# Assessment of Data and Applying Normalization on Abalone Dataset

#### **Libraries Utilized:**

- numpy
- pandas
- seaborn
- matplotlib
- scipy
- scikit-learn

## Importing Libraries

```
In [1]:
         import pandas as pd
         import random
         import seaborn as sns
         import numpy as np
         from sklearn import neighbors
         from sklearn.model selection import train test split
         from sklearn.metrics import accuracy score
         from scipy import stats
         import matplotlib.pyplot as plt
         import warnings
         from sklearn import neighbors, datasets, preprocessing
         from sklearn.neighbors import KNeighborsClassifier
         from sklearn import metrics
         warnings.filterwarnings("ignore")
         from sklearn.decomposition import PCA
         from sklearn.manifold import TSNE
         from sklearn.discriminant analysis import LinearDiscriminantAnalysis as LDA
         from sklearn.model_selection import StratifiedKFold
         from sklearn.model selection import KFold
         from sklearn.tree import DecisionTreeClassifier
         from sklearn.ensemble import RandomForestClassifier
         from sklearn.ensemble import GradientBoostingClassifier
         from sklearn.naive bayes import ComplementNB
         from sklearn.naive_bayes import MultinomialNB
```

from sklearn.model selection import GridSearchCV

from sklearn.preprocessing import MinMaxScaler

from sklearn.manifold import TSNE

# Loading the Abalone Dataset

```
In [2]:
    N = ['Length', 'Diameter', 'Height', 'Whole_weight', 'Shucked_weight', 'Visce
    df1 = pd.read_csv("abalone.csv", sep=',',names = ['Sex','Length', 'Diameter',
```

# Exploring the features, their ranges and distribution

In [3]:	df1.head(5)													
Out[3]:		Sex	Length	Diameter	Height	Whole_weight	Shucked_weight	Viscera_weight	Shell_weigl					
	0	М	0.455	0.365	0.095	0.5140	0.2245	0.1010	0.15					
	1	М	0.350	0.265	0.090	0.2255	0.0995	0.0485	0.07					
	2	F	0.530	0.420	0.135	0.6770	0.2565	0.1415	0.2′					
	3	М	0.440	0.365	0.125	0.5160	0.2155	0.1140	0.15					
	4	1	0.330	0.255	0.080	0.2050	0.0895	0.0395	0.05					

We can see that all of the attributes, with the exception of "Sex," are numerical in nature. Sex is a categorical variable with three potential outcomes. We will tackle that with a one hot encoding. The labels are all of the integer type

# Missing data

```
In [4]: df1.describe()
```

Out[4]:		Length	Diameter	Height	Whole_weight	Shucked_weight	Viscera_weight
	count	4177.000000	4177.000000	4177.000000	4177.000000	4177.000000	4177.000000
	mean	0.523992	0.407881	0.139516	0.828742	0.359367	0.180594
	std	0.120093	0.099240	0.041827	0.490389	0.221963	0.109614
	min	0.075000	0.055000	0.000000	0.002000	0.001000	0.000500
	25%	0.450000	0.350000	0.115000	0.441500	0.186000	0.093500
	50%	0.545000	0.425000	0.140000	0.799500	0.336000	0.171000
	75%	0.615000	0.480000	0.165000	1.153000	0.502000	0.253000
	max	0.815000	0.650000	1.130000	2.825500	1.488000	0.760000

As seen from the above table, it is clear that our data does not contain missing values. This is clear from the fact that count of all the features are the same. Further evidence for this is shown below. </span>

```
In [5]:
        df1.info()
        <class 'pandas.core.frame.DataFrame'>
       RangeIndex: 4177 entries, 0 to 4176
        Data columns (total 9 columns):
            Column
                           Non-Null Count Dtype
                            _____
                                           ____
         0
                            4177 non-null
                                           object
            Sex
         1
           Length
                           4177 non-null
                                           float64
                           4177 non-null
         2
           Diameter
                                           float64
            Height
                            4177 non-null
                                           float64
         4 Whole weight 4177 non-null
                                           float64
            Shucked weight 4177 non-null
                                           float64
            Viscera_weight 4177 non-null
                                           float64
         7
            Shell weight
                            4177 non-null
                                           float64
            Rings
                            4177 non-null
                                           int64
       dtypes: float64(7), int64(1), object(1)
       memory usage: 293.8+ KB
```

As we can see, it is clear that there are no null values in each feature.

# Handling Categorical features using One Hot Encoding

```
In [6]:
#one hot encoding
one_hot_enc = pd.get_dummies(df1.Sex, prefix='Sex')
df1['Sex_F'] = one_hot_enc['Sex_F']
df1['Sex_I'] = one_hot_enc['Sex_I']
df1['Sex_M'] = one_hot_enc['Sex_M']
df1 = df1.drop(columns = ["Sex"])
```

Here, we are performing one hot encoding of the feature "Sex" so that it is easier for us to handle. On that note, we split Sex into 3 distinct features (Male,Female,Infant)

```
In [7]: df1.isna().sum()
```

```
Out[7]: Length
                           0
                           0
        Diameter
                           0
        Height
        Whole_weight
        Shucked_weight
        Viscera_weight
                           0
        Shell_weight
        Rings
                           0
        Sex F
        Sex I
                           0
        Sex M
                           0
        dtype: int64
```

# Performing Min-Max Normalization on Abalone Dataset

Min-max normalization is used to scale the data such that the minimum value of the feature is set to 0 and the maximum value of the feature is set to 1

```
In [8]:
#min-max normalization
df1_minmax= df1[:].copy()
for d in df1_minmax[:]:
    if d in ['Rings']:
        continue
    df1_minmax[d] = (df1_minmax[d] - df1_minmax[d].min()) / (df1_minmax[d].max
```

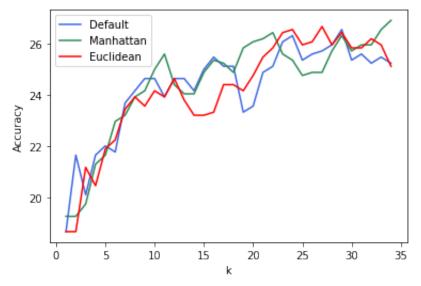
# Improving KNN with Min-Max Normalization

# Data preparation

Performing K-NN classfier using Defaults values, Manhattan distance & Euclidean distance to derive k-value of the best performance

```
knn.fit(X train, y train.values.ravel())
    y pred = knn.predict(X test)
    accuracy = metrics.accuracy_score(y_test, y_pred)*100
    if accuracy>perf['Acc']:
        perf['Acc'] = accuracy
        perf['k'] = k
        perf['dist'] = 'Euclidean'
        perf['weights'] = 'Uniform'
    mm acc default.append(accuracy)
plt.plot(k list, mm acc default,color="royalblue")
#KNN for Manhatten distance
mm acc manhatten = []
for k in k list:
    knn = KNeighborsClassifier(n_neighbors=k, weights = 'distance', p = 1, me
    knn.fit(X_train, y_train.values.ravel())
    y pred = knn.predict(X test)
    accuracy = metrics.accuracy score(y test, y pred)*100
    if accuracy>perf['Acc']:
        perf['Acc'] = accuracy
        perf['k'] = k
        perf['dist'] = 'Manhattan'
        perf['weights'] = 'Distance'
    mm acc manhatten.append(accuracy)
plt.plot(k list, mm acc manhatten,color="seagreen")
#KNN for Euclidean distance
mm acc euclidean = []
for k in k list:
    knn = KNeighborsClassifier(n neighbors=k, weights = 'distance', p = 2, me
    knn.fit(X train, y train.values.ravel())
    y pred = knn.predict(X test)
    accuracy = metrics.accuracy score(y test, y pred)*100
    if accuracy>perf['Acc']:
        perf['Acc'] = accuracy
        perf['k'] = k
        perf['dist'] = 'Euclidean'
        perf['weights'] = 'Distance'
    mm acc euclidean.append(accuracy)
plt.plot(k_list, mm_acc_euclidean,color="red")
plt.legend(["Default", "Manhattan", "Euclidean"])
plt.xlabel('k')
plt.ylabel('Accuracy')
print("Best performance is ",perf['Acc']," at k = ",perf['k']," | weights = ",pe
```

Best performance is 26.913875598086122 at  $k = 34 \mid weights = Distance \mid distance = Manhattan$ 



Using Manhattan Distance metric we get the highest accuracy of 26.91% for K=34. Manhattan Distance is used to calculate the distance between two data points in a grid-like path

# **Best performing KNN configuration**

Selecting the Best Value for K which provides best accuracy scores

```
In [11]:
    knn = KNeighborsClassifier(n_neighbors=34, weights = 'distance', p = 1, metric
    knn.fit(X_train, y_train.values.ravel())
    y_pred = knn.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, y_pred)*100
    print(accuracy)
```

26.913875598086122

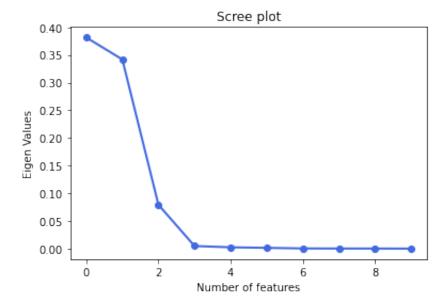
The value K=34 provides an overall accuracy of 26.91

# 1. Representation Learning

# **PCA**

PCA is an unsupervised method of dimensionality reduction technique hence, we drop the target variables and carry out PCA on the remaining 7 attributes to find principal components that capture the variances in the given data.

Out[12]: Text(0.5, 1.0, 'Scree plot')

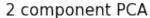


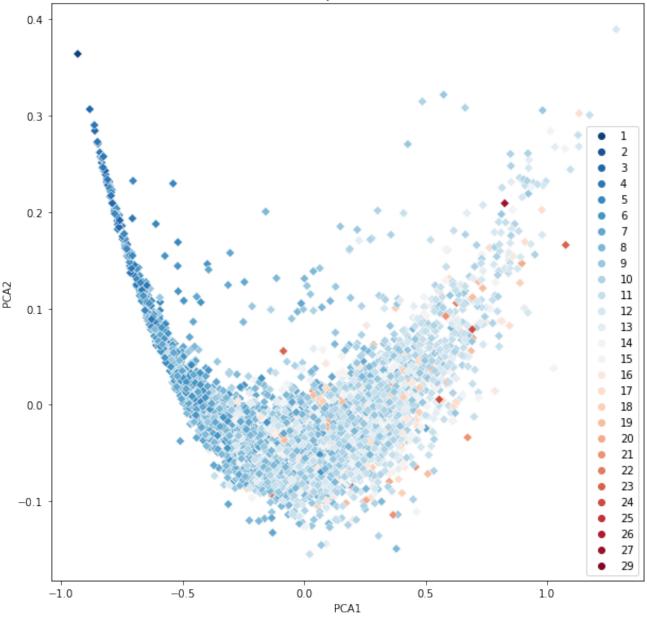
The above plot indicates the Eigen values w.r.t number of features. As the number of Features increases the Eigen value decreased and reached solidity beyond 3 features.

The scree plot is a plot between the number of features and the magnitude of the eigen values which explains the quantum of spread along a particular principle component. Based on this plot, it is clear that the amount of spread explained quickly tends to zero. This is quite useful for us, since this shows that we can drop majority of the dimensions and still be able to explain much of the data.

```
In [13]:
    D = ['Length', 'Diameter', 'Height', 'Whole_weight', 'Shucked_weight', 'Visce
    pca_model_2dims = PCA(n_components=2)
    pca_model_2dims.fit(X_train[D])
    X2d = pca_model_2dims.transform(X[D])
    df_2d_pca = pd.DataFrame(X2d, columns = ["PCA1", "PCA2"])
    df_2d_pca["Label"] = df1["Rings"]
    fig = plt.figure(figsize = (10,10))
    sns.scatterplot(x = df_2d_pca["PCA1"].values, y = df_2d_pca["PCA2"].values, m
    plt.xlabel('PCA1', fontsize = 10)
    plt.ylabel('PCA2', fontsize = 10)
    plt.title('2 component PCA', fontsize = 15)
    print(pca_model_2dims.explained_variance_ratio_)
```

#### [0.93686675 0.03205275]





From the plot we observe that first principal component is responsible for maximum variance. With principle component PCA1 we are able to explain close to 93% of the data and 3% with principle component PCA2. This is an attractive trade-off!

