Coursework One - Q3 - Wisconsin Cancer - Student

Please List Members of Team and Student IDs below:

Member 1: Marcel Santos de Carvalho 79083

Member 2: Loris Baudry 79794

Member 3: Alejandro Palacios García 73713

Which member of the team is responsible for this notebook: Alejandro Palacios García

Instructions

This is a well-known dataset on predicting cancer. It involves the analysis of tumours. A tumour can be benign (not cancerous) or malignant (cancerous). Using various geometrical measurements of actual tumours, the objective is to determine whether or not a tumour is benign or malignant.

The purpose of this question is to find the best model for predicting malignancy correctly. The data is provided by Sklearn using

from sklearn.datasets import load_breast_cancer

Some of the data fields are differently scaled values. In the following you are to

1. Load the data from Scikit learn using

from sklearn.datasets import load_breast_cancer

data = load_breast_cancer()

1. **Examine the dataframe for missing data and decide how to treat these**
2. **Try to see which features have the best explanatory power.**
3. **Also, deal with categorical data and use feature standardization**
4. **Choose metrics for model evaluation**
5. **Use the following models - Logistic Regression, KNN (test for different values of K), Decision Tree and SVM Classifier**
6. **Use training and testing to identify the best model**
7. **Write a summary explaining your results.**

In [3]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
plt.style.use('seaborn')
```

```
%matplotlib inline
%pip install graphviz
```

```
Requirement already satisfied: graphviz in c:\users\apala\anaconda3\lib\site-packages
(0.17)
Note: you may need to restart the kernel to use updated packages.
```

1.- Data import

In [5]:
```
from sklearn.datasets import load_breast_cancer
data=load_breast_cancer()
```

2.- Data Visualization and Analysis

2.1 Data Description

The Breast Cancer Dataset is comprised by 569 observations of 30 features and 2 labels. The classes are Malignant (0) and Bening (1). From the 30 features, all of them are numerical and there is no missing date in any of the features observations. Nonetheless, the scale of some features largly differs so we will standardize the features magnitude with the MinMax Scaling Method.

In [6]:
```
print(data.DESCR)
```

```
.. _breast_cancer_dataset:

Breast cancer wisconsin (diagnostic) dataset
--------------------------------------------

**Data Set Characteristics:**

    :Number of Instances: 569

    :Number of Attributes: 30 numeric, predictive attributes and the class

    :Attribute Information:
        - radius (mean of distances from center to points on the perimeter)
        - texture (standard deviation of gray-scale values)
        - perimeter
        - area
        - smoothness (local variation in radius lengths)
        - compactness (perimeter^2 / area - 1.0)
        - concavity (severity of concave portions of the contour)
        - concave points (number of concave portions of the contour)
        - symmetry
        - fractal dimension ("coastline approximation" - 1)

        The mean, standard error, and "worst" or largest (mean of the three
        worst/largest values) of these features were computed for each image,
        resulting in 30 features.  For instance, field 0 is Mean Radius, field
        10 is Radius SE, field 20 is Worst Radius.
```

- class:
    - WDBC-Malignant
    - WDBC-Benign

:Summary Statistics:

	Min	Max
radius (mean):	6.981	28.11
texture (mean):	9.71	39.28
perimeter (mean):	43.79	188.5
area (mean):	143.5	2501.0
smoothness (mean):	0.053	0.163
compactness (mean):	0.019	0.345
concavity (mean):	0.0	0.427
concave points (mean):	0.0	0.201
symmetry (mean):	0.106	0.304
fractal dimension (mean):	0.05	0.097
radius (standard error):	0.112	2.873
texture (standard error):	0.36	4.885
perimeter (standard error):	0.757	21.98
area (standard error):	6.802	542.2
smoothness (standard error):	0.002	0.031
compactness (standard error):	0.002	0.135
concavity (standard error):	0.0	0.396
concave points (standard error):	0.0	0.053
symmetry (standard error):	0.008	0.079
fractal dimension (standard error):	0.001	0.03
radius (worst):	7.93	36.04
texture (worst):	12.02	49.54
perimeter (worst):	50.41	251.2
area (worst):	185.2	4254.0
smoothness (worst):	0.071	0.223
compactness (worst):	0.027	1.058
concavity (worst):	0.0	1.252
concave points (worst):	0.0	0.291
symmetry (worst):	0.156	0.664
fractal dimension (worst):	0.055	0.208

:Missing Attribute Values: None

:Class Distribution: 212 - Malignant, 357 - Benign

:Creator: Dr. William H. Wolberg, W. Nick Street, Olvi L. Mangasarian

:Donor: Nick Street

:Date: November, 1995

This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
https://goo.gl/U2Uwz2

Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image.

Separating plane described above was obtained using Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree

```
Construction Via Linear Programming." Proceedings of the 4th
Midwest Artificial Intelligence and Cognitive Science Society,
pp. 97-101, 1992], a classification method which uses linear
programming to construct a decision tree.  Relevant features
were selected using an exhaustive search in the space of 1-4
features and 1-3 separating planes.

The actual linear program used to obtain the separating plane
in the 3-dimensional space is that described in:
[K. P. Bennett and O. L. Mangasarian: "Robust Linear
Programming Discrimination of Two Linearly Inseparable Sets",
Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:

ftp ftp.cs.wisc.edu
cd math-prog/cpo-dataset/machine-learn/WDBC/

.. topic:: References

   - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction
     for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on
     Electronic Imaging: Science and Technology, volume 1905, pages 861-870,
     San Jose, CA, 1993.
   - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and
     prognosis via linear programming. Operations Research, 43(4), pages 570-577,
     July-August 1995.
   - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques
     to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77 (1994)
     163-171.
```

In [7]:

```
x=pd.DataFrame(data.data)
```

In [8]:

```
x.shape
```

Out[8]:

```
(569, 30)
```

In [9]:

```
x.head()
```

Out[9]:

	0	1	2	3	4	5	6	7	8	9	...	20	21
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07871	...	25.38	17.33
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05667	...	24.99	23.41
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05999	...	23.57	25.53
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09744	...	14.91	26.50
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05883	...	22.54	16.67

5 rows × 30 columns

In [10]:

```
data.feature_names
```

Out[10]:

```
array(['mean radius', 'mean texture', 'mean perimeter', 'mean area',
       'mean smoothness', 'mean compactness', 'mean concavity',
       'mean concave points', 'mean symmetry', 'mean fractal dimension',
       'radius error', 'texture error', 'perimeter error', 'area error',
       'smoothness error', 'compactness error', 'concavity error',
       'concave points error', 'symmetry error',
       'fractal dimension error', 'worst radius', 'worst texture',
       'worst perimeter', 'worst area', 'worst smoothness',
       'worst compactness', 'worst concavity', 'worst concave points',
       'worst symmetry', 'worst fractal dimension'], dtype='<U23')
```

In [11]:

```
x.columns=data.feature_names
```

In [12]:

```
x.head()
```

Out[12]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	n fr dimer
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.0
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.0
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.0
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.0
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.0

5 rows × 30 columns

In [13]:

```
y=data.target
```

In [14]:

```
print(y)
```

```
[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 1 0 0 0 0 0 0 0 0 1 0 1 1 1 1 1 0 0 1 0 0 1 1 1 1 0 1 0 0 1 1 1 1 0 1 0 0
 1 0 1 0 0 1 1 1 0 0 1 0 0 0 1 1 1 0 1 1 0 0 1 1 1 0 0 1 1 1 1 0 1 1 0 1 1
 1 1 1 1 1 1 0 0 0 1 0 0 1 1 1 0 0 1 0 1 0 0 1 0 0 1 1 0 1 1 0 1 1 1 1 0 1
 1 1 1 1 1 1 1 1 0 1 1 1 1 0 0 1 0 1 1 0 0 1 1 0 0 1 1 1 1 0 1 1 0 0 0 1 0
 1 0 1 1 1 0 1 1 0 0 1 0 0 0 0 1 0 0 0 1 0 1 0 1 1 0 1 0 0 0 0 1 1 0 0 1 1
 1 0 1 1 1 1 1 0 0 1 1 0 1 1 0 0 1 0 1 1 1 1 0 1 1 1 1 1 0 1 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 1 1 1 1 1 1 0 1 0 1 1 0 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1
 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 0 1 0 1 1 1 1 0 0 0 1 1
 1 1 0 1 0 1 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 1 0 0
 0 1 0 0 1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 0 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1
 1 0 1 1 1 1 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 1 1 1 1 0 1 1
 0 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1
 1 1 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 0 0 1 0 1 0 1 1 1 1 1 0 1 1 0 1 0 1 0 0
 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 0 0 0 0 0 0 1]
```

In [15]:

```
print(data.target_names)
```

```
['malignant' 'benign']
```

In [16]:
```
types = []
for i in y:
    name = data['target_names'][i]
    types.append(name)
```

In [17]:
```
x['types'] = types
```

In [18]:
```
x.head()
```

Out[18]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	m fr dimer
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.0
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.0
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.0
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.0
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.0

5 rows × 31 columns

In [19]:
```
x.tail()
```

Out[19]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	dim
564	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0.1726	0
565	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0.1752	0
566	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0.1590	0
567	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0.2397	0
568	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0.1587	0

5 rows × 31 columns

In [20]:
```
x.isna().count()
```

Out[20]:
```
mean radius            569
mean texture           569
mean perimeter         569
mean area              569
mean smoothness        569
```

```
mean compactness           569
mean concavity             569
mean concave points        569
mean symmetry              569
mean fractal dimension     569
radius error               569
texture error              569
perimeter error            569
area error                 569
smoothness error           569
compactness error          569
concavity error            569
concave points error       569
symmetry error             569
fractal dimension error    569
worst radius               569
worst texture              569
worst perimeter            569
worst area                 569
worst smoothness           569
worst compactness          569
worst concavity            569
worst concave points       569
worst symmetry             569
worst fractal dimension    569
types                      569
dtype: int64
```

In [21]:

```
x.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   mean radius              569 non-null    float64
 1   mean texture             569 non-null    float64
 2   mean perimeter           569 non-null    float64
 3   mean area                569 non-null    float64
 4   mean smoothness          569 non-null    float64
 5   mean compactness         569 non-null    float64
 6   mean concavity           569 non-null    float64
 7   mean concave points      569 non-null    float64
 8   mean symmetry            569 non-null    float64
 9   mean fractal dimension   569 non-null    float64
 10  radius error             569 non-null    float64
 11  texture error            569 non-null    float64
 12  perimeter error          569 non-null    float64
 13  area error               569 non-null    float64
 14  smoothness error         569 non-null    float64
 15  compactness error        569 non-null    float64
 16  concavity error          569 non-null    float64
 17  concave points error     569 non-null    float64
 18  symmetry error           569 non-null    float64
 19  fractal dimension error  569 non-null    float64
 20  worst radius             569 non-null    float64
 21  worst texture            569 non-null    float64
 22  worst perimeter          569 non-null    float64
 23  worst area               569 non-null    float64
 24  worst smoothness         569 non-null    float64
```

```
 25  worst compactness        569 non-null    float64
 26  worst concavity          569 non-null    float64
 27  worst concave points     569 non-null    float64
 28  worst symmetry           569 non-null    float64
 29  worst fractal dimension  569 non-null    float64
 30  types                    569 non-null    object
dtypes: float64(30), object(1)
memory usage: 137.9+ KB
```

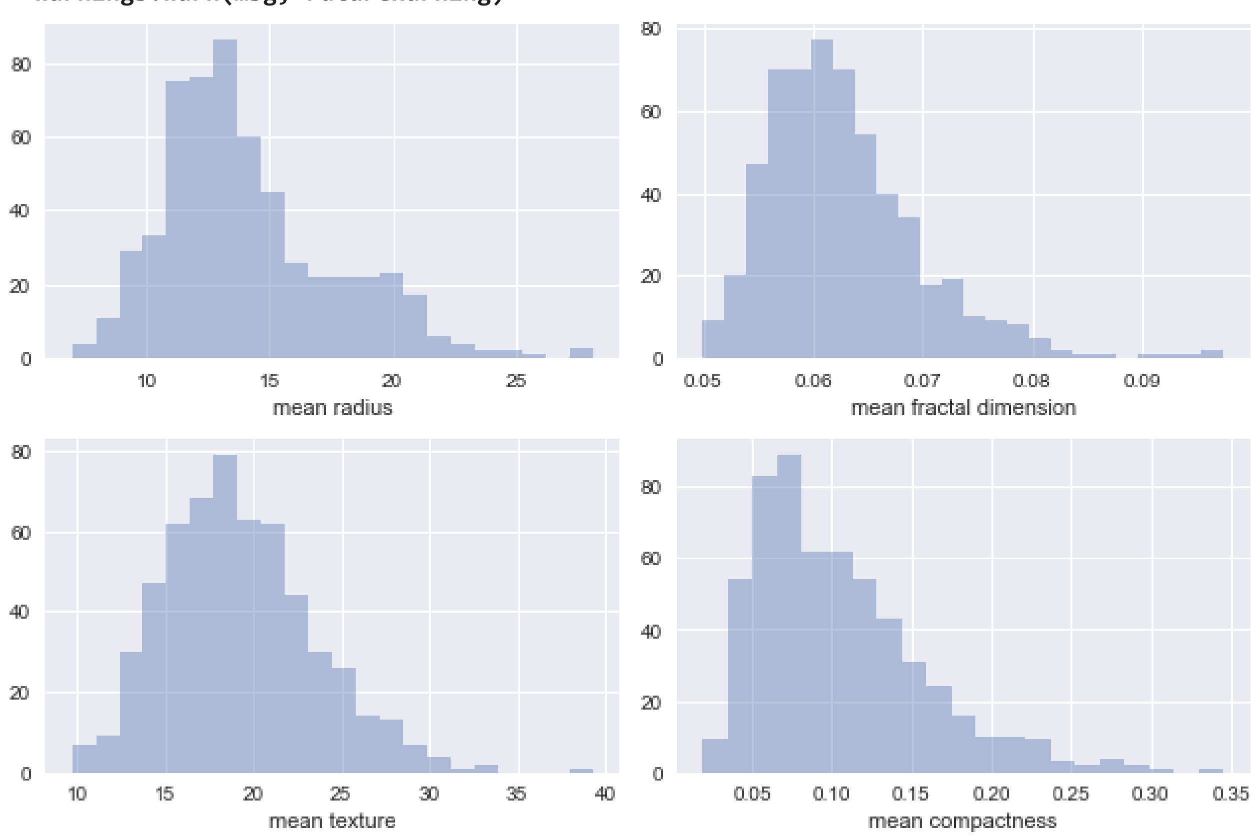
2.1 Feature Standardadization

We chose 4 randome feautres to show the difference in the scale of the features and how the MinMa Scaling method helped us to fix that problem by replotting the rescaled features

In [23]:

```
import seaborn as sns
x_hist = x[['mean radius', 'mean fractal dimension', 'mean texture', 'mean compactness'

fig, ax = plt.subplots(ncols=2, nrows=2, figsize=(9, 6))
index=0
ax = ax.flatten()

for col, values in x_hist.items():
    sns.distplot(values, ax=ax[index], kde=False)
    index += 1
plt.tight_layout()
```

```
C:\Users\apala\anaconda3\lib\site-packages\seaborn\distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please adap
t your code to use either `displot` (a figure-level function with similar flexibility) o
r `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



In [24]:
```python
from sklearn.preprocessing import MinMaxScaler
x.iloc[:,0:-1] = MinMaxScaler().fit_transform(x.iloc[:,0:-1])
```

In [25]:
```python
x.head()
```

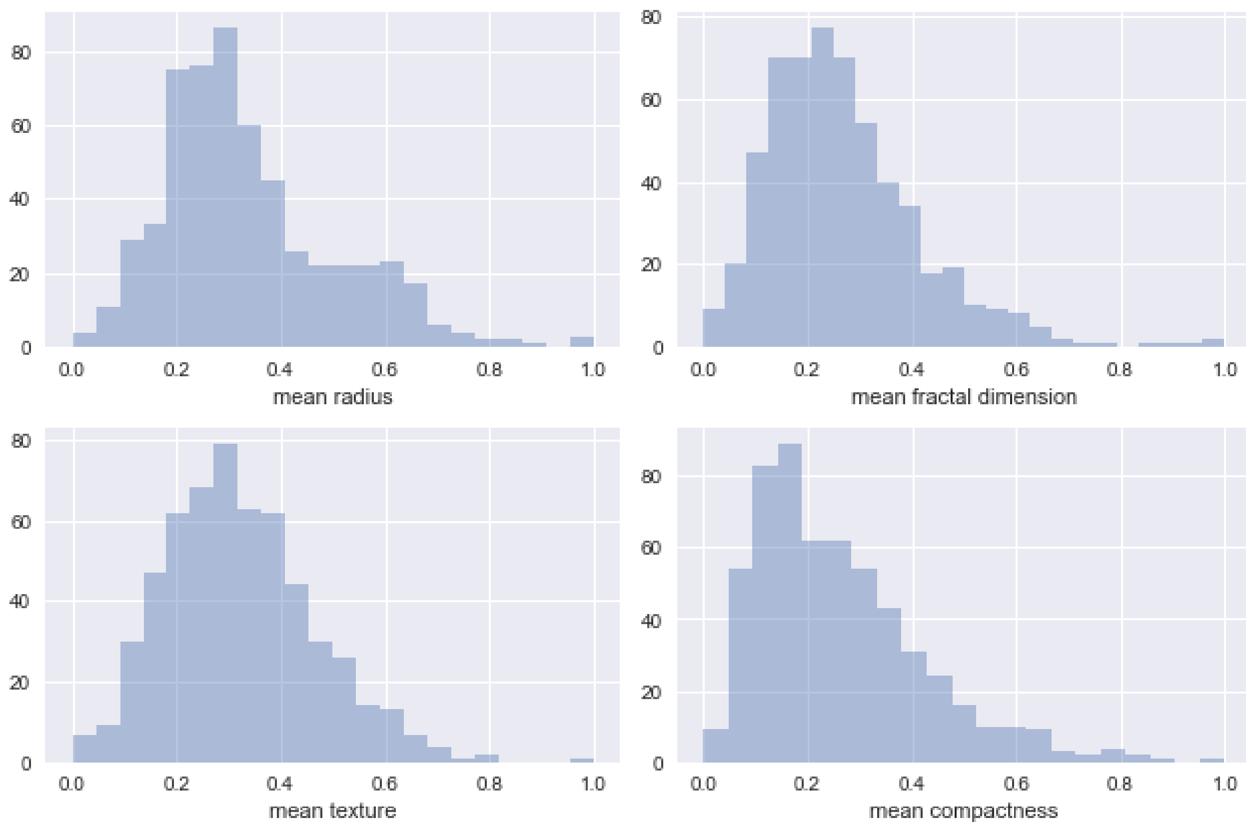
Out[25]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry
0	0.521037	0.022658	0.545989	0.363733	0.593753	0.792037	0.703140	0.731113	0.686364
1	0.643144	0.272574	0.615783	0.501591	0.289880	0.181768	0.203608	0.348757	0.379798
2	0.601496	0.390260	0.595743	0.449417	0.514309	0.431017	0.462512	0.635686	0.509596
3	0.210090	0.360839	0.233501	0.102906	0.811321	0.811361	0.565604	0.522863	0.776263
4	0.629893	0.156578	0.630986	0.489290	0.430351	0.347893	0.463918	0.518390	0.378283

5 rows × 31 columns

In [26]:
```python
x_hist = x[['mean radius', 'mean fractal dimension', 'mean texture', 'mean compactness'

fig, ax = plt.subplots(ncols=2, nrows=2, figsize=(9, 6))
index=0
ax = ax.flatten()

for col, values in x_hist.items():
    sns.distplot(values, ax=ax[index], kde=False)
    index += 1
plt.tight_layout()
```

```
C:\Users\apala\anaconda3\lib\site-packages\seaborn\distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please adap
t your code to use either `displot` (a figure-level function with similar flexibility) o
r `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```



In [27]:

```
#from sklearn.preprocessing import StandardScaler
#x.iloc[:,0:-1] = StandardScaler().fit_transform(x.iloc[:,0:-1])
#x["mean radius"].hist()
```

In [28]:

```
#x.head()
```

3.- Explanatory Power Analysis

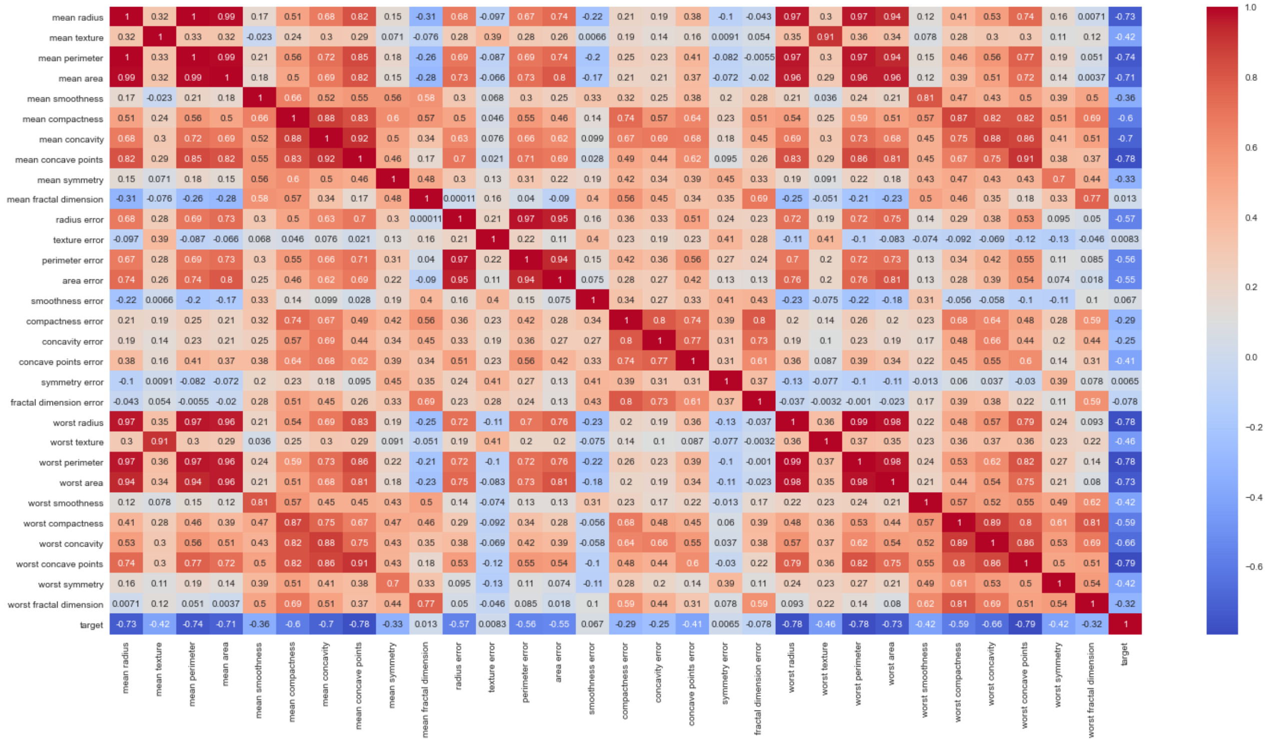
3.1 Correlations Analysis and P-values

As part of the data analysis, we will look for hihgly correlated features as having multicollinearity implies that there might be some regressors not adding much information to the model. We will try to idenify those variables that seem not to have high explanatory power and to create a second sample set without them. For the remaining of the work we will do each analysis with two samples to compare the results

In [29]:

```
## Plot a correlation matrix to see the correlations between (i) features x label and (
x['target']=y
import seaborn as sns
corr = x.corr()
plt.figure(figsize=(25,12.5))
sns.heatmap(corr, annot=True, cmap='coolwarm')
```

Out[29]: <AxesSubplot:>



From the correlation matrix is easy to see that some variables are hihgly correlated and others have veyr low correlation regarding the targe variable:

```
1.- Mean Perimeter, mean area, worst radius, worst perimeter and worst
area are highly correlated with mean radius
2.- Worst texture is highly correlated with mean texture
3.- Mean concavity is highly correlated with mean concave points
4.- Worst concave points is highly correlated with mean concave points
5.- Perimeter error and area error are highly correlated with radius
error
6.- Perimeter error is highly correlate with area error
7.- Worst perimeter and worst area are highly correlated with worst
radius
8.- Worst area is highly correlated with worst perimeter
9.- Mean fractal dimension, texture error, smoothness error, symmetry
error, fractal dimension error, have very low correlation with target.
```

Let us see how the correlation matrix shows after removing the following features:

```
 - Mean concave points, mean texture, perimeter error, area error, worst
perimeter, worst area, mean perimeter, mean area, worst radius, worst
perimeter and worst area, mean fractal dimension, texture error,
smoothness error, symmetry error, fractal dimension error
```

In [30]:

```
x1=x.drop(["mean concave points", "mean texture", "perimeter error", "area error", "wor
x1.shape
```

Out[30]:

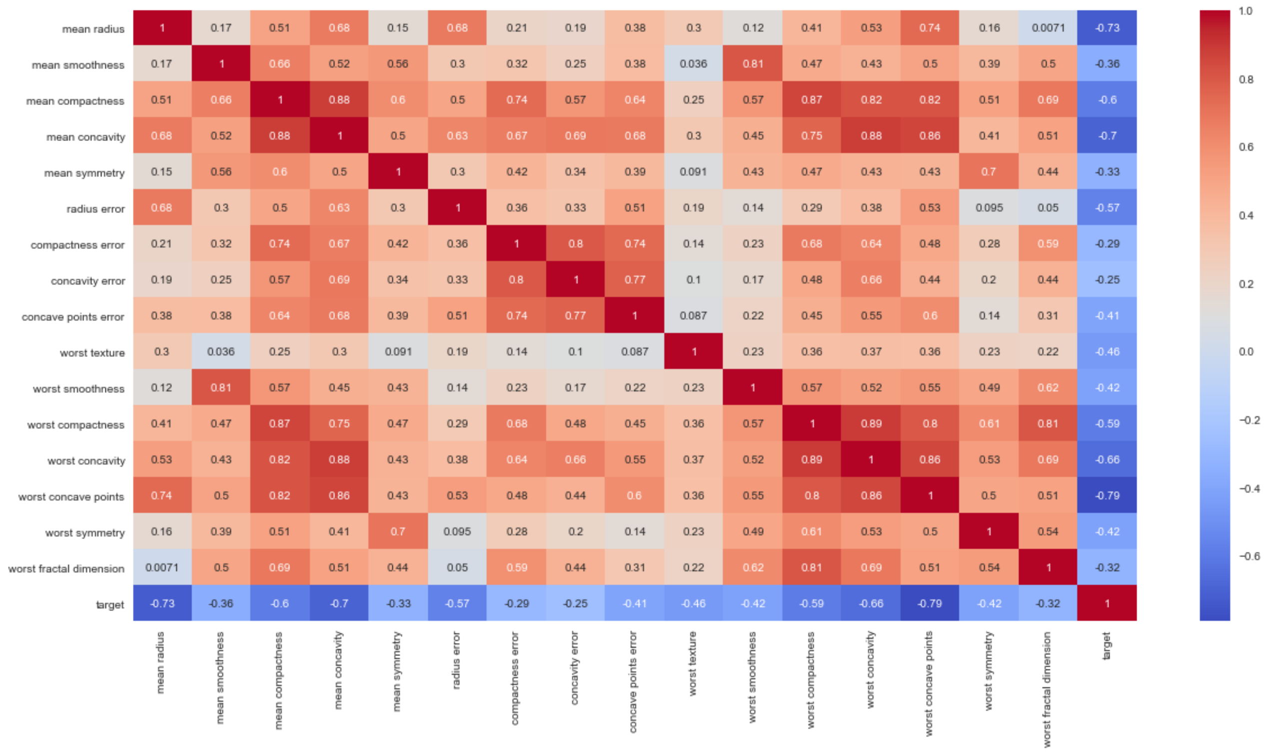
```
(569, 18)
```

In [31]:

```python
corr = x1.corr()
plt.figure(figsize=(20,10))
sns.heatmap(corr, annot=True, cmap='coolwarm')
```

Out[31]:

```
<AxesSubplot:>
```



We also compute the p-values of the regressors. Noramlly, a p-value higher than 5% (the common significance level) means that the regressor coefficient is not statistically different from zero. In other words, you could erase that regressor. From the analysis below, it seems that "mean compactness", "concavity error", "worst area" and "worst radius" are the variables with the highest explanatory power.

In [32]:

```python
import statsmodels.api as sm
xt=x.drop(["types","target"],axis=1)
xt2= sm.add_constant(xt)
est = sm.OLS(y, xt2,hasconstant=True)
est2 = est.fit()
print(est2.summary(alpha=0.05))
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:                      y   R-squared:                       0.774
Model:                            OLS   Adj. R-squared:                  0.762
Method:                 Least Squares   F-statistic:                     61.53
Date:                Sun, 17 Oct 2021   Prob (F-statistic):          6.05e-153
Time:                        08:36:11   Log-Likelihood:                 29.650
No. Observations:                 569   AIC:                             2.699
Df Residuals:                     538   BIC:                             137.4
Df Model:                          30
Covariance Type:            nonrobust
=================================================================================
===
                              coef    std err          t      P>|t|      [0.025      0.9
75]
```

```
------------------------------------------------------------------------------------
---
const                      1.7323      0.104     16.580      0.000       1.527       1.
937
mean radius                4.6013      3.666      1.255      0.210      -2.600      11.
803
mean texture              -0.1344      0.235     -0.572      0.567      -0.596       0.
327
mean perimeter            -3.4354      3.632     -0.946      0.345     -10.570       3.
699
mean area                 -0.7493      1.238     -0.605      0.545      -3.182       1.
683
mean smoothness           -0.0094      0.223     -0.042      0.967      -0.448       0.
430
mean compactness           1.3765      0.435      3.166      0.002       0.522       2.
231
mean concavity            -0.5967      0.446     -1.337      0.182      -1.474       0.
280
mean concave points       -0.4309      0.398     -1.082      0.280      -1.213       0.
351
mean symmetry             -0.0203      0.147     -0.138      0.890      -0.309       0.
269
mean fractal dimension    -0.0016      0.265     -0.006      0.995      -0.521       0.
518
radius error              -1.2011      0.857     -1.401      0.162      -2.885       0.
483
texture error              0.0306      0.167      0.183      0.855      -0.297       0.
358
perimeter error            0.4779      0.873      0.548      0.584      -1.236       2.
192
area error                 0.4943      0.748      0.660      0.509      -0.976       1.
964
smoothness error          -0.4664      0.195     -2.393      0.017      -0.849      -0.
084
compactness error         -0.0086      0.289     -0.030      0.976      -0.576       0.
559
concavity error            1.4119      0.515      2.741      0.006       0.400       2.
424
concave points error      -0.5579      0.288     -1.938      0.053      -1.123       0.
007
symmetry error            -0.1206      0.194     -0.622      0.534      -0.501       0.
260
fractal dimension error    0.2069      0.338      0.612      0.541      -0.457       0.
871
worst radius              -5.4866      1.629     -3.367      0.001      -8.688      -2.
286
worst texture             -0.2686      0.261     -1.030      0.303      -0.781       0.
244
worst perimeter            0.4889      1.192      0.410      0.682      -1.852       2.
830
worst area                 4.1145      1.301      3.163      0.002       1.559       6.
669
worst smoothness          -0.0822      0.217     -0.378      0.705      -0.509       0.
345
worst compactness         -0.0692      0.395     -0.175      0.861      -0.845       0.
706
worst concavity           -0.4773      0.336     -1.419      0.156      -1.138       0.
183
worst concave points      -0.1351      0.266     -0.508      0.612      -0.658       0.
387
worst symmetry            -0.2825      0.251     -1.126      0.260      -0.775       0.
```

```
210
worst fractal dimension    -0.6561      0.363     -1.806      0.072      -1.370       0.
058
==============================================================================
Omnibus:                       32.654   Durbin-Watson:                   1.794
Prob(Omnibus):                  0.000   Jarque-Bera (JB):               36.690
Skew:                          -0.603   Prob(JB):                     1.08e-08
Kurtosis:                       3.302   Cond. No.                         923.
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specifi
ed.
```

3.2 Features distribution by class

We will create a distribution plot to see how differentiated are each feature in term of the labels, this will also give us an idea of which features my have higher explanatory power such as mean perimeter. Even though, in the middle of the plot there is no celar difference between classes, this feature is clearly differentiated at the limits of the x-axis

In [33]:

```
plt_idx = 1
plt.figure(figsize=(20, 15))

for index1 in range(0,30):
        f1 = x.columns[index1]
        xp = x[f1]
        plt.subplot(6,5,plt_idx,label=f1)
        plt.scatter(xp,y,c = 'red')
        plt.xlabel(f1,labelpad=-75)
        plt_idx = plt_idx+1
```

4.- Metrics for model evaluation

For the model evaluation we will be using the next metrics:

$$Accuracy=\frac{TP+TN}{FP+FN+TP+TN}$$

$$Precision=\frac{TP}{TP+FP}$$

$$Recall=\frac{TP}{TP+FN}$$

$$F1=2\times\frac{Precision\times Recall}{Precision+Recall}$$

5.- Model Fitting

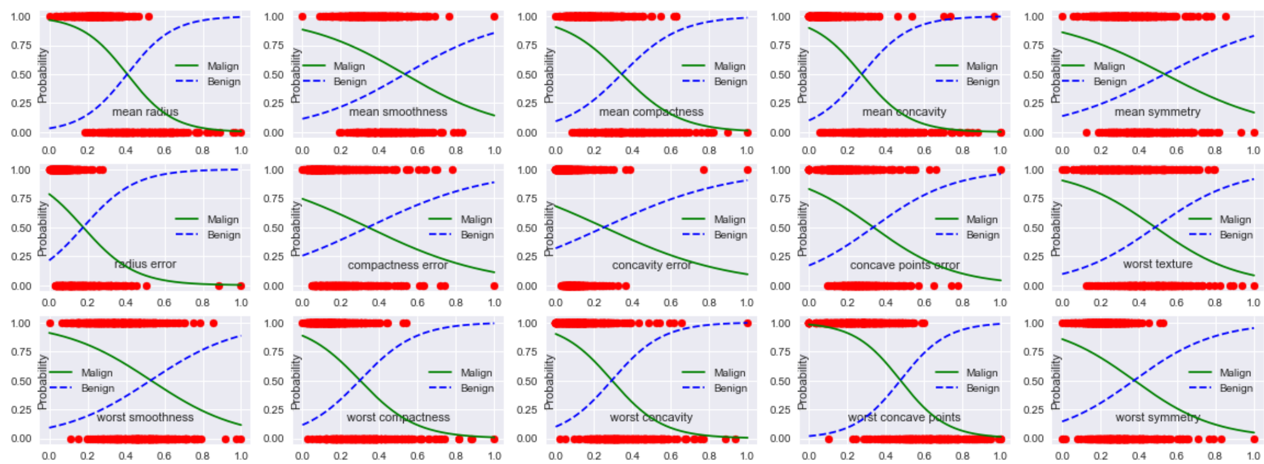
We will now fit different models to our data. We will apply each model twice. One for the original data and one for the second set in which we remove some variables. We will fit the model to a train set (70% of total data randomly selected) and then predict values for the rest 30%. The models we will aplly are Logistic Regression, K-Nearest Neighbor, Decision Tree and Supported Vector Machine

5.1 Logistic Regression

In [34]:

```
from sklearn.linear_model import LogisticRegression
```

```python
log_reg = LogisticRegression(solver='liblinear')
plt_idx = 1
plt.figure(figsize=(20, 15))

for index1 in range(0,15):
        f1 = x1.columns[index1]
        xp = x1[f1].values.reshape(569,1)
        log_reg.fit(xp,y)
        X_new = np.linspace(xp.min(),xp.max(),1000).reshape(-1,1)
        y_proba = log_reg.predict_proba(X_new)
        plt.subplot(6,5,plt_idx)
        plt.scatter(xp,y,c = 'red')
        plt.plot(X_new,y_proba[:,1],"g-",label="Malign",)
        plt.plot(X_new,y_proba[:,0],"b--",label="Benign")
        plt.xlabel(f1,labelpad=-45,loc='center')
        plt.ylabel('Probability',loc='center',labelpad=-35)
        plt.legend()
        plt_idx = plt_idx+1
```



After cleaning for high correlated variables, its easy to observe that some features do not have high explanatory power when isolated, as the classes ar not clearly differentiated. We will fit the model now with all the features at the same time.

We will define a function generation a confusion matrix, which has on the diagonal the correct prections to show graphically how well the model fit the data. Afterwards, there is a another function that we create so that the data are split between train and test set, the model is fit on the train set and the the metrics described before are applied to evaluate the model

In [35]:

```python
from sklearn.metrics import plot_confusion_matrix
import matplotlib as mpl

def plot_cm(clf, X, y, labs):

    mpl.rcParams.update({'font.size': 16})
    cm = plot_confusion_matrix(clf, X, y, display_labels=labs,cmap=mpl.cm.Blues);
```

In [36]:

```python
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
```

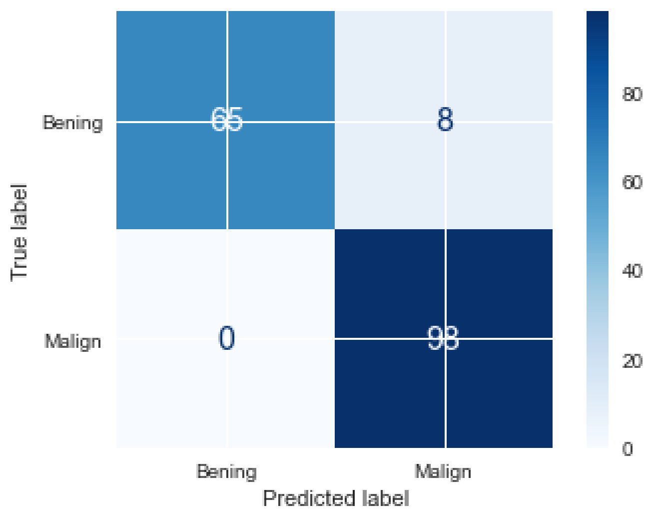
```
from sklearn.metrics import f1_score

def train(model, z, w):
    x_train, x_test, y_train, y_test = train_test_split(z, w, test_size=.30, random_sta
    model.fit(x_train, y_train)
    y_pred = model.predict(x_test)

    print('Model Report')
    print('Accuracy: ', np.around(accuracy_score(y_test, y_pred,normalize=True),4))
    print('Precision: ', np.around(precision_score(y_test, y_pred),4))
    print('Recall: ', np.around(recall_score(y_test, y_pred),4))
    print('f1: ', np.around(f1_score(y_test, y_pred),4))
    plot_cm(model, x_test, y_test, labs=('Bening', 'Malign'))
```

5.1.1 Logistic regression full sample

In [38]:

```
xt=x.drop(["types","target"],axis=1)
model = LogisticRegression(solver='liblinear')
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9532
Precision:  0.9245
Recall:  1.0
f1:  0.9608
```

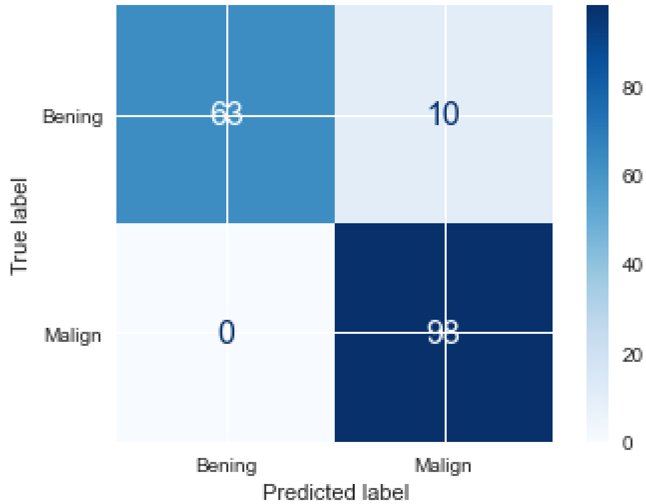


5.1.2 Logistic regression subsample

In [40]:

```
xt=x1.drop(["types","target"],axis=1)
model = LogisticRegression(solver='liblinear')
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9415
Precision:  0.9074
Recall:  1.0
f1:  0.9515
```



The results actually worsen after removing the selected variables, although not by much.

5.2 K-Nearest Neighbor

5.2.1 K-Nearest Neighbor full sample

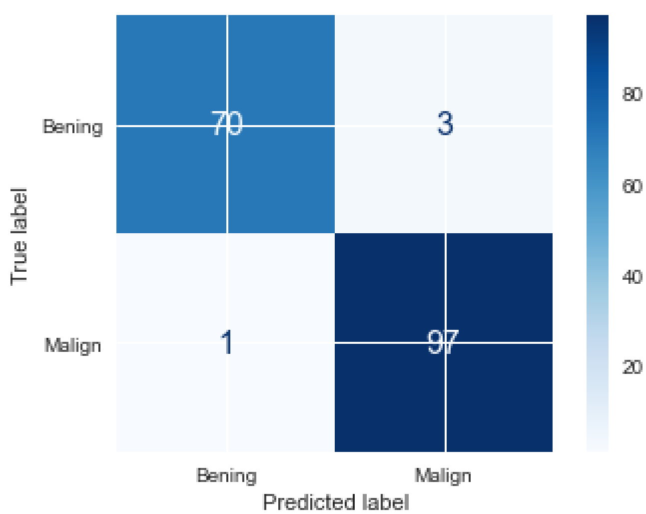
In [41]:

```
from sklearn.neighbors import KNeighborsClassifier
```

In [42]:

```
K=3
model = KNeighborsClassifier(K,p=2)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9766
Precision:  0.97
Recall:  0.9898
f1:  0.9798
```

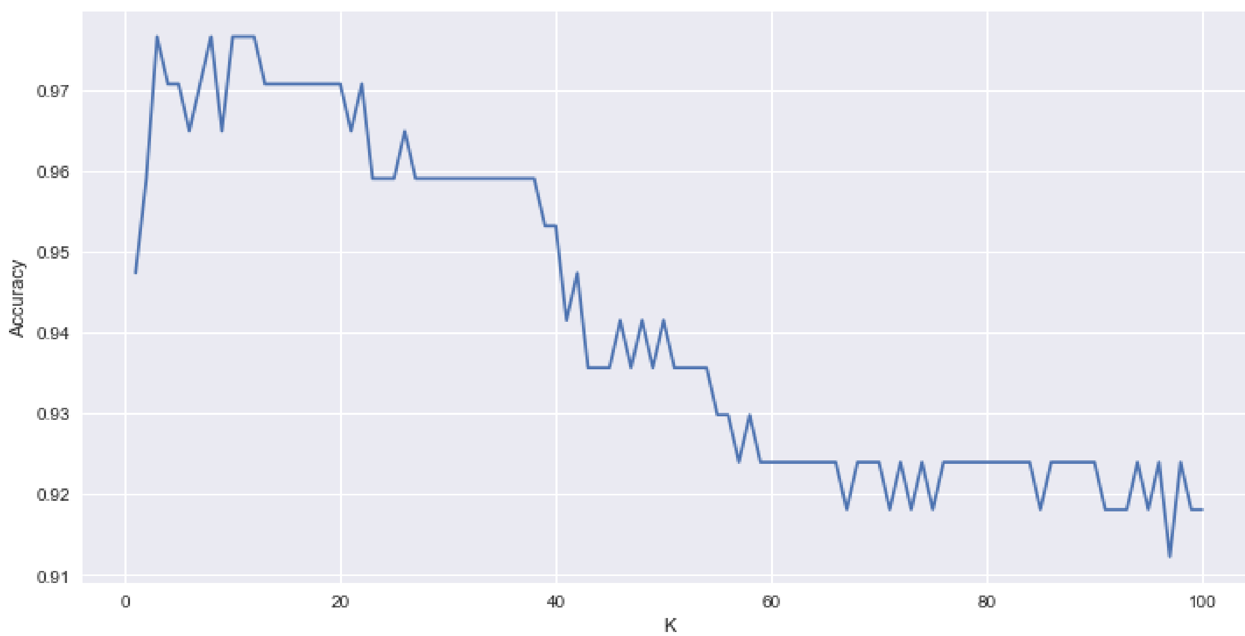


5.2.1.2 K variation analysis

We will see how the accuracy of our prediction changes as we vary the number of neighbors taken to fit the model

In [43]:

```
from sklearn.metrics import confusion_matrix
accs = []
ks = []
xt=x.drop(["types","target"],axis=1)
for k in range(1,101,1):
    x_train, x_test, y_train, y_test = train_test_split(xt, y, test_size=0.30, random_s
    knn = KNeighborsClassifier(n_neighbors = k, p=2)
    knn.fit(x_train, y_train)
    y_pred = knn.predict(x_test)
    cm = confusion_matrix(y_test, y_pred)
    acc = (cm[0][0]+cm[1][1])/len(y_test)
    ks.append(k)
    accs.append(acc)

plt.figure(figsize=(12, 6))
plt.xlabel("K")
plt.ylabel("Accuracy")
plt.plot(ks,accs);
```



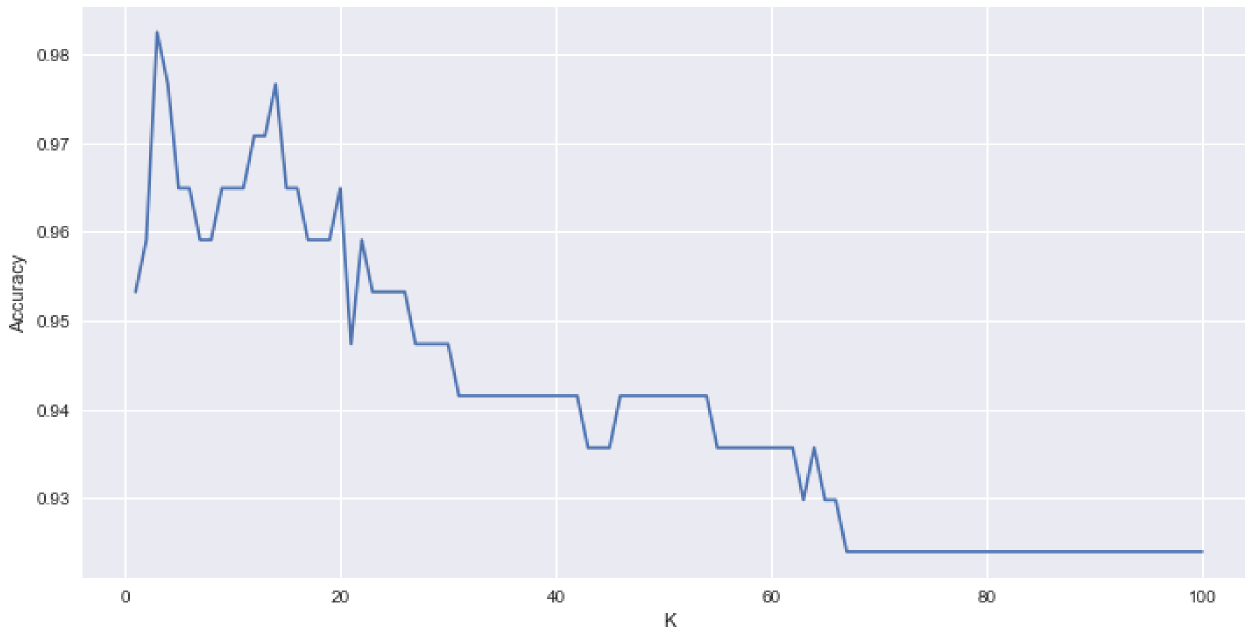
5.2.1.2 Check Analysis

Is easy to see that when K=3 we reach the highest accuracy. We will now see how the graph changes when wee change the method to measure the distance. The first method used above was the Euclidean method (p=2). Now we will use the Manhattan method (p=1). Finally, we decided to use the Manhattan method as it reaches the highest accuracy. Now, we will corroborate that accuracy decays as k increases by fittign the model for different ks

In [44]:

```
from sklearn.metrics import confusion_matrix
accs = []
ks = []
xt=x.drop(["types","target"],axis=1)
for k in range(1,101,1):
```

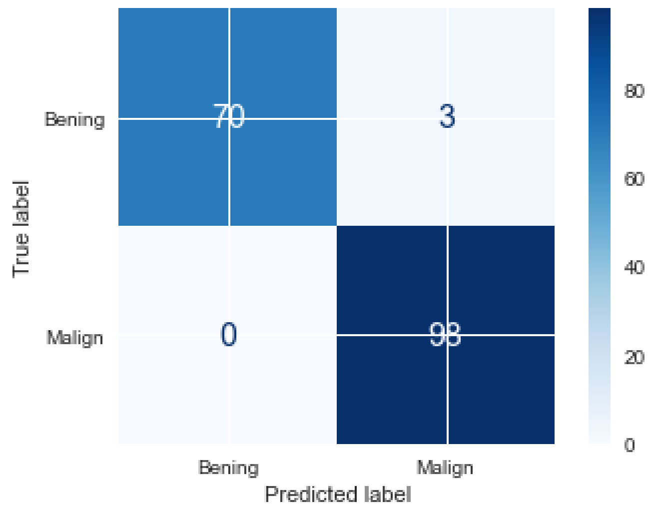
```
    x_train, x_test, y_train, y_test = train_test_split(xt, y, test_size=0.30, random_s
    knn = KNeighborsClassifier(n_neighbors = k, p=1)
    knn.fit(x_train, y_train)
    y_pred = knn.predict(x_test)
    cm = confusion_matrix(y_test, y_pred)
    acc = (cm[0][0]+cm[1][1])/len(y_test)
    ks.append(k)
    accs.append(acc)

plt.figure(figsize=(12, 6))
plt.xlabel("K")
plt.ylabel("Accuracy")
plt.plot(ks,accs);
```



In [45]:

```
K=3
model = KNeighborsClassifier(K,p=1)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

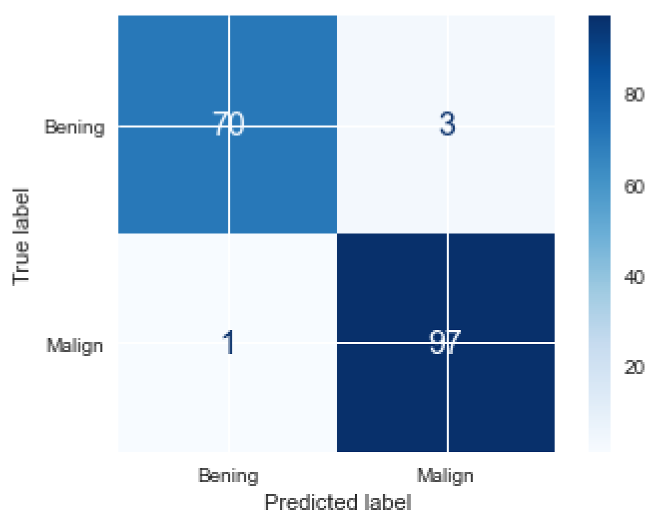
```
Model Report
Accuracy:  0.9825
Precision:  0.9703
Recall:  1.0
f1:  0.9849
```



In [47]:

```
K=4
model = KNeighborsClassifier(K,p=1)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

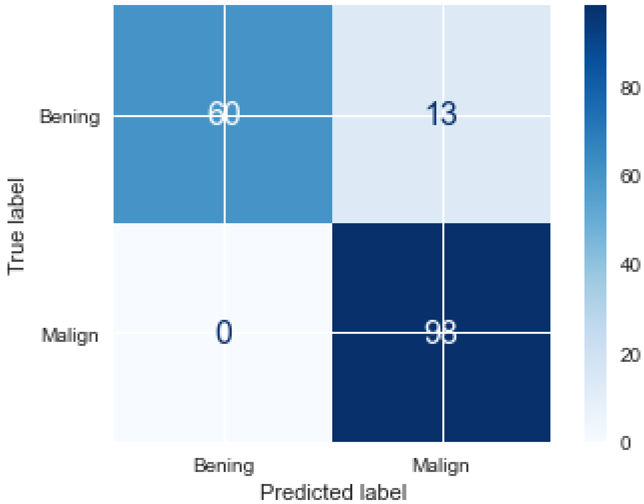
```
Model Report
Accuracy:  0.9766
Precision:  0.97
Recall:  0.9898
f1:  0.9798
```



In [48]:

```
K=70
model = KNeighborsClassifier(K,p=1)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.924
Precision:  0.8829
Recall:  1.0
f1:  0.9378
```

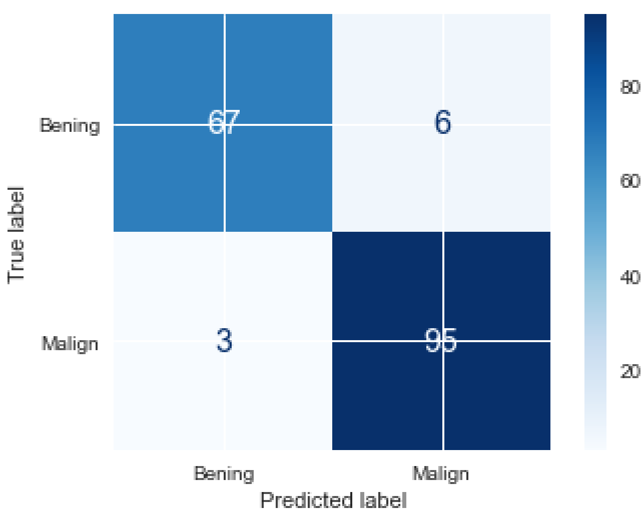


5.2.2 K-Nearest Neighbor subsample

In [49]:

```
K=3
model = KNeighborsClassifier(K,p=2)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9474
Precision:  0.9406
Recall:  0.9694
f1:  0.9548
```



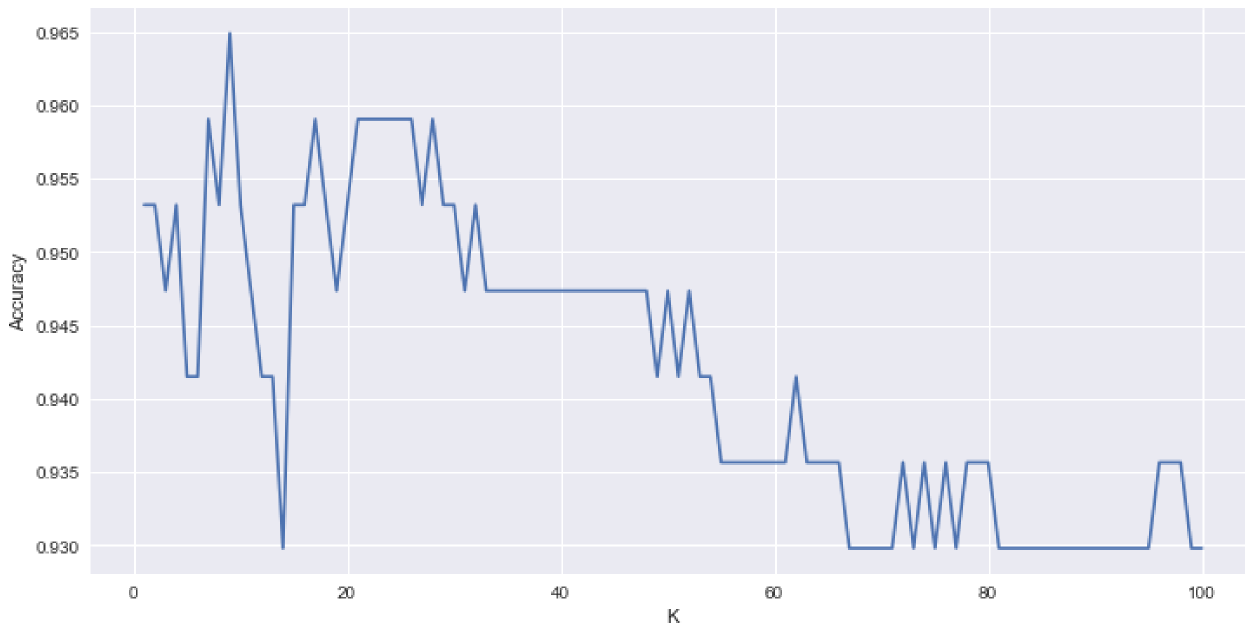
5.2.2.2 K variation analysis

We will see again how the accuracy of our prediction changes as we vary the number of neighbors taken to fit the model

In [50]:

```
from sklearn.metrics import confusion_matrix
accs = []
ks = []
xt=x1.drop(["types","target"],axis=1)
for k in range(1,101,1):
    x_train, x_test, y_train, y_test = train_test_split(xt, y, test_size=0.30, random_s
```

```
    knn = KNeighborsClassifier(n_neighbors = k, p=2)
    knn.fit(x_train, y_train)
    y_pred = knn.predict(x_test)
    cm = confusion_matrix(y_test, y_pred)
    acc = (cm[0][0]+cm[1][1])/len(y_test)
    ks.append(k)
    accs.append(acc)

plt.figure(figsize=(12, 6))
plt.xlabel("K")
plt.ylabel("Accuracy")
plt.plot(ks,accs);
```



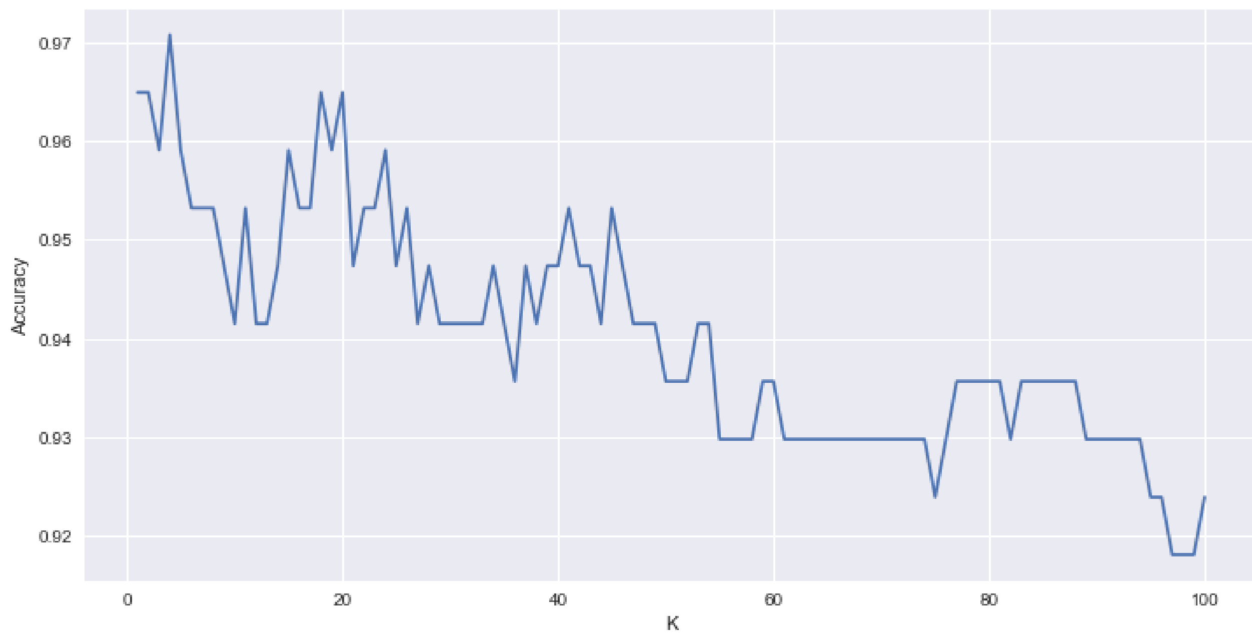
5.2.1.2 Check Analysis

In this case, when K=3 we reach again the highest accuracy. We will repeat the same step before to seehow the graph changes when we change the method to measure the distance. In this case, we decided again to use the Manhattan method as it reaches the highest accuracy. Now, we will corroborate that accuracy decays as k increases by fittign the model for different ks

In [51]:

```
from sklearn.metrics import confusion_matrix
accs = []
ks = []
xt=x1.drop(["types","target"],axis=1)
for k in range(1,101,1):
    x_train, x_test, y_train, y_test = train_test_split(xt, y, test_size=0.30, random_s
    knn = KNeighborsClassifier(n_neighbors = k, p=1)
    knn.fit(x_train, y_train)
    y_pred = knn.predict(x_test)
    cm = confusion_matrix(y_test, y_pred)
    acc = (cm[0][0]+cm[1][1])/len(y_test)
    ks.append(k)
    accs.append(acc)

plt.figure(figsize=(12, 6))
plt.xlabel("K")
```

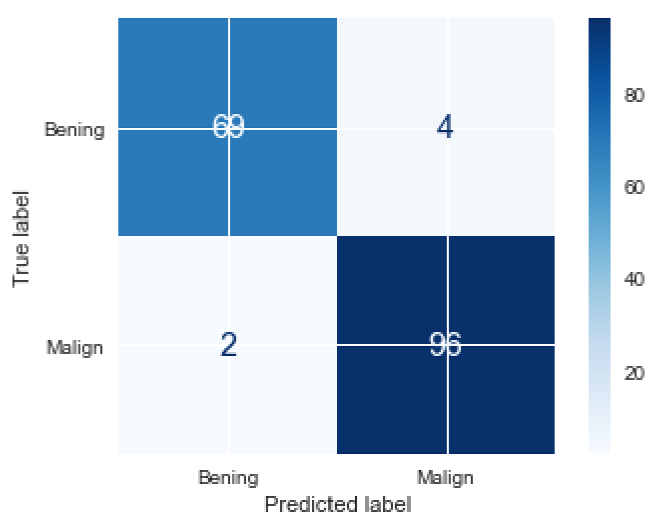
```
plt.ylabel("Accuracy")
plt.plot(ks,accs);
```



In [52]:

```
K=1
model = KNeighborsClassifier(K,p=1)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9649
Precision:  0.96
Recall:  0.9796
f1:  0.9697
```

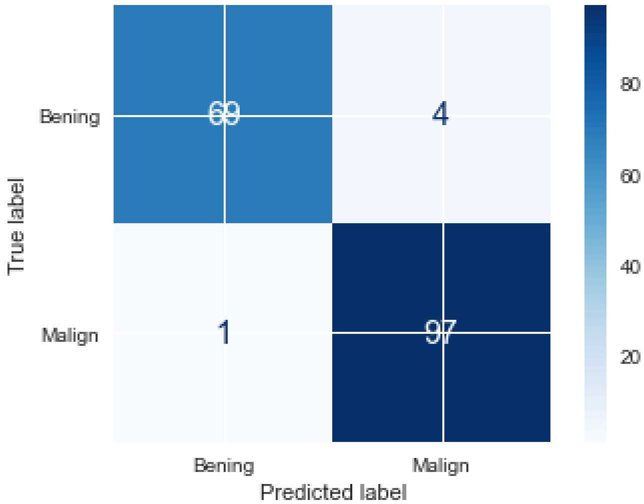


In [53]:

```
K=4
model = KNeighborsClassifier(K,p=1)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9708
```

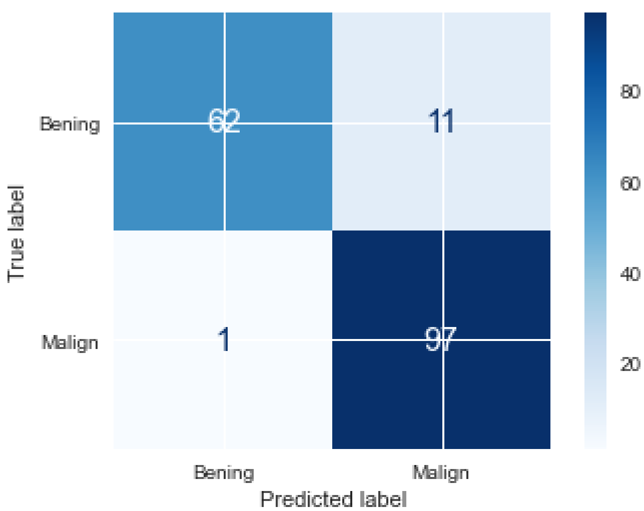
```
Precision:  0.9604
Recall:  0.9898
f1:  0.9749
```



In [54]:

```python
K=70
model = KNeighborsClassifier(K,p=1)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9298
Precision:  0.8981
Recall:  0.9898
f1:  0.9417
```



Similarly as the logistic regression case, the metrics worsen after removing the selected variables but not in a significant way

5.3 Decision Tree

We will now fit the Decision Tree model, setting a maximum depth of ramifications.

In [55]:

```python
from sklearn.metrics import classification_report
from sklearn.tree import DecisionTreeClassifier
```

```python
from sklearn.metrics import confusion_matrix
```

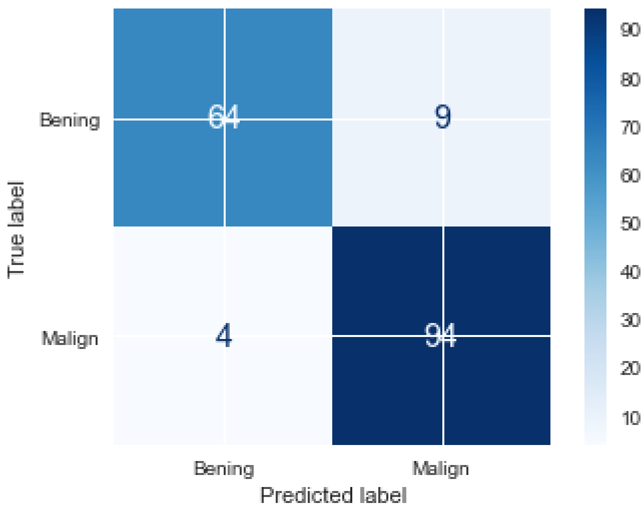
5.3.1 Decision Tree full sample

As we can see, all the final leafs have gini meausres equal to 0 meaning that the model has exactly fitted the data

In [57]:

```python
model = DecisionTreeClassifier(random_state=235, max_depth=10)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

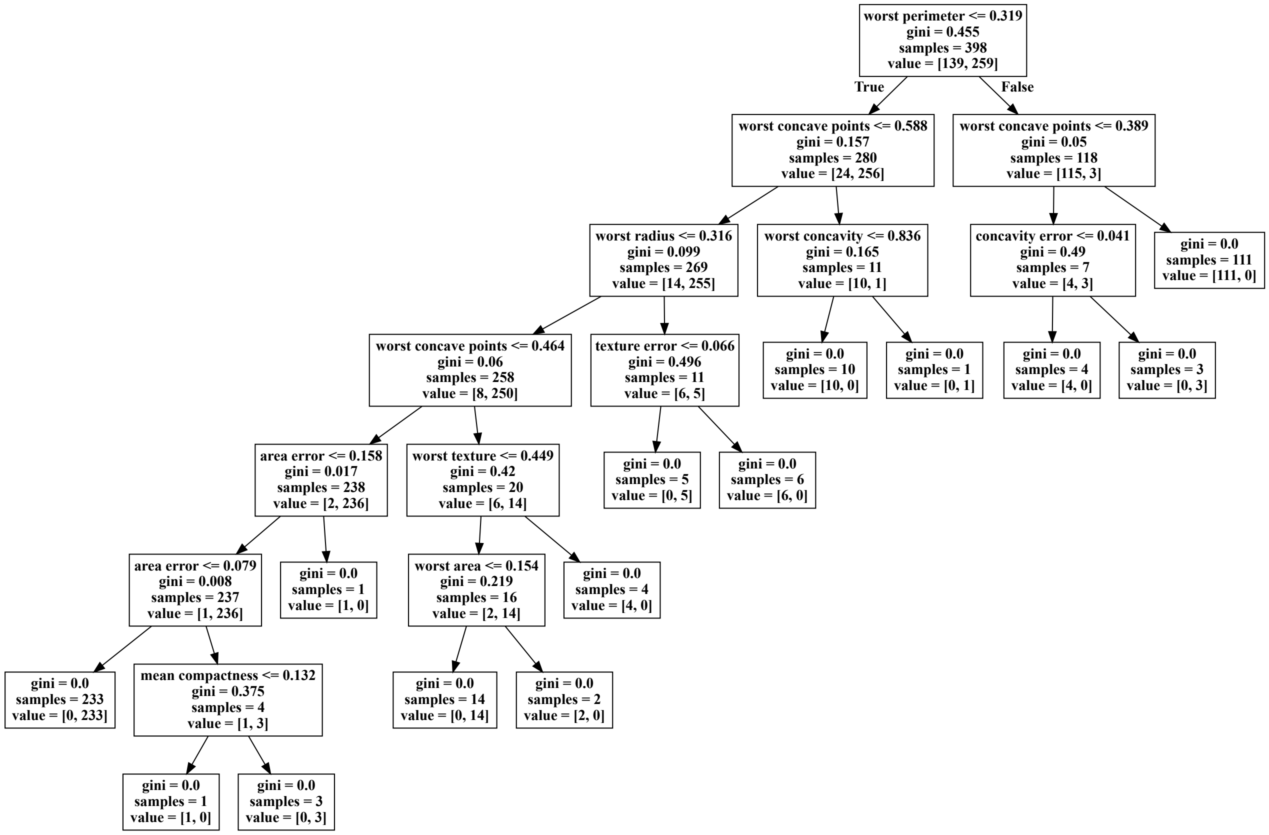
```
Model Report
Accuracy:  0.924
Precision:  0.9126
Recall:  0.9592
f1:  0.9353
```



In [58]:

```python
from sklearn.tree import export_graphviz
from os import system
from graphviz import Source
from IPython.display import SVG
graph = Source(export_graphviz(model, out_file=None, feature_names = xt.columns))
SVG(graph.pipe(format='svg'))
```

Out[58]:



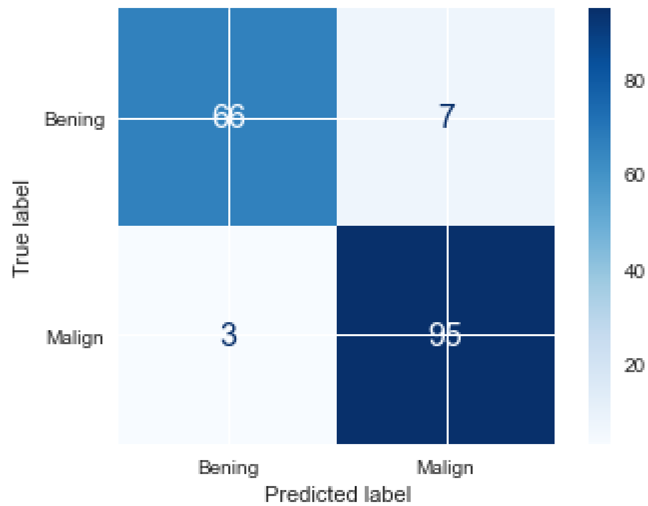
5.3.2 Decision Tree subsample

In this case, the gini metrics are all equal to zero in the final leafs, so the model fitted the data exacly again. In this case, the subsample actually allowed for an improvement in the perfomance measures, although they are still lower that the ones obtained in the previos two methods

In [59]:

```
model = DecisionTreeClassifier(random_state=235, max_depth=10)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

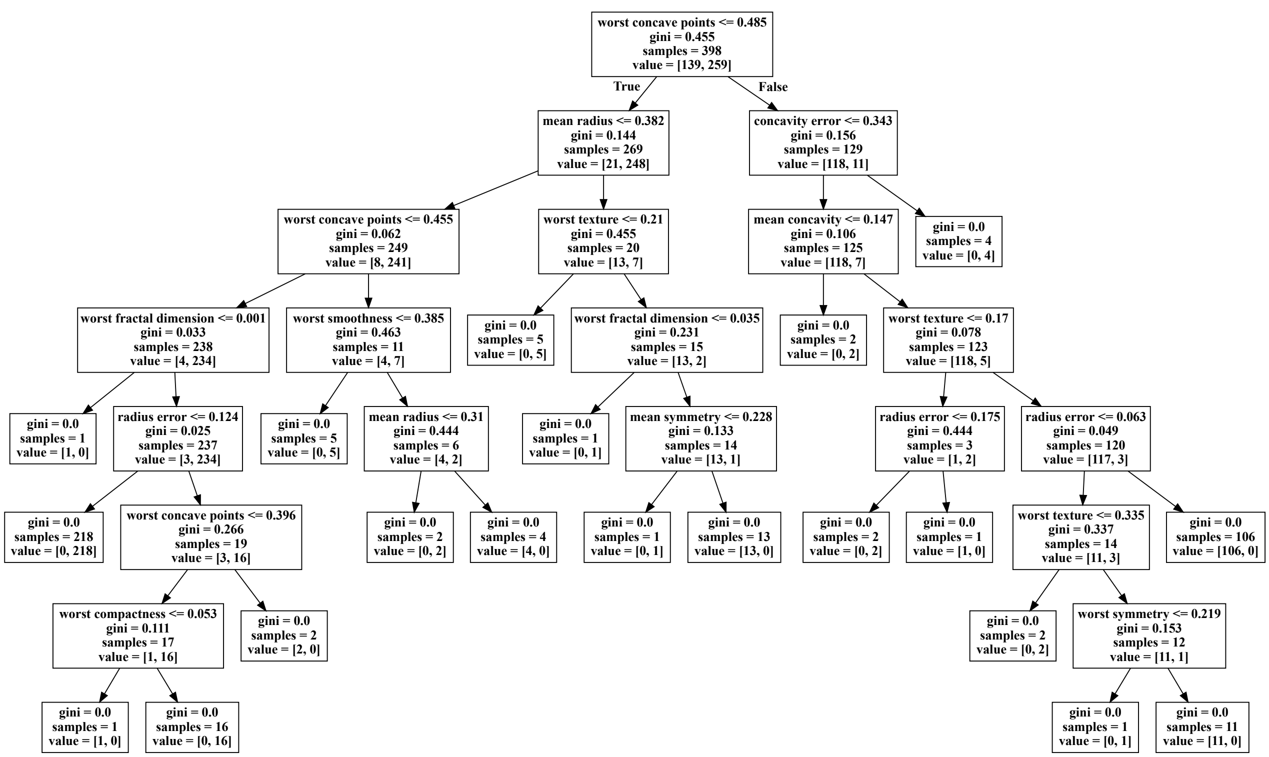
```
Model Report
Accuracy:  0.9415
Precision:  0.9314
Recall:  0.9694
f1:  0.95
```



In [60]:

```
from sklearn.tree import export_graphviz
from os import system
from graphviz import Source
from IPython.display import SVG
graph = Source(export_graphviz(model, out_file=None, feature_names = xt.columns))
SVG(graph.pipe(format='svg'))
```

Out[60]:



5.4 Support Vector Machines

In [61]:

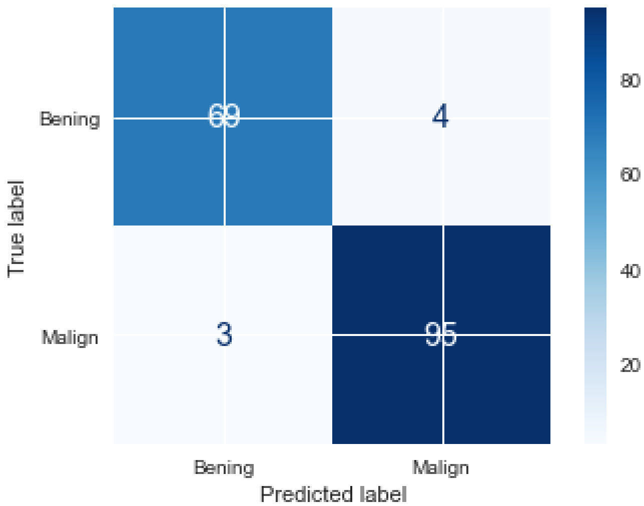
```
from sklearn.svm import SVC
```

5.4.1 Support Vector Machines full sample

We will fit the model using a linear, radial basis and polynomial kernels (mapping methods)

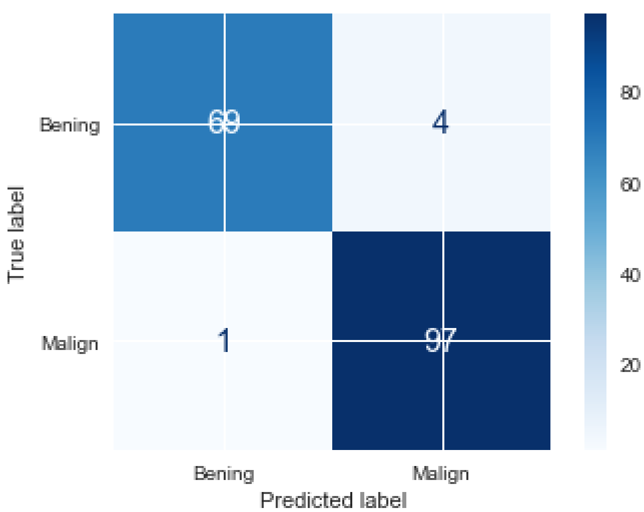
In [63]:
```python
model = SVC(kernel = 'linear', C=1000)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9591
Precision:  0.9596
Recall:  0.9694
f1:  0.9645
```



In [64]:
```python
model = SVC(kernel = 'rbf', C=1000)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

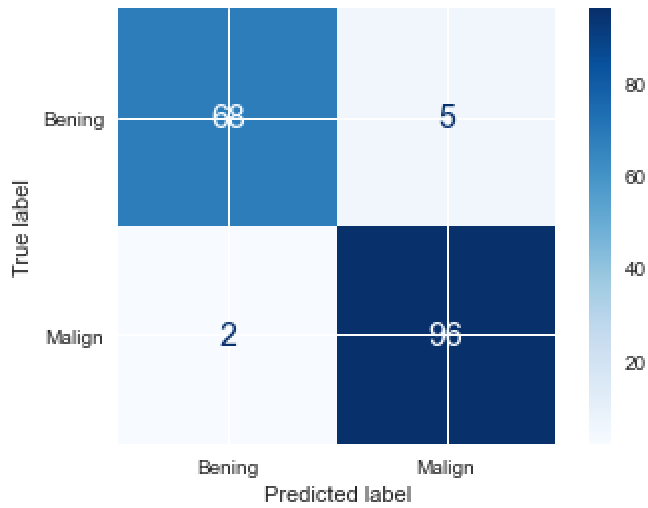
```
Model Report
Accuracy:  0.9708
Precision:  0.9604
Recall:  0.9898
f1:  0.9749
```



In [65]:
```python
model = SVC(kernel = 'poly', C=1000)
xt=x.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9591
```

```
Precision:  0.9505
Recall:  0.9796
f1:  0.9648
```



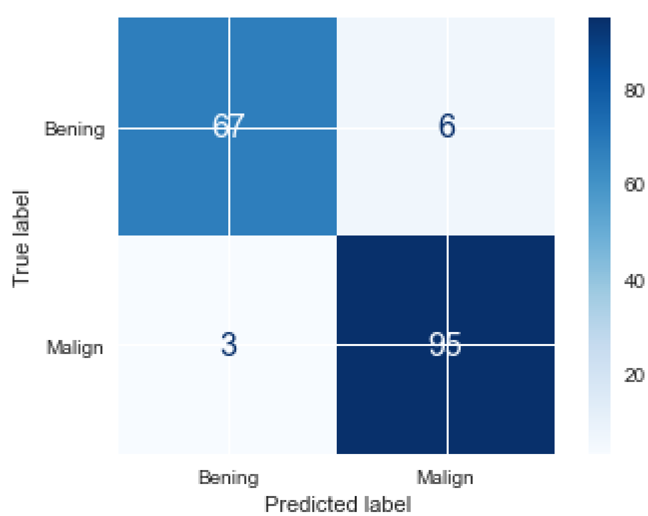
The radial basis kernel yields the best metrics. Let us explore what happens when we dropped the selected variables

5.4.2 Support Vector Machines subsample

In [66]:

```python
model = SVC(kernel = 'linear', C=1000)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9474
Precision:  0.9406
Recall:  0.9694
f1:  0.9548
```

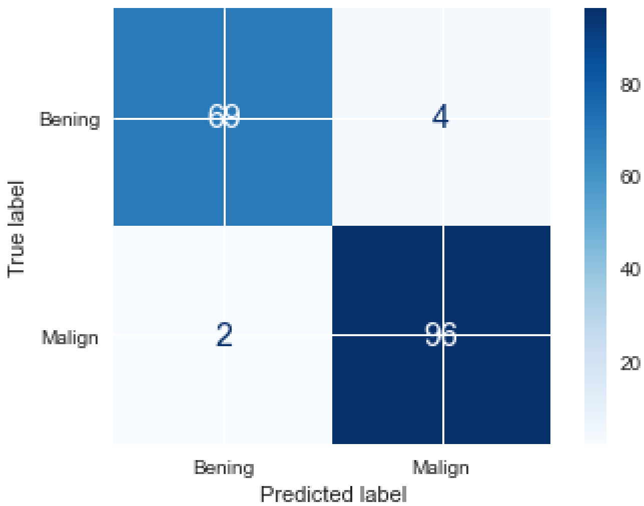


In [67]:

```python
model = SVC(kernel = 'rbf', C=1000)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9649
```

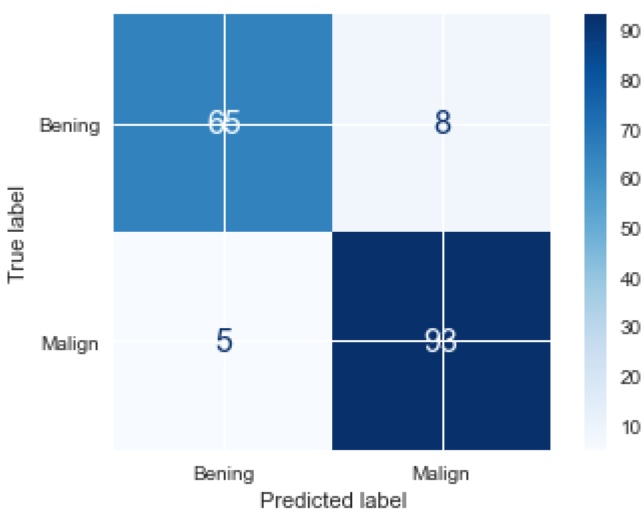
```
Precision:  0.96
Recall:  0.9796
f1:  0.9697
```



In [68]:

```python
model = SVC(kernel = 'poly', C=1000)
xt=x1.drop(["types","target"],axis=1)
train(model, xt, y)
```

```
Model Report
Accuracy:  0.924
Precision:  0.9208
Recall:  0.949
f1:  0.9347
```



We obtained the same results, the radial basis kernel yields the best result. Also, the analysis is consistent with the logistic and the K-neares neighvor methods, as dropping the selected variables actually worsen the performance

6.- Identify the best method

For selecting the best method, we compile in one talbe the performance metrics for the best case in each method. The best method was the K-Nearest Neighbor with the Manhattan method and K=3 (full sample). The next better ones were the Logistic Regression and the

Support Vector Machines with very little difference between them (full sample). Is interesting to see that the worst method was the one that actually performed better with the subsample.

In [71]:

```
L = {'Logistic Regression':[0.9532,0.9245, 1.000, 0.9608], 'KNN':[0.9825,0.9703, 1.0000

df_results = pd.DataFrame(L, index=['Accuracy', 'Precision', 'Recall', 'F1'])

df_results
```

Out[71]:

	Logistic Regression	KNN	Decision Tree	SVM
Accuracy	0.9532	0.9825	0.9240	0.9708
Precision	0.9245	0.9703	0.9126	0.9604
Recall	1.0000	1.0000	0.9592	0.9898
F1	0.9608	0.9849	0.9353	0.9749

7.- Variable significance analysis

We will perform the next analysis with the best model from the table above. We will remove one variable at a time and see how the performance measure of the model changes

In [72]:

```
results = pd.DataFrame(index=['Accuracy', 'Precision', 'Recall', 'F1'])
def train_2(model, x, y, name='Feature'):
    x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=.30, random_sta
    model.fit(x_train, y_train)
    y_pred = model.predict(x_test)

    stats = [np.around(accuracy_score(y_test, y_pred),4),np.around(precision_score(y_te
        np.around(recall_score(y_test, y_pred),4), np.around(f1_score(y_test, y_pred),4
    results[name] = stats
```

In [74]:

```
K=3
model = KNeighborsClassifier(K,p=1)
xt=x.drop(["types","target"],axis=1)
i = 0
for i in range(0, len(data.feature_names)):
    train_2(model, xt.drop(data.feature_names[i],axis=1), y, name = data.feature_names[
    i = i + 1

results.sort_values(by="Accuracy",axis=1)
```

Out[74]:

	mean texture	worst texture	concave points error	mean radius	worst concavity	worst compactness	worst perimeter	worst radius	concavity error	co
Accuracy	0.9708	0.9708	0.9708	0.9766	0.9766	0.9766	0.9766	0.9766	0.9766	
Precision	0.9604	0.9697	0.9604	0.9700	0.9608	0.9608	0.9700	0.9700	0.9608	
Recall	0.9898	0.9796	0.9898	0.9898	1.0000	1.0000	0.9898	0.9898	1.0000	

	mean texture	worst texture	concave points error	mean radius	worst concavity	worst compactness	worst perimeter	worst radius	concavity error	co
F1	0.9749	0.9746	0.9749	0.9798	0.9800	0.9800	0.9798	0.9798	0.9800	

4 rows × 30 columns

The less significant measures are "mean symmetry", "worst area", "mean concave points", "fractal dimension error", "mean compactness", "mean smoothness", "symmetry error", "worst concave points", "mean fractal dimension" and "worst smoothness" as the performance measures are the highest when removing them. The name of the column in the table above indictes which feature has been removed. We will fit the model again now removing those variables

In [75]:

```
results=[]
results = pd.DataFrame(index=['Accuracy', 'Precision', 'Recall', 'F1'])
K=4
model = KNeighborsClassifier(K,p=1)
xt=x.drop(["types","target","mean symmetry", "worst area", "mean concave points", "frac
names=list(xt.columns)
i = 0
for i in range(0, len(names)):
    train_2(model, xt.drop(names[i],axis=1), y, name = names[i])
    i = i + 1

results.sort_values(by="Accuracy",axis=1)
```

Out[75]:

	worst texture	worst symmetry	worst fractal dimension	mean texture	mean concavity	radius error	perimeter error	concave points error	compactness error
Accuracy	0.9591	0.9649	0.9708	0.9708	0.9708	0.9708	0.9708	0.9708	0.9708
Precision	0.9596	0.9792	0.9794	0.9794	0.9697	0.9697	0.9697	0.9794	0.9794
Recall	0.9694	0.9592	0.9694	0.9694	0.9796	0.9796	0.9796	0.9694	0.9694
F1	0.9645	0.9691	0.9744	0.9744	0.9746	0.9746	0.9746	0.9744	0.9744

Is interesting how if we remove "Worst Perimeter", we get a better performance measures that without removing any variable

In [76]:

```
results=[]
results = pd.DataFrame(index=['Accuracy', 'Precision', 'Recall', 'F1'])
K=4
model = KNeighborsClassifier(K,p=1)
xt=x.drop(["types","target","mean symmetry", "worst area", "mean concave points", "frac
names=list(xt.columns)
i = 0
for i in range(0, len(names)):
    train_2(model, xt.drop(names[i],axis=1), y, name = names[i])
    i = i + 1
```

```
results.sort_values(by="Accuracy",axis=1)
```

Out[76]:

	worst texture	worst symmetry	mean texture	worst fractal dimension	worst compactness	worst concavity	mean concavity	radius error	perimete erro
Accuracy	0.9649	0.9649	0.9708	0.9766	0.9766	0.9825	0.9825	0.9825	0.982
Precision	0.9600	0.9694	0.9794	0.9796	0.9796	0.9703	0.9798	0.9703	0.970
Recall	0.9796	0.9694	0.9694	0.9796	0.9796	1.0000	0.9898	1.0000	1.000
F1	0.9697	0.9694	0.9744	0.9796	0.9796	0.9849	0.9848	0.9849	0.984

Finally, we will repeat the analysis by removing the variables we selected from the correlation analysis

In [77]:

```
results=[]
results = pd.DataFrame(index=['Accuracy', 'Precision', 'Recall', 'F1'])
K=3
model = KNeighborsClassifier(K,p=1)
xt=x1.drop(["types","target"],axis=1)
names=list(xt.columns)
i = 0
for i in range(0, len(names)):
    train_2(model, xt.drop(names[i],axis=1), y, name = names[i])
    i = i + 1

results.sort_values(by="Accuracy",axis=1)
```

Out[77]:

	mean radius	worst smoothness	mean smoothness	mean symmetry	worst texture	worst concavity	worst concave points	mean compactness	con
Accuracy	0.9474	0.9474	0.9532	0.9532	0.9532	0.9532	0.9532	0.9591	0
Precision	0.9320	0.9238	0.9327	0.9327	0.9412	0.9327	0.9327	0.9417	0
Recall	0.9796	0.9898	0.9898	0.9898	0.9796	0.9898	0.9898	0.9898	0
F1	0.9552	0.9557	0.9604	0.9604	0.9600	0.9604	0.9604	0.9652	0

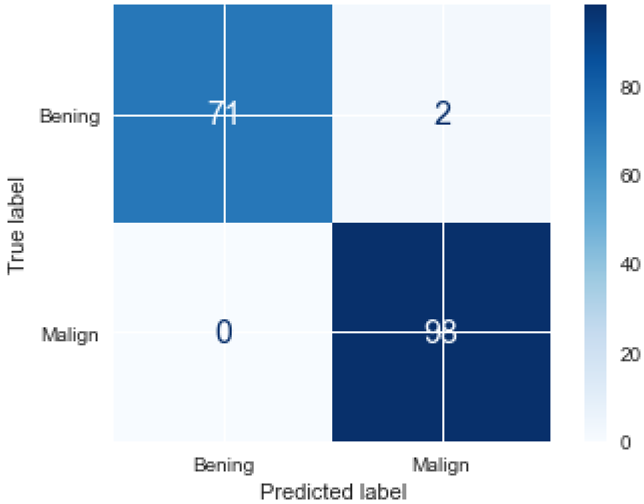
The results are better when we remove the variables selected in the last feature selection analysis

In [78]:

```
K=4
model = KNeighborsClassifier(K,p=1)
xt=x.drop(["types","target","mean symmetry", "worst area", "mean concave points", "frac
train(model, xt, y)
```

```
Model Report
Accuracy:  0.9883
Precision:  0.98
```

```
Recall:  1.0
f1:  0.9899
```



8.- Conclusion

Even though, all classifiers methods actually performed very well, the K-Nearest Neighbor seems to be the most effective. Nevertheless, given thi high number of variables, the model may have been overfitted. We discard this possibility as we removed several features at a time and the explanatory power remained quite high as reflected by the performance measures yielded when fitting the model on the subsample data. We can conclude that some features, when highly correlated to other variables, do not add much to our classifiers methods, so the most efficient choice is to delete them. Finally, given the performance measures obtained we could rely without doubt into our classifiers to do predicitons regarding the Breast Cancer. A larger sampel would be helpful to have more solid basis.

In [79]:

```
#alejandro.palacios@edhec.com
```