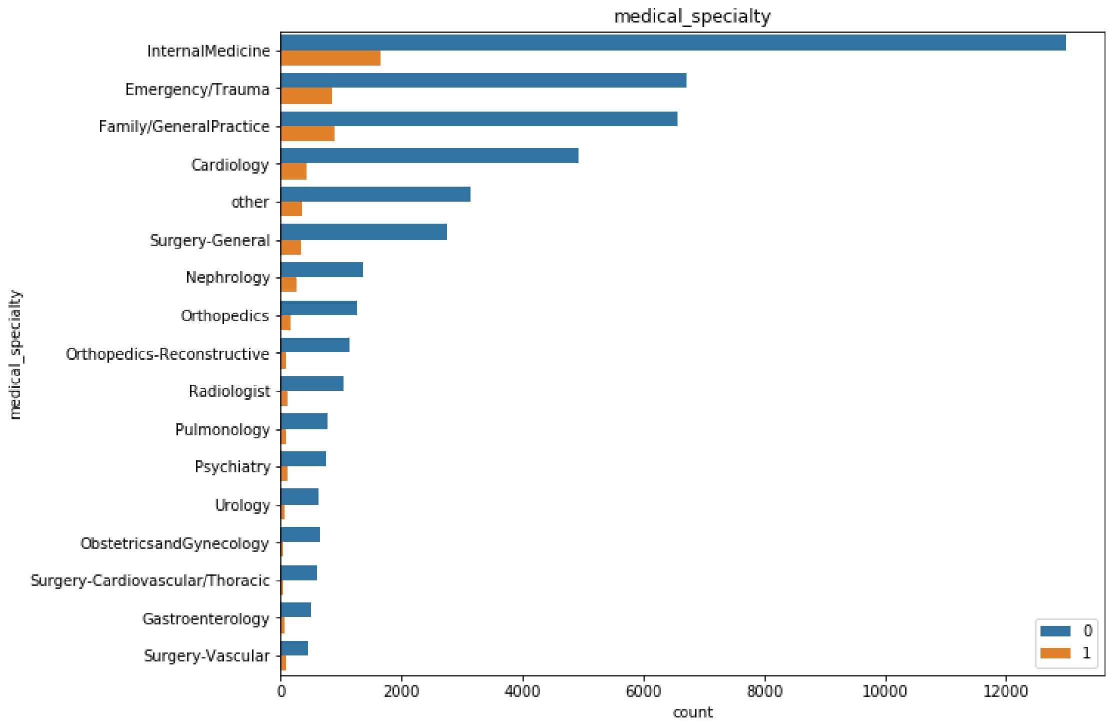

weight
[75-100)
[50-75)
[100-125)
[125-150)
[25-50)
[0-25)
[150-175)
[175-200)
>200
weight
0
1
0
200
400
600
800
1000
1200
count

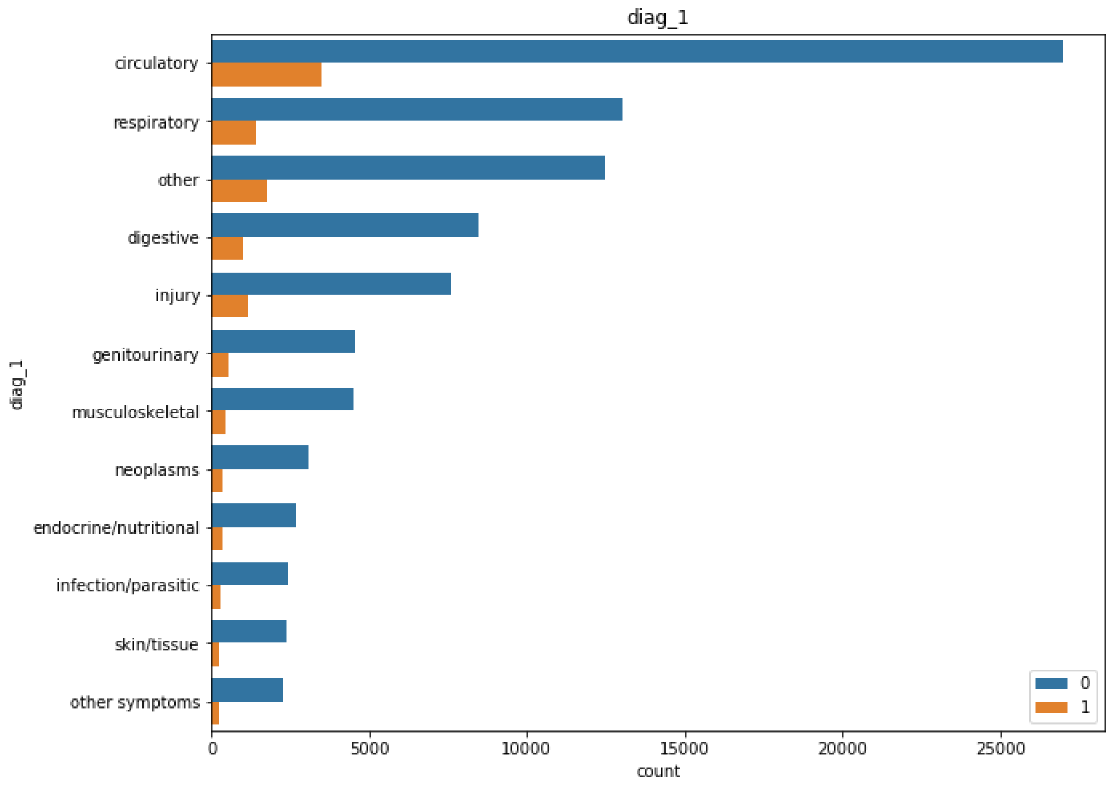

admission_type_id
1
3
2
6
5
8
7
4
admission_type_id
0
10000
20000
30000
40000
50000
count
0
1

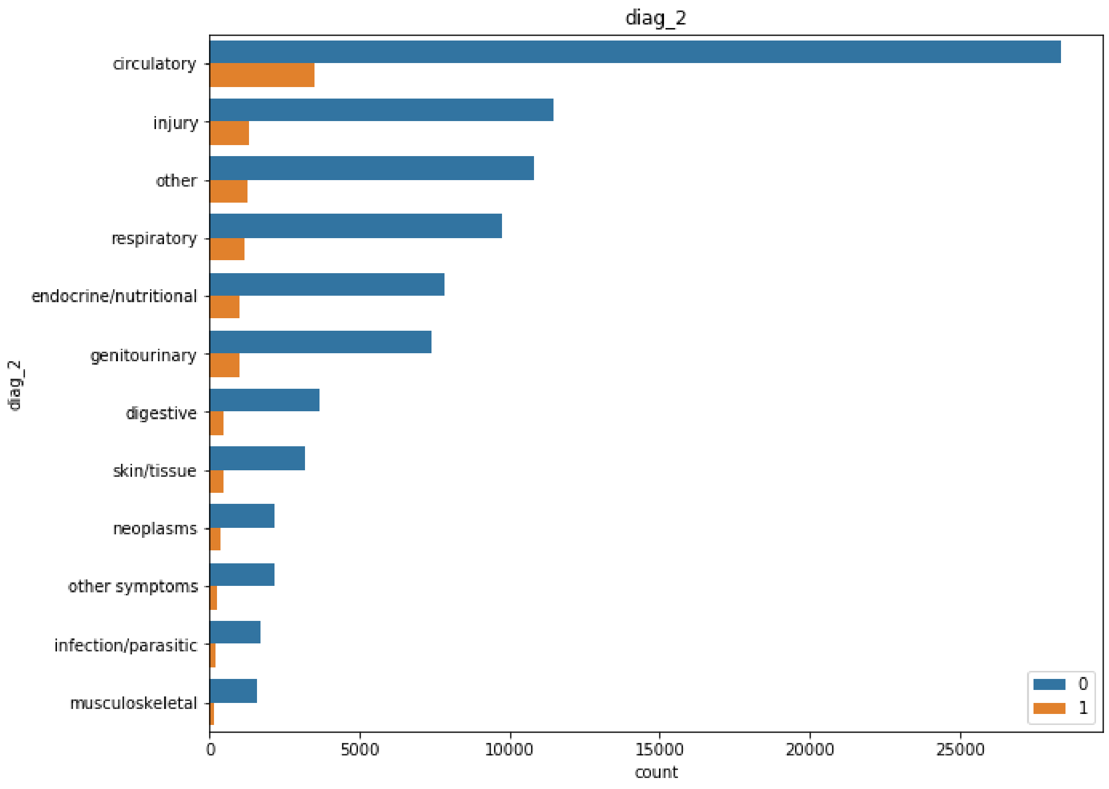

discharge_disposition_id
discharge_disposition_id
1
3
6
18
2
22
11
5
25
4
7
23
13
14
28
8
15
24
9
17
16
19
10
27
12
20
0
10000
20000
30000
40000
50000
count
0
1

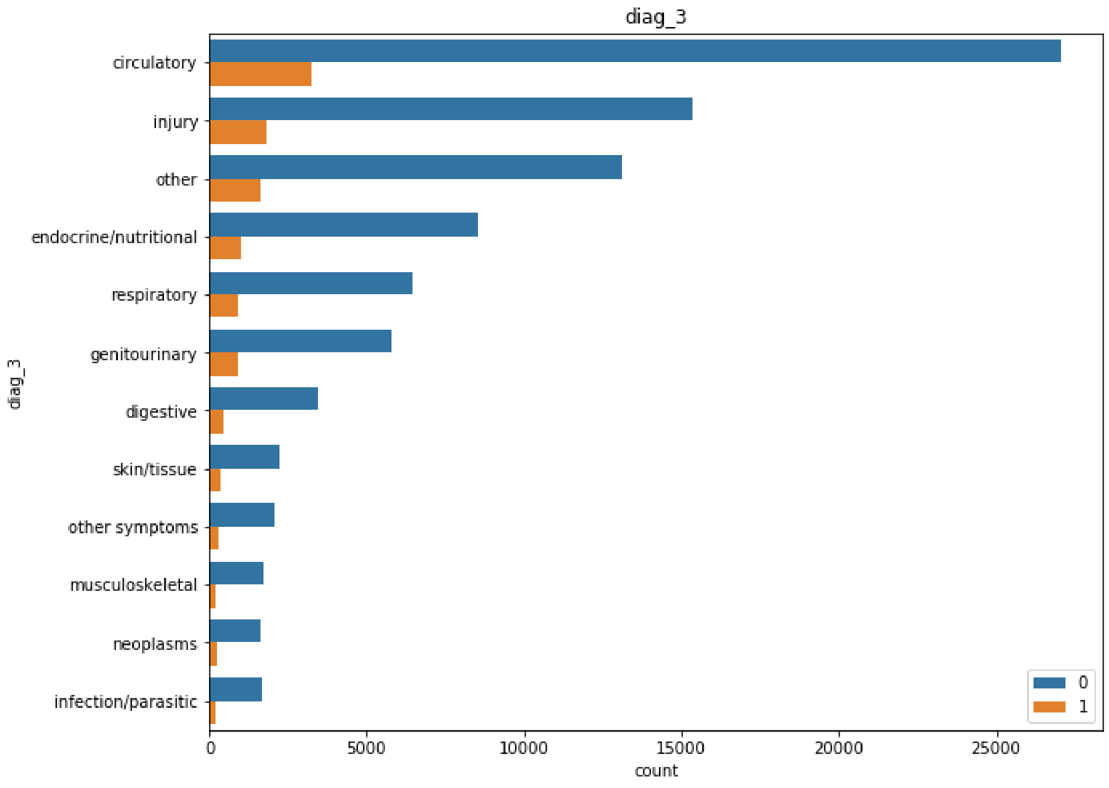

admission_source_id
7
1
17
4
6
2
5
3
20
9
8
22
10
25
11
14
13
admission_source_id
0
10000
20000
30000
40000
50000
count
0
1

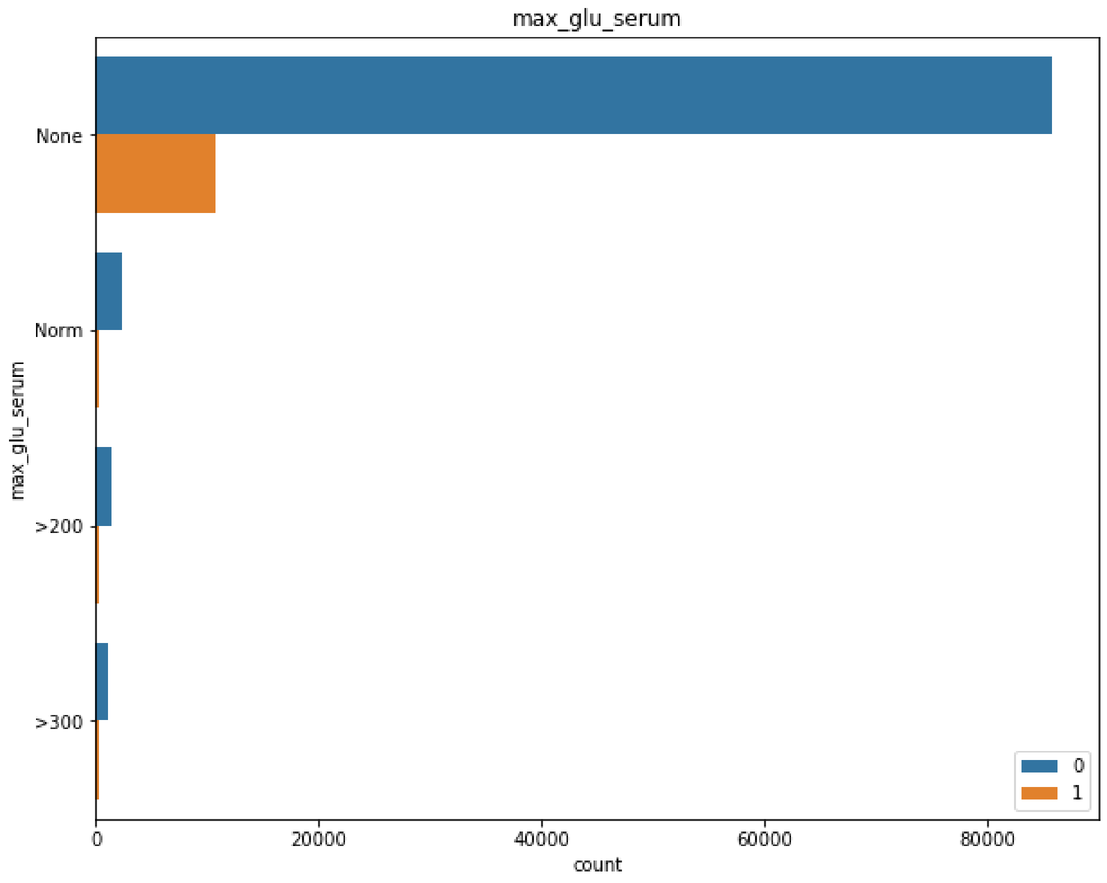

payer_code
MC
HM
SP
BC
MD
CP
UN
CM
OG
PO
DM
CH
WC
OT
MP
SI
FR
payer_code
0
5000
10000
15000
20000
25000
30000
count
0
1

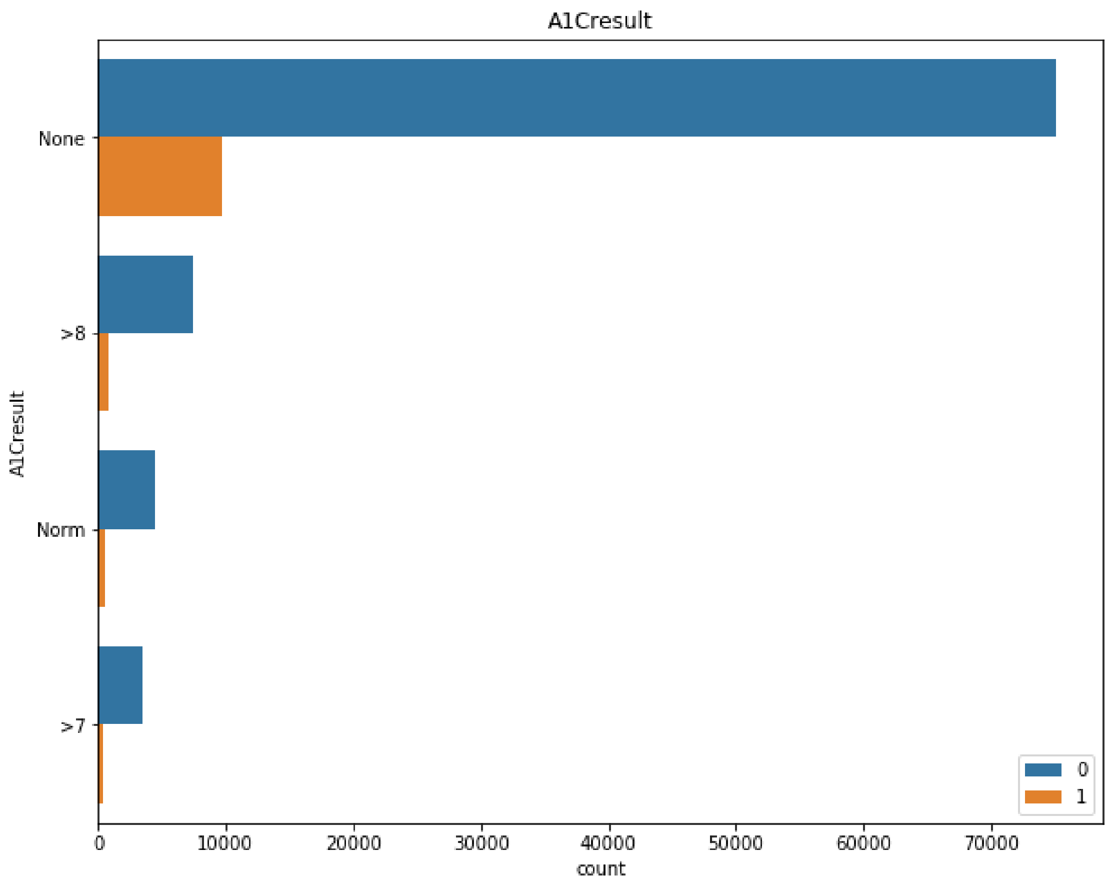

medical_specialty
InternalMedicine
Emergency/Trauma
Family/GeneralPractice
Cardiology
other
Surgery-General
Nephrology
Orthopedics
Orthopedics-Reconstructive
Radiologist
Pulmonology
Psychiatry
Urology
ObstetricsandGynecology
Surgery-Cardiovascular/Thoracic
Gastroenterology
Surgery-Vascular
medical_specialty
0
2000
4000
6000
8000
10000
12000
count
0
1