#### **TSNE**

T-SNE is another dimensionality reduction concept that is well suited to effectively visualize high dimensional data. Since us humans can visualize and discern data in a 2-D or 3-D space plots the natural choice for dimension is either 2 or 3. For our experimentation, we'll primarily be using n\_components set at 2 because of the following reasons,

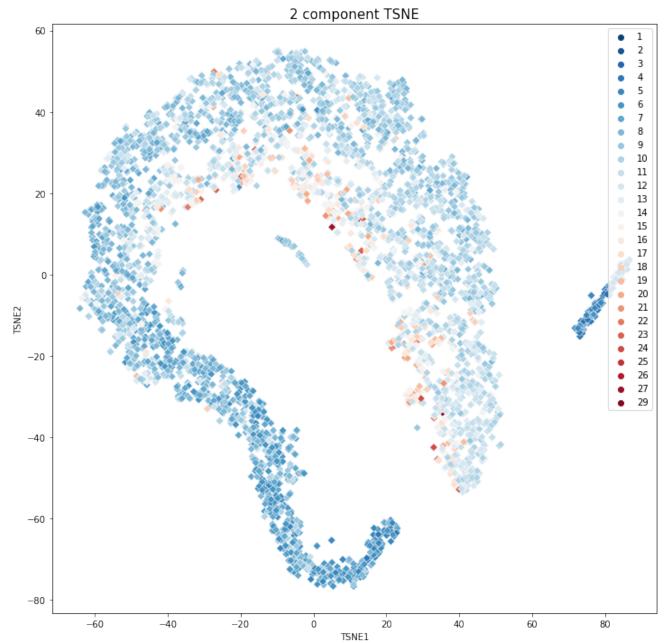
It is convenient to visualize and analyze points in a 2D plots

Easy to work with 2D plots without having to expend too much on computing

We can notice a decent amount of grouping of same class data points where local neighbourhood information is preserved.

```
In [14]:
    D = ['Length', 'Diameter', 'Height', 'Whole_weight', 'Shucked_weight', 'Visce
    tsne_2d = TSNE(n_components=2)
    X2d_tsne = tsne_2d.fit_transform(X[D])

    df_2d_tsne = pd.DataFrame(X2d_tsne, columns = ["TSNE1", "TNSE2"])
    df_2d_tsne["Label"] = df1["Rings"]
    fig = plt.figure(figsize = (12,12))
    plt.xlabel('TSNE1', fontsize = 10)
    plt.ylabel('TSNE2', fontsize = 10)
    plt.title('2 component TSNE', fontsize = 15)
    sns.scatterplot(x = df_2d_tsne["TSNE1"].values, y = df_2d_tsne["TNSE2"].value
```



Feature of t-SNE is a tuneable parameter, "perplexity," which says how to balance attention between local and global aspects of your data. The parameter is a guess about the number of close neighbors each point has. The results of the T-SNE shows evident grouping between classes.

## **LDA**

Linear Discriminant Analysis (LDA) is a supervised approach for identifying the linear discriminants that reflect the axes that optimise separation between various classes. Each class is given a Gaussian density by the model, which assumes that all classes have the same covariance matrix.

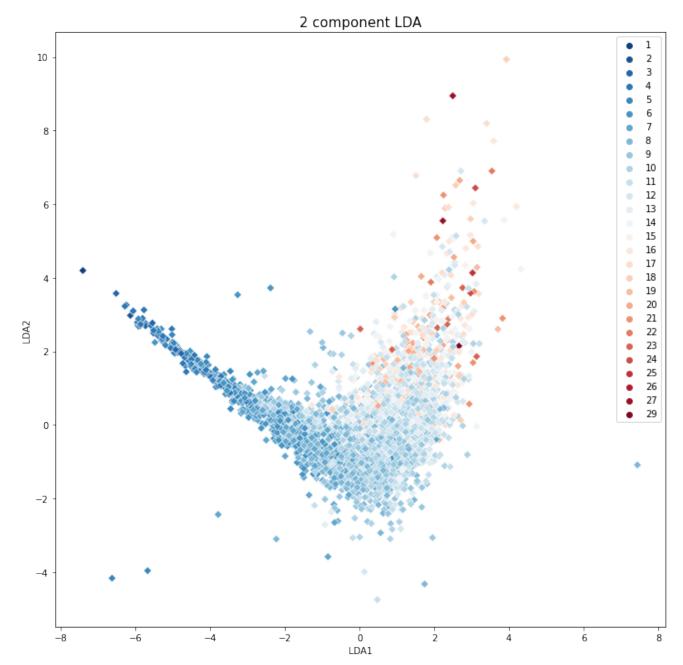
Since the labels in the dataset are unbalanced, Rings is the most balanced continuous datset, so it should be easier to train and hence we get better results with LDA.

```
In [15]:
    D = ['Length', 'Diameter', 'Height', 'Whole_weight', 'Shucked_weight', 'Visce.

    lda_2d = LDA(n_components=2)
    X2d_lda = lda_2d.fit_transform(X[D], y = y)

    df_2d_lda = pd.DataFrame(X2d_lda, columns = ["LDA1", "LDA2"])
    df_2d_lda["Label"] = df1["Rings"]
    fig = plt.figure(figsize = (12,12))
    plt.xlabel('LDA1', fontsize = 10)
    plt.ylabel('LDA2', fontsize = 10)
    plt.title('2 component LDA', fontsize = 15)
    sns.scatterplot(x = df_2d_lda["LDA1"].values, y = df_2d_lda["LDA2"].values, h
```

Out[15]: <AxesSubplot:title={'center':'2 component LDA'}, xlabel='LDA1', ylabel='LDA2'>

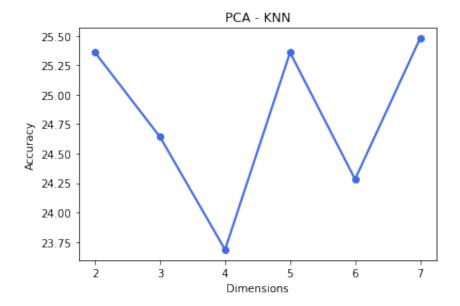


LDA focuses on the seperation of the different classes and it is evident in the above plot.

# KNN performance by varying dimensions in PCA

```
In [16]:
          dims = []
          acc = []
          for d in range(2,len(D)+1):
              dims.append(d)
              pca_model = PCA(n_components=d)
              pca model.fit(X train[D])
              Xnew = pca model.transform(X[D])
              Xtrain, Xtest, ytrain, ytest = train test split(Xnew, y, test size=0.2, random
              knn = KNeighborsClassifier(n_neighbors=24, weights = 'uniform', p = 2, me
              knn.fit(Xtrain, ytrain.values.ravel())
              y pred = knn.predict(Xtest)
              accuracy = metrics.accuracy score(ytest, y pred)*100
              acc.append(accuracy)
          plt.plot(dims,acc,'o-', linewidth=2, color='royalblue')
          plt.title("PCA - KNN")
          plt.xlabel("Dimensions")
          plt.ylabel("Accuracy")
```

#### Out[16]: Text(0, 0.5, 'Accuracy')

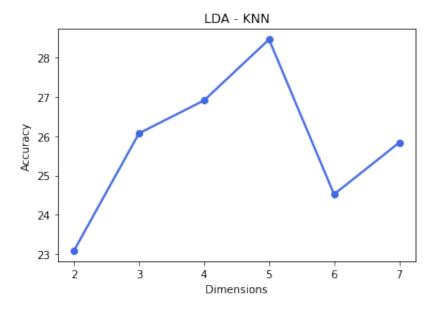


For 2 number of dimensions we get maximum accuracy of 25.35%. We opt for the lower dimensions rather than higher dimensions since we can save computational expenses.

# KNN performance by varying dimensions in LDA

```
In [17]:
          dims = []
          acc = []
          for d in range(2,len(D)+1):
              dims.append(d)
              lda_model = LDA(n_components=d)
              Xnew = lda model.fit_transform(X[D], y = y)
              Xtrain, Xtest, ytrain, ytest = train test split(Xnew, y, test size=0.2, random
              knn = KNeighborsClassifier(n neighbors=24, weights = 'uniform', p = 2, me
              knn.fit(Xtrain, ytrain.values.ravel())
              y pred = knn.predict(Xtest)
              accuracy = metrics.accuracy score(ytest, y pred)*100
              acc.append(accuracy)
          plt.plot(dims,acc,'o-', linewidth=2, color='royalblue')
          plt.title("LDA - KNN")
          plt.xlabel("Dimensions")
          plt.ylabel("Accuracy")
```

#### Out[17]: Text(0, 0.5, 'Accuracy')



For 5 number of dimensions we get maximum accuracy of 28.5%

## Dataset - Abalone

```
In [18]:
    pca_dim = 5
    lda_dim = 5
    pca_model = PCA(n_components = pca_dim)
    lda_model = LDA(n_components = lda_dim)

# Raw data
X_raw = X.to_numpy()
y_raw = y.to_numpy()

#Best PCA
X_pca = pca_model.fit_transform(X)

#Best LDA
X_lda = lda_model.fit_transform(X,y)
```

# 2. Naive Bayes

## Multinomial NB

Original Feature Space is used for this classification. Hyper parameter tuning is performed using 5-fold cross validation on each label.

Naive Bayes classifier which uses a multinomial distribution for each of the features is Multinomial NB. It is inefficient when the datasets are imbalanced.

#### Multinomial NB | Raw Abalone Dataset

```
In [19]:
    kf = KFold(n_splits=5, random_state=26, shuffle = True)
    acc = []
    for train_idx, test_idx in kf.split(X_raw,y_raw):
        xtrain = X_raw[train_idx]
        ytrain = y_raw[train_idx]
        xtest = X_raw[test_idx]
        ytest = y_raw[test_idx]
        mnb_raw = MultinomialNB()
        mnb_raw.fit(xtrain, ytrain)
        ypred = mnb_raw.predict(xtest)
        accuracy = metrics.accuracy_score(ytest, ypred)*100
        acc.append(accuracy)

print("Multinomial NB | Raw dataset | Abalone | Accuracy : ", sum(acc)/len(accuracy)
```

# Multinomial NB | PCA Abalone Dataset

```
In [20]:
          kf = KFold(n splits=5, random state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X_pca)
          X_pca_scaled = scaler.transform(X_pca)
          for train_idx, test_idx in kf.split(X_pca_scaled,y_raw):
              xtrain = X pca scaled[train idx]
              ytrain = y raw[train idx]
              xtest = X pca scaled[test idx]
              ytest = y raw[test idx]
              mnb raw = MultinomialNB()
              mnb raw.fit(xtrain, ytrain)
              ypred = mnb raw.predict(xtest)
              accuracy = metrics.accuracy score(ytest, ypred)*100
              acc.append(accuracy)
          print("Multinomial NB | PCA dataset | Abalone | Accuracy : ", sum(acc)/len(ac
```

Multinomial NB | PCA dataset | Abalone | Accuracy: 16.83075953356445

#### Multinomial NB | LDA Abalone Dataset

```
In [21]:
          kf = KFold(n splits=5, random state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X_lda)
          X_lda_scaled = scaler.transform(X_lda)
          for train idx, test idx in kf.split(X lda scaled,y raw):
              xtrain = X lda scaled[train idx]
              ytrain = y_raw[train_idx]
              xtest = X lda scaled[test idx]
              ytest = y_raw[test_idx]
              mnb raw = MultinomialNB()
              mnb raw.fit(xtrain, ytrain)
              ypred = mnb_raw.predict(xtest)
              accuracy = metrics.accuracy score(ytest, ypred)*100
              acc.append(accuracy)
          print("Multinomial NB | LDA dataset | Abalone | Accuracy : ", sum(acc)/len(ac
```

Multinomial NB | LDA dataset | Abalone | Accuracy : 16.49545884307939

## **Complement NB**

Complement NB is efficient when the datasets are imbalanced and can be considered as an adaptation of the multinomial naive bayes where the datapoints belonging to all classes are calculated.

#### Complement NB | Raw Abalone dataset

Complement NB | Raw dataset | Abalone | Accuracy: 18.38661433114632

## Complement NB | PCA Abalone dataset

```
In [23]:
          kf = KFold(n splits=5, random state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X pca)
          X pca scaled = scaler.transform(X pca)
          for train_idx, test_idx in kf.split(X_pca_scaled,y_raw):
              xtrain = X pca scaled[train idx]
              ytrain = y_raw[train_idx]
              xtest = X pca scaled[test idx]
              ytest = y_raw[test_idx]
              cmp_ = ComplementNB()
              cmp_.fit(xtrain, ytrain)
              ypred = cmp .predict(xtest)
              accuracy = metrics.accuracy_score(ytest, ypred)*100
              acc.append(accuracy)
          print("Complement NB | PCA dataset | Abalone | Accuracy : ", sum(acc)/len(acc
```

Complement NB | PCA dataset | Abalone | Accuracy : 17.261152336475373

#### Complement NB | LDA Abalone dataset

```
In [24]:
          kf = KFold(n splits=5, random state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X lda)
          X lda scaled = scaler.transform(X lda)
          for train idx, test idx in kf.split(X lda scaled,y raw):
              xtrain = X_lda_scaled[train_idx]
              ytrain = y_raw[train_idx]
              xtest = X_lda_scaled[test_idx]
              ytest = y_raw[test_idx]
              cmp_ = ComplementNB()
              cmp .fit(xtrain, ytrain)
              ypred = cmp .predict(xtest)
              accuracy = metrics.accuracy_score(ytest, ypred)*100
              acc.append(accuracy)
          print("Complement NB | LDA dataset | Abalone | Accuracy : ", sum(acc)/len(acc
```

Complement NB | LDA dataset | Abalone | Accuracy: 21.49889694295619

Multinomial naive bayes outperforms complement naive bayes with the raw abalone dataset. However, The complement naive bayes outperforms the multinomial naive bayes with LDA,PCA dataset. This may be contradictory to the fact that complement NB performs better with unbalanced dataset in this scenario owing to the following reasons:

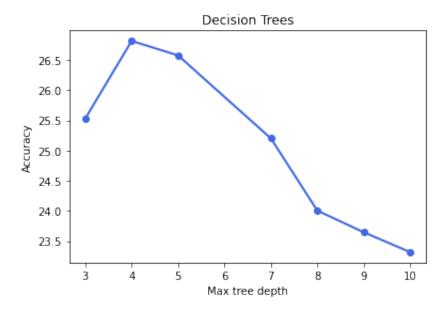
- 1. Nature of the datasets
- 2. Non-Removal of Outliers (as per instruction)
- 3. Z-scaling could not be performed due to occurances of negative values. Hence, Min-Max scaling was performed. Min-Max scaling without removal of outliers might have bad effects.

## 3. Decision Tree Classfication

- 1. Original Feature Space is used for this classification
- 2. Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for Max Depth

```
In [25]:
          X_train, X_test, y_train, y_test=train_test_split(X, y, test_size=0.2, random_state
          param_grid = {'max_depth': [3, 4, 5, 7, 8, 9, 10]}
          tree = DecisionTreeClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
          grid_search.fit(X_train, y_train)
          print(grid search.best params )
          print(grid search.best score )
          plt.title("Decision Trees")
          plt.plot( param_grid['max_depth'],grid_search.cv_results_['mean_test_score']*
          plt.xlabel("Max tree depth")
          plt.ylabel("Accuracy")
         {'max depth': 4}
         0.26817665118194106
         Text(0, 0.5, 'Accuracy')
```

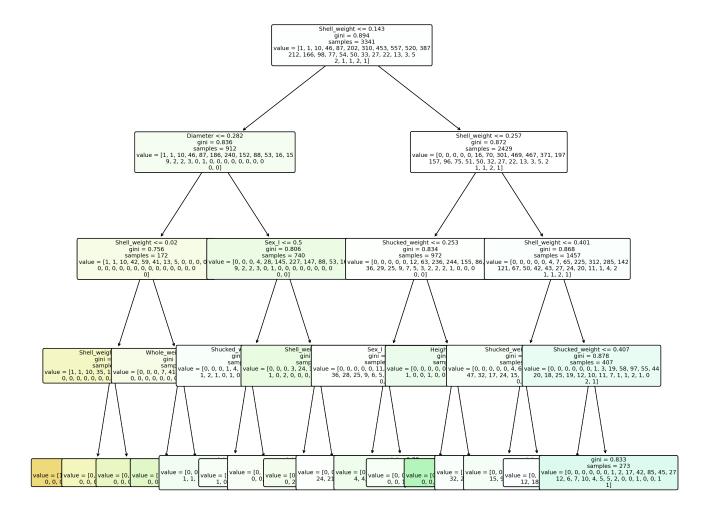
#### Out[25]:



Therefore, Max Depth value of 4 gives the best accuracy of 26.80%. When increasing the maximum depth after the value 5, the accuracy decreases as the Tree depth increases.

```
In [26]:
          from sklearn import tree
          dtree = DecisionTreeClassifier(random state=27, max depth = 4)
          dtree.fit(X train, y train)
          ypred = dtree.predict(X test)
          accuracy = metrics.accuracy_score(y_test, ypred)*100
          print(accuracy)
          fig, axes = plt.subplots(nrows = 1,ncols = 1,figsize = (12,12), dpi=300)
          tree.plot tree(dtree, feature names=list(X.columns), filled=True, fontsize=7, rou
          #plt.figure()
          plt.show()
```

#### 25.358851674641148



## Interpretability:

We can observe from the splitting pattern that, Gini Impurity is preferred to Information Gain because it does not contain logarithms which are computationally intensive. For each split, the Gini Impurity of each child node is individually calculated. The split with the lowest value of Gini Impurity is selected. We can observe that the root node was first split at Shell\_weight <=0.143 and gini impurity value of 0.894.Next split is at Diameter <= 0.282 on the left and Shell\_weight <= 0.257 on the right which is further split into Shell\_weight, Shucked\_weight and Sex. The splitting is unbalanced with more splitting and branching on the right side of root node than the left This splitting continues similarly until each of the resulting child nodes end up with 2 leaf nodes or 1 leaf node. In the final splitting, the pattern that can be observed is that the final child node splits are either on Shell\_weight, Whole\_weight, Shucked\_weight, Height and Sex on every branch. An interesting observation is that these 7 features were the subset of features selected to perform PCA.

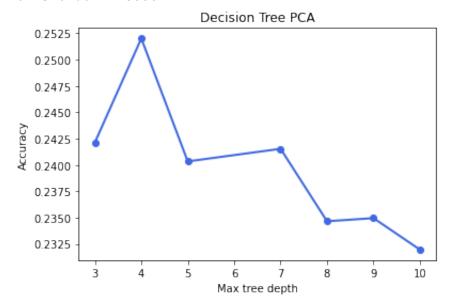
Decision Trees take a shorter time to compute morever the decision tree can prove substantially why the predictions are in a particular manner by tracing the tree unlike in PCA where the contextual information is lost in the process.

## Decision Tree | PCA ABALONE DATASET

- 1. Original Feature Space is used for this classification
- 2. Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for Max Depth

```
In [27]:
          X_train, X_test, y_train, y_test=train_test_split(X_pca, y, test_size=0.2, random_s
          param grid = {'max depth': [3, 4, 5, 7, 8, 9, 10]}
          tree = DecisionTreeClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param grid=param grid, cv=5)
          grid search.fit(X train, y train)
          print(grid search.best params )
          print(grid search.best score )
          plt.title("Decision Tree PCA")
          plt.xlabel("Max tree depth")
          plt.ylabel("Accuracy")
          plt.plot( param_grid['max_depth'],grid_search.cv_results_['mean_test_score'],
          dtree = DecisionTreeClassifier(random state=27, max depth = 4)
          dtree.fit(X_train, y_train)
          ypred = dtree.predict(X_test)
          accuracy = metrics.accuracy_score(y_test, ypred)*100
```

# {'max\_depth': 4} 0.2520170421488861



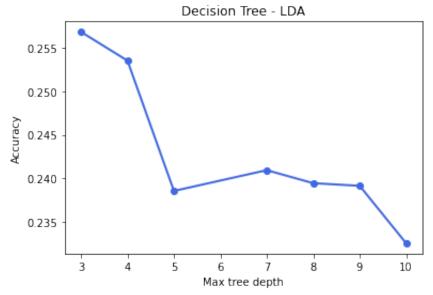
With the above plot Max Depth value of 4 gives the best accuracy of 25.20%. When increasing the maximum depth after the value 4, the accuracy decreases till tree depth of 5 and there is a slight increase in accuracy for Tree depth value of 7 after which the accuracy score goes on decreasing with increasing depth of tree

#### Decision Tree | LDA ABALONE DATASET

- 1. Original Feature Space is used for this classification
- 2. Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for Max Depth

```
In [28]:
          X train, X test, y train, y test=train test split(X lda, y, test size=0.2, random s
          param grid = {'max depth': [3, 4, 5, 7, 8, 9, 10]}
          tree = DecisionTreeClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param grid=param grid, cv=5)
          grid_search.fit(X_train, y_train)
          print(grid search.best params )
          print(grid search.best score )
          plt.title("Decision Tree - LDA")
          plt.xlabel("Max tree depth")
          plt.ylabel("Accuracy")
          plt.plot( param grid['max depth'],grid_search.cv_results_['mean_test_score'],
          dtree = DecisionTreeClassifier(random state=27, max depth = 4)
          dtree.fit(X train, y train)
          ypred = dtree.predict(X test)
          accuracy = metrics.accuracy score(y test, ypred)*100
          print("Test Accuracy is ", accuracy)
```

```
{'max depth': 3}
0.2568114891293646
Test Accuracy is 25.837320574162682
```



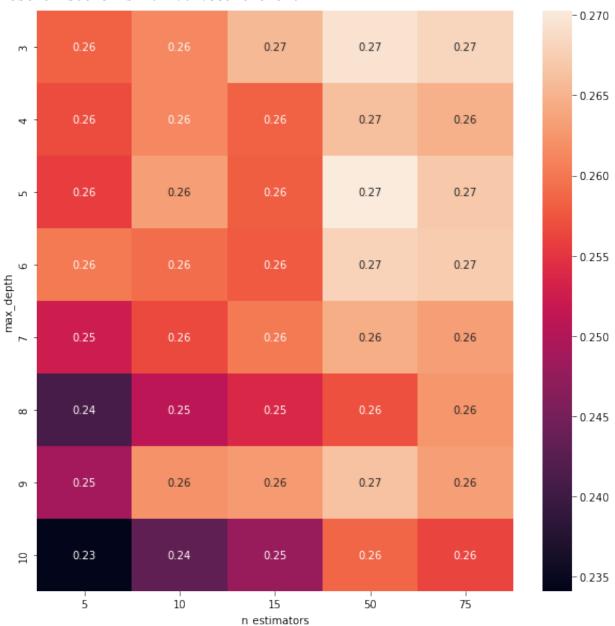
With the above plot Max Depth value of 3 gives the best accuracy of 25.83%. When increasing the maximum depth after the value 4, the accuracy decreases as the Tree depth increases

