Cardiovascular Disease Prediction

Data description

There are 3 types of input features:
Objective: factual information;
Examination: results of medical examination;
Subjective: information given by the patient.

12 Features:

1. Age | Objective Feature | age | int (days)
2. Height | Objective Feature | height | int (cm) |
3. Weight | Objective Feature | weight | float (kg) |
4. Gender | Objective Feature | gender | categorical code |
5. Systolic blood pressure | Examination Feature | ap_hi | int |
6. Diastolic blood pressure | Examination Feature | ap_lo | int |
7. Cholesterol | Examination Feature | cholesterol | 1: normal, 2: above normal, 3: well above normal |
8. Glucose | Examination Feature | gluc | 1: normal, 2: above normal, 3: well above normal |
9. Smoking | Subjective Feature | smoke | binary |
10. Alcohol intake | Subjective Feature | alco | binary |
11. Physical activity | Subjective Feature | active | binary |
12. Presence or absence of cardiovascular disease | Target Variable | cardio | binary |

All of the dataset values were collected at the moment of medical examination.

The dataset consists of 70 000 records of patients data. The target class "cardio" equals to 1, when patient has cardiovascular desease, and it's 0, if patient is healthy. The task is to predict the presence or absence of cardiovascular disease (CVD) using the patient examination results.

Most of the code was taken from https://www.kaggle.com/benanakca/cardiovascular-disease-prediction

In [1]:
```
# Import libraries
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
from matplotlib import pyplot as plt
```

```
import seaborn as sns
import scipy.stats as stats
import sklearn
import os
import warnings
warnings.filterwarnings('ignore')
```

EDA

```
In [2]: # Load the data and first few rows
        data_raw = pd.read_csv("cardio.csv", sep=";")
        data_raw.head()

Out[2]:    id    age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
        0   0  18393       2     168    62.0    110     80            1     1      0
        1   1  20228       1     156    85.0    140     90            3     1      0
        2   2  18857       1     165    64.0    130     70            3     1      0
        3   3  17623       2     169    82.0    150    100            1     1      0
        4   4  17474       1     156    56.0    100     60            1     1      0

           alco  active  cardio
        0     0       1       0
        1     0       1       1
        2     0       0       1
        3     0       1       1
        4     0       0       0

In [3]: # Further info about the data
        data_raw.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70000 entries, 0 to 69999
Data columns (total 13 columns):
id             70000 non-null int64
age            70000 non-null int64
gender         70000 non-null int64
height         70000 non-null int64
weight         70000 non-null float64
ap_hi          70000 non-null int64
ap_lo          70000 non-null int64
cholesterol    70000 non-null int64
gluc           70000 non-null int64
smoke          70000 non-null int64
alco           70000 non-null int64
active         70000 non-null int64
cardio         70000 non-null int64
dtypes: float64(1), int64(12)
```

```
memory usage: 6.9 MB
```

All features are numerical, 12 integers and 1 decimal number (weight). The second column gives us an idea how big is the dataset and how many non-null values are there for each field.

```
In [4]: # Dropping useless column
        data_raw.drop("id",axis=1,inplace=True)
```

Checking Duplication and Missing Values

Before visualization and outlier checks it is very important to handle duplicate and missing values.

```
In [5]: print("There is {} duplicated values in data frame".format(data_raw.duplicated().sum()))

There is 24 duplicated values in data frame
```

```
In [6]: duplicated = data_raw[data_raw.duplicated(keep=False)]
        duplicated = duplicated.sort_values(by=['age', "gender", "height"], ascending= False)
        # Sort the values to see duplication clearly

        duplicated.head(2) # Show 1 duplication out of 24

Out[6]:          age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
        2677   22077       1     175    69.0    120     80            1     1      0
        45748  22077       1     175    69.0    120     80            1     1      0

               alco  active  cardio
        2677      0       1       1
        45748     0       1       1
```

We can drop the duplicates because they have no any effect of training of model.

```
In [7]: data_raw.drop_duplicates(inplace=True)
        print("There is {} duplicated values in data frame".format(data_raw.duplicated().sum()))

There is 0 duplicated values in data frame
```

```
In [8]: print("There is {} missing values in data frame".format(data_raw.isnull().sum().sum()))

There is 0 missing values in data frame
```

Visualization

Detecting outlier and handling them can increase our accuracy score.

In [9]:
```
x = data_raw.copy(deep=True)
x.describe()
```

Out[9]:

```
                age        gender        height        weight         ap_hi  \
count  69976.000000  69976.000000  69976.000000  69976.000000  69976.000000
mean   19468.950126      1.349648    164.359152     74.208519    128.820453
std     2467.374620      0.476862      8.211218     14.397211    154.037729
min    10798.000000      1.000000     55.000000     10.000000   -150.000000
25%    17664.000000      1.000000    159.000000     65.000000    120.000000
50%    19703.000000      1.000000    165.000000     72.000000    120.000000
75%    21327.000000      2.000000    170.000000     82.000000    140.000000
max    23713.000000      2.000000    250.000000    200.000000  16020.000000

              ap_lo   cholesterol          gluc         smoke          alco  \
count  69976.000000  69976.000000  69976.000000  69976.000000  69976.000000
mean      96.636261      1.366997      1.226535      0.088159      0.053790
std      188.504581      0.680333      0.572353      0.283528      0.225604
min      -70.000000      1.000000      1.000000      0.000000      0.000000
25%       80.000000      1.000000      1.000000      0.000000      0.000000
50%       80.000000      1.000000      1.000000      0.000000      0.000000
75%       90.000000      2.000000      1.000000      0.000000      0.000000
max    11000.000000      3.000000      3.000000      1.000000      1.000000

             active        cardio
count  69976.000000  69976.000000
mean       0.803718      0.499771
std        0.397187      0.500004
min        0.000000      0.000000
25%        1.000000      0.000000
50%        1.000000      0.000000
75%        1.000000      1.000000
max        1.000000      1.000000
```

Columns of “age”, “height”, “weight”, “ap_hi”, “ap_lo” may have outlier. In order to compare them on same scale we need to standartize firstly.

Their Standart Scalar Function

In [10]:
```
s_list = ["age", "height", "weight", "ap_hi", "ap_lo"]
def standartization(x):
    x_std = x.copy(deep=True)
    for column in s_list:
        x_std[column] = (x_std[column]-x_std[column].mean())/x_std[column].std()
    return x_std
x_std=standartization(x)
x_std.head()
```

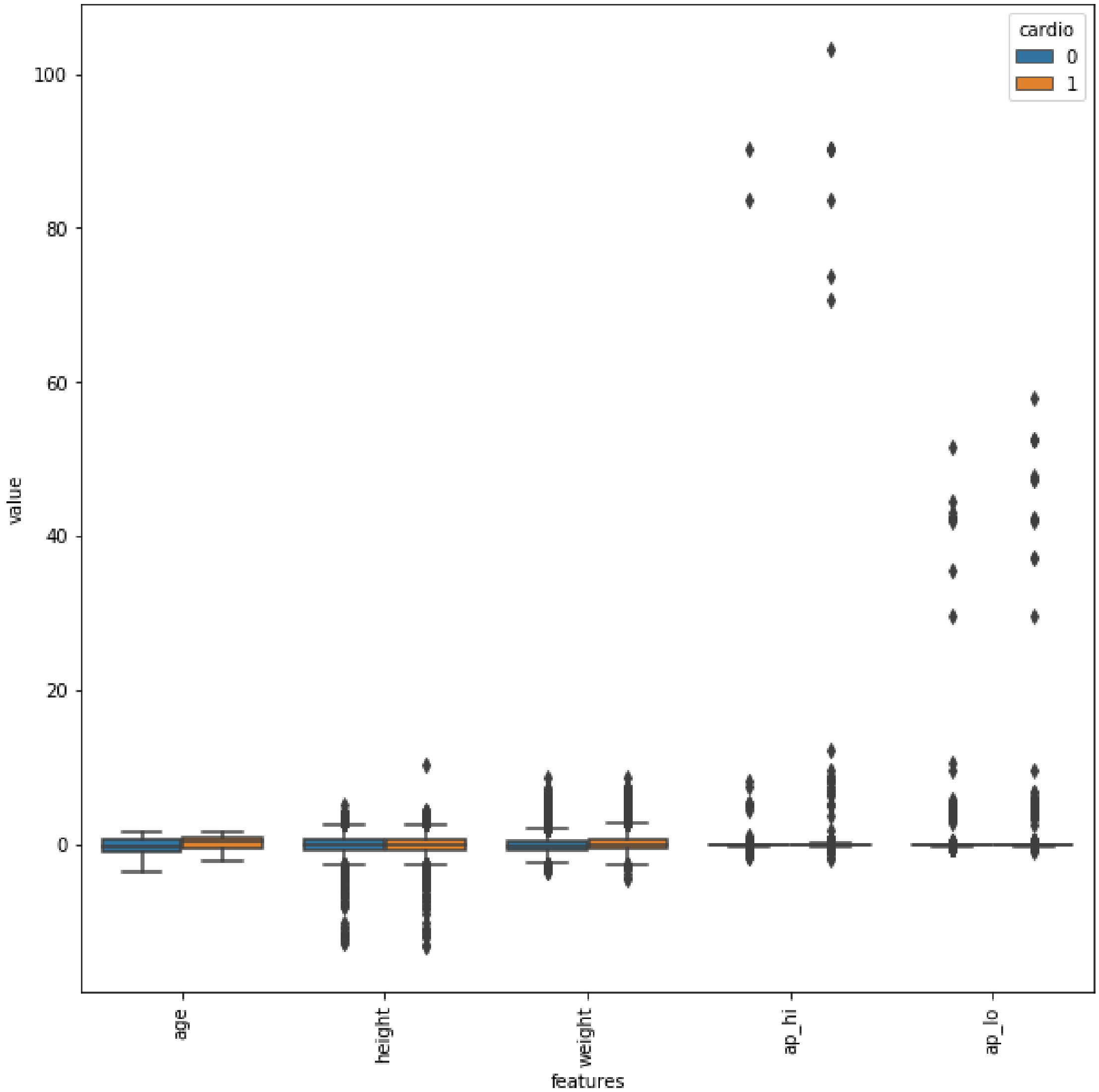
```
Out[10]:          age  gender    height    weight     ap_hi     ap_lo  cholesterol  \
         0 -0.436071       2  0.443399 -0.847978 -0.122181 -0.088254            1
         1  0.307635       1 -1.018016  0.749554  0.072577 -0.035205            3
         2 -0.248017       1  0.078045 -0.709062  0.007658 -0.141303            3
         3 -0.748143       2  0.565184  0.541180  0.137496  0.017844            1
         4 -0.808532       1 -1.018016 -1.264725 -0.187100 -0.194352            1

            gluc  smoke  alco  active  cardio
         0     1      0     0       1       0
         1     1      0     0       1       1
         2     1      0     0       0       1
         3     1      0     0       1       1
         4     1      0     0       0       0
```

In order to use the multi box graph plot we need to melt out data.

```
In [11]: x_melted = pd.melt(frame=x_std, id_vars="cardio", value_vars=s_list, var_name="features
```

```
In [12]: plt.figure(figsize=(10,10))
         sns.boxplot(x="features", y="value", hue="cardio", data=x_melted)
         plt.xticks(rotation=90)
```

```
Out[12]: (array([0, 1, 2, 3, 4]), <a list of 5 Text xticklabel objects>)
```



There are some outliers in the dataset, but as seen above there is an unusual outlier in ap_hi and ap_lo features.

Let us calculate the low bound and high bound of ap_lo and ap_hi features.

```
In [13]: ap_list = ["ap_hi", "ap_lo"]
         boundary = pd.DataFrame(index=["lower_bound","upper_bound"]) # We created an empty data
         for each in ap_list:
             Q1 = x[each].quantile(0.25)
             Q3 = x[each].quantile(0.75)
             IQR = Q3 - Q1

             lower_bound = Q1- 1.5*IQR
             upper_bound = Q3 + 1.5*IQR
```

```
        boundary[each] = [lower_bound, upper_bound ]
    boundary
```

Out[13]:

	ap_hi	ap_lo
lower_bound	90.0	65.0
upper_bound	170.0	105.0

We can select the index of outlier data by using boundaries we calculated. Normally we should analyze both upper outliers and below outliers but in this case, they considered to handle just uppers because of their extremely higher values.

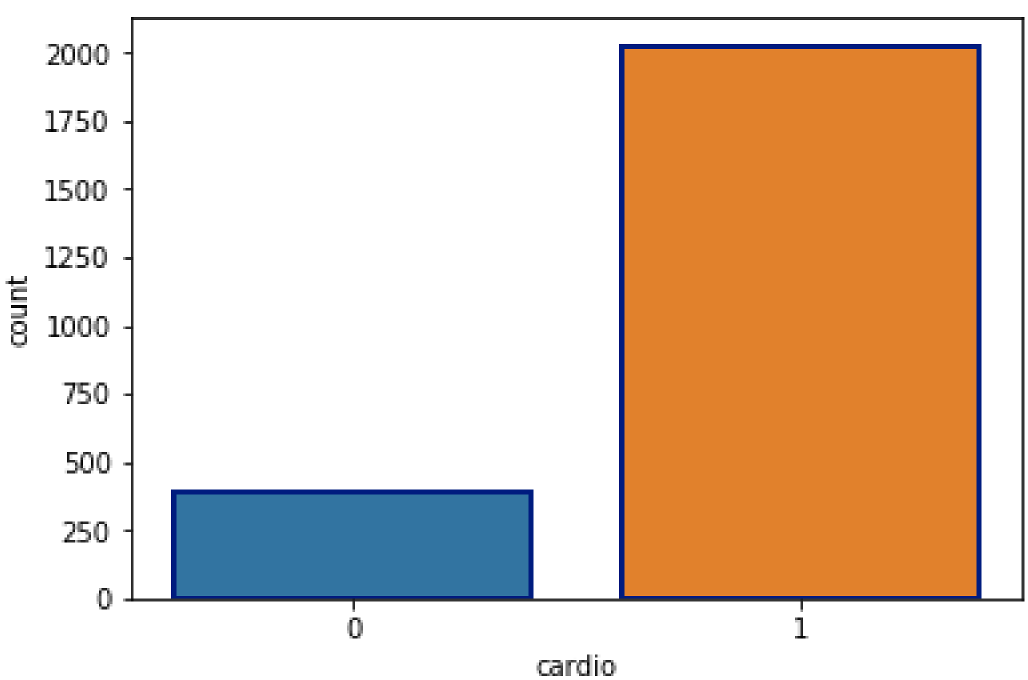
In [14]:
```
ap_hi_filter = (x["ap_hi"] > boundary["ap_hi"][1])
ap_lo_filter = (x["ap_lo"] > boundary["ap_lo"][1])
outlier_filter = (ap_hi_filter | ap_lo_filter)
x_outliers = x[outlier_filter]
x_outliers["cardio"].value_counts()
```

Out[14]:
```
1    2025
0     388
Name: cardio, dtype: int64
```

Cardiovascular disease is present in 83 percent of the ap_hi and ap_lo outlier data. Because of ap_hi and ap_lo symbolizes high blood pressure, the high rate of disease is consistent with real life. For this reason, we drop medically impossible data from the dataset.

In [15]:
```
sns.countplot(x='cardio',data=x_outliers,linewidth=2,edgecolor=sns.color_palette("dark"
```

Out[15]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x1a18924a58>
```



“If one’s systolic pressure (ap_hi) exceeds 180 or diastolic pressure (ap_lo) crosses 120, it is a stage that requires immediate medical attention.” A study published by doctors in NCBI NLM recorded a maximum blood pressure of 370/360 mm Hg. This study was performed by recording blood pressure in 10 male athletes through radial artery catheterization. Thus we can drop the ap_hi outlier values over 250 and ap_lo outlier values over 200, without fear of missing data.

```
In [16]: out_filter = ((x["ap_hi"]>250) | (x["ap_lo"]>200) )
         print("There are {} outliers".format(x[out_filter]["cardio"].count()))
```

```
There are 993 outliers
```

```
In [17]: x = x[~out_filter]
```

```
In [18]: corr = x.corr()
         f, ax = plt.subplots(figsize = (15,15))
         sns.heatmap(corr, annot=True, fmt=".3f", linewidths=0.5, ax=ax)
```

```
Out[18]: <matplotlib.axes._subplots.AxesSubplot at 0x104ffc278>
```

We can see from correlation map easily; cholesterol, blood pressure (ap_hi and ap_low both) and age have a powerful relationship with cardiovascular diseases. Glucogen and cholesterol have a strong relationship among them.

Feature Engineering

In [19]:
```
# Height and weight seems uncorrelated with the cardio feature
# but Body Mass Index could be helpful to train our model.

def bmi_calc(w, h):
    return w/(h**2)
```

In [20]:
```
x["bmi"] = x["weight"]/ (x["height"]/100)**2
```

In [21]: x.head()

Out[21]:

```
     age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
0  18393       2     168    62.0    110     80            1     1      0
1  20228       1     156    85.0    140     90            3     1      0
2  18857       1     165    64.0    130     70            3     1      0
3  17623       2     169    82.0    150    100            1     1      0
4  17474       1     156    56.0    100     60            1     1      0

   alco  active  cardio        bmi
0     0       1       0  21.967120
1     0       1       1  34.927679
2     0       0       1  23.507805
3     0       1       1  28.710479
4     0       0       0  23.011177
```

In [22]:

```python
# Detecting genders of patients

a = x[x["gender"]==1]["height"].mean()
b = x[x["gender"]==2]["height"].mean()
if a > b:
    gender = "male"
    gender2 = "female"
else:
    gender = "female"
    gender2 = "male"
print("Gender:1 is "+ gender +" & Gender:2 is " + gender2)
```

```
Gender:1 is female & Gender:2 is male
```

Women have many of the same risk factors with men for heart disease as men, such as smoking, high blood pressure, and high cholesterol especially after 65. Thus we shouldn't categorize them into 1 and 2 because of 2 is always numerically bigger than 1, the model would take into account that and give a bigger ratio to men for having a disease. We did not change other categorical code to one hot encoding because they express really hierarchical size. An example from describtion of dataset : Cholesterol | 1: normal, 2: above normal, 3: well above normal

In [23]:

```python
x["gender"] = x["gender"] % 2
x["gender"].head()
```

Out[23]:

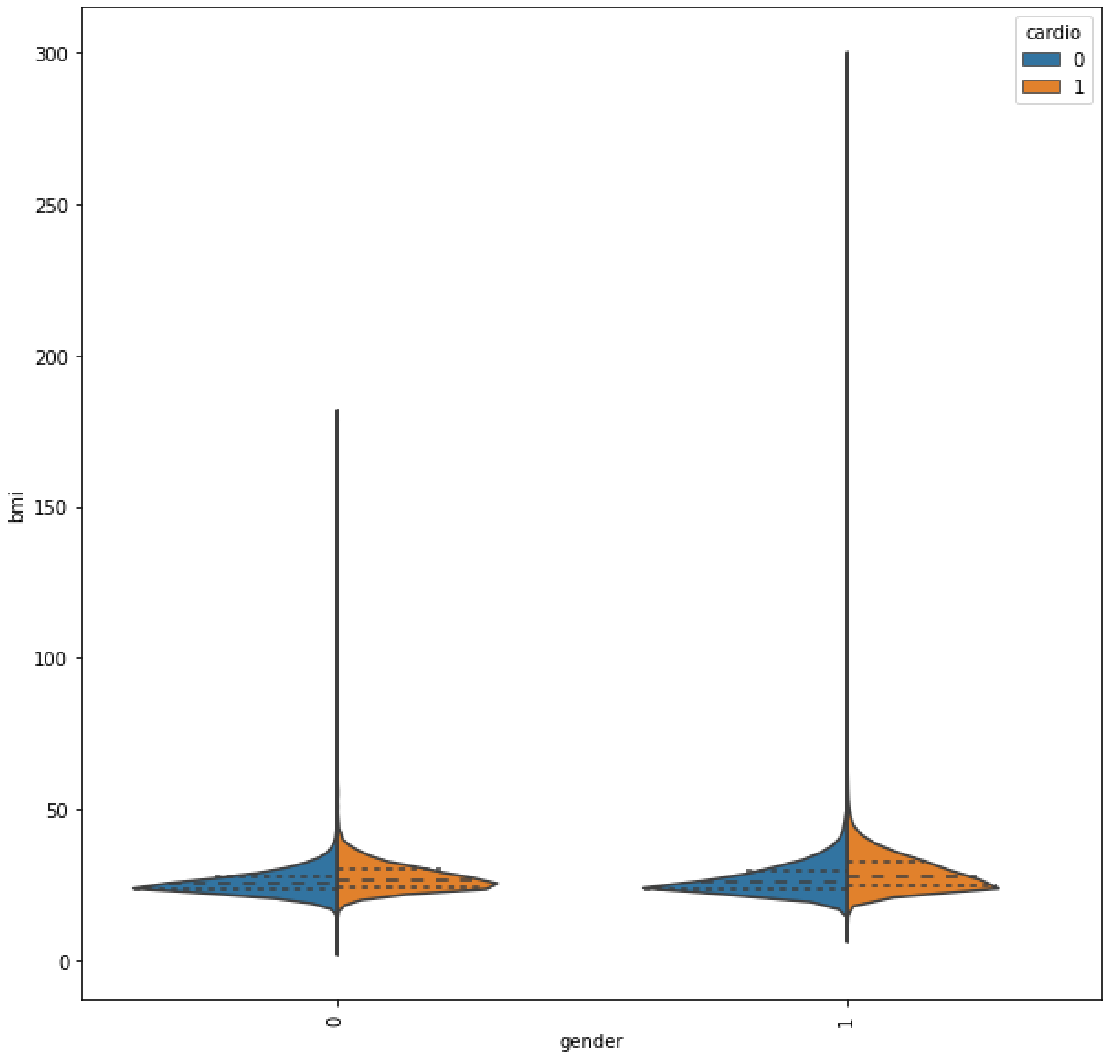
```
0    0
1    1
2    1
3    0
4    1
Name: gender, dtype: int64
```

In [24]:

```python
from sklearn.preprocessing import StandardScaler
x_std = standartization(x)
```

```
data = pd.melt(x_std,id_vars="cardio",
                    var_name="features",
                    value_name='value')
plt.figure(figsize=(10,10))
sns.violinplot(x="gender", y="bmi", hue="cardio", data=x,split=True, inner="quart")
plt.xticks(rotation=90)
```

Out[24]: (array([0, 1]), <a list of 2 Text xticklabel objects>)



If we interpret the violin plot, the median and quartiles of bmi distribution of patients is slightly higher than non-patients.

Preparing the Training and Test Sets

In [25]:
```
y = x["cardio"]
y.shape
```

```
Out[25]: (68983,)

In [26]: x.drop("cardio", axis=1,inplace=True)
         x.head()

Out[26]:      age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
         0  18393       0     168    62.0    110     80            1     1      0
         1  20228       1     156    85.0    140     90            3     1      0
         2  18857       1     165    64.0    130     70            3     1      0
         3  17623       0     169    82.0    150    100            1     1      0
         4  17474       1     156    56.0    100     60            1     1      0

            alco  active        bmi
         0     0       1  21.967120
         1     0       1  34.927679
         2     0       0  23.507805
         3     0       1  28.710479
         4     0       0  23.011177

In [27]: from sklearn.model_selection import train_test_split
         x_train,x_test, y_train, y_test = train_test_split(x,y,test_size=0.3)
```

Data Normalization

```
In [28]: from sklearn.preprocessing import normalize
         x_train = normalize(x_train)
         x_test = normalize(x_test)
         x = normalize(x)
```

Machine Learning Models

Random Guess

```
In [29]: data_size = x.shape[0]
         is_positive = np.sum(y == 1)/data_size #probability that y=1
         is_negative = np.sum(y == 0)/data_size

         # Accuracy
         print("Accuracy is", '%.03f' %is_negative)

         # AUROC
         print("AUROC is 0.5")

         #AUPRC
         print("AUPRC is", '%.03f' %is_positive)

Accuracy is 0.505
AUROC is 0.5
AUPRC is 0.495
```

DT, Random Forest, kNN, SVM, NB and Logistic Regression

In [30]:
```
# finding the best parameters for logistic regression using grid search
from sklearn.model_selection import GridSearchCV
from sklearn.linear_model import LogisticRegression
log_reg = LogisticRegression(random_state=42,solver="liblinear", max_iter=200)
grid = {"penalty" : ["l1", "l2"],
         "C" : np.arange(60,80,2)} # (60,62,64 ... 78)
log_reg_cv = GridSearchCV(log_reg, grid, cv=3)
log_reg_cv.fit(x_train, y_train)

# Print hyperparameter
print("Tuned hyperparameter n_estimators: {}".format(log_reg_cv.best_params_))
```

```
Tuned hyperparameter n_estimators: {'C': 68, 'penalty': 'l1'}
```

In [31]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.naive_bayes import GaussianNB
import sklearn.metrics as metrics
from sklearn.metrics import precision_recall_curve
from sklearn.metrics import auc
from sklearn.metrics import f1_score
from sklearn.metrics import log_loss

dec = DecisionTreeClassifier(random_state=42)
ran = RandomForestClassifier(random_state=42,n_estimators=100)
knn = KNeighborsClassifier(n_neighbors=100)
svm = SVC(random_state=42,probability=True)
naive = GaussianNB()
lg = log_reg_cv.best_estimator_

models = {"Decision tree" : dec,
          "Random forest" : ran,
          "KNN" : knn,
          "SVM" : svm,
          "Naive bayes" : naive,
          "Logistic regression" : lg}
acc_scores = { }
auroc = { }
auprc = { }
logloss = { }
F1 = { }

for key, value in models.items():
    model = value
```

```
        model.fit(x_train, y_train)
        acc_scores[key] = model.score(x_test, y_test)
        probs = model.predict_proba(x_test)
        preds = probs[:,1]
        fpr, tpr, threshold = metrics.roc_curve(y_test, preds)
        auroc[key] = metrics.auc(fpr, tpr)
        precision, recall, thresholds = precision_recall_curve(y_test, preds)
        auprc[key] = auc(recall, precision)
        predict = model.predict(x_test)
        logloss[key] = log_loss(y_test, probs)
        F1[key] = f1_score(y_test, predict)
```

Table of scores:

```
In [32]: scores_frame = pd.DataFrame([acc_scores,auroc,auprc,logloss,F1],
                                     index=["Accuracy Score", "AUROC","AUPRC", "log_loss", "F1"]
         scores_frame.sort_values(by=["Accuracy Score"], axis=0 ,ascending=False, inplace=True)
         scores_frame
```

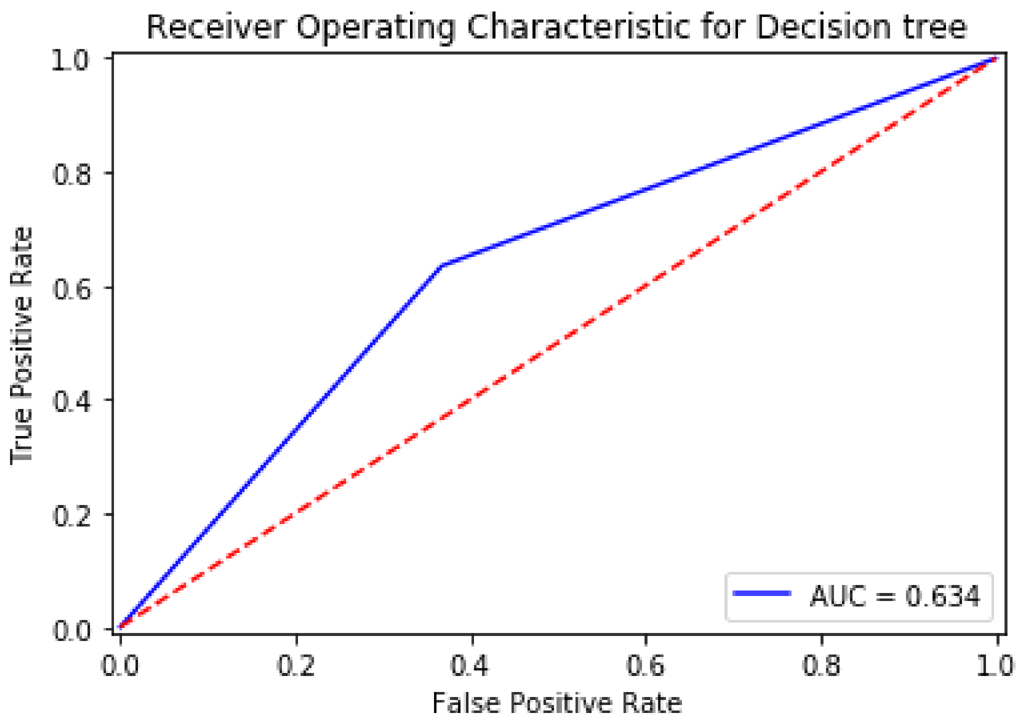
Out[32]:

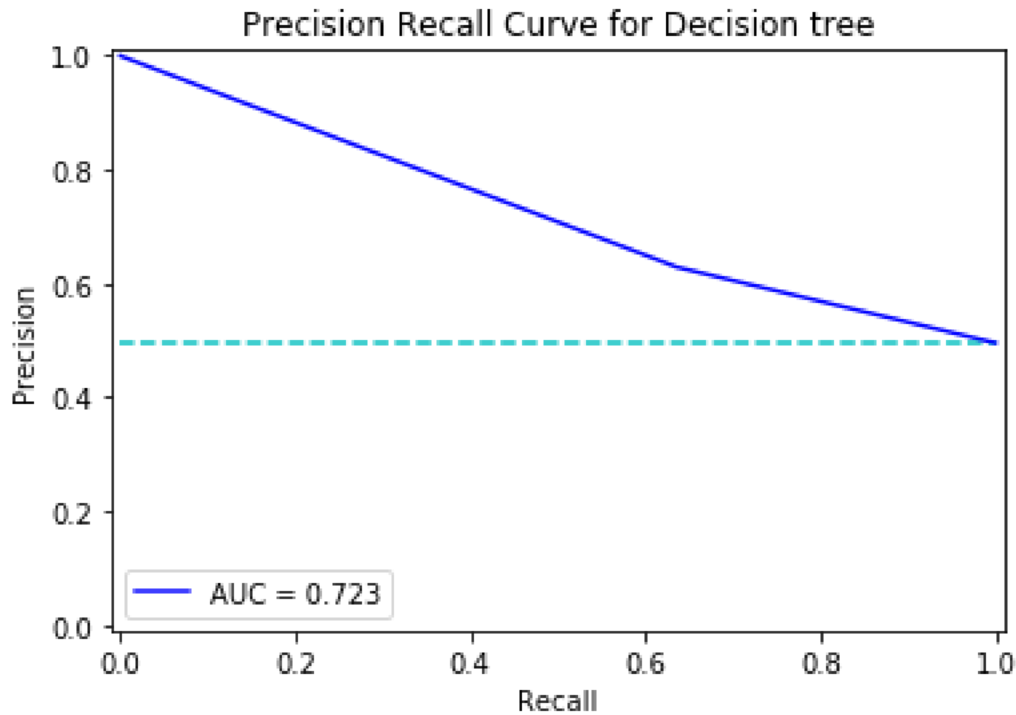
	Accuracy Score	AUROC	AUPRC	log_loss	F1
Logistic regression	0.722445	0.784962	0.766436	0.569936	0.706219
Random forest	0.715004	0.774994	0.759608	0.579101	0.704716
KNN	0.709640	0.772245	0.754992	0.572025	0.684451
Naive bayes	0.639140	0.703851	0.665866	0.707888	0.576596
Decision tree	0.633728	0.633733	0.722523	12.649020	0.632039
SVM	0.504470	0.737721	0.720255	0.677803	0.000000

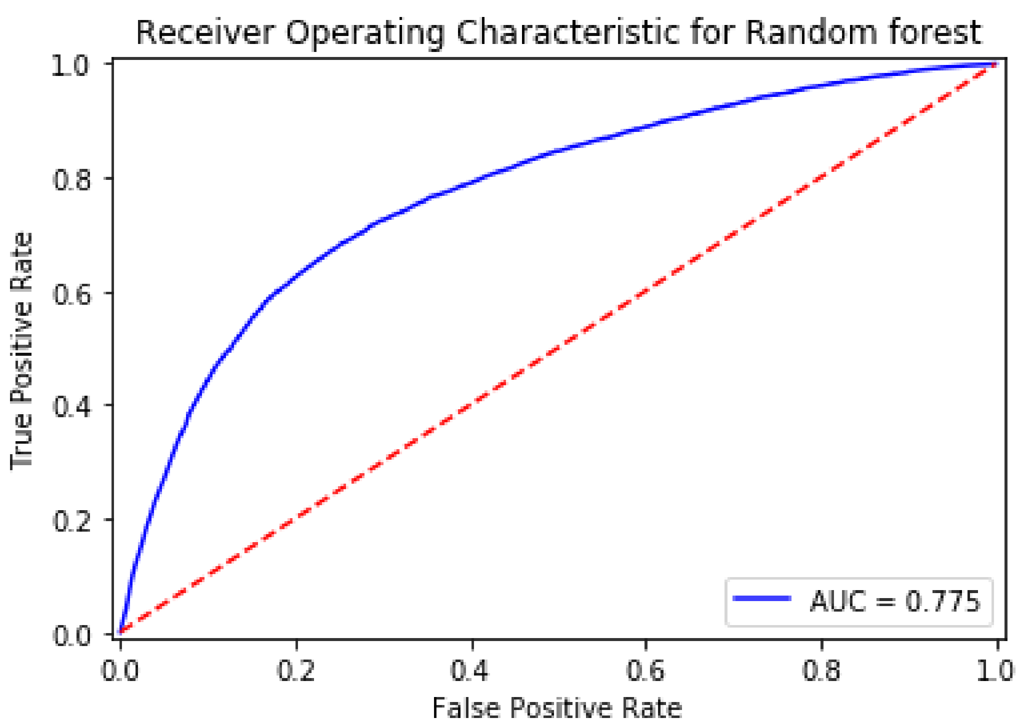
ROC and PR curves for each classifier

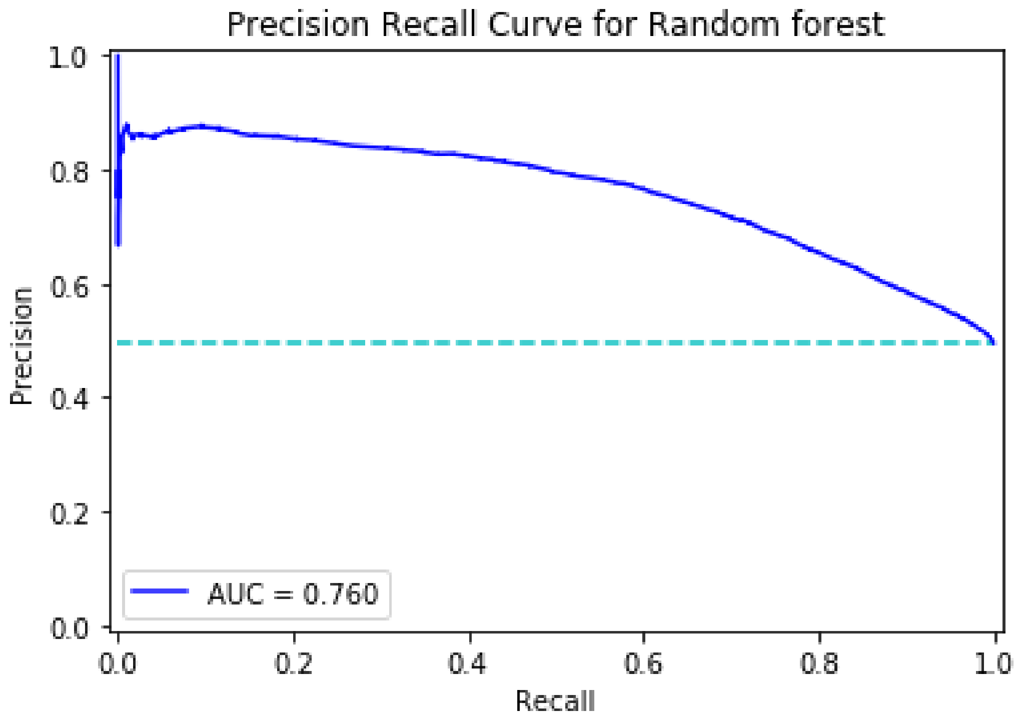
```
In [33]: for key, value in models.items():
             probs = value.predict_proba(x_test)
             preds = probs[:,1]
             fpr, tpr, threshold = metrics.roc_curve(y_test, preds)
             roc_auc = metrics.auc(fpr, tpr)

             plt.title('Receiver Operating Characteristic for {}'.format(key))
             plt.plot(fpr, tpr, 'b', label = 'AUC = %0.3f' % roc_auc)
             plt.legend(loc = 'lower right')
             plt.plot([0, 1], [0, 1],'r--')
             plt.xlim([-0.01, 1.01])
             plt.ylim([-0.01, 1.01])
             plt.ylabel('True Positive Rate')
             plt.xlabel('False Positive Rate')
             plt.show()

             precision, recall, thresholds = precision_recall_curve(y_test, preds)

             plt.title('Precision Recall Curve for {}'.format(key))
```

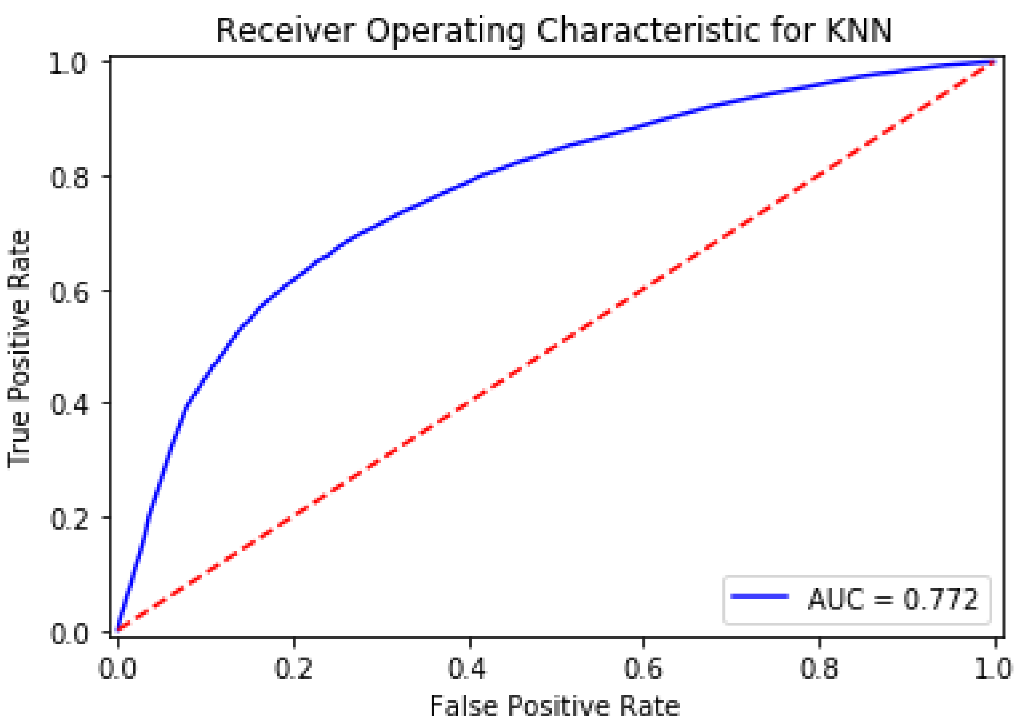
```
plt.plot(recall, precision, 'b', label = 'AUC = %0.3f' % auc(recall, precision))
plt.hlines(is_positive, 0, 1, colors = 'c', linestyle = 'dashed')
plt.legend(loc = 'lower left')
plt.xlim([-0.01, 1.01])
plt.ylim([-0.01, 1.01])
plt.ylabel('Precision')
plt.xlabel('Recall')
plt.show()
```

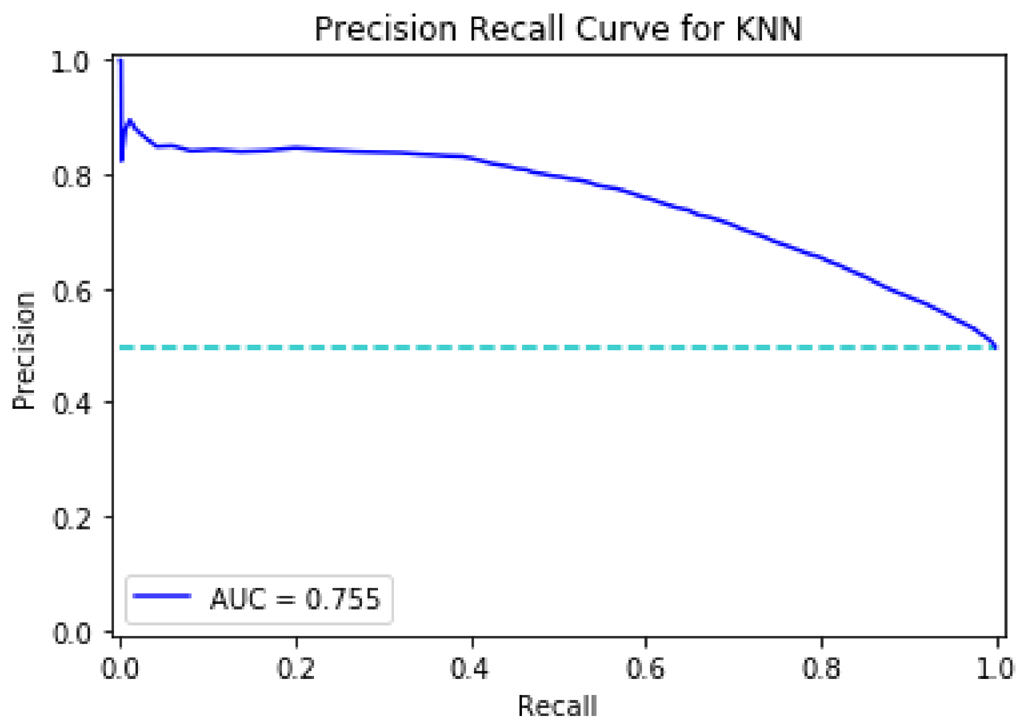


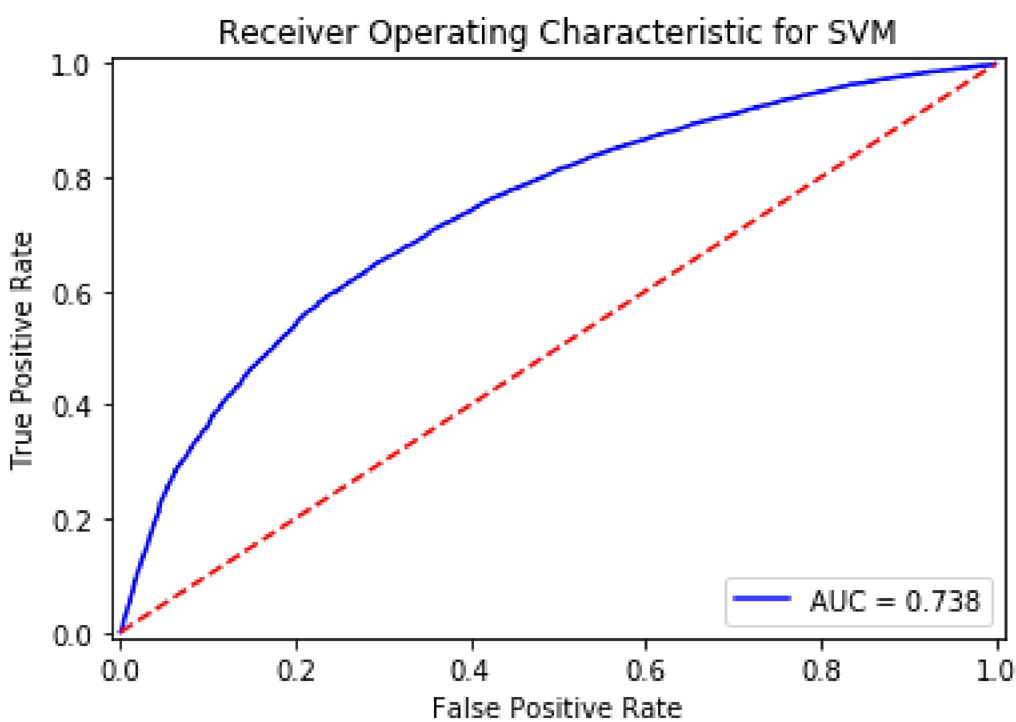

Precision Recall Curve for Decision tree
1.0
0.8
0.6
0.4
0.2
0.0
Precision
AUC = 0.723
0.0
0.2
0.4
0.6
0.8
1.0
Recall

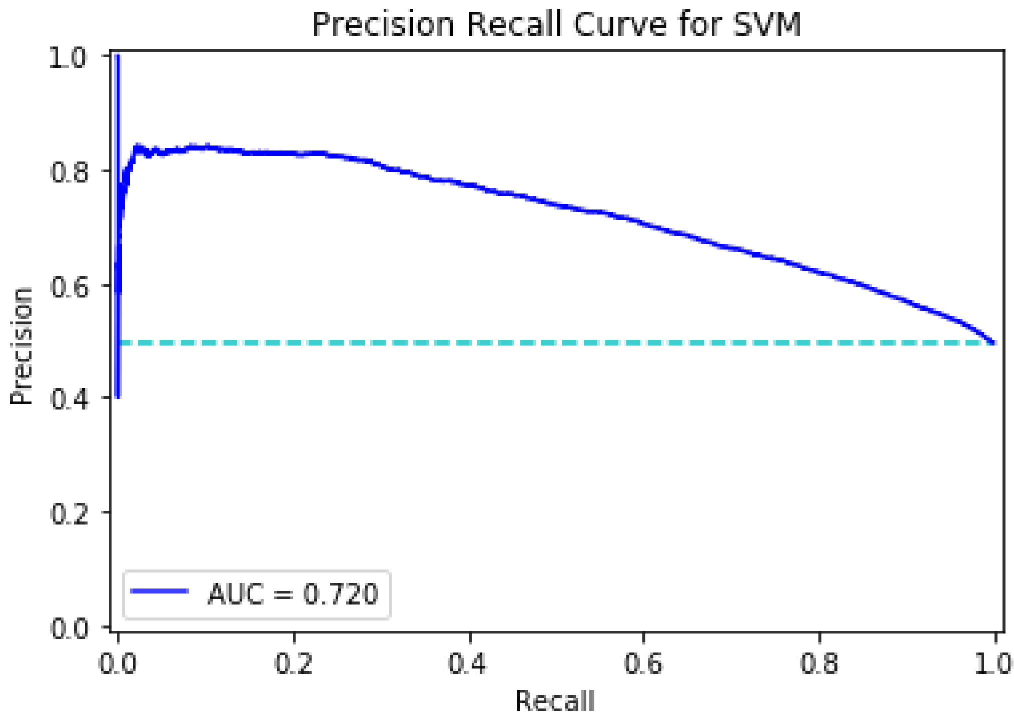

Receiver Operating Characteristic for Random forest
1.0
0.8
0.6
0.4
0.2
0.0
True Positive Rate
AUC = 0.775
0.0
0.2
0.4
0.6
0.8
1.0
False Positive Rate

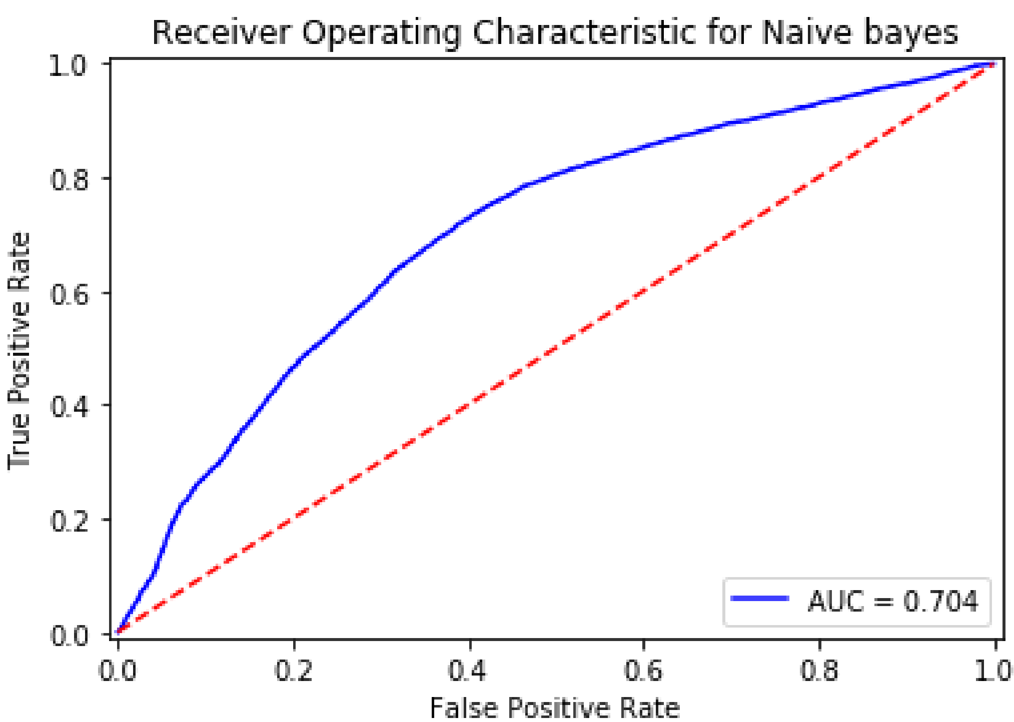

Precision Recall Curve for Random forest
1.0
0.8
0.6
0.4
0.2
0.0
Precision
AUC = 0.760
0.0
0.2
0.4
0.6
0.8
1.0
Recall

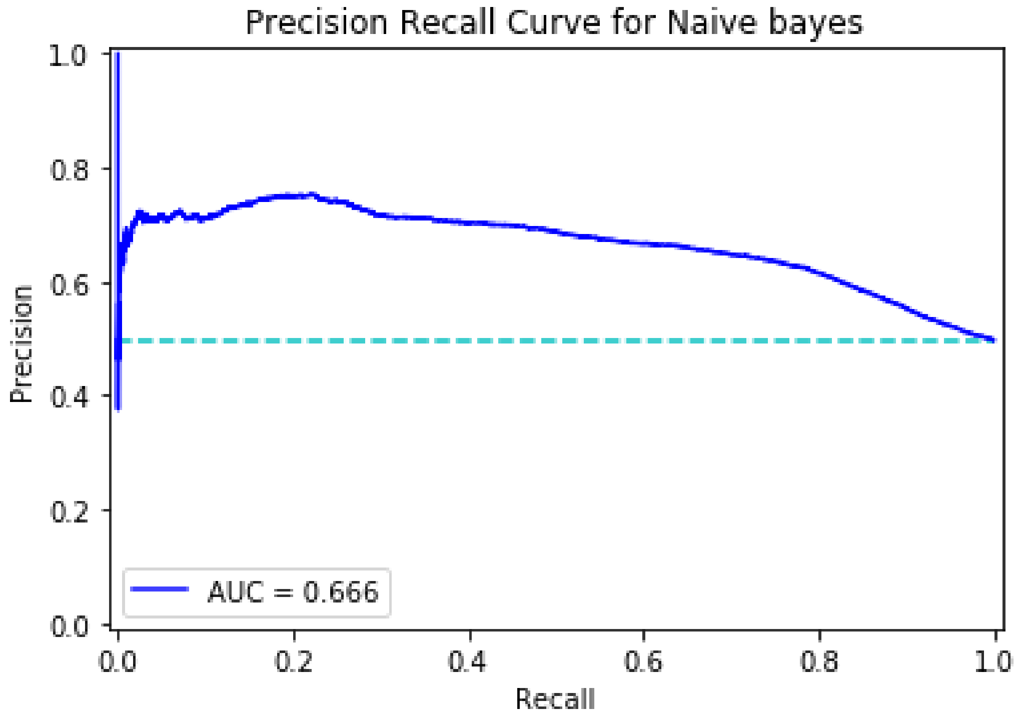

Receiver Operating Characteristic for KNN
1.0
0.8
0.6
0.4
0.2
0.0
True Positive Rate
AUC = 0.772
0.0
0.2
0.4
0.6
0.8
1.0
False Positive Rate

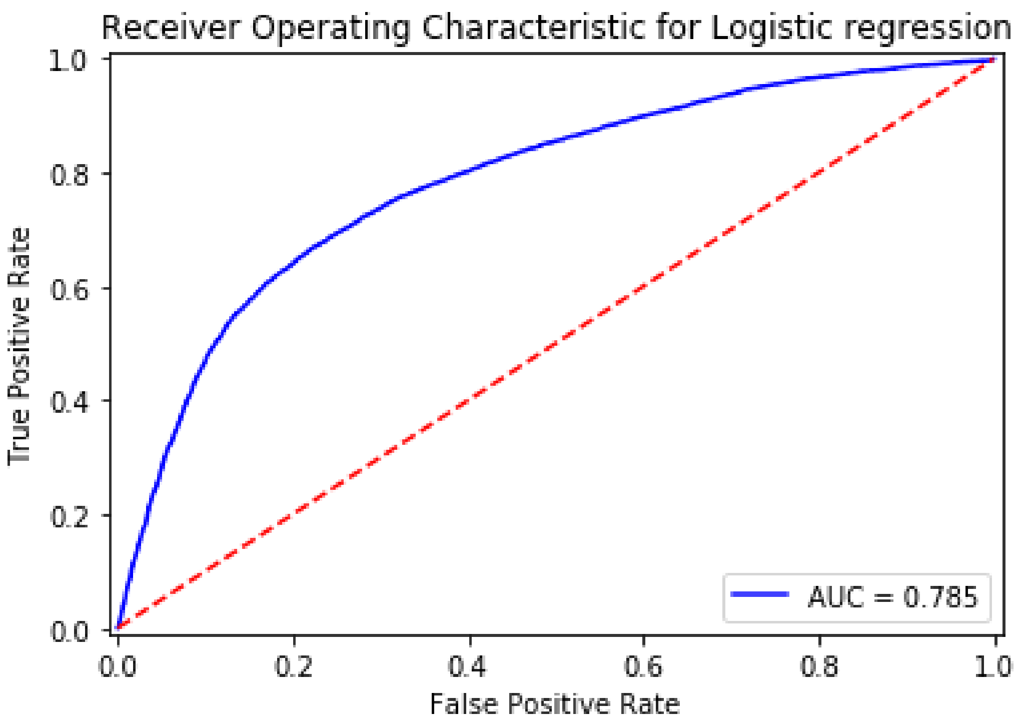

Precision Recall Curve for KNN
Precision
Recall
AUC = 0.755
0.0
0.2
0.4
0.6
0.8
1.0

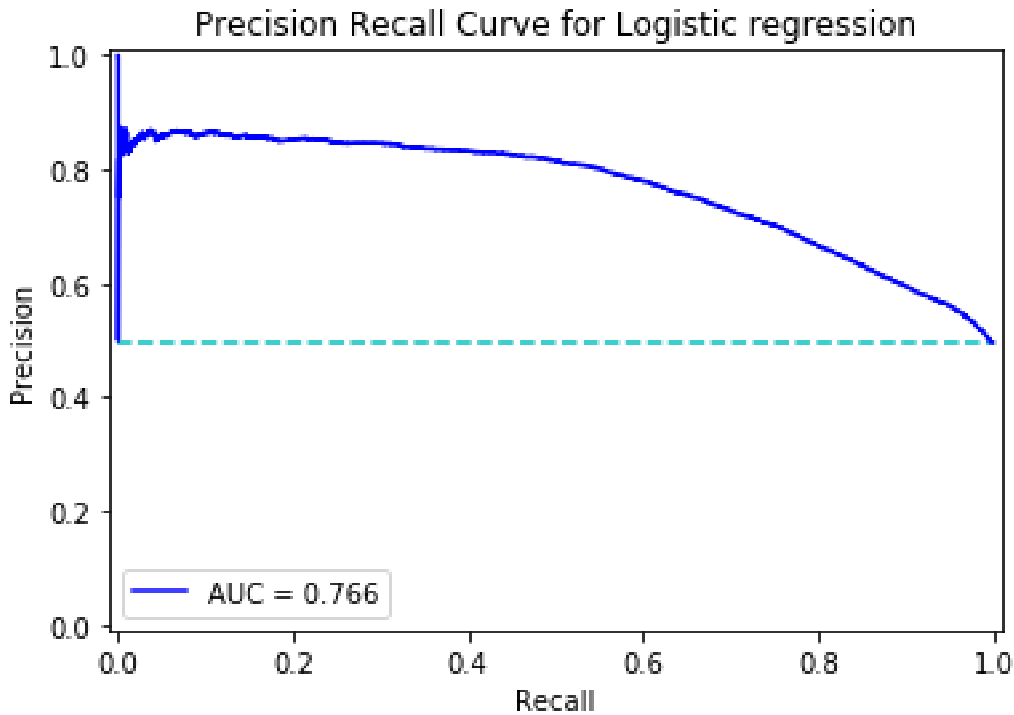

Receiver Operating Characteristic for SVM
True Positive Rate
False Positive Rate
AUC = 0.738
0.0
0.2
0.4
0.6
0.8
1.0


Precision Recall Curve for SVM
Precision
Recall
AUC = 0.720
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0


Receiver Operating Characteristic for Naive bayes
True Positive Rate
False Positive Rate
AUC = 0.704
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0


Precision Recall Curve for Naive bayes
1.0
0.8
0.6
0.4
0.2
0.0
Precision
AUC = 0.666
0.0
0.2
0.4
0.6
0.8
1.0
Recall


Receiver Operating Characteristic for Logistic regression
1.0
0.8
0.6
0.4
0.2
0.0
True Positive Rate
AUC = 0.785
0.0
0.2
0.4
0.6
0.8
1.0
False Positive Rate



Overall Analysis

From the table above we can see that the best classifier for this problem is Logistic Regression. Most of the measures agree with the second best classifier being Random Forest, except log_loss which votes for KNN. Hence, all measures pick a good classifier well.

However, there are some disagreements in what classifier should not be used for this problem. For example, SVM are very bad according to accuracy but not that bad according to AUROC, AUPRC and log_loss. In F1, SVM scores zero. This is probably because F1 choses a threshold when recall is zero. Hence, F1 here is not very useful measure. On the other hand, both AUROC and log_loss vote for Decision Tree as the worst classifier. However, in AUPRC, Decision Tree scores quite high. According to AUPRC, Naive Bayes is the worst classifier, disagreeing with AUROC.

In conclusion, it is very hard to say which classifier is the best by just looking at the table. Perhaps looking at ROC and PR curves will give us more idea. PR curves for SVM and Naive Bayes do go below the baseline for a bit. PR curves for Logistic Regression, SVM, Naive Bayes and Random Forest are very unstable in the beginning. I do not know why this is the case. ROC curves are smooth for all classifiers.

Overall, it is very hard to compare measures just by analysing the table and shape of the curves. We will need to do more reasearch in the future.