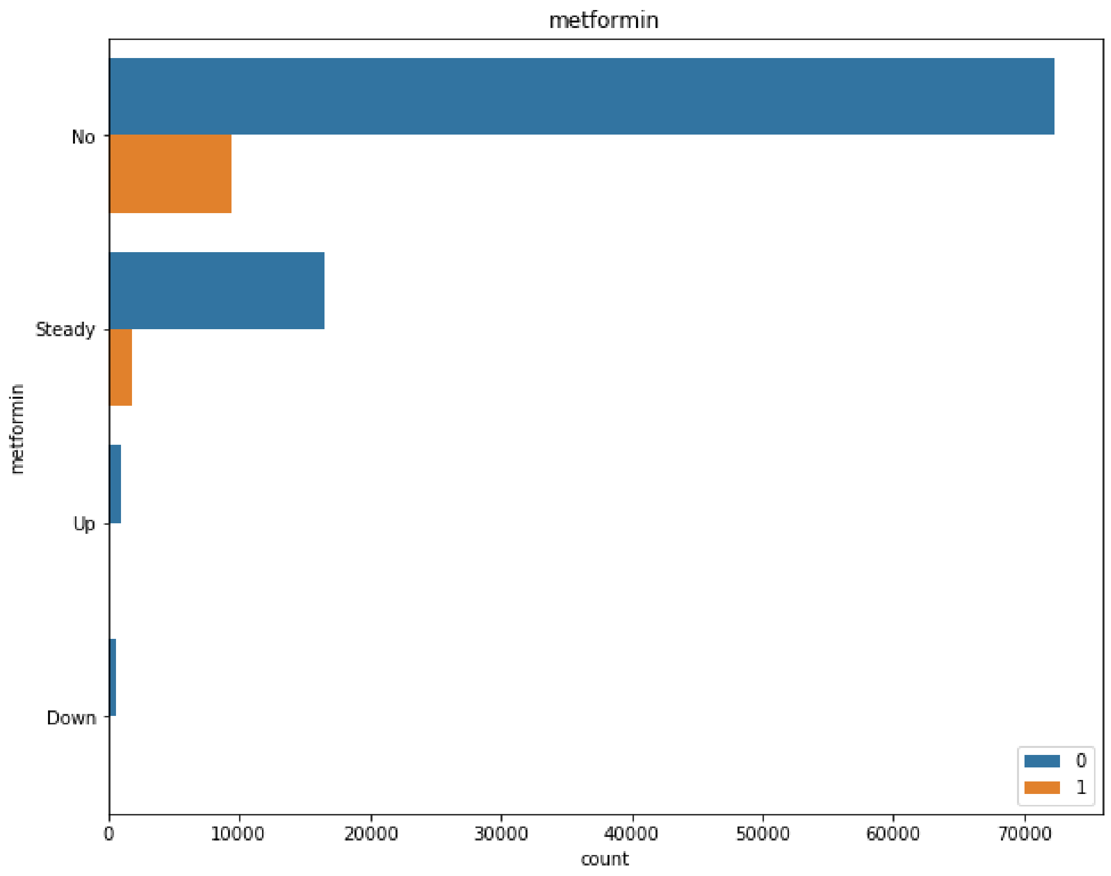

diag_1
circulatory
respiratory
other
digestive
injury
genitourinary
musculoskeletal
neoplasms
endocrine/nutritional
infection/parasitic
skin/tissue
other symptoms
diag_1
0
5000
10000
15000
20000
25000
count
0
1

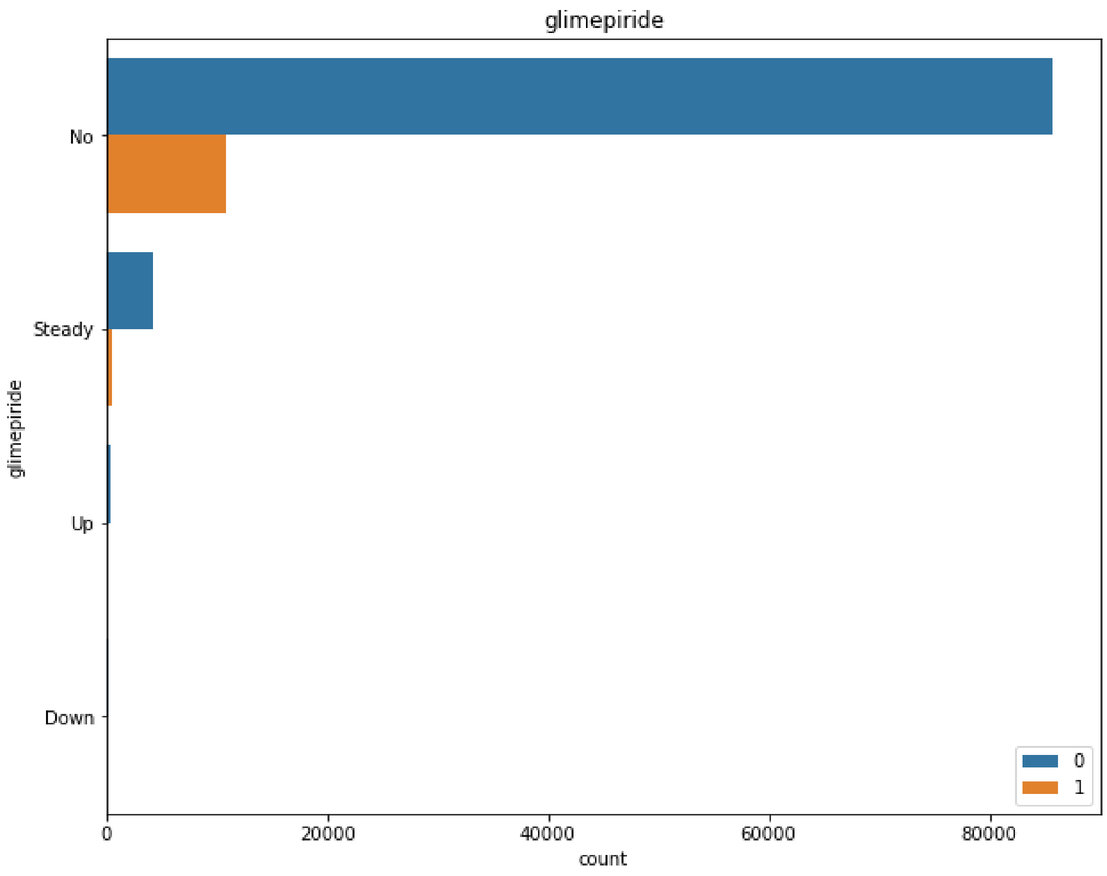

diag_2
circulatory
injury
other
respiratory
endocrine/nutritional
genitourinary
digestive
skin/tissue
neoplasms
other symptoms
infection/parasitic
musculoskeletal
diag_2
0
1
0
5000
10000
15000
20000
25000
count

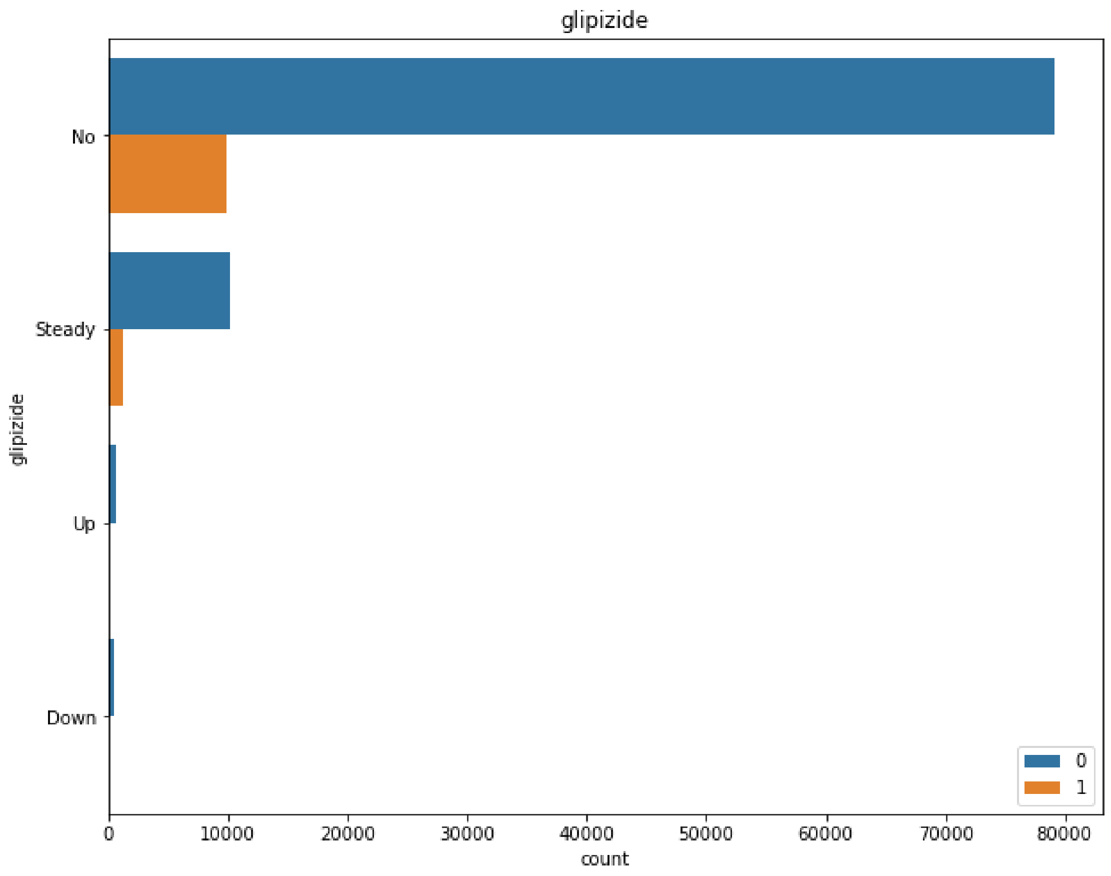

diag_3
circulatory
injury
other
endocrine/nutritional
respiratory
genitourinary
digestive
skin/tissue
other symptoms
musculoskeletal
neoplasms
infection/parasitic
diag_3
0
1
0
5000
10000
15000
20000
25000
count

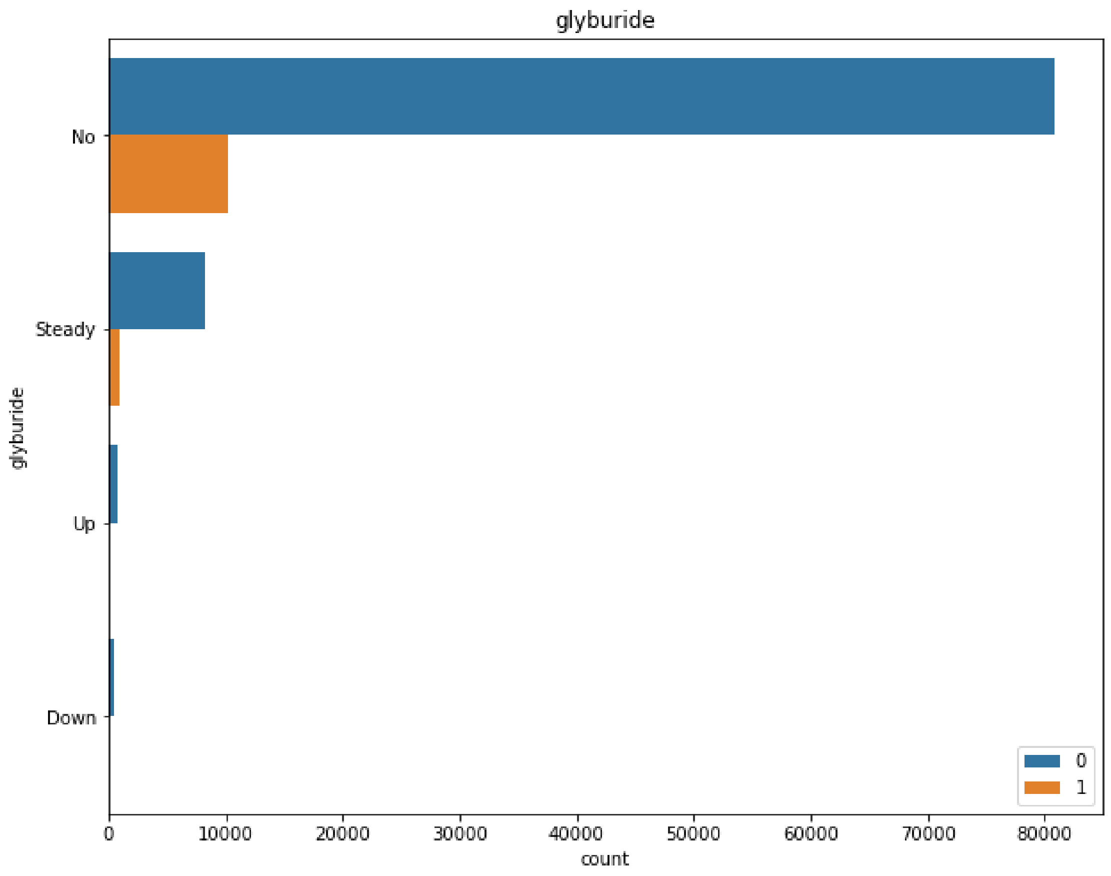

max_glu_serum
None
Norm
>200
>300
max_glu_serum
0
20000
40000
60000
80000
count
0
1

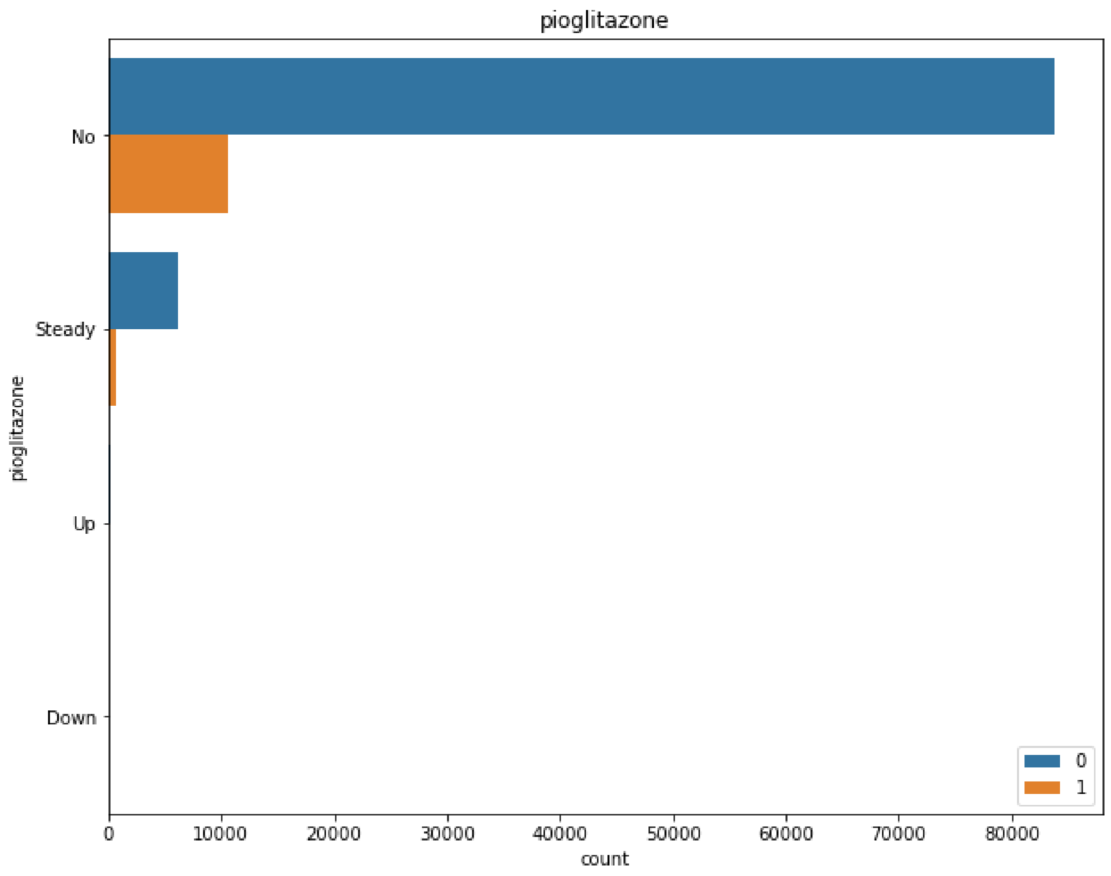

A1Cresult
None
>8
Norm
>7
A1Cresult
0
1
0
10000
20000
30000
40000
50000
60000
70000
count

