Breast Cancer Prediction

Libraries to Import

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import KFold
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV
from sklearn.svm import SVC
from pandas.plotting import scatter_matrix

%matplotlib inline
```

In [96]:
```
# Citation Request:
#   This breast cancer databases was obtained from the University of Wisconsin
#   Hospitals, Madison from Dr. William H. Wolberg.  If you publish results
#   when using this database, then please include this information in your
#   acknowledgements.  Also, please cite one or more of:

#   1. O. L. Mangasarian and W. H. Wolberg: "Cancer diagnosis via linear
#      programming", SIAM News, Volume 23, Number 5, September 1990, pp 1 & 18.

#   2. William H. Wolberg and O.L. Mangasarian: "Multisurface method of
#      pattern separation for medical diagnosis applied to breast cytology",
#      Proceedings of the National Academy of Sciences, U.S.A., Volume 87,
#      December 1990, pp 9193-9196.

#   3. O. L. Mangasarian, R. Setiono, and W.H. Wolberg: "Pattern recognition
#      via linear programming: Theory and application to medical diagnosis",
#      in: "Large-scale numerical optimization", Thomas F. Coleman and Yuying
#      Li, editors, SIAM Publications, Philadelphia 1990, pp 22-30.

#   4. K. P. Bennett & O. L. Mangasarian: "Robust linear programming
#      discrimination of two linearly inseparable sets", Optimization Methods
#      and Software 1, 1992, 23-34 (Gordon & Breach Science Publishers).

# URL to load data
source = "https://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wisconsin/breast-cance

# Adding names to CSV columns
colNames = ['id', 'clumpThickness', 'uniformCellSize', 'uniformCellShape',
    'marginalAdhesion', 'singleEpithelialSize', 'bareNuclei',
```

```
    'blandChromatin', 'normalNucleoli', 'mitoses', 'class']

bCancerDF = pd.read_csv(source, names=colNames)
bCancerDF.head()
```

Out[96]:

	id	clumpThickness	uniformCellSize	uniformCellShape	marginalAdhesion	singleEpithelialSize
0	1000025	5	1	1	1	2
1	1002945	5	4	4	5	7
2	1015425	3	1	1	1	2
3	1016277	6	8	8	1	3
4	1017023	4	1	1	3	2

In [3]:

```
# checking number of rows & columns
bCancerDF.shape
```

Out[3]: (699, 11)

Preprocessing

In [4]:

```
# droping index column
bCancerDF.drop(['id'],axis=1,inplace = True)
bCancerDF.columns
```

Out[4]:

```
Index(['clumpThickness', 'uniformCellSize', 'uniformCellShape',
       'marginalAdhesion', 'singleEpithelialSize', 'bareNuclei',
       'blandChromatin', 'normalNucleoli', 'mitoses', 'class'],
      dtype='object')
```

Handling Missing Values

In [5]:

```
# Dataframe Information
bCancerDF.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 10 columns):
 #   Column           Non-Null Count  Dtype 
---  ------           --------------  ----- 
 0   clumpThickness   699 non-null    int64 
 1   uniformCellSize  699 non-null    int64 
 2   uniformCellShape 699 non-null    int64 
 3   marginalAdhesion 699 non-null    int64 
 4   singleEpithelialSize 699 non-null  int64 
 5   bareNuclei       699 non-null    object
 6   blandChromatin   699 non-null    int64 
 7   normalNucleoli   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
```

In [6]:
```
#Diagnosis class:
# 2 is for Benign
# 4 is for Malignant

# Total number of Benign and Maglinant cases from the dataset
bCancerDF['class'].value_counts()
```

Out[6]:
```
2   458
4   241
Name: class, dtype: int64
```

In [7]:
```
# counting number of rows for bareNuclei from 1 to 10
bCancerDF['bareNuclei'].value_counts()
```

Out[7]:
```
1    402
10   132
2     30
5     30
3     28
8     21
4     19
?     16
9      9
7      8
6      4
Name: bareNuclei, dtype: int64
```

In [9]:
```
# finding unknowns
bCancerDF[bCancerDF['bareNuclei'] == '?']
```

Out[9]:

	clumpThickness	uniformCellSize	uniformCellShape	marginalAdhesion	singleEpithelialSize	bareNu
23	8	4	5	1	2	
40	6	6	6	9	6	
139	1	1	1	1	1	
145	1	1	3	1	2	
158	1	1	2	1	3	
164	5	1	1	1	2	
235	3	1	4	1	2	
249	3	1	1	1	2	
275	3	1	3	1	2	
292	8	8	8	1	2	
294	1	1	1	1	2	
297	5	4	3	1	2	
315	4	6	5	6	7	

	clumpThickness	uniformCellSize	uniformCellShape	marginalAdhesion	singleEpithelialSize	bareNu
321	3	1	1	1	2	
411	1	1	1	1	1	
617	1	1	1	1	1	

In [10]:
```
# getting sum of values for each feature (column) with unknown values
bCancerDF[bCancerDF['bareNuclei'] == '?'].sum()
```

Out[10]:
```
clumpThickness                54
uniformCellSize               39
uniformCellShape              46
marginalAdhesion              29
singleEpithelialSize          39
bareNuclei          ??????????????????
blandChromatin                50
normalNucleoli                44
mitoses                       16
class                         36
dtype: object
```

In [11]:
```
# replace nan with '?'
bCancerDF.replace('?',np.nan,inplace=True)

# checking data at index 23 for the confirmation of replacement
bCancerDF.loc[23,:]
```

Out[11]:
```
clumpThickness          8
uniformCellSize         4
uniformCellShape        5
marginalAdhesion        1
singleEpithelialSize    2
bareNuclei            NaN
blandChromatin          7
normalNucleoli          3
mitoses                 1
class                   4
Name: 23, dtype: object
```

In [12]:
```
# Number of records with Null values
bCancerDF.isna().sum()
```

Out[12]:
```
clumpThickness          0
uniformCellSize         0
uniformCellShape        0
marginalAdhesion        0
singleEpithelialSize    0
bareNuclei             16
blandChromatin          0
normalNucleoli          0
mitoses                 0
class                   0
dtype: int64
```

In [13]:
```
# filling null values with 'ffill'
# that propagates last valid observation forward
bCancerDF.fillna(method='ffill', inplace=True)

#now you can see that there isn't any null value
bCancerDF.isna().sum()
```

Out[13]:
```
clumpThickness       0
uniformCellSize      0
uniformCellShape     0
marginalAdhesion     0
singleEpithelialSize 0
bareNuclei           0
blandChromatin       0
normalNucleoli       0
mitoses              0
class                0
dtype: int64
```

In [14]:
```
bCancerDF.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 10 columns):
 #   Column           Non-Null Count  Dtype 
---  ------           --------------  ----- 
 0   clumpThickness   699 non-null    int64 
 1   uniformCellSize  699 non-null    int64 
 2   uniformCellShape 699 non-null    int64 
 3   marginalAdhesion 699 non-null    int64 
 4   singleEpithelialSize 699 non-null  int64 
 5   bareNuclei       699 non-null    object
 6   blandChromatin   699 non-null    int64 
 7   normalNucleoli   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
```

In [15]:
```
#changing bareNuclei datatype to int64
bCancerDF['bareNuclei'] = bCancerDF['bareNuclei'].astype('int64')
```

Exploratory Data Analysis (EDA)

In [20]:
```
# dataframe information
bCancerDF.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 10 columns):
 #   Column           Non-Null Count  Dtype 
---  ------           --------------  ----- 
 0   clumpThickness   699 non-null    int64 
 1   uniformCellSize  699 non-null    int64 
 2   uniformCellShape 699 non-null    int64 
 3   marginalAdhesion 699 non-null    int64 
 4   singleEpithelialSize 699 non-null  int64 
```

```
 5  bareNuclei          699 non-null    int64
 6  blandChromatin      699 non-null    int64
 7  normalNucleoli      699 non-null    int64
 8  mitoses             699 non-null    int64
 9  class               699 non-null    int64
dtypes: int64(10)
memory usage: 54.7 KB
```

In [21]:
```
# describing statistical values for numeric data
bCancerDF.describe()
```

Out[21]:

	clumpThickness	uniformCellSize	uniformCellShape	marginalAdhesion	singleEpithelialSize	bareN
count	699.000000	699.000000	699.000000	699.000000	699.000000	699.0(
mean	4.417740	3.134478	3.207439	2.806867	3.216023	3.5
std	2.815741	3.051459	2.971913	2.855379	2.214300	3.6
min	1.000000	1.000000	1.000000	1.000000	1.000000	1.0(
25%	2.000000	1.000000	1.000000	1.000000	2.000000	1.0(
50%	4.000000	1.000000	1.000000	1.000000	2.000000	1.0(
75%	6.000000	5.000000	5.000000	4.000000	4.000000	6.0(
max	10.000000	10.000000	10.000000	10.000000	10.000000	10.0(

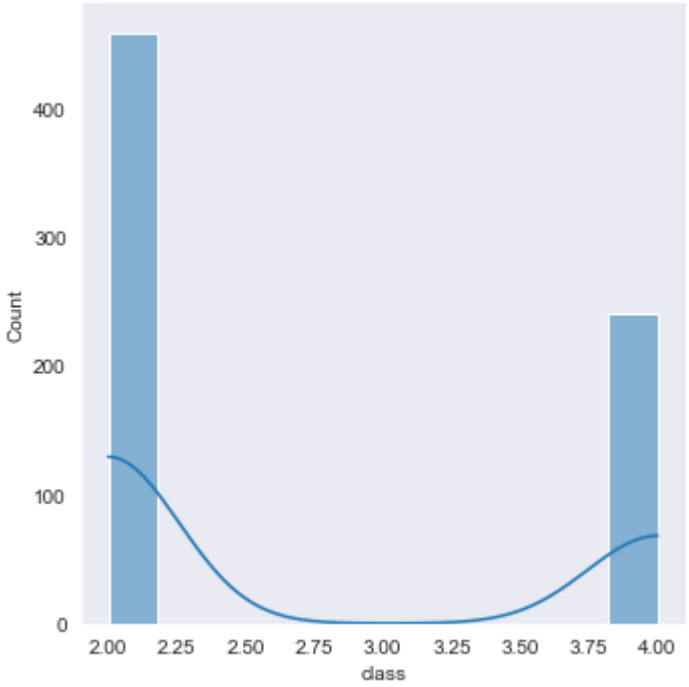
Data Visualization

1. Bivariate Data Analysis

Histogram plot with KDE

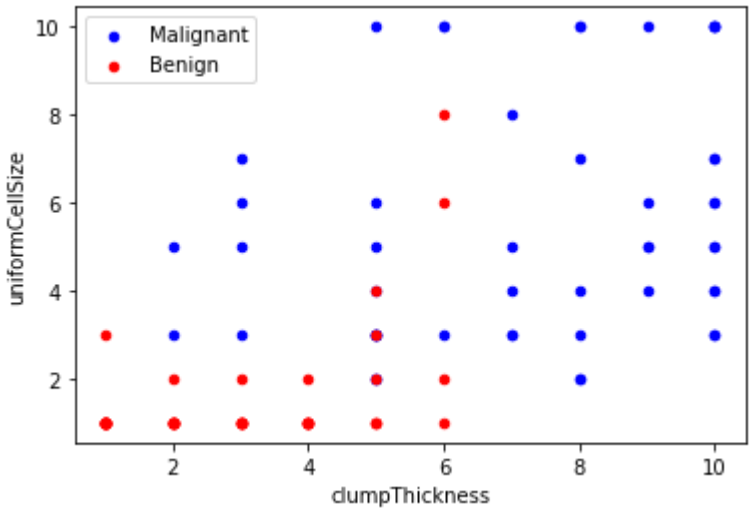
In [38]:
```
sns.displot(bCancerDF['class'],kde=True)
```

Out[38]:
```
<seaborn.axisgrid.FacetGrid at 0x12eb24ca620>
```



Scatter plot with hue

In [23]:
```
# showing scatter plot for clumpThickness and unifromCellSize between the two classes
ax = bCancerDF[bCancerDF['class'] == 4][0:50].plot(kind='scatter', x='clumpThickness', y='uniformCellSiz
bCancerDF[bCancerDF['class'] == 2][0:50].plot(kind='scatter', x='clumpThickness', y='uniformCellSize', co
plt.show()
```

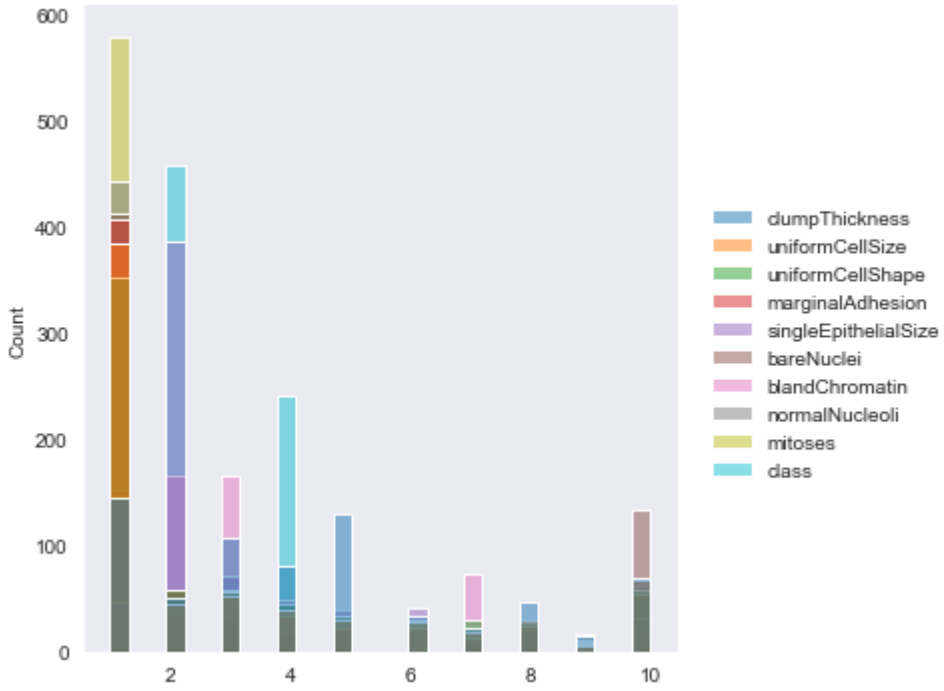


2. Multivariate Data Analysis

single histogram for all variables

In [40]:
```
sns.displot(data=bCancerDF)
```

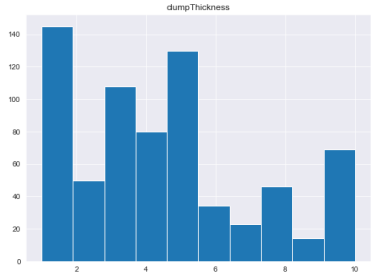
Out[40]:
```
<seaborn.axisgrid.FacetGrid at 0x12eb8328190>
```

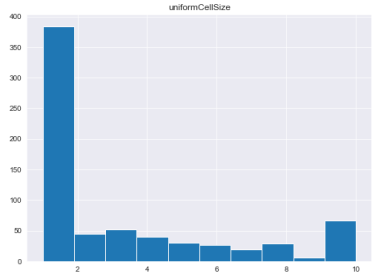


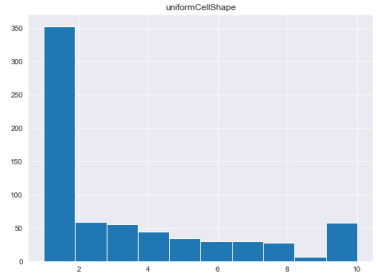
Histograms for each attribute

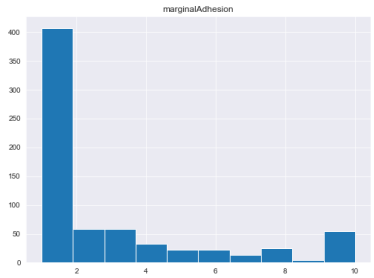
In [41]:

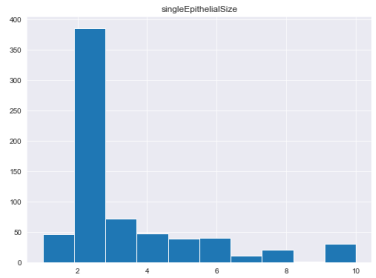
```
sns.set_style('dark')
bCancerDF.hist(figsize=(30,30))
plt.show()
```

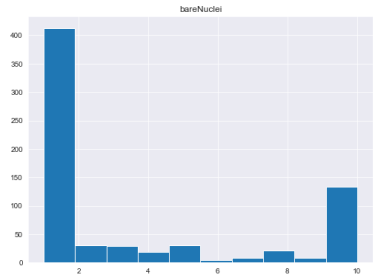


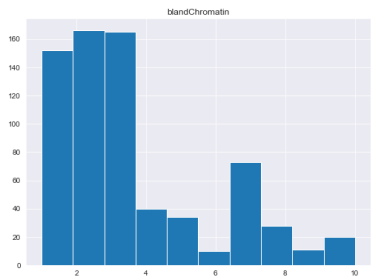


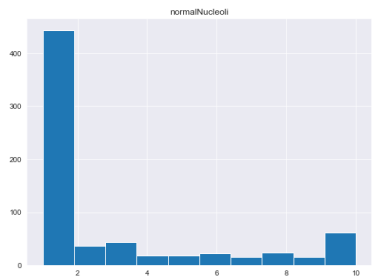


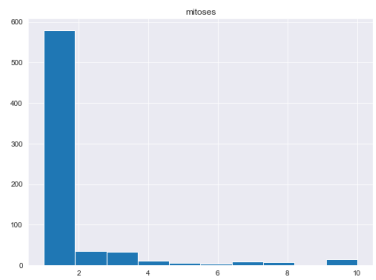


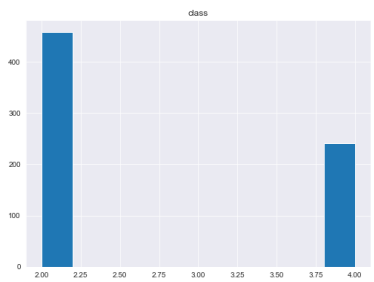








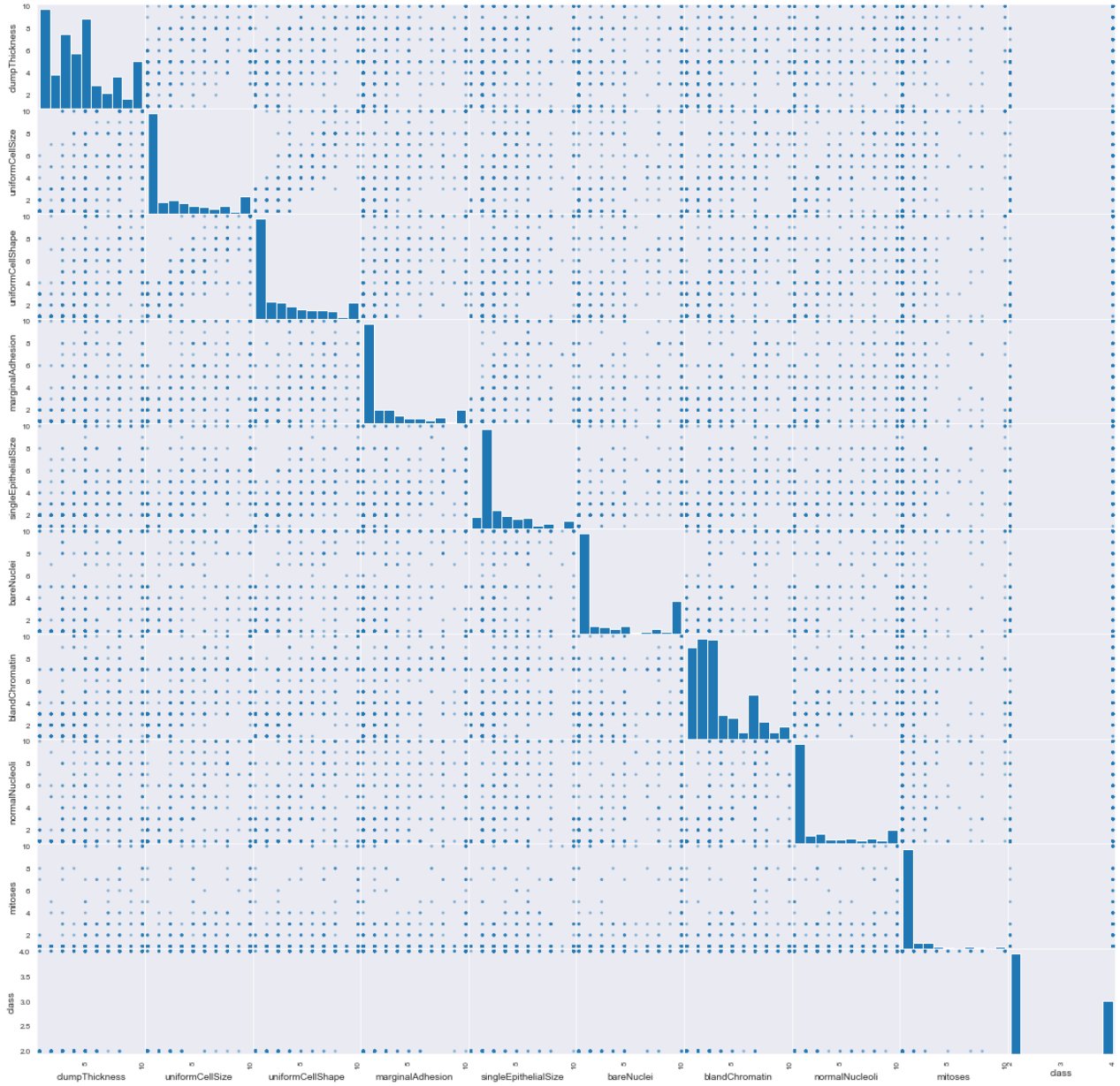




Scatter plot matrix

In [42]:

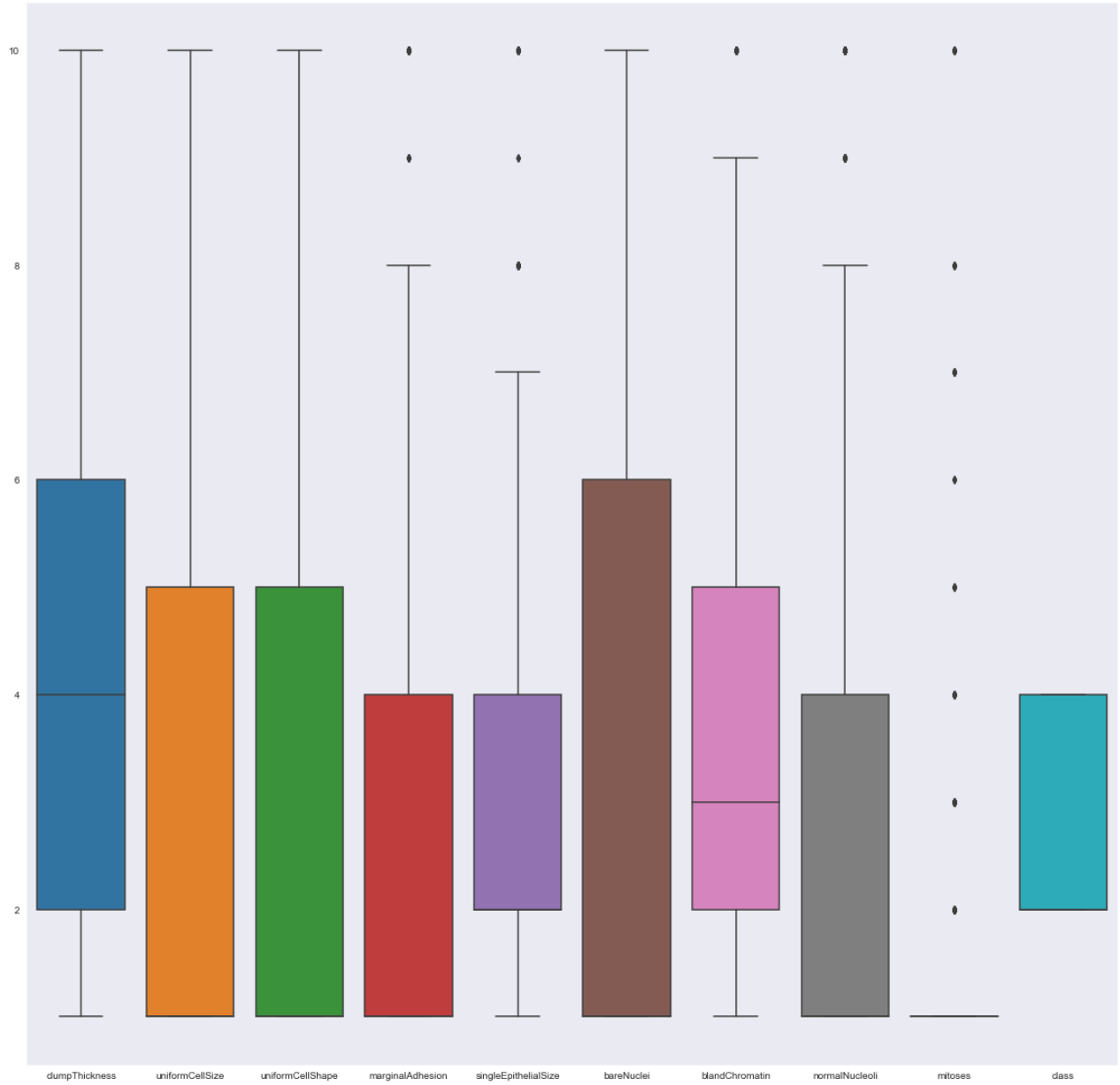
```
scatter_matrix(bCancerDF, figsize = (20,20))
plt.show()
```



Box plot (vertial orientation)

In [44]:
```
plt.figure(figsize=(20,20))
sns.boxplot(data=bCancerDF)
```

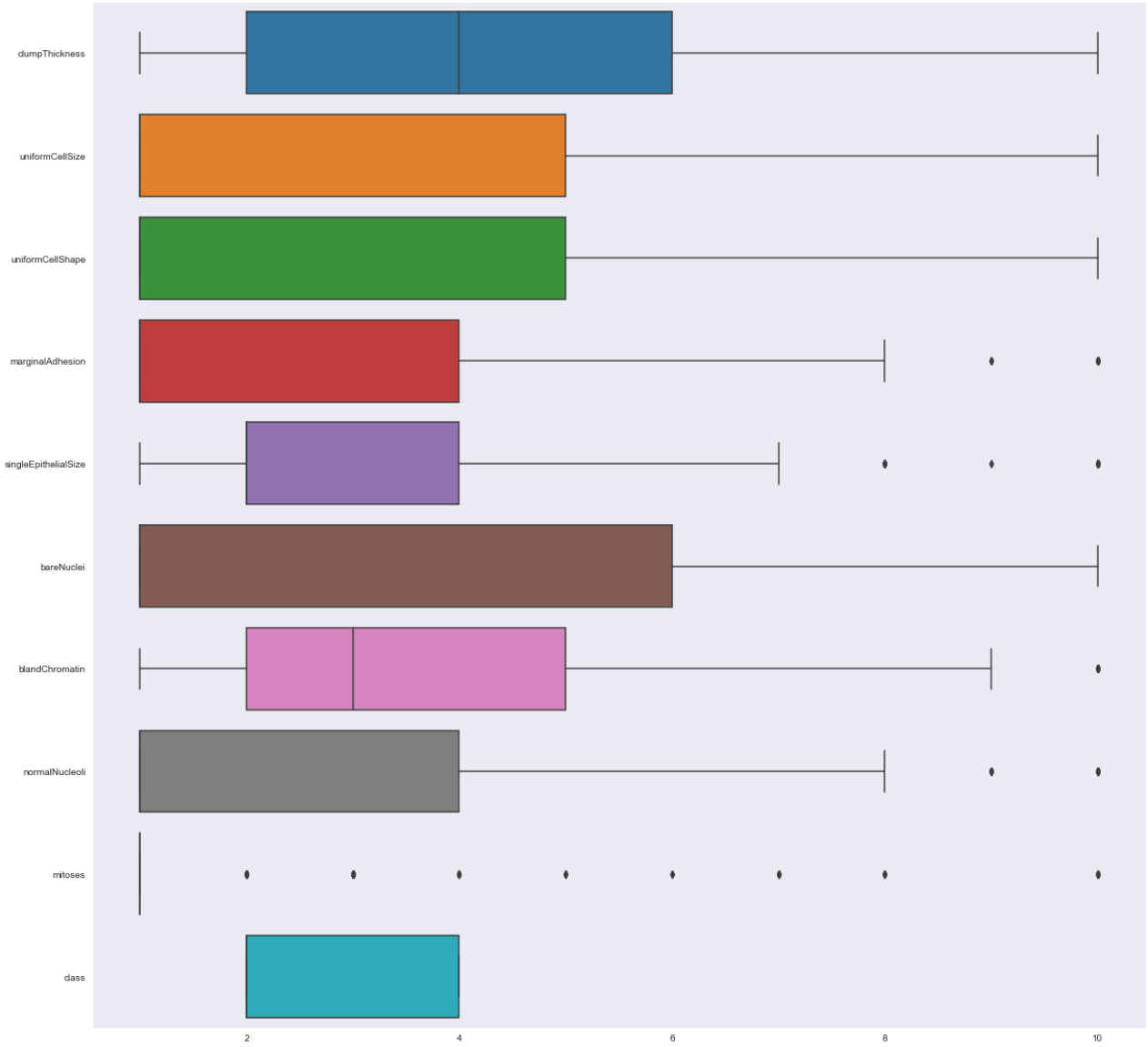
Out[44]: <AxesSubplot:>



Box plot with horizontal orientation

In [45]:
```
plt.figure(figsize=(20,20))
sns.boxplot(data=bCancerDF, orient='h')
```

Out[45]: <AxesSubplot:>



Feature selection

Correlation chart

In [47]:
```
coR = bCancerDF.corr()
coR
```

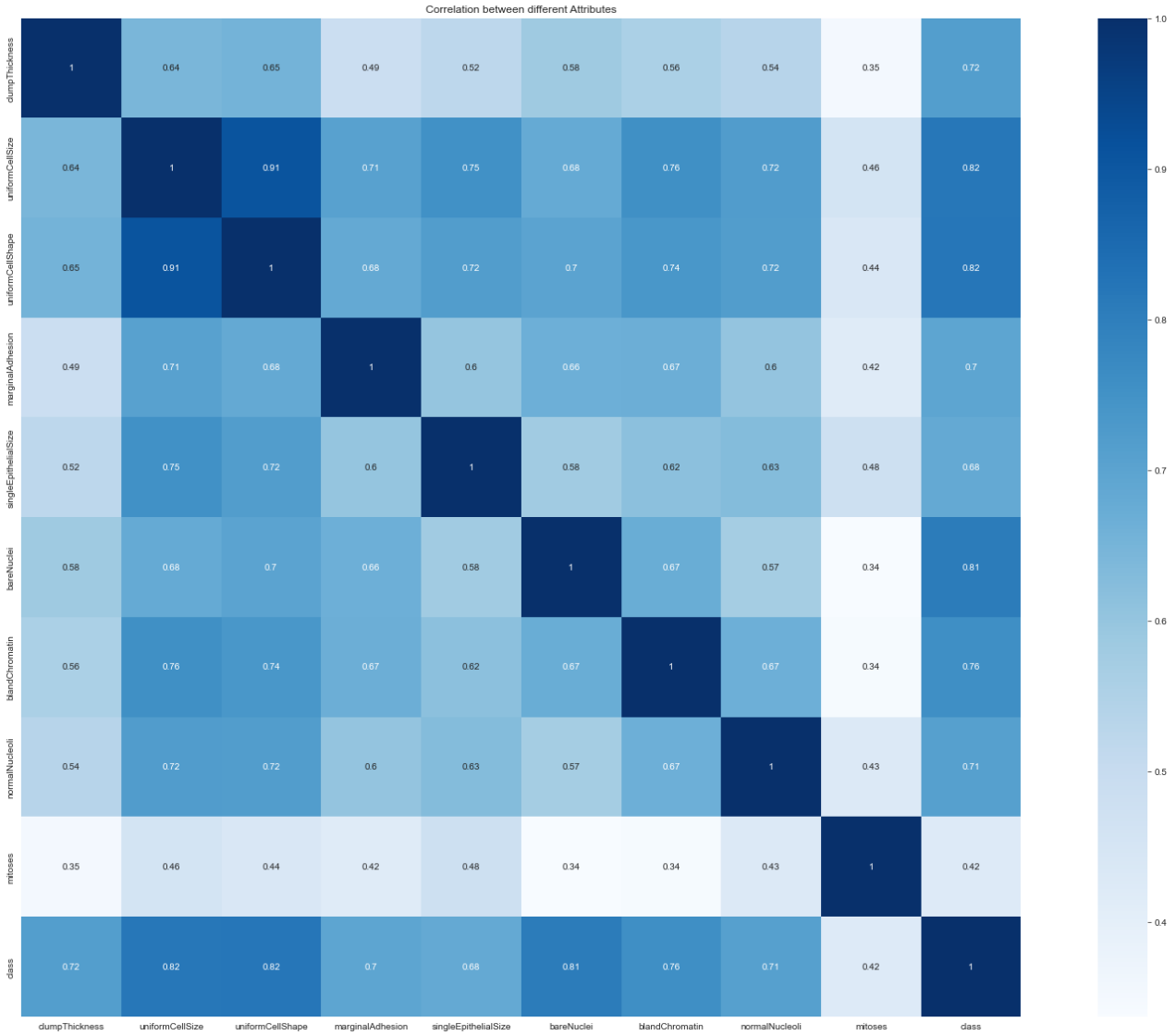
Out[47]:

	clumpThickness	uniformCellSize	uniformCellShape	marginalAdhesion	singleEpitheli
clumpThickness	1.000000	0.644913	0.654589	0.486356	0.5
uniformCellSize	0.644913	1.000000	0.906882	0.705582	0.7
uniformCellShape	0.654589	0.906882	1.000000	0.683079	0.7
marginalAdhesion	0.486356	0.705582	0.683079	1.000000	0.5
singleEpithelialSize	0.521816	0.751799	0.719668	0.599599	1.0
bareNuclei	0.583571	0.681309	0.701137	0.663669	0.5
blandChromatin	0.558428	0.755721	0.735948	0.666715	0.6

	clumpThickness	uniformCellSize	uniformCellShape	marginalAdhesion	singleEpitheli
normalNucleoli	0.535835	0.722865	0.719446	0.603352	0.6
mitoses	0.350034	0.458693	0.438911	0.417633	0.4
class	0.716001	0.817904	0.818934	0.696800	0.6

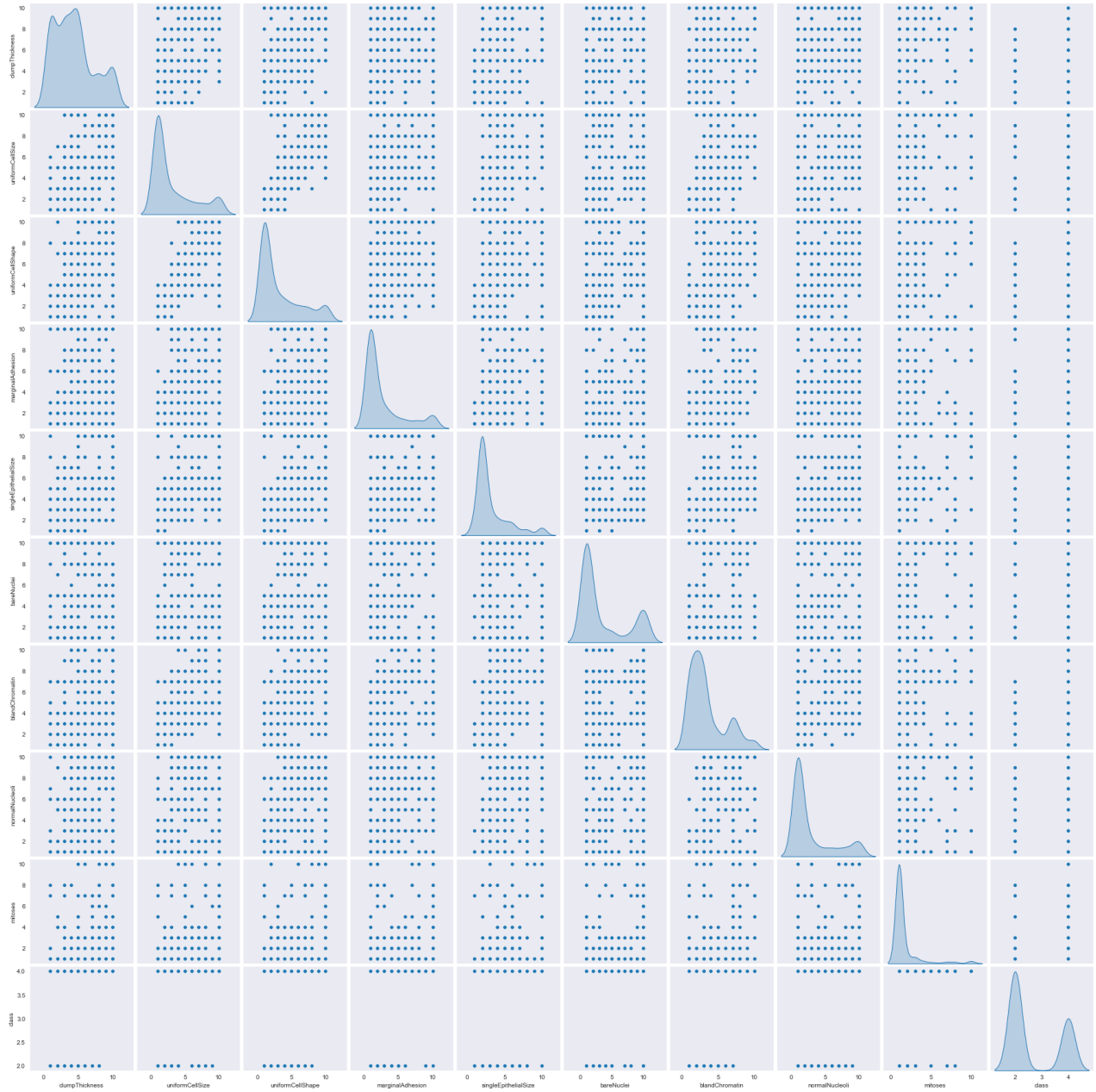
Heatmap

In [49]:
```
plt.figure(figsize=(30,20))
sns.heatmap(coR,vmax=1, square = True, annot=True, cmap=plt.cm.Blues)
plt.title('Correlation between different Attributes')
plt.show()
```



Pairplot

In [50]:
```
sns.pairplot(bCancerDF,diag_kind='kde')
plt.show()
```



Correlation with output

Correlation with output variable

In [51]:
```
cor_target = abs(coR["class"])
#Selecting highly correlated features
relevant_features = cor_target[cor_target>0]
relevant_features
```

Out[51]:
```
clumpThickness       0.716001
uniformCellSize      0.817904
uniformCellShape     0.818934
marginalAdhesion     0.696800
singleEpithelialSize 0.682785
bareNuclei           0.807394
blandChromatin       0.756616
normalNucleoli       0.712244
mitoses              0.423170
```

```
class           1.000000
Name: class, dtype: float64
```

Train and Test Model

Splitting

In [53]:
```
# Split the data first into predictor and target variable
# Then by train and test sets.

# everything except 'Class' attribute
X = bCancerDF.drop('class', axis=1).values
Y = bCancerDF['class'].values

# Splitting by 70% for train and 30% for test
X_train, X_test, Y_train, Y_test = train_test_split (X, Y, test_size = 0.30, random_state=21)
```

In [58]:
```
# Testing Options
scoring = 'accuracy'
```

Model Selection

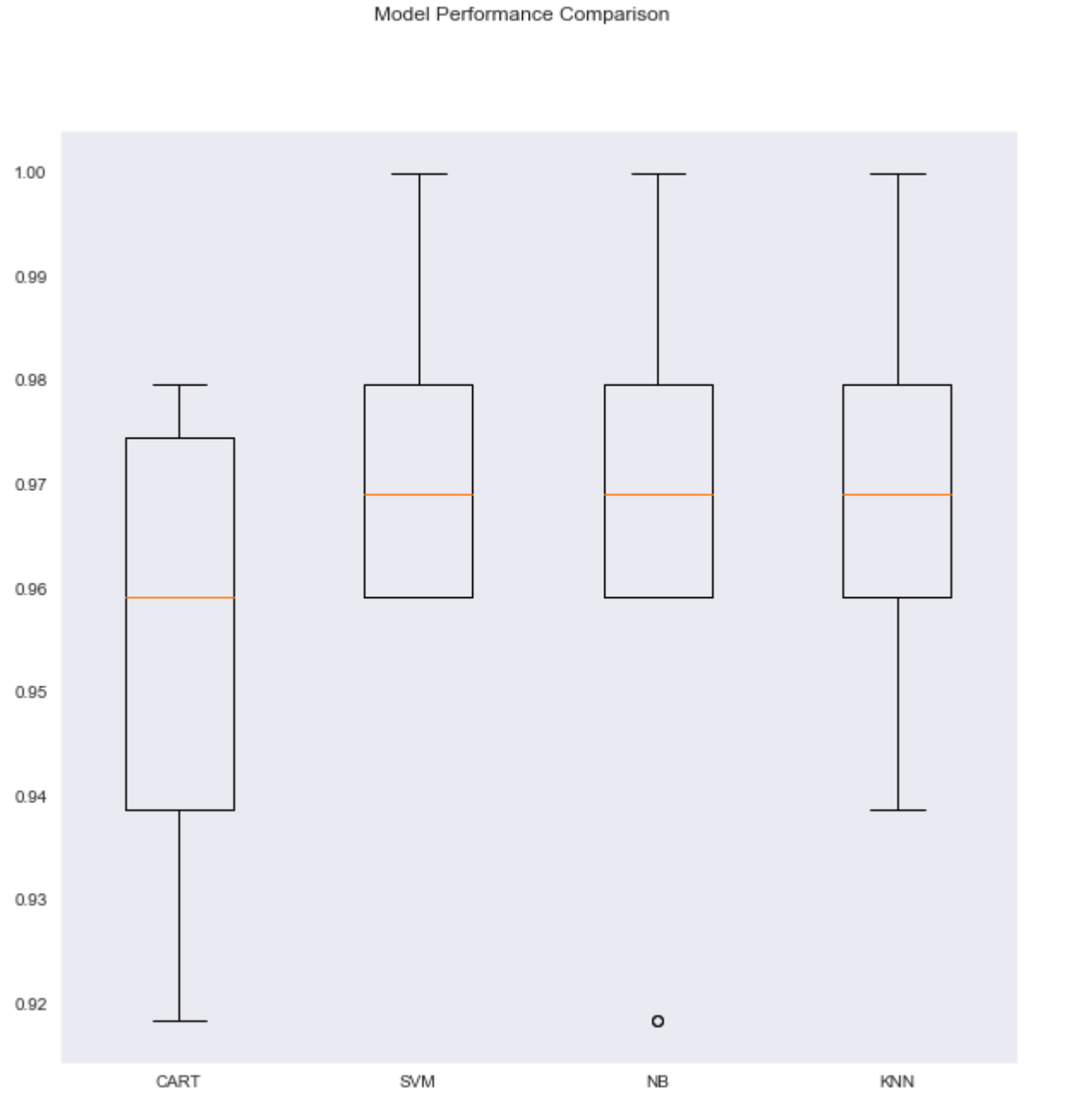
1. Decision Tree
2. support Vector Machine
3. Gaussian Naive Bayes
4. KNN', K-Nearest Neighbors

In [61]:
```
# Define models to train
models= []
models.append(('CART', DecisionTreeClassifier()))
models.append(('SVM', SVC()))
models.append(('NB', GaussianNB()))
models.append(('KNN', KNeighborsClassifier()))

# evaluate each model in turn
results = []
names = []

for name, model in models:
   kfold = KFold(n_splits=10)
   cv_results = cross_val_score(model, X_train, Y_train, cv=kfold, scoring=scoring)
   results.append(cv_results)
   names.append(name)
   msg = "For %s Model:Mean accuracy is %f (Std accuracy is %f)" % (name, cv_results.mean(), cv_results.st
   print(msg)
```

```
For CART Model:Mean accuracy is 0.954974 (Std accuracy is 0.020103)
For SVM Model:Mean accuracy is 0.971386 (Std accuracy is 0.013512)
For NB Model:Mean accuracy is 0.963223 (Std accuracy is 0.025463)
For KNN Model:Mean accuracy is 0.969345 (Std accuracy is 0.016428)
```

In [64]:
```
fig = plt.figure(figsize=(10,10))
```

```
fig.suptitle('Model Performance Comparison')
ax = fig.add_subplot(111)
plt.boxplot(results)
ax.set_xticklabels(names)
plt.show()
```



In [65]:

```
# Make predictions on validation dataset

for name, model in models:
    model.fit(X_train, Y_train)
    predictions = model.predict(X_test)
    print("\nModel:",name)
    print("Accuracy score:",accuracy_score(Y_test, predictions))
    print("Classification report:\n",classification_report(Y_test, predictions))

# Accuracy - ratio of correctly predicted observation to the total observations.
# Precision - (false positives) ratio of correctly predicted positive observations to the total predicted positiv
```

```
# Recall (Sensitivity) - (false negatives) ratio of correctly predicted positive observations to the all observat
# F1 score - F1 Score is the weighted average of Precision and Recall. Therefore, this score takes both false p
```

Model: CART
Accuracy score: 0.9047619047619048
Classification report:

	precision	recall	f1-score	support
2	0.90	0.96	0.93	133
4	0.93	0.81	0.86	77
accuracy			0.90	210
macro avg	0.91	0.88	0.89	210
weighted avg	0.91	0.90	0.90	210

Model: SVM
Accuracy score: 0.9714285714285714
Classification report:

	precision	recall	f1-score	support
2	0.98	0.98	0.98	133
4	0.96	0.96	0.96	77
accuracy			0.97	210
macro avg	0.97	0.97	0.97	210
weighted avg	0.97	0.97	0.97	210

Model: NB
Accuracy score: 0.9523809523809523
Classification report:

	precision	recall	f1-score	support
2	0.96	0.96	0.96	133
4	0.94	0.94	0.94	77
accuracy			0.95	210
macro avg	0.95	0.95	0.95	210
weighted avg	0.95	0.95	0.95	210

Model: KNN
Accuracy score: 0.9571428571428572
Classification report:

	precision	recall	f1-score	support
2	0.96	0.97	0.97	133
4	0.95	0.94	0.94	77
accuracy			0.96	210
macro avg	0.96	0.95	0.95	210
weighted avg	0.96	0.96	0.96	210

Support Vector Machine

AS SVC has the highest accuracy score in prediction, we are selecting it for test score

Test Accuracy

In [93]:
```
clf = SVC()

clf.fit(X_train, Y_train)
accuracy = clf.score(X_test, Y_test)
print("Test Accuracy:",accuracy)

predict = clf.predict(X_test)
```

Test Accuracy: 0.9714285714285714

Example Prediction

In [86]:
```
example_measures = [[4,2,1,9,1,2,3,2,9]]
prediction = clf.predict(example_measures)
prediction
```

Out[86]: array([4], dtype=int64)

Bengin or Malignant?

In [87]:
```
if (prediction == 2):
    print('Benign')
else:
    print('Malignant')
```

Malignant

Confusion Matrix

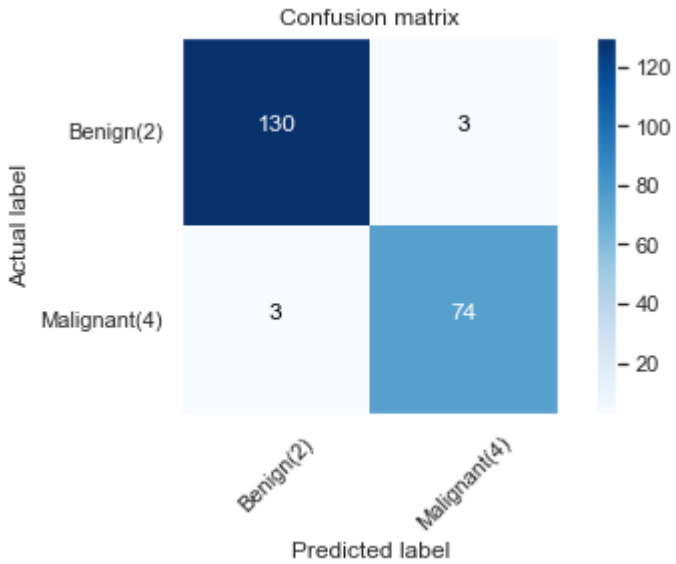
In [94]:
```
import itertools
sns.set_theme(style="dark")
def plot_confusion_matrix(cm, classes, normalize=False,title='Confusion matrix', cmap=plt.cm.Blues):
    """
    Prints and plots the confusion matrix.
    Normalization can be applied by setting `normalize=True`.
    """

    if normalize:
        cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
        print("Normalized confusion matrix")
    else:
        print('Confusion matrix, without normalization')

    print(cm)

    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.title(title)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    fmt = '.2f' if normalize else 'd'
```

```
    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, format(cm[i, j], fmt),
                 horizontalalignment="center",
                 color="white" if cm[i, j] > thresh else "black")

    plt.tight_layout()
    plt.ylabel('Actual label')
    plt.xlabel('Predicted label')
```

In [92]:

```
# Compute confusion matrix
cnf_matrix = confusion_matrix(Y_test, predict, labels=[2,4])
np.set_printoptions(precision=2)

print (classification_report(Y_test, predict))

# Plot non-normalized confusion matrix
plt.figure()
plot_confusion_matrix(cnf_matrix, classes=['Benign(2)','Malignant(4)'],normalize= False,  title='Confusio
```

```
              precision    recall  f1-score   support

           2       0.98      0.98      0.98       133
           4       0.96      0.96      0.96        77

    accuracy                           0.97       210
   macro avg       0.97      0.97      0.97       210
weighted avg       0.97      0.97      0.97       210

Confusion matrix, without normalization
[[130   3]
 [  3  74]]
```



Conclusion

We had Wisconsin Breast Cancer Database with 699 records on 11 columns.

Attributes at column indices 2 through 10 have been used to represent instances.

- Each instance has one of 2 possible classes: benign or malignant.
- These classes was included as attribute at column index 11

Class distribution was:

1. Benign: 458 (65.5%)
2. Malignant: 241 (34.5%)

After processing data and obtaining analysis from it, we split the dataset into train-test of 70%-30%. we trained four models. By far, SVM model had highest accuracy for training and test data.