Group Assignment, M1.

Group Members:

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Subject: Mushroom classification through machine learning techniques

```
#Import necessary libraries
import pandas as pd
import numpy as np
from matplotlib import pyplot as plt
import seaborn as sns
```

```
#For our dataset, we define the headers, because they have an un-logic header
#when loading in the .csv file from url. (like 'x' as 'cap-shape').
column_names = ['class',
                'cap-shape',
                'cap-surface',
                'cap-color',
                'bruises?',
                'odor',
                'gill-attachment',
                'gill-spacing',
                'gill-size',
                'gill-color',
                'stalk-shape',
                'stalk-root',
                'stalk-surface-above-ring',
                'stalk-surface-below-ring',
                'stalk-color-above-ring',
                'stalk-color-below-ring',
                'veil-type',
                'veil-color',
                'ring-number',
                'ring-type',
                'spore-print-color',
                'population',
                'habitat']

#Read in .CSV file and display the first five columns.
url = 'https://archive.ics.uci.edu/ml/machine-learning-databases/mushroom/agaricus-lepiota.d
data = pd.read_csv(url, names=column_names)
data.head()
```

	class	cap-shape	cap-surface	cap-color	bruises?	odor	gill-attachment	gill-spacing	gill-size	gill-color
0	p	x	s	n	t	p	f	c	n	k
1	e	x	s	y	t	a	f	c	b	k
2	e	b	s	w	t	l	f	c	b	n
3	p	x	y	w	t	p	f	c	n	n
4	e	x	s	g	f	n	f	w	b	k

PREPROCESSING

```
#Check the info of the dataset, to see if there are missing values etc.
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8124 entries, 0 to 8123
Data columns (total 23 columns):
class                       8124 non-null object
cap-shape                   8124 non-null object
cap-surface                 8124 non-null object
cap-color                   8124 non-null object
bruises?                    8124 non-null object
odor                        8124 non-null object
gill-attachment             8124 non-null object
gill-spacing                8124 non-null object
gill-size                   8124 non-null object
gill-color                  8124 non-null object
stalk-shape                 8124 non-null object
stalk-root                  8124 non-null object
stalk-surface-above-ring    8124 non-null object
stalk-surface-below-ring    8124 non-null object
stalk-color-above-ring      8124 non-null object
stalk-color-below-ring      8124 non-null object
veil-type                   8124 non-null object
veil-color                  8124 non-null object
ring-number                 8124 non-null object
ring-type                   8124 non-null object
spore-print-color           8124 non-null object
population                  8124 non-null object
habitat                     8124 non-null object
dtypes: object(23)
memory usage: 1.4+ MB
```

```
#Check if dataset contains null-values
data.isnull().sum()
```

```
class                       0
cap-shape                   0
cap-surface                 0
cap-color                   0
bruises?                    0
odor                        0
gill-attachment             0
gill-spacing                0
gill-size                   0
gill-color                  0
stalk-shape                 0
stalk-root                  0
stalk-surface-above-ring    0
stalk-surface-below-ring    0
stalk-color-above-ring      0
stalk-color-below-ring      0
veil-type                   0
veil-color                  0
ring-number                 0
ring-type                   0
spore-print-color           0
population                  0
habitat                     0
dtype: int64
```

```
#The column 'class' consists of a label of either 'p' for poisonous, or 'e'
#for edible.
data['class'].unique()
```

```
array(['p', 'e'], dtype=object)
```

```
#Data.shape tells us the shape of the dataframe. In this dataframe we got 8124
#observations, and 23 features.
data.shape
```

```
(8124, 23)
```

```
#All the data in the dataframe, contains string values. For easier to be able to
#calculate using the data-observations, we convert them to integer values.
#We do this with LabelEncoder function.
from sklearn.preprocessing import LabelEncoder

labelencoder = LabelEncoder()

#we fit_transform each column to labelencoder.
for col in data.columns:
  data[col] = labelencoder.fit_transform(data[col])

#print the dataset, to see if the data has been encoded.
data.head()
```

