KNN Classifier (Breat Cancer Detection)

Import Libraries

In [2]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

In [3]:
```
import os
for dirname, _, filenames in os.walk(r"C:\Users\Prachi\Documents\VS Code Files\Mach
    for filename in filenames:
        print(os.path.join(dirname, filename))
```

In [4]:
```
import warnings
warnings.filterwarnings('ignore')
```

Import Dataset

In [5]:
```
data = r"C:\Users\Prachi\Documents\VS Code Files\Machine Learning\Classification\KN

df = pd.read_csv(data, header=None)
```

Exploratory Data Analysis

In [6]:
```
df.head()
```

Out[6]:

	0	1	2	3	4	5	6	7	8	9	10
0	1000025	5	1	1	1	2	1	3	1	1	2
1	1002945	5	4	4	5	7	10	3	2	1	2
2	1015425	3	1	1	1	2	2	3	1	1	2
3	1016277	6	8	8	1	3	4	3	7	1	2
4	1017023	4	1	1	3	2	1	3	1	1	2

In [7]:
```
df.shape
```

Out[7]:
```
(699, 11)
```

Rename column names

In [8]:
```
col_names = ['Id', 'Clump_thickness', 'Uniformity_Cell_Size', 'Uniformity_Cell_Shap
             'Single_Epithelial_Cell_Size', 'Bare_Nuclei', 'Bland_Chromatin', 'Norm


```

```
df.columns = col_names

df.columns
```

Out[8]:
```
Index(['Id', 'Clump_thickness', 'Uniformity_Cell_Size',
       'Uniformity_Cell_Shape', 'Marginal_Adhesion',
       'Single_Epithelial_Cell_Size', 'Bare_Nuclei', 'Bland_Chromatin',
       'Normal_Nucleoli', 'Mitoses', 'Class'],
      dtype='object')
```

In [9]:
```
df.head()
```

Out[9]:

	Id	Clump_thickness	Uniformity_Cell_Size	Uniformity_Cell_Shape	Marginal_Adhesion	Sing
0	1000025	5	1	1	1	
1	1002945	5	4	4	5	
2	1015425	3	1	1	1	
3	1016277	6	8	8	1	
4	1017023	4	1	1	3	

Drop redundant columns

In [10]:
```
df.drop('Id', axis=1, inplace=True)
```

View summary of daaset

In [11]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 10 columns):
 #   Column                       Non-Null Count  Dtype 
---  ------                       --------------  ----- 
 0   Clump_thickness              699 non-null    int64 
 1   Uniformity_Cell_Size         699 non-null    int64 
 2   Uniformity_Cell_Shape        699 non-null    int64 
 3   Marginal_Adhesion            699 non-null    int64 
 4   Single_Epithelial_Cell_Size  699 non-null    int64 
 5   Bare_Nuclei                  699 non-null    object
 6   Bland_Chromatin              699 non-null    int64 
 7   Normal_Nucleoli              699 non-null    int64 
 8   Mitoses                      699 non-null    int64 
 9   Class                        699 non-null    int64 
dtypes: int64(9), object(1)
memory usage: 54.7+ KB
```

Frequency distribution of values in variables

In [12]:
```
for var in df.columns:
    print(df[var].value_counts())
```

```
Clump_thickness
1     145
5     130
3     108
4      80
10     69
2      50
8      46
6      34
7      23
9      14
Name: count, dtype: int64
Uniformity_Cell_Size
1     384
10     67
3      52
2      45
4      40
5      30
8      29
6      27
7      19
9       6
Name: count, dtype: int64
Uniformity_Cell_Shape
1     353
2      59
10     58
3      56
4      44
5      34
6      30
7      30
8      28
9       7
Name: count, dtype: int64
Marginal_Adhesion
1     407
3      58
2      58
10     55
4      33
8      25
5      23
6      22
7      13
9       5
Name: count, dtype: int64
Single_Epithelial_Cell_Size
2     386
3      72
4      48
1      47
6      41
5      39
10     31
8      21
7      12
9       2
Name: count, dtype: int64
Bare_Nuclei
1     402
10    132
2      30
```

```
5      30
3      28
8      21
4      19
?      16
9       9
7       8
6       4
Name: count, dtype: int64
Bland_Chromatin
2     166
3     165
1     152
7      73
4      40
5      34
8      28
10     20
9      11
6      10
Name: count, dtype: int64
Normal_Nucleoli
1     443
10     61
3      44
2      36
8      24
6      22
5      19
4      18
7      16
9      16
Name: count, dtype: int64
Mitoses
1     579
2      35
3      33
10     14
4      12
7       9
8       8
5       6
6       3
Name: count, dtype: int64
Class
2    458
4    241
Name: count, dtype: int64
```

Convert data type of Bare_Nuclei to integer

In [13]:
```
df['Bare_Nuclei'] = pd.to_numeric(df['Bare_Nuclei'],errors='coerce')
```

check data types of columns of dataframe

In [14]:
```
df.dtypes
```

Out[14]:
```
Clump_thickness                int64
Uniformity_Cell_Size           int64
Uniformity_Cell_Shape          int64
Marginal_Adhesion              int64
Single_Epithelial_Cell_Size    int64
Bare_Nuclei                  float64
Bland_Chromatin                int64
Normal_Nucleoli                int64
Mitoses                        int64
Class                          int64
dtype: object
```

In [15]:
```
# check missing values in variables

df.isnull().sum()
```

Out[15]:
```
Clump_thickness               0
Uniformity_Cell_Size          0
Uniformity_Cell_Shape         0
Marginal_Adhesion             0
Single_Epithelial_Cell_Size   0
Bare_Nuclei                  16
Bland_Chromatin               0
Normal_Nucleoli               0
Mitoses                       0
Class                         0
dtype: int64
```

In [16]:
```
# check `na` values in the dataframe

df.isna().sum()
```

Out[16]:
```
Clump_thickness               0
Uniformity_Cell_Size          0
Uniformity_Cell_Shape         0
Marginal_Adhesion             0
Single_Epithelial_Cell_Size   0
Bare_Nuclei                  16
Bland_Chromatin               0
Normal_Nucleoli               0
Mitoses                       0
Class                         0
dtype: int64
```

In [17]:
```
# check frequency distribution of `Bare_Nuclei` column

df['Bare_Nuclei'].value_counts()
```

Out[17]:
```
Bare_Nuclei
1.0     402
10.0    132
2.0      30
5.0      30
3.0      28
8.0      21
4.0      19
9.0       9
7.0       8
6.0       4
Name: count, dtype: int64
```

In [18]:
```
df['Bare_Nuclei'].unique()
```

Out[18]:
```
array([ 1., 10.,  2.,  4.,  3.,  9.,  7., nan,  5.,  8.,  6.])
```

In [19]:
```
df['Bare_Nuclei'].isna().sum()
```

Out[19]:
```
16
```

In [20]:
```
df['Class'].value_counts()
```

Out[20]:
```
Class
2    458
4    241
Name: count, dtype: int64
```

In [21]:
```
# view percentage of frequency distribution of values in `Class` variable

df['Class'].value_counts()/float(len(df))
```

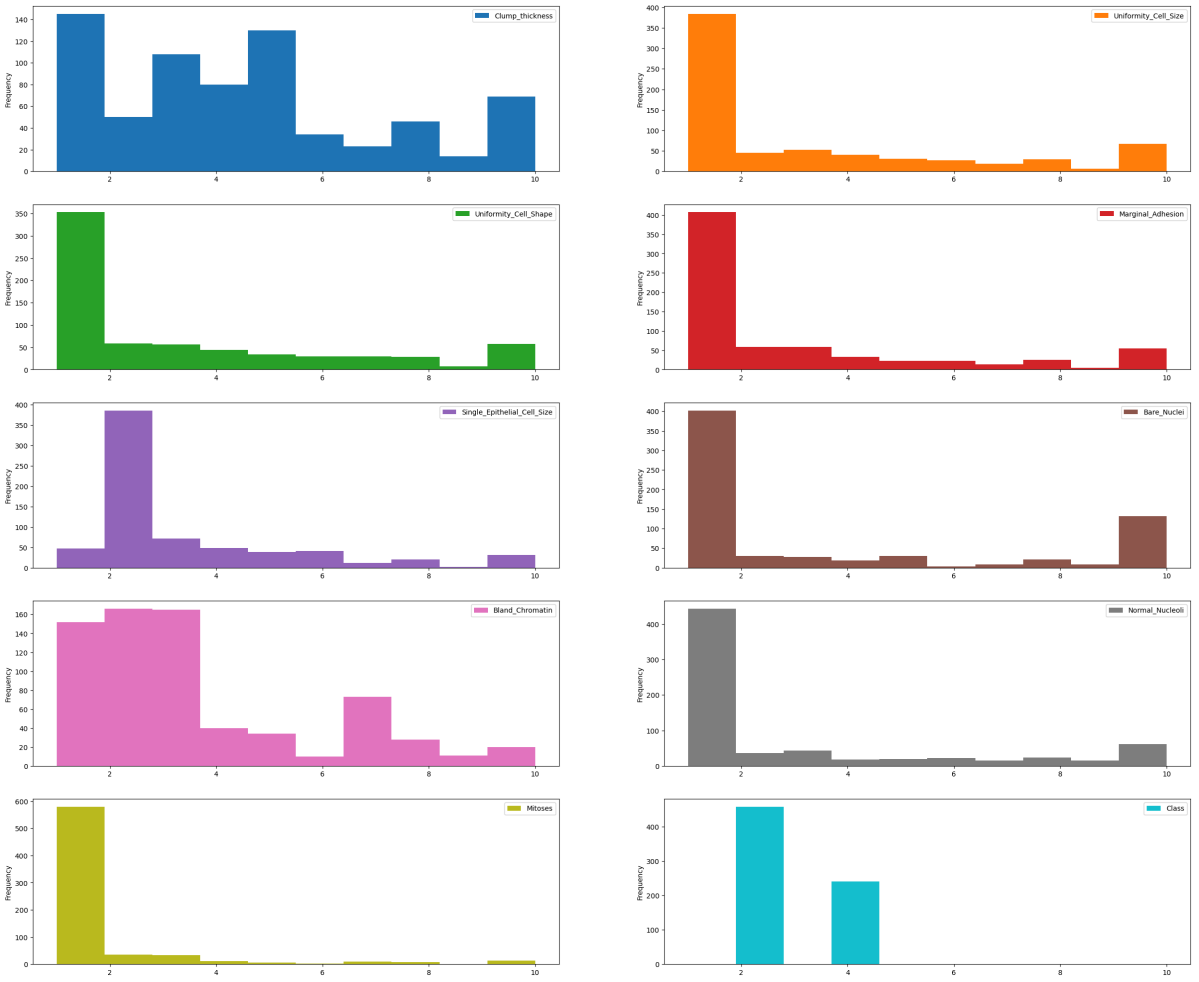
Out[21]:
```
Class
2    0.655222
4    0.344778
Name: count, dtype: float64
```

In [22]:
```
print(round(df.describe(),2))
```

```
       Clump_thickness  Uniformity_Cell_Size  Uniformity_Cell_Shape  \
count           699.00                699.00                 699.00
mean              4.42                  3.13                   3.21
std               2.82                  3.05                   2.97
min               1.00                  1.00                   1.00
25%               2.00                  1.00                   1.00
50%               4.00                  1.00                   1.00
75%               6.00                  5.00                   5.00
max              10.00                 10.00                  10.00

       Marginal_Adhesion  Single_Epithelial_Cell_Size  Bare_Nuclei  \
count             699.00                       699.00       683.00
mean                2.81                         3.22         3.54
std                 2.86                         2.21         3.64
min                 1.00                         1.00         1.00
25%                 1.00                         2.00         1.00
50%                 1.00                         2.00         1.00
75%                 4.00                         4.00         6.00
max                10.00                        10.00        10.00

       Bland_Chromatin  Normal_Nucleoli  Mitoses   Class
count           699.00           699.00   699.00  699.00
mean              3.44             2.87     1.59    2.69
std               2.44             3.05     1.72    0.95
min               1.00             1.00     1.00    2.00
25%               2.00             1.00     1.00    2.00
50%               3.00             1.00     1.00    2.00
75%               5.00             4.00     1.00    4.00
max              10.00            10.00    10.00    4.00
```

Data Visualisation

In [23]:
```
# plot histograms of the variables

plt.rcParams['figure.figsize']=(30,25)

df.plot(kind='hist', bins =10, subplots=True, layout=(5,2), sharex=False, sharey=Fa

plt.show()
```



Multivariate Plots

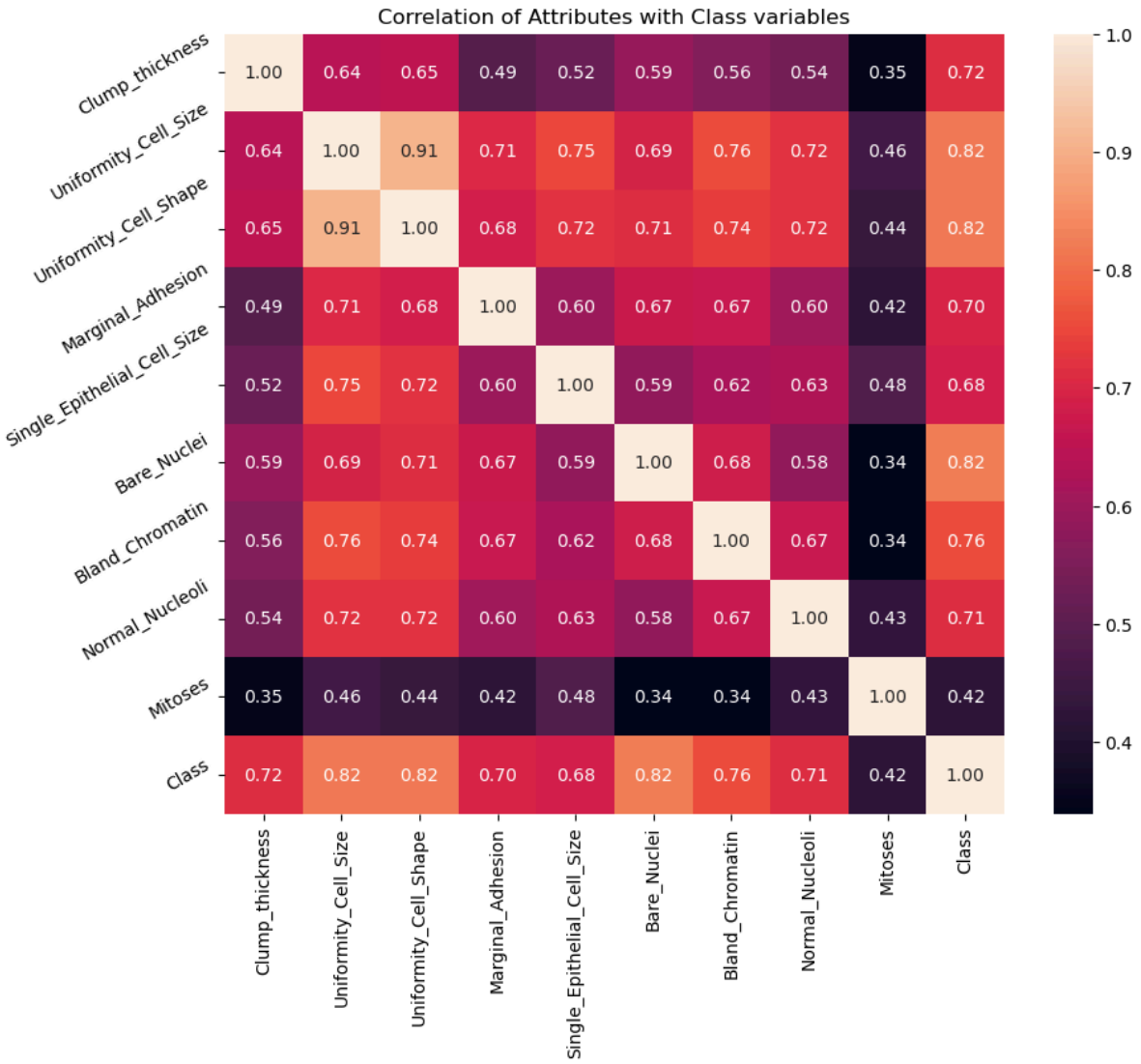
In [24]:
```
# Estimating correlation coefficients
correlation = df.corr()
```

In [25]:
```
correlation['Class'].sort_values(ascending=False)
```

Out[25]:
```
Class                          1.000000
Bare_Nuclei                    0.822696
Uniformity_Cell_Shape          0.818934
Uniformity_Cell_Size           0.817904
Bland_Chromatin                0.756616
Clump_thickness                0.716001
Normal_Nucleoli                0.712244
Marginal_Adhesion              0.696800
Single_Epithelial_Cell_Size    0.682785
Mitoses                        0.423170
Name: Class, dtype: float64
```

Correlation Heat Map

In [26]:
```
plt.figure(figsize =(10,8))
plt.title('Correlation of Attributes with Class variables')
a= sns.heatmap(correlation, square=True, annot=True, fmt='.2f', linecolor='white')
a.set_xticklabels(a.get_xticklabels(), rotation=90)
a.set_yticklabels(a.get_yticklabels(), rotation=30)
plt.show()
```



In [27]:
```
X = df.drop(['Class'], axis=1)
y = df['Class']
```

In [28]:
```
# split X and y into training and testing sets

from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_s
```

In [29]:
```
# check the shape of X_train and X_test
X_train.shape, X_test.shape
```

Out[29]:
```
((559, 9), (140, 9))
```

Fetaure Engineering

In [30]:
```
# check data types in X_train

X_train.dtypes
```

Out[30]:
```
Clump_thickness                int64
Uniformity_Cell_Size           int64
Uniformity_Cell_Shape          int64
Marginal_Adhesion              int64
Single_Epithelial_Cell_Size    int64
Bare_Nuclei                  float64
Bland_Chromatin                int64
Normal_Nucleoli                int64
Mitoses                        int64
dtype: object
```

In [31]:
```
# check missing values in numerical variables in X_train

X_train.isnull().sum()
```

Out[31]:
```
Clump_thickness                0
Uniformity_Cell_Size           0
Uniformity_Cell_Shape          0
Marginal_Adhesion              0
Single_Epithelial_Cell_Size    0
Bare_Nuclei                   13
Bland_Chromatin                0
Normal_Nucleoli                0
Mitoses                        0
dtype: int64
```

In [32]:
```
X_test.isnull().sum()
```

Out[32]:
```
Clump_thickness                0
Uniformity_Cell_Size           0
Uniformity_Cell_Shape          0
Marginal_Adhesion              0
Single_Epithelial_Cell_Size    0
Bare_Nuclei                    3
Bland_Chromatin                0
Normal_Nucleoli                0
Mitoses                        0
dtype: int64
```

In [33]:
```
# print percentage of missing values in the numerical variables in training set

for col in X_train.columns:
    if X_train[col].isnull().mean()>0:
        print(col, round(X_train[col].isnull().mean(),4))
```

```
Bare_Nuclei 0.0233
```

In [34]:
```
# impute missing values in X_train and X_test with respective column median in X_tr

for df1 in [X_train, X_test]:
    for col in X_train.columns:
        col_median=X_train[col].median()
        df1[col].fillna(col_median, inplace=True)
```

In [35]:
```
X_train.isnull().sum()
```

Out[35]:
```
Clump_thickness               0
Uniformity_Cell_Size          0
Uniformity_Cell_Shape         0
Marginal_Adhesion             0
Single_Epithelial_Cell_Size   0
Bare_Nuclei                   0
Bland_Chromatin               0
Normal_Nucleoli               0
Mitoses                       0
dtype: int64
```

In [36]:
```
X_test.isnull().sum()
```

Out[36]:
```
Clump_thickness               0
Uniformity_Cell_Size          0
Uniformity_Cell_Shape         0
Marginal_Adhesion             0
Single_Epithelial_Cell_Size   0
Bare_Nuclei                   0
Bland_Chromatin               0
Normal_Nucleoli               0
Mitoses                       0
dtype: int64
```

In [37]:
```
X_train.head()
```

Out[37]:

	Clump_thickness	Uniformity_Cell_Size	Uniformity_Cell_Shape	Marginal_Adhesion	Single_Epith
293	10	4	4	6	
62	9	10	10	1	
485	1	1	1	3	
422	4	3	3	1	
332	5	2	2	2	

In [38]:
```
X_test.head()
```

Out[38]:

	Clump_thickness	Uniformity_Cell_Size	Uniformity_Cell_Shape	Marginal_Adhesion	Single_Epith
476	4	1	2	1	
531	4	2	2	1	
40	6	6	6	9	
432	5	1	1	1	
14	8	7	5	10	

Feature Scaling

In [39]:
```
cols = X_train.columns
```

In [40]:
```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

In [41]:
```
X_train = pd.DataFrame(X_train, columns=[cols])
```

In [42]:
```
X_test = pd.DataFrame(X_test, columns=[cols])
```

In [43]:
```
X_train.head()
```

Out[43]:

	Clump_thickness	Uniformity_Cell_Size	Uniformity_Cell_Shape	Marginal_Adhesion	Single_Epitheli
0	2.028383	0.299506	0.289573	1.119077	
1	1.669451	2.257680	2.304569	-0.622471	
2	-1.202005	-0.679581	-0.717925	0.074148	
3	-0.125209	-0.026856	-0.046260	-0.622471	
4	0.233723	-0.353219	-0.382092	-0.274161	

Fit K Neighbours Classifier to the Training

In [44]:
```
# import KNeighbors ClaSSifier from sklearn
from sklearn.neighbors import KNeighborsClassifier


# instantiate the model
knn = KNeighborsClassifier(n_neighbors=3)


# fit the model to the training set
knn.fit(X_train, y_train)
```

Out[44]:

KNeighborsClassifier

KNeighborsClassifier(n_neighbors=3)

Predict test-set results

In [45]:
```
y_pred = knn.predict(X_test)
y_pred
```

Out[45]:
```
array([2, 2, 4, 2, 4, 2, 4, 2, 4, 2, 2, 2, 4, 4, 4, 2, 2, 4, 4, 2, 4, 4,
       2, 2, 2, 4, 2, 2, 4, 4, 2, 2, 2, 2, 2, 2, 2, 4, 2, 2, 2, 2, 2, 2,
       4, 4, 2, 4, 2, 4, 4, 2, 2, 4, 2, 2, 2, 2, 2, 2, 4, 2, 2, 4, 4, 4,
       4, 2, 2, 4, 2, 2, 4, 4, 2, 2, 2, 2, 4, 2, 2, 2, 4, 2, 2, 2, 4, 2,
       4, 4, 2, 2, 2, 4, 2, 2, 2, 4, 2, 4, 4, 2, 2, 2, 4, 2, 2, 2, 2, 2,
       4, 4, 4, 2, 2, 2, 2, 2, 4, 4, 4, 4, 2, 4, 2, 2, 4, 4, 4, 4, 4, 2,
       2, 4, 4, 2, 2, 4, 2, 2], dtype=int64)
```

In [46]:
```
# probability of getting output as 2 - benign cancer

knn.predict_proba(X_test)[:,0]
```

Out[46]:
```
array([1.        , 1.        , 0.33333333, 1.        , 0.        ,
       1.        , 0.        , 1.        , 0.        , 0.66666667,
       1.        , 1.        , 0.        , 0.33333333, 0.        ,
       1.        , 1.        , 0.        , 0.        , 1.        ,
       0.        , 0.        , 1.        , 1.        , 1.        ,
       0.        , 1.        , 1.        , 0.        , 0.        ,
       1.        , 1.        , 1.        , 1.        , 1.        ,
       0.66666667, 1.        , 0.        , 1.        , 1.        ,
       1.        , 1.        , 1.        , 1.        , 0.        ,
       0.        , 1.        , 0.        , 1.        , 0.        ,
       0.        , 1.        , 1.        , 0.        , 1.        ,
       1.        , 1.        , 1.        , 0.66666667, 1.        ,
       0.        , 1.        , 1.        , 0.        , 0.        ,
       0.33333333, 0.        , 1.        , 1.        , 0.        ,
       1.        , 1.        , 0.        , 0.        , 1.        ,
       1.        , 1.        , 1.        , 0.        , 1.        ,
       1.        , 1.        , 0.        , 1.        , 1.        ,
       1.        , 0.        , 1.        , 0.        , 0.        ,
       1.        , 1.        , 0.66666667, 0.        , 1.        ,
       1.        , 1.        , 0.        , 1.        , 0.        ,
       0.        , 1.        , 1.        , 1.        , 0.        ,
       1.        , 1.        , 1.        , 1.        , 1.        ,
       0.        , 0.33333333, 0.        , 1.        , 1.        ,
       1.        , 1.        , 1.        , 0.        , 0.        ,
       0.        , 0.33333333, 1.        , 0.        , 1.        ,
       1.        , 0.33333333, 0.33333333, 0.        , 0.        ,
       0.        , 1.        , 1.        , 0.33333333, 0.        ,
       1.        , 1.        , 0.        , 1.        , 1.        ])
```

In [47]:
```
# probability of getting output as 4 - malignant cancer

knn.predict_proba(X_test)[:,1]
```

Out[47]:
```
array([0.        , 0.        , 0.66666667, 0.        , 1.        ,
       0.        , 1.        , 0.        , 1.        , 0.33333333,
       0.        , 0.        , 1.        , 0.66666667, 1.        ,
       0.        , 0.        , 1.        , 1.        , 0.        ,
       1.        , 1.        , 0.        , 0.        , 0.        ,
       1.        , 0.        , 0.        , 1.        , 1.        ,
       0.        , 0.        , 0.        , 0.        , 0.        ,
       0.33333333, 0.        , 1.        , 0.        , 0.        ,
       0.        , 0.        , 0.        , 0.        , 1.        ,
       1.        , 0.        , 1.        , 0.        , 1.        ,
       1.        , 0.        , 0.        , 1.        , 0.        ,
       0.        , 0.        , 0.        , 0.33333333, 0.        ,
       1.        , 0.        , 0.        , 1.        , 1.        ,
       0.66666667, 1.        , 0.        , 0.        , 1.        ,
       0.        , 0.        , 1.        , 1.        , 0.        ,
       0.        , 0.        , 0.        , 1.        , 0.        ,
       0.        , 0.        , 1.        , 0.        , 0.        ,
       0.        , 1.        , 0.        , 1.        , 1.        ,
       0.        , 0.        , 0.33333333, 1.        , 0.        ,
       0.        , 0.        , 1.        , 0.        , 1.        ,
       1.        , 0.        , 0.        , 0.        , 1.        ,
       0.        , 0.        , 0.        , 0.        , 0.        ,
       1.        , 0.66666667, 1.        , 0.        , 0.        ,
       0.        , 0.        , 0.        , 1.        , 1.        ,
       1.        , 0.66666667, 0.        , 1.        , 0.        ,
       0.        , 0.66666667, 0.66666667, 1.        , 1.        ,
       1.        , 0.        , 0.        , 0.66666667, 1.        ,
       0.        , 0.        , 1.        , 0.        , 0.        ])
```

check accuracy score

In [48]:
```
from sklearn.metrics import accuracy_score
print('Model accuracy score:  {0:0.4f}'.format(accuracy_score(y_test, y_pred)))
```

```
Model accuracy score:  0.9714
```

Comapre the train-set and test-set accuracy

In [49]:
```
y_pred_train = knn.predict(X_train)
```

In [50]:
```
print('Training-set accuracy score: {0:0.4f}'. format(accuracy_score(y_train, y_pre
```

```
Training-set accuracy score: 0.9821
```

Check for overfitting and underfitting

In [51]:
```
# print the scores on training and test set

print('Training set score: {:.4f}'.format(knn.score(X_train, y_train)))
print('Test set score: {:.4f}'.format(knn.score(X_test, y_test)))
```

```
Training set score: 0.9821
Test set score: 0.9714
```

Compare model accuracy with null accuracy

In [52]:
```
# check class distribution in test set

y_test.value_counts()
```

Out[52]:
```
Class
2    85
4    55
Name: count, dtype: int64
```

In [53]:
```
# check null accuracy score
null_accuracy = (85/(85+55))
print('Null accuracy score: {0:0.4f}'.format(null_accuracy))
```

```
Null accuracy score: 0.6071
```

Rebuild kNN Classification model using different values of k

Rebuild kNN Classification model using k=5

In [54]:
```
# instantiate the model with k=5
knn_5 = KNeighborsClassifier(n_neighbors=5)

# fit the model to the training set
knn_5.fit(X_train, y_train)
```

```
# Predict on the test-set
y_pred_5 = knn_5.predict(X_test)

print('Model accuracy score with k=5: {0:0.4f}'.format(accuracy_score(y_test,y_pred
```

```
Model accuracy score with k=5: 0.9714
```

Rebuild kNN Classification model using k=6

In [55]:
```
# instantiate the model with k=6
knn_6 = KNeighborsClassifier(n_neighbors=6)

# fit the model to the training set
knn_6.fit(X_train, y_train)

# Predict on the test-set
y_pred_6 = knn_6.predict(X_test)

print('Model accuracy score with k=5: {0:0.4f}'.format(accuracy_score(y_test,y_pred
```

```
Model accuracy score with k=5: 0.9786
```

Rebuild kNN Classification model using k=7

In [56]:
```
# instantiate the model with k=7
knn_7 = KNeighborsClassifier(n_neighbors=7)

# fit the model to the training set
knn_7.fit(X_train, y_train)

# Predict on the test-set
y_pred_7 = knn_7.predict(X_test)

print('Model accuracy score with k=7: {0:0.4f}'.format(accuracy_score(y_test,y_pred
```

```
Model accuracy score with k=7: 0.9786
```

Rebuild kNN Classification model using k=8

In [57]:
```
# instantiate the model with k=8
knn_8 = KNeighborsClassifier(n_neighbors=8)


# fit the model to the training set
knn_8.fit(X_train, y_train)


# predict on the test-set
y_pred_8 = knn_8.predict(X_test)


print('Model accuracy score with k=8 : {0:0.4f}'. format(accuracy_score(y_test, y_p
```

```
Model accuracy score with k=8 : 0.9786
```

Rebuild kNN Classification model using k=9

In [58]:
```
# instantiate the model with k=9
knn_9 = KNeighborsClassifier(n_neighbors=9)


# fit the model to the training set
knn_9.fit(X_train, y_train)


# predict on the test-set
y_pred_9 = knn_9.predict(X_test)


print('Model accuracy score with k=9 : {0:0.4f}'. format(accuracy_score(y_test, y_p
```

```
Model accuracy score with k=9 : 0.9714
```

Confusion matrix

In [59]:
```
# Print the confusion Matrix with k=3 and slice it into four pieces

from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_pred)

print('Confusion matrix\n\n', cm)

print('\n True Positive (TP)= ', cm[0,0])

print('\nTrue Negatives(TN) = ', cm[1,1])

print('\nFalse Positives(FP) = ', cm[0,1])

print('\nFalse Negatives(FN) = ', cm[1,0])
```

```
Confusion matrix

 [[83  2]
 [ 2 53]]

 True Positive (TP)=  83

True Negatives(TN) =  53

False Positives(FP) =  2

False Negatives(FN) =  2
```

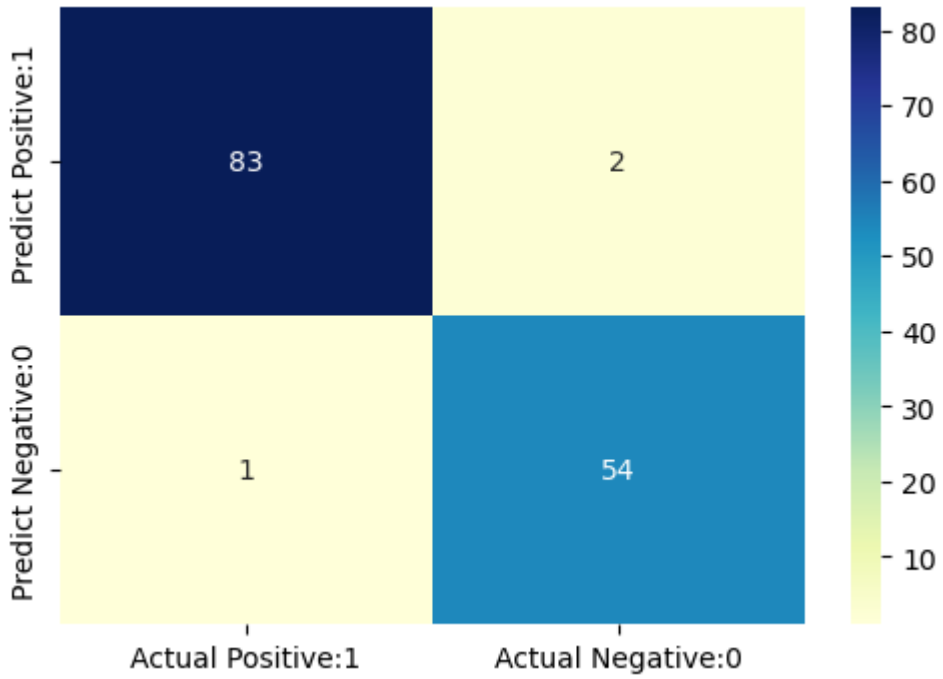
In [60]:
```
# Print the Confusion Matrix with k =7 and slice it into four pieces

cm_7 = confusion_matrix(y_test, y_pred_7)

print('Confusion matrix\n\n', cm_7)

print('\nTrue Positives(TP) = ', cm_7[0,0])
```

```
print('\nTrue Negatives(TN) = ', cm_7[1,1])

print('\nFalse Positives(FP) = ', cm_7[0,1])

print('\nFalse Negatives(FN) = ', cm_7[1,0])
```

```
Confusion matrix

 [[83  2]
 [ 1 54]]

True Positives(TP) =  83

True Negatives(TN) =  54

False Positives(FP) =  2

False Negatives(FN) =  1
```

In [61]:
```
# visualize confusion matrix with seaborn heatmap

plt.figure(figsize=(6,4))

cm_matrix = pd.DataFrame(data=cm_7, columns=['Actual Positive:1', 'Actual Negative:
                                             index=['Predict Positive:1', 'Predict N

sns.heatmap(cm_matrix, annot=True, fmt = 'd', cmap='YlGnBu')
```

Out[61]:
```
<Axes: >
```



Classification metrics

Classification Report

In [62]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test, y_pred_7))
```

```
              precision    recall  f1-score   support

           2       0.99      0.98      0.98        85
           4       0.96      0.98      0.97        55

    accuracy                           0.98       140
   macro avg       0.98      0.98      0.98       140
weighted avg       0.98      0.98      0.98       140
```

Classification accuracy

In [63]:
```
TP = cm_7[0,0]
TN = cm_7[1,1]
FP = cm_7[0,1]
FN = cm_7[1,0]
```

In [64]:
```
# print classifiction accuracy

classification_accuracy = (TP+TN) / float(TP+TN+FP+FN)

print('Classification accuracy : {0:0.4f}'.format(classification_accuracy))
```

```
Classification accuracy : 0.9786
```

Classification error

In [65]:
```
# print classification error

classification_error = (FP+FN) / float(TP+TN+FP+FN)

print('Classification error: {0:0.4f}'.format(classification_error))
```

```
Classification error: 0.0214
```

Precision

In [66]:
```
# print precision score

precision = TP / float(TP+FP)

print('Precision : {0:0.4f}'.format(precision))
```

```
Precision : 0.9765
```

Recall

In [69]:
```
recall = TP/ float(TP + FN)
print('Recall or Sensitivity : {0:0.4f}'.format(recall))
```

```
Recall or Sensitivity : 0.9881
```

True Positive Rate

In [70]:
```
true_positive_rate = TP / float(TP + FN)


print('True Positive Rate : {0:0.4f}'.format(true_positive_rate))
```

```
True Positive Rate : 0.9881
```

False Positive Rate

In [71]:
```
false_positive_rate = FP / float(FP + TN)


print('False Positive Rate : {0:0.4f}'.format(false_positive_rate))
```

```
False Positive Rate : 0.0357
```

Specificity

In [72]:
```
specificity = TN/(TN + FP)
print('Specificity : {0:0.4f}'.format(specificity))
```

```
Specificity : 0.9643
```

f1 - score

Adjusting the classification threshold level

In [73]:
```
# print the first 10 predicted probabilities of two classes- 2 and 4

y_pred_prob = knn.predict_proba(X_test)[0:10]

y_pred_prob
```

Out[73]:
```
array([[1.        , 0.        ],
       [1.        , 0.        ],
       [0.33333333, 0.66666667],
       [1.        , 0.        ],
       [0.        , 1.        ],
       [1.        , 0.        ],
       [0.        , 1.        ],
       [1.        , 0.        ],
       [0.        , 1.        ],
       [0.66666667, 0.33333333]])
```

In [74]:
```
# store the probabilities in dataframe

y_pred_prob_df = pd.DataFrame(data=y_pred_prob, columns=['Prob of - benign cancer (

y_pred_prob_df
```

Out[74]:

	Prob of - benign cancer (2)	Prob of - malignant cancer (4)
0	1.000000	0.000000
1	1.000000	0.000000
2	0.333333	0.666667
3	1.000000	0.000000
4	0.000000	1.000000
5	1.000000	0.000000
6	0.000000	1.000000
7	1.000000	0.000000
8	0.000000	1.000000
9	0.666667	0.333333

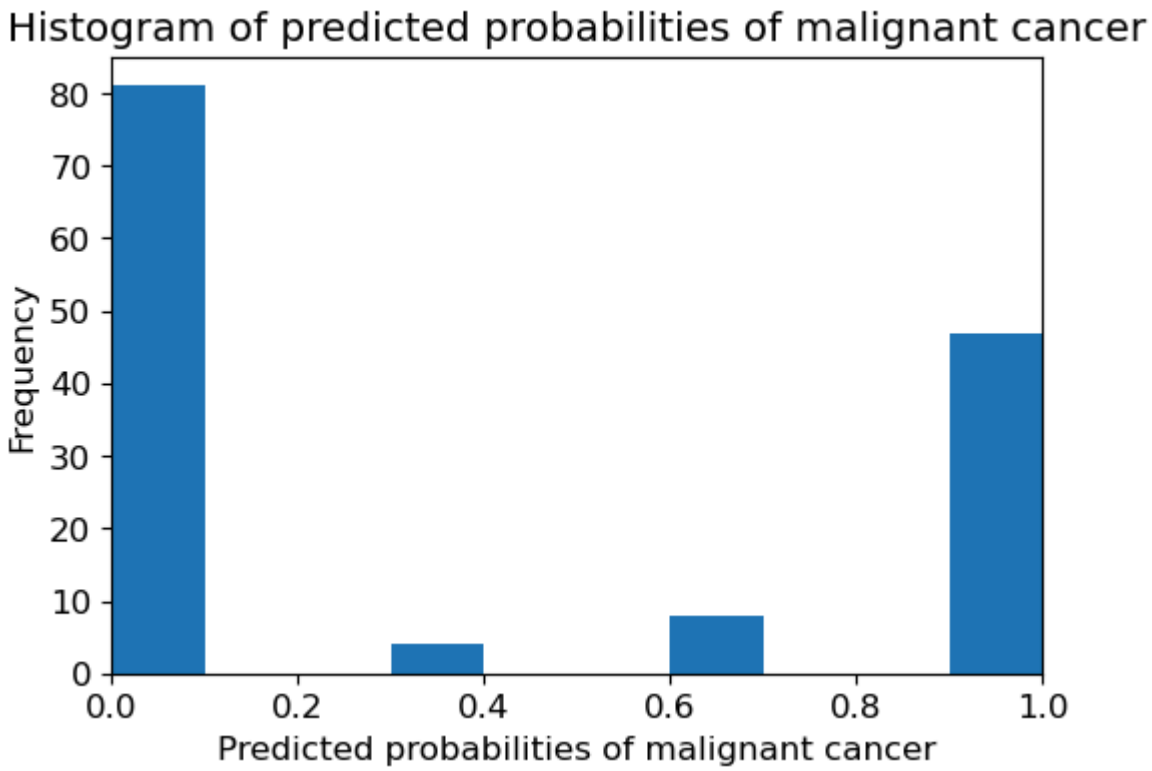
In [75]:
```
# print the first 10 predicted probabilities for class 4 - Probability of malignant

knn.predict_proba(X_test)[0:10, 1]
```

Out[75]:
```
array([0.        , 0.        , 0.66666667, 0.        , 1.        ,
       0.        , 1.        , 0.        , 1.        , 0.33333333])
```

In [76]:
```
# store the predicted probabilities for class 4 - Probability of malignant cancer

y_pred_1 = knn.predict_proba(X_test)[:, 1]
```

In [77]:
```
# plot histogram of predicted probabilities

# adjust figure size
plt.figure(figsize=(6,4))

# adjust the font size
plt.rcParams['font.size'] = 12


# plot histogram with 10 bins
plt.hist(y_pred_1, bins = 10)


# set the title of predicted probabilities
plt.title('Histogram of predicted probabilities of malignant cancer')


# set the x-axis limit
plt.xlim(0,1)


# set the title
plt.xlabel('Predicted probabilities of malignant cancer')
plt.ylabel('Frequency')
```

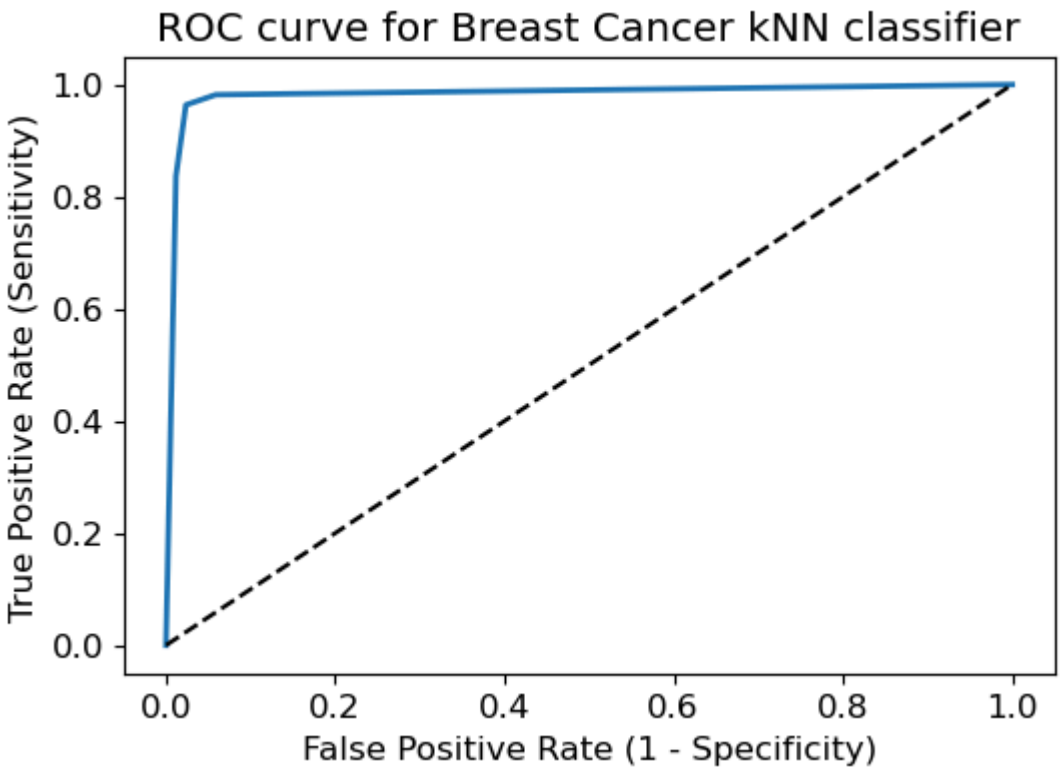
Out[77]:
```
Text(0, 0.5, 'Frequency')
```



ROC - AOC

In [79]:

```
from sklearn.metrics import roc_curve

fpr, tpr, thresholds = roc_curve(y_test, y_pred_1, pos_label=4)

plt.figure(figsize=(6,4))

plt.plot(fpr, tpr, linewidth=2)

plt.plot([0,1], [0,1], 'k--' )

plt.rcParams['font.size'] = 12

plt.title('ROC curve for Breast Cancer kNN classifier')

plt.xlabel('False Positive Rate (1 - Specificity)')

plt.ylabel('True Positive Rate (Sensitivity)')

plt.show()
```



ROC AUC

In [80]:
```
# compute ROC AUC

from sklearn.metrics import roc_auc_score

ROC_AUC = roc_auc_score(y_test, y_pred_1)

print('ROC AUC : {:.4f}'.format(ROC_AUC))
```

```
ROC AUC : 0.9825
```

In [81]:
```
# calculate cross-validated ROC AUC

from sklearn.model_selection import cross_val_score

Cross_validated_ROC_AUC = cross_val_score(knn_7, X_train, y_train, cv=5, scoring='r

print('Cross validated ROC AUC : {:.4f}'.format(Cross_validated_ROC_AUC))
```

```
Cross validated ROC AUC : 0.9910
```

k-fold cross validation

In [83]:
```
# Applying 10-fold cross validation

from sklearn.model_selection import cross_val_score

scores = cross_val_score(knn_7, X_train, y_train, cv = 10, scoring='accuracy')

print('Cross -Validation Scores: {}'.format(scores))
```

```
Cross -Validation Scores: [0.875      0.96428571 0.94642857 0.98214286 0.96428571
0.96428571
 0.98214286 0.98214286 1.         0.98181818]
```

In [84]:
```
# compute Average cross-validation score

print('Average cross-validation score: {:.4f}'.format(scores.mean()))
```

```
Average cross-validation score: 0.9643
```

Results and Conclusion

21. Results and Conclusion

Table of Contents

1. In this project, I build a kNN classifier model to classify the patients suffering from breast cancer. The model yields very good performance as indicated by the model accuracy which was found to be 0.9786 with k=7.

2. With k=3, the training-set accuracy score is 0.9821 while the test-set accuracy to be 0.9714. These two values are quite comparable. So, there is no question of overfitting.

3. I have compared the model accuracy score which is 0.9714 with null accuracy score which is 0.6071. So, we can conclude that our K Nearest Neighbors model is doing a very good job in predicting the class labels.

4. Our original model accuracy score with k=3 is 0.9714. Now, we can see that we get same accuracy score of 0.9714 with k=5. But, if we increase the value of k further, this would result in enhanced accuracy. With k=6,7,8 we get accuracy score of 0.9786. So, it results in performance improvement. If we increase k to 9, then accuracy decreases again to 0.9714. So, we can conclude that our optimal value of k is 7.

5. kNN Classification model with k=7 shows more accurate predictions and less number of errors than k=3 model. Hence, we got performance improvement with k=7.

6. ROC AUC of our model approaches towards 1. So, we can conclude that our classifier does a good job in predicting whether it is benign or malignant cancer.

7. Using the mean cross-validation, we can conclude that we expect the model to be around 96.46 % accurate on average.

8. If we look at all the 10 scores produced by the 10-fold cross-validation, we can also conclude that there is a relatively high variance in the accuracy between folds, ranging from 100% accuracy to 87.72% accuracy. So, we can conclude that the model is very dependent on the particular folds used for training, but it also be the consequence of the small size of the dataset.