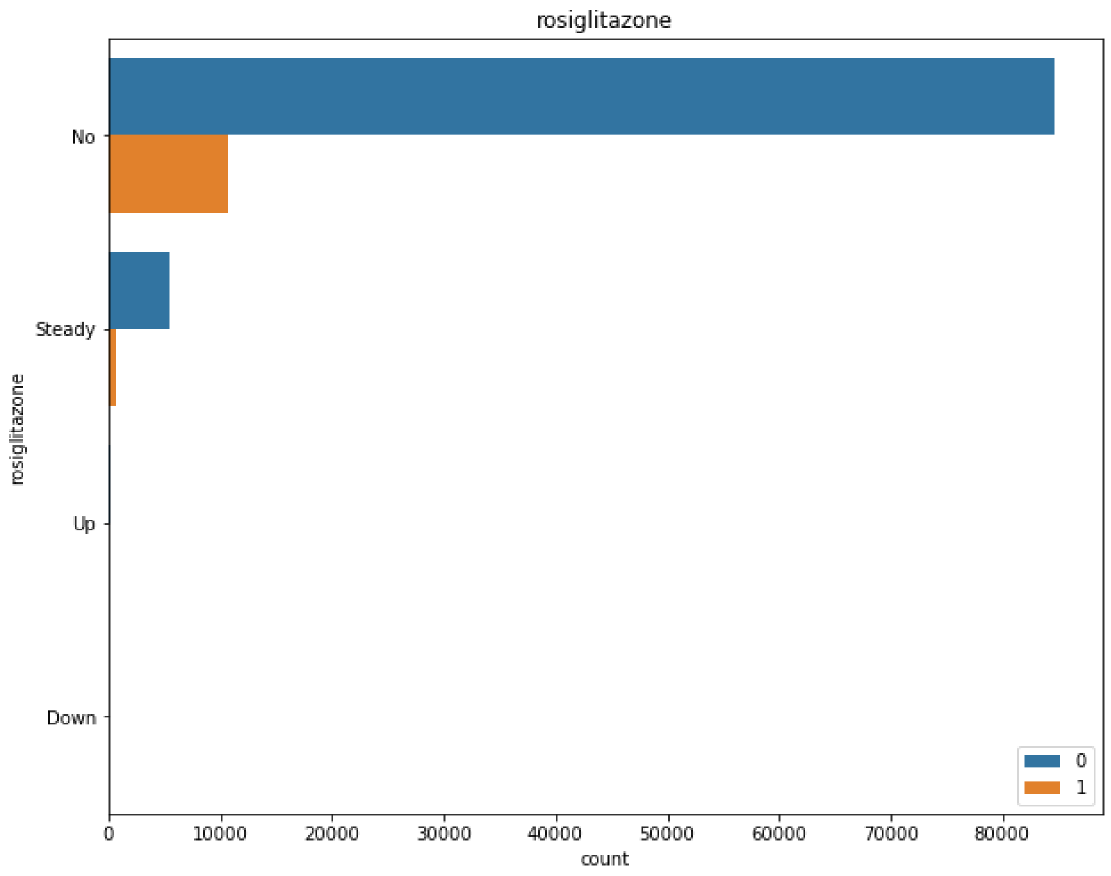

metformin
No
Steady
Up
Down
metformin
0
10000
20000
30000
40000
50000
60000
70000
count
0
1

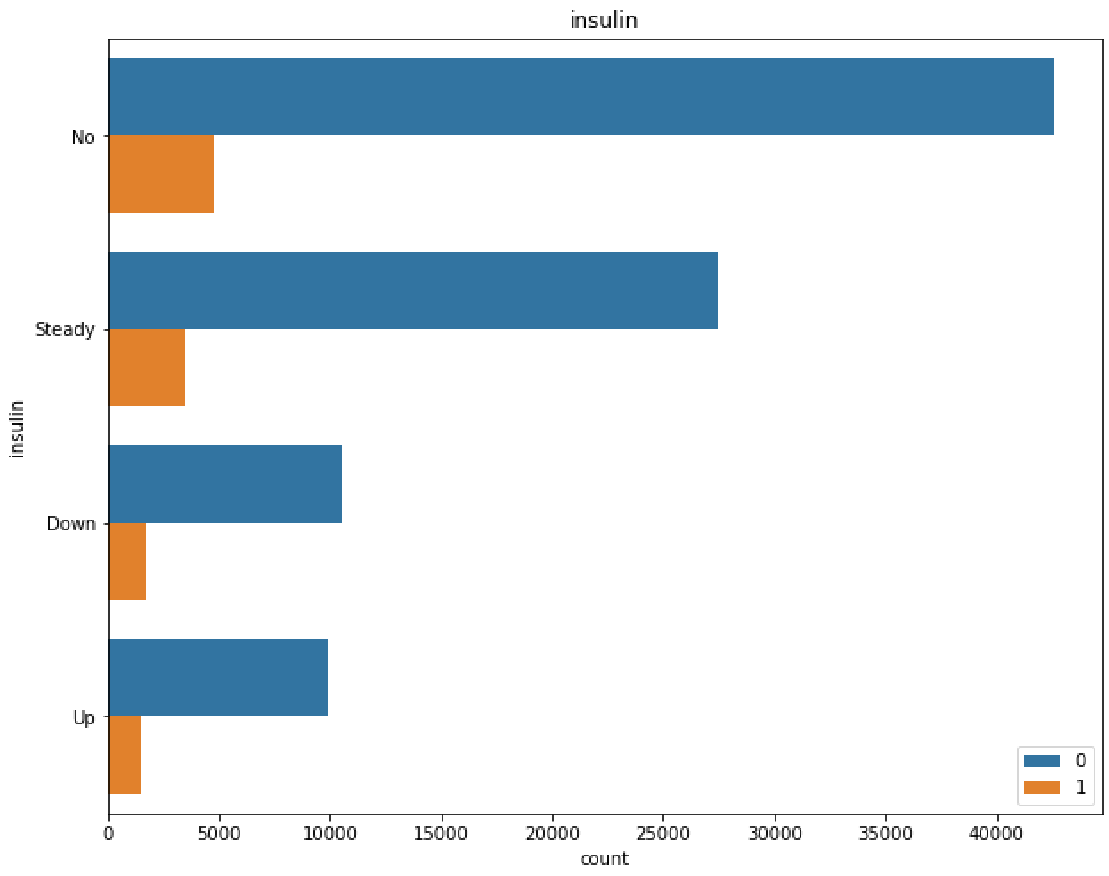

glimepiride
No
Steady
Up
Down
glimepiride
count
0
20000
40000
60000
80000
0
1

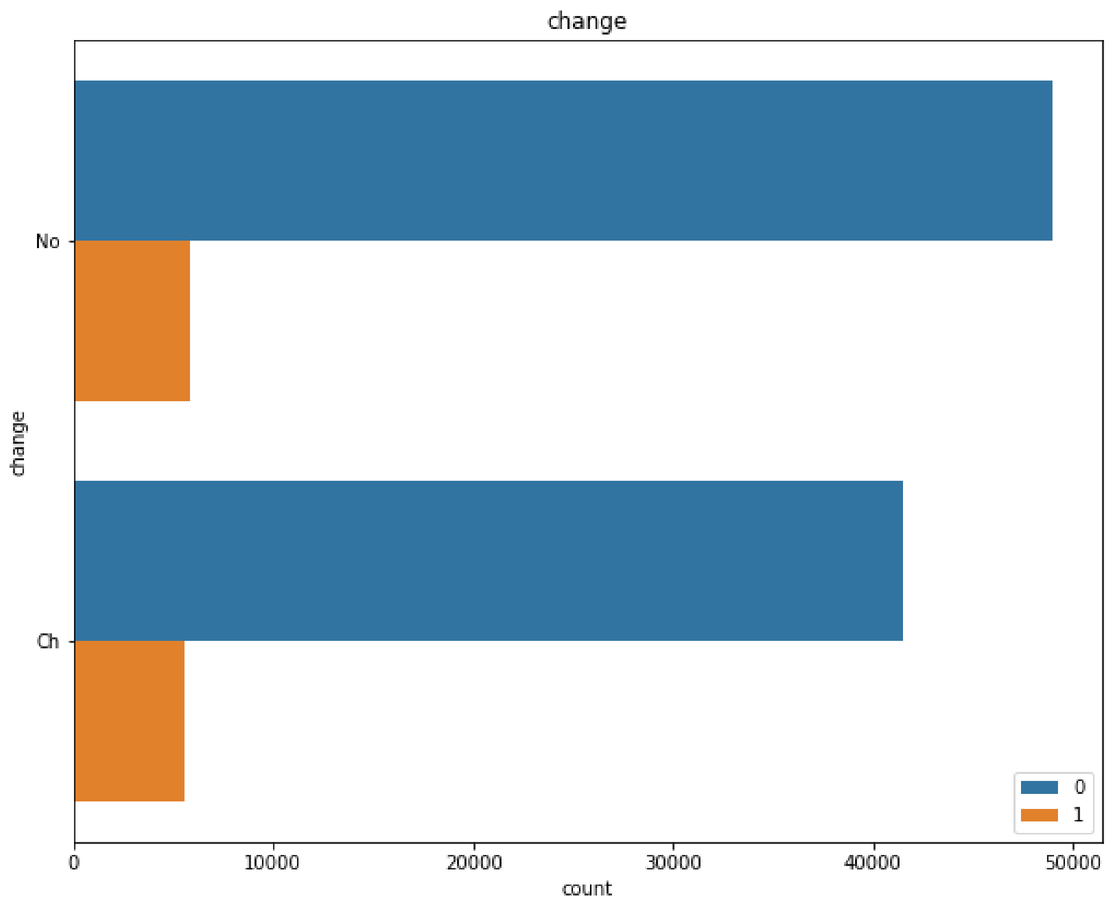

glipizide
No
Steady
Up
Down
glipizide
0
1
0
10000
20000
30000
40000
50000
60000
70000
80000
count


glyburide
No
Steady
Up
Down
glyburide
0
10000
20000
30000
40000
50000
60000
70000
80000
count
0
1

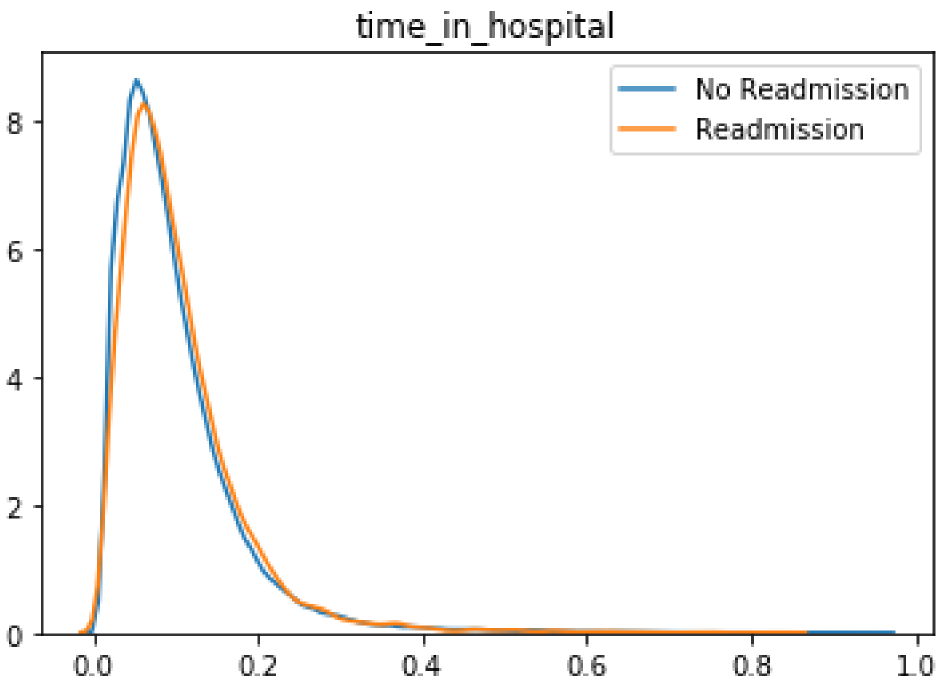

pioglitazone
No
Steady
Up
Down
pioglitazone
count
0
10000
20000
30000
40000
50000
60000
70000
80000
0
1

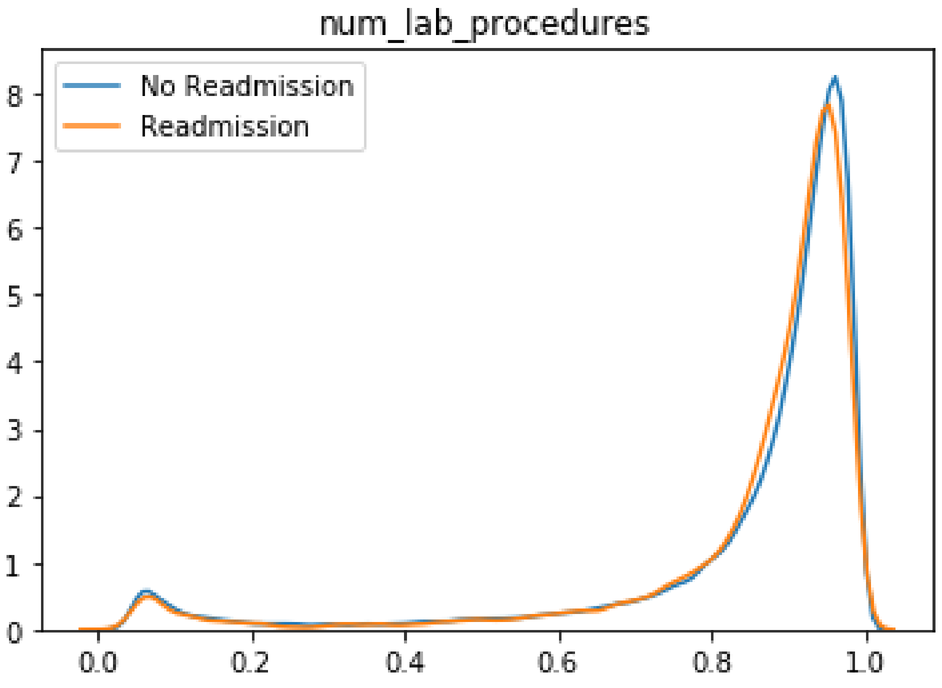

rosiglitazone
No
Steady
Up
Down
rosiglitazone
count
0
10000
20000
30000
40000
50000
60000
70000
80000
0
1

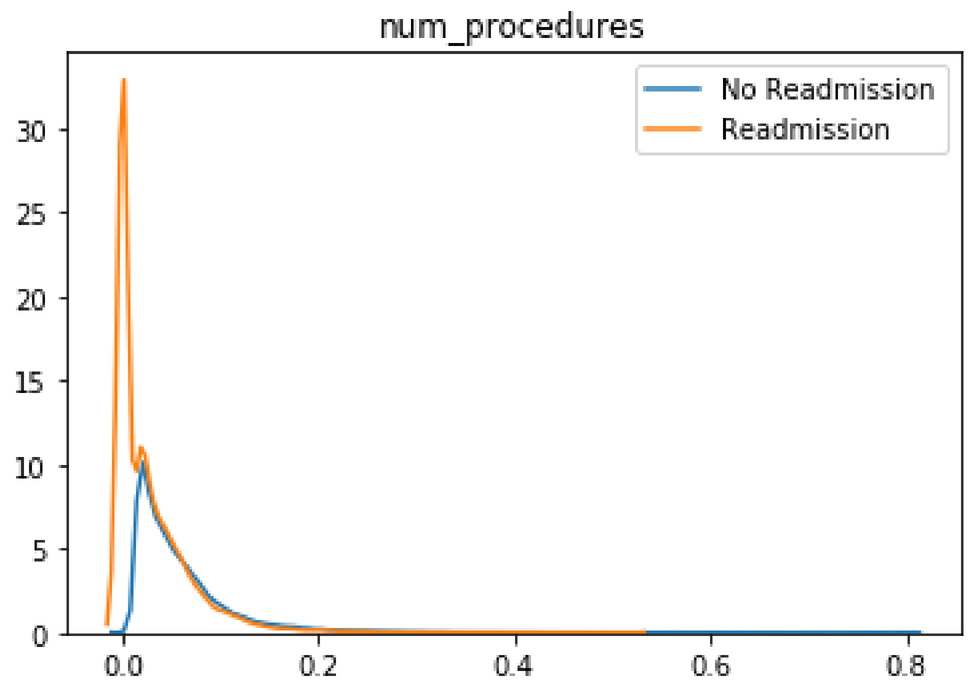

insulin
No
Steady
Down
Up
insulin
0
5000
10000
15000
20000
25000
30000
35000
40000
count
0
1

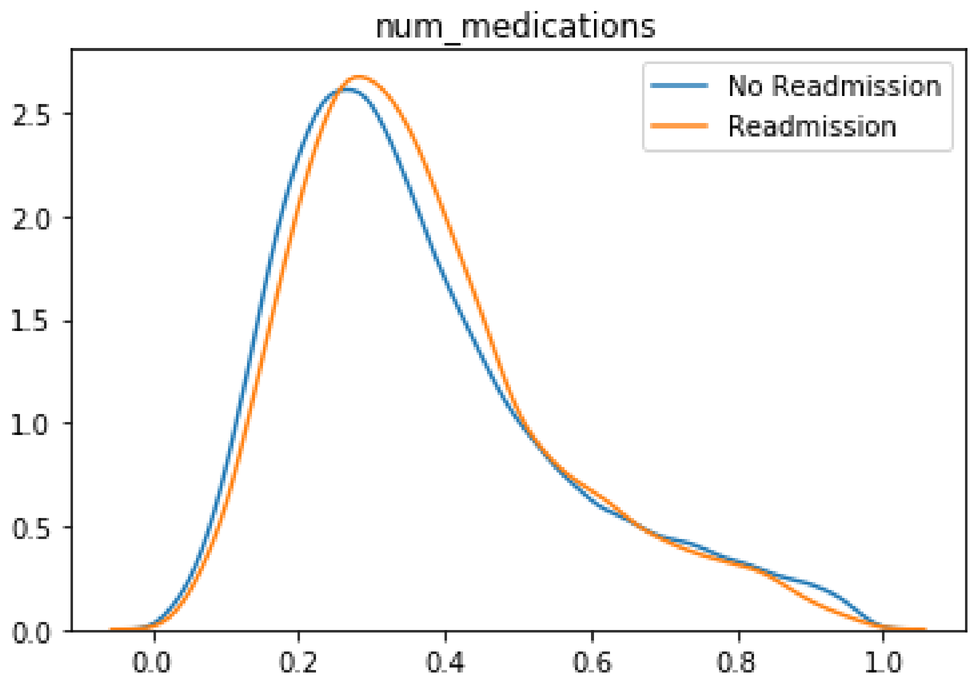


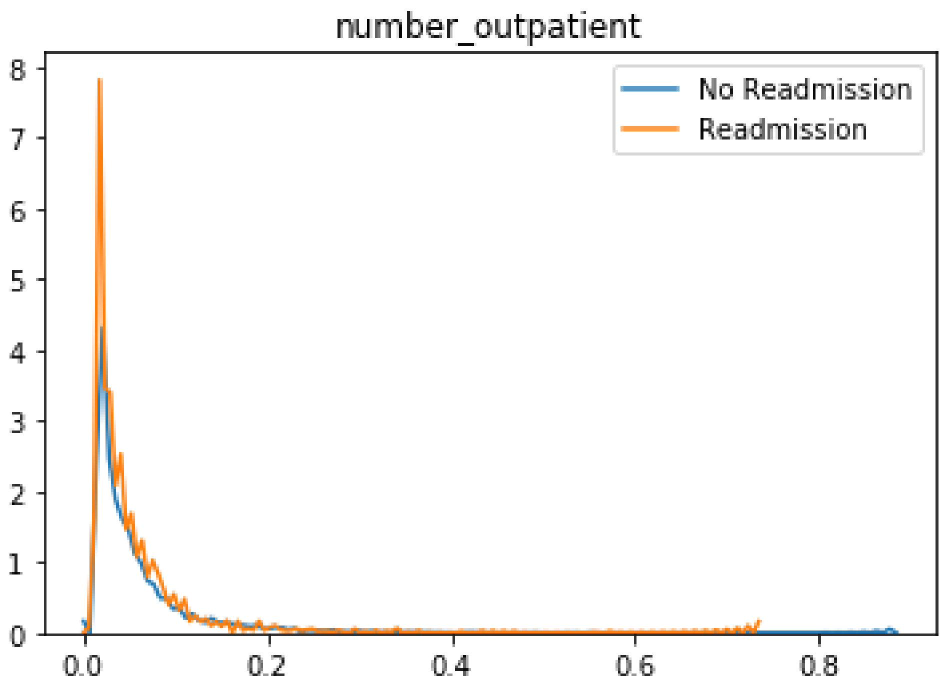
```
In [21]: # Plot continuous features by readmission label
         for i in num_feats:
             sns.kdeplot(df.loc[df.readmitted == 0, i])
             sns.kdeplot(df.loc[df.readmitted == 1, i])
             plt.title(i)
             plt.legend(['No Readmission', 'Readmission'])
             plt.show()
```

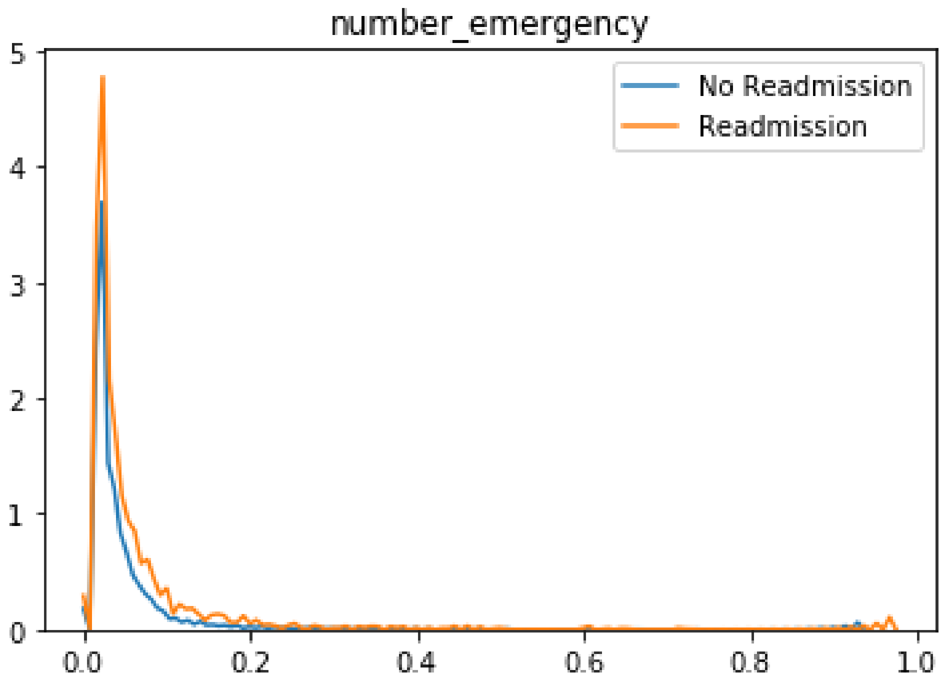

time_in_hospital
No Readmission
Readmission
8
6
4
2
0
0.0
0.2
0.4
0.6
0.8
1.0

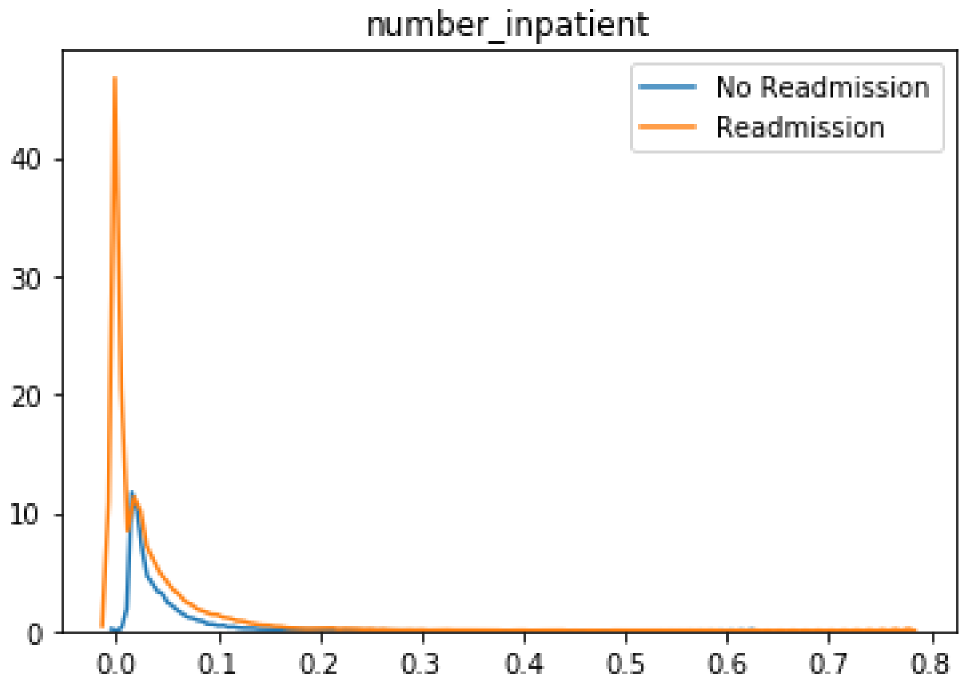

num_lab_procedures
No Readmission
Readmission
8
7
6
5
4
3
2
1
0
0.0
0.2
0.4
0.6
0.8
1.0

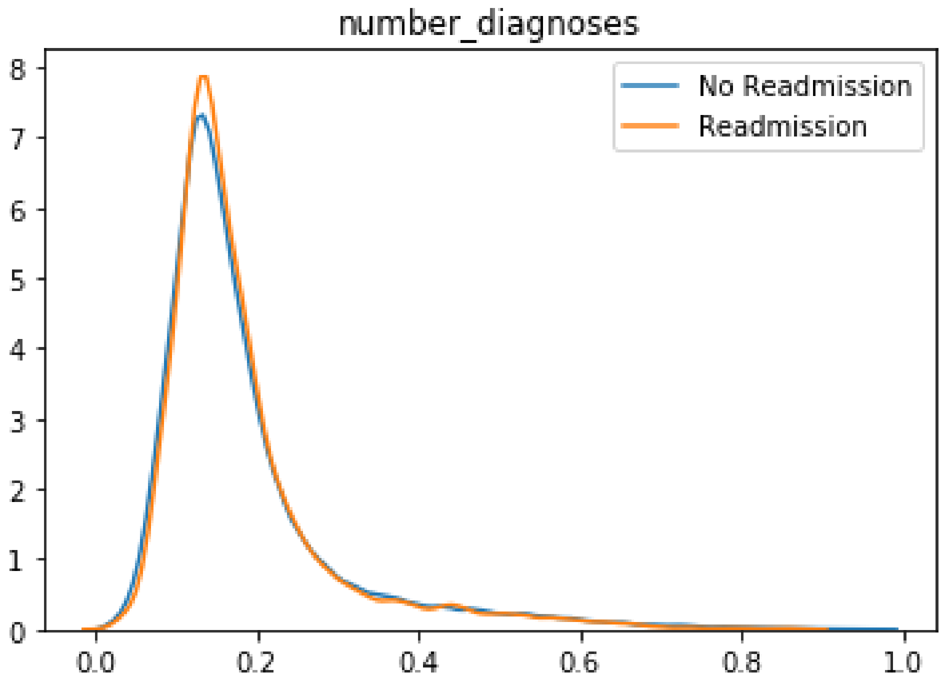

num_procedures
No Readmission
Readmission
30
25
20
15
10
5
0
0.0
0.2
0.4
0.6
0.8


num_medications
No Readmission
Readmission
2.5
2.0
1.5
1.0
0.5
0.0
0.0
0.2
0.4
0.6
0.8
1.0


number_outpatient
No Readmission
Readmission
0
1
2
3
4
5
6
7
8
0.0
0.2
0.4
0.6
0.8


number_emergency
No Readmission
Readmission
0
1
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0

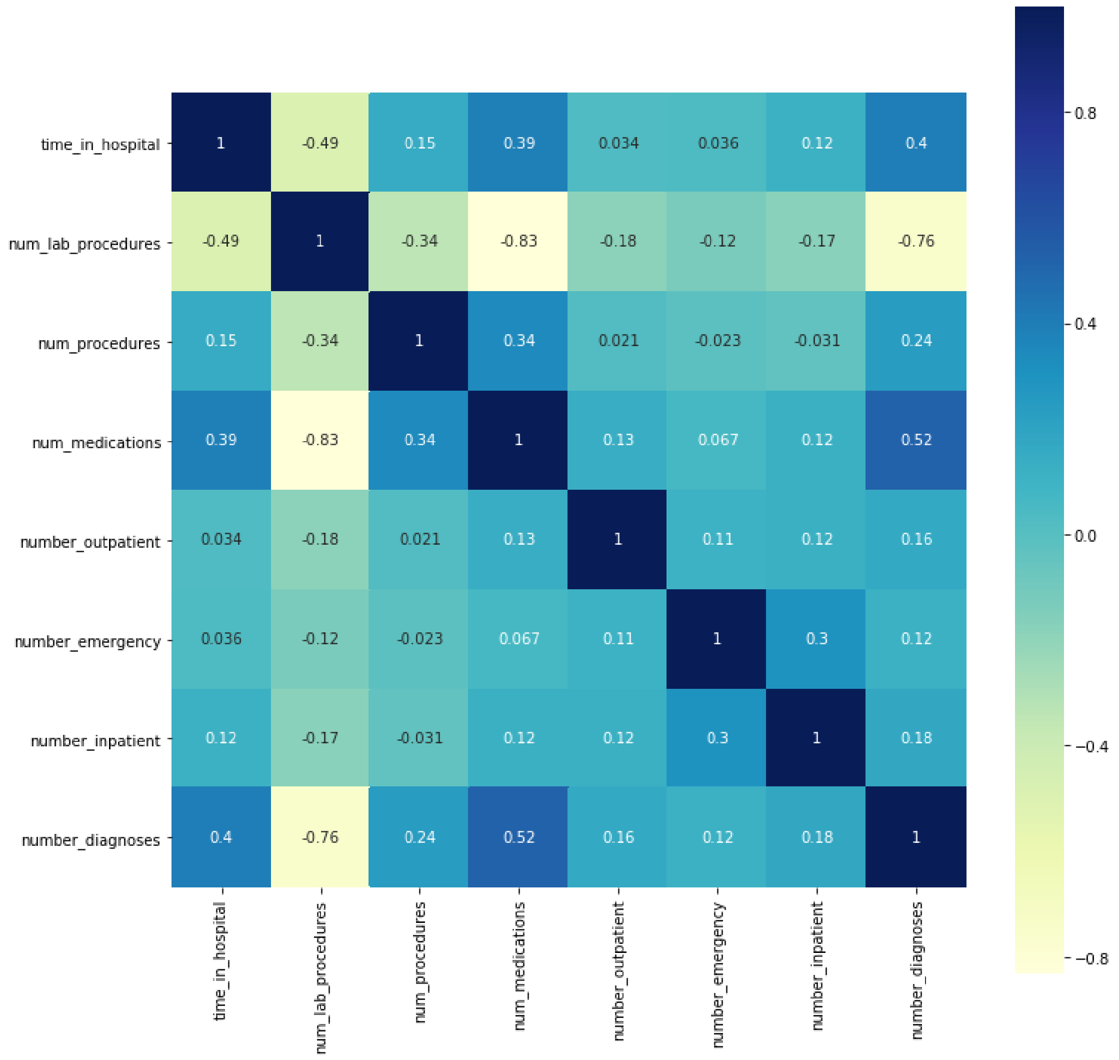

number_inpatient
No Readmission
Readmission
0
10
20
30
40
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8


number_diagnoses
No Readmission
Readmission
0
1
2
3
4
5
6
7
8
0.0
0.2
0.4
0.6
0.8
1.0

## 2.2 Correlation of Features

The following heatmap shows the correlation of continous features.

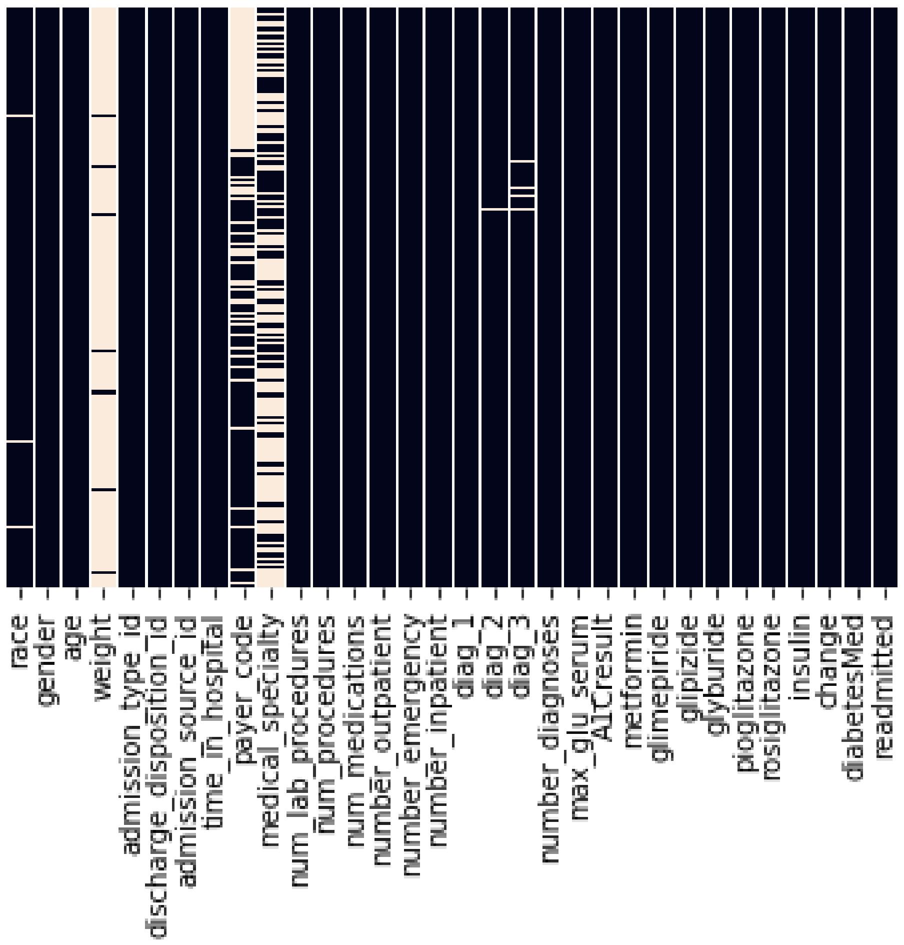
```
In [22]: # Plot the correlation of features
         fig, ax = plt.subplots(figsize=(12,12))
         sns.heatmap(df[num_feats].corr(), annot = True, cmap="YlGnBu", square = True, ax = ax)
         plt.show()
```



|  | time_in_hospital | num_lab_procedures | num_procedures | num_medications | number_outpatient | number_emergency | number_inpatient | number_diagnoses |
|---|---|---|---|---|---|---|---|---|
| time_in_hospital | 1 | -0.49 | 0.15 | 0.39 | 0.034 | 0.036 | 0.12 | 0.4 |
| num_lab_procedures | -0.49 | 1 | -0.34 | -0.83 | -0.18 | -0.12 | -0.17 | -0.76 |
| num_procedures | 0.15 | -0.34 | 1 | 0.34 | 0.021 | -0.023 | -0.031 | 0.24 |
| num_medications | 0.39 | -0.83 | 0.34 | 1 | 0.13 | 0.067 | 0.12 | 0.52 |
| number_outpatient | 0.034 | -0.18 | 0.021 | 0.13 | 1 | 0.11 | 0.12 | 0.16 |
| number_emergency | 0.036 | -0.12 | -0.023 | 0.067 | 0.11 | 1 | 0.3 | 0.12 |
| number_inpatient | 0.12 | -0.17 | -0.031 | 0.12 | 0.12 | 0.3 | 1 | 0.18 |
| number_diagnoses | 0.4 | -0.76 | 0.24 | 0.52 | 0.16 | 0.12 | 0.18 | 1 |

## 2.3 Missing Data

```
In [23]: # Display the null features in the dataset using a heat map
         sns.heatmap(df.isnull(), cbar=False, yticklabels=False)
         plt.show()
```



There is a lot of missing data in 3 columns. Let's look at how much exactly is missing.

```
In [24]: # Find the percentage of missing data in the dataset
         null_columns=df.columns[df.isnull().any()]
         100*df[null_columns].isnull().sum()/df.shape[0]
```

```
Out[24]: race                  2.233555
         weight               96.858479
         payer_code           39.557416
         medical_specialty    49.082208
         diag_1                0.020636
         diag_2                0.351787
         diag_3                1.398306
         dtype: float64
```

The weight column is missing data in 96% of its records. Drop it. The payer code and medical specialty column have moderate missing data. The race and diags columns have little missing data. Fill in missing data using a random forest.

```
In [25]: # Drop the weight column
         df = df.drop('weight', 1)
         cat_feats.remove('weight')
```

## 2.4 Missing Data - Random Forest

```
In [26]: # A function to impute missing values using a RF classifier
         def missing_val_rf(old_df):

             df_rf = old_df.copy()
             for col in df_rf.columns[df_rf.isnull().any()]:
                 Y = df_rf.loc[:,col]
                 X = pd.get_dummies(df_rf.loc[:, df_rf.columns != col])

                 Xtrain = X.loc[~Y.isnull()]
                 Xtest = X.loc[Y.isnull()]
                 Ytrain = Y.loc[~Y.isnull()]
                 Ytest = Y.loc[Y.isnull()]

                 clf = RandomForestClassifier(n_estimators=5)
                 clf.fit(Xtrain, Ytrain)

                 p = clf.predict(Xtest)
                 Ytest = pd.DataFrame(p, index = Xtest.index)
                 new_col = pd.concat([Ytrain, Ytest])
                 df_rf[col] = new_col
             return df_rf
```

```
In [27]: # Fill in missing values
         df_rf_filled = missing_val_rf(df)
```

## 2.5 Combine numerical and categorical data along with class label into one dataframe

```
In [28]: # A function to combine data into a clean dataframe
         def combineData(df, cat, num, label):
             return pd.concat([pd.get_dummies(df.loc[:,cat_feats]),
                               df.loc[:, num], df.loc[:, label]], axis = 1)
```

## 2.6 Encode Features

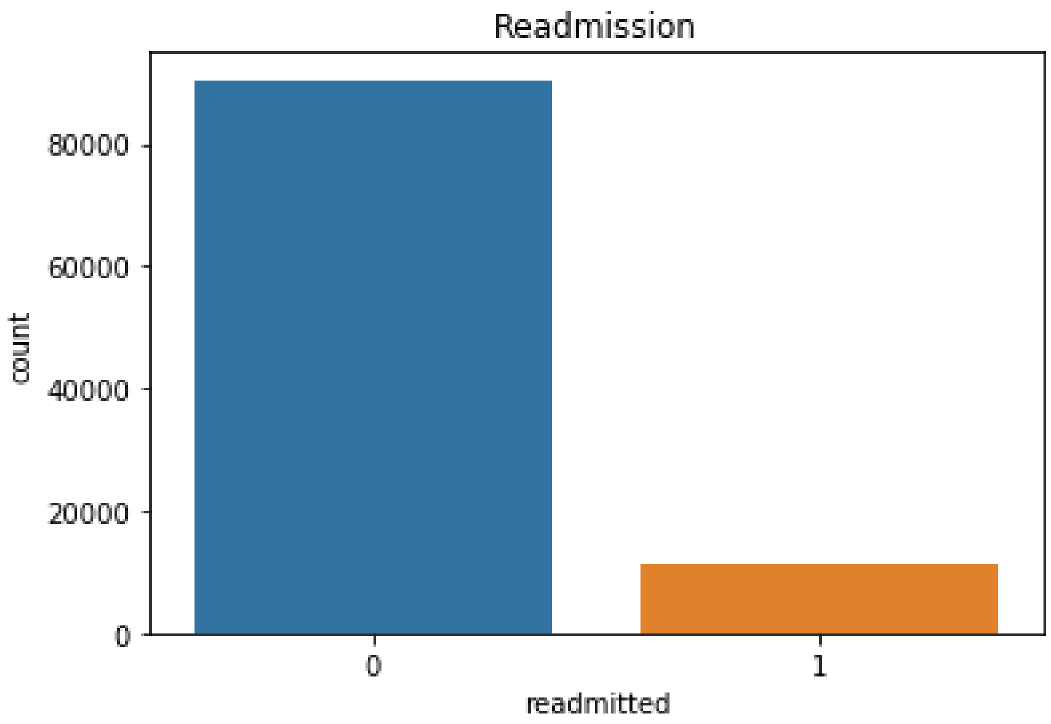
Encode the categorical features and concat it with the numerical features and class label.

```
In [29]: # Encode the categorical features and combine it with the continuous features
         feat_lab_rf = combineData(df_rf_filled, cat_feats, num_feats, "readmitted")
```

## 2.7 Class Label Distribution

Look at the distribution of the class label.

```
In [30]: # Plot the counts of the readmission label
         sns.countplot(df.readmitted)
         plt.title("Readmission")
         plt.show()
```



There are a lot more cases of non-readmission than readmission. This is an imbalanced dataset. To fix this, use undersampling, oversampling and SMOTE to equate the class labels.

### 2.8 Split Feature Label

```
In [31]: # A function to split the X and Y from a dataset
         def split_features_label(df):
             X = df.iloc[:,:-1]
             Y = df.iloc[:,-1]
             return X,Y
```

## 3 Feature Selection and Oversampling Solutions

Before thinking about getting the class label counts to be equal, appropriate features must be selected first so that it does not affect the SMOTE oversampling algorithm afterwards. Feature selection will be run on the dataset with missing values imputed using random forest. The features will be selected by choosing the top 30% that is related to the class label via a $\chi^2$ test. After the features are selected, it will be joined with the class labels for the oversampling solutions. Imbalancing will then be solved using the SMOTE algorithm.

```
In [32]: # Split the dataset into Xs and Y
         Xrf, Yrf = split_features_label(feat_lab_rf)

         # Get the top 33% relevant features
         Xrf_rev = pd.DataFrame(SelectPercentile(chi2,
                                                 percentile = 33).fit_transform(Xrf, Yrf))

         # Oversample using SMOTE
         sm = SMOTE(random_state = 42)
         Xrf_smote, Yrf_smote = sm.fit_sample(Xrf_rev, Yrf)
         Xrf_smote = pd.DataFrame(Xrf_smote)
         Yrf_smote = pd.Series(Yrf_smote)
```

## 3.1 Model for 1 Classifier

```
In [33]: # A function to runn k-fold cross validation using 1 classifier
         def kfoldcv1Model(X, Y, clf):

             start = time.time()
             kf = KFold(n_splits=5, random_state = 42)
             total_tn, total_fp, total_fn, total_tp = 0, 0, 0, 0
             acc = []

             for train_index, test_index in kf.split(X):
                 Xtrain, Xtest = X.iloc[train_index], X.iloc[test_index]
                 Ytrain, Ytest = Y.iloc[train_index], Y.iloc[test_index]

                 clf.fit(Xtrain, Ytrain)
                 Ypred = clf.predict(Xtest)
                 acc_score = accuracy_score(Ytest, Ypred)
                 acc.append(acc_score)

                 tn, fp, fn, tp = confusion_matrix(Ytest, Ypred).ravel()
                 total_tn += tn
                 total_fp += fp
                 total_fn += fn
                 total_tp += tp

             cm = np.array([[total_tn, total_fp], [total_fn, total_tp]])
             sns.heatmap(cm, annot = True, fmt='g', cmap="Blues",
                         square = True, annot_kws={"size": 20})
             plt.title("Confusion Matrix")
             plt.xlabel("Predicted Value")
             plt.ylabel("True Value")
             plt.show()

             print("Classification Report for", clf)
             precision = total_tp / (total_tp + total_fp)
```

```
            recall = total_tp / (total_tp + total_fn)
            F1 = 2 * (precision * recall) / (precision + recall)
            print("Accuracy:", np.mean(acc))
            print("Precision: ", precision)
            print("Recall: ", recall)
            print("F1 Score: ", F1)

            end = time.time()
            print("Time Elapsed: ", end - start, " secs")

            return np.mean(acc), F1, end - start
```

## 3.2 Ensemble Model of 3 Classifiers

```
In [34]: # A function to run k-fold cross validation using an ensemble of
         # 3 given models
         def kfoldcv3Models(X, Y, modelA, modelB, modelC):

             start = time.time()
             kf = KFold(n_splits=5, random_state = 42)
             total_tn, total_fp, total_fn, total_tp = 0, 0, 0, 0
             acc = []

             for train_index, test_index in kf.split(X):
                 Xtrain, Xtest = X.iloc[train_index], X.iloc[test_index]
                 Ytrain, Ytest = Y.iloc[train_index], Y.iloc[test_index]

                 clf = VotingClassifier(estimators =
                                     [('modelA', modelA), ('modelB', modelB),
                                     ('modelC', modelC)], voting = 'hard')

                 clf.fit(Xtrain, Ytrain)
                 Ypred = clf.predict(Xtest)
                 acc_score = accuracy_score(Ytest, Ypred)
                 acc.append(acc_score)

                 tn, fp, fn, tp = confusion_matrix(Ytest, Ypred).ravel()
                 total_tn += tn
                 total_fp += fp
                 total_fn += fn
                 total_tp += tp

             cm = np.array([[total_tn, total_fp], [total_fn, total_tp]])
             sns.heatmap(cm, annot = True, fmt='g', cmap="BuPu",
                         square = True, annot_kws={"size": 20})
             plt.title("Confusion Matrix")
             plt.xlabel("Predicted Value")
             plt.ylabel("True Value")
```

```
        plt.show()

        print("Classification Report for ", modelA, modelB, modelC)
        precision = total_tp / (total_tp + total_fp)
        recall = total_tp / (total_tp + total_fn)
        F1 = 2 * (precision * recall) / (precision + recall)
        print("Accuracy:", np.mean(acc))
        print("Precision: ", precision)
        print("Recall: ", recall)
        print("F1 Score: ", F1)

        end = time.time()
        print("Time Elapsed: ", end - start, " secs")

        return np.mean(acc), F1, end - start
```

### 3.3 Ensemble Model of 5 Classifiers

```
In [35]: # A function to run k-fold cross validation using an
         # ensemble of 5 models
         def kfoldcv5Models(X, Y):

             start = time.time()
             kf = KFold(n_splits=5, random_state = 42)
             total_tn, total_fp, total_fn, total_tp = 0, 0, 0, 0
             acc = []

             for train_index, test_index in kf.split(X):
                 Xtrain, Xtest = X.iloc[train_index], X.iloc[test_index]
                 Ytrain, Ytest = Y.iloc[train_index], Y.iloc[test_index]

                 cl1 = Perceptron(random_state = 42)
                 cl2 = GaussianNB()
                 cl3 = DecisionTreeClassifier(random_state = 42)
                 cl4 = LinearSVC(dual = False, C = 0.3, random_state = 42)
                 cl5 = ExtraTreeClassifier(random_state = 42)

                 clf = VotingClassifier(estimators =
                                     [('P', cl1), ('NB', cl2),
                                     ('DT', cl3), ('SVC', cl4),
                                     ('ET', cl5)], voting = 'hard')

                 clf.fit(Xtrain, Ytrain)
                 Ypred = clf.predict(Xtest)
                 acc_score = accuracy_score(Ytest, Ypred)
                 acc.append(acc_score)

                 tn, fp, fn, tp = confusion_matrix(Ytest, Ypred).ravel()
```

```
            total_tn += tn
            total_fp += fp
            total_fn += fn
            total_tp += tp

        cm = np.array([[total_tn, total_fp], [total_fn, total_tp]])
        sns.heatmap(cm, annot = True, fmt='g', cmap="Greens",
                    square = True, annot_kws={"size": 20})
        plt.title("Confusion Matrix")
        plt.xlabel("Predicted Value")
        plt.ylabel("True Value")
        plt.show()

        print("Classification Report for all 5 Classifiers")
        precision = total_tp / (total_tp + total_fp)
        recall = total_tp / (total_tp + total_fn)
        F1 = 2 * (precision * recall) / (precision + recall)
        print("Accuracy:", np.mean(acc))
        print("Precision: ", precision)
        print("Recall: ", recall)
        print("F1 Score: ", F1)

        end = time.time()
        print("Time Elapsed: ", end - start, " secs")

        return np.mean(acc), F1, end - start
```

### 3.4 Ensemble Model of Random Forest

```
In [36]: # A function to run k-Fold cross validation using
         # random forest classifier
         def kfoldcvRF(X, Y, n = 10):

             start = time.time()
             kf = KFold(n_splits=5, random_state = 42)
             total_tn, total_fp, total_fn, total_tp = 0, 0, 0, 0
             acc = []

             for train_index, test_index in kf.split(X):
                 Xtrain, Xtest = X.iloc[train_index], X.iloc[test_index]
                 Ytrain, Ytest = Y.iloc[train_index], Y.iloc[test_index]

                 clf = RandomForestClassifier(n_estimators = n)

                 clf.fit(Xtrain, Ytrain)
                 Ypred = clf.predict(Xtest)
                 acc_score = accuracy_score(Ytest, Ypred)
                 acc.append(acc_score)
```

```
            tn, fp, fn, tp = confusion_matrix(Ytest, Ypred).ravel()
            total_tn += tn
            total_fp += fp
            total_fn += fn
            total_tp += tp

        cm = np.array([[total_tn, total_fp], [total_fn, total_tp]])
        sns.heatmap(cm, annot = True, fmt='g', cmap="Greens",
                    square = True, annot_kws={"size": 20})
        plt.title("Confusion Matrix")
        plt.xlabel("Predicted Value")
        plt.ylabel("True Value")
        plt.show()

        print("Classification Report for Random Forest")
        precision = total_tp / (total_tp + total_fp)
        recall = total_tp / (total_tp + total_fn)
        F1 = 2 * (precision * recall) / (precision + recall)
        print("Accuracy:", np.mean(acc))
        print("Precision: ", precision)
        print("Recall: ", recall)
        print("F1 Score: ", F1)

        end = time.time()
        print("Time Elaped: ", end - start, " secs")

        return np.mean(acc), F1, end - start
```

### 3.4.1 Classifiers

The 5 classifiers are:

- Perceptron
- Naive Bayes
- Decision Tree
- Linear SVC
- Extra Tree

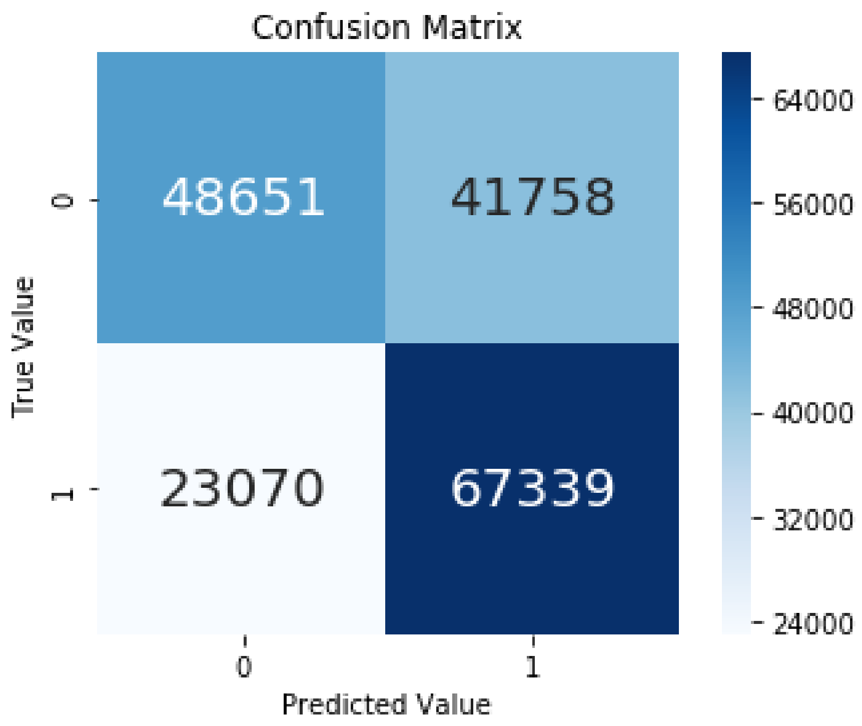
Each of these five classifiers will be used individually to create a model. Then several ensemble models will be made. There are 5 classifications algorithms to choose 3 from for each ensemble model. In total, there are 10 combinations.

The 10 combinations will be: - Perceptron, Naive Bayes, Decision Tree - Perceptron, Naive Bayes, Linear SVC - Perceptron, Naive Bayes, Extra Tree - Perceptron, Decision Tree, Linear SVC - Perceptron, Decision Tree, Extra Tree - Perceptron, Linear SVC, Extra Tree - Naive Bayes, Decision Tree, Linear SVC - Naive Bayes, Decision Tree, Extra Tree - Naive Bayes, Linear SVC, Extra Tree - Decision Tree, Linear SVC, Extra Tree

In addition, an ensemble model of all 5 classifiers and an ensemble model of random forests will be created.

### 3.5 One Classifier Model: Perceptron

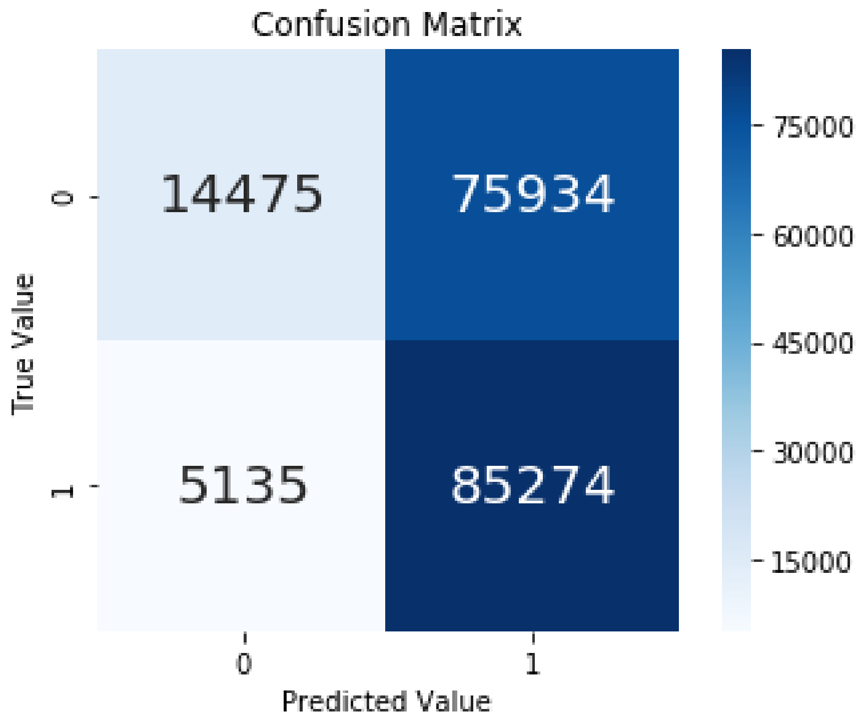
```
In [37]: accuracy_1, f1_1, T1 = kfoldcv1Model(Xrf_smote, Yrf_smote, Perceptron())
```



```
Classification Report for Perceptron(alpha=0.0001, class_weight=None, early_stopping=False, eta0
      fit_intercept=True, max_iter=None, n_iter=None, n_iter_no_change=5,
      n_jobs=None, penalty=None, random_state=0, shuffle=True, tol=None,
      validation_fraction=0.1, verbose=0, warm_start=False)
Accuracy: 0.6414753913372047
Precision:  0.6172397041165202
Recall:  0.7448262894180889
F1 Score:  0.6750573917576413
Time Elapsed:  1.2549679279327393  secs
```

### 3.6 One Classifier Model: Naive Bayes

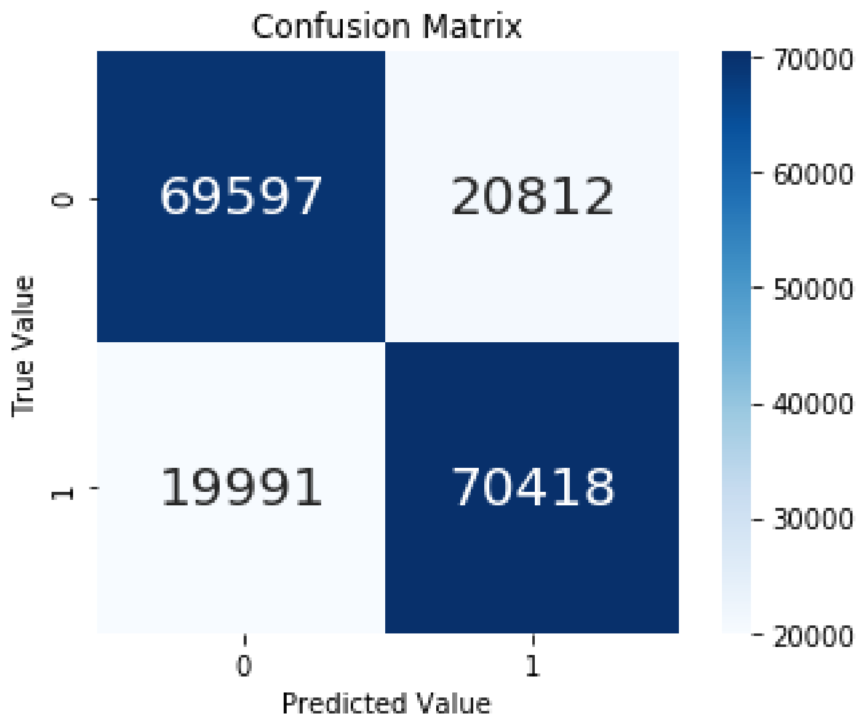
```
In [38]: accuracy_2, f1_2, T2 = kfoldcv1Model(Xrf_smote, Yrf_smote, GaussianNB())
```



```
Classification Report for GaussianNB(priors=None, var_smoothing=1e-09)
Accuracy: 0.5516585558212638
Precision:  0.528968785668205
Recall:  0.9432025572675287
F1 Score:  0.6778079382553643
Time Elapsed:  1.0086472034454346  secs
```

## 3.7 One Classifier Model: Decision Tree

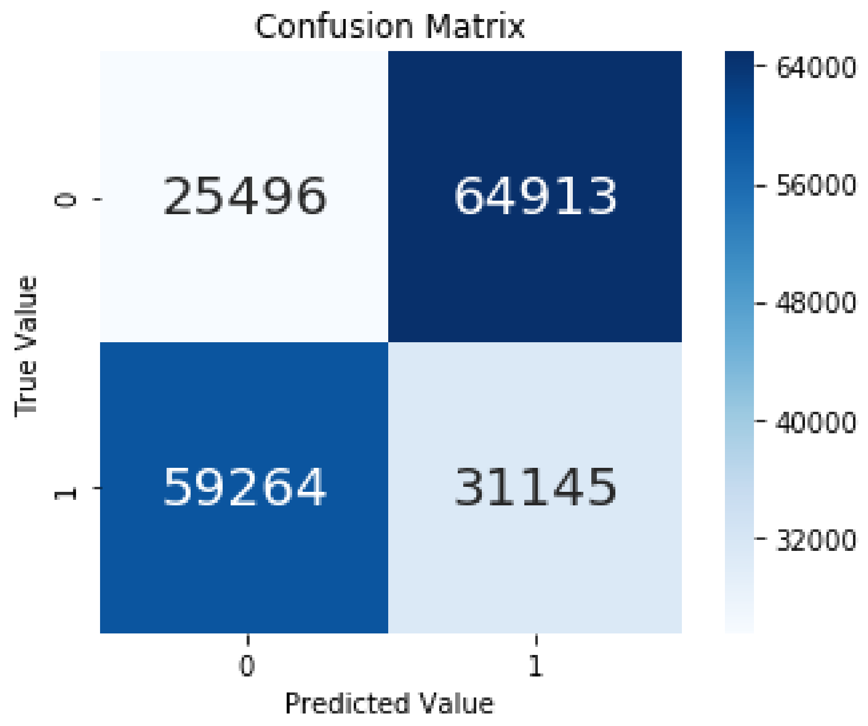
```
In [39]: accuracy_3, f1_3, T3 = kfoldcv1Model(Xrf_smote, Yrf_smote, DecisionTreeClassifier())
```



```
Classification Report for DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best')
Accuracy: 0.7743425755210167
Precision:  0.7718732872958457
Recall:  0.7788826333661472
F1 Score:  0.7753621193686376
Time Elapsed:  8.58218002319336  secs
```

### 3.8 One Classifier Model: Linear SVC

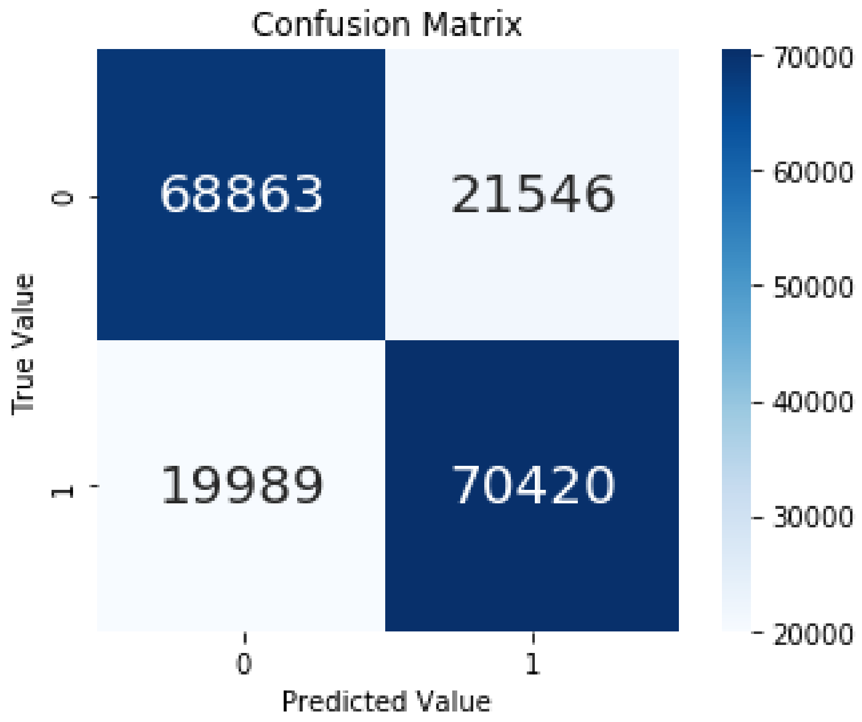
```
In [40]: accuracy_4, f1_4, T4 = kfoldcv1Model(Xrf_smote, Yrf_smote, LinearSVC(dual = False, C =
```



```
Classification Report for LinearSVC(C=0.3, class_weight=None, dual=False, fit_intercept=True,
     intercept_scaling=1, loss='squared_hinge', max_iter=1000,
     multi_class='ovr', penalty='l2', random_state=None, tol=0.0001,
     verbose=0)
Accuracy: 0.313247699952656
Precision:  0.3242311936538341
Recall:  0.3444900397084361
F1 Score:  0.33405374677556887
Time Elapsed:  6.577644109725952  secs
```

### 3.9 One Classifier Model: Extra Tree

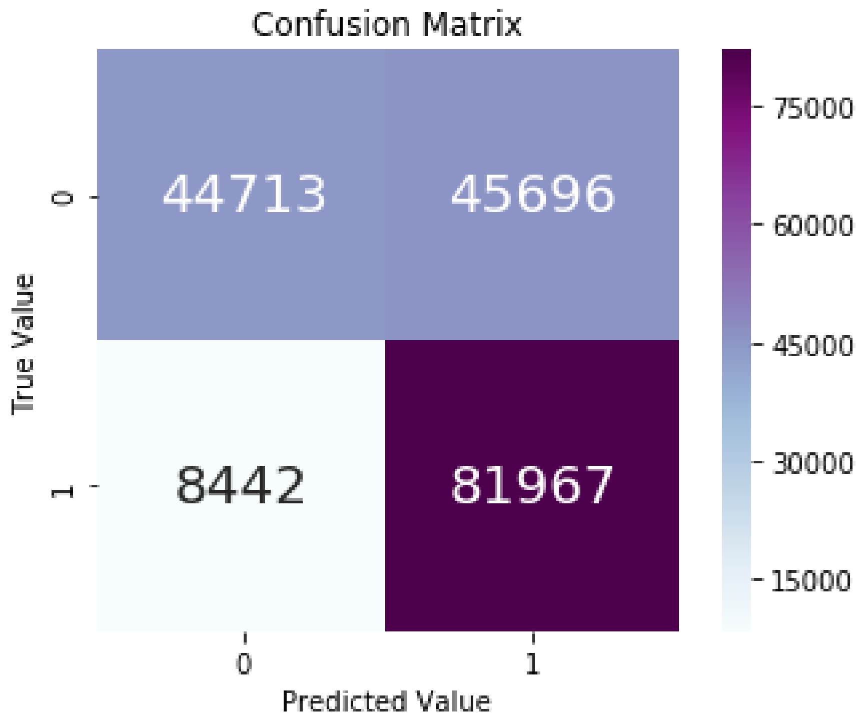
```
In [41]: accuracy_5, f1_5, T5 = kfoldcv1Model(Xrf_smote, Yrf_smote, ExtraTreeClassifier())
```



```
Classification Report for ExtraTreeClassifier(class_weight=None, criterion='gini', max_depth=Non
          max_features='auto', max_leaf_nodes=None,
          min_impurity_decrease=0.0, min_impurity_split=None,
          min_samples_leaf=1, min_samples_split=2,
          min_weight_fraction_leaf=0.0, random_state=None,
          splitter='random')
Accuracy: 0.7702941288675298
Precision:  0.7657177652610747
Recall:  0.7789047550575717
F1 Score:  0.7722549691569568
Time Elapsed:  2.0421249866485596  secs
```

### 3.10 Ensemble Model 1: Perceptron, Naive Bayes, Decision tree

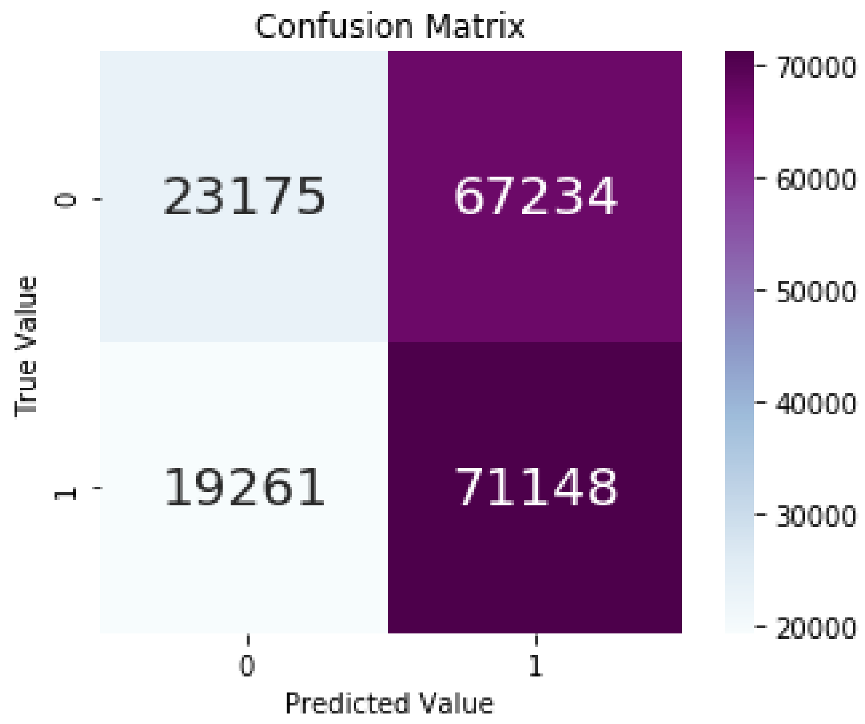
```
In [42]: accuracy_6, f1_6, T6 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                               Perceptron(),
                                               GaussianNB(),
                                               DecisionTreeClassifier())
```



```
Classification Report for  Perceptron(alpha=0.0001, class_weight=None, early_stopping=False, eta
      fit_intercept=True, max_iter=None, n_iter=None, n_iter_no_change=5,
      n_jobs=None, penalty=None, random_state=0, shuffle=True, tol=None,
      validation_fraction=0.1, verbose=0, warm_start=False) GaussianNB(priors=None, var_smoothin
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best')
Accuracy: 0.7005965922591214
Precision:  0.6420576047876049
Recall:  0.9066243404970744
F1 Score:  0.7517425437470194
Time Elapsed:  11.300517797470093  secs
```

### 3.11 Ensemble Model 2: Perceptron, Naive Bayes, Linear SVC

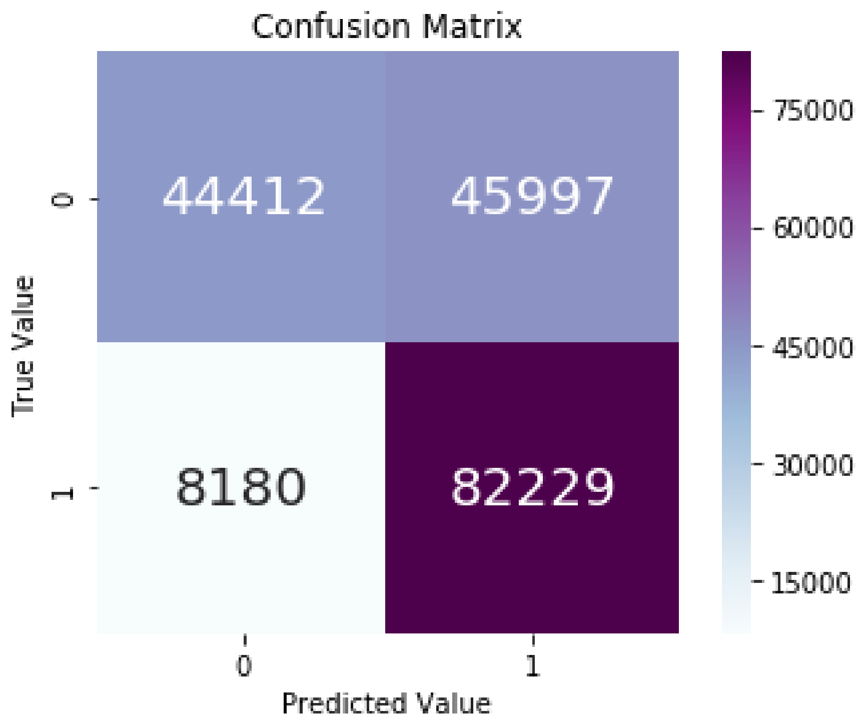
```
In [43]: accuracy_7, f1_7, T7 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                               Perceptron(),
                                               GaussianNB(),
                                               LinearSVC(dual = False, C = 0.3))
```



```
Classification Report for  Perceptron(alpha=0.0001, class_weight=None, early_stopping=False, eta
      fit_intercept=True, max_iter=None, n_iter=None, n_iter_no_change=5,
      n_jobs=None, penalty=None, random_state=0, shuffle=True, tol=None,
      validation_fraction=0.1, verbose=0, warm_start=False) GaussianNB(priors=None, var_smoothin
     intercept_scaling=1, loss='squared_hinge', max_iter=1000,
     multi_class='ovr', penalty='l2', random_state=None, tol=0.0001,
     verbose=0)
Accuracy: 0.52164885001586
Precision:  0.5141420126895117
Recall:  0.7869570507360992
F1 Score:  0.6219475416428094
Time Elapsed:  9.104327201843262  secs
```

## 3.12 Ensemble Model 3: Perceptron, Naive Bayes, Extra Tree

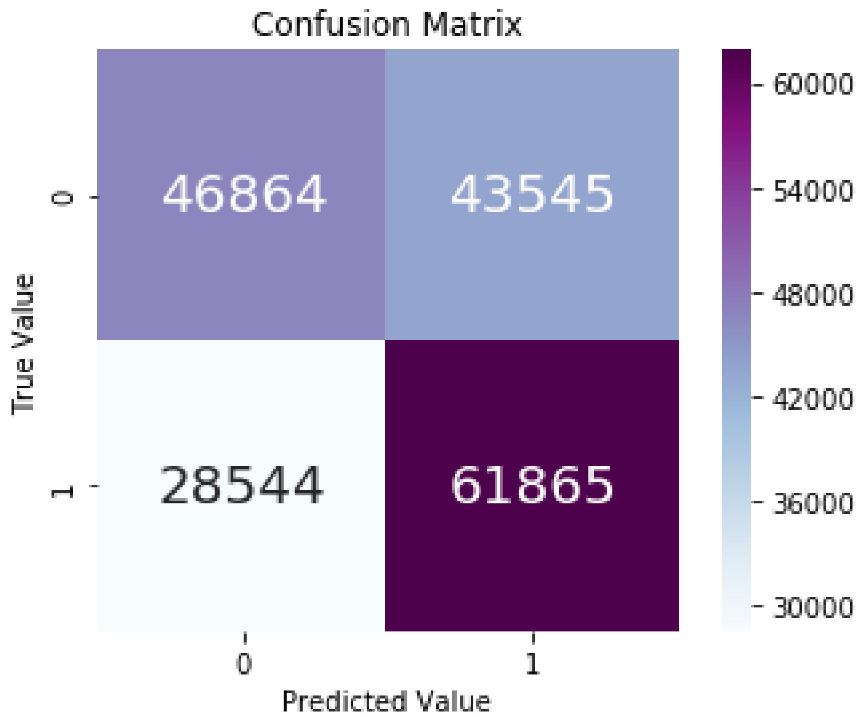
```
In [44]: accuracy_8, f1_8, T8 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                               Perceptron(),
                                               GaussianNB(),
                                               ExtraTreeClassifier())
```



```
Classification Report for  Perceptron(alpha=0.0001, class_weight=None, early_stopping=False, eta
      fit_intercept=True, max_iter=None, n_iter=None, n_iter_no_change=5,
      n_jobs=None, penalty=None, random_state=0, shuffle=True, tol=None,
      validation_fraction=0.1, verbose=0, warm_start=False) GaussianNB(priors=None, var_smoothin
          max_features='auto', max_leaf_nodes=None,
          min_impurity_decrease=0.0, min_impurity_split=None,
          min_samples_leaf=1, min_samples_split=2,
          min_weight_fraction_leaf=0.0, random_state=None,
          splitter='random')
Accuracy: 0.7003808540166102
Precision:  0.6412817993230702
Recall:  0.9095222820736873
F1 Score:  0.7522034440963249
Time Elapsed:  4.454015016555786  secs
```

### 3.13 Ensemble Model 4: Perceptron, Decision Tree, Linear SVC

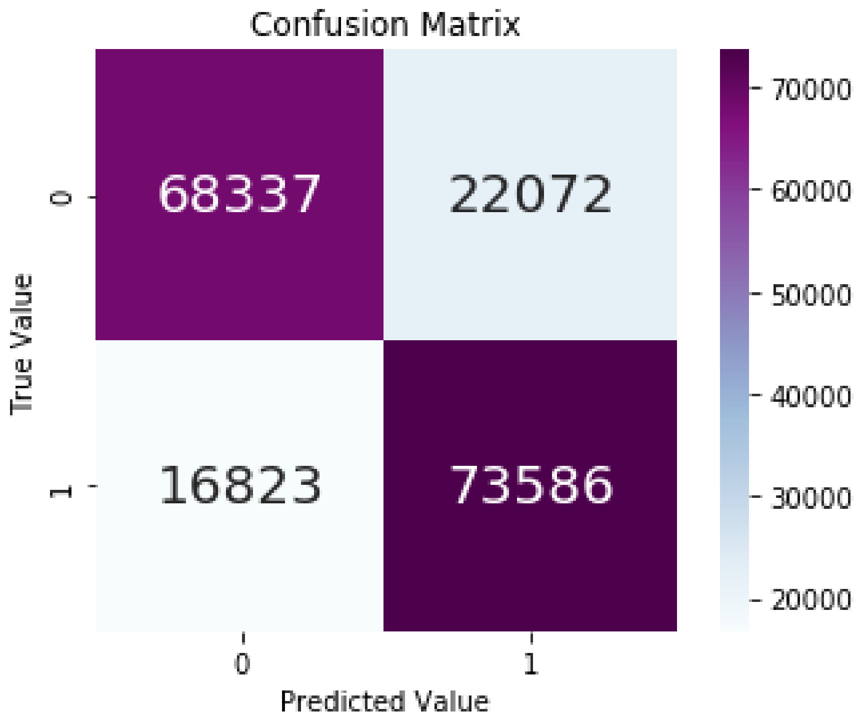
```
In [45]: accuracy_9, f1_9, T9 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                               Perceptron(),
                                               DecisionTreeClassifier(),
                                               LinearSVC(dual = False, C = 0.3))
```



```
Classification Report for  Perceptron(alpha=0.0001, class_weight=None, early_stopping=False, eta
      fit_intercept=True, max_iter=None, n_iter=None, n_iter_no_change=5,
      n_jobs=None, penalty=None, random_state=0, shuffle=True, tol=None,
      validation_fraction=0.1, verbose=0, warm_start=False) DecisionTreeClassifier(class_weight=
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best') LinearSVC(C=0.3, class_weight=None, dual=False, fit_intercept=True,
     intercept_scaling=1, loss='squared_hinge', max_iter=1000,
     multi_class='ovr', penalty='l2', random_state=None, tol=0.0001,
     verbose=0)
Accuracy: 0.601318141972323
Precision:  0.586898776207191
Recall:  0.6842792199891604
F1 Score:  0.6318590126596499
Time Elapsed:  17.514384746551514  secs
```

### 3.14 Ensemble Model 5: Perceptron, Decision Tree, Extra Tree

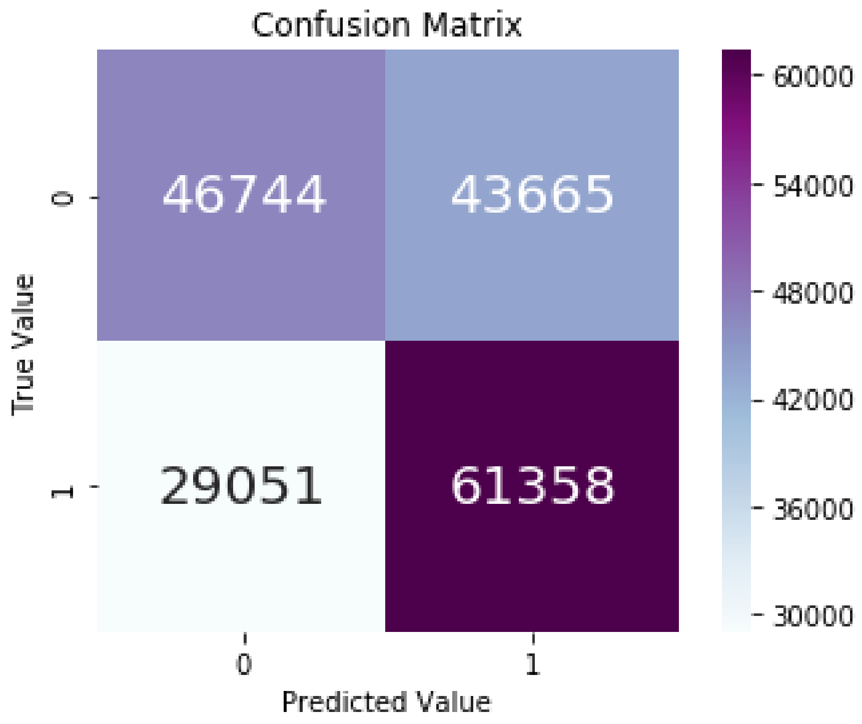
```
In [46]: accuracy_10, f1_10, T10 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                                  Perceptron(),
                                                  DecisionTreeClassifier(),
                                                  ExtraTreeClassifier())
```



```
Classification Report for  Perceptron(alpha=0.0001, class_weight=None, early_stopping=False, eta
      fit_intercept=True, max_iter=None, n_iter=None, n_iter_no_change=5,
      n_jobs=None, penalty=None, random_state=0, shuffle=True, tol=None,
      validation_fraction=0.1, verbose=0, warm_start=False) DecisionTreeClassifier(class_weight=
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best') ExtraTreeClassifier(class_weight=None, criterion='gini', max_depth=
          max_features='auto', max_leaf_nodes=None,
          min_impurity_decrease=0.0, min_impurity_split=None,
          min_samples_leaf=1, min_samples_split=2,
          min_weight_fraction_leaf=0.0, random_state=None,
          splitter='random')
Accuracy: 0.7848948529183923
Precision:  0.7692613268100943
Recall:  0.8139233925825968
F1 Score:  0.7909623952662213
Time Elapsed:  12.664221048355103  secs
```

### 3.15 Ensemble Model 6: Perceptron, Linear SVC, Extra Tree

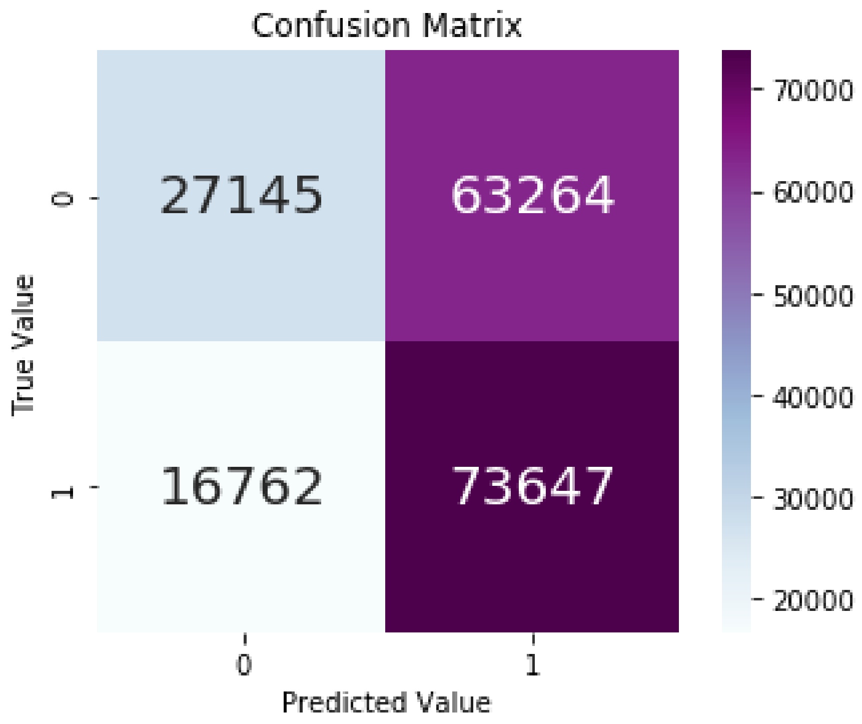
```
In [47]: accuracy_11, f1_11, T11 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                                  Perceptron(),
                                                  LinearSVC(dual = False, C = 0.3),
                                                  ExtraTreeClassifier())
```



```
Classification Report for  Perceptron(alpha=0.0001, class_weight=None, early_stopping=False, eta
      fit_intercept=True, max_iter=None, n_iter=None, n_iter_no_change=5,
      n_jobs=None, penalty=None, random_state=0, shuffle=True, tol=None,
      validation_fraction=0.1, verbose=0, warm_start=False) LinearSVC(C=0.3, class_weight=None,
     intercept_scaling=1, loss='squared_hinge', max_iter=1000,
     multi_class='ovr', penalty='l2', random_state=None, tol=0.0001,
     verbose=0) ExtraTreeClassifier(class_weight=None, criterion='gini', max_depth=None,
          max_features='auto', max_leaf_nodes=None,
          min_impurity_decrease=0.0, min_impurity_split=None,
          min_samples_leaf=1, min_samples_split=2,
          min_weight_fraction_leaf=0.0, random_state=None,
          splitter='random')
Accuracy: 0.5978504489022551
Precision:  0.5842339297106348
Recall:  0.678671371213043
F1 Score:  0.6279217323672683
Time Elapsed:  9.86362910270691  secs
```

## 3.16 Ensemble Model 7: Naive Bayes, Decision Tree, Linear SVC

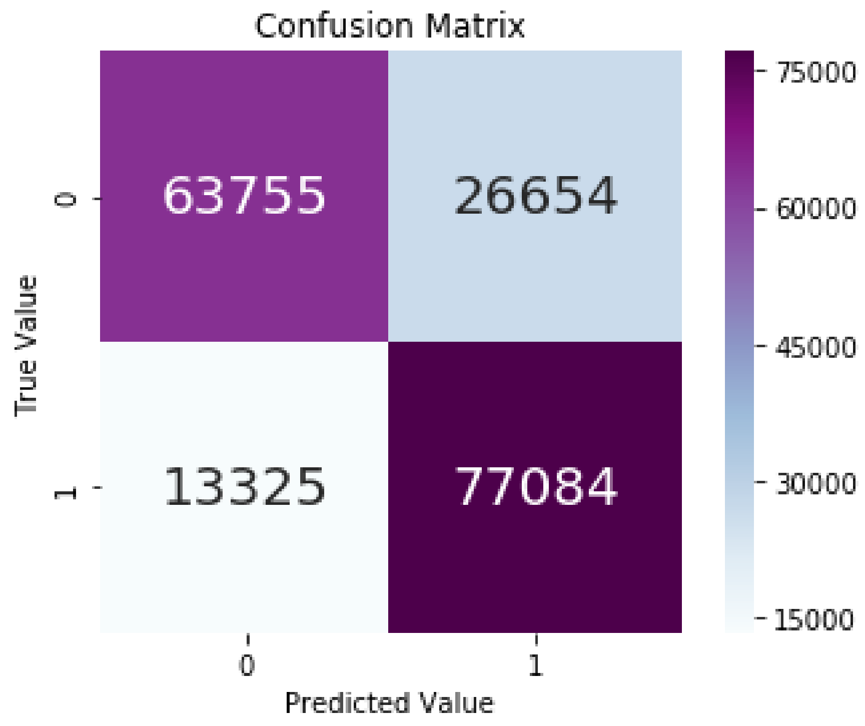
```
In [48]: accuracy_12, f1_12, T12 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                                  GaussianNB(),
                                                  DecisionTreeClassifier(),
                                                  LinearSVC(dual = False, C = 0.3))
```



```
Classification Report for  GaussianNB(priors=None, var_smoothing=1e-09) DecisionTreeClassifier(c
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best') LinearSVC(C=0.3, class_weight=None, dual=False, fit_intercept=True,
     intercept_scaling=1, loss='squared_hinge', max_iter=1000,
     multi_class='ovr', penalty='l2', random_state=None, tol=0.0001,
     verbose=0)
Accuracy: 0.5574250359496449
Precision:  0.5379187939610404
Recall:  0.814598104171045
F1 Score:  0.6479588245644906
Time Elapsed:  18.16699719429016  secs
```

### 3.17 Ensemble Model 8: Naive Bayes, Decision Tree, Extra Tree

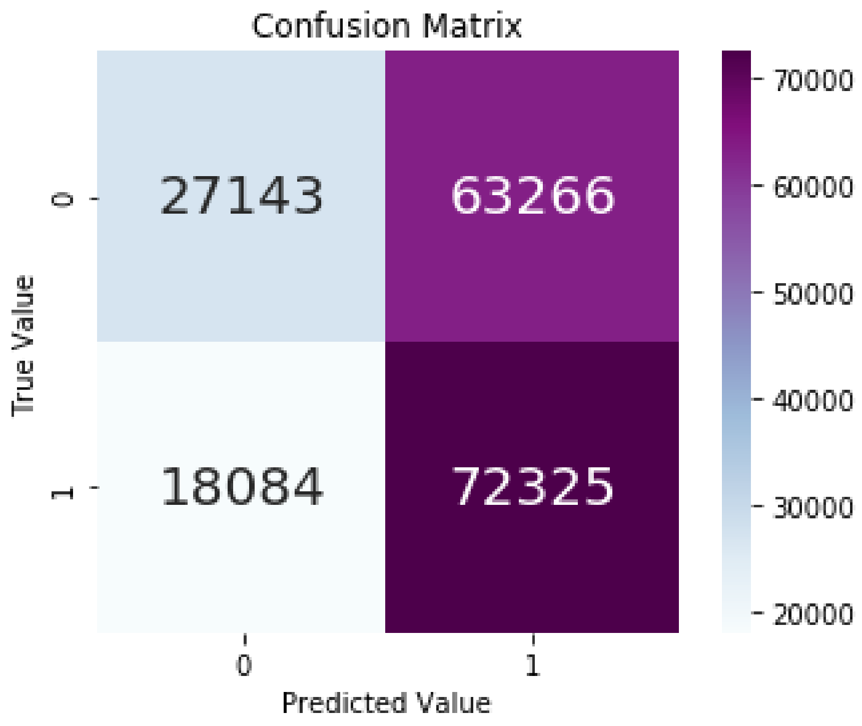
```
In [49]: accuracy_13, f1_13, T13 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                                  GaussianNB(),
                                                  DecisionTreeClassifier(),
                                                  ExtraTreeClassifier())
```



```
Classification Report for  GaussianNB(priors=None, var_smoothing=1e-09) DecisionTreeClassifier(c
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best') ExtraTreeClassifier(class_weight=None, criterion='gini', max_depth=
          max_features='auto', max_leaf_nodes=None,
          min_impurity_decrease=0.0, min_impurity_split=None,
          min_samples_leaf=1, min_samples_split=2,
          min_weight_fraction_leaf=0.0, random_state=None,
          splitter='random')
Accuracy: 0.7789002893757202
Precision:  0.7430642580346642
Recall:  0.8526142308840934
F1 Score:  0.7940787135521022
Time Elapsed:  12.008816003799438  secs
```

### 3.18 Ensemble Model 9: Naive Bayes, Linear SVC, Extra Tree

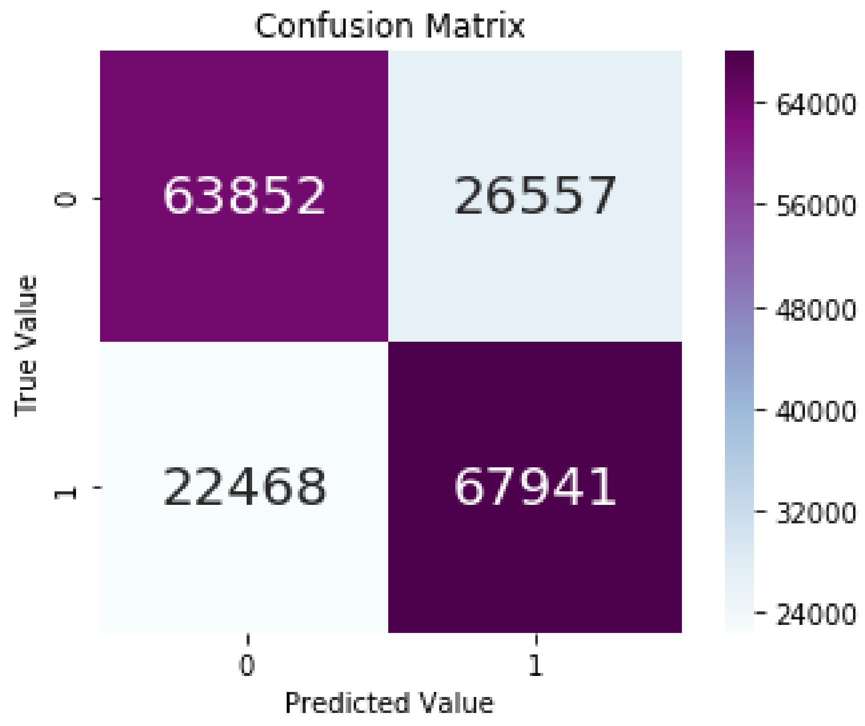
```
In [50]: accuracy_14, f1_14, T14 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                                  GaussianNB(),
                                                  LinearSVC(dual = False, C = 0.3),
                                                  ExtraTreeClassifier())
```



```
Classification Report for  GaussianNB(priors=None, var_smoothing=1e-09) LinearSVC(C=0.3, class_w
     intercept_scaling=1, loss='squared_hinge', max_iter=1000,
     multi_class='ovr', penalty='l2', random_state=None, tol=0.0001,
     verbose=0) ExtraTreeClassifier(class_weight=None, criterion='gini', max_depth=None,
          max_features='auto', max_leaf_nodes=None,
          min_impurity_decrease=0.0, min_impurity_split=None,
          min_samples_leaf=1, min_samples_split=2,
          min_weight_fraction_leaf=0.0, random_state=None,
          splitter='random')
Accuracy: 0.5501026067671704
Precision:  0.5334056095168558
Recall:  0.799975666139433
F1 Score:  0.6400442477876106
Time Elapsed:  9.441408157348633  secs
```

### 3.19 Ensemble Model 10: Decision Tree, Linear SVC, Extra Tree

```
In [51]: accuracy_15, f1_15, T15 = kfoldcv3Models(Xrf_smote, Yrf_smote,
                                                   DecisionTreeClassifier(),
                                                   LinearSVC(dual = False, C = 0.3),
                                                   ExtraTreeClassifier())
```

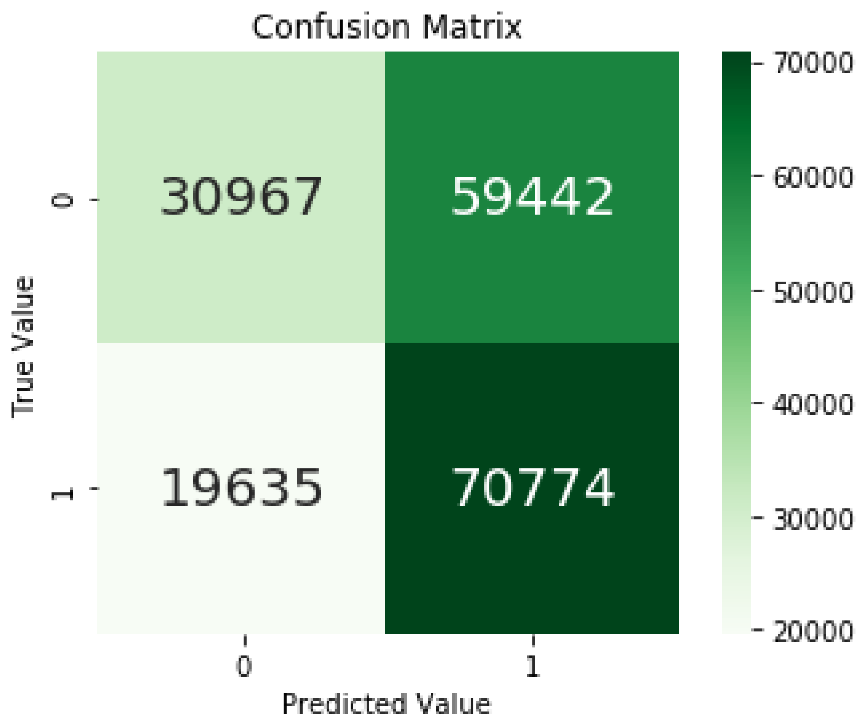


```
Classification Report for  DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best') LinearSVC(C=0.3, class_weight=None, dual=False, fit_intercept=True,
     intercept_scaling=1, loss='squared_hinge', max_iter=1000,
     multi_class='ovr', penalty='l2', random_state=None, tol=0.0001,
     verbose=0) ExtraTreeClassifier(class_weight=None, criterion='gini', max_depth=None,
          max_features='auto', max_leaf_nodes=None,
          min_impurity_decrease=0.0, min_impurity_split=None,
          min_samples_leaf=1, min_samples_split=2,
          min_weight_fraction_leaf=0.0, random_state=None,
          splitter='random')
Accuracy: 0.7288712613616449
Precision:  0.7189675971978243
Recall:  0.7514849185368714
```

```
F1 Score:  0.7348667167819498
Time Elapsed:  16.692336082458496  secs
```

### 3.20 Ensemble Model 11: All 5 Classifiers

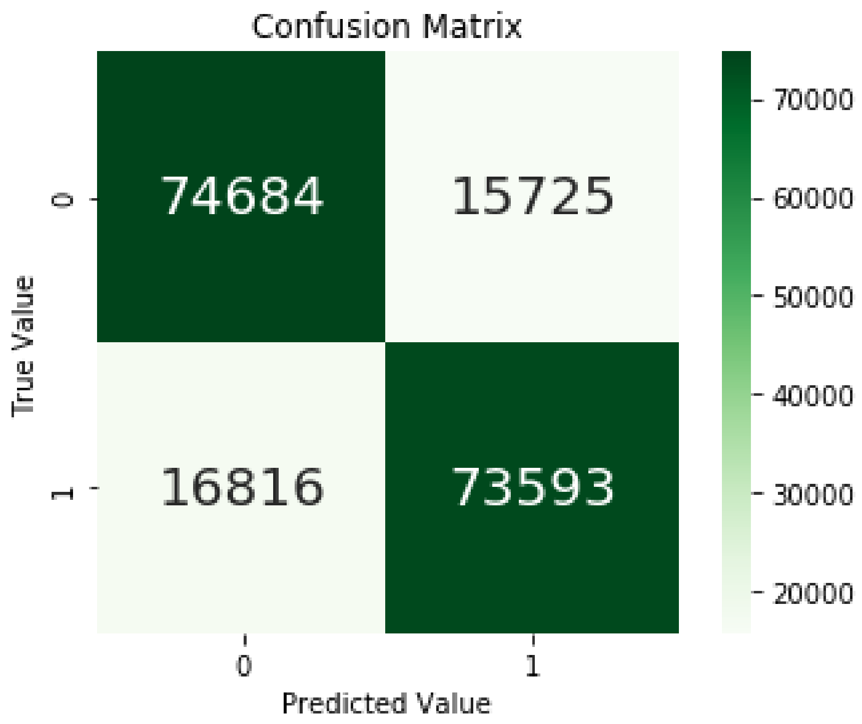
```
In [52]: accuracy_16, f1_16, T16 = kfoldcv5Models(Xrf_smote, Yrf_smote)
```



```
Classification Report for all 5 Classifiers
Accuracy: 0.562672877862983
Precision:  0.5435123179947164
Recall:  0.7828202944397129
F1 Score:  0.6415773371104816
Time Elapsed:  18.246505975723267  secs
```

### 3.21 Ensemble Model 12: Random Forest

```
In [53]: accuracy_17, f1_17, T17 = kfoldcvRF(Xrf_smote, Yrf_smote)
```

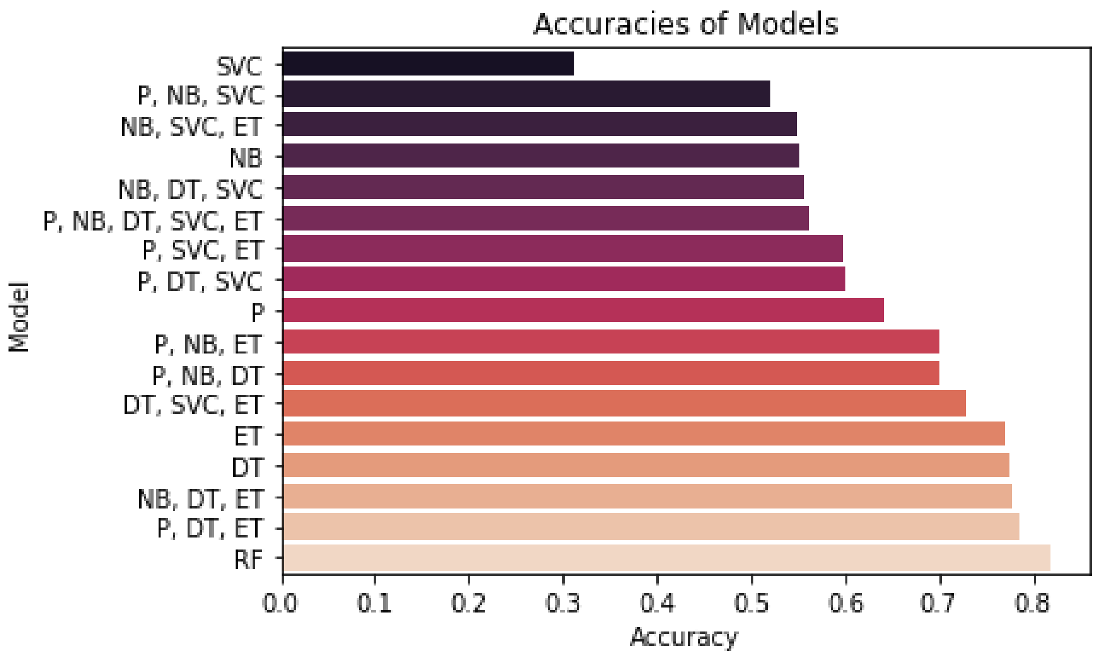


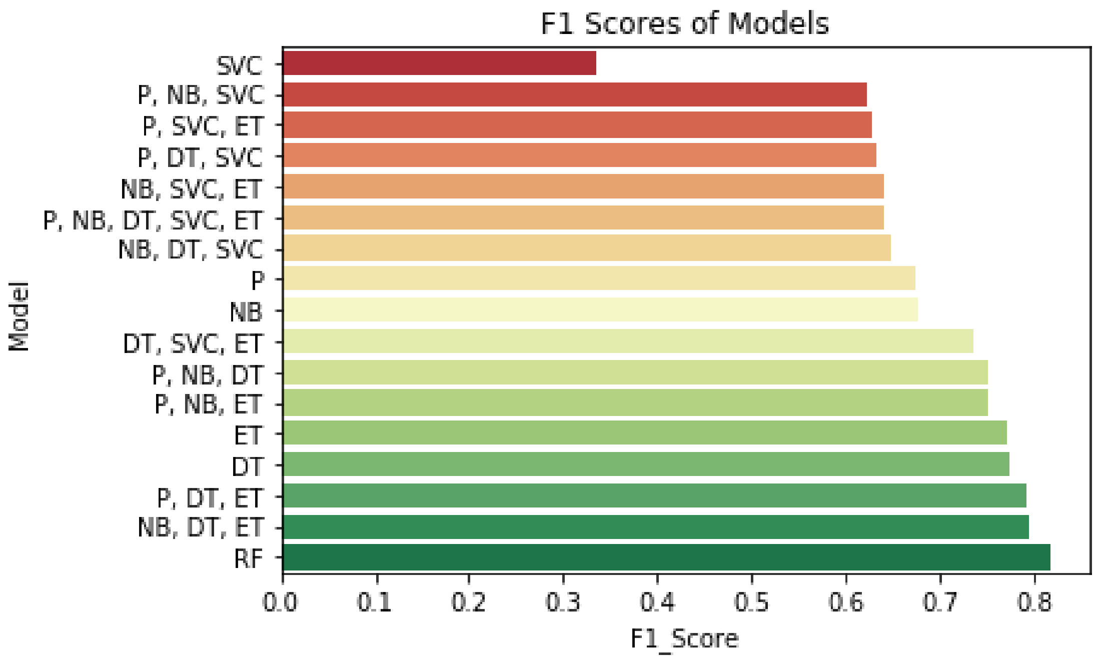
```
Classification Report for Random Forest
Accuracy: 0.8200348623674916
Precision:  0.823943661971831
Recall:  0.8140008185025827
F1 Score:  0.81894206212756
Time Elaped:  9.729307174682617  secs
```

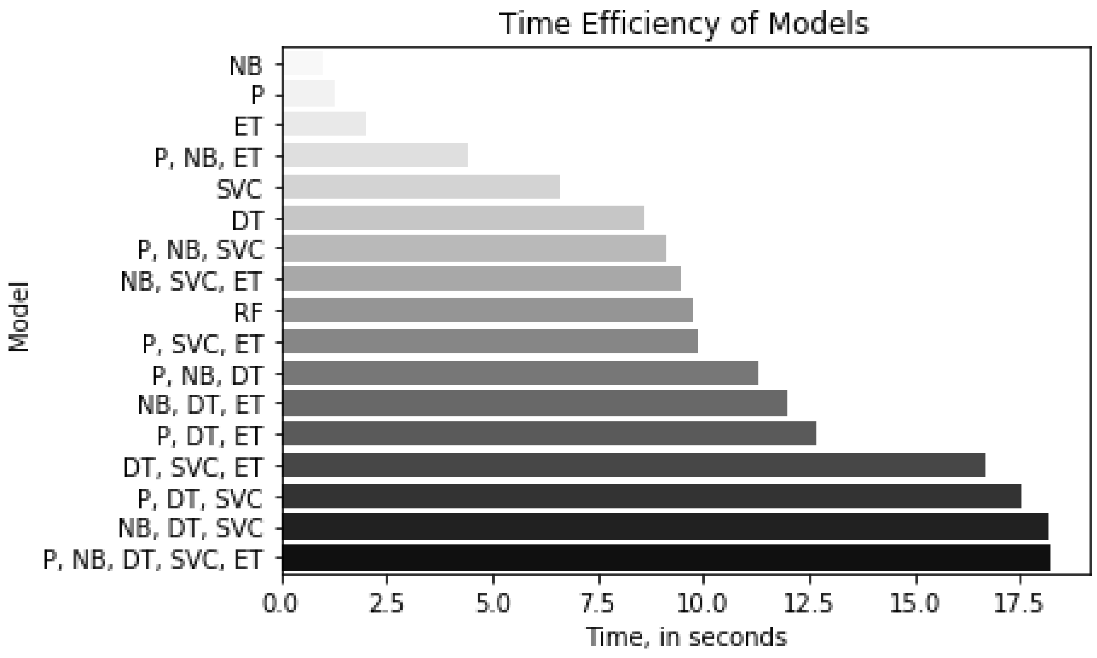
```
In [54]: # Create lists of accuracies, F1 scores, times, and labels
         ensemble_accuracy = [accuracy_1, accuracy_2, accuracy_3, accuracy_4,
                              accuracy_5, accuracy_6,accuracy_7, accuracy_8,
                              accuracy_9, accuracy_10, accuracy_11, accuracy_12,
                              accuracy_13, accuracy_14, accuracy_15, accuracy_16, accuracy_17]
         ensemble_f1 = [f1_1, f1_2, f1_3, f1_4, f1_5, f1_6, f1_7, f1_8,
                        f1_9, f1_10, f1_11, f1_12, f1_13, f1_14, f1_15, f1_16, f1_17]
         ensemble_time = [T1, T2, T3, T4, T5, T6, T7, T8,
                          T9, T10, T11, T12, T13, T14, T15, T16, T17]

         ensemble_label = ['P', 'NB', 'DT', 'SVC', 'ET',
                           'P, NB, DT', 'P, NB, SVC', 'P, NB, ET', 'P, DT, SVC',
                           'P, DT, ET', 'P, SVC, ET', 'NB, DT, SVC', 'NB, DT, ET',
                           'NB, SVC, ET', 'DT, SVC, ET', 'P, NB, DT, SVC, ET', 'RF']
```

```
In [55]: # Create a dataframe to store each type of data
         sorted_accuracy = pd.DataFrame({'Accuracy':ensemble_accuracy},
                         index =ensemble_label).reset_index().sort_values('Accuracy')
         sorted_f1 = pd.DataFrame({'F1_Score':ensemble_f1},
                         index = ensemble_label).reset_index().sort_values('F1_Score')
         sorted_time = pd.DataFrame({'Time':ensemble_time},
                         index = ensemble_label).reset_index().sort_values('Time')
```

```
In [56]: # Plot the accuracies, F1 scores and time efficiency
         # on 3 different plots
         sns.barplot(y = 'index', x = 'Accuracy', data = sorted_accuracy, palette = 'rocket')
         plt.ylabel("Model")
         plt.title("Accuracies of Models")
         plt.show()
         sns.barplot(y = 'index', x = 'F1_Score', data = sorted_f1, palette = 'RdYlGn')
         plt.ylabel("Model")
         plt.title("F1 Scores of Models")
         plt.show()
         sns.barplot(y = 'index', x = 'Time', data = sorted_time, palette = 'Greys')
         plt.ylabel("Model")
         plt.xlabel("Time, in seconds")
         plt.title("Time Efficiency of Models")
         plt.show()
```




F1 Scores of Models
Model
SVC
P, NB, SVC
P, SVC, ET
P, DT, SVC
NB, SVC, ET
P, NB, DT, SVC, ET
NB, DT, SVC
P
NB
DT, SVC, ET
P, NB, DT
P, NB, ET
ET
DT
P, DT, ET
NB, DT, ET
RF
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
F1_Score


Time Efficiency of Models
Model
NB
P
ET
P, NB, ET
SVC
DT
P, NB, SVC
NB, SVC, ET
RF
P, SVC, ET
P, NB, DT
NB, DT, ET
P, DT, ET
DT, SVC, ET
P, DT, SVC
NB, DT, SVC
P, NB, DT, SVC, ET
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
Time, in seconds