Midterm report: Heartdisease

Shuangyi Tan s1889983

Shuangyi Tan's dataset is about heart disease. And it came from Kaggle.

The source dataset is publicly available on the Kaggle website from an ongoing cardiovascular study of residents of Framingham, Massachusetts. The purpose of the classification is to predict whether the patient has a 10-year risk of future coronary heart disease (CHD).[1]

Data processing and analysis

1. import librarys and supress Warnings

[3]:
```
import warnings
warnings.filterwarnings('ignore')
import numpy as np
import pandas as pd
import scipy.stats as st
import statsmodels.api as sm
import matplotlib.pyplot as plt
from statsmodels.tools import add_constant as add_constant
```

2. Read the data, drop some information, rename columns

[4]:
```
heart_df=pd.read_csv("framingham_heart_disease.csv")
heart_df.head()
```

[4]:

	male	age	education	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp	diabetes	totChol	sysBP	diaBP	BMI	heartRate	glucose	TenYearCHD
0	1	39	4.0	0	0.0	0.0	0	0	0	195.0	106.0	70.0	26.97	80.0	77.0	0
1	0	46	2.0	0	0.0	0.0	0	0	0	250.0	121.0	81.0	28.73	95.0	76.0	0
2	1	48	1.0	1	20.0	0.0	0	0	0	245.0	127.5	80.0	25.34	75.0	70.0	0
3	0	61	3.0	1	30.0	0.0	0	1	0	225.0	150.0	95.0	28.58	65.0	103.0	1
4	0	46	3.0	1	23.0	0.0	0	0	0	285.0	130.0	84.0	23.10	85.0	85.0	0

[5]:
```
heart_df.describe()
```

[5]:

	male	age	education	currentSmoker	cigsPerDay
count	4238.000000	4238.000000	4133.000000	4238.000000	4209.000000
mean	0.429212	49.584946	1.978950	0.494101	9.003089
std	0.495022	8.572160	1.019791	0.500024	11.920094
min	0.000000	32.000000	1.000000	0.000000	0.000000
25%	0.000000	42.000000	1.000000	0.000000	0.000000
50%	0.000000	49.000000	2.000000	0.000000	0.000000
75%	1.000000	56.000000	3.000000	1.000000	20.000000
max	1.000000	70.000000	4.000000	1.000000	70.000000

	BPMeds	prevalentStroke	prevalentHyp	diabetes	totChol
count	4185.000000	4238.000000	4238.000000	4238.000000	4188.000000
mean	0.029630	0.005899	0.310524	0.025720	236.721585
std	0.169584	0.076587	0.462763	0.158316	44.590334
min	0.000000	0.000000	0.000000	0.000000	107.000000
25%	0.000000	0.000000	0.000000	0.000000	206.000000
50%	0.000000	0.000000	0.000000	0.000000	234.000000
75%	0.000000	0.000000	1.000000	0.000000	263.000000
max	1.000000	1.000000	1.000000	1.000000	696.000000

	sysBP	diaBP	BMI	heartRate	glucose
count	4238.000000	4238.000000	4219.000000	4237.000000	3850.000000
mean	132.352407	82.893464	25.802008	75.878924	81.966753
std	22.038097	11.910850	4.080111	12.026596	23.959998
min	83.500000	48.000000	15.540000	44.000000	40.000000
25%	117.000000	75.000000	23.070000	68.000000	71.000000
50%	128.000000	82.000000	25.400000	75.000000	78.000000
75%	144.000000	89.875000	28.040000	83.000000	87.000000
max	295.000000	142.500000	56.800000	143.000000	394.000000

	TenYearCHD
count	4238.000000
mean	0.151958
std	0.359023
min	0.000000
25%	0.000000
50%	0.000000
75%	0.000000
max	1.000000

From above, we could see that the original dataset has 14 variables, 2 classes and 4238 samples. From original dataset description, we have:

Demographic:

Sex: male or female(Nominal)

Age: Age of the patient;(Continuous - Although the recorded ages have been truncated to whole numbers, the concept of age is continuous)

Behavioral:

Current Smoker: whether or not the patient is a current smoker (Nominal)

Cigs Per Day: the number of cigarettes that the person smoked on average in one day.(can be considered continuous as one can have any number of cigarettes, even half a cigarette.)

Medical(history):

BP Meds: whether or not the patient was on blood pressure medication (Nominal)

Prevalent Stroke: whether or not the patient had previously had a stroke (Nominal)

Prevalent Hyp: whether or not the patient was hypertensive (Nominal)

Diabetes: whether or not the patient had diabetes (Nominal)

Tot Chol: total cholesterol level (Continuous)

Sys BP: systolic blood pressure (Continuous)

Dia BP: diastolic blood pressure (Continuous)

BMI: Body Mass Index (Continuous)

Heart Rate: heart rate (Continuous - In medical research, variables such as heart rate though in fact discrete, yet are considered continuous because of large number of possible values.)

Glucose: glucose level (Continuous) Predict variable (desired target)

Class:

10 year risk of coronary heart disease CHD (binary: "1", means "Yes", "0" means "No")

[6]:
```
heart_df.drop(['education'],axis=1,inplace=True)
heart_df.rename(columns={'male':'Sex_male'},inplace=True)
```

From basic information, we could know education has nearly no relationship with heart disease. so we drop it here. ### 3. Handle the missing values

[7]:
```
count=0
for i in heart_df.isnull().sum(axis=1):
    if i>0:
        count=count+1
print('Total number of rows with missing values is ', count)
print('since it is only',round((count/len(heart_df.index))*100), 'percent of the␣
 ↪entire dataset the rows with missing values are excluded.')
heart_df.dropna(axis=0,inplace=True)
pd.set_option('display.max_columns', 1000)
pd.set_option('display.width', 1000)
heart_df.describe()
```

```
Total number of rows with missing values is  489
since it is only 12 percent of the entire dataset the rows with missing values
are excluded.
```

[7]:

	Sex_male	age	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp	diabetes	totChol	sysBP	diaBP	BMI	heartRate	glucose	TenYearCHD
count	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000	3749.000000
mean	0.445185	49.578821	0.488397	9.005335	0.030408	0.005601	0.311816	0.027207	236.952787	132.365964	82.933716				

```
25.809651    75.703921    81.883169     0.152574
std       0.497053     8.569322       0.499932    11.922440     0.171730
0.074643      0.463297     0.162709    44.610417    22.051951    11.933321
4.065894    11.957763    23.888039     0.359624
min       0.000000    32.000000       0.000000     0.000000     0.000000
0.000000      0.000000     0.000000   113.000000    83.500000    48.000000
15.540000    44.000000    40.000000     0.000000
25%       0.000000    42.000000       0.000000     0.000000     0.000000
0.000000      0.000000     0.000000   206.000000   117.000000    75.000000
23.090000    68.000000    71.000000     0.000000
50%       0.000000    49.000000       0.000000     0.000000     0.000000
0.000000      0.000000     0.000000   234.000000   128.000000    82.000000
25.410000    75.000000    78.000000     0.000000
75%       1.000000    56.000000       1.000000    20.000000     0.000000
0.000000      1.000000     0.000000   264.000000   144.000000    90.000000
28.060000    82.000000    87.000000     0.000000
max       1.000000    70.000000       1.000000    70.000000     1.000000
1.000000      1.000000     1.000000   696.000000   295.000000   142.500000
56.800000   143.000000   394.000000     1.000000
```

Firstly, we check the proportion of missing values and find that total number of rows with missing values is 489, which is 12 percent of entire dataset.

As a result, here we do the complete analysis for the dataset, which means that we drop all samples with missing values.

Then we will have a dataset with values all observed. The new dataset has 3749 samples.

4. Add a constant

Here we add a constant for each sample, which make things more convenient for using several models.

[8]:
```
heart_df_constant = add_constant(heart_df)
heart_df_constant.head()
```

[8]:
```
   const  Sex_male  age  currentSmoker  cigsPerDay  BPMeds  prevalentStroke
prevalentHyp  diabetes  totChol  sysBP  diaBP    BMI  heartRate  glucose
TenYearCHD
0    1.0         1   39              0         0.0     0.0               0
0         0    195.0  106.0   70.0  26.97       80.0     77.0           0
1    1.0         0   46              0         0.0     0.0               0
0         0    250.0  121.0   81.0  28.73       95.0     76.0           0
2    1.0         1   48              1        20.0     0.0               0
0         0    245.0  127.5   80.0  25.34       75.0     70.0           0
3    1.0         0   61              1        30.0     0.0               0
1         0    225.0  150.0   95.0  28.58       65.0    103.0           1
4    1.0         0   46              1        23.0     0.0               0
0         0    285.0  130.0   84.0  23.10       85.0     85.0           0
```

5. Choose relative features we need to use

[9]:
```
st.chisqprob = lambda chisq, df: st.chi2.sf(chisq, df)
cols = heart_df_constant.columns[:-1]
model = sm.Logit(heart_df.TenYearCHD,heart_df_constant[cols])
result = model.fit()
print(result.summary())

# Define back_feature_selection
def back_feature_elem (data_frame,dep_var,col_list):
    while len(col_list)>0 :
        model = sm.Logit(dep_var,data_frame[col_list])
        result = model.fit(disp=0)
        largest_pvalue = round(result.pvalues,3).nlargest(1)
        if largest_pvalue[0]<(0.05):
            return result
            break
        else:
            col_list=col_list.drop(largest_pvalue.index)

# Use back_feature_selection to select features, if p > 0.05, we delete the␣
 ↪feature
result=back_feature_elem(heart_df_constant,heart_df.TenYearCHD,cols)

#Interpreting the results: Odds Ratio, Confidence Intervals and Pvalues
params = np.exp(result.params)
conf = np.exp(result.conf_int())
conf['OR'] = params
pvalue=round(result.pvalues,3)
conf['pvalue']=pvalue
conf.columns = ['CI 95%(2.5%)', 'CI 95%(97.5%)', 'Odds Ratio','pvalue']
print (conf)

new_features=heart_df[['age','Sex_male','cigsPerDay','totChol','sysBP','glucose','TenYearCHD']]
```

```
Optimization terminated successfully.
         Current function value: 0.377199
         Iterations 7
                           Logit Regression Results
==============================================================================
Dep. Variable:             TenYearCHD   No. Observations:                 3749
Model:                          Logit   Df Residuals:                     3734
Method:                           MLE   Df Model:                           14
Date:                Mon, 11 Nov 2019   Pseudo R-squ.:                 0.1169
Time:                        23:12:32   Log-Likelihood:                -1414.1
converged:                       True   LL-Null:                       -1601.4
Covariance Type:            nonrobust   LLR p-value:                2.922e-71
==============================================================================
```

```
===
                       coef    std err          z      P>|z|      [0.025
0.975]
------------------------------------------------------------------------------
---
const               -8.6463      0.687    -12.577      0.000      -9.994
-7.299
Sex_male             0.5740      0.107      5.343      0.000       0.363
0.785
age                  0.0640      0.007      9.787      0.000       0.051
0.077
currentSmoker        0.0732      0.155      0.473      0.636      -0.230
0.376
cigsPerDay           0.0184      0.006      3.003      0.003       0.006
0.030
BPMeds               0.1446      0.232      0.622      0.534      -0.311
0.600
prevalentStroke      0.7191      0.489      1.471      0.141      -0.239
1.677
prevalentHyp         0.2146      0.136      1.574      0.116      -0.053
0.482
diabetes             0.0025      0.312      0.008      0.994      -0.609
0.614
totChol              0.0022      0.001      2.074      0.038       0.000
0.004
sysBP                0.0153      0.004      4.080      0.000       0.008
0.023
diaBP               -0.0039      0.006     -0.619      0.536      -0.016
0.009
BMI                  0.0103      0.013      0.820      0.412      -0.014
0.035
heartRate           -0.0023      0.004     -0.550      0.583      -0.010
0.006
glucose              0.0076      0.002      3.408      0.001       0.003
0.012
==============================================================================
===
             CI 95%(2.5%)  CI 95%(97.5%)  Odds Ratio  pvalue
const            0.000044       0.000274    0.000109   0.000
Sex_male         1.454877       2.198166    1.788313   0.000
age              1.054409       1.080897    1.067571   0.000
cigsPerDay       1.011730       1.028128    1.019896   0.000
totChol          1.000150       1.004386    1.002266   0.036
sysBP            1.013299       1.021791    1.017536   0.000
glucose          1.004343       1.010895    1.007614   0.000
```

Feature Selection: Backward elemination (P-value approach)
Here we use backward elemination to select relative features.

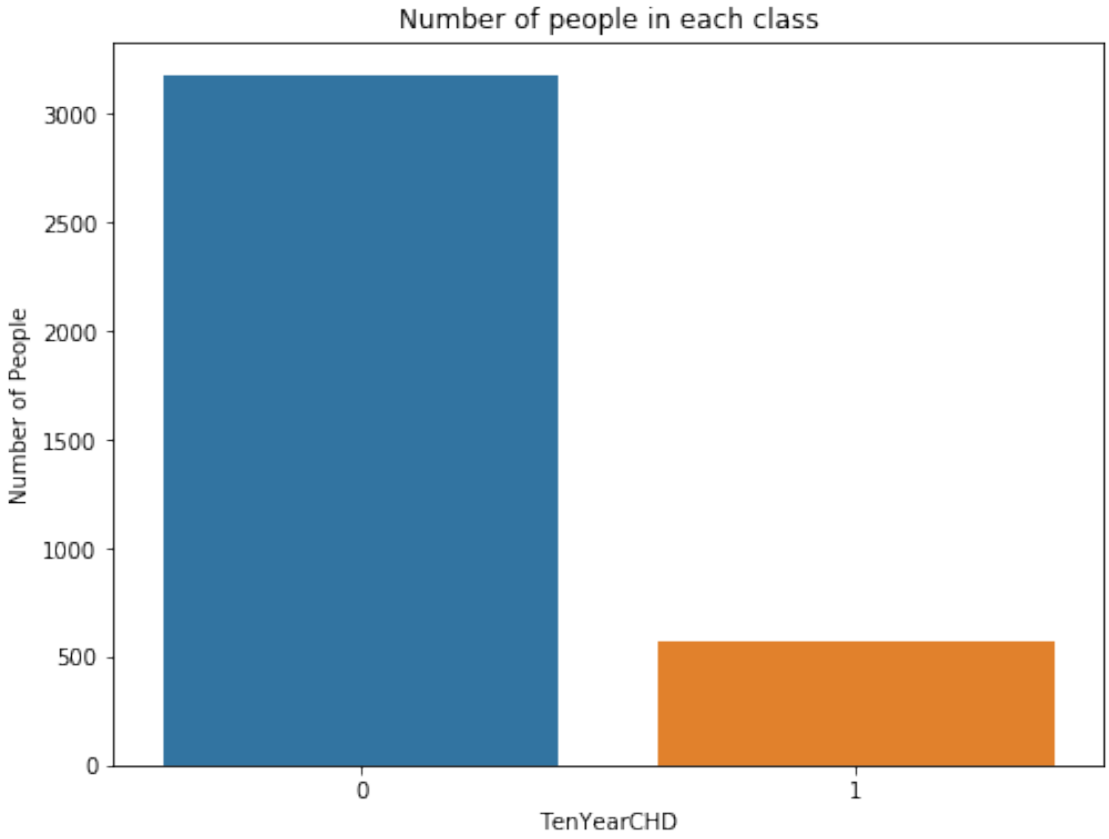
Statistically speaking, if some attributes have the P values are higher than the preferred alpha (5%), there is a very low statistically significant relationship between these attributes and the probability of heart disease.

The backward elimination method is used to delete those attributes with the highest P value at a time, and then run the learning repeatedly until the P values of all the attributes are less than 0.05.

So finally we choose 'age','Sex_male','cigsPerDay','totChol','sysBP' and 'glucose' these six features which are most relative to the heart disease due to the low p-values. We use these six features and the class variable to form a new dataset named 'new_features' here.

6. Plot basis features of new dataset

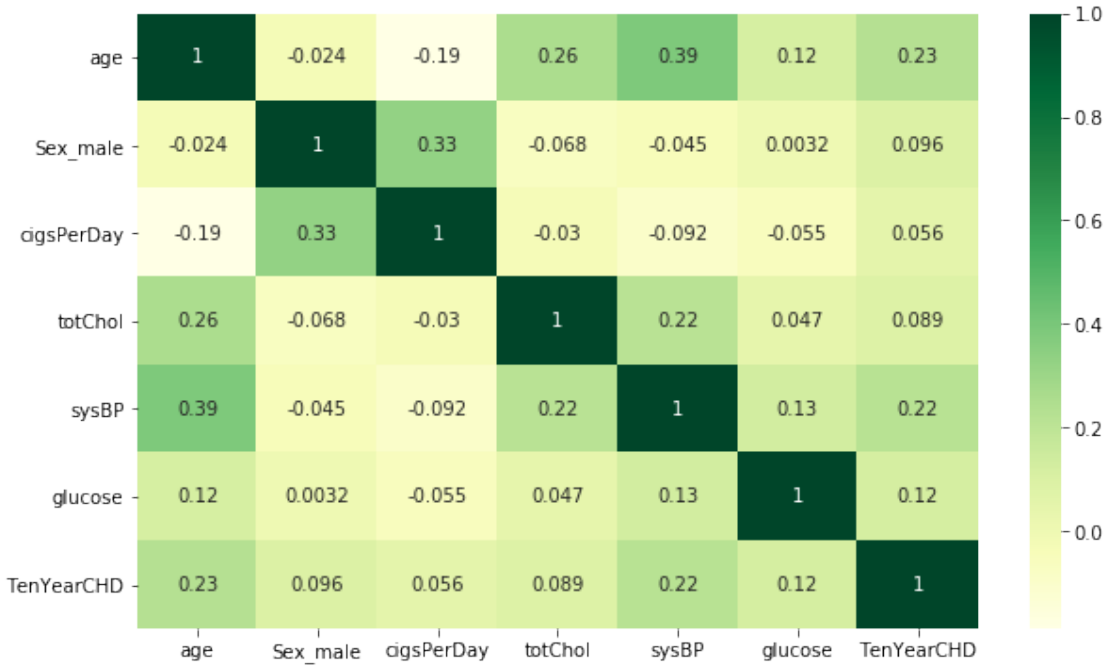
[10]:
```
import seaborn as sns
plt.figure(figsize=(8,6))
sns.countplot(x='TenYearCHD',data=new_features)
plt.title('Number of people in each class')
plt.ylabel('Number of People')
plt.savefig('Class.png')
plt.show()

print()
count = new_features.TenYearCHD.value_counts()
print(count)
print()
```




```
0    3177
1     572
Name: TenYearCHD, dtype: int64
```

Firstly, from what is stated above, there are 2 classes. 0 shows that the participant has no has 10-year risk of future coronary heart disease(CHD) and 1 otherwise. From the result above, we could see that the dataset is extremely unbalanced.

[11]:
```
plt.figure(figsize=(10,6))
sns.heatmap(new_features.corr(),cmap='YlGn',annot=True)
plt.savefig('Corr.png')
plt.show()
```



From the graph above, we could see that the correlation between features are small, which means that the features we choose here describe the dataset to the utmost extent.

[12]:
```
# Plot out the distribution, which will take a long time
y_target = new_features['TenYearCHD']
new_features['target'] = new_features['TenYearCHD'].map({0:'NH',1:'H'})
g = sns.pairplot(new_features.drop('TenYearCHD', axis = 1), hue="target",␣
 ↪palette='prism');
plt.savefig('Distribution.png')
plt.show()
```

From the pairplot above, we could see that the data is very mixed in every dimension. That is, the problem here is a complex problem, which means that the classifier can't easily reach a high accuracy.

7. Split training data and testing data

[18]:
```
new_features=heart_df[['age','Sex_male','cigsPerDay','totChol','sysBP','glucose','TenYearCHD']]
x = new_features.iloc[:,:-1]
y = new_features.iloc[:,-1]
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test = train_test_split(x,y,test_size=.
 ↪20,random_state=5)
```

This module is aiming to generate 2 sets, one for testing and another for training. The proposition here we use is training set : testing set = 4:1.

8. Training different classifier and test result analysis

Firstly we focus on the random guess classifier, which also will be a baseline.

The AUROC of random guess will be 0.5 and the AUPRC of it should be $\frac{572}{3177+572} \approx 0.15257$.

[31]:
```
# Create a list to show the Acc, AUROC and AUPRC for different classifiers
table = pd.DataFrame(index=["Logistic Regression","SVM","KNN","Naive␣
 ↪Bayes","Desicion Tree","Random Forest"], columns=["AUROC", "AUPRC", "ACC",␣
 ↪"log_loss", "F1"])

# Fit the model and predict y with it
from sklearn.linear_model import LogisticRegression
logreg = LogisticRegression()
log_y_score = logreg.fit(x_train, y_train).decision_function(x_test)
log_y_pred = logreg.predict(x_test)

from sklearn import svm
SvM = svm.SVC()
SVM_y_score = SvM.fit(x_train, y_train).decision_function(x_test)
SVM_y_pred = SvM.predict(x_test)

from sklearn.neighbors import KNeighborsClassifier
neigh = KNeighborsClassifier(n_neighbors=10)
KNN_y_score = neigh.fit(x_train, y_train).predict_proba(x_test)[:, 1]
KNN_y_pred = neigh.predict(x_test)

from sklearn.naive_bayes import GaussianNB
gnb = GaussianNB()
NB_y_score = gnb.fit(x_train, y_train).predict_proba(x_test)[:, 1]
NB_y_pred = gnb.predict(x_test)

from sklearn import tree
dt = tree.DecisionTreeClassifier()
DT_y_score = dt.fit(x_train, y_train).predict_proba(x_test)[:, 1]
DT_y_pred = dt.predict(x_test)


from sklearn.ensemble import RandomForestClassifier
rf = RandomForestClassifier(n_estimators=100, max_depth=2, random_state=0)
RF_y_score = rf.fit(x_train, y_train).predict_proba(x_test)[:, 1]
RF_y_pred = rf.predict(x_test)


# AUROC
from sklearn.metrics import roc_auc_score
log_AUROC = roc_auc_score(y_test,log_y_score)
table.values[0][0] = log_AUROC
```

```
SVM_AUROC = roc_auc_score(y_test,SVM_y_score)
table.values[1][0] = SVM_AUROC

KNN_AUROC = roc_auc_score(y_test,KNN_y_score)
table.values[2][0] = KNN_AUROC

NB_AUROC = roc_auc_score(y_test,NB_y_score)
table.values[3][0] = NB_AUROC

DT_AUROC = roc_auc_score(y_test,DT_y_score)
table.values[4][0] = DT_AUROC

RF_AUROC = roc_auc_score(y_test,RF_y_score)
table.values[5][0] = RF_AUROC


# AUPRC

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import auc

def AUPRC(y_test,y_pred_proba):
    precision, recall, thresholds = precision_recall_curve(y_test,y_pred_proba)
    auprc = auc(recall, precision)
    return auprc

log_AUPRC = AUPRC(y_test,log_y_score)
table.values[0][1] = log_AUPRC
SVM_AUPRC = AUPRC(y_test,SVM_y_score)
table.values[1][1] = SVM_AUPRC
KNN_AUPRC = AUPRC(y_test,KNN_y_score)
table.values[2][1] = KNN_AUPRC
NB_AUPRC = AUPRC(y_test,NB_y_score)
table.values[3][1] = NB_AUPRC
DT_AUPRC = AUPRC(y_test,DT_y_score)
table.values[4][1] = DT_AUPRC
RF_AUPRC = AUPRC(y_test,RF_y_score)
table.values[5][1] = RF_AUPRC


# Model accuracy
from sklearn.metrics import accuracy_score
log_Acc = accuracy_score(y_test, log_y_pred)
table.values[0][2] = log_Acc
SVM_Acc = accuracy_score(y_test, SVM_y_pred)
table.values[1][2] = SVM_Acc
KNN_Acc = accuracy_score(y_test, KNN_y_pred)
```

```
table.values[2][2] = KNN_Acc
NB_Acc = accuracy_score(y_test, NB_y_pred)
table.values[3][2] = NB_Acc
DT_Acc = accuracy_score(y_test, DT_y_pred)
table.values[4][2] = DT_Acc
RF_Acc = accuracy_score(y_test, RF_y_pred)
table.values[5][2] = RF_Acc

#neg_log loss
from sklearn.metrics import log_loss
log_neg_log = log_loss(y_test, log_y_pred)
table.values[0][3] = log_neg_log
SVM_neg_log = log_loss(y_test, SVM_y_pred)
table.values[1][3] = SVM_neg_log
KNN_neg_log = log_loss(y_test, KNN_y_pred)
table.values[2][3] = KNN_neg_log
NB_neg_log = log_loss(y_test, NB_y_pred)
table.values[3][3] = NB_neg_log
DT_neg_log = log_loss(y_test, DT_y_pred)
table.values[4][3] = DT_neg_log
RF_neg_log = log_loss(y_test, RF_y_pred)
table.values[5][3] = RF_neg_log

#F1
from sklearn.metrics import f1_score
log_f1 = f1_score(y_test, log_y_pred, average='weighted')
table.values[0][4] = log_f1
SVM_f1 = f1_score(y_test, SVM_y_pred, average='weighted')
table.values[1][4] = SVM_f1
KNN_f1 = f1_score(y_test, KNN_y_pred, average='weighted')
table.values[2][4] = KNN_f1
NB_f1 = f1_score(y_test, NB_y_pred, average='weighted')
table.values[3][4] = NB_f1
DT_f1 = f1_score(y_test, DT_y_pred, average='weighted')
table.values[4][4] = DT_f1
RF_f1 = f1_score(y_test, RF_y_pred, average='weighted')
table.values[5][4] = RF_f1

# Show the conclu table
print(table.head(7))
```

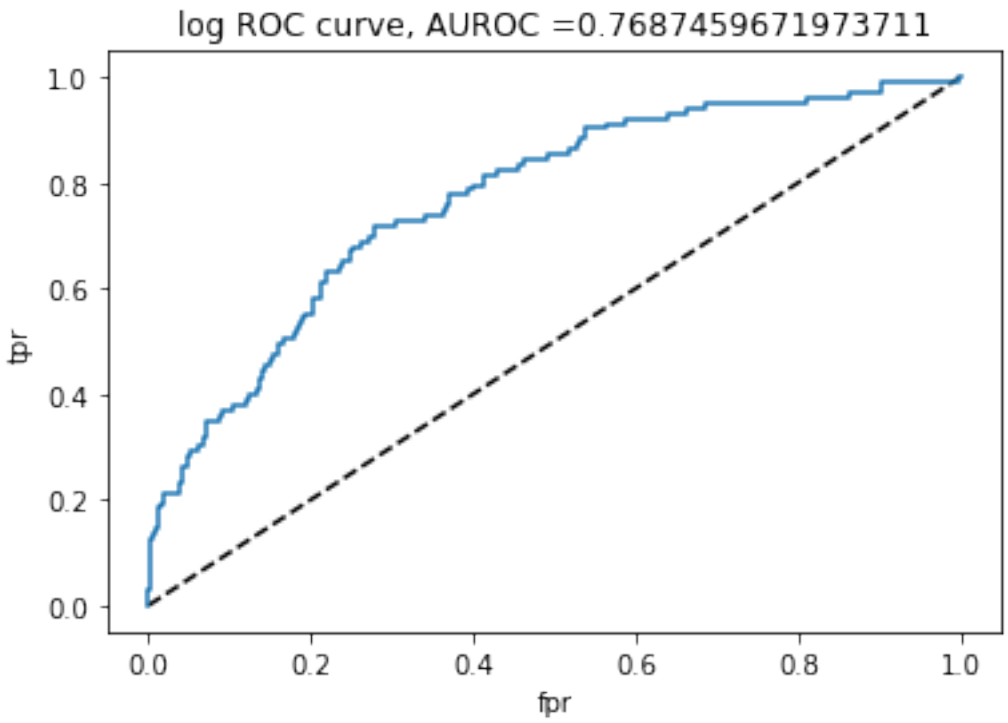
```
                       AUROC     AUPRC       ACC log_loss        F1
Logistic Regression  0.768746   0.40626  0.866667  4.60517  0.810866
SVM                   0.59786  0.159508  0.862667  4.74333  0.799063
KNN                   0.66192  0.225833  0.857333  4.92754  0.809676
Naive Bayes          0.776121  0.386426  0.861333   4.7894  0.834652
Desicion Tree        0.527753  0.246352  0.762667  8.19731   0.76892
```

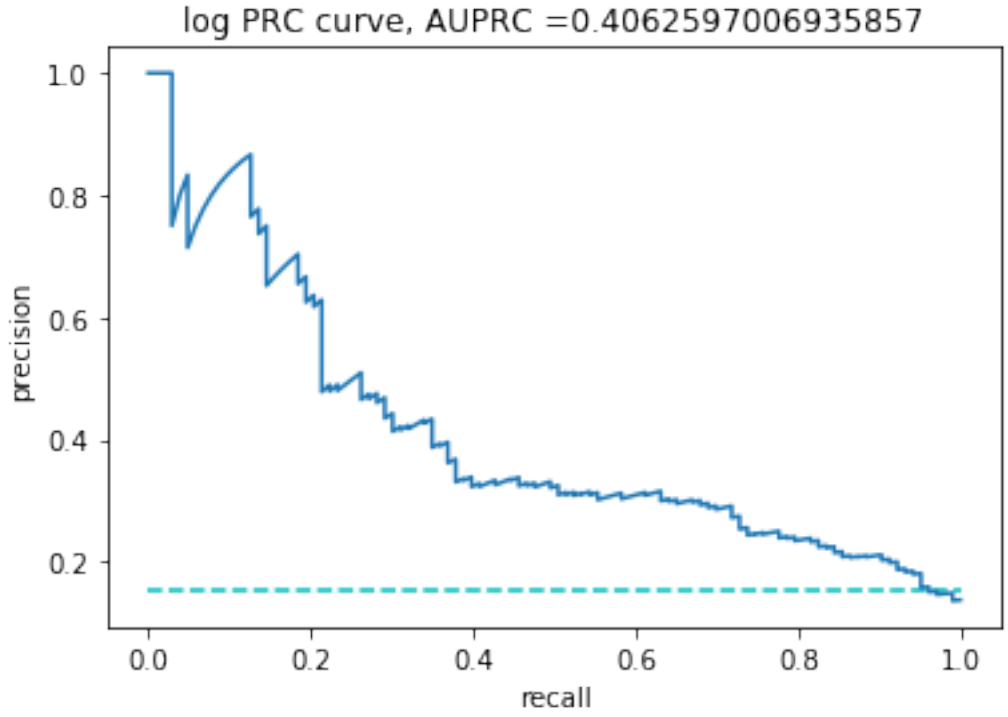
```
Random Forest        0.759758  0.355428  0.862667  4.74333  0.799063
```

Here we choose Logistic regression, Support Vector Machine, KNN, Naive Bayes, Decision Tree and Random Forest these 6 classifiers for experiments. Also, we choose AUROC, AUPRC, accuracy, log loss and F1 score as measurements.

The first one is Logistic regression, here we use built-in preset parameters for the classifier. The ROC and PRC are shown below.

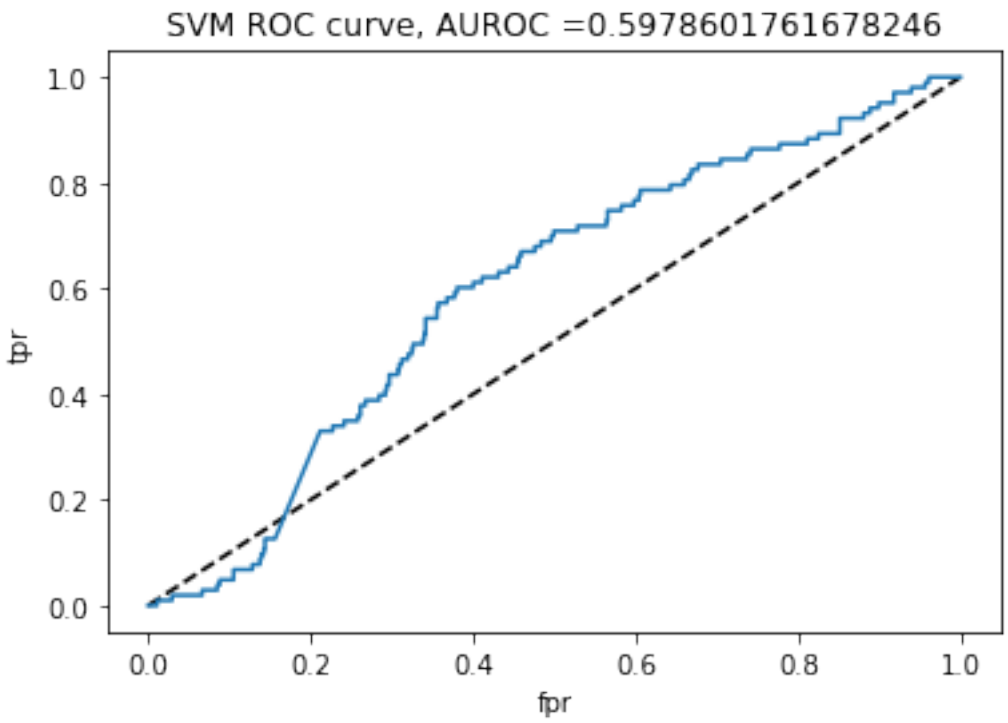
[34]:
```
from sklearn.metrics import roc_curve
y_pred_proba = log_y_score ###############
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba)
#Area under ROC curve
from sklearn.metrics import roc_auc_score
auroc = roc_auc_score(y_test,y_pred_proba)
plt.plot([0,1],[0,1],'k--')
plt.plot(fpr,tpr, label='log') ##############
plt.xlabel('fpr')
plt.ylabel('tpr')
title_name = 'log ROC curve, AUROC ='+str(auroc) ############
plt.title(title_name)
plt.savefig('log ROC curve.png') ####################
plt.show()

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

auprc = auc(recall, precision)
plt.hlines(572/(3177+572), 0, 1, colors = "c", linestyles = "dashed")
plt.plot(recall,precision, label='log') ####################
plt.xlabel('recall')
plt.ylabel('precision')
title_name = 'log PRC curve, AUPRC ='+str(auprc) ###############
plt.title(title_name)
plt.savefig('log PRC curve.png') ######################
plt.show()
```

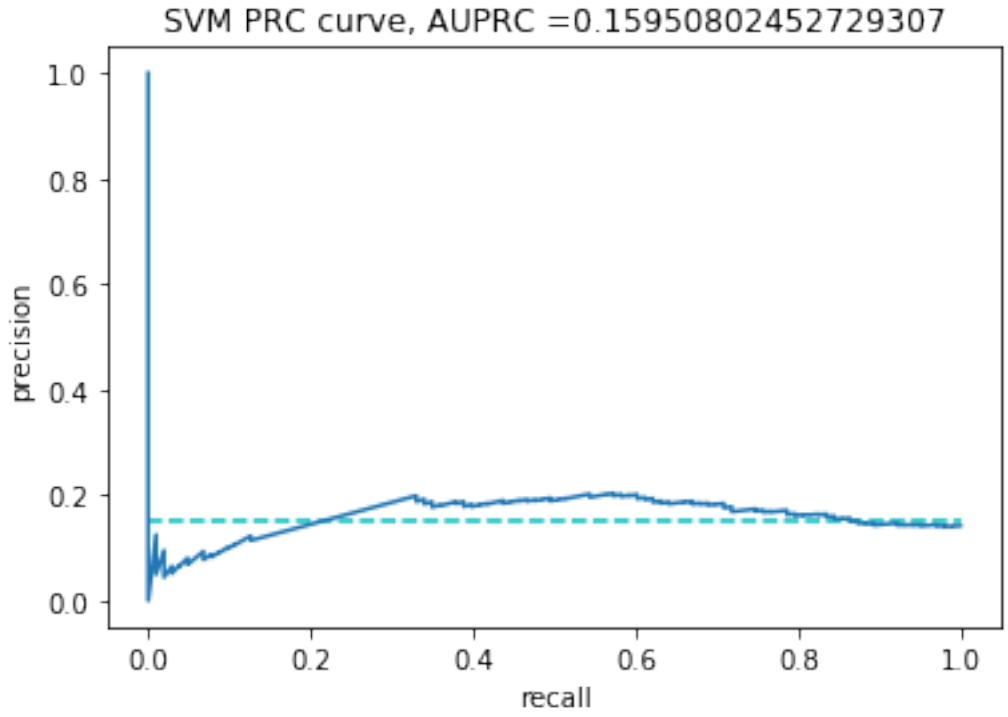

log ROC curve, AUROC =0.7687459671973711
tpr
fpr
0.0
0.2
0.4
0.6
0.8
1.0


log PRC curve, AUPRC =0.4062597006935857
precision
recall
0.0
0.2
0.4
0.6
0.8
1.0

The second one is Support Vector Machine, here we use built-in preset parameters for the classifier. The ROC and PRC are shown below.

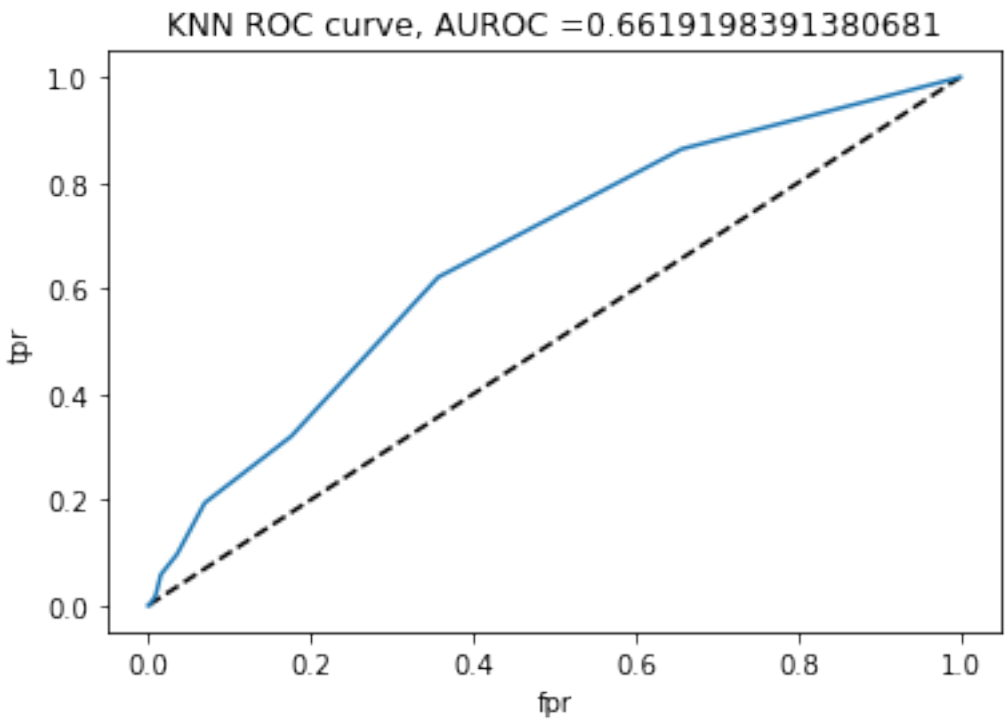
[35]:
```
from sklearn.metrics import roc_curve
y_pred_proba = SVM_y_score ###############
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba)
#Area under ROC curve
from sklearn.metrics import roc_auc_score
auroc = roc_auc_score(y_test,y_pred_proba)
plt.plot([0,1],[0,1],'k--')
plt.plot(fpr,tpr, label='SVM') ##############
plt.xlabel('fpr')
plt.ylabel('tpr')
title_name = 'SVM ROC curve, AUROC ='+str(auroc) ############
plt.title(title_name)
plt.savefig('SVM ROC curve.png') ####################
plt.show()

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

auprc = auc(recall, precision)
plt.hlines(572/(3177+572), 0, 1, colors = "c", linestyles = "dashed")
plt.plot(recall,precision, label='SVM') ####################
plt.xlabel('recall')
plt.ylabel('precision')
title_name = 'SVM PRC curve, AUPRC ='+str(auprc) ###############
plt.title(title_name)
plt.savefig('SVM PRC curve.png') ######################
plt.show()
```

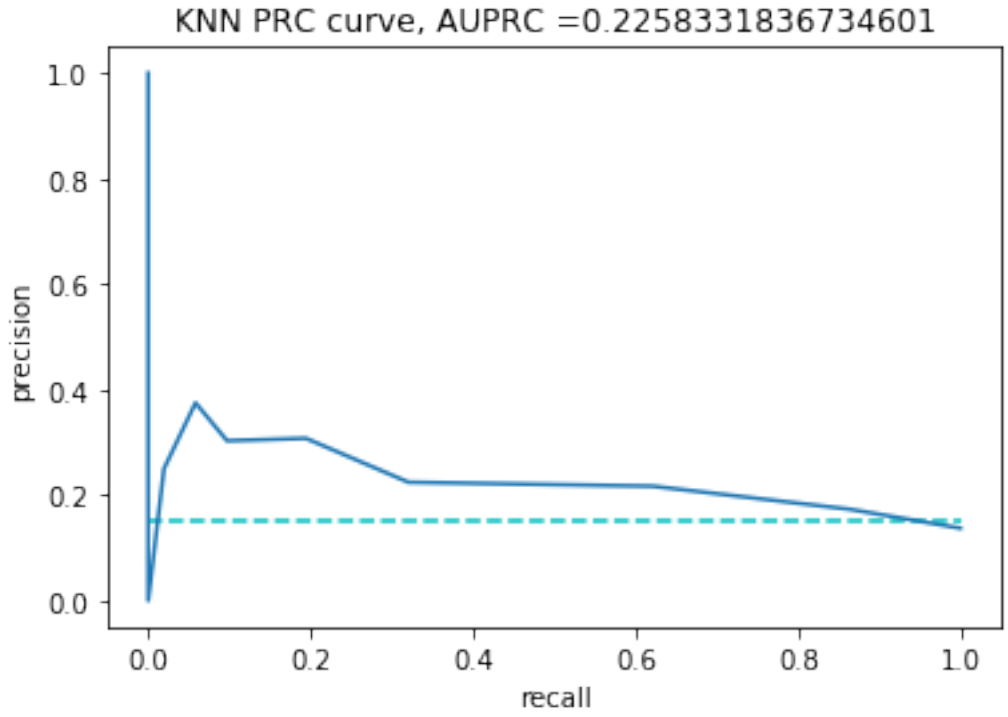

SVM ROC curve, AUROC =0.5978601761678246
tpr
fpr
0.0
0.2
0.4
0.6
0.8
1.0


SVM PRC curve, AUPRC =0.15950802452729307
precision
recall
0.0
0.2
0.4
0.6
0.8
1.0

The third one is KNN(K = 10), here for other parameters we use built-in preset ones for the classifier. The ROC and PRC are shown below.

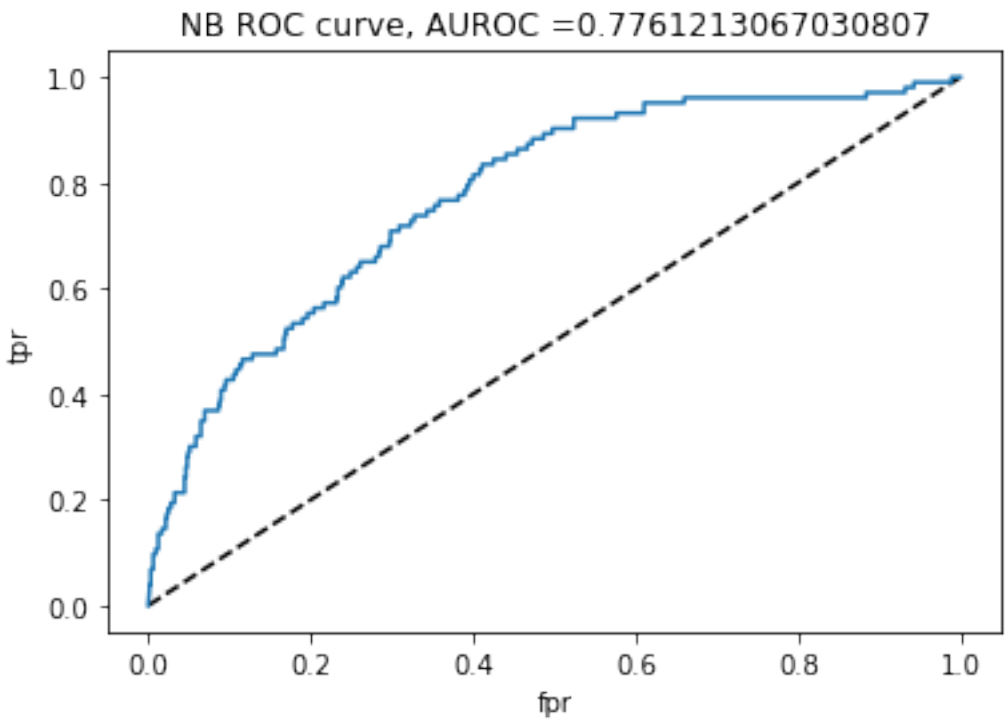
[36]:
```
from sklearn.metrics import roc_curve
y_pred_proba = KNN_y_score ###############
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba)
#Area under ROC curve
from sklearn.metrics import roc_auc_score
auroc = roc_auc_score(y_test,y_pred_proba)
plt.plot([0,1],[0,1],'k--')
plt.plot(fpr,tpr, label='KNN') ##############
plt.xlabel('fpr')
plt.ylabel('tpr')
title_name = 'KNN ROC curve, AUROC ='+str(auroc) ############
plt.title(title_name)
plt.savefig('KNN ROC curve.png') ####################
plt.show()

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

auprc = auc(recall, precision)
plt.hlines(572/(3177+572), 0, 1, colors = "c", linestyles = "dashed")
plt.plot(recall,precision, label='KNN') ####################
plt.xlabel('recall')
plt.ylabel('precision')
title_name = 'KNN PRC curve, AUPRC ='+str(auprc) ###############
plt.title(title_name)
plt.savefig('KNN PRC curve.png') ######################
plt.show()
```

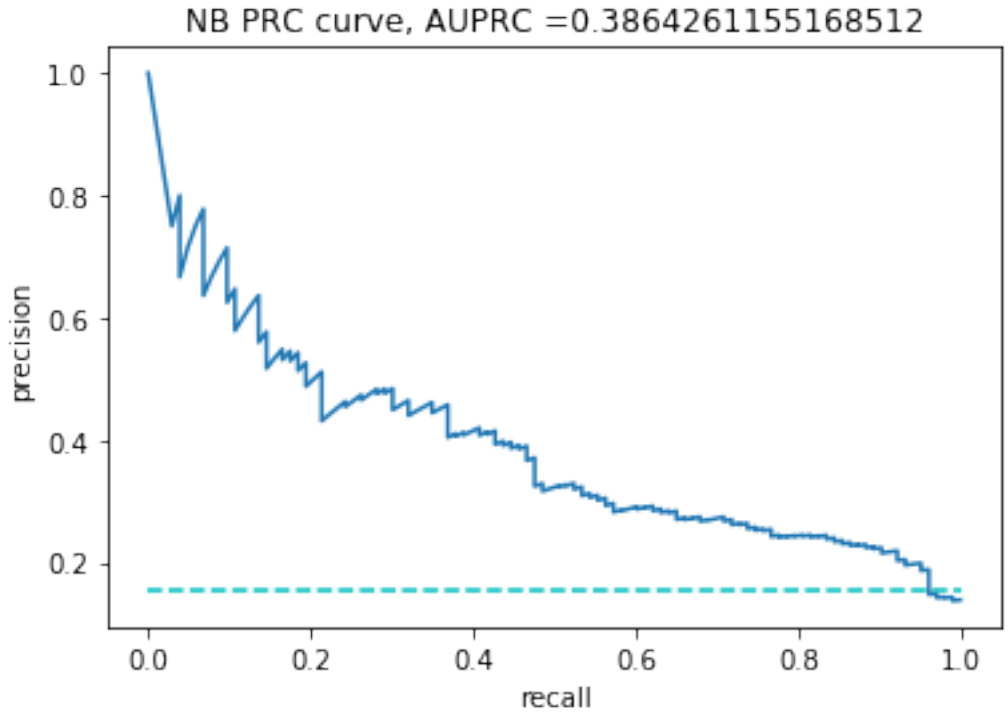

KNN ROC curve, AUROC =0.6619198391380681
tpr
fpr
0.0
0.2
0.4
0.6
0.8
1.0


KNN PRC curve, AUPRC =0.2258331836734601
precision
recall
0.0
0.2
0.4
0.6
0.8
1.0

The fourth one is Naive Bayes, here we use built-in preset parameters for the classifier. The ROC and PRC are shown below.

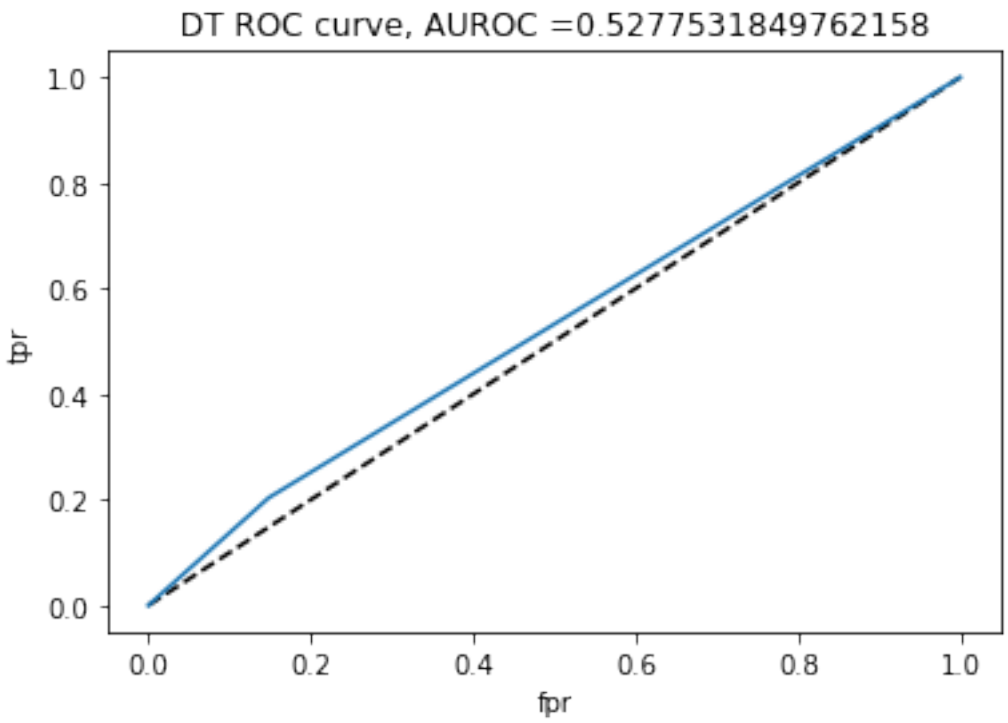
[37]:
```
from sklearn.metrics import roc_curve
y_pred_proba = NB_y_score ###############
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba)
#Area under ROC curve
from sklearn.metrics import roc_auc_score
auroc = roc_auc_score(y_test,y_pred_proba)
plt.plot([0,1],[0,1],'k--')
plt.plot(fpr,tpr, label='NB') ##############
plt.xlabel('fpr')
plt.ylabel('tpr')
title_name = 'NB ROC curve, AUROC ='+str(auroc) ############
plt.title(title_name)
plt.savefig('NB ROC curve.png') ####################
plt.show()

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

auprc = auc(recall, precision)
plt.hlines(572/(3177+572), 0, 1, colors = "c", linestyles = "dashed")
plt.plot(recall,precision, label='NB') ####################
plt.xlabel('recall')
plt.ylabel('precision')
title_name = 'NB PRC curve, AUPRC ='+str(auprc) ###############
plt.title(title_name)
plt.savefig('NB PRC curve.png') ######################
plt.show()
```

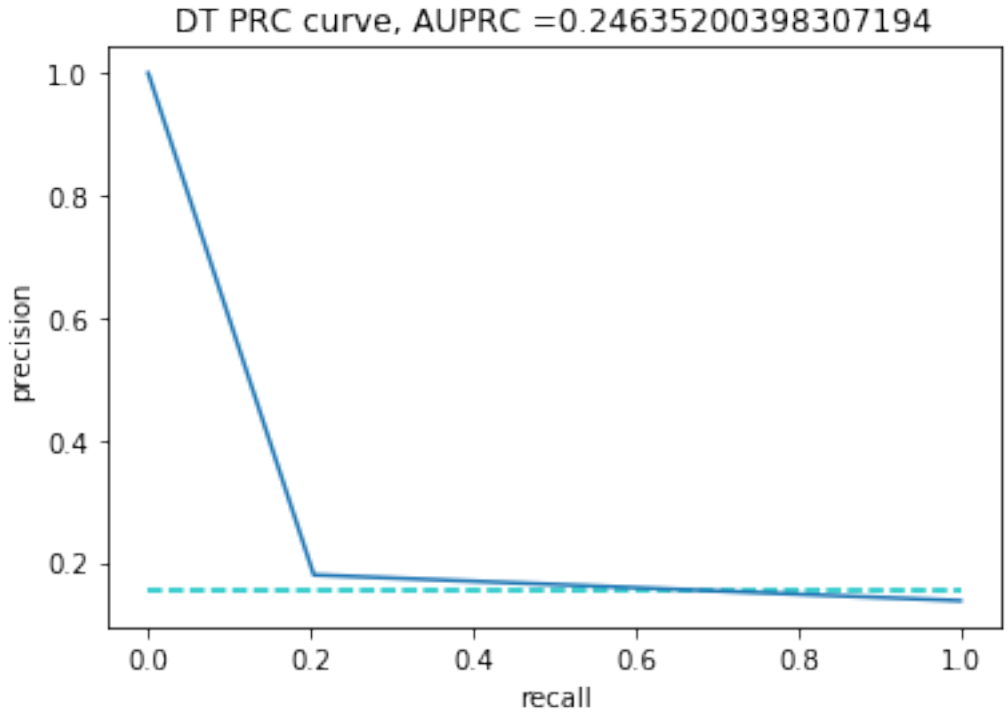

NB ROC curve, AUROC =0.7761213067030807
tpr
fpr
0.0
0.2
0.4
0.6
0.8
1.0


NB PRC curve, AUPRC =0.3864261155168512
precision
recall
0.0
0.2
0.4
0.6
0.8
1.0

The fifth one is Decision Tree, here we use built-in preset parameters for the classifier. The ROC and PRC are shown below.

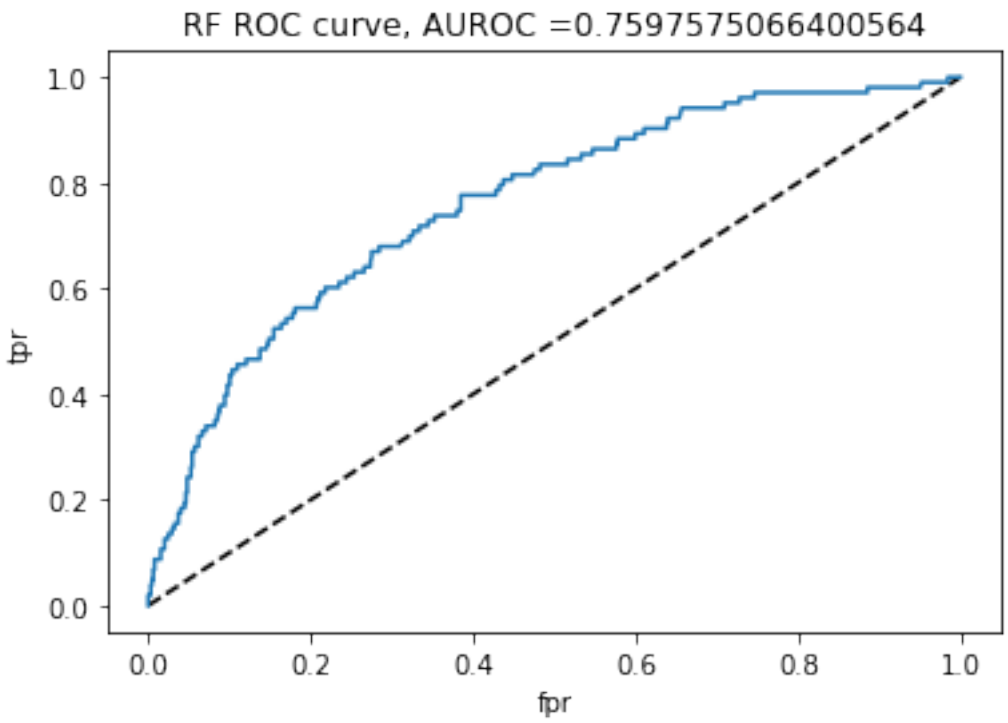
[38]:
```
from sklearn.metrics import roc_curve
y_pred_proba = DT_y_score ###############
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba)
#Area under ROC curve
from sklearn.metrics import roc_auc_score
auroc = roc_auc_score(y_test,y_pred_proba)
plt.plot([0,1],[0,1],'k--')
plt.plot(fpr,tpr, label='DT') ##############
plt.xlabel('fpr')
plt.ylabel('tpr')
title_name = 'DT ROC curve, AUROC ='+str(auroc) ############
plt.title(title_name)
plt.savefig('DT ROC curve.png') ####################
plt.show()

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

auprc = auc(recall, precision)
plt.hlines(572/(3177+572), 0, 1, colors = "c", linestyles = "dashed")
plt.plot(recall,precision, label='DT') ####################
plt.xlabel('recall')
plt.ylabel('precision')
title_name = 'DT PRC curve, AUPRC ='+str(auprc) ###############
plt.title(title_name)
plt.savefig('DT PRC curve.png') ########################
plt.show()
```

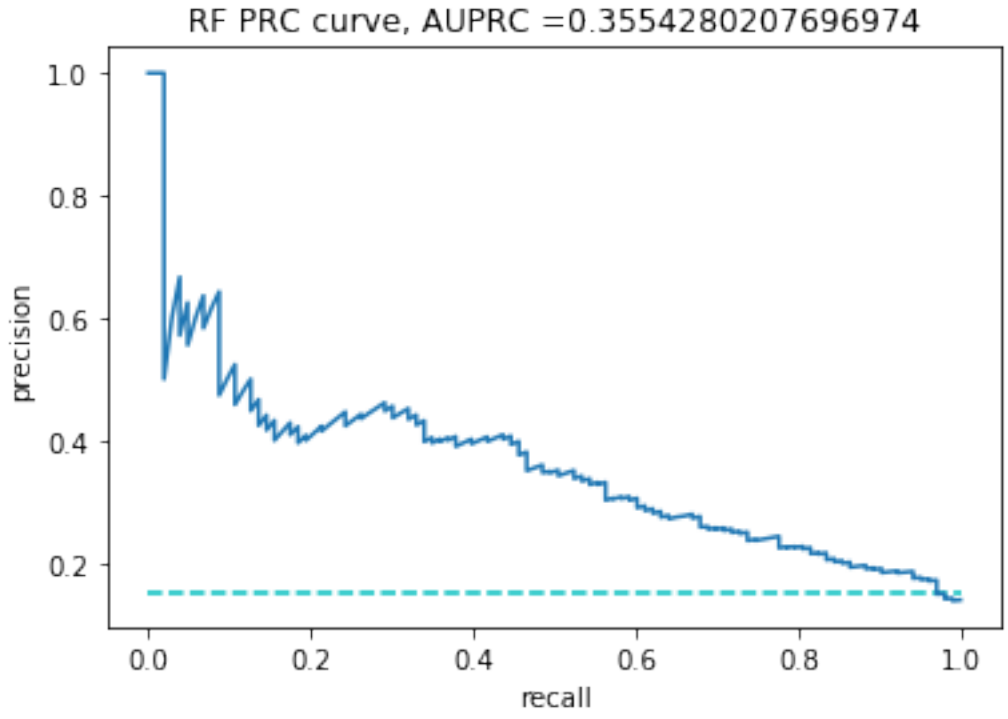

DT ROC curve, AUROC =0.5277531849762158
tpr
fpr
0.0
0.2
0.4
0.6
0.8
1.0


DT PRC curve, AUPRC =0.24635200398307194
precision
recall
0.0
0.2
0.4
0.6
0.8
1.0

The sixth one is Random Forest with n_estimators=100, max_depth=2,and random_state=0. The ROC and PRC are shown below.

[39]:
```
from sklearn.metrics import roc_curve
y_pred_proba = RF_y_score ###############
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba)
#Area under ROC curve
from sklearn.metrics import roc_auc_score
auroc = roc_auc_score(y_test,y_pred_proba)
plt.plot([0,1],[0,1],'k--')
plt.plot(fpr,tpr, label='RF') ##############
plt.xlabel('fpr')
plt.ylabel('tpr')
title_name = 'RF ROC curve, AUROC ='+str(auroc) ############
plt.title(title_name)
plt.savefig('RF ROC curve.png') ####################
plt.show()

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

auprc = auc(recall, precision)
plt.hlines(572/(3177+572), 0, 1, colors = "c", linestyles = "dashed")
plt.plot(recall,precision, label='RF') ####################
plt.xlabel('recall')
plt.ylabel('precision')
title_name = 'RF PRC curve, AUPRC ='+str(auprc) ###############
plt.title(title_name)
plt.savefig('RF PRC curve.png') ########################
plt.show()
```


RF ROC curve, AUROC =0.7597575066400564
tpr
fpr
0.0
0.2
0.4
0.6
0.8
1.0


RF PRC curve, AUPRC =0.3554280207696974
precision
recall
0.0
0.2
0.4
0.6
0.8
1.0

Overall analysis:

From the table above, we could see that all the classifier we use here have higher accuracy than random guess.

As for which classifier is better, AUROC votes for:

Naive Bayes ≈ Logistic Regression > Random Forest >> KNN > SVM > Decision Tree.

AUPRC votes for:

Logistic Regression > Naive Bayes > Random Forest >> Decision Tree > KNN > SVM.

Accuracy votes for:

Logistic Regression ≈ SVM = Random Forest > Naive Bayes > KNN > Decision Tree.

Log_loss votes for:

Logistic Regression > SVM = Random Forest > Naive Bayes > KNN >> Decision Tree.

F1 score votes for:

Naive Bayes > Logistic Regression > KNN > SVM > Random Forest = Decision Tree.

For the majority vote, Logistic regression is the best classifier and Naive Bayes is the second best. Among these measurements, AUPRC seems has a similar pattern to the result achieved by the majority vote. However, from the majority vote, we also could see that the performance of Decision Tree is the worst and the performance of KNN is the second worst. For this situation, AUROC gives out the similar result. As for accuracy and F1 score, there is one more thing we need to mention. That is, the accuracy or F1 score of different classifier have no significant difference, which means they are not suitable for measuring performance of classifier for this dataset.

For the graphs above, we could see that PRC works well for "good" classifier (which means that the classifier works well), but for "bad" ones, the curve becomes unstable. At the same time, ROC shows similarly for "good" ones but clearly expresses the poor performance of those "bad" classifier.

So for this dataset, AUPRC should be a better measurement for evaluate the performance of "good" classifier than AUROC, while AUROC works well for evaluate the performance of "bad" classifier. They both works much better than accuracy and F1 score. As for log_loss, the result it gives out seems quite different from the majority vote, especially for the the Naive Bayes and SVM. To reach a conclusion, AUPRC and AUROC should be used together for choosing classifiers. That is, AUPRC should be use to evaluate which classifier is accurate, while AUROC should be used to measure how inaccurate a classifier is.