# 4. Random Forest Classification

Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for number of trees and Max Depth

```
In [29]:
          # find best value for max depth & number of trees parameters using gridsearch
          X train, X test, y train, y test=train test split(X, y, test size=0.2, random state
          param grid = {'max depth': [3, 4, 5, 6, 7, 8, 9, 10], 'n estimators': [5, 10,
          tree = RandomForestClassifier(random state=27)
          grid_search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
          grid search.fit(X train, y train)
          print(grid_search.best_params_)
          print("Best CV score is ",grid_search.best_score_)
          plt.figure(figsize = (10,10))
          cv_score = grid_search.cv_results_['mean_test_score']
          data1 = pd.DataFrame(grid search.cv results ['params'])
          data1['cv_score'] = cv_score
          data pivoted = datal.pivot("max depth", "n_estimators", "cv_score")
          sns.heatmap(data pivoted, annot = True)
          plt.show()
```

{'max\_depth': 5, 'n\_estimators': 50}
Best CV score is 0.2702755923131316



```
dtree = RandomForestClassifier(random_state=27, max_depth = 5, n_estimators =
    dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

Test Accuracy is 27.631578947368425

We can conclude from the heat map that max depth of 5 with 50 n-estimators provides the best accuracy of 27.63%

#### Random Forest Classification | PCA Abalone dataset

In [31]: # find best value for max depth & number of trees parameters using gridsearch X\_train, X\_test, y\_train, y\_test=train\_test\_split(X\_pca, y, test\_size=0.2, random\_s param grid = {'max depth': [3, 4, 5, 6, 7, 8, 9, 10], 'n estimators': [5, 10, tree = RandomForestClassifier(random state=27) grid search = GridSearchCV(estimator=tree, param\_grid=param\_grid, cv=5) grid search.fit(X train, y train) print(grid search.best params ) print("Best CV score is ",grid\_search.best\_score\_) plt.figure(figsize = (10,10)) cv\_score = grid\_search.cv\_results\_['mean\_test\_score'] data1 = pd.DataFrame(grid\_search.cv\_results\_['params']) data1['cv score'] = cv score data pivoted = data1.pivot("max depth", "n estimators", "cv score") sns.heatmap(data pivoted, annot = True) plt.show()

{'max\_depth': 5, 'n\_estimators': 15}
Best CV score is 0.2732785549976281



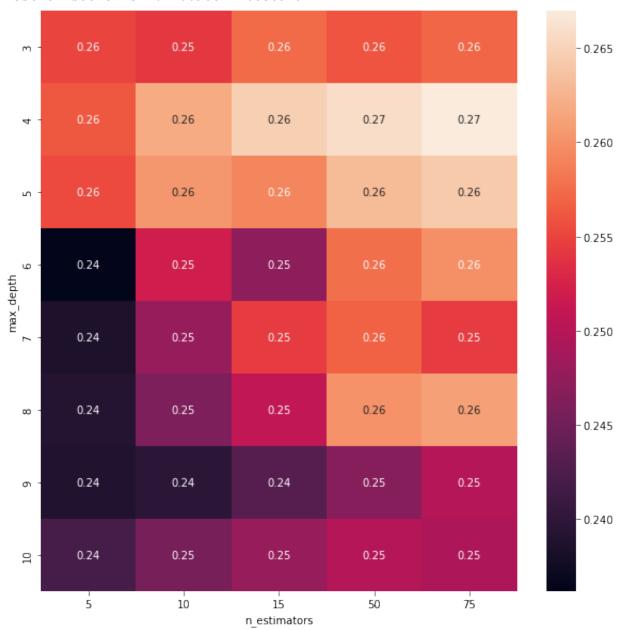
Test Accuracy is 26.435406698564595

We can conclude from the heat map that max depth of 5 with 15 n-estimators provides the best accuracy of 26.43%

#### Random Forest Classification | LDA Abalone dataset

In [33]: # find best value for max depth & number of trees parameters using gridsearch X\_train, X\_test, y\_train, y\_test=train\_test\_split(X\_lda, y, test\_size=0.2, random\_s param grid = {'max depth': [3, 4, 5, 6, 7, 8, 9, 10], 'n estimators': [5, 10, tree = RandomForestClassifier(random state=27) grid search = GridSearchCV(estimator=tree, param\_grid=param\_grid, cv=5) grid search.fit(X train, y train) print(grid search.best params ) print("Best CV score is ",grid\_search.best\_score\_) plt.figure(figsize = (10,10)) cv\_score = grid\_search.cv\_results\_['mean\_test\_score'] data1 = pd.DataFrame(grid\_search.cv\_results\_['params']) data1['cv score'] = cv score data pivoted = data1.pivot("max depth", "n estimators", "cv score") sns.heatmap(data pivoted, annot = True) plt.show()

{'max\_depth': 4, 'n\_estimators': 75}
Best CV score is 0.2669884446353929



Test Accuracy is 26.913875598086122

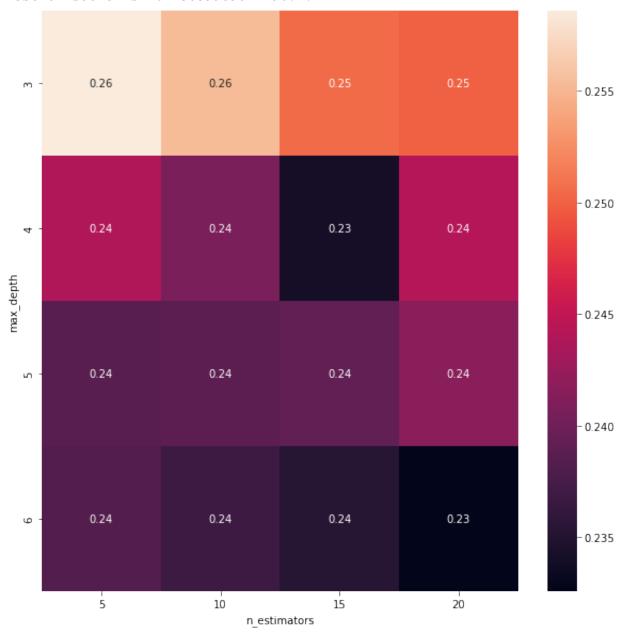
We can conclude from the heat map that max depth of 5 with 75 n-estimators provides the best accuracy of 26.91%

# 5. Gradient Boosting

Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for number of estimators

```
In [35]:
          # find best value for max depth & number of trees parameters using gridsearch
          X_train, X_test, y_train, y_test=train_test_split(X, y, test_size=0.2, random_state
          param grid = {'max depth': [3, 4, 5, 6],'n estimators' :[5, 10, 15, 20]}
          tree = GradientBoostingClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param grid=param grid, cv=5)
          grid search.fit(X train, y train)
          print(grid search.best params )
          print("Best CV score is ",grid search.best score )
          plt.figure(figsize = (10,10))
          cv_score = grid_search.cv_results_['mean_test_score']
          data1 = pd.DataFrame(grid search.cv results ['params'])
          data1['cv score'] = cv score
          data pivoted = datal.pivot("max depth", "n_estimators", "cv_score")
          sns.heatmap(data pivoted, annot = True)
          plt.show()
```

{'max\_depth': 3, 'n\_estimators': 5}
Best CV score is 0.25859939314196717



Best value for number of estimators=3 with accuracy=25.71%

Test Accuracy is 25.717703349282296

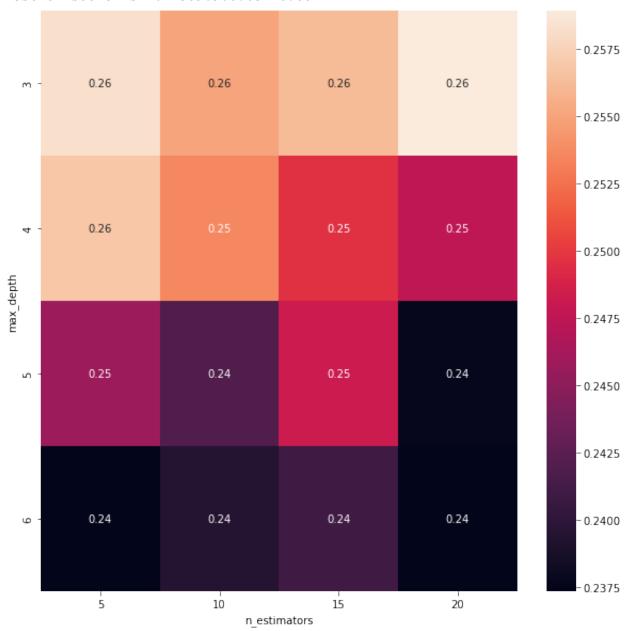
## **Gradient Tree Boosting | PCA Abalone Dataset**

```
In [37]:
```

```
# find best value for max depth & number of trees parameters using gridsearch
X_train,X_test,y_train,y_test=train_test_split(X_pca,y,test_size=0.2,random_s
param_grid = {'max_depth': [3, 4, 5, 6],'n_estimators': [5, 10, 15, 20]}
tree = GradientBoostingClassifier(random_state=27)
grid_search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
grid_search.fit(X_train, y_train)
print(grid_search.best_params_)
print("Best CV score is ",grid_search.best_score_)

plt.figure(figsize = (10,10))
cv_score = grid_search.cv_results_['mean_test_score']
datal = pd.DataFrame(grid_search.cv_results_['params'])
datal['cv_score'] = cv_score
data_pivoted = datal.pivot("max_depth", "n_estimators", "cv_score")
sns.heatmap(data_pivoted, annot = True)
plt.show()
```

{'max\_depth': 3, 'n\_estimators': 20}
Best CV score is 0.25890908765428783



```
dtree = GradientBoostingClassifier(random_state=27, max_depth = 3, n_estimator
dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

Test Accuracy is 25.478468899521534

Best value for number of estimators=20 with accuracy=25.47%

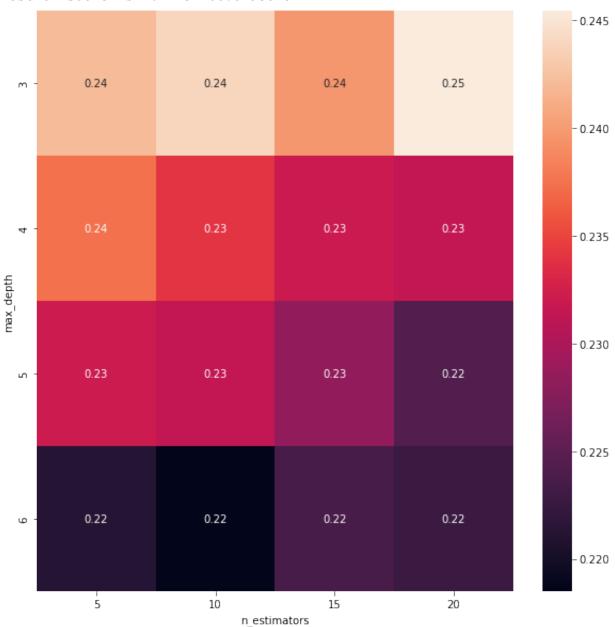
## **Gradient Tree Boosting | LDA Abalone Dataset**

```
In [39]:
```

```
# find best value for max depth & number of trees parameters using gridsearch
X_train,X_test,y_train,y_test=train_test_split(X_lda,y,test_size=0.2,random_s
param_grid = {'max_depth': [3, 4, 5, 6],'n_estimators': [5, 10, 15, 20]}
tree = GradientBoostingClassifier(random_state=27)
grid_search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
grid_search.fit(X_train, y_train)
print(grid_search.best_params_)
print("Best CV score is ",grid_search.best_score_)

plt.figure(figsize = (10,10))
cv_score = grid_search.cv_results_['mean_test_score']
datal = pd.DataFrame(grid_search.cv_results_['params'])
datal['cv_score'] = cv_score
data_pivoted = datal.pivot("max_depth", "n_estimators", "cv_score")
sns.heatmap(data_pivoted, annot = True)
plt.show()
```

{'max\_depth': 3, 'n\_estimators': 20}
Best CV score is 0.24542887319531342



Test Accuracy is 28.11004784688995

Best value for number of estimators=20 with accuracy=28.11%

In [41]:

#### **OBSERVATIONS: Gradient Tree Boosting**

```
1. Raw Abalone data ---- No of estimators = 03, Accuracy = 25.71%
```

- 2. PCA Abalone data ---- No of estimators = 20, Accuracy = 25.47%
- 3. LDA Abalone data ---- No of estimators = 20, Accuracy = 28.11%

## Wine Dataset

## Importing libraries

import os

```
from sklearn.preprocessing import StandardScaler
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix, accuracy_score,classification_r.
# libraries
import numpy as np
import pandas as pd
import random
import seaborn as sns
sns.set(style="ticks", color_codes=True)
from sklearn import neighbors
from sklearn.model_selection import train_test_split
from scipy import stats
import matplotlib.pyplot as plt
import warnings
from sklearn import neighbors, datasets, preprocessing
```

from sklearn.discriminant analysis import LinearDiscriminantAnalysis as LDA

from sklearn.tree import DecisionTreeClassifier

from sklearn.naive\_bayes import MultinomialNB
from sklearn.model\_selection import GridSearchCV

from sklearn.model selection import train test split

from sklearn.metrics import f1 score, roc auc score

from sklearn.model selection import StratifiedKFold

warnings.filterwarnings("ignore")

from sklearn.decomposition import PCA
from sklearn.manifold import TSNE

from sklearn.model selection import KFold

from sklearn.preprocessing import MinMaxScaler

```
In [42]:
    D = ['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar', 'c'
    L = 'quality'
    C = 'color'

#Loading Data set
    wine_r = pd.read_csv("winequality-red.csv", sep=';')
    #Loading Data set
    wine_w = pd.read_csv("winequality-white.csv", sep=';')
    wine_w = wine_w.copy()
    wine_w[C] = np.zeros(wine_w.shape[0])
    wine_r[C] = np.ones(wine_r.shape[0])
    wine = pd.concat([wine_w,wine_r]).reset_index()

X=wine.drop('quality',axis=1)
    Y=wine['quality'].values
```

# Preliminary analysis on the data

# **Normalization**

Min-max normalization is used to scale the data such that the minimum value of the feature is set to 0 and the maximum value of the feature is set to 1

```
In [44]:
#Normalizing data using Min-Max method
wine_MinMax = wine[:].copy()
for d in wine_MinMax[:]:
    if d in ['quality']:
        continue
    wine_MinMax[d] = (wine_MinMax[d] - wine_MinMax[d].min()) / (wine_MinMax[d])
```

## KNN with Min-Max Normalization

### Data preparation

Performing K-NN classfier using Defaults values, Manhattan distance & Euclidean distance to derive k-value of the best performance

```
In [45]:
    from sklearn.model_selection import train_test_split
    from sklearn.neighbors import KNeighborsClassifier
    from sklearn import metrics

#Preparing the data
X = wine_MinMax
drop_columns = ['quality']
y = wine['quality']
X = X.drop(columns = drop_columns)

#Splitting the data
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.2,random_state)
```

### KNN with default parameters

```
In [46]:
    knn = KNeighborsClassifier()
    knn.fit(X_train, y_train.values.ravel())
    y_pred = knn.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, y_pred)*100
    print("For KNN default settings, the accuracy is ",accuracy)

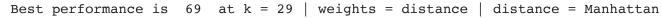
For KNN default settings, the accuracy is 55.15384615384615

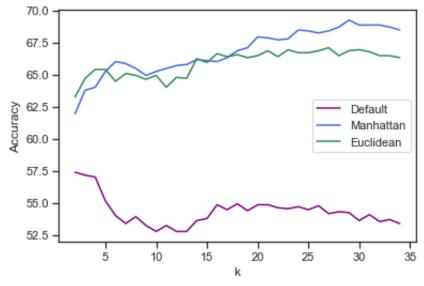
In [47]:

#KNN for default
    perf = {"Acc" : 0, "k":0, "dist": "Manhattan", "weights": "uniform"}
    k_list = list(range(2,35))
    m_acc_default = []
    for k in k_list:
        knn = KNeighborsClassifier(n_neighbors=k, weights = 'uniform', p = 2, met)
```

knn.fit(X\_train, y\_train.values.ravel())

```
y pred = knn.predict(X test)
    accuracy = metrics.accuracy score(y test, y pred)*100
    if accuracy>perf['Acc']:
        perf['Acc'] = accuracy
        perf['k'] = k
        perf['dist'] = 'Euclidean'
        perf['weights'] = 'Uniform'
    m acc default.append(accuracy)
plt.plot(k_list, m_acc_default,color="purple")
#KNN for Manhatten distance
m acc manhatten = []
for k in k list:
    knn = KNeighborsClassifier(n neighbors=k, weights = 'distance', p = 1, me
    knn.fit(X_train, y_train.values.ravel())
    y pred = knn.predict(X test)
    accuracy = metrics.accuracy_score(y_test, y_pred)*100
    if accuracy>perf['Acc']:
        perf['Acc'] = accuracy
        perf['k'] = k
        perf['dist'] = 'Manhattan'
        perf['weights'] = 'distance'
    m_acc_manhatten.append(accuracy)
plt.plot(k_list, m_acc_manhatten,color="royalblue")
#KNN for Euclidean distance
m acc euclidean = []
for k in k list:
    knn = KNeighborsClassifier(n neighbors=k, weights = 'distance', p = 2, me
    knn.fit(X train, y train.values.ravel())
    y pred = knn.predict(X test)
    accuracy = metrics.accuracy score(y test, y pred)*100
    if accuracy>perf['Acc']:
        perf['Acc'] = accuracy
        perf['k'] = k
        perf['dist'] = 'Euclidean'
        perf['weights'] = 'distance'
    m acc euclidean.append(accuracy)
plt.plot(k list, m acc euclidean,color="seagreen")
plt.legend(["Default", "Manhattan", "Euclidean"])
plt.xlabel('k')
plt.ylabel('Accuracy')
print("Best performance is ",round(perf['Acc'])," at k = ",perf['k']," | weight
```





Using Manhattan Distance metric we get the highest accuracy of 69% for K=29. Manhattan Distance is used to calculate the distance between two data points in a grid-like path

# Best performing KNN configuration

Selecting the Best Value for K which provides best accuracy scores

```
In [48]:
    knn = KNeighborsClassifier(n_neighbors=29, weights = 'distance', p = 1, metricknn.fit(X_train, y_train.values.ravel())
    y_pred = knn.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, y_pred)*100
    print(accuracy)
```

69.23076923076923

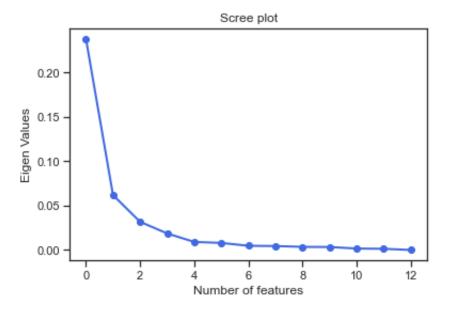
The value K=29 provides an overall accuracy of 69.23

# 1. Representation Learning

### **PCA**

PCA is an unsupervised form of learning hence, we drop the target variables and carry out PCA on the remaining 11 attributes to find principal components with highest cumulative covariance.

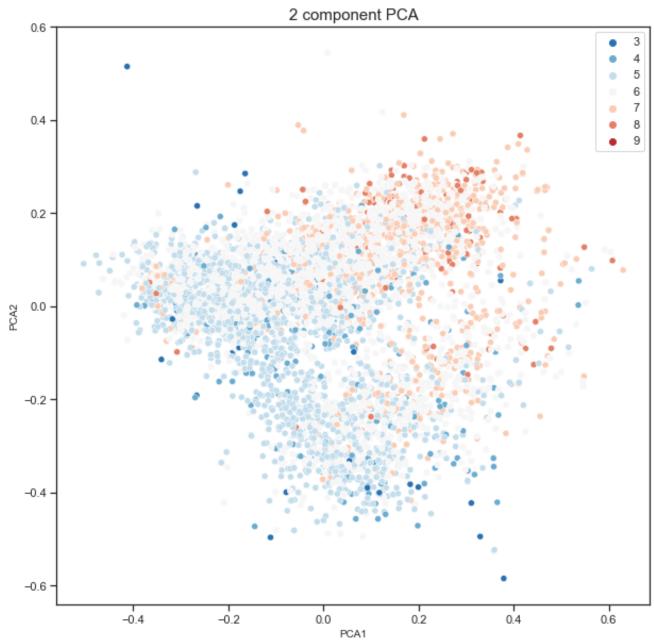
Out[49]: Text(0.5, 1.0, 'Scree plot')



The above plot indicates the Eigen values w.r.t number of features. As the number of Features increases the Eigen value decreased and reached solidity beyond 4 features.

```
In [50]:
    D = ['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar', 'c
    pca_model_2dims = PCA(n_components=2)
    pca_model_2dims.fit(X_train[D])
    X2d = pca_model_2dims.transform(X[D])
    wine_2d_pca = pd.DataFrame(X2d, columns = ["PCA1", "PCA2"])
    wine_2d_pca["Label"] = wine["quality"]
    fig = plt.figure(figsize = (10,10))
    sns.scatterplot(x = wine_2d_pca["PCA1"].values, y = wine_2d_pca["PCA2"].value
    plt.xlabel('PCA1', fontsize = 10)
    plt.ylabel('PCA2', fontsize = 10)
    plt.title('2 component PCA', fontsize = 15)
    print(pca_model_2dims.explained_variance_ratio_)
```

[0.32279011 0.2374186 ]



The scree plot is a plot between the number of features and the magnitude of the eigen values which explains the quantum of spread along a particular principle component. Based on this plot, the datapoints are wide spread and portrays that the first two components adds up to only 55% of the total features and hence it may not be efficient and other PCA components may have to be added.

### **TSNE**

T-SNE is another dimensionality reduction concept that is well suited to effectively visualize high dimensional data. Since us humans can visualize and discern data in a 2-D or 3-D space plots the natural choice for dimension is either 2 or 3. For our experimentation, we'll primarily be using n\_components set at 2 because of the following reasons,

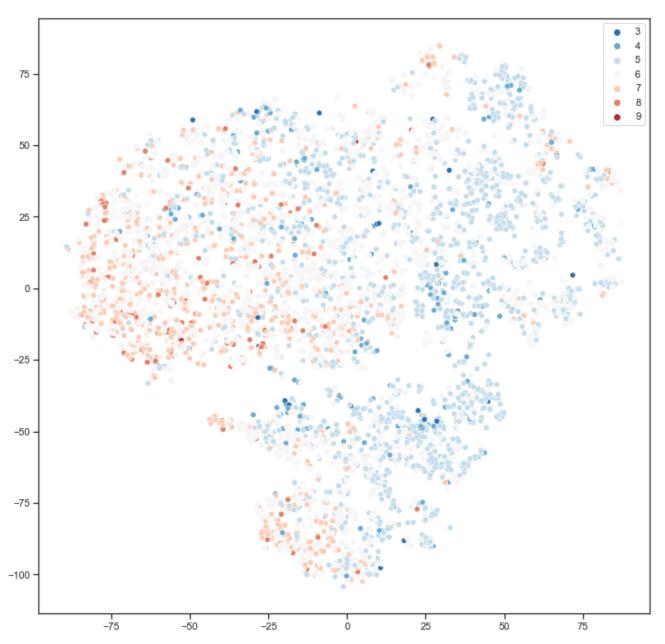
It is convenient to visualize and analyze points in a 2D plots

Easy to work with 2D plots without having to expend too much on computing

```
In [51]:
    D = ['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar', 'c
    tsne_2d = TSNE(n_components=2)
    X2d_tsne = tsne_2d.fit_transform(X[D])

wine_2d_tsne = pd.DataFrame(X2d_tsne, columns = ["TSNE1", "TNSE2"])
wine_2d_tsne["Label"] = wine["quality"]
fig = plt.figure(figsize = (12,12))
sns.scatterplot(x = wine_2d_tsne["TSNE1"].values, y = wine_2d_tsne["TNSE2"].v
```

### Out[51]: <AxesSubplot:>



Feature of t-SNE is a tuneable parameter, "perplexity," which says how to balance attention between local and global aspects of your data. The parameter is a guess about the number of close neighbors each point has. The results of the T-SNE shows evident grouping between classes however it is not distinct and difficult to infer from the plot.

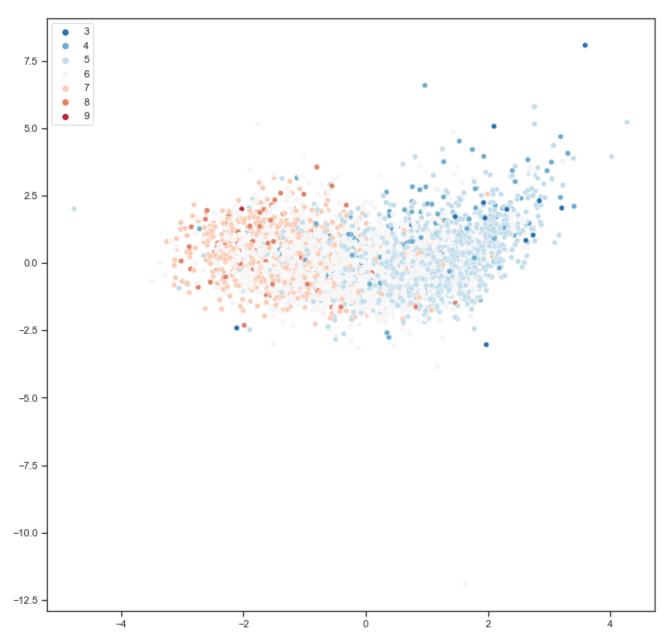
### **LDA**

Linear Discriminant Analysis (LDA) is a supervised approach for identifying the linear discriminants that reflect the axes that optimise separation between various classes. Each class is given a Gaussian density by the model, which assumes that all classes have the same covariance matrix.

```
In [52]:
    D = ['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar', 'c
    lda_2d = LDA(n_components=2)
    X2d_lda = lda_2d.fit_transform(X[D], y = y)

wine_2d_lda = pd.DataFrame(X2d_lda, columns = ["LDA1", "LDA2"])
    wine_2d_lda["Label"] = wine["quality"]
    fig = plt.figure(figsize = (12,12))
    sns.scatterplot(x = wine_2d_lda["LDA1"].values, y = wine_2d_lda["LDA2"].value
```

Out[52]: <AxesSubplot:>

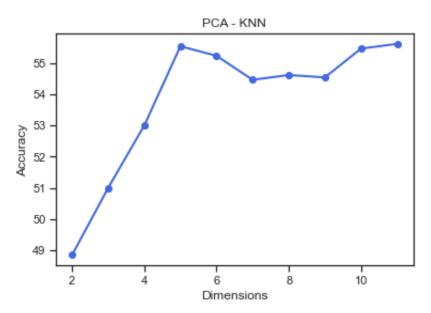


LDA focuses on the seperation of the different classes and it is evident in the above plot.

# KNN performance by varying dimensions in PCA

```
In [53]:
          dims = []
          acc = []
          for d in range(2,len(D)+1):
              dims.append(d)
              pca_model = PCA(n_components=d)
              pca model.fit(X train[D])
              Xnew = pca model.transform(X[D])
              Xtrain, Xtest, ytrain, ytest = train test split(Xnew, y, test size=0.2, random
              knn = KNeighborsClassifier(n_neighbors=26, weights = 'uniform', p = 2, me
              knn.fit(Xtrain, ytrain.values.ravel())
              y pred = knn.predict(Xtest)
              accuracy = metrics.accuracy score(ytest, y pred)*100
              acc.append(accuracy)
          plt.plot(dims,acc, 'o-', linewidth=2, color='royalblue')
          plt.title("PCA - KNN")
          plt.xlabel("Dimensions")
          plt.ylabel("Accuracy")
```

#### Out[53]: Text(0, 0.5, 'Accuracy')

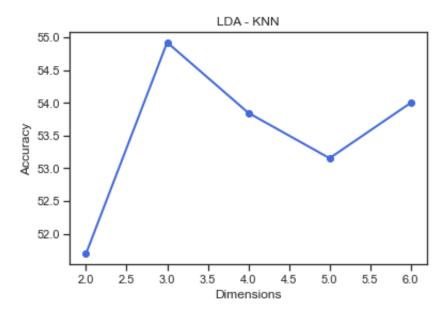


The accuracy for 5 dimensions for the KNN-PCA is 56%

### KNN performance by varying dimensions in LDA

```
In [54]:
          dims = []
          acc = []
          for d in range(2,7):
              dims.append(d)
              lda_model = LDA(n_components=d)
              Xnew = lda model.fit_transform(X[D], y = y)
              Xtrain, Xtest, ytrain, ytest = train test split(Xnew, y, test size=0.2, random
              knn = KNeighborsClassifier(n neighbors=26, weights = 'uniform', p = 2, me
              knn.fit(Xtrain, ytrain.values.ravel())
              y pred = knn.predict(Xtest)
              accuracy = metrics.accuracy score(ytest, y pred)*100
              acc.append(accuracy)
          plt.plot(dims,acc, 'o-', linewidth=2, color='royalblue')
          plt.title("LDA - KNN")
          plt.xlabel("Dimensions")
          plt.ylabel("Accuracy")
```

#### Out[54]: Text(0, 0.5, 'Accuracy')



The accuracy for 3 dimensions for the LDA-KNN is 54.8%

## Dataset - Wine

```
In [55]:
    pca_dim = 5
    lda_dim = 3
    pca_model = PCA(n_components = pca_dim)
    lda_model = LDA(n_components = lda_dim)

# Raw data
X_raw = X.to_numpy()
y_raw = y.to_numpy()

#Best PCA
X_pca = pca_model.fit_transform(X)

#Best LDA
X_lda = lda_model.fit_transform(X,y)
```

# 2. Naive Bayes

## **Multinomial Naive Bayes**

Original Feature Space is used for this classification. Hyper parameter tuning is performed using 5-fold cross validation on each label.

Naive Bayes classifier which uses a multinomial distribution for each of the features is Multinomial NB. It is inefficient when the datasets are imbalanced.

#### Multinomial NB | Raw Wine dataset

Multinomial NB | Raw dataset | Wine | Accuracy : 47.03685675371587

### Multinomial NB | PCA Wine dataset

```
In [57]:
          kf = KFold(n splits=5, random state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X pca)
          X pca scaled = scaler.transform(X pca)
          for train idx, test idx in kf.split(X pca scaled,y raw):
              xtrain = X pca scaled[train idx]
              ytrain = y raw[train idx]
              xtest = X pca scaled[test idx]
              ytest = y raw[test idx]
              mnb_raw = MultinomialNB()
              mnb raw.fit(xtrain, ytrain)
              ypred = mnb_raw.predict(xtest)
              accuracy = metrics.accuracy_score(ytest, ypred)*100
              acc.append(accuracy)
          print("Multinomial NB | PCA dataset | Wine | Accuracy : ", sum(acc)/len(acc))
```

Multinomial NB | PCA dataset | Wine | Accuracy: 43.650595132350325

#### Multinomial NB | LDA Wine dataset

```
In [58]:
          kf = KFold(n_splits=3, random_state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X lda)
          X lda scaled = scaler.transform(X lda)
          for train_idx, test_idx in kf.split(X_lda_scaled,y_raw):
              xtrain = X lda scaled[train idx]
              ytrain = y raw[train idx]
              xtest = X_lda_scaled[test_idx]
              ytest = y raw[test idx]
              mnb raw = MultinomialNB()
              mnb raw.fit(xtrain, ytrain)
              ypred = mnb raw.predict(xtest)
              accuracy = metrics.accuracy_score(ytest, ypred)*100
              acc.append(accuracy)
          print("Multinomial NB | LDA dataset | Wine | Accuracy : ", sum(acc)/len(acc))
         Multinomial NB | LDA dataset | Wine | Accuracy: 43.6507591250319
```

## Complement Naive Bayes

#### Complement NB | Raw Wine dataset

Complement NB | Raw dataset | Wine | Accuracy: 43.604666311363765

#### Complement NB | PCA Wine dataset

```
In [60]:
          kf = KFold(n_splits=5, random_state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X_pca)
          X pca scaled = scaler.transform(X pca)
          for train_idx, test_idx in kf.split(X_pca_scaled,y_raw):
              xtrain = X pca scaled[train idx]
              ytrain = y raw[train idx]
              xtest = X_pca_scaled[test idx]
              ytest = y raw[test idx]
              cmp = ComplementNB()
              cmp .fit(xtrain, ytrain)
              ypred = cmp_.predict(xtest)
              accuracy = metrics.accuracy_score(ytest, ypred)*100
              acc.append(accuracy)
          print("Complement NB | PCA dataset | Wine | Accuracy : ", sum(acc)/len(acc))
```

Complement NB | PCA dataset | Wine | Accuracy : 39.74158820394386

### Complement NB | LDA Wine dataset

```
In [61]:
          kf = KFold(n splits=3, random state=26, shuffle=True)
          acc = []
          scaler = MinMaxScaler()
          scaler.fit(X lda)
          X_lda_scaled = scaler.transform(X_lda)
          for train idx, test idx in kf.split(X lda scaled,y raw):
              xtrain = X lda_scaled[train_idx]
              ytrain = y raw[train idx]
              xtest = X lda scaled[test idx]
              ytest = y_raw[test_idx]
              cmp_ = ComplementNB()
              cmp .fit(xtrain, ytrain)
              ypred = cmp .predict(xtest)
              accuracy = metrics.accuracy_score(ytest, ypred)*100
              acc.append(accuracy)
          print("Complement NB | LDA dataset | Wine | Accuracy : ", sum(acc)/len(acc))
```

Complement NB | LDA dataset | Wine | Accuracy: 42.95843027202543

Multinomial naive bayes outperforms complement naive bayes with the all datasets. This may be contradictory to the fact that complement NB performs better with unbalanced dataset in this scenario owing to the following reasons: Nature of the datasets Non-Removal of Outliers Z-scaling could not be performed due to occurances of negative values. Hence, Min-Max scaling was performed

### 3. Decision Tree Classification

Original Feature Space is used for this classification.

Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for Max Depth

```
In [62]:

X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.2,random_state=param_grid = {'max_depth': [3, 4, 5, 7, 8, 9, 10]}

tree = DecisionTreeClassifier(random_state=27)

grid_search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)

grid_search.fit(X_train, y_train)

print(grid_search.best_params_)

print(grid_search.best_score_)

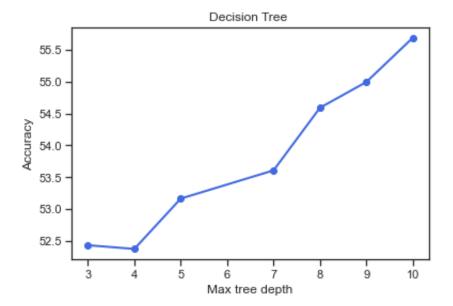
plt.plot( param_grid['max_depth'],grid_search.cv_results_['mean_test_score']*

plt.title("Decision Tree ")

plt.xlabel("Max_tree_depth")

plt.ylabel("Accuracy")
```

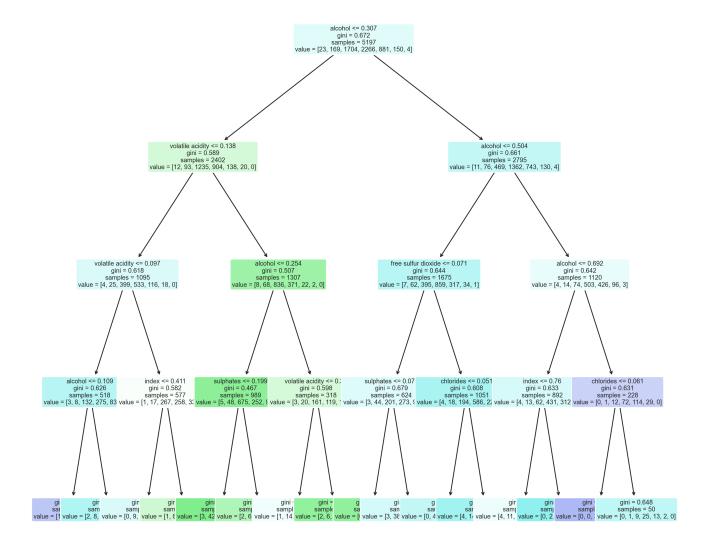
```
{'max_depth': 10}
0.5568555193603316
Out[62]: Text(0, 0.5, 'Accuracy')
```



Therefore, Max Depth value of 10 gives the best accuracy of 55.68 %. With reference to the plot the as the Depth of tree increases the accuracy of the classfier also increases Linearly

```
from sklearn import tree
    dtree = DecisionTreeClassifier(random_state=27, max_depth = 4)
    dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print(accuracy)
    fig, axes = plt.subplots(nrows = 1,ncols = 1,figsize = (12,12), dpi=300)
    tree.plot_tree(dtree,feature_names=list(X.columns),filled=True,fontsize=7,rou
#plt.figure()
    plt.show()
```

#### 52.307692307692314

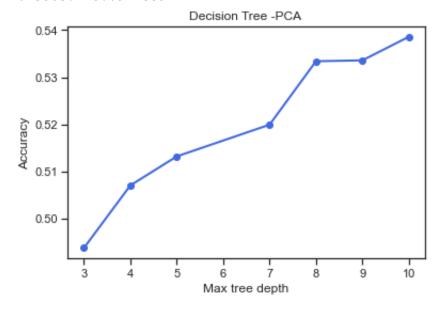


We can observe from the splitting pattern that, Gini Impurity is preferred to Information Gain because it does not contain logarithms which are computationally intensive. For each split, the Gini Impurity of each child node is individually calculated. The split with the lowest value of Gini Impurity is selected. We can observe that the root node was first split at alcohol <=0.307 and gini impurity value of 0.672 .Next split is at volatile acidity <= 0.138 on the left and alcohol <= 0.504 on the right which is further split into volatile acidity, alcohol and free sulphur dioxide. The splitting is balanced with continous and regularised splitting at nodes. This splitting continues similarly until each of the resulting child nodes end up with 2 leaf nodes. In the final splitting, the pattern that can be observed is that the final child node splits are either on alcohol, sulphates, volatile acidity and chlorides on every branch. An interesting observation is that these features were the subset of features selected to perform PCA.

#### **Decision Tree | PCA WINE DATASET**

```
In [64]:
          X_train,X_test,y_train,y_test=train_test_split(X_pca,y,test_size=0.2,random_s
          param_grid = {'max_depth': [3, 4, 5, 7, 8, 9, 10]}
          tree = DecisionTreeClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param grid=param grid, cv=5)
          grid search.fit(X train, y train)
          print(grid search.best params )
          print(grid_search.best_score_)
          plt.plot( param_grid['max_depth'],grid_search.cv_results_['mean_test_score'],
          plt.title("Decision Tree -PCA ")
          plt.xlabel("Max tree depth")
          plt.ylabel("Accuracy")
          dtree = DecisionTreeClassifier(random_state=27, max_depth = 10)
          dtree.fit(X_train, y_train)
          ypred = dtree.predict(X test)
          accuracy = metrics.accuracy_score(y_test, ypred)*100
```

{'max\_depth': 10}
0.5385742577922559



With the above plot Max Depth value of 10 gives the best accuracy of 53.85%. With reference to the plot above as there is linear increase in Accuracy with respect to depth of the tree

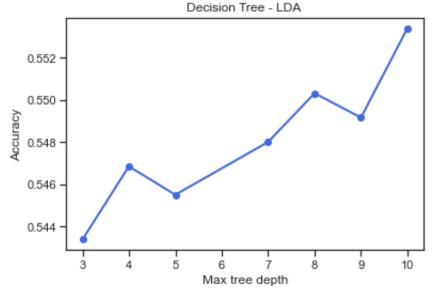
#### **Decision Tree | LDA WINE DATASET**

Original Feature Space is used for this classification

Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for Max Depth

```
In [65]:
          X_train, X_test, y_train, y_test=train_test_split(X_lda, y, test_size=0.2, random_s
          param grid = {'max depth': [3, 4, 5, 7, 8, 9, 10]}
          tree = DecisionTreeClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param grid=param grid, cv=5)
          grid search.fit(X train, y train)
          print(grid search.best params )
          print(grid search.best score )
          plt.plot( param grid['max depth'], grid search.cv results ['mean test score'],
          plt.title("Decision Tree - LDA ")
          plt.xlabel("Max tree depth")
          plt.ylabel("Accuracy")
          dtree = DecisionTreeClassifier(random state=27, max depth = 10)
          dtree.fit(X_train, y_train)
          ypred = dtree.predict(X_test)
          accuracy = metrics.accuracy_score(y_test, ypred)*100
          print("Test Accuracy is ", accuracy)
```

```
{'max depth': 10}
0.5534002739320353
Test Accuracy is 54.307692307692314
```



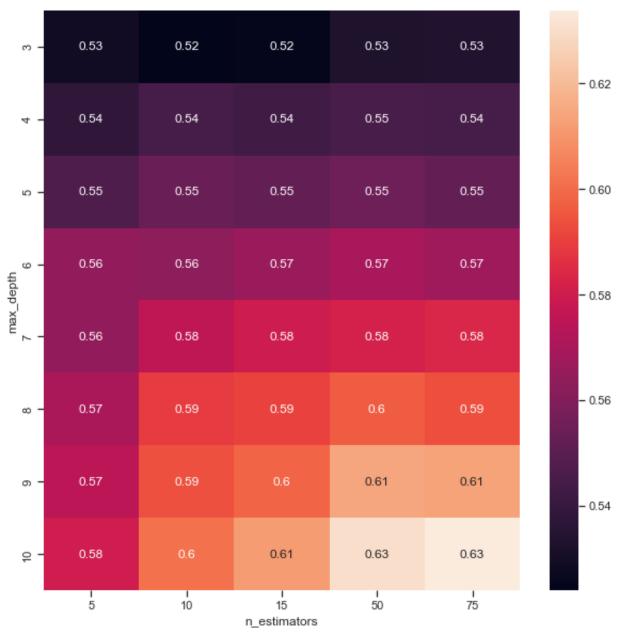
With the above plot Max Depth value of 10 gives the best accuracy of 55.41%. With reference to the plot above as there is linear increase in Accuracy with respect to depth of the tree. There is a difference in the above case where a decrease in the accuracy is observed at tree depth value of 5.

### Random Forest

Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for number of trees and Max Depth

```
In [66]:
          # find best value for max depth & number of trees parameters using gridsearch
          X_train, X_test, y_train, y_test=train_test_split(X, y, test_size=0.2, random_state
          param_grid = {'max_depth': [3, 4, 5, 6, 7, 8, 9, 10], 'n_estimators' :[5, 10,
          tree = RandomForestClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
          grid_search.fit(X_train, y_train)
          print(grid_search.best_params_)
          print("Best CV score is ",grid_search.best_score_)
          plt.figure(figsize = (10,10))
          cv score = grid search.cv results ['mean test score']
          data1 = pd.DataFrame(grid search.cv results ['params'])
          data1['cv score'] = cv score
          data pivoted = data1.pivot("max depth", "n estimators", "cv_score")
          sns.heatmap(data_pivoted, annot = True)
          plt.show()
```

{'max\_depth': 10, 'n\_estimators': 75}
Best CV score is 0.6338235729621677



```
In [67]:
    dtree = RandomForestClassifier(random_state=27, max_depth = 10, n_estimators
    dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

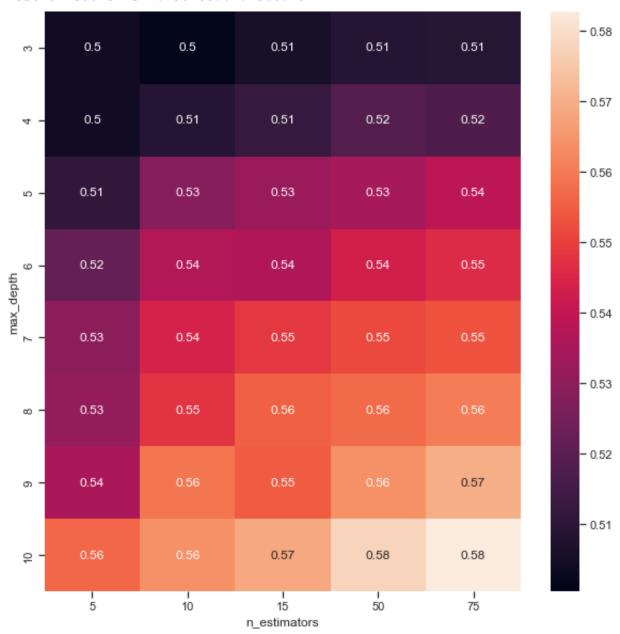
Test Accuracy is 64.38461538461539

We can conclude from the heat map that max depth of 10 with 75 n-estimators provides the best accuracy of 64.38 %

#### Random Forest | PCA WINE DATASET

```
In [68]:
          # find best value for max depth & number of trees parameters using gridsearch
          X train, X test, y train, y test=train_test_split(X_pca, y, test_size=0.2, random_s
          param grid = {'max depth': [3, 4, 5, 6, 7, 8, 9, 10], 'n estimators': [5, 10,
          tree = RandomForestClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param grid=param grid, cv=5)
          grid search.fit(X train, y train)
          print(grid_search.best_params_)
          print("Best CV score is ",grid_search.best_score_)
          plt.figure(figsize = (10,10))
          cv score = grid search.cv results ['mean test score']
          data1 = pd.DataFrame(grid_search.cv_results_['params'])
          data1['cv_score'] = cv_score
          data pivoted = datal.pivot("max depth", "n estimators", "cv score")
          sns.heatmap(data pivoted, annot = True)
          plt.show()
```

{'max\_depth': 10, 'n\_estimators': 75}
Best CV score is 0.5828370474568743



```
dtree = RandomForestClassifier(random_state=27, max_depth = 10, n_estimators
    dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

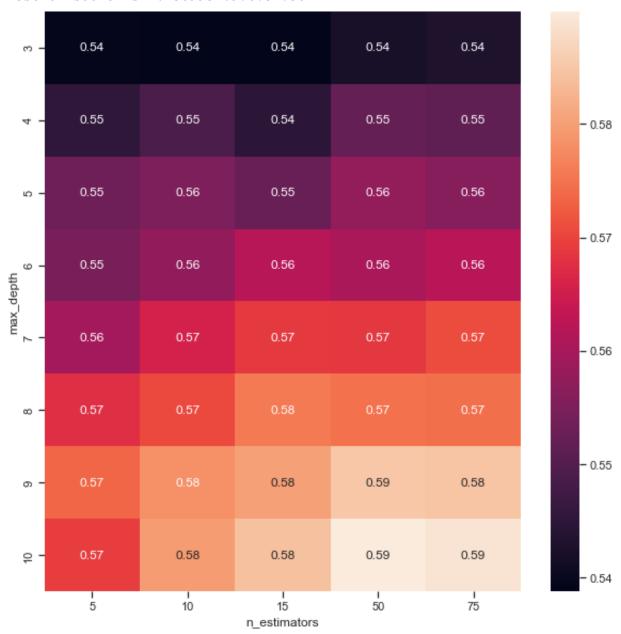
Test Accuracy is 58.46153846153847

We can conclude from the heat map that max depth of 10 with 75 n-estimators provides the best accuracy of 58.46 %

### Random Forest Classification | LDA Wine dataset

```
In [70]:
          # find best value for max depth & number of trees parameters using gridsearch
          X train, X test, y train, y test=train test split(X lda, y, test size=0.2, random s
          param_grid = {'max_depth': [3, 4, 5, 6, 7, 8, 9, 10], 'n_estimators' :[5, 10,
          tree = RandomForestClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param grid=param grid, cv=5)
          grid search.fit(X train, y train)
          print(grid_search.best_params_)
          print("Best CV score is ",grid_search.best_score_)
          plt.figure(figsize = (10,10))
          cv score = grid search.cv results ['mean test score']
          data1 = pd.DataFrame(grid_search.cv_results_['params'])
          data1['cv_score'] = cv_score
          data pivoted = datal.pivot("max depth", "n estimators", "cv score")
          sns.heatmap(data pivoted, annot = True)
          plt.show()
```

{'max\_depth': 10, 'n\_estimators': 50}
Best CV score is 0.5899540978751758



```
dtree = RandomForestClassifier(random_state=27, max_depth = 10, n_estimators
    dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

Test Accuracy is 58.61538461538461

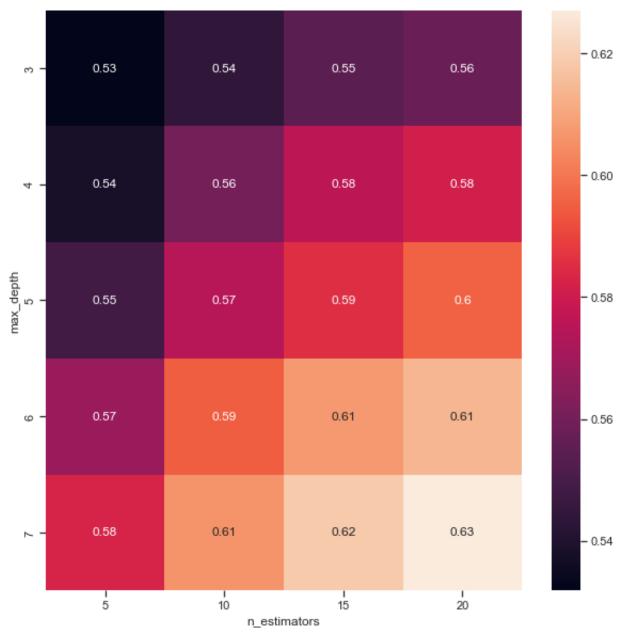
We can conclude from the heat map that max depth of 10 with 75 n-estimators provides the best accuracy of 58.76 %

# **Gradient Boosting**

Hyper parameter tuning is performed using 5-fold cross validation on each label to evaluate the best value for number of estimators

```
In [72]:
          # find best value for max depth & number of trees parameters using gridsearch
          X_train, X_test, y_train, y_test=train_test_split(X, y, test_size=0.2, random_state
          param grid = {'max depth': [3, 4, 5, 6, 7], 'n estimators' :[5, 10, 15, 20]}
          tree = GradientBoostingClassifier(random state=27)
          grid search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
          grid search.fit(X train, y train)
          print(grid search.best params )
          print("Best CV score is ",grid search.best score )
          plt.figure(figsize = (10,10))
          cv_score = grid_search.cv_results_['mean_test_score']
          data1 = pd.DataFrame(grid search.cv results ['params'])
          data1['cv score'] = cv score
          data pivoted = datal.pivot("max depth", "n_estimators", "cv_score")
          sns.heatmap(data pivoted, annot = True)
          plt.show()
```

{'max\_depth': 7, 'n\_estimators': 20}
Best CV score is 0.6270844747168135



```
In [73]:
    dtree = GradientBoostingClassifier(random_state=27, max_depth = 7, n_estimator
    dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

Test Accuracy is 58.07692307692308

Best value for number of estimators=20 with accuracy= 55 %

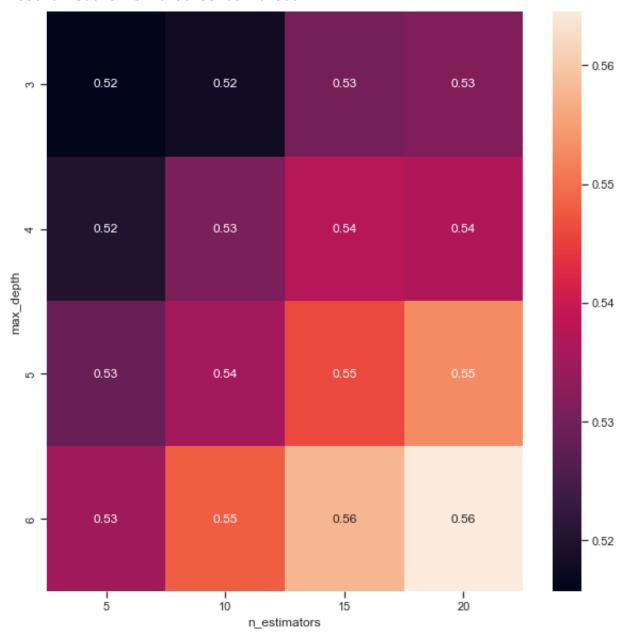
# **Gradient Tree Boosting | PCA Wine Dataset**

```
In [74]:
```

```
# find best value for max depth & number of trees parameters using gridsearch
X_train,X_test,y_train,y_test=train_test_split(X_pca,y,test_size=0.2,random_s
param_grid = {'max_depth': [3, 4, 5, 6],'n_estimators': [5, 10, 15, 20]}
tree = GradientBoostingClassifier(random_state=27)
grid_search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
grid_search.fit(X_train, y_train)
print(grid_search.best_params_)
print("Best CV score is ",grid_search.best_score_)

plt.figure(figsize = (10,10))
cv_score = grid_search.cv_results_['mean_test_score']
datal = pd.DataFrame(grid_search.cv_results_['params'])
datal['cv_score'] = cv_score
data_pivoted = datal.pivot("max_depth", "n_estimators", "cv_score")
sns.heatmap(data_pivoted, annot = True)
plt.show()
```

{'max\_depth': 6, 'n\_estimators': 20}
Best CV score is 0.5645520841045384



```
In [75]:
    dtree = GradientBoostingClassifier(random_state=27, max_depth = 6, n_estimator
    dtree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

Test Accuracy is 53.15384615384615

Best value for number of estimators=20 with accuracy= 55.15 %

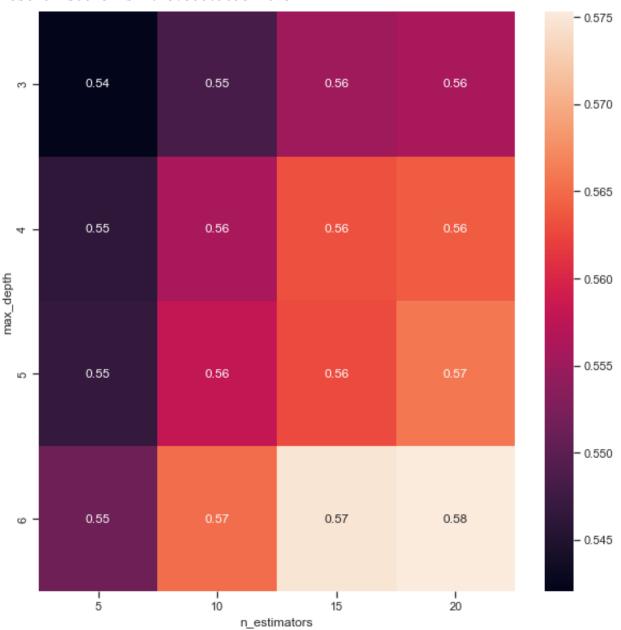
## **Gradient Tree Boosting | LDA Wine Dataset**

In [76]:

```
# find best value for max depth & number of trees parameters using gridsearch
X_train,X_test,y_train,y_test=train_test_split(X_lda,y,test_size=0.2,random_s
param_grid = {'max_depth': [3, 4, 5, 6],'n_estimators': [5, 10, 15, 20]}
tree = GradientBoostingClassifier(random_state=27)
grid_search = GridSearchCV(estimator=tree, param_grid=param_grid, cv=5)
grid_search.fit(X_train, y_train)
print(grid_search.best_params_)
print("Best CV score is ",grid_search.best_score_)

plt.figure(figsize = (10,10))
cv_score = grid_search.cv_results_['mean_test_score']
datal = pd.DataFrame(grid_search.cv_results_['params'])
datal['cv_score'] = cv_score
data_pivoted = datal.pivot("max_depth", "n_estimators", "cv_score")
sns.heatmap(data_pivoted, annot = True)
plt.show()
```

{'max\_depth': 6, 'n\_estimators': 20}
Best CV score is 0.5753309395128452



```
dtree = GradientBoostingClassifier(random_state=27, max_depth = 6 , n_estimated tree.fit(X_train, y_train)
    ypred = dtree.predict(X_test)
    accuracy = metrics.accuracy_score(y_test, ypred)*100
    print("Test Accuracy is ", accuracy)
```

Test Accuracy is 57.230769230769226

Test Accuracy is 56.84615384615385 Best value for number of estimators=20 with accuracy= 56.84 %

#### **OBSERVATIONS: Gradient Tree Boosting**

- 1. Raw Wine data ---- No of estimators = 20 , Accuracy = 55.00%
- 2. PCA Wine data ---- No of estimators = 20, Accuracy = 55.15%
- 3. LDA Wine data ---- No of estimators = 20, Accuracy = 56.84%

#### **Abalone Dataset**

Classifier	Setting	Abalone-raw	Abalone-pca	Abalone-Ida
kNN	k = 35	26.91 %	25.35 %	28.5 %
Multinomial Naive Bayes	MultinomialNB	21.33 %	16.83 %	16.49 %
Complement Naive Bayes	ComplementNB	18.3 %	17.26 %	21.49 %
Decision Tree Classifier	Grid Search CV=5	26.80 %	25.20 %	25.83 %
Random Forest Classifier	Grid Search CV=5	27.63 %	26.43 %	26.91 %
Gradient Tree Boosting	Grid Search CV=5	25.71 %	25.47 %	28.11 %

#### Wine Dataset

Classifier	Setting	Wine-raw	Wine-pca	Wine-Ida
kNN	k = 29	69.23 %	56.00 %	54.8 %
Multinomial Naive Bayes	MultinomialNB	47.03 %	43.63 %	43.65 %
Complement Naive Bayes	ComplementNB	43.60 %	39.74 %	42.95 %
Decision Tree Classifier	Grid Search CV=5	55.68 %	53.85 %	55.41 %
Random Forest Classifier	Grid Search CV=5	64.38 %	58.46 %	58.76 %
Gradient Tree Boosting	Grid Search CV=5	55.00 %	55.15 %	56.84 %

#### **ABALONE DATASET:**

- 1. For the abalone dataset, the KNN classifier performs the best with 26.91% accuracy in the raw-dataset and 25.35% and 28.5% for PCA and LDA respectively.
- 2. With the aid of dimensionality reduction, accuracy results portrays evident increase in the PCA and LDA datasets when the complement Naive bayes is applied when compared with raw dataset
- 3. The same scenario occurs in the case of gradient tree boosting wherein the accuracy increases.

#### **WINE DATASET**

- 1. For the wine dataset, the the KNN classifier performs the best with 69.23% accuracy in the raw-dataset and 56% and 54.8% for PCA and LDA respectively.
- 2. With the aid of dimensionality reduction, accuracy results portrays decrease in the PCA and LDA datasets when the KNN or Random Forest Classifier is applied when compared with raw dataset.

## References

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