	class	cap-shape	cap-surface	cap-color	bruises?	odor	gill-attachment	gill-spacing	gill-size	gill-color
0	1	5	2	4	1	6	1	0	1	4
1	0	5	2	9	1	0	1	0	0	4
2	0	0	2	8	1	3	1	0	0	5
3	1	5	3	8	1	6	1	0	1	5
4	0	5	2	3	0	5	1	1	0	4

```
#Convert the 'class' column from integer values to a boolean representation of
#whether the mushroom is poisonous or not.
data['class'] = data['class'].astype('bool')

#Print the dataset, to see if 'class' column holds a boolean value for
#poisonous or edible mushrooms.
data.head()
```

	class	cap-shape	cap-surface	cap-color	bruises?	odor	gill-attachment	gill-spacing	gill-size	gill-color
0	True	5	2	4	1	6	1	0	1	4
1	False	5	2	9	1	0	1	0	0	4
2	False	0	2	8	1	3	1	0	0	5
3	True	5	3	8	1	6	1	0	1	5
4	False	5	2	3	0	5	1	1	0	4

```
#Run data.describe() to get a glimpse of the data.
data.describe()
```

	cap-shape	cap-surface	cap-color	bruises?	odor	gill-attachment	sp
count	8124.000000	8124.000000	8124.000000	8124.000000	8124.000000	8124.000000	8124.0
mean	3.348104	1.827671	4.504677	0.415559	4.144756	0.974151	0.1
std	1.604329	1.229873	2.545821	0.492848	2.103729	0.158695	0.3
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.0
25%	2.000000	0.000000	3.000000	0.000000	2.000000	1.000000	0.0
50%	3.000000	2.000000	4.000000	0.000000	5.000000	1.000000	0.0
75%	5.000000	3.000000	8.000000	1.000000	5.000000	1.000000	0.0
max	5.000000	3.000000	9.000000	1.000000	8.000000	1.000000	1.0

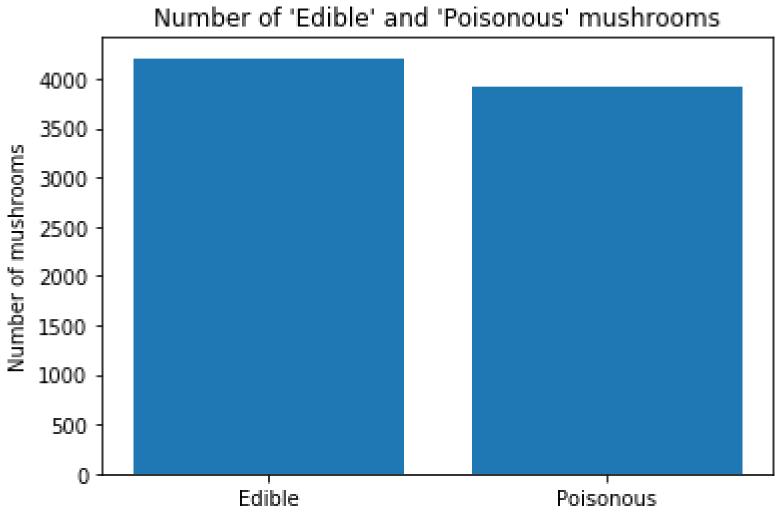
```
#This shows us, that the column 'veil-type' is always 0. Therefore we can
#drop this column, since it holds no values. We use inplace=True to
#impact and make the changes to the original dataset.
data.drop('veil-type', axis=1, inplace=True)

#Print the dataset, to see if 'veil-type' column is removed.
data.head()
```

	class	cap-shape	cap-surface	cap-color	bruises?	odor	gill-attachment	gill-spacing	gill-size	gill-color
0	True	5	2	4	1	6	1	0	1	4
1	False	5	2	9	1	0	1	0	0	4
2	False	0	2	8	1	3	1	0	0	5
3	True	5	3	8	1	6	1	0	1	5
4	False	5	2	3	0	5	1	1	0	4

```
#We want to store the poisonous and edible mushroom observations in the two
#variables 'poisonous' and 'edible' and print the length of each, to see how
#many poisonous and edible mushrooms are in the dataset.
poisonous = data[data['class'] == True]
edible = data[data['class'] == False]
print(len(poisonous))
print(len(edible))

#This shows us there are 3916 poisonous and 4208 edible mushrooms in the dataset.
```

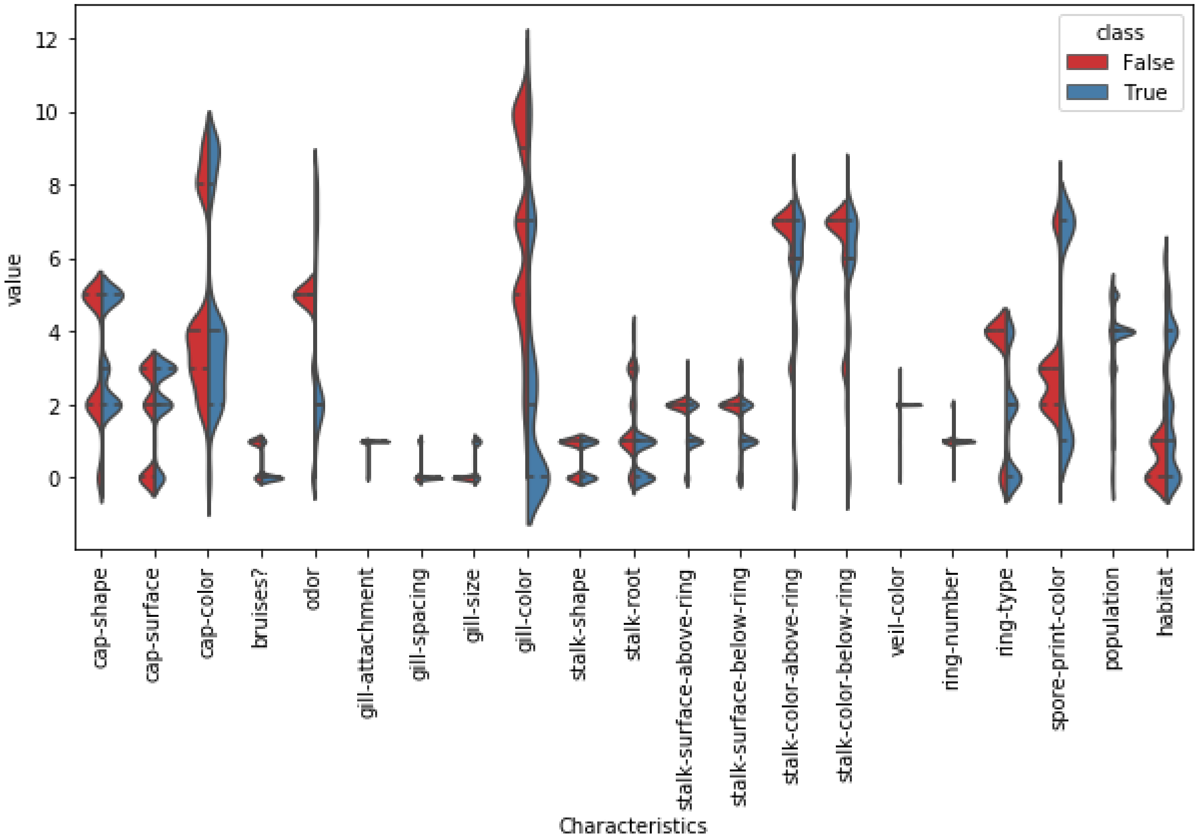
```
3916
4208
```

```
#We define the two mushroom types
types = ('Edible', 'Poisonous')

#Position 'Edible' first, 'Poisonous' as second.
y_pos = np.arange(len(types))

#Define 'numbers' as the number of 'edible' and 'poisonous' mushrooms.
numbers = [len(edible), len(poisonous)]

#Plot as barchart using matplotlib, with types and numbers of mushrooms.
plt.bar(y_pos, numbers)

#Set x ticks as 'Edible' and 'Poisonous'
plt.xticks(y_pos, types)

#Set y-label and title of visualization.
plt.ylabel("Number of mushrooms")
plt.title("Number of 'Edible' and 'Poisonous' mushrooms")

#Show barchart.
plt.show()
```



```
#For further investigation we create a violin-plot, to see if there are any
#correlation between edible and poisonous characteristics in the
#mushroom dataset.

#We create 'data_div' which melts the dataset, 'class' column and var_name
#as 'Characteristics'.
data_div = pd.melt(data, "class", var_name="Characteristics")

#'fig' and 'ax' is created as subplot with figsize(10,5).
fig, ax = plt.subplots(figsize=(10,5))

#Now we create 'p' as Seaborn violinplot, which contains ax, 'Characteristics'
#as x (all columns), 'value' as y and hued by 'class' (edible or poisonous).
p = sns.violinplot(ax = ax, x="Characteristics", y="value", hue="class",
                   split = True, data=data_div, inner = 'quartile',
                   palette = 'Set1')

#The dataset should not contain 'class' as characteristics in the violin-plot.
#Therefore we drop the column 'class' and store it as 'data_no_class'.
data_no_class = data.drop(["class"],axis = 1)
```

```
#Set labels as 90 degree rotation (for better view), and as list without 'class'
p.set_xticklabels(rotation = 90, labels = list(data_no_class.columns));

#As a result, we can see in the violin plot, that there is some correlation
#between characteristics for edible and poisonous mushrooms in e.g. 'gill-color'

#This characteristic show us, that mushrooms with gill-color 0 to ~4 tend to be
#more poisonous than mushrooms with gill-color above 4. (the numbers are a
#representation of a color in the original dataset).
```



Double-click (or enter) to edit

The violinplot suggest that there might be a correlation between gill-color and if a mushroom is poisonous or edible.

```
#To see which gill-color most poisonous mushrooms have, we print out the gill-
#color column from the poisonous data, and sort by 'value_counts()' to sort in
#descending order.
poisonous['gill-color'].value_counts()

#This shows us that 1728 of the poisonous mushrooms have gill-color 0 and so on
```

```
#To see which gill-color most edible mushrooms have, we print out the gill-
#color column from the edible data, and sort by 'value_counts()' to sort in
#descending order.
edible['gill-color'].value_counts()

#This show us that gill-color 10 is the color of most
#edible mushrooms.
```

UNSUPERVISED MACHINE LEARNING

```
#To be able to perform unsupervised machine learning on our dataset,
#we scale our data using StandardScaler. This function scales our data so the data
#is represented within the same scale. This removes the mean and scales the
#relation within the dataset. StandardScaler divides the values with the
#standard diviation in order to perform better calculations on the dataset.

#Import StandardScaler from SciKit Learn
from sklearn.preprocessing import StandardScaler

#Define variable 'scaler' as StandardScaler function.
scaler = StandardScaler()

#Define variable 'X_scaled' as scaler.fit_transform on dataset 'data'.
X_scaled = scaler.fit_transform(data)

#print(X_scaled)
print(X_scaled)
```

```
#We perform a Principal Component Analysis (PCA), which is a statistical
#procedure to convert a set of observations of possibly correlated variables
#into a set of values of linearly uncorrelated variables called Principal
#Components. We import this function from sklearn.decomposition.
from sklearn.decomposition import PCA

#Set 'pca' as 'PCA()'
pca = PCA()

#Now we fit_transform our 'X_scaled' data to pca.
X_scaled = pca.fit_transform(X_scaled)
```

```
#We print out the explained variance ratio, that shows us how much each
#pca explains of the variance.
explained_variance=pca.explained_variance_ratio_

explained_variance

#This show us that the first pca explains 19% of the variance in the dataset and so on.
```

```
#Below we plot the individual explained variance from the pca analysis.
plt.figure(figsize=(8, 8))

#we plot the explained variance as a barchart and set x and y labels.
plt.bar(range(22), explained_variance,
        label='individual explained variance')
plt.ylabel('Explained variance ratio')
plt.xlabel('Principal components')
plt.legend(loc='best')

#From the  graph below we can see, that the first 15 pca's explain much
#variance in the dataset. The last 6 pca's doesn't contribute very much
#to the overall explanation so we will sort them out.
```

```
#We create a new PCA, with pre-defined number of components as 15.
pca = PCA(n_components=15)

#We fit_transform the 'X_scaled' data to pca
X_scaled = pca.fit_transform(X_scaled)

#We print out the sum of the explained variance ratio, to see how much of the
#variance is explained in the pca analysis.
pca.explained_variance_ratio_.sum()

#This shows us, that with a PCA analysis with 15 components, we are able to
#explain 94,68% of the variance in the dataset.
```

```
#To perform a cluster analysis we import KMeans from sklearn.cluster.
from sklearn.cluster import KMeans

#We create a 'inertia'-variable as an empty array.
inertia = []

#In the below for-loop we create a KMeans with 'i'-numbers of cluster (from 1
#to 10, since the set a range equal to 10 units). At the end of each loop, we
#append the fitted KMeans of 'X_scaled' function to the 'inertia' array.
for i in range(1,11):
  k_means = KMeans(n_clusters=i)
  inertia.append(k_means.fit(X_scaled).inertia_)

#We create a Seaborn lineplot, where y is the 'inertia' array, and x as
#range of 10
sns.lineplot(y = inertia, x = range(1,11))

#From this lineplot, we can spot a tiny elbow point at the second range.
```

```
#From the first elbow point of the two clusters we create a new KMeans with two
#clusters and random state as 42. We create two clusters in order to see if the
#algorithm can separate poisonous and edible mushrooms.
k_means = KMeans(n_clusters=2, random_state=42)
k_means.fit(X_scaled)

plt.figure(figsize=(8,8))

#We create a scatterplot with two clusters.
g = sns.scatterplot(X_scaled[:,0], X_scaled[:,1], hue = k_means.labels_, legend='full',
                    palette='viridis')

#Below scatterplot shows the two clusters.
```

```
#We create a new column in the dataset, called 'cluster', which represents which
#cluster each mushroom in represented in. This will in our further analysis
#give us an indication of whether the clusters is separated in
#poisonous or edible mushrooms.
data['cluster'] = k_means.labels_
data.head()
```

```
#we print out a count of edible and
#poisonous mushrooms in each cluster using itertools.
import itertools
from collections import Counter

cluster0 = Counter(list(itertools.chain(data[data.cluster == 0]['class'])))
cluster1 = Counter(list(itertools.chain(data[data.cluster == 1]['class'])))
```

```
#Using 'most_common()' method, we print out the number of edible and poisonous
#mushrooms in cluster 0.
cluster0.most_common()

#This show us that all edible mushrooms and ~half of the poisonous mushrooms
#are represented in this cluster.
```

```
#Using 'most_common()' method, we print out the number of edible and poisonous
#mushrooms in cluster 1.
cluster1.most_common()

#This shows us that 1756 of the poisonous mushrooms are represented in this
#cluster, and there are no edible mushrooms in this cluster. This must be a sign
#of characteristics that is unique for poisonous mushrooms, but the algorithm
#was not able to separete the poisonous from the edible mushrooms
```

SUPERVISED MACHINE LEARNING

Train- / Testset preparation

```
#We define variable 'x' as all rows in the dataset and all columns beside the
#'class' and 'cluster' columns.
x = data.loc[:, (data.columns != 'class') & (data.columns != 'cluster')]

#We define 'y' as all rows in the dataset and the column 'class'. This is our
#target variable.
y = data.loc[:,'class']
```

```
#Import train_test_split from sklearn.model_selection.
from sklearn.model_selection import train_test_split
#Define variables 'X_train', 'X_test', 'y_train', 'y_test' as train_test_split
#function of 'X_scaled, 'y_enc, with test size of 25% and random state as 42
X_train, X_test, y_train, y_test = train_test_split(x, y,
test_size=0.25,
random_state=42)
```

```
#We import cross_val_score, classification_report and LogisticRegression
#from sklearn.
from sklearn.model_selection import cross_val_score
from sklearn.metrics import classification_report
from sklearn.linear_model import LogisticRegression

#We define 'model' as LogisticRegression()
model = LogisticRegression()

#Fit the training data to the logistic regression model.
model.fit(X_train, y_train)

#We create 'y_pred' as a prediction of 'X_test' on the logisticregression model
y_pred = model.predict(X_test)

#We print out a classification_report of test data and 'y_pred', to see the
#precision of our datamodel.
print(classification_report(y_test, y_pred))

#we import confusion_matrix from mlxtend and sklearn, to be able to create a
#confusion matrix.
from mlxtend.plotting import plot_confusion_matrix
from sklearn.metrics import confusion_matrix

#Define variable confmatrix as a confusion matrix of 'y_test' and 'y_pred'
confmatrix = confusion_matrix(y_test,y_pred)

#Plot the confmatrix variable.
plot_confusion_matrix(conf_mat=confmatrix,
                                colorbar=True,
                                show_absolute=True,
                                show_normed=True)

#The classification report shows, that the accuracy/precision of the Logistic
#Regression model is 95%, and it classifies 1040 mushrooms as edible and
#991 mushrooms as poisonous.

#In the confusion matrix we can evaluate, that the algorithm predicted 1037
#mushrooms as edible, where 49 were poisonous. Further the algorithm predicted 994
#mushrooms as poisonous, whereas 52 were edible.
```

```
#We define 'scores' as cross_val_score function on KNearestNeighbor on
#training dataset. We set cross-validation number as 5. This means, that the
#training dataset is divided into (in this case) 5 sets, and runs 5 times, where
#in each run, a new set will be used as test-set.
scores = cross_val_score(model, X_train, y_train, cv=5)
```

```
#Print the mean of the k-fold cross-validation (scores)
print(np.mean(scores))

#This shows us the score (accuracy) on our training dataset as 94,96%.
```

```
#We import KNearestNeighbor from sklearn as second algorithm.
#This model predicts the value of the testrow based on its nearest neighbors
#value.
from sklearn.neighbors import KNeighborsClassifier

#We create 'classifies' as KNeighborsClassifier, with number of neighbors as 5.
classifier = KNeighborsClassifier(n_neighbors=5)

#Fit the training set to the KNearestNeighbor model.
classifier.fit(X_train, y_train)

#We create 'y_pred' as a prediction of 'X_test' on the KNearestNeighbor model
y_pred = classifier.predict(X_test)

#We print out a classification_report of test data and 'y_pred', to see the
#precision of our datamodel.
print(classification_report(y_test, y_pred))

#Define variable confmatrix as a confusion matrix of 'y_test' and 'y_pred'
confmatrix = confusion_matrix(y_test,y_pred)

#Plot the confmatrix variable.
plot_confusion_matrix(conf_mat=confmatrix,
                                colorbar=True,
                                show_absolute=True,
                                show_normed=True)

#The classification report shows, that the accuracy/precision of the
#KNearestNeighbor model is 100%/99%, and it classifies 1040 mushrooms as edible
#and 991 mushrooms as poisonous.

#In the confusion matrix, we can evaluate, that the second algorithm predicted
#1034 mushrooms as edible, where 1 were poisonous. Further 997
#mushrooms was predicted as poisonous and 7 as edible.
```

```
#We define 'scores' as cross_val_score function on KNearestNeighbor on the
#training dataset. We set cross-validation to 5. This means, that the
#training dataset is divided into (in this case) 5 sets, and runs 5 times, where
#in each run, a new set will be used as test-set.
scores = cross_val_score(classifier, X_train, y_train, cv=5)

#Print the mean of the k-fold cross-validation (scores)
print(np.mean(scores))

#This shows us the score (accuracy) on our training dataset is 99,81%.
```

```
#cross-validation workflow, model fitting, prediction and evaluation
#for Decision Tree Classifier

#Import DecisionTreeClassifier from sklearn.tree
from sklearn.tree import DecisionTreeClassifier

#Define variable 'model' as DecisionTreeClassifier()
```

```
tree = DecisionTreeClassifier()

#Fit the 'X' and 'y' values to the tree variable.
tree.fit(X_train, y_train)

#We create 'y_pred' as a prediction of 'X_test' on the DecisionTree model
y_pred = tree.predict(X_test)

#We print out a classification_report of test data and 'y_pred', to see the
#precision of our datamodel.
print(classification_report(y_test, y_pred))

#Define variable confmatrix as a confusion matrix of 'y_test' and 'y_pred'
confmatrix = confusion_matrix(y_test,y_pred)

#Plot the confmatrix variable.
plot_confusion_matrix(conf_mat=confmatrix,
                                colorbar=True,
                                show_absolute=True,
                                show_normed=True)

#The classification report shows, that the accuracy/precision of the
#DecisionTree model is 100%, and it classifies 1040 mushrooms as edible
#and 991 mushrooms as poisonous.

#In the confusion matrix, we can evaluate that the algorithm predicted 1040
#mushrooms as edible and 0 were poisonous. Further the algortihm predicted 991
#mushrooms as poisonous and 0 as edible.
```

```
#We define 'scores' as cross_val_score function on KNearestNeighbor on the
#training dataset. We set cross-validation to 5. This means that the
#training dataset is divided into (in this case) 5 sets, and runs 5 times, where
#in each run, a new set will be used as test-set.
scores = cross_val_score(tree, X_train, y_train, cv=5)
```

```
#Print the mean of the k-fold cross-validation (scores)
print(np.mean(scores))

#This shows us the score (accuracy) on our training dataset is 100%.
```