Project 2 - Binary Classification Comparative Methods

For this project we're going to attempt a binary classification of a dataset using multiple methods and compare results.

Our goals for this project will be to introduce you to several of the most common classification techniques, how to perform them and tweek parameters to optimize outcomes, how to produce and interpret results, and compare performance. You will be asked to analyze your findings and provide explanations for observed performance.

DEFINITIONS

Binary Classification: In this case a complex dataset has an added 'target' label with one of two options. Your learning algorithm will try to assign one of these labels to the data.

Supervised Learning: This data is fully supervised, which means it's been fully labeled and we can trust the veracity of the labeling.

Submission Details

Project is due May 17th at 12:00 pm (Wednesday Noon). To submit the project, please save the notebook as a pdf file and submit the assignment via Gradescope. In addition, make sure that all figures are legible and sufficiently large. For best pdf results, we recommend downloading [Latex (https://www.latex-project.org/)](https://www.latex-project.org/) and print the notebook using Latex.

Loading Essentials and Helper Functions

In [1]:
```
#Here are a set of libraries we imported to complete this assignment.
#Feel free to use these or equivalent libraries for your implementation
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import matplotlib.pyplot as plt # this is used for the plot the graph
import matplotlib
import os
import time
#Sklearn classes
from sklearn.model_selection import train_test_split, cross_val_score, GridSearchCV, KFold
from sklearn import metrics
from sklearn.svm import SVC  #SVM classifier
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier

from sklearn.metrics import confusion_matrix
import sklearn.metrics.cluster as smc

from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler, OneHotEncoder, Normalizer, MinMaxScaler
from sklearn.compose import ColumnTransformer, make_column_transformer



from matplotlib import pyplot
import itertools

%matplotlib inline

#Sets random seed
import random
random.seed(42)
```

In [2]:
```
# Helper function allowing you to export a graph
def save_fig(fig_id, tight_layout=True, fig_extension="png", resolution=300):
    path = os.path.join(fig_id + "." + fig_extension)
    print("Saving figure", fig_id)
    if tight_layout:
        plt.tight_layout()
    plt.savefig(path, format=fig_extension, dpi=resolution)
```

In [3]:
```
# Helper function that allows you to draw nicely formatted confusion matrices
def draw_confusion_matrix(y, yhat, classes):
    '''
        Draws a confusion matrix for the given target and predictions
        Adapted from scikit-learn and discussion example.
    '''
    plt.cla()
    plt.clf()
    matrix = confusion_matrix(y, yhat)
    plt.imshow(matrix, interpolation='nearest', cmap=plt.cm.YlOrBr)
    plt.title("Confusion Matrix")
    plt.colorbar()
    num_classes = len(classes)
    plt.xticks(np.arange(num_classes), classes, rotation=90)
    plt.yticks(np.arange(num_classes), classes)

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

    plt.ylabel('True label')
    plt.xlabel('Predicted label')
    plt.tight_layout()
    plt.show()
```

In [4]:
```python
def heatmap(data, row_labels, col_labels, figsize = (20,12), cmap = "YlGn",
            cbar_kw={}, cbarlabel="", valfmt="{x:.2f}",
            textcolors=("black", "white"), threshold=None):
    """
    Create a heatmap from a numpy array and two lists of labels.

    Taken from matplotlib example.

    Parameters
    ----------
    data
        A 2D numpy array of shape (M, N).
    row_labels
        A list or array of length M with the labels for the rows.
    col_labels
        A list or array of length N with the labels for the columns.
    ax
        A `matplotlib.axes.Axes` instance to which the heatmap is plotted.  If
        not provided, use current axes or create a new one.  Optional.
    cmap
        A string that specifies the colormap to use. Look at matplotlib docs for information.
        Optional.
    cbar_kw
        A dictionary with arguments to `matplotlib.Figure.colorbar`.  Optional.
    cbarlabel
        The label for the colorbar.  Optional.
    valfmt
        The format of the annotations inside the heatmap.  This should either
        use the string format method, e.g. "$ {x:.2f}", or be a
        `matplotlib.ticker.Formatter`.  Optional.
    textcolors
        A pair of colors.  The first is used for values below a threshold,
        the second for those above.  Optional.
    threshold
        Value in data units according to which the colors from textcolors are
        applied.  If None (the default) uses the middle of the colormap as
    """

    plt.figure(figsize = figsize)
    ax = plt.gca()

    # Plot the heatmap
    im = ax.imshow(data,cmap=cmap)

    # Create colorbar
    cbar = ax.figure.colorbar(im, ax=ax, **cbar_kw)
    cbar.ax.set_ylabel(cbarlabel, rotation=-90, va="bottom")

    # Show all ticks and label them with the respective list entries.
    ax.set_xticks(np.arange(data.shape[1]), labels=col_labels)
    ax.set_yticks(np.arange(data.shape[0]), labels=row_labels)

    # Let the horizontal axes labeling appear on top.
    ax.tick_params(top=True, bottom=False,
                   labeltop=True, labelbottom=False)

    # Rotate the tick labels and set their alignment.
    plt.setp(ax.get_xticklabels(), rotation=-30, ha="right",
             rotation_mode="anchor")

    # Turn spines off and create white grid.
    ax.spines[:].set_visible(False)

    ax.set_xticks(np.arange(data.shape[1]+1)-.5, minor=True)
    ax.set_yticks(np.arange(data.shape[0]+1)-.5, minor=True)
    ax.grid(which="minor", color="w", linestyle='-', linewidth=3)
    ax.tick_params(which="minor", bottom=False, left=False)


    # Normalize the threshold to the images color range.
    if threshold is not None:
        threshold = im.norm(threshold)
    else:
        threshold = im.norm(data.max())/2.

    # Set default alignment to center, but allow it to be
    # overwritten by textkw.
    kw = dict(horizontalalignment="center",
              verticalalignment="center")

    # Get the formatter in case a string is supplied
    if isinstance(valfmt, str):
        valfmt = matplotlib.ticker.StrMethodFormatter(valfmt)

    # Loop over the data and create a `Text` for each "pixel".
    # Change the text's color depending on the data.
```

```
    texts = []
    for i in range(data.shape[0]):
        for j in range(data.shape[1]):
            kw.update(color=textcolors[int(im.norm(data[i, j]) > threshold)])
            text = im.axes.text(j, i, valfmt(data[i, j], None), **kw)
            texts.append(text)
```

In [5]:

```
def make_meshgrid(x, y, h=0.02):
    """Create a mesh of points to plot in

    Parameters
    ----------
    x: data to base x-axis meshgrid on
    y: data to base y-axis meshgrid on
    h: stepsize for meshgrid, optional

    Returns
    -------
    xx, yy : ndarray
    """
    x_min, x_max = x.min() - 1, x.max() + 1
    y_min, y_max = y.min() - 1, y.max() + 1
    xx, yy = np.meshgrid(np.arange(x_min, x_max, h), np.arange(y_min, y_max, h))
    return xx, yy


def plot_contours(clf, xx, yy, **params):
    """Plot the decision boundaries for a classifier.

    Parameters
    ----------
    ax: matplotlib axes object
    clf: a classifier
    xx: meshgrid ndarray
    yy: meshgrid ndarray
    params: dictionary of params to pass to contourf, optional
    """
    Z = clf.predict(np.c_[xx.ravel(), yy.ravel()])
    Z = Z.reshape(xx.shape)
    out = plt.contourf(xx, yy, Z, **params)
    return out

def draw_contour(x,y,clf, class_labels = ["Negative", "Positive"]):
    """
    Draws a contour line for the predictor

    Assumption that x has only two features. This functions only plots the first two columns of x.

    """

    X0, X1 = x[:, 0], x[:, 1]
    xx0, xx1 = make_meshgrid(X0,X1)

    plt.figure(figsize = (10,6))
    plot_contours(clf, xx0, xx1, cmap="PiYG", alpha=0.8)
    scatter=plt.scatter(X0, X1, c=y, cmap="PiYG", s=30, edgecolors="k")
    plt.legend(handles=scatter.legend_elements()[0], labels=class_labels)

    plt.xlim(xx0.min(), xx0.max())
    plt.ylim(xx1.min(), xx1.max())
```

Example Project

In this part, we will go over how to perform a Binary classification task using a variety of models. We will provide examples of how to train and evaluate these models.

Dataset Description

Healthcare is an important industry that uses machine learning to aid doctors in diagnosing many different kinds of illnesses and diseases. For this example project, we will be using the [Breast Cancer Wisconsin Dataset (https://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data)](https://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data) to determine whether a mass found in a body is benign or malignant.

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.

Feature Information:

Column 1: ID number

Column 2: Diagnosis (M = malignant, B = benign)

Ten real-valued features are computed for each cell nucleus:

```
1. radius (mean of distances from center to points on the perimeter)
2. texture (standard deviation of gray-scale values)
3. perimeter
4. area
5. smoothness (local variation in radius lengths)
6. compactness (perimeter^2 / area - 1.0)
7. concavity (severity of concave portions of the contour)
8. concave points (number of concave portions of the contour)
9. symmetry
10. fractal dimension ("coastline approximation" - 1)
```

Due to the statistical nature of the test, we are not able to get exact measurements of the previous values. Instead, the dataset contains the mean and standard error of the real-valued features.

Columns 3-12 present the mean of the measured values

Columns 13-22 present the standard error of the measured values

Load and Analyze the dataset

In [6]:
```
#Load Data
data = pd.read_csv('datasets/breast_cancer_data.csv')
```

Always look at your dataset after loading it. Use information from .describe and .info to learn more about the dataset.

In [7]:
```
data.head(5)
```

Out[7]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	...
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	...
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	...
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	...
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	...

5 rows × 22 columns

In [8]:
```
data.describe()
```

Out[8]:

	id	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symm
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.088799	0.048919	
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.079720	0.038803	
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.000000	0.000000	
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.029560	0.020310	
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.061540	0.033500	
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.130700	0.074000	
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.426800	0.201200	

8 rows × 21 columns

In [9]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 22 columns):
 #   Column                  Non-Null Count  Dtype  
---  ------                  --------------  -----  
 0   id                      569 non-null    int64  
 1   diagnosis               569 non-null    object 
 2   radius_mean             569 non-null    float64
 3   texture_mean            569 non-null    float64
 4   perimeter_mean          569 non-null    float64
 5   area_mean               569 non-null    float64
 6   smoothness_mean         569 non-null    float64
 7   compactness_mean        569 non-null    float64
 8   concavity_mean          569 non-null    float64
 9   concave points_mean     569 non-null    float64
 10  symmetry_mean           569 non-null    float64
 11  fractal_dimension_mean  569 non-null    float64
 12  radius_se               569 non-null    float64
 13  texture_se              569 non-null    float64
 14  perimeter_se            569 non-null    float64
 15  area_se                 569 non-null    float64
 16  smoothness_se           569 non-null    float64
 17  compactness_se          569 non-null    float64
 18  concavity_se            569 non-null    float64
 19  concave points_se       569 non-null    float64
 20  symmetry_se             569 non-null    float64
 21  fractal_dimension_se    569 non-null    float64
dtypes: float64(20), int64(1), object(1)
memory usage: 97.9+ KB
```

While .info shows that every entry has 569 non-null and there are 569 entries, it is good to explicitly check for nulls.

In [10]:
```
data.isnull().sum()
```

Out[10]:
```
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
dtype: int64
```

Awesome! No need for imputation!

While we are looking at the dataset, we shall remove the "id" column.

In [11]:
```
data = data.drop(["id"],axis= 1)
```

Looking at the target labels

For this project, we wish to classify the diagnosis column.

In [12]:
```
data["diagnosis"]
```

Out[12]:
```
0      M
1      M
2      M
3      M
4      M
      ..
564    M
565    M
566    M
567    M
568    B
Name: diagnosis, Length: 569, dtype: object
```

We need to transform this column into numerical column so that we may use them in our models. To do this, we will employ the LabelEncoder to automatically transform all the target label.

In [13]:
```
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

data['diagnosis'] = le.fit_transform(data['diagnosis'])
print(le.classes_)
```

```
['B' 'M']
```

In [14]:
```
data['diagnosis']
```

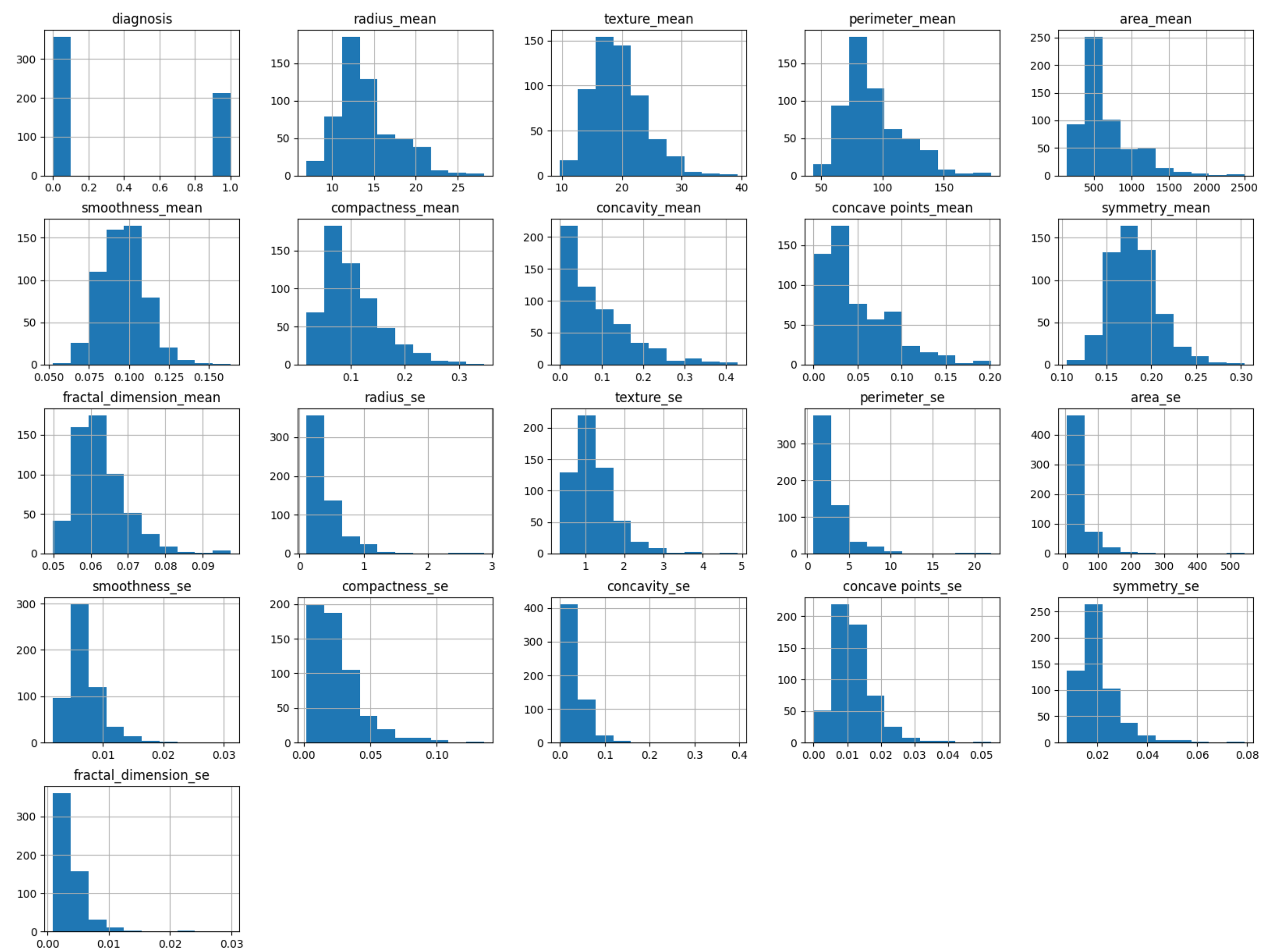
Out[14]:
```
0      1
1      1
2      1
3      1
4      1
      ..
564    1
565    1
566    1
567    1
568    0
Name: diagnosis, Length: 569, dtype: int64
```

Let's look at a histogram of the full dataset.

Its always good to get a global view of your datasets by looking at their histograms. You might see some interesting trends.

In [15]:
```python
data.hist(figsize = (20,15))
```

Out[15]:
```
array([[<AxesSubplot: title={'center': 'diagnosis'}>,
        <AxesSubplot: title={'center': 'radius_mean'}>,
        <AxesSubplot: title={'center': 'texture_mean'}>,
        <AxesSubplot: title={'center': 'perimeter_mean'}>,
        <AxesSubplot: title={'center': 'area_mean'}>],
       [<AxesSubplot: title={'center': 'smoothness_mean'}>,
        <AxesSubplot: title={'center': 'compactness_mean'}>,
        <AxesSubplot: title={'center': 'concavity_mean'}>,
        <AxesSubplot: title={'center': 'concave points_mean'}>,
        <AxesSubplot: title={'center': 'symmetry_mean'}>],
       [<AxesSubplot: title={'center': 'fractal_dimension_mean'}>,
        <AxesSubplot: title={'center': 'radius_se'}>,
        <AxesSubplot: title={'center': 'texture_se'}>,
        <AxesSubplot: title={'center': 'perimeter_se'}>,
        <AxesSubplot: title={'center': 'area_se'}>],
       [<AxesSubplot: title={'center': 'smoothness_se'}>,
        <AxesSubplot: title={'center': 'compactness_se'}>,
        <AxesSubplot: title={'center': 'concavity_se'}>,
        <AxesSubplot: title={'center': 'concave points_se'}>,
        <AxesSubplot: title={'center': 'symmetry_se'}>],
       [<AxesSubplot: title={'center': 'fractal_dimension_se'}>,
        <AxesSubplot: >, <AxesSubplot: >, <AxesSubplot: >,
        <AxesSubplot: >]], dtype=object)
```

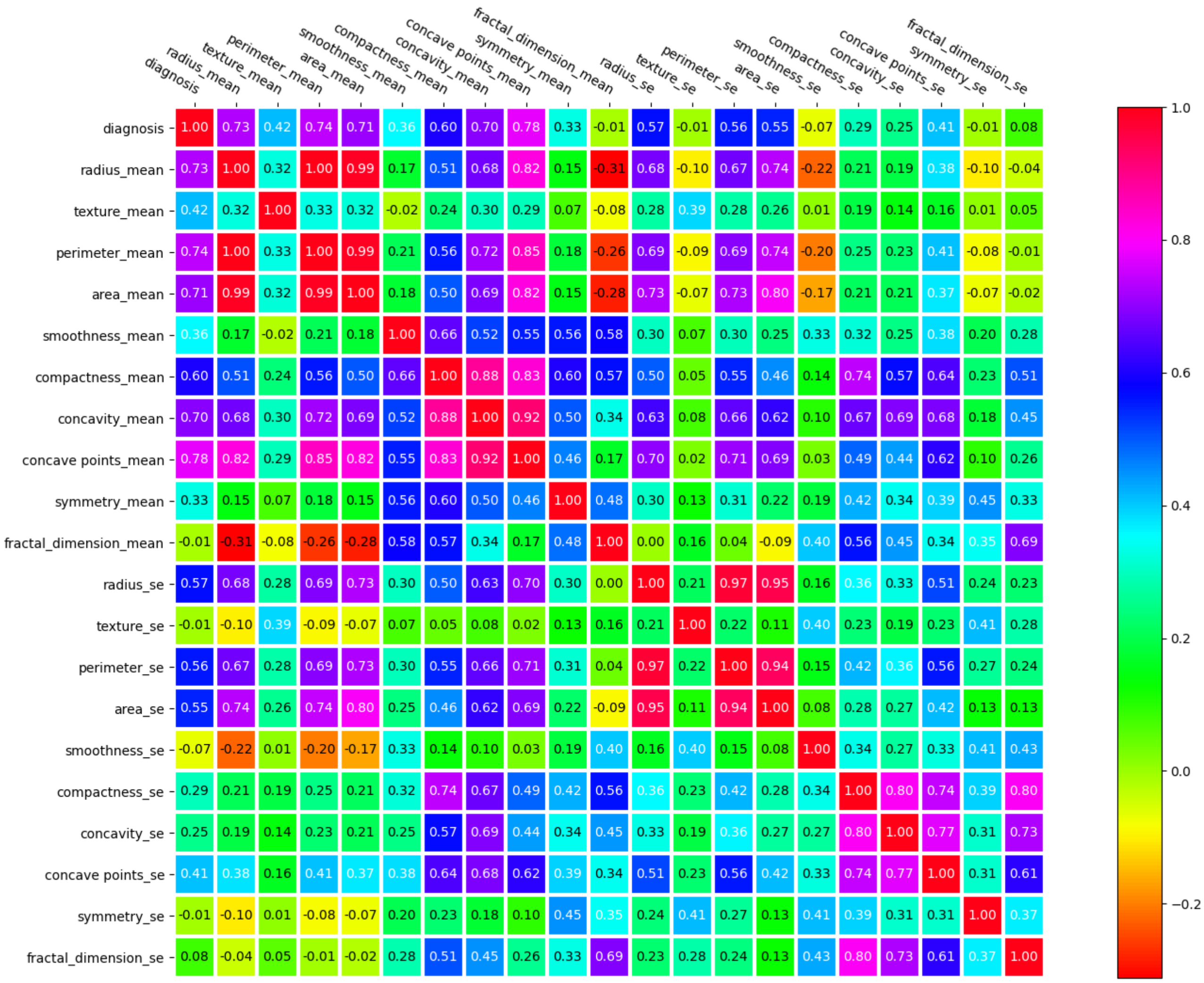


From the histograms, we can see some interesting trends. Possible observations:

- Many of the _se columns indicate a heavy skewness towards low values and have large tails
- Many of the _mean columns look more Gaussian in shape
- There is a large disparity between the ranges of certain features. For example, radius mean can go from 0 to 25 while smoothness_mean is in the range [0.050,0.150]. This indicates we will have to normalize or standardize the features if the models are sensitive to such measures.

Looking at the correlation matrix to get an idea about which features are important

In [16]:
```
correlations = data.corr()
columns = list(data)
#Creates the heatmap
heatmap(correlations.values,columns,columns,figsize = (20,12),cmap="hsv")
```



In [17]:
```
#Let's specifically look at the correlations of our target feature
correlations["diagnosis"].sort_values(ascending=False)
```

Out[17]:
```
diagnosis                 1.000000
concave points_mean       0.776614
perimeter_mean            0.742636
radius_mean               0.730029
area_mean                 0.708984
concavity_mean            0.696360
compactness_mean          0.596534
radius_se                 0.567134
perimeter_se              0.556141
area_se                   0.548236
texture_mean              0.415185
concave points_se         0.408042
smoothness_mean           0.358560
symmetry_mean             0.330499
compactness_se            0.292999
concavity_se              0.253730
fractal_dimension_se      0.077972
symmetry_se              -0.006522
texture_se               -0.008303
fractal_dimension_mean   -0.012838
smoothness_se            -0.067016
Name: diagnosis, dtype: float64
```

We can see that there is a lot of correlation between the features and the target label. Thus, we can expect to learn something from the data

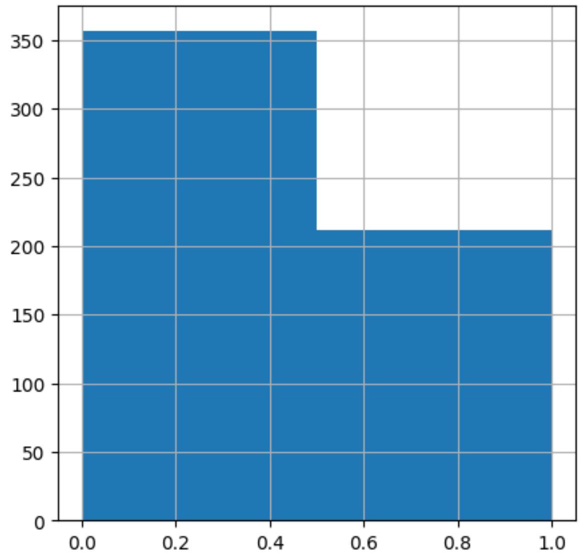
When doing classification, check if classes are heavily imbalanced.

It is important that the dataset does not prefer one class over any others. Otherwise, it may bias the model to not learn the minority classes well.

Lets use a histogram and count the number of elements in each class.

In [18]:
```
data['diagnosis'].hist(bins=2, figsize=(5,5))
data['diagnosis'].value_counts()
```

Out[18]:
```
0    357
1    212
Name: diagnosis, dtype: int64
```



There is a bit of an imbalance which is something to keep in mind if we find that our models do not perform well on the minority classes. For our purposes, this imbalance is not big enough to be an issue so we will not perform balancing techniques for this dataset.

Since the dataset is small though, we want to be careful when making training and testing splits to ensure that there is enough of each class for both splits. We will show how to perform this shortly.

Setting up the data

Before starting any model training, we have to split up the target labels from our features.

In [19]:
```
y = data["diagnosis"]
x = data.drop(["diagnosis"],axis = 1)
```

Now, we also split the data into training and testing data. To ensure that there is not an imbalance of classes in the training and testing set, we will use the stratify parameter in train_test_split to perform stratified sampling on the data (Recall from lecture how stratified sampling is performed).

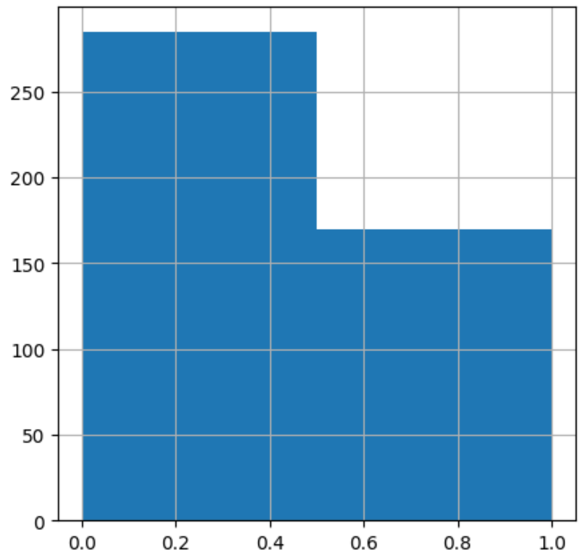
In [20]:
```
train_raw, test_raw, target, target_test = train_test_split(x,y, test_size=0.2, stratify= y, random_state=0)
```

Note that we named the input feature data as raw to indicate that there has been no pre-processing on them such as standardization. Shortly, we will show the affect that pre-processing has on the performance of the model.

Let us quickly test that the splits are somewhat balanced.

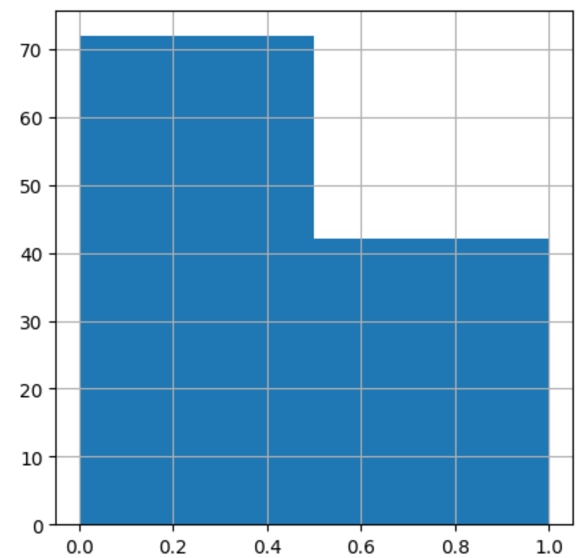
In [21]:
```
#Training classes
target.hist(bins=2, figsize=(5,5))
target.value_counts()
```

Out[21]:
```
0    285
1    170
Name: diagnosis, dtype: int64
```



In [22]:
```
#Testing classes
target_test.hist(bins=2, figsize=(5,5))
target_test.value_counts()
```

Out[22]:
```
0    72
1    42
Name: diagnosis, dtype: int64
```



We can see that the class balance is about the same as before the split. In fact, we can see that if a classifier just guessed class 0, it would have an accuracy of $100 * \frac{72}{72+42} = 63.15\%$. We can consider this the baseline accuracy to compare against.

Models for Classification: KNN

For our first model, we will use KNN classfication. This is a model we have seen many times throughout the course and it would be interesting to see how well it performs.

Simple KNN classification with K = 3

Let us try KNN on the raw data with simply 3 nearest neighbors. We use the sklearn metric library (https://scikit-learn.org/stable/modules/model_evaluation.html) to calculate the measures of interest. In this case, we focus on accuracy.

In [23]:
```
# k-Nearest Neighbors algorithm
knn = KNeighborsClassifier(n_neighbors=3)
knn.fit(train_raw, target)
predicted = knn.predict(test_raw)
```

In [24]:
```
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Accuracy:    0.877193
```

We can see that there is already a huge improvement in accuracy on comparison to the baseline of 63.15%. Let's see the effect that standardizing the input features would have on the KNN performance.

Affect of pre-processing on KNN

In [25]:
```
#Since all features are real-valued, we only have one pipeline
pipeline = Pipeline([
    ('scaler', StandardScaler())
])


#Transform raw data
train = pipeline.fit_transform(train_raw)
test = pipeline.transform(test_raw) #Note that there is no fit calls
```

In [26]:
```
# k-Nearest Neighbors algorithm
knn = KNeighborsClassifier(n_neighbors=3)
knn.fit(train, target)
testing_result = knn.predict(test)
predicted = knn.predict(test)
```

In [27]:
```
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Accuracy:    0.921053
```

We can see that with pre-processing we were able to get a much better classification accuracy.

Here we only used StandardScaler. Lets see if other pre-processing techniques could have also worked. As such, lets look at MinMaxScaler and Normalizer:

In [28]:
```

preprocessors = [StandardScaler(),MinMaxScaler(),Normalizer() ]

for pre in preprocessors:
    pipeline = Pipeline([
        ('preprocessor', pre)
    ])


    #Transform raw data
    train = pipeline.fit_transform(train_raw)
    test = pipeline.transform(test_raw) #Note that there is no fit calls
    # k-Nearest Neighbors algorithm
    knn = KNeighborsClassifier(n_neighbors=7)
    knn.fit(train, target)
    testing_result = knn.predict(test)
    predicted = knn.predict(test)

    print(pre)
    print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

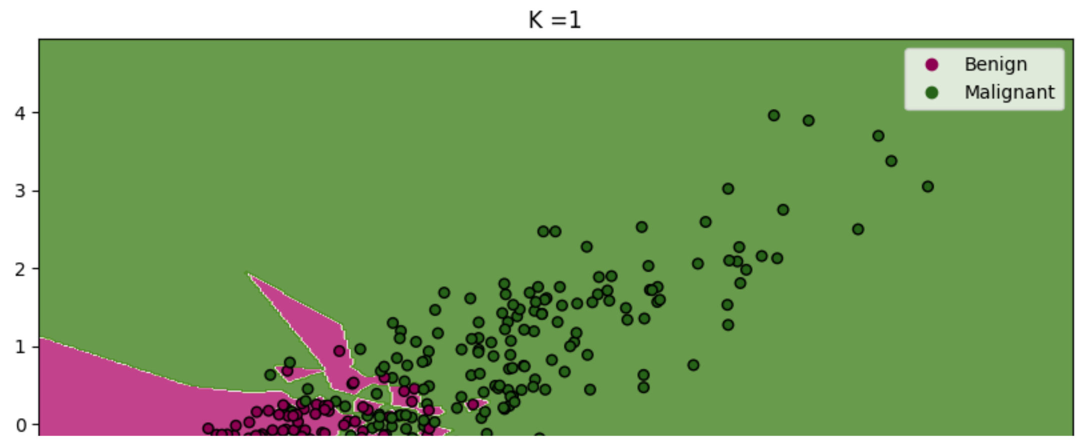
```
StandardScaler()
Accuracy:    0.903509
MinMaxScaler()
Accuracy:    0.912281
Normalizer()
Accuracy:    0.885965
```

We can see that MinMaxScaler had the same performance as StandardScaler. Yet, Normalizer did not improve the model.

Visualizing decision boundaries for KNN

Its always nice to see the decision boundaries a model decides upon. Let's see how the decision boundary changes as function of k when only using the two most correlated features to the target labels: concave_points_mean and perimeter_mean.

In [29]:
```
#Extract first two features and use the standardscaler
train_2 = StandardScaler().fit_transform(train_raw[['concave points_mean','perimeter_mean']])

k_r  = [1,3,5,7]
for k in k_r:
    knn = KNeighborsClassifier(n_neighbors=k)
    knn.fit(train_2, target)
    draw_contour(train_2,target,knn, class_labels = ['Benign', 'Malignant'])

    plt.title(f"K ={k}")
```



We can see that as k gets larger, the decision boundary gets smoother.

Models for Classification: Logistic Regression

While KNN is a very powerful model, it does come with a few issues such as

- Require storing the full training dataset
- Prediction is done by comparing new sample will all samples in training set which is time-consuming

These issues arise because KNN is a **non-parametric** model which means that it does not summarize the data into a finite set of parameters.

Let us now look at Logistic Regression which is an example of a **parametric** model.

Simple Logistic Regression

First, let us see how logistic regression performs without any regularization.

In [30]:
```
log_reg = LogisticRegression(penalty = "l2",max_iter = 1000, solver = "lbfgs", C=(10**30)/1)
#C is choosen to be high to remove regularization
#We could have chosen penalty = "none" since lbfgs supports it but this option is not possible for all solvers.

log_reg.fit(train_raw, target)
testing_result = log_reg.predict(test_raw)
predicted = log_reg.predict(test_raw)

print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Accuracy:    0.956140

/home/josh/.local/lib/python3.10/site-packages/sklearn/linear_model/_logistic.py:444: ConvergenceWarning: lbfgs fa
iled to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html (https://scikit-learn.org/stable/modules/preprocess
ing.html)
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression (https://scikit-learn.org/stabl
e/modules/linear_model.html#logistic-regression)
  n_iter_i = _check_optimize_result(
```

We can see that Logistic Regression is actually performing much better than any of the KNN models we tried. We can also see the parameters that the model learned.

In [31]:
```
#Parameters for each feature
log_reg.coef_
```

Out[31]:
```
array([[ 6.34289470e+00,  5.47849287e-01, -1.20688690e+00,
         1.85996451e-02,  4.56958906e+01,  2.53266931e+01,
         6.03823865e+01,  6.42115111e+01,  4.80889648e+01,
        -1.41499498e-01, -3.55987410e+01, -2.47759411e+00,
         6.15222166e-01,  4.59555277e-01, -1.18708808e+00,
        -4.77453177e+01, -6.90140641e+01, -7.30478909e+00,
        -1.14536151e+01, -1.04372288e+01]])
```

In [32]:
```
#Intercept term
log_reg.intercept_
```

Out[32]:
```
array([-21.84477771])
```

In [33]:
```
print("Number of Features in data:", train_raw.shape[1])
print("Number of Parameters:", len(log_reg.coef_[0]))
```

```
Number of Features in data: 20
Number of Parameters: 20
```

Since we are using Logistic Regression where we model the log odds with a linear function, it makes sense that we have a parameter/coefficient for each input feature.

Parameters for Logistic Regression

In Sci-kit Learn, the following are just some of the parameters we can pass into Logistic Regression:

- penalty: {'l1', 'l2', 'elasticnet', 'none'} default="l2"
  - Specifies the type of regularization to use. Not all penalties work for each solver.
- C: positive float, default=1
  - Inverse of the regularization strength. You can treat C as $\frac{1}{\lambda}$ as shown in lecture. Thus, as C gets smaller, the regularization strength increases.
- solver: {'newton-cg', 'lbfgs', 'liblinear', 'sag', 'saga'}, default='lbfgs'
  - Algorithm to use in the optimization problem. Each algorithms solves logistic regression using different iterative methods that are based on the gradient. Read the [sci-kit learn documentation (https://scikit-learn.org/dev/modules/linear_model.html#logistic-regression)](https://scikit-learn.org/dev/modules/linear_model.html#logistic-regression) for more information.
- max_iter: int, default=100
  - Maximum number of iterations taken for the solvers to converge.

Each parameter has a different effect on the model. Let's look at how the choose of max_iter affects the model performance on the raw data and the standardized dataset.

In [34]:
```

#Since all features are real-valued, we only have one pipeline
preprocesser = Pipeline([
    ('scaler', StandardScaler())
])


#Transform raw data
train = preprocesser.fit_transform(train_raw)
test = preprocesser.transform(test_raw) #Note that there is no fit call
```

In [35]:
```
log_reg = LogisticRegression(penalty = "l2",max_iter = 1000, solver = "lbfgs", C= 0.01)

#Train raw is the data before preprocessing
log_reg.fit(train_raw, target)
predicted = log_reg.predict(test_raw)
print("%-12s %f" % ('Raw Data Accuracy:', metrics.accuracy_score(target_test,predicted)))


#Train is the data after preprocessing (using Standard scalar)
log_reg.fit(train, target)
predicted = log_reg.predict(test)

print("%-12s %f" % ('Preprocessed Data Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Raw Data Accuracy: 0.938596
Preprocessed Data Accuracy: 0.947368
```

We see that the accuraccies are pretty close to each other. Lets see what happens when we decrease the max_iter.

In [36]:
```
log_reg = LogisticRegression(penalty = "l2",max_iter = 70, solver = "lbfgs", C= 0.01)

#Train raw is the data before preprocessing
log_reg.fit(train_raw, target)
predicted = log_reg.predict(test_raw)
print("%-12s %f" % ('Raw Data Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Raw Data Accuracy: 0.921053

/home/josh/.local/lib/python3.10/site-packages/sklearn/linear_model/_logistic.py:444: ConvergenceWarning: lbfgs fa
iled to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html (https://scikit-learn.org/stable/modules/preprocess
ing.html)
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression (https://scikit-learn.org/stabl
e/modules/linear_model.html#logistic-regression)
  n_iter_i = _check_optimize_result(
```

Ooops! The model did not seem to converge. Its seem that the scale of the features strongly affects the convergence speed of the iterative algorithm. As suggested, we can fix this issue by increaing the max_iter, re-scaling the data, or using a different solver.

In [37]:
```
#Train is the data after preprocessing (using Standard scalar)
log_reg.fit(train, target)
predicted = log_reg.predict(test)

print("%-12s %f" % ('Preprocessed Data Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Preprocessed Data Accuracy: 0.947368
```

Cross Validation for Logistic Regression

Let us do a little experiment using cross validation to see how each term affects the logistic regression. We will perform this example on the standardized data.

In [38]:
```


#You may even do Cross validation for classification

from sklearn.model_selection import GridSearchCV

#Note that this a list of dict
#Each dict describes the combination of parameters to check
parameters = [
    {"penalty": ["l2"],
    "C": [0.01,1,100],
    "solver": ["lbfgs","liblinear"]},#These solvers support penalty = "l2"
    {"penalty": ["none"],
    "C": [1], #Specified to prevent error message
    "solver": ["lbfgs","newton-cg"]},#These solvers support penalty = "none"
]

#instantiate model


#Implementing cross validation

k = 3
kf = KFold(n_splits=k, random_state=None)

log_reg = LogisticRegression(penalty = "none",max_iter = 1000, solver = "lbfgs") #will change parameters during CV
grid = GridSearchCV(log_reg , parameters, cv = kf, scoring = "accuracy")
grid.fit(train,target)
```

```
/home/josh/.local/lib/python3.10/site-packages/scipy/optimize/_linesearch.py:305: LineSearchWarning: The line sear
ch algorithm did not converge
  warn('The line search algorithm did not converge', LineSearchWarning)
/home/josh/.local/lib/python3.10/site-packages/sklearn/utils/optimize.py:203: UserWarning: Line Search failed
  warnings.warn("Line Search failed")
```

Out[38]:
```
▸ GridSearchCV
▸ estimator: LogisticRegression
  ▸ LogisticRegression
```

In [39]:
```
#Put results into Dataframe
res= pd.DataFrame(grid.cv_results_)
res
```

Out[39]:

	mean_fit_time	std_fit_time	mean_score_time	std_score_time	param_C	param_penalty	param_solver	params	split0_test_score	split1_test_score	split
0	0.010789	0.004541	0.003772	0.004006	0.01	l2	lbfgs	{'C': 0.01, 'penalty': 'l2', 'solver': 'lbfgs'}	0.914474	0.927632	
1	0.003817	0.001406	0.000981	0.000110	0.01	l2	liblinear	{'C': 0.01, 'penalty': 'l2', 'solver': 'liblin...	0.921053	0.953947	
2	0.013168	0.001413	0.002027	0.001604	1	l2	lbfgs	{'C': 1, 'penalty': 'l2', 'solver': 'lbfgs'}	0.960526	0.960526	
3	0.002684	0.000223	0.000959	0.000170	1	l2	liblinear	{'C': 1, 'penalty': 'l2', 'solver': 'liblinear'}	0.960526	0.960526	
4	0.036103	0.008450	0.000634	0.000080	100	l2	lbfgs	{'C': 100, 'penalty': 'l2', 'solver': 'lbfgs'}	0.947368	0.947368	
5	0.003319	0.000470	0.000643	0.000036	100	l2	liblinear	{'C': 100, 'penalty': 'l2', 'solver': 'libline...	0.947368	0.953947	
6	0.101528	0.062953	0.000873	0.000098	1	none	lbfgs	{'C': 1, 'penalty': 'none', 'solver': 'lbfgs'}	0.940789	0.953947	
7	0.059927	0.017233	0.001042	0.000414	1	none	newton-cg	{'C': 1, 'penalty': 'none', 'solver': 'newton-...	0.940789	0.953947	

In [40]:
```
#Extract the columns that specify the score and the parameters for each row
res[["rank_test_score","param_C","param_penalty","param_solver","mean_test_score"]]
```

Out[40]:

	rank_test_score	param_C	param_penalty	param_solver	mean_test_score
0	8	0.01	l2	lbfgs	0.916463
1	5	0.01	l2	liblinear	0.934051
2	2	1	l2	lbfgs	0.956024
3	1	1	l2	liblinear	0.958232
4	7	100	l2	lbfgs	0.934007
5	4	100	l2	liblinear	0.936200
6	6	1	none	lbfgs	0.934007
7	3	1	none	newton-cg	0.938422

We can see that the choice of these parameters can stronlgy affect performance of the classifier. Lets check the performance of the best parameters on the test set.

In [41]:
```

#Train raw is the data before preprocessing
predicted = grid.predict(test)
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Accuracy:    0.938596
```

Note that this test accuracy is not as good as some of the other logistic regression examples we've shown.

Speedtest between KNN and Logistic Regression

Lets see how long KNN and Logistic Regression take to perform training and testing.

In [42]:
```
scaler = StandardScaler()
train = scaler.fit_transform(train_raw)
test = scaler.fit_transform(test_raw)


log_reg = LogisticRegression(penalty = "none",max_iter = 1000)
knn = KNeighborsClassifier(n_neighbors=3)

t0 = time.time()
knn.fit(train, target)
t1 = time.time()
print("KNN Training Time : ", t1-t0)

t0 = time.time()
log_reg.fit(train, target)
t1 = time.time()
print("Logistic Regression Training Time : ", t1-t0)
```

```
KNN Training Time :  0.002641439437866211
Logistic Regression Training Time :  0.22118496894836426
```

In [43]:
```
t0 = time.time()
knn.predict(test)
t1 = time.time()
print("KNN Testing Time : ", t1-t0)

t0 = time.time()
log_reg.predict(test)
t1 = time.time()
print("Logistic Regression Testing Time : ", t1-t0)
```

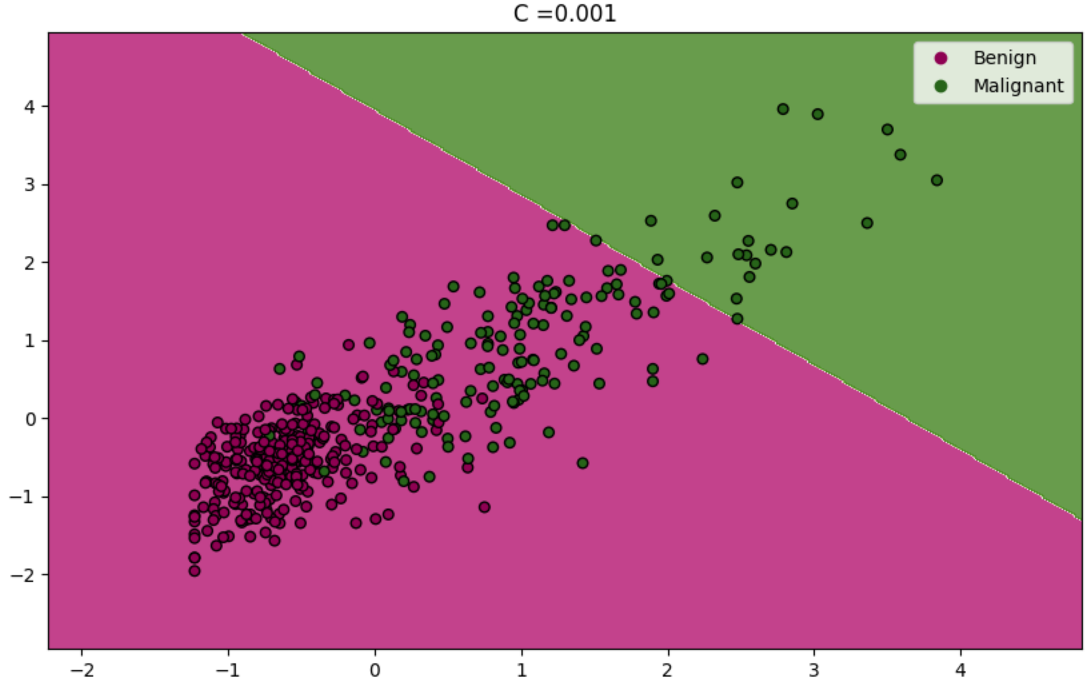
```
KNN Testing Time :  0.031116962432861328
Logistic Regression Testing Time :  0.0003840923309326172
```

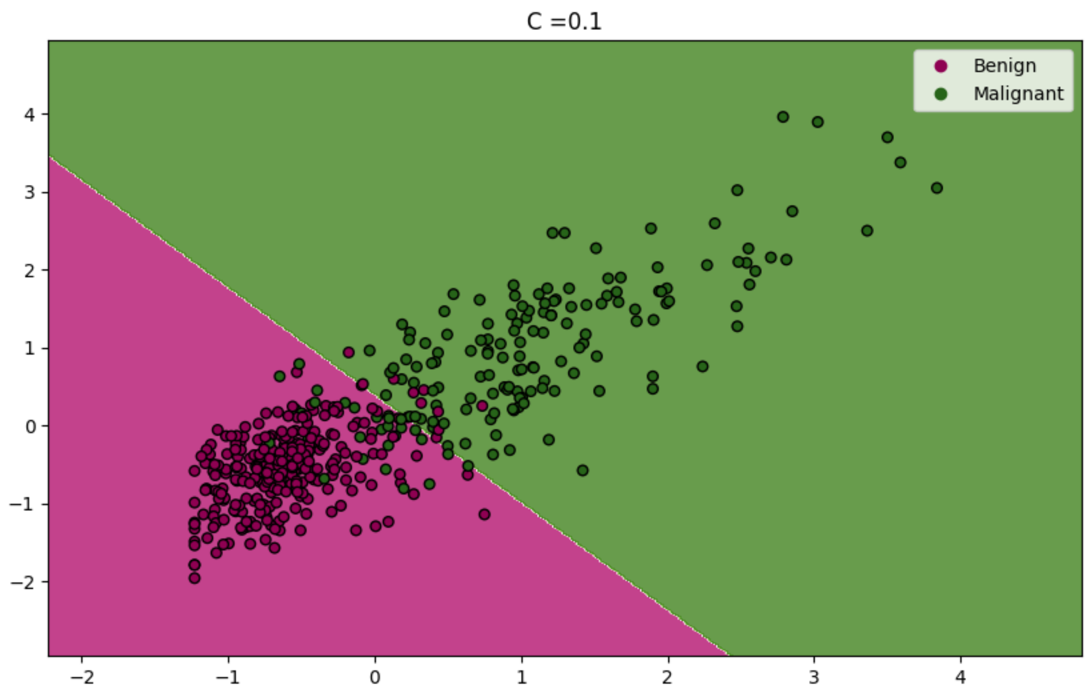
This simple test shows that Logistic Regression is slower than KNN during Training time but is much faster during testing time.

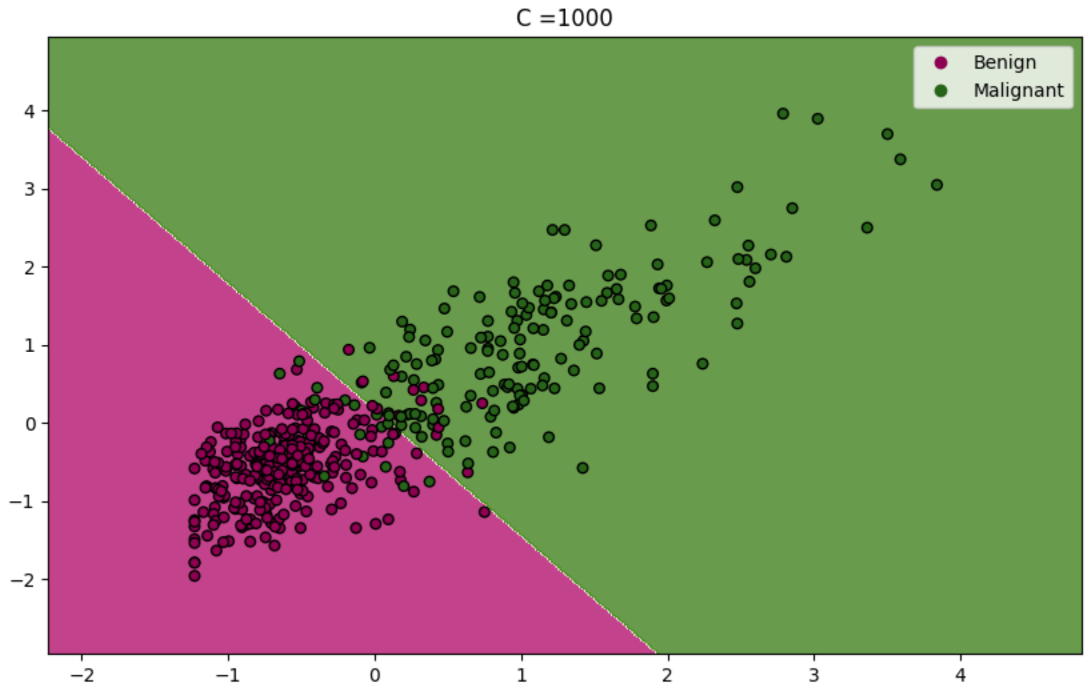
Visualizing decision boundaries for Logistic Regression

Now, lets look at the decision boundary caused by Logistic Regression. Same as for KNN, we use the two most correlated features to the target labels: concave_points_mean and perimeter_mean. This way, we can visualize the 2D decision boundary.

In [44]:
```
#Extract first two feature and use the standardscaler
train_2 = StandardScaler().fit_transform(train_raw[['concave points_mean','perimeter_mean']])

Cs  = [0.001,0.1,1000]
for C in Cs:
    log_reg = LogisticRegression(penalty = "l2",max_iter = 1000, solver = "lbfgs", C=C) #will change parameters dur
    log_reg.fit(train_2, target)

    draw_contour(train_2,target,log_reg, class_labels = ['Benign', 'Malignant'])
    plt.title(f"C ={C}")
```





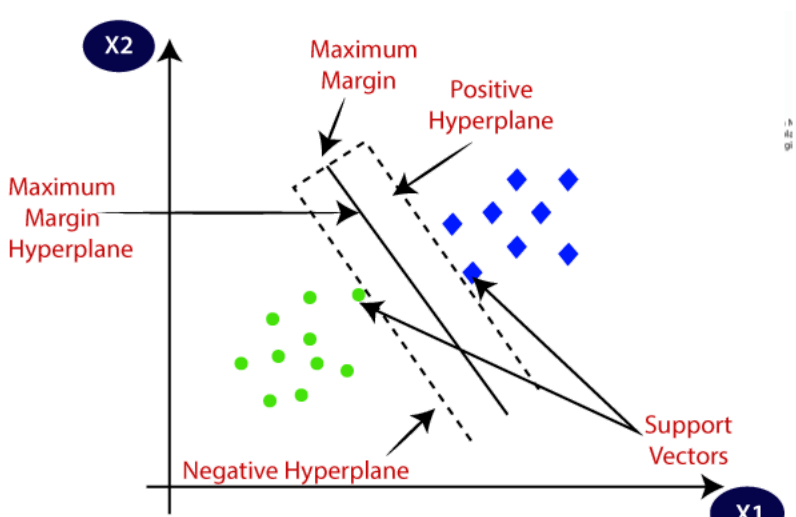


We can see as the regularization strength changes, the decision boundary moves as well. Additionally, we can clearly see that the decision boundary is a line since this is a linear model.

Models for Classification: SVM

We now discuss another type of linear classification model known as Support Vector Machines (SVM). Where Logistic Regression was motivated probability theory, SVM is motivated by geometeric arguments. Specifcally, SVM finds a separating hyperline that maximizes the margin (i.e. distance from each class). The hyperplane is used to classify the points by designating every sample on of side of the hyperplane as the positive class and the other side as the negative class.

The hyperplane is determine by a few sample points known as support vectors that uniquely characterize the hyperplane.



Note that it may not always be possible to find a hyperplane that completely separates the classes. Thus, we use what is known as Soft-Margin SVM which aims to maximize the margin while minizming the distance on the classes that are on the wrong side.

All Sci-kit learn implementations of SVM that we use are soft-margin SVM.

Simple SVM classification

In [45]:
```
svm = SVC()
svm.fit(train, target)
predicted = svm.predict(test)
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```

```
Accuracy:    0.921053
```

Parameters for SVM

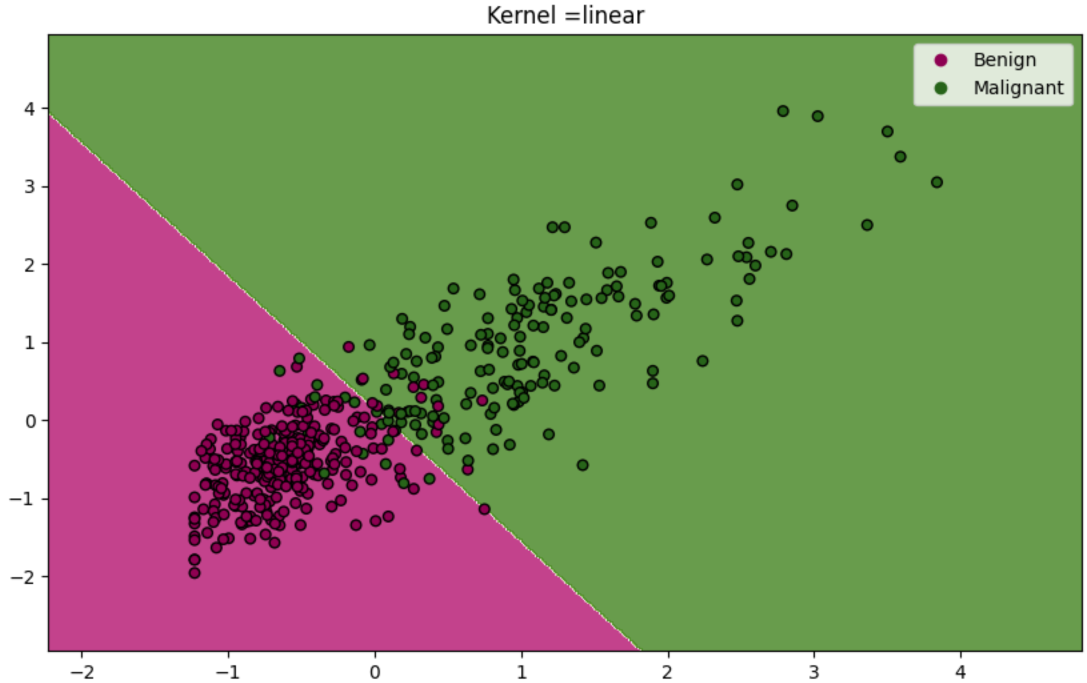
In Sci-kit Learn, the following are just some of the parameters we can pass into Logistic Regression:

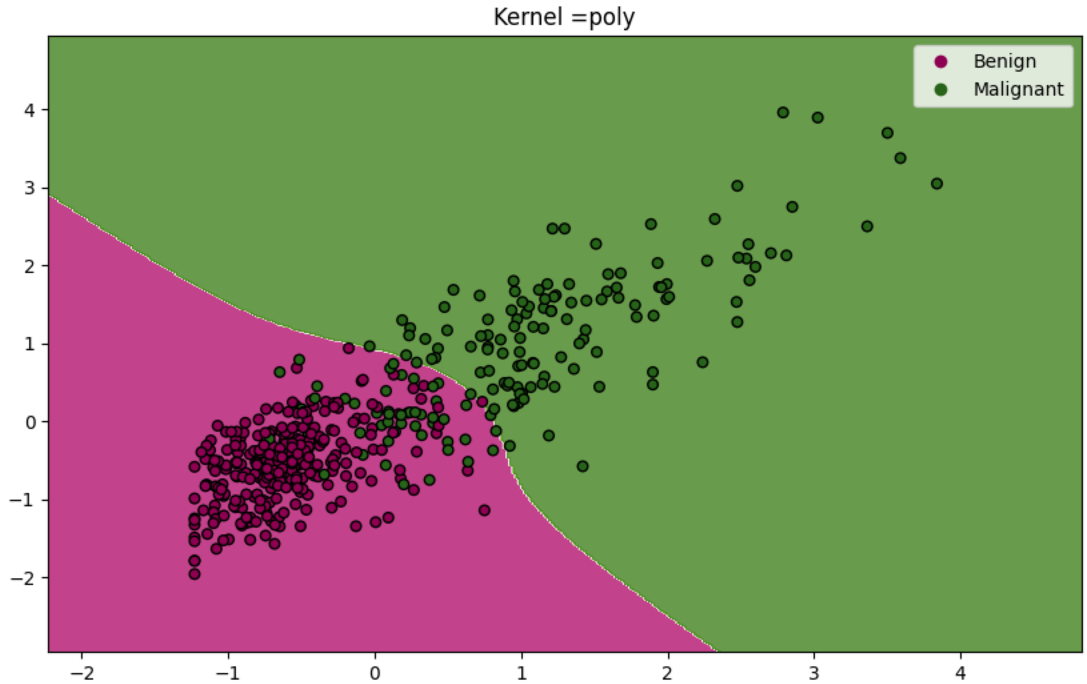
- C: positive float, default=1
  - Inverse of the regularization strength. You can treat C as $\frac{1}{\lambda}$ as shown in lecture. Thus, as C gets smaller, the regularization strength increases. SVM only uses the L2 regularization.
- kernel: {‘linear’, ‘poly’, ‘rbf’, ‘sigmoid’}, default=’rbf’
  - Specifies the kernel type to be used in the algorithm. A kernel specifies a mapping into a higher dimension space to allow for non-linear decision boundaries.
- degree: int, default=3
  - Degree of the polynomial kernel function (‘poly’). Ignored by all other kernels.

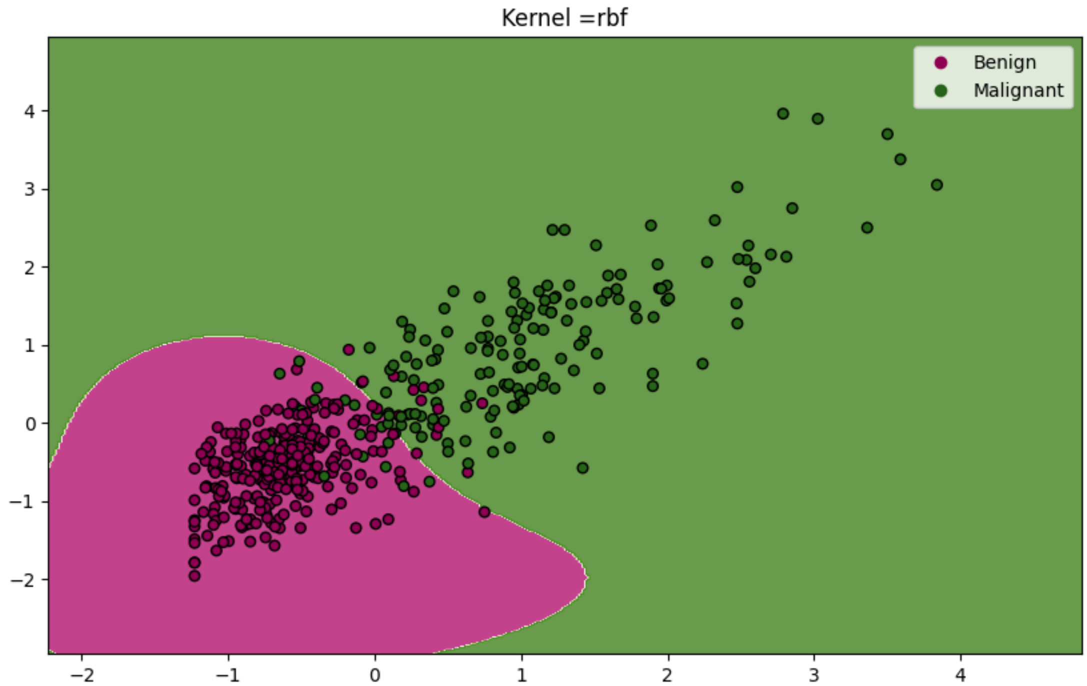
Visualizing decision boundaries for SVM

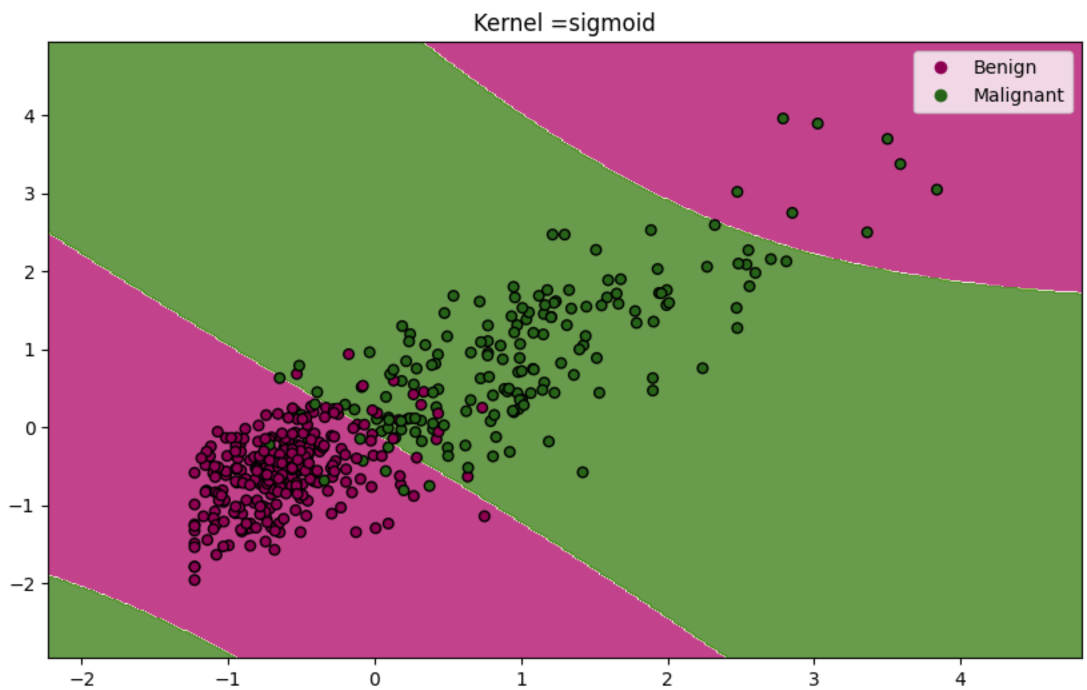
Now, lets look at the decision boundary caused by SVM with different kernels. Same as for KNN and Logistic Regression, we use the two most correlated features to the target labels: concave_points_mean and perimeter_mean. This way, we can visualize the 2D decision boundary.

In [46]:
```
#Extract first two feature and use the standardscaler
train_2 = StandardScaler().fit_transform(train_raw[['concave points_mean','perimeter_mean']])

kernel  = ['linear', 'poly', 'rbf',  'sigmoid']
for ker in kernel:
    svm = SVC(kernel = ker) #will change parameters during CV
    svm.fit(train_2, target)
    draw_contour(train_2,target,svm,class_labels = ['Benign', 'Malignant'])

    plt.title(f"Kernel ={ker}")
```









We can see that the decision boundary is not always linear because we are using non-linear kernels.

Important Measures for Classifications

Now that we have gone over a few models for binary classification, let's explore the different ways we can measure the performance of these models.

In [47]:
```
#Example classifier
log_reg = LogisticRegression(max_iter = 1000)
log_reg.fit(train_raw, target)
predicted = log_reg.predict(test_raw)
```

Here are just some of the most important measures of interest. We use the convention to refer to the class labeled as 1 as the positive class.

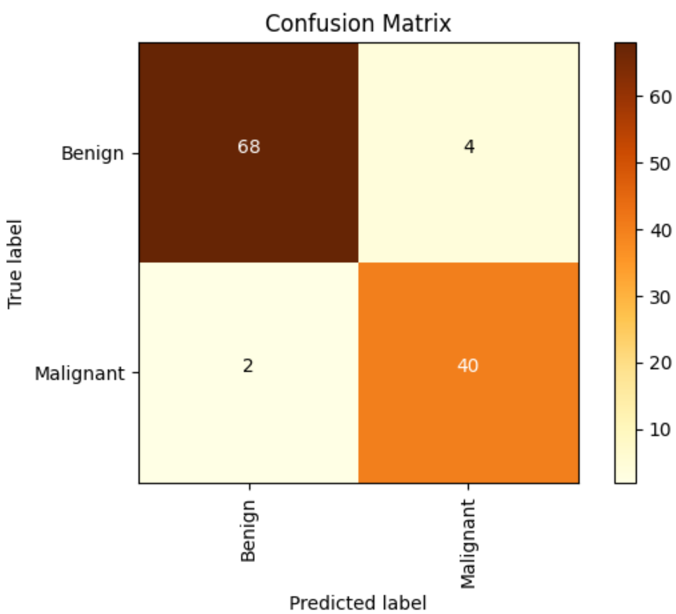
- **Accuracy:** The percentage of predictions that are correct. Use metrics.accuracy_score
- **Precision:** $\frac{\text{Number of labels correctly classified as positive}}{\text{Number of labels classified as positives}}$. Percentage of predictions that are correctly positive among all the predictions that were classified as positive. Use metrics.precision_score

- **Recall:** $\frac{\text{Number of labels correctly classified as positive}}{\text{Number of labels where the true class is positive}}$. Percentage of predictions that are correctly positive among all the labels where the true class is positive. Also known as the probability of detecting when a class is positive. Use metrics.recall_score
- **F1 Score:** Harmonic mean of the precision and recall. Highest value is 1 when both precision and recall are 1, i.e. perfect. Lowest value is 0 when either precision or recall is zero. Provides an aggregate score to analyze both precision and recall. Use metrics.f1_score

We can calculate these measures by using a confusion matrix as well.

In [48]:
```
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
print("%-12s %f" % ('Precision:', metrics.precision_score(target_test,predicted, labels=None, pos_label=1, average=
print("%-12s %f" % ('Recall:', metrics.recall_score(target_test,predicted, labels=None, pos_label=1, average='binar
print("%-12s %f" % ('F1 Score:', metrics.f1_score(target_test,predicted, labels=None, pos_label=1, average='binary'
print("Confusion Matrix: \n", metrics.confusion_matrix(target_test,predicted))

#Draws confusion matrix
draw_confusion_matrix(target_test, predicted, ['Benign', 'Malignant'])
```

```
Accuracy:    0.947368
Precision:   0.909091
Recall:      0.952381
F1 Score:    0.930233
Confusion Matrix:
 [[68  4]
 [ 2 40]]
```



TODO: Using classification methods to classify heart disease

Now that you have some examples of the classifiers that Sci-kit learn has to offers, let try to apply them to a new dataset.

Background: The Dataset

For this exercise we will be using a subset of the UCI Heart Disease dataset, leveraging the fourteen most commonly used attributes. All identifying information about the patient has been scrubbed. You will be asked to classify whether a **patient is suffering from heart disease** based on a host of potential medical factors.

The dataset includes 14 columns. The information provided by each column is as follows:

- **age:** Age in years
- **sex:** (1 = male; 0 = female)
- **cp:** Chest pain type (0 = asymptomatic; 1 = atypical angina; 2 = non-anginal pain; 3 = typical angina)
- **trestbps:** Resting blood pressure (in mm Hg on admission to the hospital)
- **chol:** cholesterol in mg/dl
- **fbs** Fasting blood sugar > 120 mg/dl (1 = true; 0 = false)
- **restecg:** Resting electrocardiographic results (0= showing probable or definite left ventricular hypertrophy by Estes' criteria; 1 = normal; 2 = having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV))
- **thalach:** Maximum heart rate achieved
- **exang:** Exercise induced angina (1 = yes; 0 = no)
- **oldpeak:** Depression induced by exercise relative to rest
- **slope:** The slope of the peak exercise ST segment (0 = downsloping; 1 = flat; 2 = upsloping)
- **ca:** Number of major vessels (0-3) colored by flourosopy

- **thal:** 1 = normal; 2 = fixed defect; 7 = reversable defect
- **sick:** Indicates the presence of Heart disease (True = Disease; False = No disease)

[25 pts] Part 1. Load the Data and Analyze

Let's first load our dataset so we'll be able to work with it. (correct the relative path if your notebook is in a different directory than the csv file.)

In [49]:
```
data = pd.read_csv('datasets/heartdisease.csv')
```

[5 pts] Looking at the data

Now that our data is loaded, let's take a closer look at the dataset we're working with. Use the head method, the describe method, and the info method to display some of the rows so we can visualize the types of data fields we'll be working with.

In [50]:
```
data.head(5)
```

Out[50]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	sick
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	False
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	False
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	False
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	False
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	False

In [51]:
```
data.describe()
```

Out[51]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515	0.528053	149.646865	0.326733	1.039604	1.399340	0.729373	2
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.905161	0.469794	1.161075	0.616226	1.022606	0
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	0.000000	0.000000	0
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000	0.000000	1.000000	0.000000	2
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000	0.000000	0.800000	1.000000	0.000000	2
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.000000	1.000000	1.600000	2.000000	1.000000	3
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	2.000000	4.000000	3

In [52]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       303 non-null    int64  
 1   sex       303 non-null    int64  
 2   cp        303 non-null    int64  
 3   trestbps  303 non-null    int64  
 4   chol      303 non-null    int64  
 5   fbs       303 non-null    int64  
 6   restecg   303 non-null    int64  
 7   thalach   303 non-null    int64  
 8   exang     303 non-null    int64  
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64  
 11  ca        303 non-null    int64  
 12  thal      303 non-null    int64  
 13  sick      303 non-null    bool   
dtypes: bool(1), float64(1), int64(12)
memory usage: 31.2 KB
```

Sometimes data will be stored in different formats (e.g., string, date, boolean), but many learning methods work strictly on numeric inputs. Additionally, some numerical features can represent categorical features which need to be pre-processed. Are there any columns that need to be transformed and why?

We would need to transform cp, restecg, slope, thal, and sick as these are all categorical data points that are not already one-hot encoded.

Determine if we're dealing with any null values. If so, report on which columns?

In [53]:
```
data.isnull().sum()
```

Out[53]:
```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
sick        0
dtype: int64
```

No null values we need to deal with.

[5 pts] Transform target label into numerical value

Before we begin our analysis, we need to fix the field(s) that will be problematic. Specifically, convert our boolean "sick" variable into a binary numeric target variable (values of either '0' or '1') using the [label encoder from scikit-learn (https://scikit-learn.org/stable/modules/generated/sklearn.preprocessing.LabelEncoder.html)](https://scikit-learn.org/stable/modules/generated/sklearn.preprocessing.LabelEncoder.html), place this new array into a new column of the DataFrame named "target", and then drop the original "sick" column from the dataframe. Afterward, use .head to print the first 5 rows

In [54]:
```
le = LabelEncoder()

data['target'] = le.fit_transform(data['sick'])
data = data.drop(["sick"],axis= 1)
#print(le.classes_)
data.head(5)
```

Out[54]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	0
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	0
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	0
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	0
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	0

In [55]:
```
data['target']
```

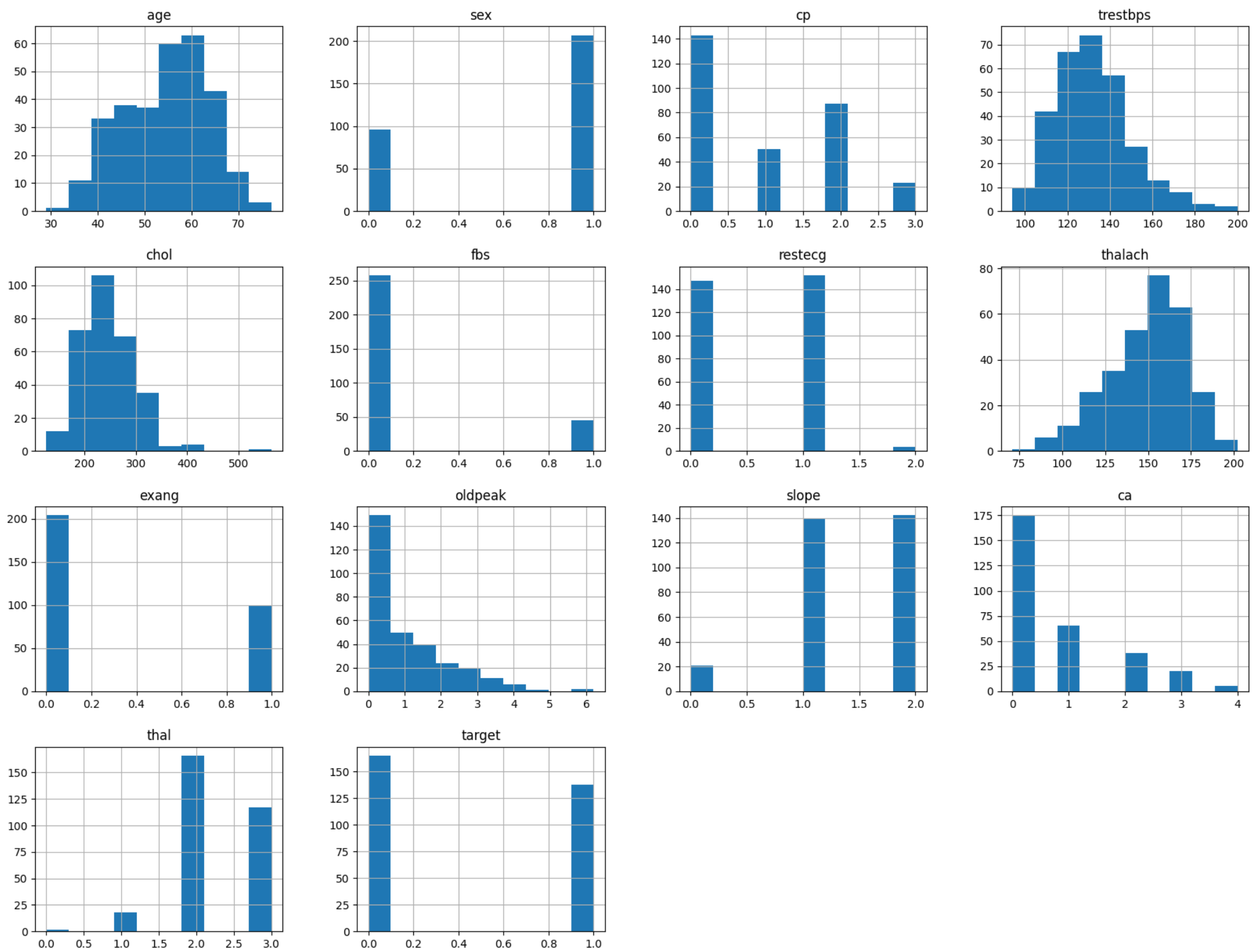
Out[55]:
```
0      0
1      0
2      0
3      0
4      0
      ..
298    1
299    1
300    1
301    1
302    1
Name: target, Length: 303, dtype: int64
```

[5 pts] Plotting histogram of data

Now that we have a feel for the data-types for each of the variables, plot histograms of each field.

In [56]:
```
data.hist(figsize = (20,15))
```

Out[56]:
```
array([[<AxesSubplot: title={'center': 'age'}>,
        <AxesSubplot: title={'center': 'sex'}>,
        <AxesSubplot: title={'center': 'cp'}>,
        <AxesSubplot: title={'center': 'trestbps'}>],
       [<AxesSubplot: title={'center': 'chol'}>,
        <AxesSubplot: title={'center': 'fbs'}>,
        <AxesSubplot: title={'center': 'restecg'}>,
        <AxesSubplot: title={'center': 'thalach'}>],
       [<AxesSubplot: title={'center': 'exang'}>,
        <AxesSubplot: title={'center': 'oldpeak'}>,
        <AxesSubplot: title={'center': 'slope'}>,
        <AxesSubplot: title={'center': 'ca'}>],
       [<AxesSubplot: title={'center': 'thal'}>,
        <AxesSubplot: title={'center': 'target'}>, <AxesSubplot: >,
        <AxesSubplot: >]], dtype=object)
```

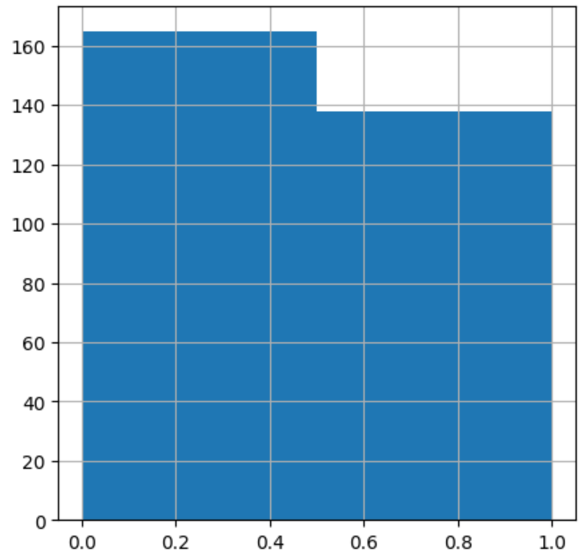


[5 pts] Looking at class balance

We also want to make sure we are dealing with a balanced dataset. In this case, we want to confirm whether or not we have an equitable number of sick and healthy individuals to ensure that our classifier will have a sufficiently balanced dataset to adequately classify the two. Plot a histogram specifically of the sick target, and conduct a count of the number of sick and healthy individuals and report on the results:

In [57]:
```
data['target'].hist(bins=2, figsize=(5,5))
data['target'].value_counts()
```

Out[57]:
```
0    165
1    138
Name: target, dtype: int64
```



The data seems to be fairy evenly balanced with 54% not sick.

Balanced datasets are important to ensure that classifiers train adequately and don't overfit, however arbitrary balancing of a dataset might introduce its own issues.

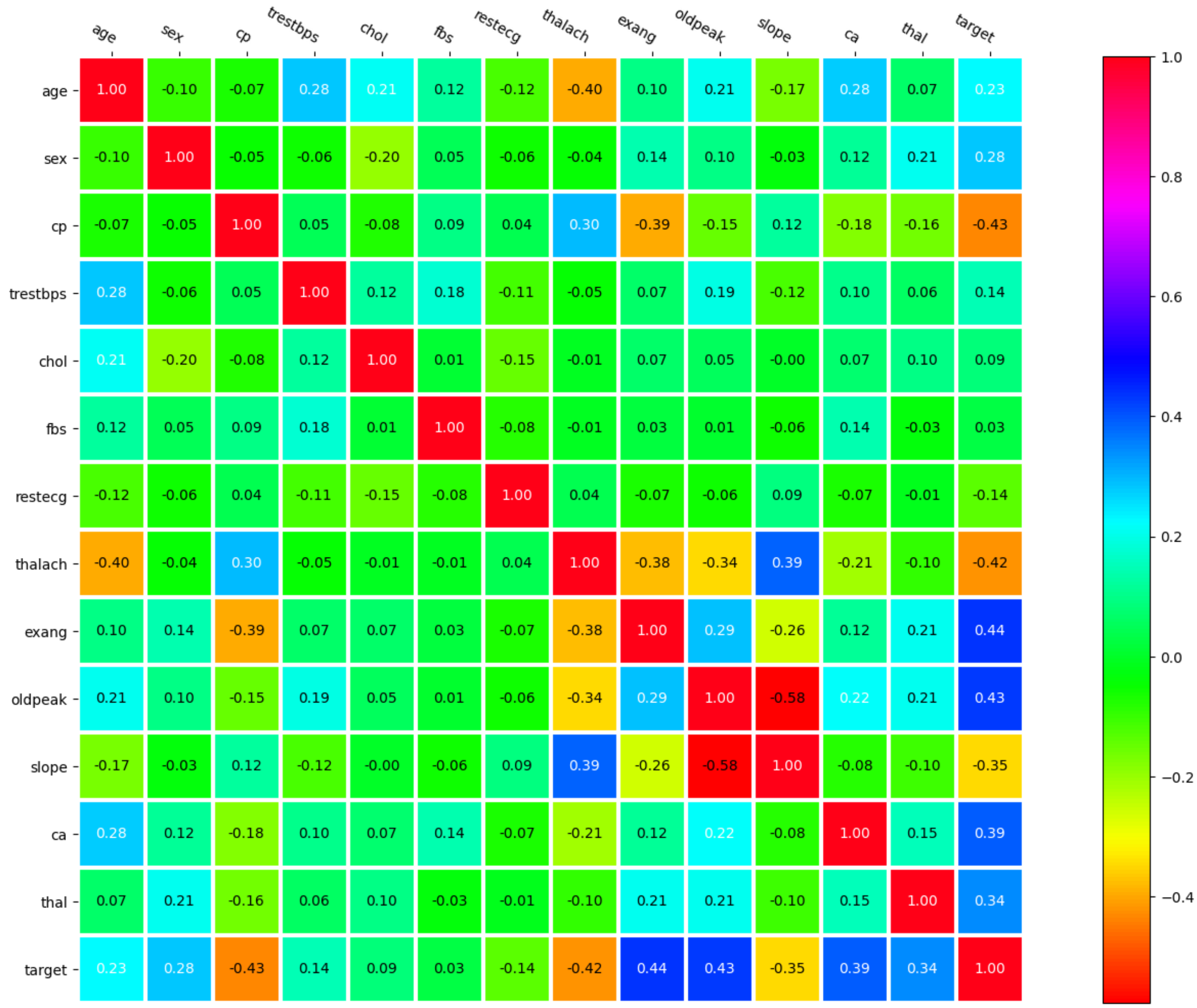
Discuss some of the problems that might arise by artificially balancing a dataset.

The main issue one may arise is the introduction of bias. We may accidently balance towards certain values when we remove/add data points.

[5 pts] Looking at Data Correlation

Now that we have our dataframe prepared let's start analyzing our data. For this next question let's look at the correlations of our variables to our target value. First, use the heatmap function to plot the correlations of the data.

In [58]:
```
correlations = data.corr()
columns = list(data)
#Creates the heatmap
heatmap(correlations.values,columns,columns,figsize = (20,12),cmap="hsv")
```



Next, show the correlation to the "target" feature only and sorr them in descending order.

In [59]:
```
#Let's specifically look at the correlations of our target feature
correlations["target"].sort_values(ascending=False)
```

Out[59]:
```
target      1.000000
exang       0.436757
oldpeak     0.430696
ca          0.391724
thal        0.344029
sex         0.280937
age         0.225439
trestbps    0.144931
chol        0.085239
fbs         0.028046
restecg    -0.137230
slope      -0.345877
thalach    -0.421741
cp         -0.433798
Name: target, dtype: float64
```

From the heatmap values and the description of the features, why do you think some variables correlate more highly than others? (This question is just to get you thinking and there is no perfect answer since we have no medical background)

The angina (or chest pain) related features seem to be highly correlated as the pain is due to exercise which would stress the heart. Some of the features that arent too correlated like blood sugar and cholesteral levels seem to be metrics not that related to heart performance.

[25 pts] Part 2. Prepare the Data and run a KNN Model

Before running our various learning methods, we need to do some additional prep to finalize our data. Specifically you'll have to cut the classification target from the data that will be used to classify, and then you'll have to divide the dataset into training and testing cohorts.

Specifically, we're going to ask you to prepare 2 batches of data. The first batch will simply be the raw numeric data that hasn't gone through any additional pre-processing. The second batch will be data that you will pipeline using pre-processing methods. We will then feed both of these datasets into a classifier to showcase just how important this step can be!

[2 pts] Separate target labels from data

Save the label column as a separate array and then make a new dataframe without the target.

In [60]:
```
y = data["target"]
x = data.drop(["target"],axis = 1)
```

[5 pts] Balanced Train Test Split

Now, create your 'Raw' unprocessed training data by dividing your dataframe into training and testing cohorts, with your training cohort consisting of 60% of your total dataframe. To ensure that the train and test sets have balanced classes, use the [stratify command of train_test_split (https://scikit-learn.org/stable/modules/generated/sklearn.model_selection.train_test_split.html)](https://scikit-learn.org/stable/modules/generated/sklearn.model_selection.train_test_split.html). Output the resulting shapes of your training and testing samples to confirm that your split was successful. Additionally, output the class counts for the training and testing cohorts to confirm that there is no artifical class imbalance.

Note: Use randomstate = 0 to ensure that the same train/test split happens everytime for ease of grading.

In [61]:
```
train_raw, test_raw, target, target_test = train_test_split(x,y, test_size=0.4, stratify= y, random_state=0)
```

In [62]:
```
#Training classes
target.value_counts()
```

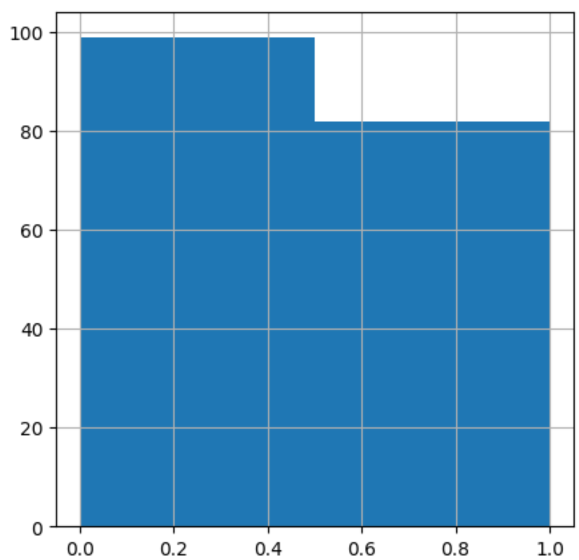
Out[62]:
```
0    99
1    82
Name: target, dtype: int64
```

In [63]:
```
target.shape
```

Out[63]:
```
(181,)
```

In [64]:
```
target.hist(bins=2, figsize=(5,5))
```

Out[64]:
```
<AxesSubplot: >
```



In [65]:
```
#Test class
target_test.shape
```

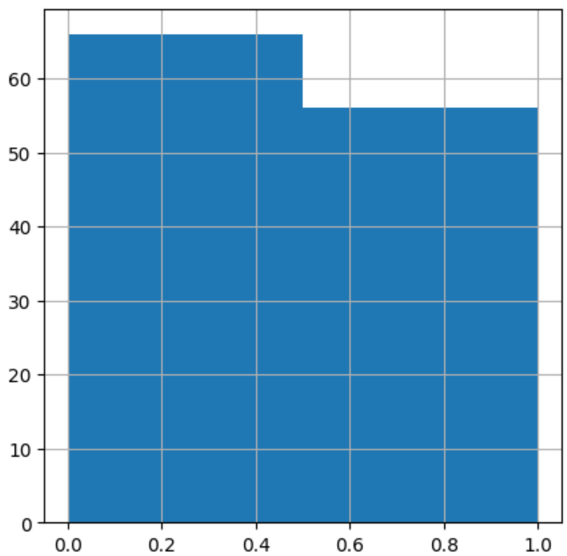
Out[65]:
```
(122,)
```

In [66]:
```
target_test.value_counts()
```

Out[66]:
```
0    66
1    56
Name: target, dtype: int64
```

In [67]:
```
target_test.hist(bins=2, figsize=(5,5))
```

Out[67]:
```
<AxesSubplot: >
```



[5 pts] KNN on raw data

Now, let's try a classification model on this data. We'll first use KNN since it is the one we are most familiar with.

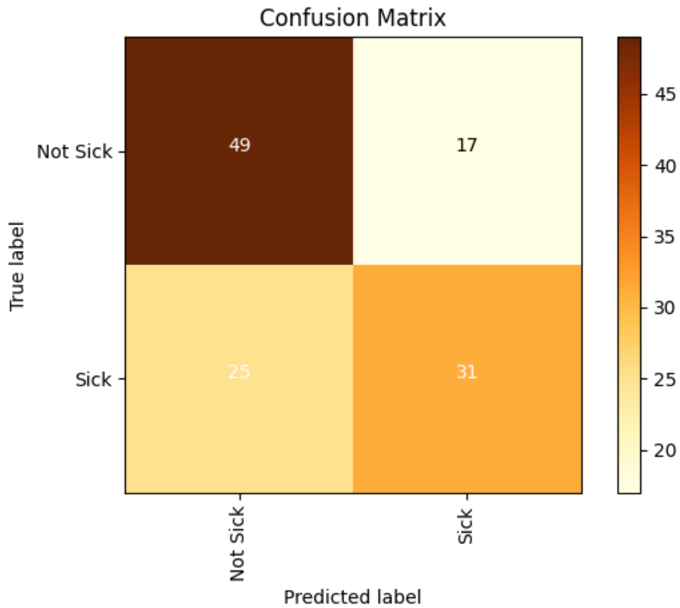
One thing we noted in class was that because KNN relies on Euclidean distance, it is highly sensitive to the relative magnitude of different features. Let's see that in action! Implement a K-Nearest Neighbor algorithm on our data and report the results. For this initial implementation, simply use the default settings. Refer to the [KNN Documentation (https://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KNeighborsClassifier.html)](https://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KNeighborsClassifier.html) for details on implementation. **Report on the test accuracy of the resulting model and print out the confusion matrix.**

Recall that accurracy can be calculated easily using metrics.accuracy_score and that we have a helper function to draw the confusion matrix.

In [68]:
```
# k-Nearest Neighbors algorithm
knn = KNeighborsClassifier()
knn.fit(train_raw, target)
testing_result = knn.predict(test_raw)
predicted = knn.predict(test_raw)
```

In [69]:
```
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))

#Draws confusion matrix
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
```

```
Accuracy:    0.655738
```



[5 pts] KNN on preprocessed data

Now lets implement a pipeline to preprocess the data. For the pipeline, use StandardScaler on the numerical features and one-hot encoding on the categorical features. For reference on how to make a pipeline, please look at project 1.

For reference, the categorical features are ['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca','thal'].

In [70]:
```
numerical_features = ["age", "trestbps", "chol", "thalach", "oldpeak"]
categorical_features = ['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca','thal']
num_pipeline = Pipeline([('std_scaler', StandardScaler())])

full_pipeline = ColumnTransformer([
    ("num", num_pipeline, numerical_features),
    ("cat", OneHotEncoder(), categorical_features),
])


#Transform raw data
train = full_pipeline.fit_transform(train_raw)
test = full_pipeline.transform(test_raw)
```

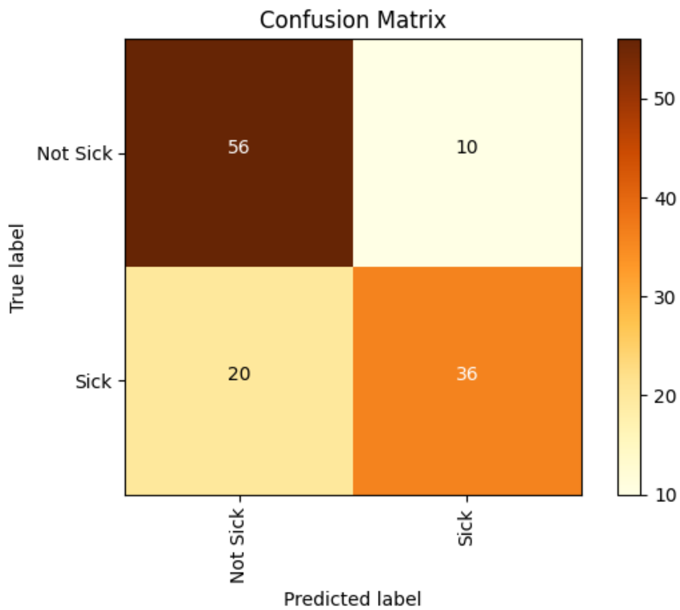
Now use the pipeline to transform the data and then apply the same KNN classifier with this new training/testing data. Report the test accuraccy. Discuss the implications of the different results you are obtaining.

Note: Remember to use fit_transform on the training data and transform on the testing data.

In [71]:
```
# k-Nearest Neighbors algorithm
knn = KNeighborsClassifier()
knn.fit(train, target)
testing_result = knn.predict(test)
predicted = knn.predict(test)
```

In [72]:
```
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))

#Draws confusion matrix
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
```

```
Accuracy:    0.754098
```



10% increase in accuracy. Improvement most likely came from the multiple categorical variables that were properly encoded

[8 pts] KNN Parameter optimization for n_neighbors

The KNN Algorithm includes an n_neighbors attribute that specifies how many neighbors to use when developing the cluster. (The default value is 5, which is what your previous model used.) Lets now try n values of: 1, 2, 3, 5, 7, 9, 10, 20, and 50. Run your model for each value and report the test accuracy for each. (HINT leverage python's ability to loop to run through the array and generate results without needing to manually code each iteration).

In [73]:
```
best_n = 0
best_acc = 0
for n in [1, 2, 3, 5, 7, 9, 10, 20, 50]:
    knn = KNeighborsClassifier(n_neighbors = n)
    knn.fit(train, target)
    testing_result = knn.predict(test)
    predicted = knn.predict(test)
    print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
    if metrics.accuracy_score(target_test,predicted) > best_acc:
        best_acc = metrics.accuracy_score(target_test,predicted)
        best_n = n

print("best n = " + str(best_n))
print("%-12s %f" % ('Accuracy:', best_acc))
```

```
Accuracy:    0.770492
Accuracy:    0.745902
Accuracy:    0.754098
Accuracy:    0.754098
Accuracy:    0.762295
Accuracy:    0.778689
Accuracy:    0.778689
Accuracy:    0.778689
Accuracy:    0.778689
best n = 9
Accuracy:    0.778689
```

Comment for which value of n did the KNN model perform the best. Did the model perform strictly better or stricly worse as the value of n increased?

The model performed the best when n=9 with an accuracy of .778689. After n neighbors it plateaued. It was hoever pretty accurate with a single neighbor but dipped as n increased before rising again

So we have a model that seems to work well. But let's see if we can do better! To do so we'll employ Logistic Regression and SVM to improve upon the model and compare the results.

For the rest of the project, you will only be using the transformed data and not the raw data. DO NOT USE THE RAW DATA ANYMORE.

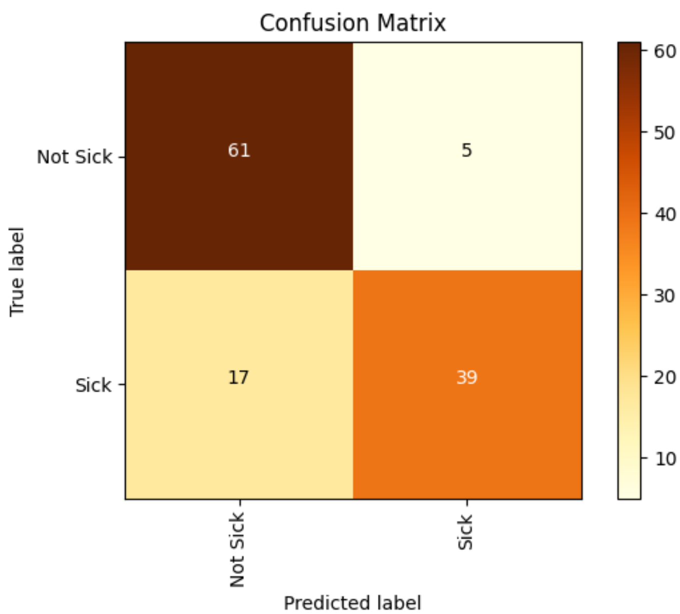
[20 pts] Part 3. Additional Learning Methods: Logistic Regression

Let's now try Logistic Regression. Recall that Logistic regression is a statistical model that in its basic form uses a logistic function to model a binary dependent variable.

[5 pts] Run the default Logistic Regression

Implement a Logistical Regression Classifier. Review the [Logistical Regression Documentation (https://scikit-learn.org/stable/modules/generated/sklearn.linear_model.LogisticRegression.html)](https://scikit-learn.org/stable/modules/generated/sklearn.linear_model.LogisticRegression.html) for how to implement the model. Use the default settings. **Report on the test accuracy and print out the confusion matrix.**

In [74]:
```
#log_reg = LogisticRegression(penalty = "l2",max_iter = 1000, solver = "lbfgs", C=(10**30)/1)
#C is choosen to be high to remove regularization
#We could have chosen penalty = "none" since lbfgs supports it but this option is not possible for all solvers.

log_reg = LogisticRegression()
log_reg.fit(train, target)
testing_result = log_reg.predict(test)
predicted = log_reg.predict(test)

#Draws confusion matrix
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```




```
Accuracy:    0.819672
```

[5 pts] Compare Logistic Regression and KNN

In your own words, describe the key differences between Logistic Regression and KNN? When would you use one over the other?

Although they are both used for classification, logistic regression is typically used when the data is linearly seperable and we want a probability of our prediction. Also, since it is parametric, the parameters can be stored and distributed easier that KNN which needs to store all its data. KNN is typically used when we know similar points have similar attributes and thus we can make predictions off similar points.

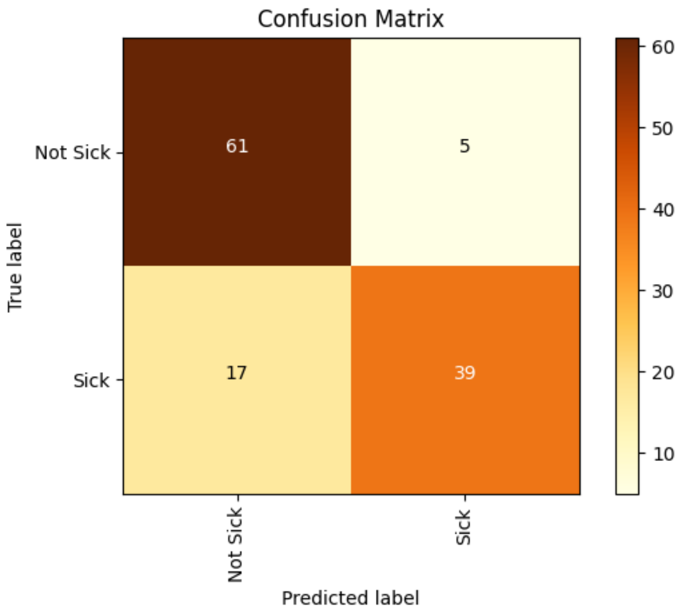
[5 pts] Tweaking the Logistic Regression

What are some parameters we can change that will affect the performance of Logistic Regression?

We can tune the regularization terms, the learning rate, the number of iterations, learning rate decay, the optimization method, and various other attributes

Implement Logistic Regression with solver= 'liblinear', max_iter= 1000, penalty = 'l2', and C=1. Report on the test accuracy and print out the confusion matrix.

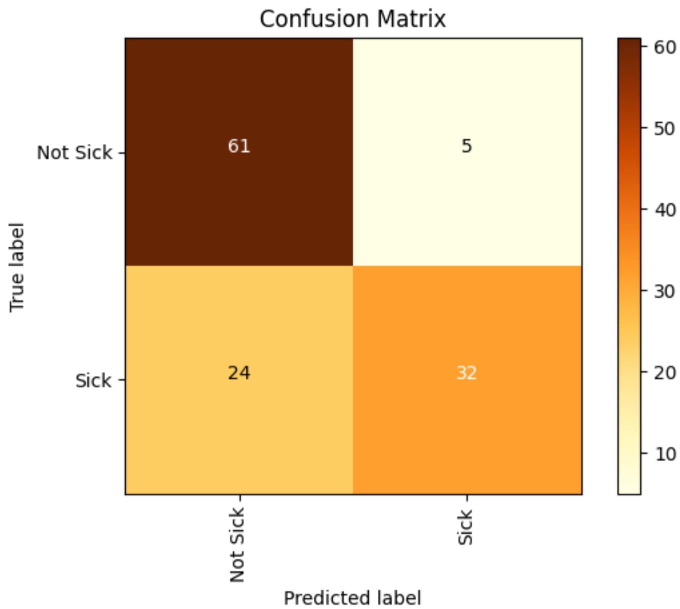
In [75]:
```
log_reg = LogisticRegression(penalty = "l2", max_iter = 1000, solver = "liblinear", C=1)
#C is choosen to be high to remove regularization
#We could have chosen penalty = "none" since lbfgs supports it but this option is not possible for all solvers.

log_reg.fit(train, target)
testing_result = log_reg.predict(test)
predicted = log_reg.predict(test)

#Draws confusion matrix
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```




```
Accuracy:    0.819672
```

Now, Implement Logistic Regression with solver= 'liblinear', max_iter= 1000, penalty = 'l2', and C=0.0001. Report on the test accuracy and print out the confusion matrix.

In [76]:
```
log_reg = LogisticRegression(penalty = "l2", max_iter = 1000, solver = "liblinear", C=.0001)
#C is choosen to be high to remove regularization
#We could have chosen penalty = "none" since lbfgs supports it but this option is not possible for all solvers.

log_reg.fit(train, target)
testing_result = log_reg.predict(test)
predicted = log_reg.predict(test)

#Draws confusion matrix
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```




```
Accuracy:    0.762295
```

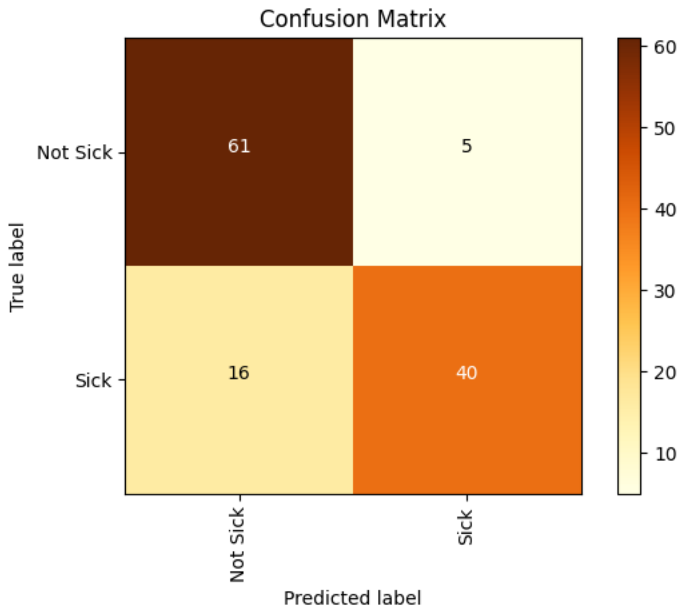
Did the accuraccy drop or improve? Why?

Accuracy most likely dropped because we are penalizing the parameters too much.

[5 pts] Trying out different penalties

Now, Implement Logistic Regression with solver= 'liblinear', max_iter= 1000, penalty = 'l1', and C=1. Report on the test accuracy and print out the confusion matrix.

In [77]:
```
log_reg = LogisticRegression(penalty = "l1", max_iter = 1000, solver = "liblinear", C=1)
#C is choosen to be high to remove regularization
#We could have chosen penalty = "none" since lbfgs supports it but this option is not possible for all solvers.

log_reg.fit(train, target)
testing_result = log_reg.predict(test)
predicted = log_reg.predict(test)

#Draws confusion matrix
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```




```
Accuracy:    0.827869
```

Describe what the purpose of a penalty term is and how the change from L2 to L1 affected the model.

L1 uses the sum of the absolute values of the weights whereas l2 uses the sum of the squared values of the weights. Thus, l2 has harsher penalties for any weights > 1

[20 pts] Part 4. Additional Learning Methods: SVM (Support Vector Machine)

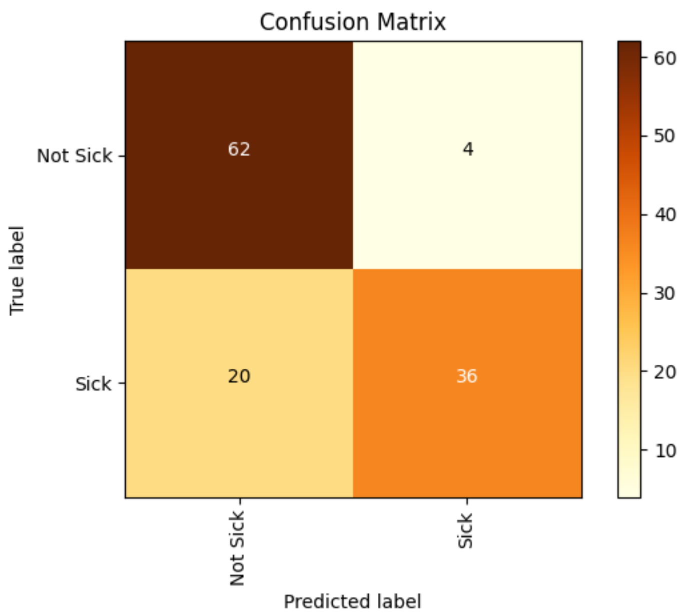
A Support Vector Machine (SVM) is a discriminative classifier formally defined by a separating hyperplane. In other words, given labeled training data (supervised learning), the algorithm outputs an optimal hyperplane which categorizes new examples. In two dimensional space this hyperplane is a line dividing a plane in two parts each corresponding to one of the two classes.

Recall that Sci-kit learn uses soft-margin SVM to account for datasets that are not separable.

[5 pts] Run default SVM classifier

Implement a Support Vector Machine classifier on your pipelined data. Review the [SVM Documentation (https://scikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html)](https://scikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html) for how to implement a model. For this implementation you can simply use the default settings. **Report on the test accuracy and print out the confusion matrix.**

In [78]:
```
svm = SVC()
svm.fit(train, target)
predicted = svm.predict(test)
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
```




```
Accuracy:    0.803279
```

Print out the number of support vectors that SVC has determined. Look at the documentation for how to get this.

In [79]:
```
svm.support_vectors_.shape[0]
```

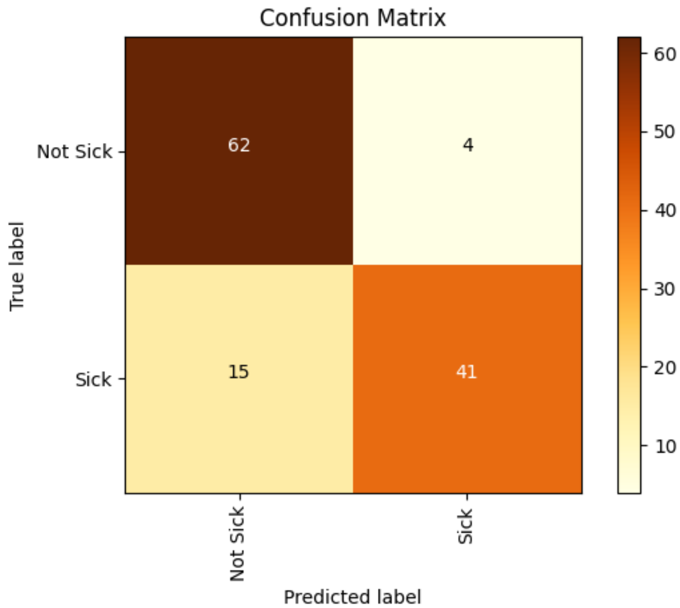
Out[79]: 106

You may find that there are quite a few support vectors. This is due in part to the small number of samples in the training set and the choice of kernel.

[5 pts] Use a Linear SVM

Rerun your SVM, but now modify your model parameter kernel to equal 'linear'. **Report on the test accuracy and print out the confusion matrix. Also, print out the number of support vectors.**

In [80]:
```
svm = SVC(kernel = 'linear')
svm.fit(train, target)
predicted = svm.predict(test)
draw_confusion_matrix(target_test, predicted, ['Not Sick', 'Sick'])
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted)))
svm.support_vectors_.shape[0]
```




```
Accuracy:    0.844262
```

Out[80]: 65

You will notice that number of support vectors has decreased significantly.

[5 pts] Compare default SVM and Linear SVM

Explain the what the new results you've achieved mean. Read the documentation to understand what you've changed about your model and explain why changing that input parameter might impact the results in the manner you've observed.

Kernels are functions that modify the input data into a different a different input space. This allowes the svm to split on that new space where it may be easier to draw line that splits the data evenly.

[5 pts] Compare SVM and Logistic Regression

Both logistic regression and linear SVM are trying to classify data points using a linear decision boundary but achieve it in different ways. In your own words, explain the difference between the ways that Logistic Regression and Linear SVM find the boundary?

SVM tries to find the best margin by maximizing the distance between the margin and the support vectors. Logistic regression on the other hand attempts to find the best distance for all data points, not just those near the margin.

[10 pts] Part 5: Cross Validation and Model Selection

You've sampled a number of different classification techniques and have seen their performance on the dataset. Before we draw any conclusions on which model is best, we want to ensure that our results are not the result of the random sampling of our data we did with the Train-Test-Split. To ensure otherwise, we will conduct a K-Fold Cross-Validation with GridSearch to determine which model perform best and assess its performance on the test set.

[10 pts] Model Selection

Run a GridSearchCV with 3-Fold Cross Validation. You will be running each classification model with different parameters.

KNN:

- n_neighbors = [1,3,5,7]
- metric = ["euclidean","manhattan"] #Different Distance functions

Logistic Regression:

- penalty = ["l1","l2"]

- solver = ["liblinear"]
- C = [0.0001,0.1,10]

SVM:

- kernel = ["linear","rbf"]
- C = [0.0001,0.1,10]

Make sure to train and test your model on the transformed data and not on the raw data.

After using GridSearchCV, put the results into a pandas Dataframe and print out the whole table.

In [81]:

```
#Note that this a list of dict
#Each dict describes the combination of parameters to check
parameters_knn = [
    {"n_neighbors": [1, 3, 5, 7],
    "metric": ["euclidean", "manhattan"]}
]

parameters_lr = [
    {"penalty": ["l1", "l2"],
    "C": [.0001, .1, 10],
    "solver": ["liblinear"]}
]

parameters_svm = [
    {"kernel": ["linear", "rbf"],
    "C": [.0001, .1, 10]}
]
#instantiate model


#Implementing cross validation

k = 3
kf = KFold(n_splits=k, random_state=None)
```

In [82]:

```
# k-Nearest Neighbors algorithm
knn = KNeighborsClassifier()
grid = GridSearchCV(knn , parameters_knn, cv = kf, scoring = "accuracy")
grid.fit(train, target)
knn_res = pd.DataFrame(grid.cv_results_)
knn_res
```

Out[82]:

	mean_fit_time	std_fit_time	mean_score_time	std_score_time	param_metric	param_n_neighbors	params	split0_test_score	split1_test_score	split2_
0	0.001075	0.000328	0.006065	0.001997	euclidean	1	{'metric': 'euclidean', 'n_neighbors': 1}	0.737705	0.783333	
1	0.000932	0.000087	0.050574	0.033889	euclidean	3	{'metric': 'euclidean', 'n_neighbors': 3}	0.803279	0.783333	
2	0.000810	0.000098	0.006092	0.002237	euclidean	5	{'metric': 'euclidean', 'n_neighbors': 5}	0.770492	0.833333	
3	0.000777	0.000038	0.004514	0.000136	euclidean	7	{'metric': 'euclidean', 'n_neighbors': 7}	0.754098	0.800000	
4	0.000833	0.000084	0.004317	0.000085	manhattan	1	{'metric': 'manhattan', 'n_neighbors': 1}	0.737705	0.750000	
5	0.000686	0.000019	0.004625	0.000174	manhattan	3	{'metric': 'manhattan', 'n_neighbors': 3}	0.803279	0.800000	
6	0.000812	0.000051	0.004861	0.000167	manhattan	5	{'metric': 'manhattan', 'n_neighbors': 5}	0.786885	0.833333	
7	0.000796	0.000087	0.004834	0.000297	manhattan	7	{'metric': 'manhattan', 'n_neighbors': 7}	0.770492	0.833333	

In [83]:
```
knn_res[["rank_test_score","param_n_neighbors", "param_metric","mean_test_score"]]
```

Out[83]:

	rank_test_score	param_n_neighbors	param_metric	mean_test_score
0	7	1	euclidean	0.768124
1	3	3	euclidean	0.828871
2	1	5	euclidean	0.829053
3	6	7	euclidean	0.812477
4	8	1	manhattan	0.762568
5	3	3	manhattan	0.828871
6	2	5	manhattan	0.828962
7	5	7	manhattan	0.823497

In [84]:
```
predicted_knn = grid.predict(test)
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted_knn)))
```

```
Accuracy:    0.754098
```

In [85]:
```
log_reg = LogisticRegression(penalty = "none",max_iter = 1000, solver = "lbfgs") #will change parameters during CV
grid = GridSearchCV(log_reg , parameters_lr, cv = kf, scoring = "accuracy")
grid.fit(train,target)
lr_res = pd.DataFrame(grid.cv_results_)
lr_res
```

Out[85]:

	mean_fit_time	std_fit_time	mean_score_time	std_score_time	param_C	param_penalty	param_solver	params	split0_test_score	split1_test_score	split2
0	0.004626	0.003630	0.001004	0.000220	0.0001	l1	liblinear	{'C': 0.0001, 'penalty': 'l1', 'solver': 'libl...	0.459016	0.566667	
1	0.004053	0.004004	0.000599	0.000060	0.0001	l2	liblinear	{'C': 0.0001, 'penalty': 'l2', 'solver': 'libl...	0.721311	0.783333	
2	0.007554	0.005132	0.001012	0.000264	0.1	l1	liblinear	{'C': 0.1, 'penalty': 'l1', 'solver': 'libline...	0.754098	0.733333	
3	0.001619	0.000135	0.000687	0.000044	0.1	l2	liblinear	{'C': 0.1, 'penalty': 'l2', 'solver': 'libline...	0.803279	0.833333	
4	0.002335	0.000460	0.000765	0.000108	10	l1	liblinear	{'C': 10, 'penalty': 'l1', 'solver': 'liblinear'}	0.786885	0.800000	
5	0.003886	0.002370	0.001007	0.000239	10	l2	liblinear	{'C': 10, 'penalty': 'l2', 'solver': 'liblinear'}	0.786885	0.783333	

In [86]:
```
lr_res[["rank_test_score","param_C","param_penalty","param_solver","mean_test_score"]]
```

Out[86]:

	rank_test_score	param_C	param_penalty	param_solver	mean_test_score
0	6	0.0001	l1	liblinear	0.547450
1	4	0.0001	l2	liblinear	0.779326
2	5	0.1	l1	liblinear	0.773588
3	1	0.1	l2	liblinear	0.856648
4	2	10	l1	liblinear	0.817851
5	3	10	l2	liblinear	0.817851

In [87]:
```
predicted_lr = grid.predict(test)
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted_lr)))
```

```
Accuracy:    0.827869
```

In [88]:
```
svm = SVC()
grid = GridSearchCV(svm, parameters_svm, cv = kf, scoring = "accuracy")
grid.fit(train,target)
svm_res = pd.DataFrame(grid.cv_results_)
svm_res
```

Out[88]:

	mean_fit_time	std_fit_time	mean_score_time	std_score_time	param_C	param_kernel	params	split0_test_score	split1_test_score	split2_test_score	mea
0	0.003234	0.000277	0.002942	0.001323	0.0001	linear	{'C': 0.0001, 'kernel': 'linear'}	0.459016	0.566667	0.616667	
1	0.008396	0.007282	0.006211	0.005678	0.0001	rbf	{'C': 0.0001, 'kernel': 'rbf'}	0.459016	0.566667	0.616667	
2	0.002131	0.000161	0.007883	0.005154	0.1	linear	{'C': 0.1, 'kernel': 'linear'}	0.836066	0.850000	0.900000	
3	0.003452	0.000048	0.002719	0.000086	0.1	rbf	{'C': 0.1, 'kernel': 'rbf'}	0.573770	0.766667	0.866667	
4	0.022656	0.017223	0.001151	0.000064	10	linear	{'C': 10, 'kernel': 'linear'}	0.770492	0.833333	0.900000	
5	0.003474	0.000200	0.001529	0.000041	10	rbf	{'C': 10, 'kernel': 'rbf'}	0.754098	0.750000	0.850000	

In [89]:
```
svm_res[["rank_test_score","param_C","param_kernel","mean_test_score"]]
```

Out[89]:

	rank_test_score	param_C	param_kernel	mean_test_score
0	5	0.0001	linear	0.547450
1	5	0.0001	rbf	0.547450
2	1	0.1	linear	0.862022
3	4	0.1	rbf	0.735701
4	2	10	linear	0.834608
5	3	10	rbf	0.784699

In [90]:
```
predicted_svm = grid.predict(test)
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted_svm)))
```

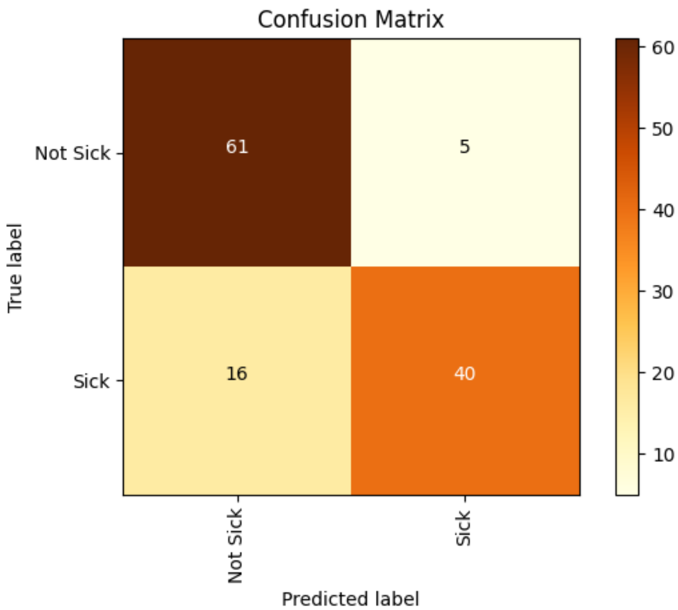
```
Accuracy:    0.811475
```

What was the best model and what was it's score?

The logistic regression model performed the best with an accuracy of .827869

Using the best model you have, report the test accuracy and print out the confusion matrix

In [91]:
```
draw_confusion_matrix(target_test, predicted_lr, ['Not Sick', 'Sick'])
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(target_test,predicted_lr)))
```




```
Accuracy:    0.827869
```

In [ ]: