# MAULANA AZAD NATIONAL INSTITUTE OF TECHNOLOGY , BHOPAL



# COMPUTER SCIENCE & ENGINEERING DEPARTMENT

MACHINE LEARNING LAB (CS 5508)
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# **SUBMITED BY:**

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**SECTION: CSE 3** 

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# **ASSIGNMENT - 06**

**QUES -** Develop a machine learning model for Pima-Indians-diabetes data set using SVM , Naive Bayes, Linear Regression, and random forest .Tune the hyper parameter to get the higher accuracy and draw graph for different accuracy .Take 5-6 variation of hyper parameter and plot the graph of confusion matrices like accuracy, recall , precision,F1 score etc.

#### DATASET DESCRIPTION

The datasets consists of several medical predictor variables and one target variable (Outcome). Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and more.

Variables Description

Pregnancies Number of times pregnant

Glucose Plasma glucose concentration in an oral glucose tolerance test

BloodPressure Diastolic blood pressure (mm Hg)

SkinThickness Triceps skinfold thickness (mm)

Insulin Two hour serum insulin

BMI Body Mass Index

DiabetesPedigreeFunction Diabetes pedigree function

Age in years

Outcome Class variable (either 0 or 1). 268 of 768 values are 1, and the

others are 0

#### **Observations & Exploratory Data Analysis:**

- 1. Age, Insulin, DiabetesPedigreeFunction and Pregnancies are right skewed.
- 2. .Zero values in blood pressure, BMI, Insulin and Glocuse clearly stands out in the plot
- 3. After removing zeros for non-zero expected columns, we see that except Insulin which is highly right skewed, all other are near to gaussian distribution.
- 4. Except for Insulin, for rest of other non-zero columns, we can take mean value.For Insulin, we took median value to fill
- 5. In Data type count plot, we can see that there are 2 int type columns and 7 float type

#### **CODE SECTION & OUTPUTS:**

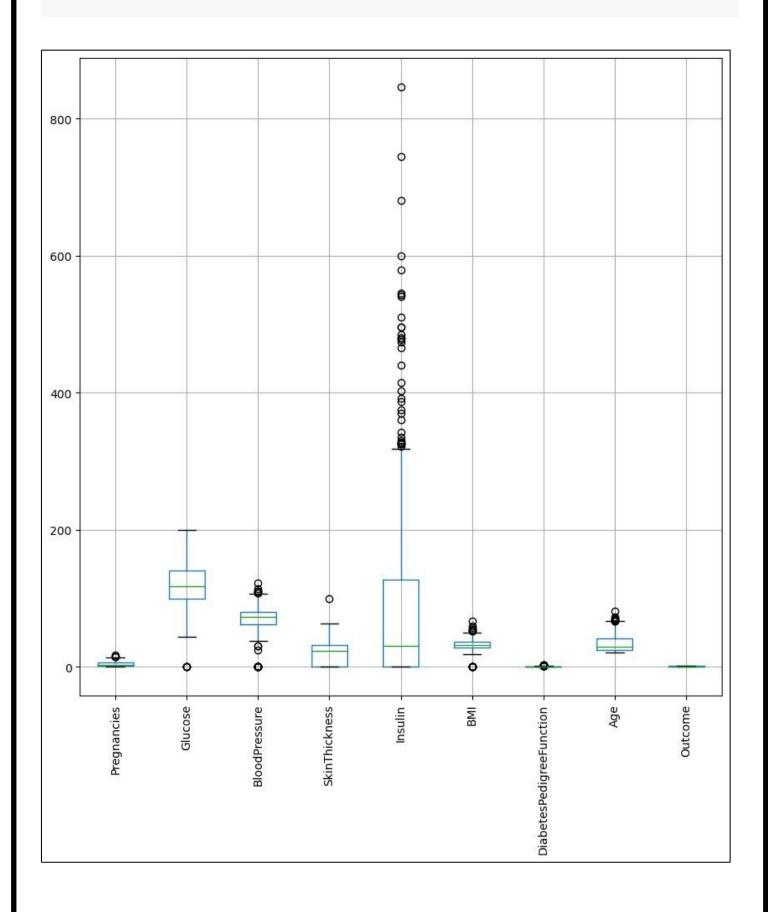
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
import copy
data_raw = pd.read_csv('../input/pima-indians-diabetes-database/diabetes.csv')
data_raw.dtypes
data_raw.shape
data_raw.sample(5)
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
    Column
                               Non-Null Count Dtype
0
   Pregnancies
                               768 non-null
                                              int64
1
    Glucose
                               768 non-null int64
                               768 non-null int64
768 non-null int64
768 non-null int64
2 BloodPressure
 3
    SkinThickness
4 Insulin
                               768 non-null
5 BMI
                                              float64
6
    DiabetesPedigreeFunction 768 non-null float64
7
    Age
                               768 non-null
                                              int64
    Outcome
                               768 non-null
                                               int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

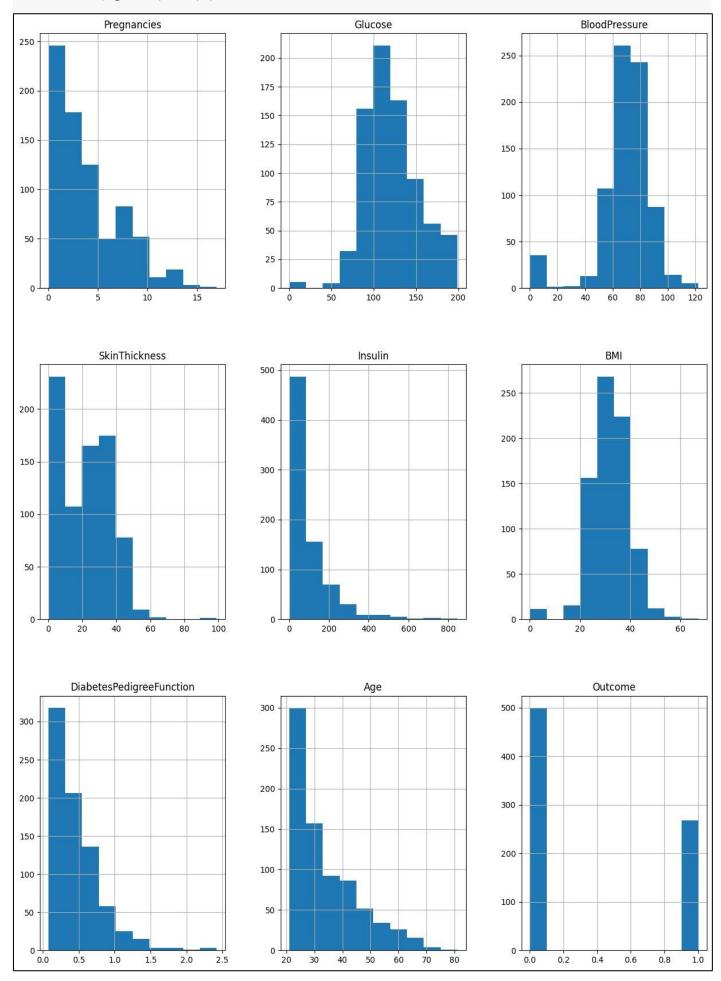
#### data\_raw.describe()

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diabetes Pedigree Function	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

data\_raw.boxplot(figsize=(10,10), rot=90)



# data\_raw.hist(figsize=(15,20),)



# **Treating Zero valued columns**

```
not_allowed_zero_cols = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']
data = copy.deepcopy(data_raw)

data[not_allowed_zero_cols] = data[not_allowed_zero_cols].replace(0, np.NaN)

data.isnull().sum()
```

Pregnancies	0
Glucose	5
BloodPressure	35
SkinThickness	227
Insulin	374
BMI	11
DiabetesPedigreeFunction	0
Age	0
Outcome	0
dtype: int64	

```
fig, ax = plt.subplots(nrows=3, ncols=2, figsize=(15,20))

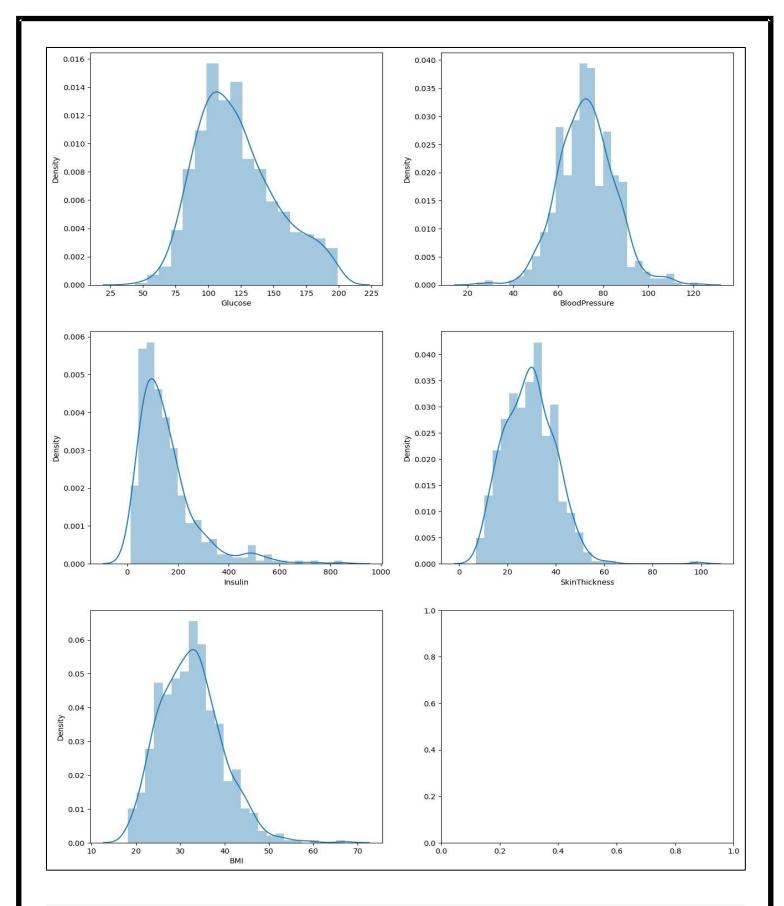
sns.distplot(data.Glucose, ax=ax[0][0])

sns.distplot(data.BloodPressure, ax=ax[0][1])

sns.distplot(data.Insulin, ax=ax[1][0])

sns.distplot(data.SkinThickness, ax=ax[1][1])

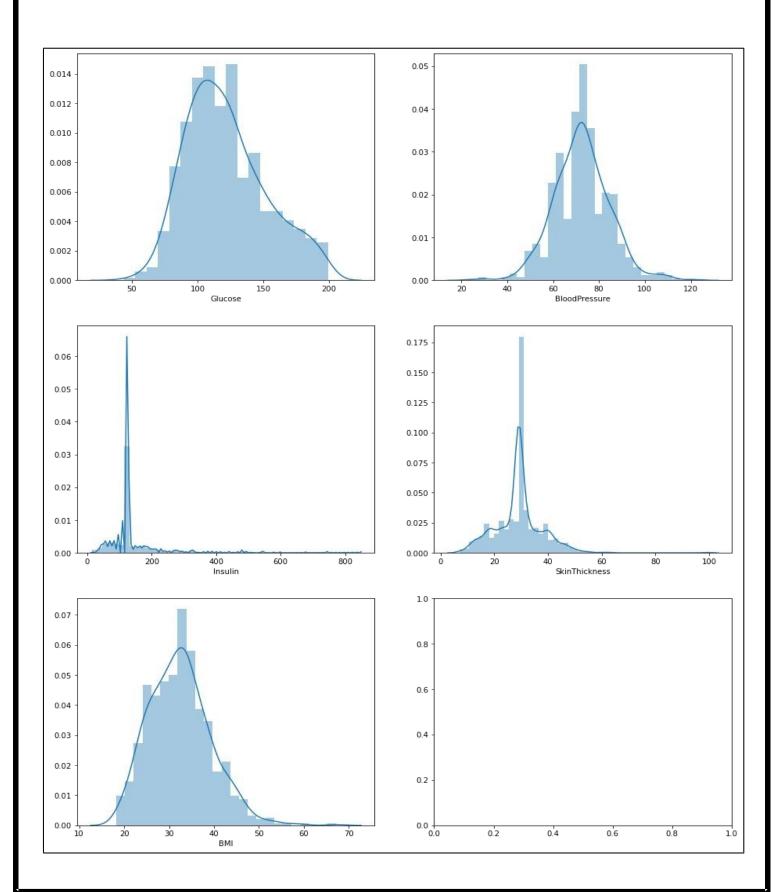
sns.distplot(data.BMI, ax=ax[2][0])
```



data['Glucose'].fillna(data.Glucose.mean(), inplace=True)
data['BloodPressure'].fillna(data.BloodPressure.mean(), inplace=True)
data['BMI'].fillna(data.BMI.mean(), inplace=True)
data['SkinThickness'].fillna(data.SkinThickness.mean(), inplace=True)
data['Insulin'].fillna(data.Insulin.median(), inplace=True)

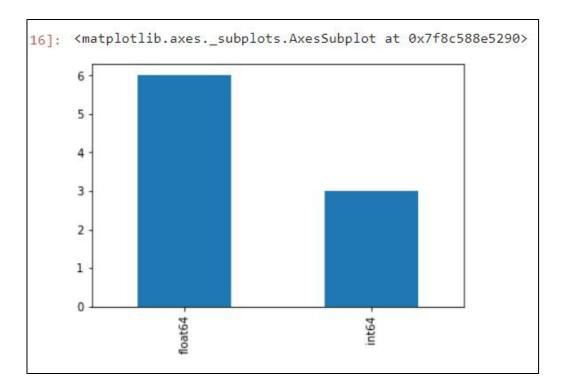
# Plots after filling the NaN values.

```
fig, ax = plt.subplots(nrows=3, ncols=2, figsize=(15,20)) sns.distplot(data.Glucose, ax=ax[0][0]) sns.distplot(data.BloodPressure, ax=ax[0][1]) sns.distplot(data.Insulin, ax=ax[1][0]) sns.distplot(data.SkinThickness, ax=ax[1][1]) sns.distplot(data.BMI, ax=ax[2][0])
```



# Plot data types

data.dtypes.value\_counts().plot(kind='bar')



#### **Observations**

It is an imbalanced dataset where positive outcomes are almost half of the negative outcomes. While creating model, we need to balance the outcomes either by oversampling the minority class or undersampling of majority class. Other workaround could be to do a weighted computation while training the model.

#### Pair plot analysis

- BMI and Skin thickness have a positive correlation
- Insulin and Glucose have a positive correlation.
- Rest other fields are uncorrelated or very weakly correlated.

# **Correlation Analysis**

- There is no strong correlation between any two fields
- The BMI-Skinthickness and Insulin-Glucose are the highest correlated in the set but they are moderately correlated
- Outcome is moderately correlated to Glucose

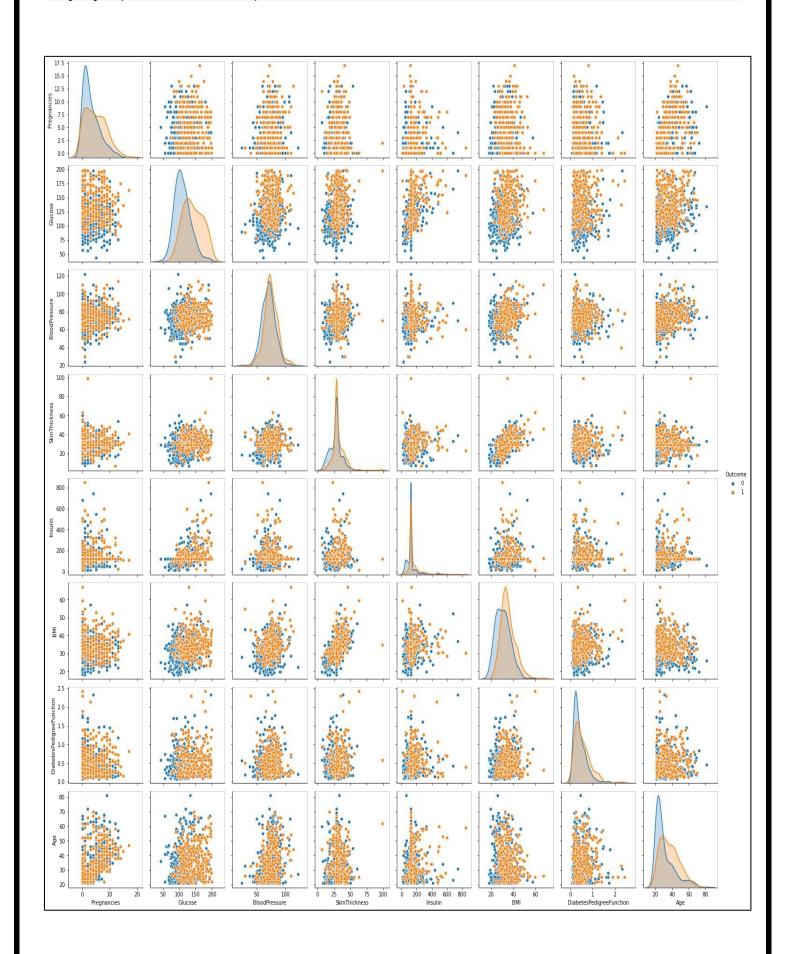
# **Checking Data balance**

sns.countplot(data.Outcome, ).set(title="Data Imbalance Check")

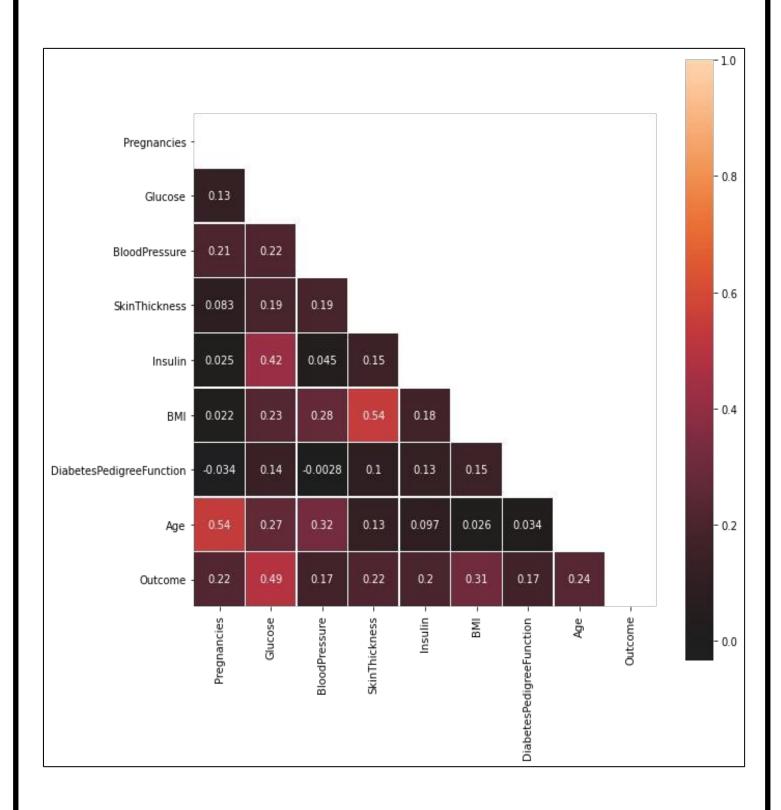


# Pair plot analysis

sns.pairplot(data, hue='Outcome')



# **Correlation analysis**



#### **OBSERVATIONS FROM DATA ANALYSIS**

This is a binary data classification problem where depending on the all the features, the model has to predict whether a person have diabetes or not. We have several ways to build the model for binary/multi-class classification. Few of them are listed below:

- 1. Logistics Regression
- 2. Naive Bayes classification
- 3. Stochastic Gradient Descent
- 4. K-Nearest Neighbours
- 5. Decision Tree
- 6. Random Forest
- 7. SVM

We are going to build four models and compare their performance on test and train dataset. We will tune the models if there is need to tune. We will use K-Fold Cross Validation to validate the models. We will plot all the models stats together and compare their performance. Of all the tuned models, we will pick up the best model. The step by step procedure can be followed below:

- A. Common Terminalogy
- B. Data Scaling & Splitting
- C. Logistic Regression
- D. Naive Bayes Classification
- E. Random Forest
- F. K Nearest Neighbours
- G. Putting it all together
  - ROC AUC Curves
  - Model Comparison

From Model Comparison, we find that KNN is the most stable classifier. All the parameters are quite good. It has best accuracy, auc, precision and f1\_score of all the models.

If we are looking for a highly sensitive model, we can take logistic regression model, which has the highest recall.

#### Scaling and splitting the data

from sklearn.model\_selection import train\_test\_split

from sklearn.metrics import classification\_report, f1\_score, accuracy\_score, mean\_squared\_error, roc\_auc\_score, confusion\_matrix, roc\_curve, recall\_score, precision\_score, f1\_score

from sklearn.preprocessing import StandardScaler

X\_scaled = StandardScaler().fit\_transform(data.drop(['Outcome'], axis='columns'))

X\_train, X\_test, y\_train, y\_test = train\_test\_split(X\_scaled, data.Outcome, random\_state=123, test\_size=.2)

#### 1- LINEAR REGRESSION

#### **AUC ROC Curve parmas computation for Linear Regression**

```
y_pred_prob_lr = lr_clf.predict_proba(X_test)[:, 1]
fpr_lr, tpr_lr , th_lr = roc_curve(y_test, y_pred_prob_lr)
gmean_lr = np.sqrt(tpr_lr * (1-fpr_lr))
ix_lr = np.argmax(gmean_lr)
```

# Tuning by AUC\_ROC Threshold

The geometric mean between TPR and FPR is an optimum value which is max for any give tpr, fpr. If our focus is to create a model that predicts both sides, then this threshold value could be choosen to be optimum threshold. The optimam threshold to classify True or False, we get at .364

```
th_lr[np.argmax(gmean_lr)]
```

```
Out[30]:
```

0.36454228797001864

```
y_roc_pred_lr = [0 if pred < th_lr[ix_lr] else 1 for pred in y_pred_prob_lr ]
print("Test classification Report With tuned threshold")
print(classification_report(y_test, y_roc_pred_lr) )
print("Test classification Report Without tuned threshold")
print(classification_report(y_test, lr_pred) )</pre>
```

		7.7	50	
	precision	recall	f1-score	support
0	0.94	0.66	0.77	96
1	0.62	0.93	0.74	58
accuracy			0.76	154
macro avg	0.78	0.79	0.76	154
eighted avg	0.82	0.76	0.76	154
est classif	ication Report	t Without	tuned the	reshold
Test classif	ication Report precision			
			f1-score	
Test classif: 0 1	precision	recall	f1-score	support
	precision 0.83 0.68	recall 0.79	f1-score 0.81	support 96
0 1	precision 0.83 0.68	recall 0.79	f1-score 0.81 0.70 0.77	support 96 58

#### 2 - NAIVE BAYES CLASSIFICATION

#### **AUC ROC for Naive Bayes classifier**

```
y_pred_prob_gnb = gnb_clf.predict_proba(X_test)[:, 1]
fpr_nb, tpr_nb , th_nb = roc_curve(y_test, y_pred_prob_gnb)
gmean_nb = np.sqrt(tpr_nb * (1-fpr_nb))ix_nb = np.argmax(gmean_nb)
print("Train Classification Report")
print(classification_report(y_train, gnb_clf.predict(X_train)) )
```

	precision	recall	f1-score	support
0	0.79	0.83	0.81	404
1	0.64	0.59	0.61	210
accuracy			0.74	614
macro avg	0.72	0.71	0.71	614
weighted avg	0.74	0.74	0.74	614

```
print("Test Classification Report")
print(classification_report(y_test, gnb_clf.predict(X_test)) )
```

	precision	recall	f1-score	support
0	0.79	0.83	0.81	96
1	0.70	0.64	0.67	58
accuracy			0.76	154
macro avg	0.75	0.74	0.74	154
eighted avg	0.76	0.76	0.76	154

#### 3 - RANDOM FOREST

	precision	recall	f1-score	support
0	1.00	1.00	1.00	404
1	1.00	1.00	1.00	210
accuracy			1.00	614
macro avg	1.00	1.00	1.00	614
eighted avg	1.00	1.00	1.00	614

```
print("\t\tTest Classification Report\n")
print(classification_report(y_test, rf_clf.predict(X_test)) )
```

Test Classification Report						
	precision	recall	f1-score	support		
0	0.81	0.82	0.82	96		
1	0.70	0.69	0.70	58		
accuracy			0.77	154		
macro avg	0.76	0.76	0.76	154		
eighted avg	0.77	0.77	0.77	154		

#### **Observation from Random Forest**

From the looks of training data, we can say that Random forest has overfitted. Due to overfitting, it may show very good responses but ultimately it is not a good model. We will tune the parmas for this. We will tune on Cost parameter and see what cost function makes the training and test data accuracy comparable.

In below code, we see only one iteration, but before coming to below values, I have done several iterations and compared trin and test errors to arrive at optimum cost value. The below iteration is to arrive at more precise cost value.

```
alphas=[]test=[]train=[]for alpha in np.linspace(.03, .05, 10):

rf = RandomForestClassifier(ccp_alpha=alpha, random_state=123)

rf.fit(X_train, y_train)

y_train_predicted = rf.predict(X_train)

y_test_predicted = rf.predict(X_test)

mse_train = mean_squared_error(y_train, y_train_predicted)

mse_test = mean_squared_error(y_test, y_test_predicted)

alphas.append(alpha)

test.append(mse_test)

train.append(mse_train)

print("Alpha: {} Train mse: {} Test mse: {}".format(alpha, mse_train, mse_test))

score=pd.DataFrame({'alpha': alphas, 'test':test, 'train': train})
```

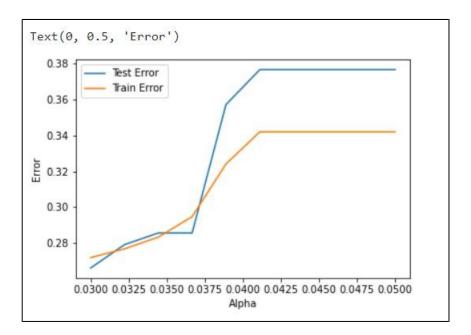
```
plt.plot(score.alpha, score.test)

plt.plot(score.alpha, score.train)

plt.legend(['Test Error', 'Train Error'])

plt.xlabel('Alpha')

plt.ylabel('Error')
```



hCV(estimator=rf\_clf\_cv, param\_distributions=random\_grid, cv=3, scoring='f1\_weighted')

from sklearn.model\_selection import RandomizedSearchCV

rscv.best\_estimator\_

rscv.fit(X\_train, y\_train)

```
print("\t\Test Classification Report\n")
print(classification_report(y_test, rscv.predict(X_test)) )
```

	Test Classification Report						
	precision	recall	f1-score	support			
0	0.86	0.78	0.82	96			
1	0.69	0.79	0.74	58			
accuracy			0.79	154			
macro avg	0.77	0.79	0.78	154			
weighted avg	0.80	0.79	0.79	154			

```
print("\t\tTrain Classification Report\n")
print(classification_report(y_train, rscv.predict(X_train)) )
```

	precision	recall	f1-score	support
0	0.86	0.77	0.81	404
0	0.63	0.77	0.69	210
accuracy			0.77	614
macro avg	0.75	0.77	0.75	614
ighted avg	0.78	0.77	0.77	614

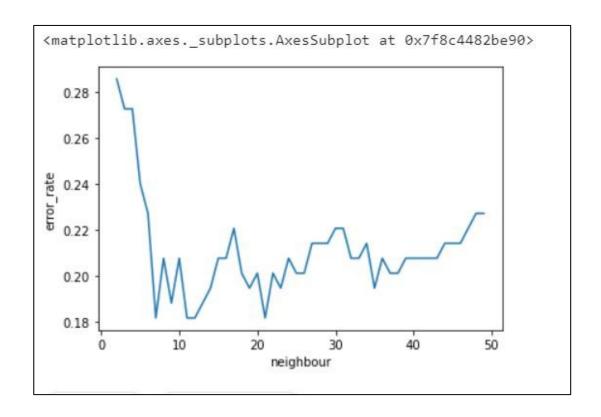
```
['accuracy',
 'adjusted mutual info score',
 'adjusted rand score',
 'average precision',
 'balanced_accuracy',
 'completeness score',
 'explained variance',
'f1',
'f1 macro',
'f1 micro',
 'f1 samples',
 'f1 weighted',
 'fowlkes mallows score',
 'homogeneity_score',
 'jaccard',
'jaccard_macro',
 'jaccard_micro',
 'jaccard_samples',
 'jaccard_weighted',
 'max error',
 'mutual info score',
 'neg brier score',
 'neg log loss',
 'neg mean absolute error',
 'neg_mean_gamma_deviance',
 'neg_mean_poisson_deviance',
 'neg mean squared error',
 'neg mean squared_log_error',
 'neg median absolute error',
 'neg_root_mean_squared_error',
 'normalized mutual info score',
 'precision',
 'precision_macro',
 'precision micro',
 'precision_samples'
 'precision weighted',
 'r2',
 'recall',
 'recall macro',
 'recall micro',
 'recall samples',
 'recall weighted',
 'roc auc',
 'roc_auc_ovo',
 'roc auc ovo weighted',
 'roc_auc_ovr',
 'roc_auc_ovr_weighted',
 'v measure score']
```

# 4 - K-Nearest Neighbour

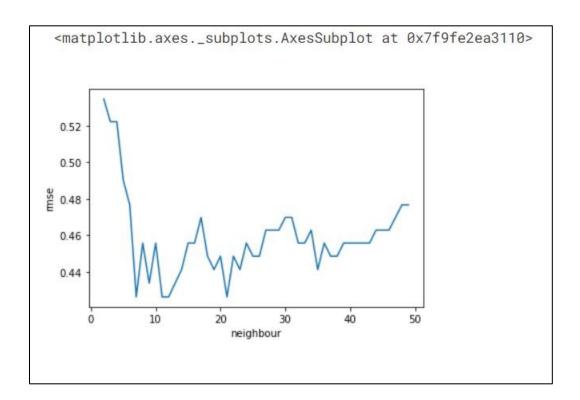
We are capturing rmse, error\_rate and accuracy for a range of nearest neighbours. We will plot all of them to observer nearest neighbours. We observe that error\_rate and rmse give same plot while accuracy gives a mirror image of other two.

```
from sklearn.neighbors import KNeighborsClassifier
nbr = []error_rmse = []error_rate = []accuracy = []for n in range(2, 50):
    knn_clf = KNeighborsClassifier(n_neighbors=n, weights='distance')
    knn_clf.fit(X_train, y_train)
    pred = knn_clf.predict(X_test)

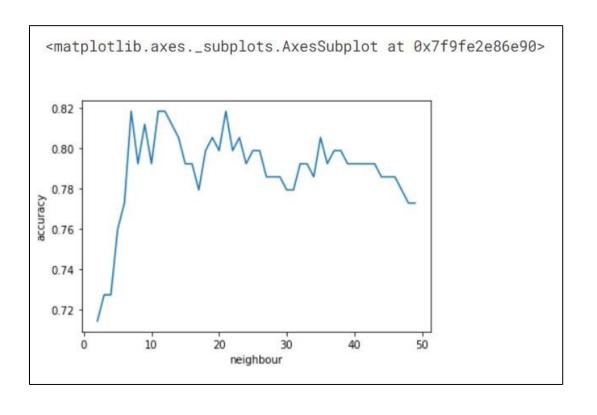
    nbr.append(n)
    error_rmse.append(mean_squared_error(y_test, pred, squared=False))
    error_rate.append(np.mean(y_test != pred))
    accuracy.append(accuracy_score(y_test, pred))
    knn_stats = pd.DataFrame({'neighbour': nbr, 'rmse': error_rmse, 'error_rate': error_rate, 'accuracy': accuracy})
sns.lineplot(x='neighbour', y='error_rate', data=knn_stats)
```



sns.lineplot(x='neighbour', y='rmse', data=knn\_stats)



sns.lineplot(x='neighbour', y='accuracy', data=knn\_stats)



knn\_stats.neighbour[knn\_stats.rmse.argmin()] knn\_stats.neighbour[[5,19,9,10]]

```
5 7
19 21
9 11
10 12
Name: neighbour, dtype: int64
```

```
knn_clf = KNeighborsClassifier(n_neighbors=7, weights='distance')
knn_clf.fit(X_train, y_train)
knn_pred = knn_clf.predict(X_test)
print(classification_report(y_test, pred))
```

	precision	recall	f1-score	support
0	0.77	0.91	0.83	96
1	0.78	0.55	0.65	58
accuracy			0.77	154
macro avg	0.78	0.73	0.74	154
weighted avg	0.77	0.77	0.76	154

#### **Tuning KNN**

We have seen that 4 values of Nearest Neighbours yeilded the same error in our earlier plot. We will tune the model with all those given values and pickup the best.

knn\_rscv.best\_params\_

```
{'weights': 'uniform',
  'n_neighbors': 11,
  'leaf_size': 50,
  'algorithm': 'kd_tree'}
```

# **Model Comparison**

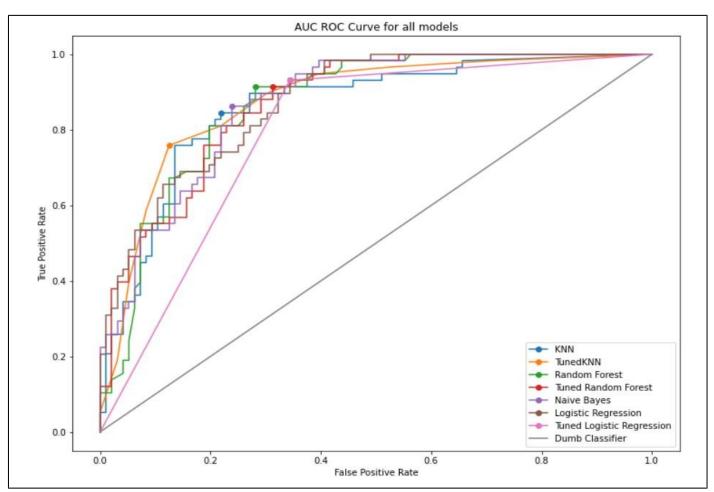
#### **Data Modeling and Observations**

I have plotted auc\_roc curve of all the models together for comparison purpose. Also, I have plotted all the model stats together, tuned and non-tuned version. We can compare the performance by looking at the plots

.

#### AUC ROC Curve of all the models put together

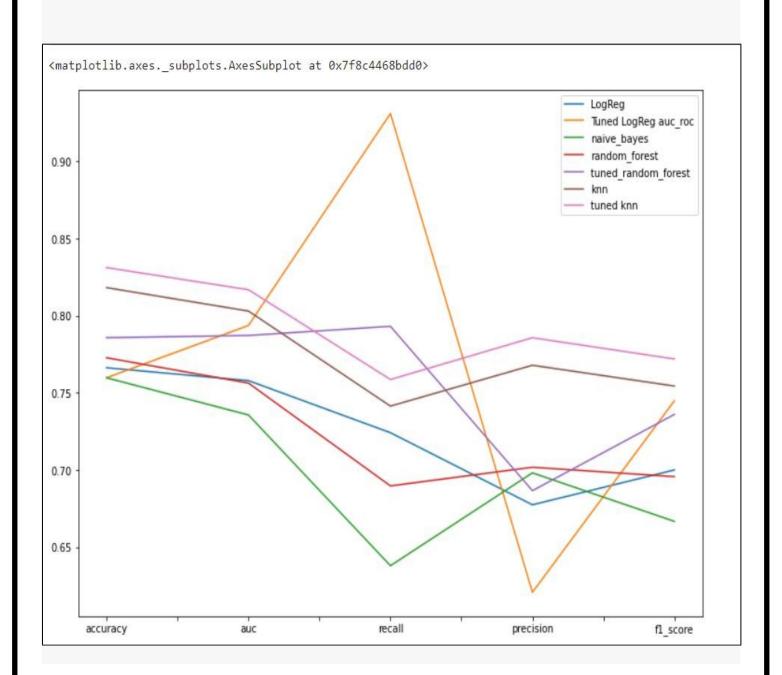
```
plt.subplots(figsize=(12,9))
plt.plot(fpr_knn, tpr_knn, marker='o', markevery=[ix_knn])
plt.plot(fpr_tknn, tpr_tknn, marker='o', markevery=[ix_tknn])
plt.plot(fpr_rf, tpr_rf, marker='o', markevery=[ix_rf])
plt.plot(fpr_trf, tpr_trf, marker='o', markevery=[ix_trf])
plt.plot(fpr_nb, tpr_nb, marker='o', markevery=[ix_nb])
plt.plot(fpr_lr, tpr_lr, marker='o', markevery=[ix_lr])
plt.plot(fpr_tlr, tpr_tlr, marker='o', markevery=[ix_tlr])
plt.plot([0,1], [0,1])plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('AUC ROC Curve for all models')
plt.legend(['KNN', 'TunedKNN', 'Random Forest', 'Tuned Random Forest', 'Naive Bayes', 'Logistic Regression', 'Tuned Logistic Regression', 'Dumb Classifier'])
plt.show()
```



# **Comparing model parameters**

```
model_stats = pd.DataFrame(data=[lr_model_vals, tlr_model_vals, gnb_model_vals, rf_model_vals, tuned_rf_model_vals, knn_model_vals, tknn_model_vals ], index=['LogReg', 'Tuned LogReg auc_roc', 'naive_bayes', 'random_forest', 'tuned_random_forest', 'knn', 'tuned knn'])
```

model\_stats.T.plot(kind='line', figsize=(12,9))



#### **FINAL OBSERVATIONS:**

I have plotted different parameters of all the models above. By a simple look, we know that recall and precision are in opposite direction for all the models. The overfitted Random Forest had similar characteristics as KNN but once that was tuned, its recall has gone up and precision came down.

Considering overall parameter values, KNN is best predictor of all the models. I have tuned KNN as well. With tuning the model performance has increased on all the parameters.

I have tuned Logistic regression as well. After tuning, TPR has gone up while precision has gone down.

If we are looking for a model with high Sensitivity, we can pick up Logistic Regression model. For over-all better performance, we can choose KNN

#### FINAL MODEL:

