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

In [2]:
```
df_bc = pd.read_csv('breast-cancer-data.csv')
```

In [3]:
```
df_bc.shape
```

Out[3]:
```
(569, 32)
```

In [4]:
```
df_bc.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 32 columns):
id                         569 non-null int64
diagnosis                  569 non-null object
radius_mean                569 non-null float64
texture_mean               569 non-null float64
perimeter_mean             569 non-null float64
area_mean                  569 non-null float64
smoothness_mean            569 non-null float64
compactness_mean           569 non-null float64
concavity_mean             569 non-null float64
concave points_mean        569 non-null float64
symmetry_mean              569 non-null float64
fractal_dimension_mean     569 non-null float64
radius_se                  569 non-null float64
texture_se                 569 non-null float64
perimeter_se               569 non-null float64
area_se                    569 non-null float64
smoothness_se              569 non-null float64
compactness_se             569 non-null float64
concavity_se               569 non-null float64
concave points_se          569 non-null float64
symmetry_se                569 non-null float64
fractal_dimension_se       569 non-null float64
radius_worst               569 non-null float64
texture_worst              569 non-null float64
perimeter_worst            569 non-null float64
area_worst                 569 non-null float64
smoothness_worst           569 non-null float64
compactness_worst          569 non-null float64
concavity_worst            569 non-null float64
concave points_worst       569 non-null float64
symmetry_worst             569 non-null float64
fractal_dimension_worst    569 non-null float64
dtypes: float64(30), int64(1), object(1)
memory usage: 142.3+ KB
```

In [5]:
```
df_bc.head()
```

Out[5]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_
0	842302	M	17.99	10.38	122.80	1001.0	0
1	842517	M	20.57	17.77	132.90	1326.0	0
2	84300903	M	19.69	21.25	130.00	1203.0	0
3	84348301	M	11.42	20.38	77.58	386.1	0
4	84358402	M	20.29	14.34	135.10	1297.0	0

5 rows × 32 columns

In [6]:
```
#Checking missing values
df_bc.isnull().sum()
```

Out[6]:
```
id                         0
diagnosis                  0
radius_mean                0
texture_mean               0
perimeter_mean             0
area_mean                  0
smoothness_mean            0
compactness_mean           0
concavity_mean             0
concave points_mean        0
symmetry_mean              0
fractal_dimension_mean     0
radius_se                  0
texture_se                 0
perimeter_se               0
area_se                    0
smoothness_se              0
compactness_se             0
concavity_se               0
concave points_se          0
symmetry_se                0
fractal_dimension_se       0
radius_worst               0
texture_worst              0
perimeter_worst            0
area_worst                 0
smoothness_worst           0
compactness_worst          0
concavity_worst            0
concave points_worst       0
symmetry_worst             0
fractal_dimension_worst    0
dtype: int64
```

In [7]:
```
#Observation:
## There are no mising values
## diagnosis column is the categorical field which says whether the dig
nosis is malignant (M) or benign (B)
# total 32 columns, but id colum can be drop that makes it to 31 column
s including the target variable = 'Diagnosis
```

In [8]:
```
#dropping the id col

df_bc.drop(['id'],axis=1,inplace=True)
```

In [9]:
```
df_bc.head(2)
```

Out[9]:

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	cor
0	M	17.99	10.38	122.8	1001.0	0.11840	
1	M	20.57	17.77	132.9	1326.0	0.08474	

2 rows × 31 columns

In [10]:
```
df_bc.shape
```

Out[10]:
```
(569, 31)
```

In [11]:
```
# checking how many malignant or benign in the dataset
df_bc['diagnosis'].value_counts()
```

Out[11]:
```
B    357
M    212
Name: diagnosis, dtype: int64
```

In [12]:
```
df_bc['diagnosis'].value_counts()/df_bc.shape[0]
```

Out[12]:
```
B    0.627417
M    0.372583
Name: diagnosis, dtype: float64
```

Observation: we have good split of the diagnosis in the data sets

63% benign

37 % malignant

In [14]:
```
# Converting the diagnosis in to column 1/0 using one hot encoding


df_bc = pd.get_dummies(columns=['diagnosis'], data=df_bc,drop_first=True)
```

In [15]:
```
df_bc.head()
```

Out[15]:

	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_
0	17.99	10.38	122.80	1001.0	0.11840	0.2
1	20.57	17.77	132.90	1326.0	0.08474	0.0
2	19.69	21.25	130.00	1203.0	0.10960	0.1
3	11.42	20.38	77.58	386.1	0.14250	0.2
4	20.29	14.34	135.10	1297.0	0.10030	0.1

5 rows × 31 columns

In [16]:
```
df_bc['diagnosis_M'].unique()
```

Out[16]:
```
array([1, 0], dtype=uint64)
```

In [17]:
```
df_bc.shape
```

Out[17]:
```
(569, 31)
```

In [21]:
```
df_bc.rename(columns={'diagnosis_M':'target'},inplace=True)
```

In [22]:
```
df_bc.head()
```

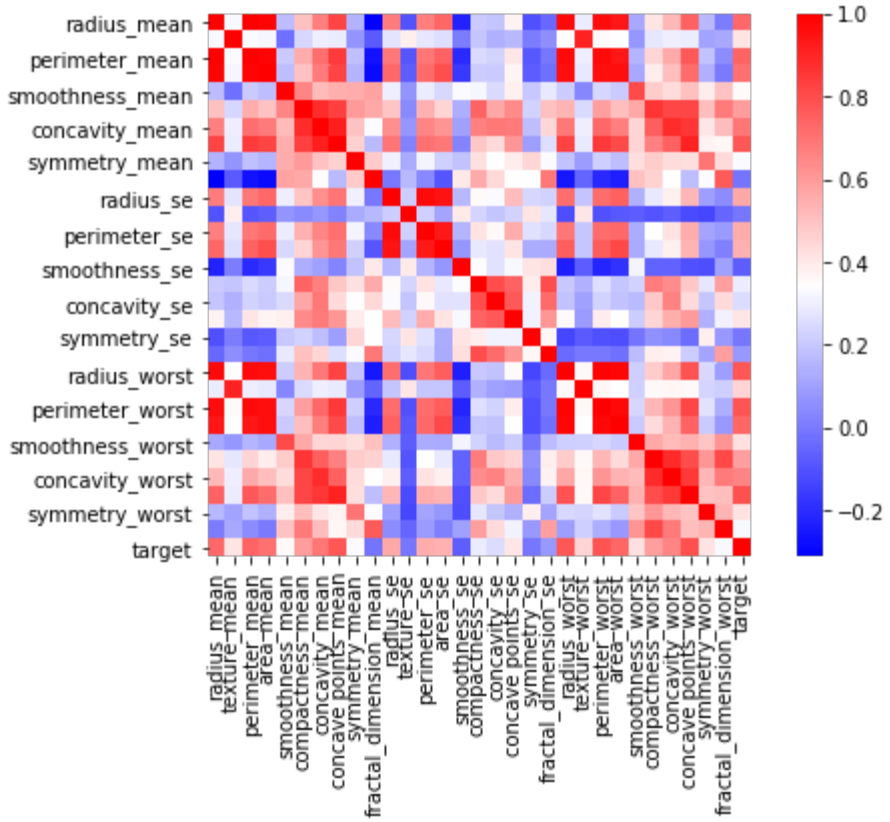
Out[22]:

	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_
0	17.99	10.38	122.80	1001.0	0.11840	0.2
1	20.57	17.77	132.90	1326.0	0.08474	0.0
2	19.69	21.25	130.00	1203.0	0.10960	0.1
3	11.42	20.38	77.58	386.1	0.14250	0.2
4	20.29	14.34	135.10	1297.0	0.10030	0.1

5 rows × 31 columns

In [24]:
```
plt.figure(figsize=(8,5))
sns.heatmap(df_bc.corr(),square=True, cmap='bwr')
plt.show
```

Out[24]:
```
<function matplotlib.pyplot.show(*args, **kw)>
```



Observations: from the chart we do see that there are quite a few variables which seems to have a high correlation among them.

In [28]:
```
X = df_bc.drop(['target'],axis=1)
y = df_bc['target']
```

In [33]:
```
print(X.shape)
print(y.shape)
```

```
(569, 30)
(569,)
```

In [26]:
```
#Scaling the data so that each feature has a single unit variance
from sklearn.preprocessing import StandardScaler
```

In [34]:
```
scaler = StandardScaler()
```

In [75]:
```
scaler.fit(X)
```

Out[75]:
```
StandardScaler(copy=True, with_mean=True, with_std=True)
```

In [76]:
```
X_scaled = scaler.transform(X)
```

In [77]:
```
X_scaled
```

Out[77]:
```
array([[ 1.09706398, -2.07333501,  1.26993369, ...,  2.29607613,
         2.75062224,  1.93701461],
       [ 1.82982061, -0.35363241,  1.68595471, ...,  1.0870843 ,
        -0.24388967,  0.28118999],
       [ 1.57988811,  0.45618695,  1.56650313, ...,  1.95500035,
         1.152255  ,  0.20139121],
       ...,
       [ 0.70228425,  2.0455738 ,  0.67267578, ...,  0.41406869,
        -1.10454895, -0.31840916],
       [ 1.83834103,  2.33645719,  1.98252415, ...,  2.28998549,
         1.91908301,  2.21963528],
       [-1.80840125,  1.22179204, -1.81438851, ..., -1.74506282,
        -0.04813821, -0.75120669]])
```

In [78]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X_scaled,y,train_si
ze=0.7, random_state=42)
```

```
C:\Users\SujitSonar\Anaconda3\lib\site-packages\sklearn\model_selecti
on\_split.py:2179: FutureWarning: From version 0.21, test_size will a
lways complement train_size unless both are specified.
  FutureWarning)
```

In [79]:
```
print(X_train.shape)
print(X_test.shape)
print(y_train.shape)
print(y_test.shape)
```

```
(398, 30)
(171, 30)
(398,)
(171,)
```

In [83]:
```
from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
lr.fit(X_train, y_train)
y_pred = lr.predict(X_test)
```

```
C:\Users\SujitSonar\Anaconda3\lib\site-packages\sklearn\linear_model\
logistic.py:433: FutureWarning: Default solver will be changed to 'lb
fgs' in 0.22. Specify a solver to silence this warning.
  FutureWarning)
```

In [84]:
```
y_pred[0:10]
```

Out[84]:
```
array([0, 1, 1, 0, 0, 1, 1, 1, 0, 0], dtype=uint8)
```

In [56]:
```
from sklearn.metrics import accuracy_score, confusion_matrix
```

In [85]:
```
print(accuracy_score(y_pred, y_test))
print(confusion_matrix(y_pred, y_test))
```

```
0.9824561403508771
[[106   1]
 [  2  62]]
```

In [54]:
```
# without any feature enginerrin we get the acuracy of 98%
```

PCA with 2 components

In [55]:
```
#Transform this data to its first 2 principal components.
```

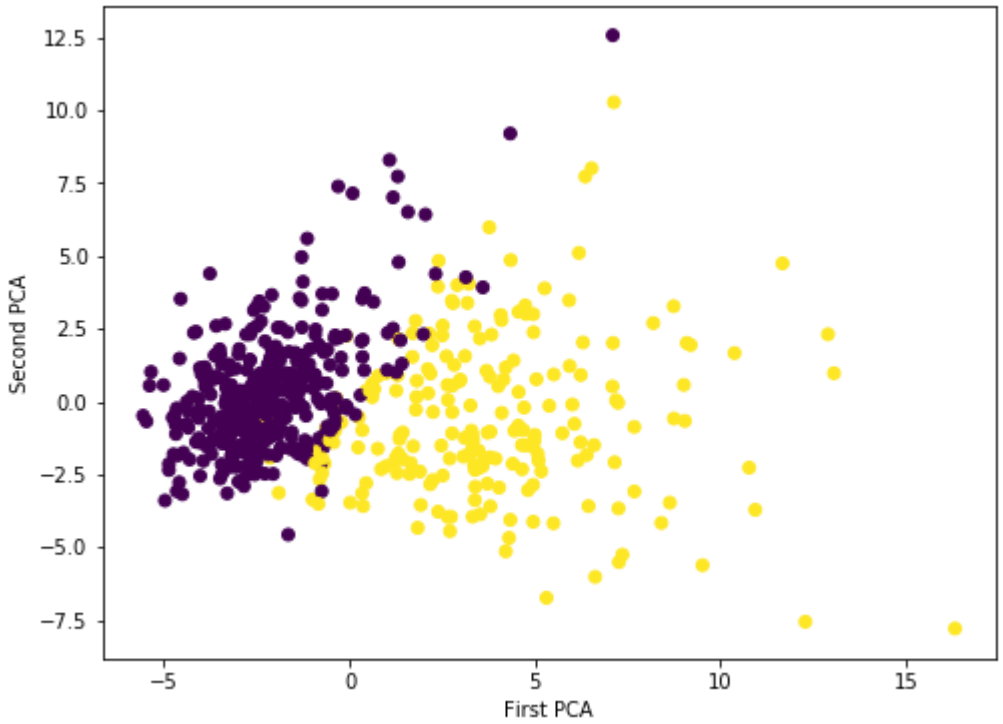
In [119]:
```
from sklearn.decomposition import PCA
pca_2 = PCA(n_components=2)
pca_2.fit(X_scaled)

X_scaled_pca_2 = pca_2.transform(X_scaled)

X_scaled_pca_2.shape
```

Out[119]:
```
(569, 2)
```

In [120]:
```
X_scaled_pca_2
```

Out[120]:
```
array([[ 9.19283683,  1.94858307],
       [ 2.3878018 , -3.76817174],
       [ 5.73389628, -1.0751738 ],
       ...,
       [ 1.25617928, -1.90229671],
       [10.37479406,  1.67201011],
       [-5.4752433 , -0.67063679]])
```

In [121]:
```
# Plot the two dimensions.
plt.figure(figsize=(8,6))
plt.scatter(X_scaled_pca_2[:,0],X_scaled_pca_2[:,1],c=y,cmap='viridis
')
plt.xlabel('First PCA')
plt.ylabel('Second PCA')
plt.show()
```



In [113]:
```
#Print the explained variance.
print(pca_2.explained_variance_)
print(pca_2.explained_variance_ratio_)
```

```
[13.30499079  5.7013746 ]
[0.44272026 0.18971182]
```

In [ ]:
```
#Modelling with 2 PCA
```

In [122]:
```
X_train_pca, X_test_pca, y_train_pca, y_test_pca = train_test_split(X_
scaled_pca_2, y, train_size=0.7, random_state=42)
```

```
C:\Users\SujitSonar\Anaconda3\lib\site-packages\sklearn\model_selecti
on\_split.py:2179: FutureWarning: From version 0.21, test_size will a
lways complement train_size unless both are specified.
  FutureWarning)
```

In [123]:
```
print(X_train_pca.shape)
print(X_test_pca.shape)
print(y_train_pca.shape)
print(y_test_pca.shape)
```

```
(398, 2)
(171, 2)
(398,)
(171,)
```

In [124]:
```
lr_pca = LogisticRegression()
lr_pca.fit(X_train_pca, y_train_pca)
y_pred_pca = lr_pca.predict(X_test_pca)
```

```
C:\Users\SujitSonar\Anaconda3\lib\site-packages\sklearn\linear_model\
logistic.py:433: FutureWarning: Default solver will be changed to 'lb
fgs' in 0.22. Specify a solver to silence this warning.
  FutureWarning)
```

In [125]:
```
print(accuracy_score(y_pred_pca,y_test_pca))
```

```
0.9707602339181286
```

PCA with 3 components

In [126]:
```
## PCA with 3 components

pca_3 = PCA(n_components=3)
pca_3.fit(X_scaled)

X_scaled_pca_3 = pca_3.transform(X_scaled)

X_scaled_pca_3.shape
```

Out[126]:
```
(569, 3)
```

In [127]:
```
X_scaled_pca_3
```

Out[127]:
```
array([[ 9.19283683,  1.94858307, -1.12316571],
       [ 2.3878018 , -3.76817174, -0.52929237],
       [ 5.73389628, -1.0751738 , -0.55174764],
       ...,
       [ 1.25617928, -1.90229671,  0.56273032],
       [10.37479406,  1.6720101 , -1.87702938],
       [-5.4752433 , -0.67063679,  1.4904437 ]])
```

In [128]:
```
#Print the explained variance.
print(pca_3.explained_variance_)
print(pca_3.explained_variance_ratio_)
```

```
[13.30499079  5.7013746   2.82291015]
[0.44272026 0.18971182 0.09393163]
```

In [129]:
```
## Modelling with 3 PCA
```

In [130]:
```
X_train_pca_3, X_test_pca_3, y_train_pca_3, y_test_pca_3 = train_test_
split(X_scaled_pca_3, y, train_size=0.7, random_state=42)
```

```
C:\Users\SujitSonar\Anaconda3\lib\site-packages\sklearn\model_selecti
on\_split.py:2179: FutureWarning: From version 0.21, test_size will a
lways complement train_size unless both are specified.
  FutureWarning)
```

In [131]:
```
lr_pca_3 = LogisticRegression()
lr_pca_3.fit(X_train_pca_3, y_train_pca_3)
y_pred_pca_3 = lr_pca_3.predict(X_test_pca_3)
```

```
C:\Users\SujitSonar\Anaconda3\lib\site-packages\sklearn\linear_model\
logistic.py:433: FutureWarning: Default solver will be changed to 'lb
fgs' in 0.22. Specify a solver to silence this warning.
  FutureWarning)
```

In [132]:
```
accuracy_score(y_pred_pca_3, y_test_pca_3)
```

Out[132]:
```
0.9707602339181286
```

In [134]:
```
# Observation: accuracy score from PCA 2 and PCA 3 has no change and a
ccuracy score (97%) is slighly low
#compared to accuracy score without any PCA ( 98%)
```

In [ ]:
```

```