Data Science and Generative AI

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Machine Learning

Machine Learning - Scale

Scale Features

When your data has different values, and even different measurement units, it can be difficult to compare them. What is kilograms compared to meters? Or altitude compared to time?

The answer to this problem is scaling. We can scale data into new values that are easier to compare.

Take a look at the table below, it is the same data set that we used in the multiple regression chapter, but this time the **volume** column contains values in*liters* instead of cm^3 (1.0 instead of 1000).

Car Model		Volume	Weight	CO2
Toyota	Aygo	1.0	790	99
Mitsubishi	Space Star	1.2	1160	95
Skoda	Citigo	1.0	929	95
Fiat	500	0.9	865	90
Mini	Cooper	1.5	1140	105
VW	Up!	1.0	929	105
Skoda	Fabia	1.4	1109	90
Mercedes	A-Class	1.5	1365	92
Ford	Fiesta	1.5	1112	98
Audi	A1	1.6	1150	99
Hyundai	I20	1.1	980	99
Suzuki	Swift	1.3	990	101
Ford	Fiesta	1.0	1112	99

Honda	Civic	1.6 1252 94
Hundai	I30	1.6 1326 97
Opel	Astra	1.6 1330 97
BMW	1	1.6 1365 99
Mazda	3	2.2 1280 104
Skoda	Rapid	1.6 1119 104
Ford	Focus	2.0 1328 105
Ford	Mondeo	1.6 1584 94
Opel	Insignia	2.0 1428 99
Mercedes	C-Class	2.1 1365 99
Skoda	Octavia	1.6 1415 99
Volvo	S60	2.0 1415 99
Mercedes	CLA	1.5 1465 102
Audi	A4	2.0 1490 104
Audi	A6	2.0 1725 114
Volvo	V70	1.6 1523 109
BMW	5	2.0 1705 114
Mercedes	E-Class	2.1 1605 115
Volvo	XC70	2.0 1746 117
Ford	B-Max	1.6 1235 104
BMW	2	1.6 1390 108
Opel	Zafira	1.6 1405 109

Mercedes SLK 2.5 1395 120

It can be difficult to compare the volume 1.0 with the weight 790, but if we scale them both into comparable values, we can easily see how much one value is compared to the other.

There are different methods for scaling data, in this we will use a method called standardization.

The standardization method uses this formula:

z = (x - u) / s

Where z is the new value, x is the original value, u is the mean and s is the standard deviation.

If you take the **weight** column from the data set above, the first value is 790, and the scaled value will be:

(790 - 1292.23) / 238.74 = -2.1

If you take the **volume** column from the data set above, the first value is 1.0, and the scaled value will be:

(1.0 - 1.61) / 0.38 = -1.59

Now you can compare -2.1 with -1.59 instead of comparing 790 with 1.0.

You do not have to do this manually, the Python sklearn module has a method called StandardScaler() which returns a Scaler object with methods for transforming data sets.

Example

Scale all values in the Weight and Volume columns:

```
import pandas
from sklearn import linear_model
from sklearn.preprocessing import StandardScaler
scale = StandardScaler()

df = pandas.read_csv("data.csv")

X = df[['Weight', 'Volume']]

scaledX = scale.fit_transform(X)
```

print(scaledX)

Result:

Note that the first two values are -2.1 and -1.59, which corresponds to our calculations:

[[-2.10389253 -1.59336644]

[-0.55407235 -1.07190106]

[-1.52166278 -1.59336644]

[-1.78973979 -1.85409913]

[-0.63784641 -0.28970299]

[-1.52166278 -1.59336644]

[-0.76769621 -0.55043568]

[0.3046118 -0.28970299]

[-0.7551301 -0.28970299]

[-0.59595938 -0.0289703]

[-1.30803892 -1.33263375]

[-1.26615189 -0.81116837]

[-0.7551301 -1.59336644]

[-0.16871166 -0.0289703]

[0.14125238 -0.0289703]

[0.15800719 -0.0289703]

[0.3046118 -0.0289703]

[-0.05142797 1.53542584]

[-0.72580918 -0.0289703]

[0.14962979 1.01396046]

[1.2219378 -0.0289703]

[0.5685001 1.01396046]

[0.3046118 1.27469315]

[0.51404696 -0.0289703]

[0.51404696 1.01396046]

[0.72348212 -0.28970299]

[0.8281997 1.01396046]

[1.81254495 1.01396046]

[0.96642691 -0.0289703]

[1.72877089 1.01396046]

[1.30990057 1.27469315]

[1.90050772 1.01396046]

[-0.23991961 -0.0289703]

[0.40932938 -0.0289703]

[0.47215993 -0.0289703]

[0.4302729 2.31762392]]

Machine Learning - Train/Test

Evaluate Your Model

In Machine Learning we create models to predict the outcome of certain event, the CO2 emission of a car when we knew the weight and engine size.

To measure if the model is good enough, we can use a method called Train/Test.

What is Train/Test

Train/Test is a method to measure the accuracy of your model.

It is called Train/Test because you split the data set into two sets: a training set and a testing set.

80% for training, and 20% for testing.

You *train* the model using the training set.

You *test* the model using the testing set.

Train the model means *create* the model.

Test the model means test the accuracy of the model.

Start With a Data Set

Start with a data set you want to test.

Our data set illustrates 100 customers in a shop, and their shopping habits.

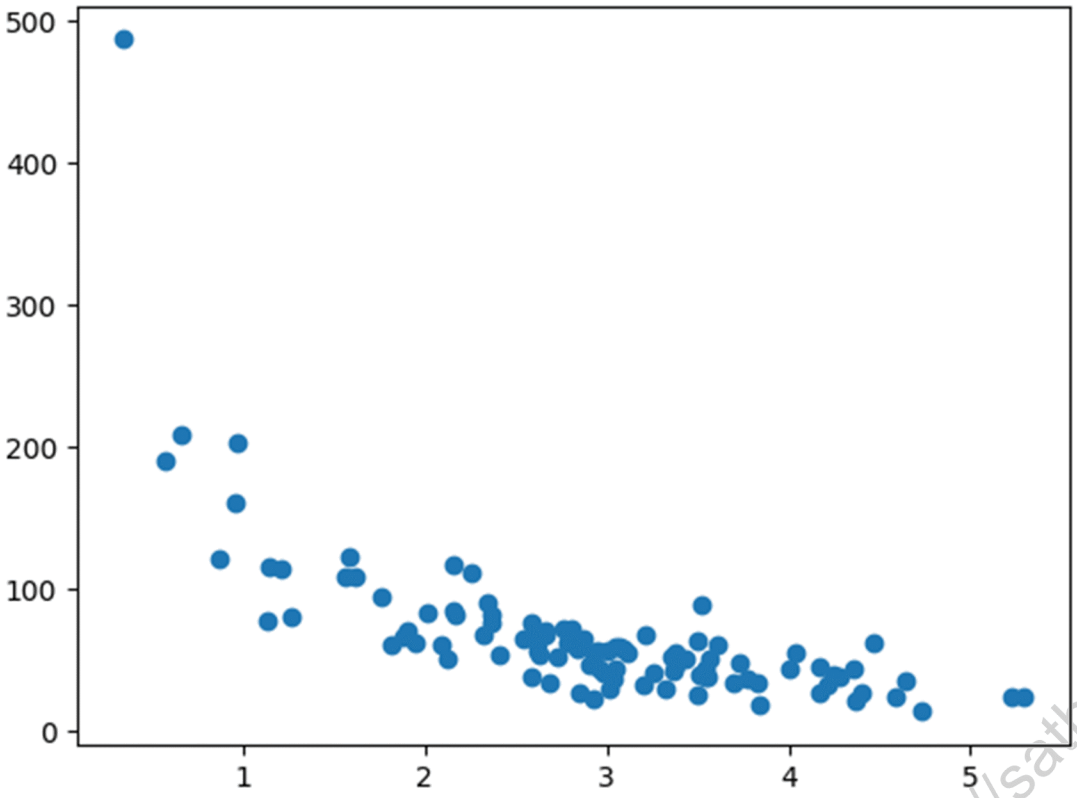
Example

```
import numpy
import matplotlib.pyplot as plt
numpy.random.seed(2)

x = numpy.random.normal(3, 1, 100)
y = numpy.random.normal(150, 40, 100) / x

plt.scatter(x, y)
plt.show()
```

Result:

The x axis represents the number of minutes before making a purchase.

The y axis represents the amount of money spent on the purchase.



Split Into Train/Test

The *training* set should be a random selection of 80% of the original data.

The *testing* set should be the remaining 20%.

```
train_x = x[:80]
train_y = y[:80]

test_x = x[80:]
test_y = y[80:]
```

Display the Training Set

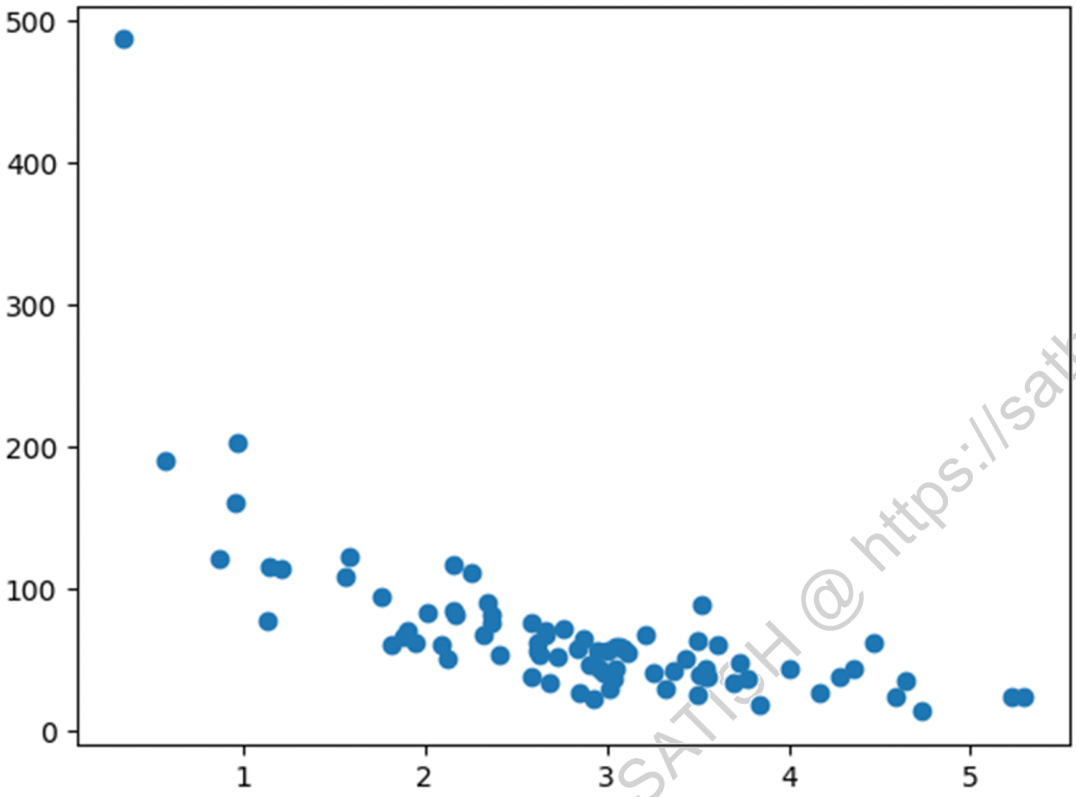
Display the same scatter plot with the training set:

Example

```
plt.scatter(train_x, train_y)
plt.show()
```

Result:

It looks like the original data set, so it seems to be a fair selection:



Display the Testing Set

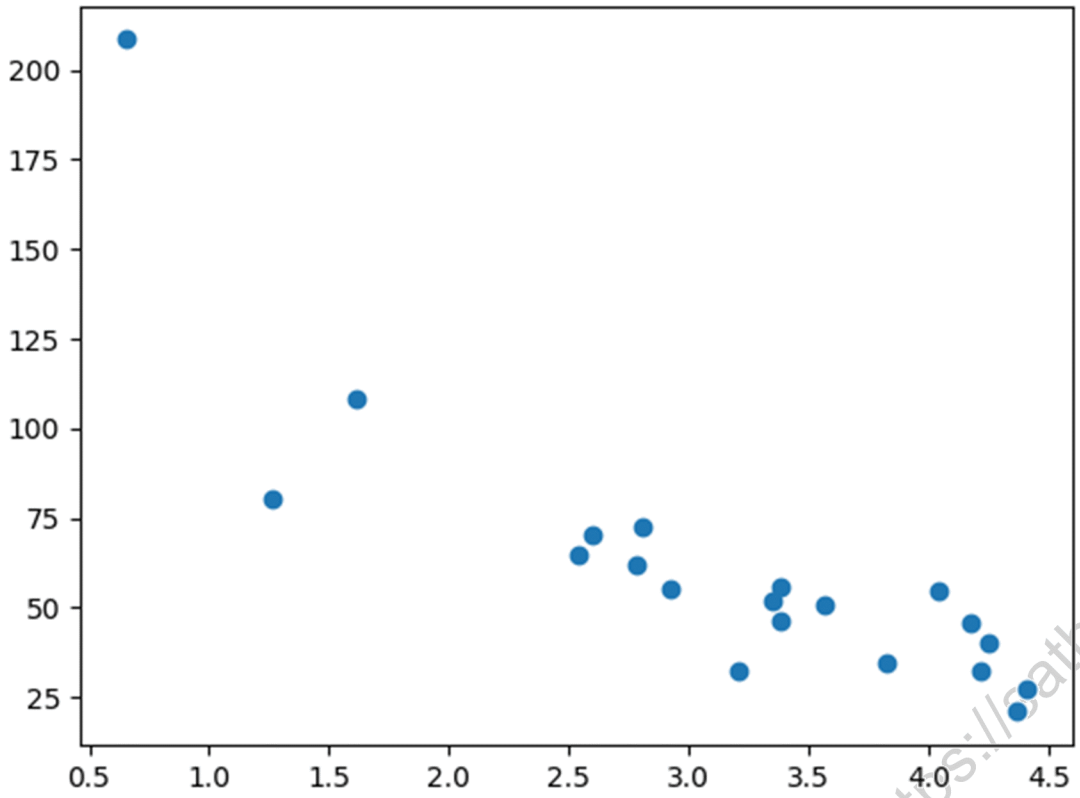
To make sure the testing set is not completely different, we will take a look at the testing set as well.

Example

```
plt.scatter(test_x, test_y)
plt.show()
```

Result:

The testing set also looks like the original data set:



Fit the Data Set

What does the data set look like? In my opinion I think the best fit would be a polynomial regression, so let us draw a line of polynomial regression.

To draw a line through the data points, we use the plot() method of the matplotlib module:

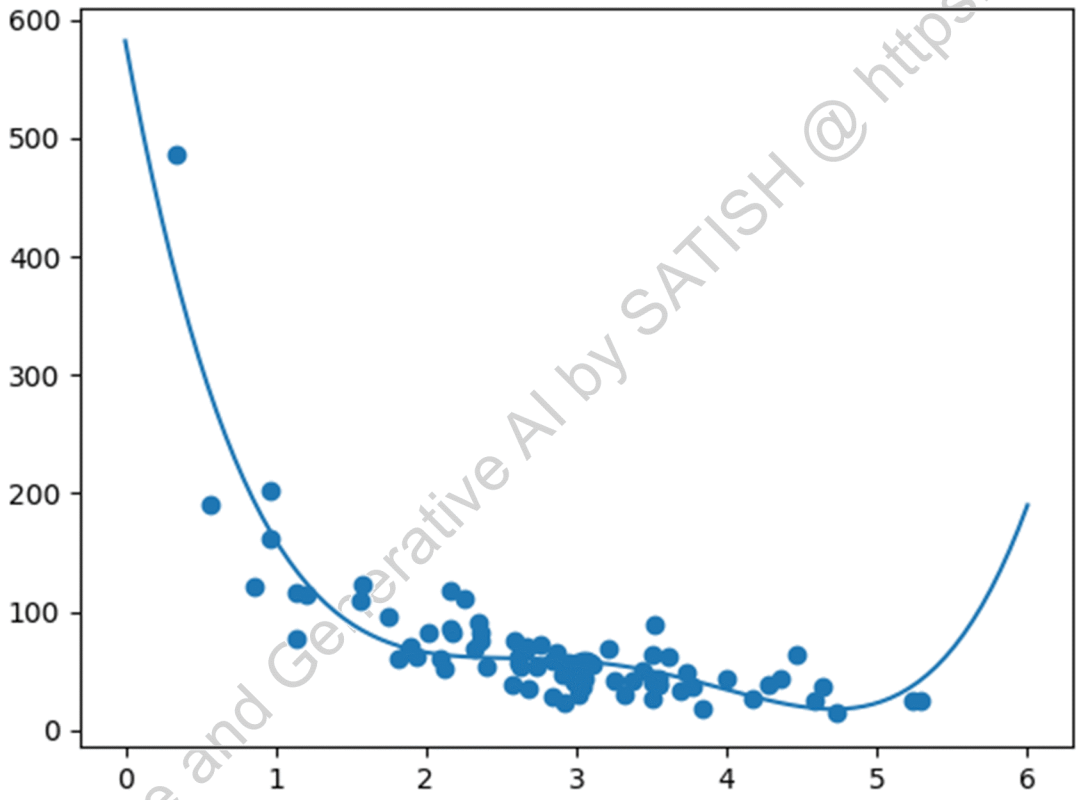
Example

Draw a polynomial regression line through the data points:

```
import numpy
import matplotlib.pyplot as plt
numpy.random.seed(2)

x = numpy.random.normal(3, 1, 100)
y = numpy.random.normal(150, 40, 100) / x
```

```
train_x = x[:80]
train_y = y[:80]

test_x = x[80:]
test_y = y[80:]

mymodel = numpy.poly1d(numpy.polyfit(train_x, train_y, 4))

myline = numpy.linspace(0, 6, 100)

plt.scatter(train_x, train_y)
plt.plot(myline, mymodel(myline))
plt.show()
```

Result:



The result can back my suggestion of the data set fitting a polynomial regression, even though it would give us some weird results if we try to predict values outside of the data

set. Example: the line indicates that a customer spending 6 minutes in the shop would make a purchase worth 200. That is probably a sign of overfitting.

But what about the R-squared score? The R-squared score is a good indicator of how well my data set is fitting the model.

R2

Remember R2, also known as R-squared?

It measures the relationship between the x axis and the y axis, and the value ranges from 0 to 1, where 0 means no relationship, and 1 means totally related.

The sklearn module has a method called r2_score() that will help us find this relationship.

In this case we would like to measure the relationship between the minutes a customer stays in the shop and how much money they spend.

Example

How well does my training data fit in a polynomial regression?

```
import numpy
from sklearn.metrics import r2_score
numpy.random.seed(2)

x = numpy.random.normal(3, 1, 100)
y = numpy.random.normal(150, 40, 100) / x

train_x = x[:80]
train_y = y[:80]

test_x = x[80:]
test_y = y[80:]

mymodel = numpy.poly1d(numpy.polyfit(train_x, train_y, 4))

r2 = r2_score(train_y, mymodel(train_x))

print(r2)
```

Note: The result 0.799 shows that there is a OK relationship.

Bring in the Testing Set

Now we have made a model that is OK, at least when it comes to training data.

Now we want to test the model with the testing data as well, to see if gives us the same result.

Example

Let us find the R2 score when using testing data:

```
import numpy
from sklearn.metrics import r2_score
numpy.random.seed(2)

x = numpy.random.normal(3, 1, 100)
y = numpy.random.normal(150, 40, 100) / x

train_x = x[:80]
train_y = y[:80]

test_x = x[80:]
test_y = y[80:]

mymodel = numpy.poly1d(numpy.polyfit(train_x, train_y, 4))

r2 = r2_score(test_y, mymodel(test_x))

print(r2)
```

Note: The result 0.809 shows that the model fits the testing set as well, and we are confident that we can use the model to predict future values.

Predict Values

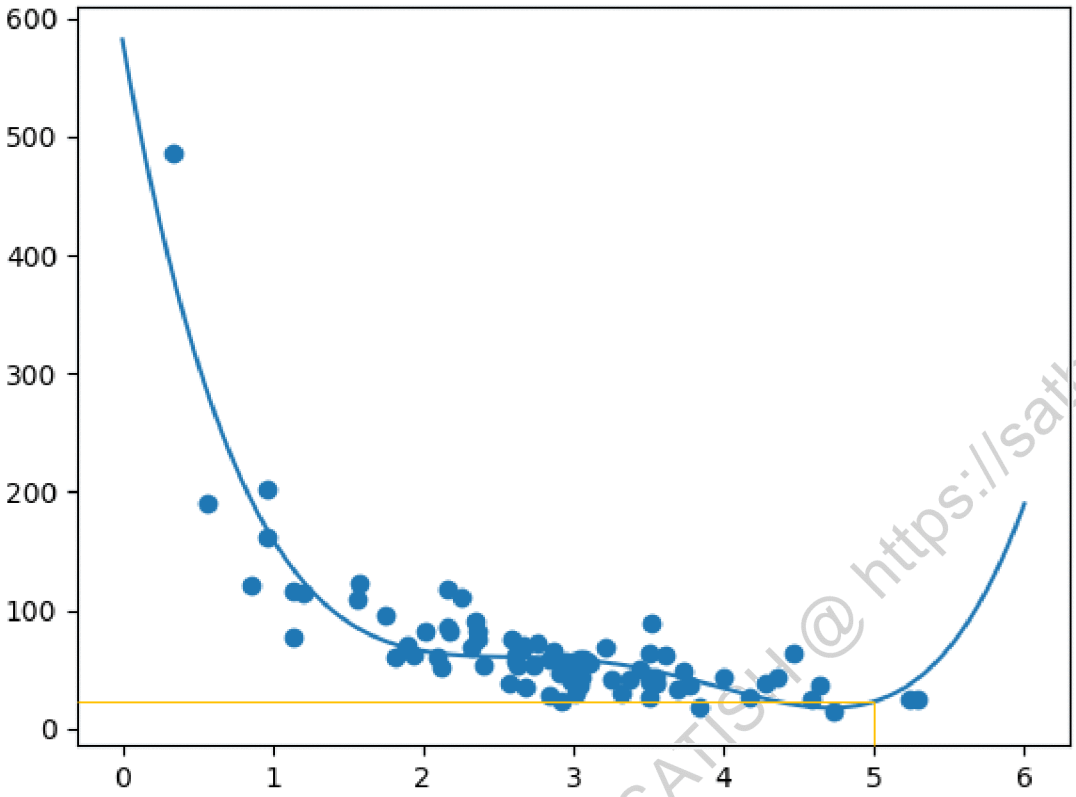
Now that we have established that our model is OK, we can start predicting new values.

Example

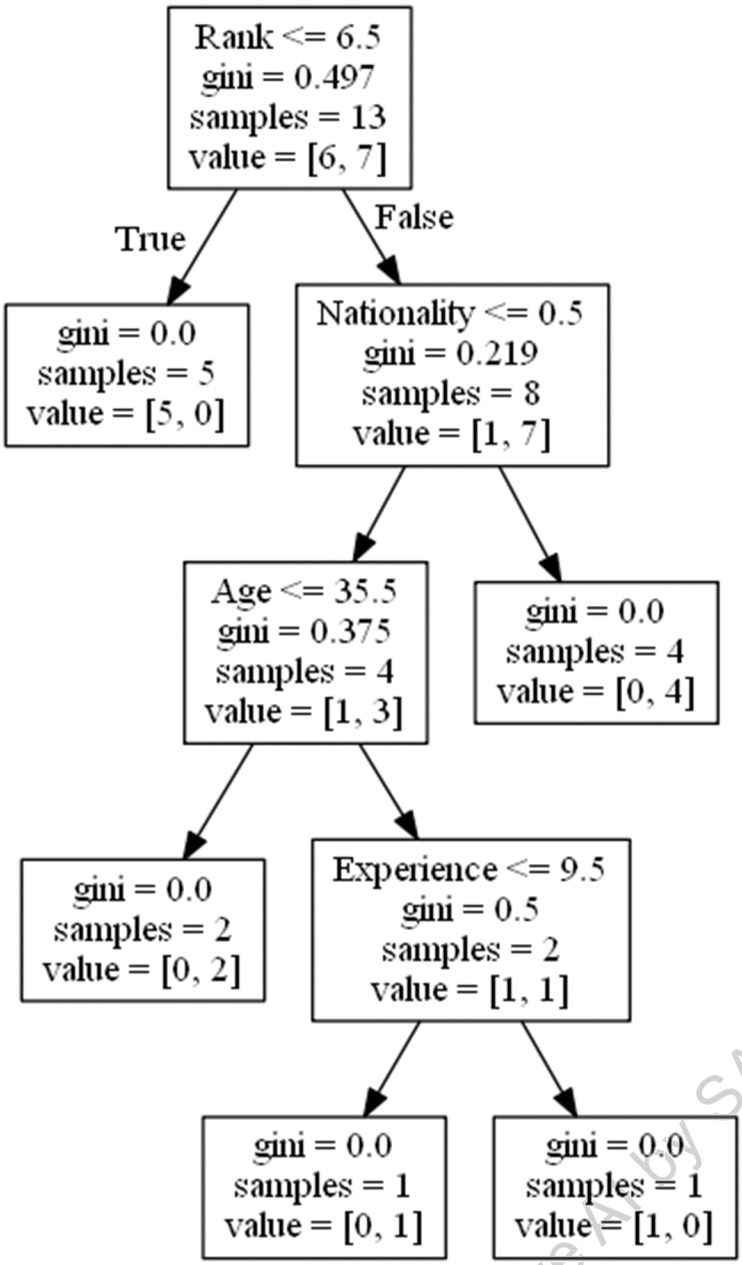
How much money will a buying customer spend, if she or he stays in the shop for 5 minutes?

print(mymodel(5))

The example predicted the customer to spend 22.88 dollars, as seems to correspond to the diagram:



Machine Learning - Decision Tree



Decision Tree

A Decision Tree is a Flow Chart, and can help you make decisions based on previous experience.

Example:

a person will try to decide if he/she should go to a comedy show or not.

Luckily our example person has registered every time there was a comedy show in town, and registered some information about the comedian, and also registered if he/she went or not.

Age	Experience	Rank	Nationality	Go
36	10	9	UK	NO
42	12	4	USA	NO
23	4	6	N	NO
52	4	4	USA	NO
43	21	8	USA	YES
44	14	5	UK	NO
66	3	7	N	YES
35	14	9	UK	YES
52	13	7	N	YES
35	5	9	N	YES
24	3	5	USA	NO
18	3	7	UK	YES
45	9	9	UK	YES

Now, based on this data set, Python can create a decision tree that can be used to decide if any new shows are worth attending to.

How Does it Work?

First, read the dataset with pandas:

Example

Read and print the data set:

```
import pandas

df = pandas.read_csv("data.csv")

print(df)
```

To make a decision tree, all data has to be numerical.

We have to convert the non numerical columns 'Nationality' and 'Go' into numerical values.

Pandas has a map() method that takes a dictionary with information on how to convert the values.

{'UK': 0, 'USA': 1, 'N': 2}

Means convert the values 'UK' to 0, 'USA' to 1, and 'N' to 2.

Example

Change string values into numerical values:

```
d = {'UK': 0, 'USA': 1, 'N': 2}
df['Nationality'] = df['Nationality'].map(d)
d = {'YES': 1, 'NO': 0}
df['Go'] = df['Go'].map(d)

print(df)
```

Then we have to separate the *feature* columns from the *target* column.

The feature columns are the columns that we try to predict *from*, and the target column is the column with the values we try to predict.

Example

X is the feature columns, y is the target column:

```
features = ['Age', 'Experience', 'Rank', 'Nationality']

X = df[features]
y = df['Go']
```

```
print(X)
print(y)
```

Now we can create the actual decision tree, fit it with our details. Start by importing the modules we need:

Example

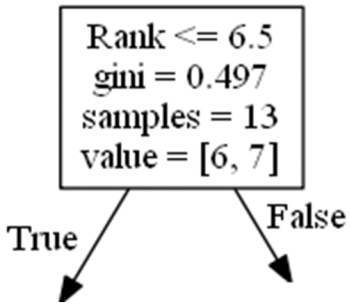
Create and display a Decision Tree:

```
import pandas
from sklearn import tree
from sklearn.tree import DecisionTreeClassifier
import matplotlib.pyplot as plt

df = pandas.read_csv("data.csv")

d = {'UK': 0, 'USA': 1, 'N': 2}
df['Nationality'] = df['Nationality'].map(d)
d = {'YES': 1, 'NO': 0}
df['Go'] = df['Go'].map(d)

features = ['Age', 'Experience', 'Rank', 'Nationality']

X = df[features]
y = df['Go']

dtree = DecisionTreeClassifier()
dtree = dtree.fit(X, y)

tree.plot_tree(dtree, feature_names=features)
```

Result Explained

The decision tree uses your earlier decisions to calculate the odds for you to wanting to go see a comedian or not.

Let us read the different aspects of the decision tree:



Rank

Rank <= 6.5 means that every comedian with a rank of 6.5 or lower will follow the True arrow (to the left), and the rest will follow the False arrow (to the right).

gini = 0.497 refers to the quality of the split, and is always a number between 0.0 and 0.5, where 0.0 would mean all of the samples got the same result, and 0.5 would mean that the split is done exactly in the middle.

samples = 13 means that there are 13 comedians left at this point in the decision, which is all of them since this is the first step.

value = [6, 7] means that of these 13 comedians, 6 will get a "NO", and 7 will get a "GO".

Gini

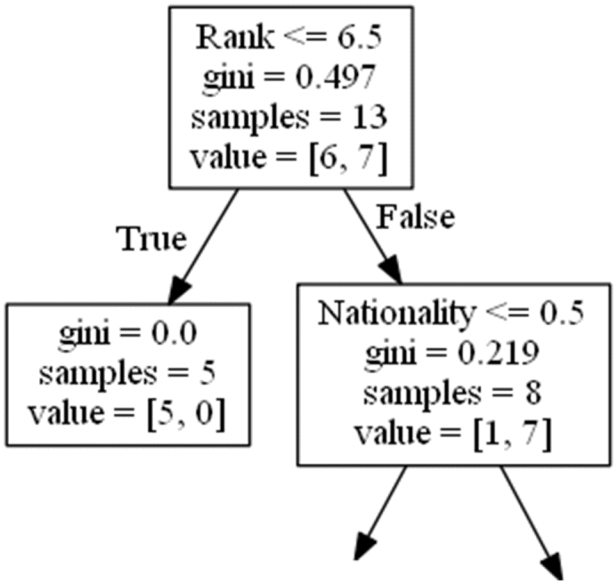
There are many ways to split the samples, we use the GINI method in this .

The Gini method uses this formula:

Gini = 1 - $(x/n)^2$ - $(y/n)^2$

Where x is the number of positive answers("GO"), n is the number of samples, and y is the number of negative answers ("NO"), which gives us this calculation:

1 - $(7 / 13)^2$ - $(6 / 13)^2$ = 0.497



The next step contains two boxes, one box for the comedians with a 'Rank' of 6.5 or lower, and one box with the rest.

True - 5 Comedians End Here:

gini = 0.0 means all of the samples got the same result.

samples = 5 means that there are 5 comedians left in this branch (5 comedian with a Rank of 6.5 or lower).

value = [5, 0] means that 5 will get a "NO" and 0 will get a "GO".

False - 8 Comedians Continue:

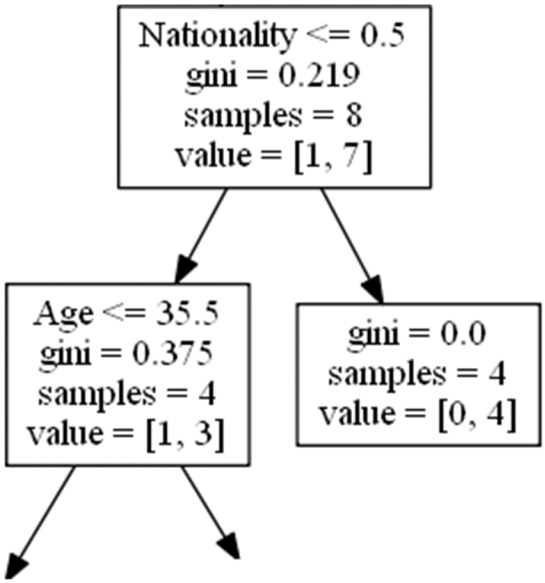
Nationality

Nationality <= 0.5 means that the comedians with a nationality value of less than 0.5 will follow the arrow to the left (which means everyone from the UK,), and the rest will follow the arrow to the right.

gini = 0.219 means that about 22% of the samples would go in one direction.

samples = 8 means that there are 8 comedians left in this branch (8 comedian with a Rank higher than 6.5).

value = [1, 7] means that of these 8 comedians, 1 will get a "NO" and 7 will get a "GO".



True - 4 Comedians Continue:

Age

Age <= 35.5 means that comedians at the age of 35.5 or younger will follow the arrow to the left, and the rest will follow the arrow to the right.

gini = 0.375 means that about 37.5% of the samples would go in one direction.

samples = 4 means that there are 4 comedians left in this branch (4 comedians from the UK).

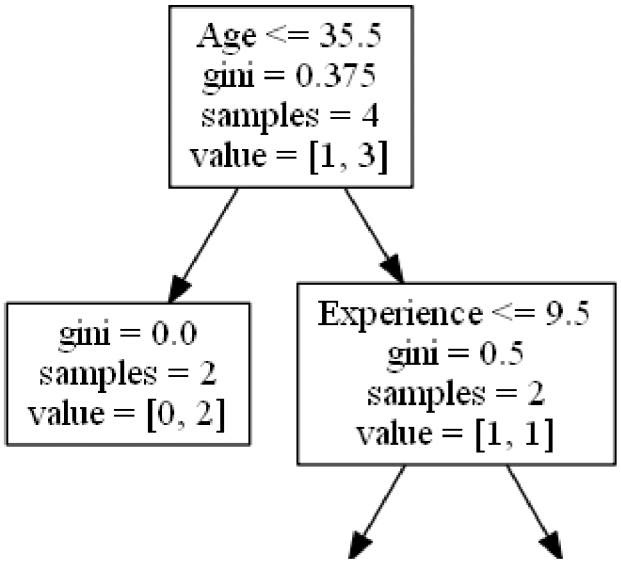
value = [1, 3] means that of these 4 comedians, 1 will get a "NO" and 3 will get a "GO".

False - 4 Comedians End Here:

gini = 0.0 means all of the samples got the same result.

samples = 4 means that there are 4 comedians left in this branch (4 comedians not from the UK).

value = [0, 4] means that of these 4 comedians, 0 will get a "NO" and 4 will get a "GO".



True - 2 Comedians End Here:

gini = 0.0 means all of the samples got the same result.

samples = 2 means that there are 2 comedians left in this branch (2 comedians at the age 35.5 or younger).

value = [0, 2] means that of these 2 comedians, 0 will get a "NO" and 2 will get a "GO".

False - 2 Comedians Continue:

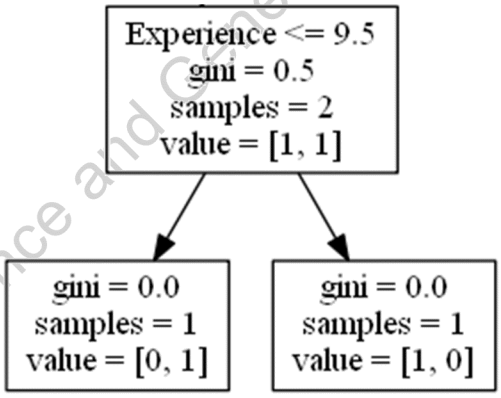
Experience

Experience <= 9.5 means that comedians with 9.5 years of experience, or less, will follow the arrow to the left, and the rest will follow the arrow to the right.

gini = 0.5 means that 50% of the samples would go in one direction.

samples = 2 means that there are 2 comedians left in this branch (2 comedians older than 35.5).

value = [1, 1] means that of these 2 comedians, 1 will get a "NO" and 1 will get a "GO".



True - 1 Comedian Ends Here:

gini = 0.0 means all of the samples got the same result.

samples = 1 means that there is 1 comedian left in this branch (1 comedian with 9.5 years of experience or less).

value = [0, 1] means that 0 will get a "NO" and 1 will get a "GO".

False - 1 Comedian Ends Here:

gini = 0.0 means all of the samples got the same result.

samples = 1 means that there is 1 comedians left in this branch (1 comedian with more than 9.5 years of experience).

value = [1, 0] means that 1 will get a "NO" and 0 will get a "GO".

Predict Values

We can use the Decision Tree to predict new values.

Example: Should I go see a show starring a 40 years old American comedian, with 10 years of experience, and a comedy ranking of 7?

Example

Use predict() method to predict new values:

```
print(dtree.predict([[40, 10, 7, 1]]))
```

Example

What would the answer be if the comedy rank was 6?

```
print(dtree.predict([[40, 10, 6, 1]]))
```

Machine Learning - Confusion Matrix

What is a confusion matrix?

It is a table that is used in classification problems to assess where errors in the model were made.

The rows represent the actual classes the outcomes should have been. While the columns represent the predictions we have made. Using this table it is easy to see which predictions are wrong.

Creating a Confusion Matrix

Confusion matrixes can be created by predictions made from a logistic regression.

For now we will generate actual and predicted values by utilizing NumPy:

```
import numpy
```

Next we will need to generate the numbers for "actual" and "predicted" values.

```
actual = numpy.random.binomial(1, 0.9, size = 1000)
predicted = numpy.random.binomial(1, 0.9, size = 1000)
```

In order to create the confusion matrix we need to import metrics from the sklearn module.

```
from sklearn import metrics
```

Once metrics is imported we can use the confusion matrix function on our actual and predicted values.

```
confusion_matrix = metrics.confusion_matrix(actual, predicted)
```

To create a more interpretable visual display we need to convert the table into a confusion matrix display.

```
cm_display = metrics.ConfusionMatrixDisplay(confusion_matrix = confusion_matrix, display_labels = [0, 1])
```

Vizualizing the display requires that we import pyplot from matplotlib.

```
import matplotlib.pyplot as plt
```

Finally to display the plot we can use the functions plot() and show() from pyplot.

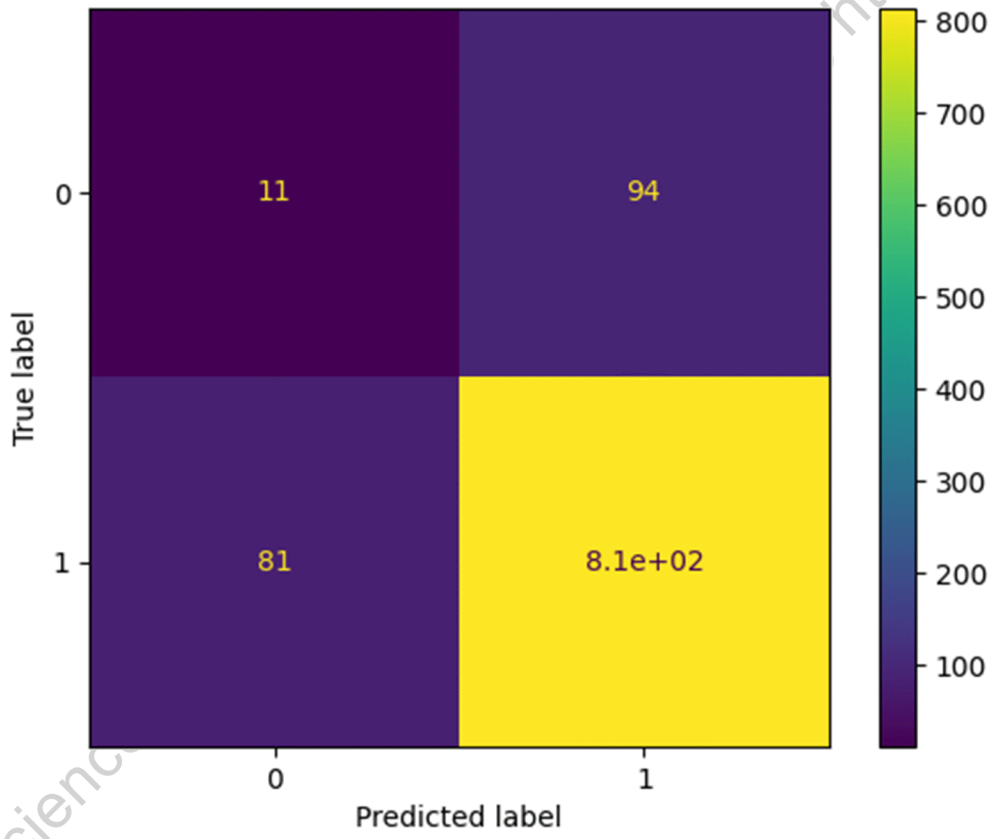
```
cm_display.plot()
plt.show()
```

See the whole example in action:

Example

```
import matplotlib.pyplot as plt
import numpy
from sklearn import metrics

actual = numpy.random.binomial(1,.9,size = 1000)
predicted = numpy.random.binomial(1,.9,size = 1000)

confusion_matrix = metrics.confusion_matrix(actual, predicted)

cm_display = metrics.ConfusionMatrixDisplay(confusion_matrix = confusion_matrix,
display_labels = [0, 1])

cm_display.plot()
plt.show()
```

Result



Results Explained

The Confusion Matrix created has four different quadrants:

True Negative (Top-Left Quadrant)
False Positive (Top-Right Quadrant)
False Negative (Bottom-Left Quadrant)
True Positive (Bottom-Right Quadrant)

True means that the values were accurately predicted, False means that there was an error or wrong prediction.

Now that we have made a Confusion Matrix, we can calculate different measures to quantify the quality of the model. First, lets look at Accuracy.

Created Metrics

The matrix provides us with many useful metrics that help us to evaluate out classification model.

The different measures include: Accuracy, Precision, Sensitivity (Recall), Specificity, and the F-score, explained below.

Accuracy

Accuracy measures how often the model is correct.

How to Calculate

(True Positive + True Negative) / Total Predictions

Example

Accuracy = metrics.accuracy_score(actual, predicted)

Precision

Of the positives predicted, what percentage is truly positive?

How to Calculate

True Positive / (True Positive + False Positive)

Precision does not evaluate the correctly predicted negative cases:

Example

Precision = metrics.precision_score(actual, predicted)

Sensitivity (Recall)

Of all the positive cases, what percentage are predicted positive?

Sensitivity (sometimes called Recall) measures how good the model is at predicting positives.

This means it looks at true positives and false negatives (which are positives that have been incorrectly predicted as negative).

How to Calculate

True Positive / (True Positive + False Negative)

Sensitivity is good at understanding how well the model predicts something is positive:

Example

Sensitivity_recall = metrics.recall_score(actual, predicted)

Specificity

How well the model is at prediciting negative results?

Specificity is similar to sensitivity, but looks at it from the persepctive of negative results.

How to Calculate

True Negative / (True Negative + False Positive)

Since it is just the opposite of Recall, we use the recall_score function, taking the opposite position label:

Example

Specificity = metrics.recall_score(actual, predicted, pos_label=0)

F-score

F-score is the "harmonic mean" of precision and sensitivity.

It considers both false positive and false negative cases and is good for imbalanced datasets.

How to Calculate

2 * ((Precision * Sensitivity) / (Precision + Sensitivity))

This score does not take into consideration the True Negative values:

Example

F1_score = metrics.f1_score(actual, predicted)

All calulations in one:

Example

#metrics
print({"Accuracy":Accuracy,"Precision":Precision,"Sensitivity_recall":Sensitivity_recall,"Specificity":Specificity,"F1_score":F1_score})

Machine Learning - Hierarchical Clustering

Hierarchical Clustering

Hierarchical clustering is an unsupervised learning method for clustering data points. The algorithm builds clusters by measuring the dissimilarities between data. Unsupervised learning means that a model does not have to be trained, and we do not need a "target" variable. This method can be used on any data to visualize and interpret the relationship between individual data points.

Here we will use hierarchical clustering to group data points and visualize the clusters using both a dendrogram and scatter plot.

How does it work?

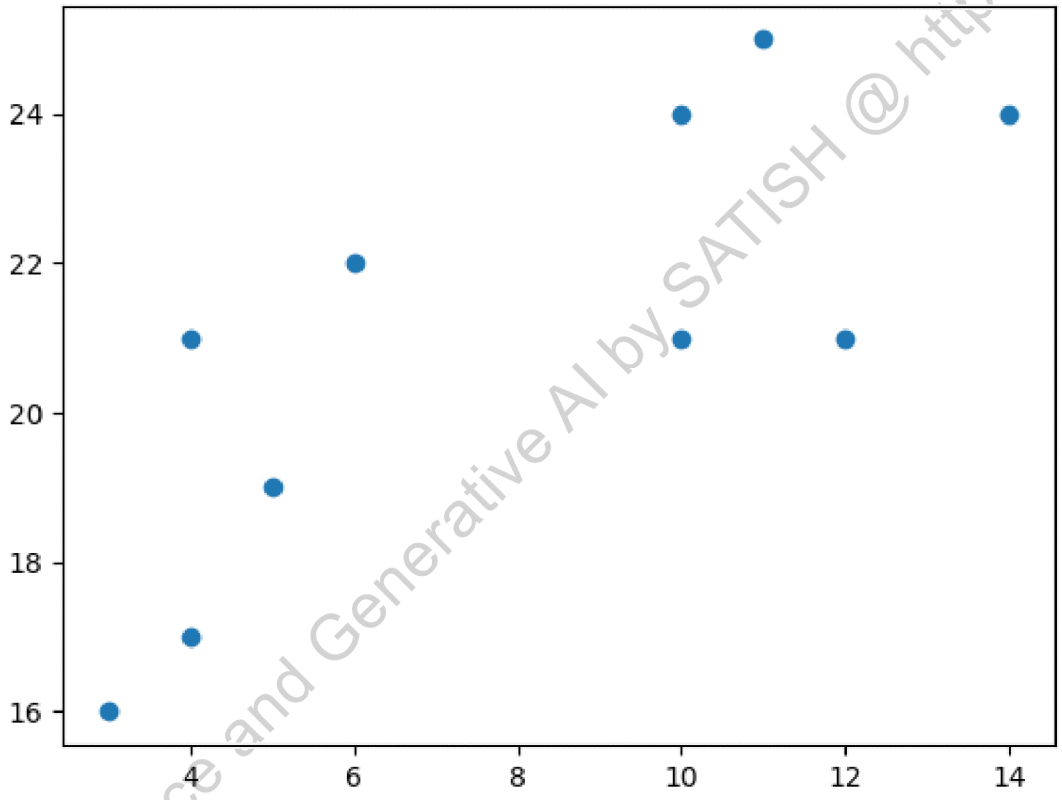
We will use Agglomerative Clustering, a type of hierarchical clustering that follows a bottom up approach. We begin by treating each data point as its own cluster. Then, we join clusters together that have the shortest distance between them to create larger clusters. This step is repeated until one large cluster is formed containing all of the data points.

Example

Start by visualizing some data points:

```
import numpy as np
import matplotlib.pyplot as plt

x = [4, 5, 10, 4, 3, 11, 14 , 6, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]
plt.scatter(x, y)
plt.show()
```

Result

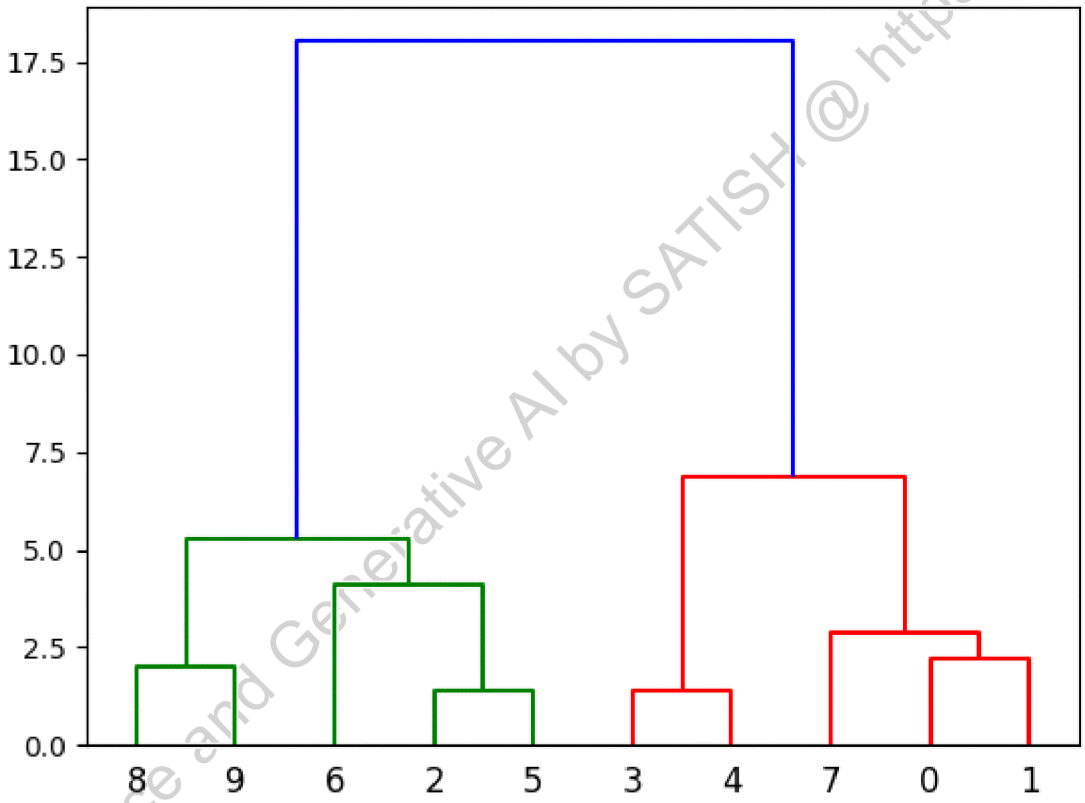


Now we compute the ward linkage using euclidean distance, and visualize it using a dendrogram:

Example

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.cluster.hierarchy import dendrogram, linkage

x = [4, 5, 10, 4, 3, 11, 14 , 6, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]

data = list(zip(x, y))

linkage_data = linkage(data, method='ward', metric='euclidean')
dendrogram(linkage_data)
plt.show()
```

Result

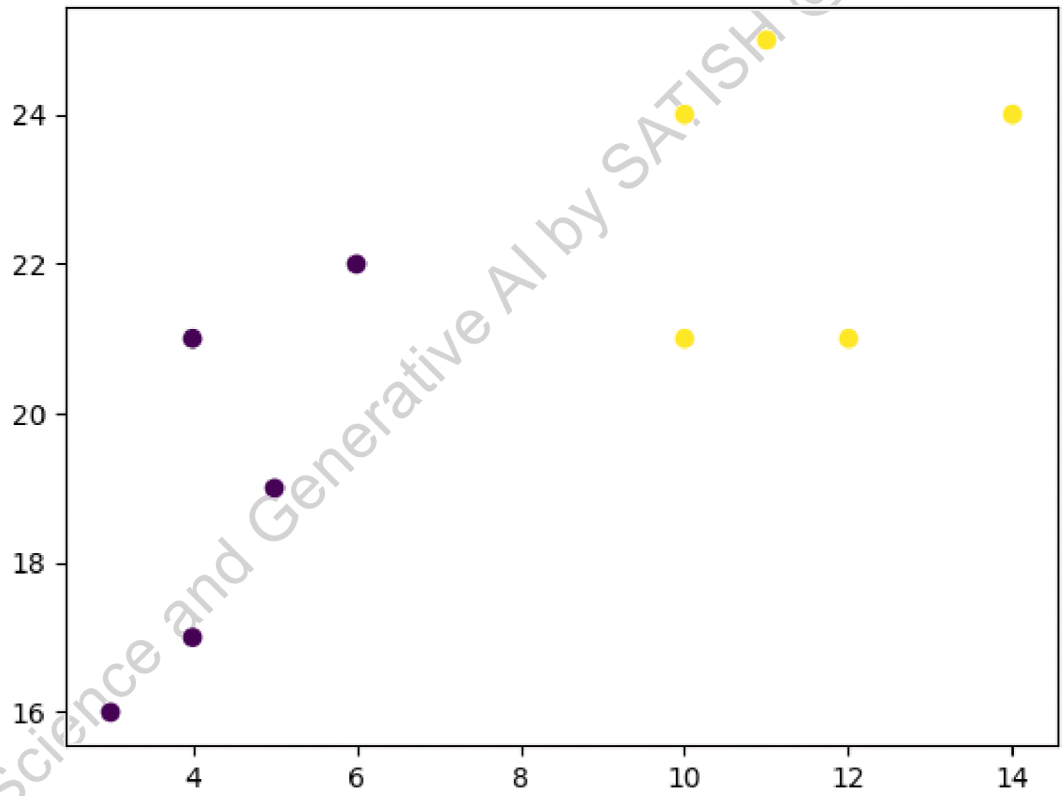


Here, we do the same thing with Python's scikit-learn library. Then, visualize on a 2-dimensional plot:

Example

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.cluster import AgglomerativeClustering

x = [4, 5, 10, 4, 3, 11, 14 , 6, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]

data = list(zip(x, y))

hierarchical_cluster = AgglomerativeClustering(n_clusters=2, affinity='euclidean',
linkage='ward')
labels = hierarchical_cluster.fit_predict(data)

plt.scatter(x, y, c=labels)
plt.show()
```

Result



Example Explained

Import the modules you need.

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.cluster.hierarchy import dendrogram, linkage
from sklearn.cluster import AgglomerativeClustering
```

scikit-learn is a popular library for machine learning.

Create arrays that resemble two variables in a dataset. Note that while we only use two variables here, this method will work with any number of variables:

```
x = [4, 5, 10, 4, 3, 11, 14 , 6, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]
```

Turn the data into a set of points:

```
data = list(zip(x, y))
print(data)
```

Result:

```
[(4, 21), (5, 19), (10, 24), (4, 17), (3, 16), (11, 25), (14, 24), (6, 22), (10, 21), (12, 21)]
```

Compute the linkage between all of the different points. Here we use a simple euclidean distance measure and Ward's linkage, which seeks to minimize the variance between clusters.

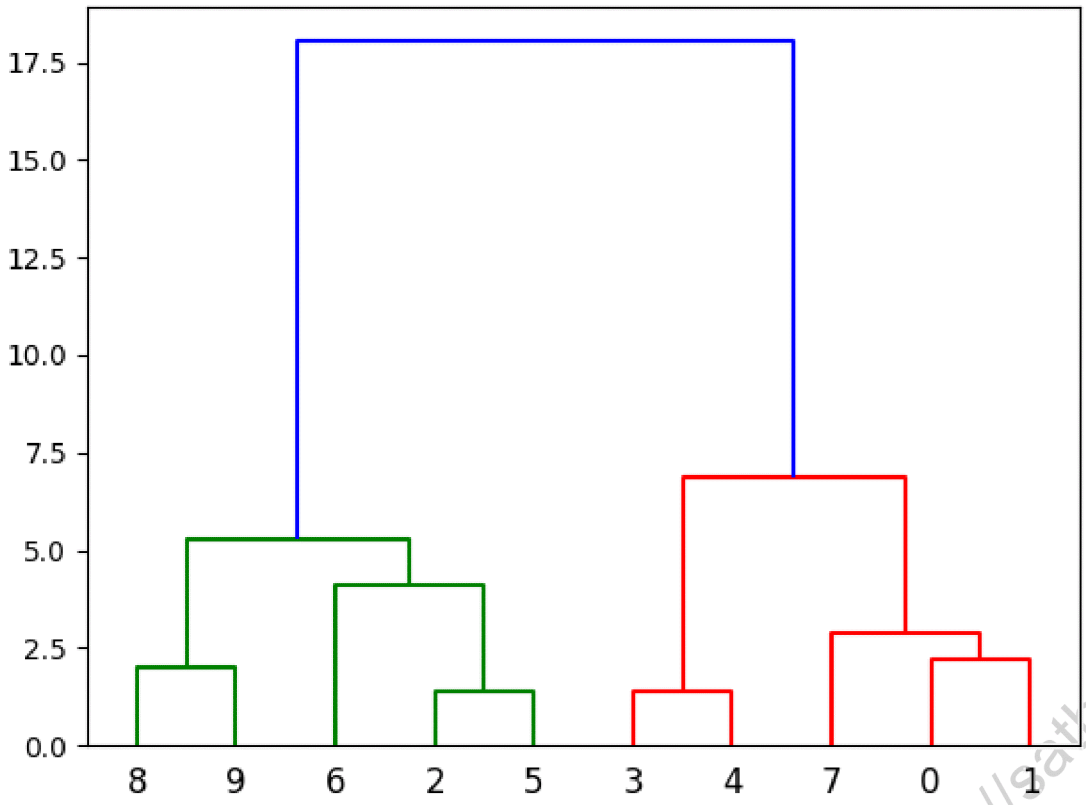
```
linkage_data = linkage(data, method='ward', metric='euclidean')
```

Finally, plot the results in a dendrogram. This plot will show us the hierarchy of clusters from the bottom (individual points) to the top (a single cluster consisting of all data points).

plt.show() lets us visualize the dendrogram instead of just the raw linkage data.

```
dendrogram(linkage_data)
plt.show()
```

Result:



The scikit-learn library allows us to use hierarchichal clustering in a different manner. First, we initialize the AgglomerativeClustering class with 2 clusters, using the same euclidean distance and Ward linkage.

hierarchical_cluster = AgglomerativeClustering(n_clusters=2, affinity='euclidean', linkage='ward')

The .fit_predict method can be called on our data to compute the clusters using the defined parameters across our chosen number of clusters.

labels = hierarchical_cluster.fit_predict(data) print(labels)

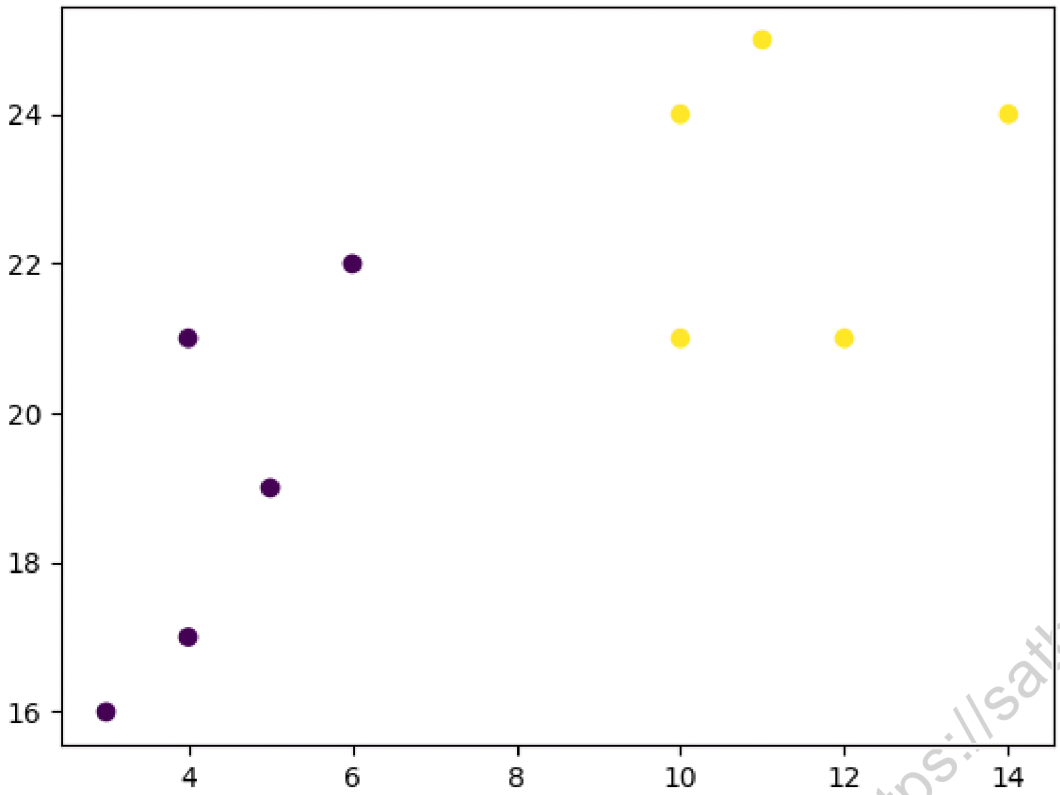
Result:

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

Finally, if we plot the same data and color the points using the labels assigned to each index by the hierarchical clustering method, we can see the cluster each point was assigned to:

```
plt.scatter(x, y, c=labels)
plt.show()
```

Result:



Machine Learning - K-means

K-means

K-means is an unsupervised learning method for clustering data points. The algorithm iteratively divides data points into K clusters by minimizing the variance in each cluster.

Here, we will show you how to estimate the best value for K using the elbow method, then use K-means clustering to group the data points into clusters.

How does it work?

First, each data point is randomly assigned to one of the K clusters. Then, we compute the centroid (functionally the center) of each cluster, and reassign each data point to the

cluster with the closest centroid. We repeat this process until the cluster assignments for each data point are no longer changing.

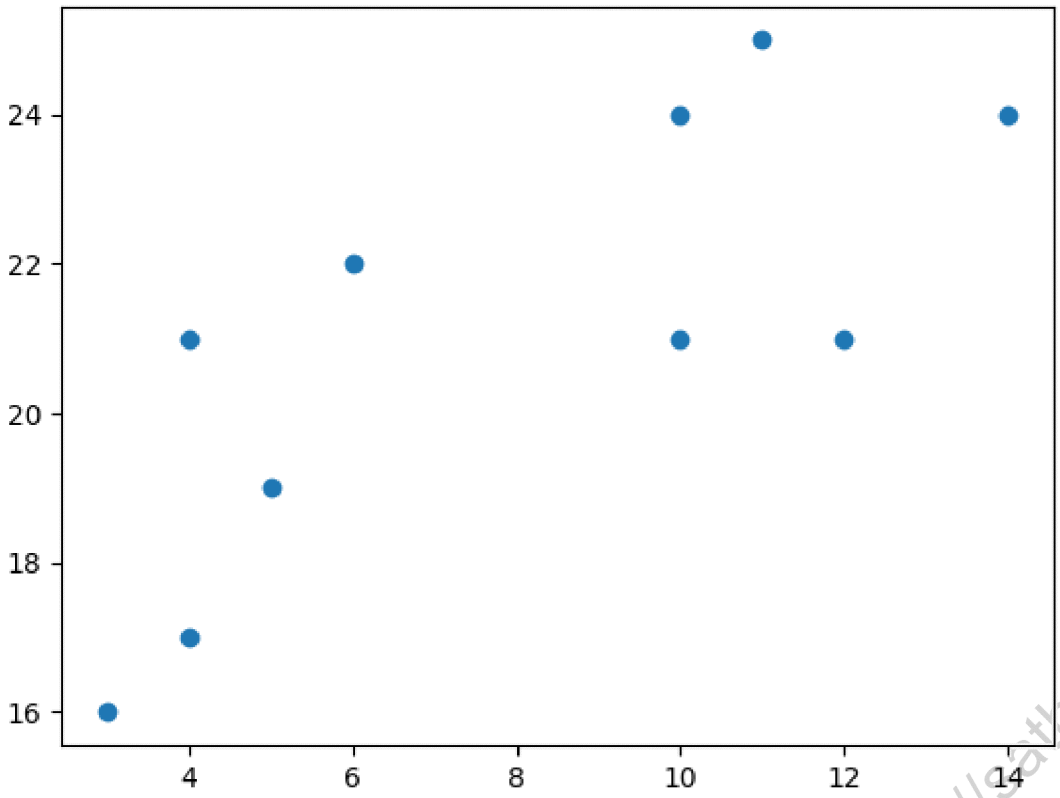
K-means clustering requires us to select K, the number of clusters we want to group the data into. The elbow method lets us graph the inertia (a distance-based metric) and visualize the point at which it starts decreasing linearly. This point is referred to as the "elbow" and is a good estimate for the best value for K based on our data.

Example

Start by visualizing some data points:

```
import matplotlib.pyplot as plt

x = [4, 5, 10, 4, 3, 11, 14 , 6, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]

plt.scatter(x, y)
plt.show()
```

Result



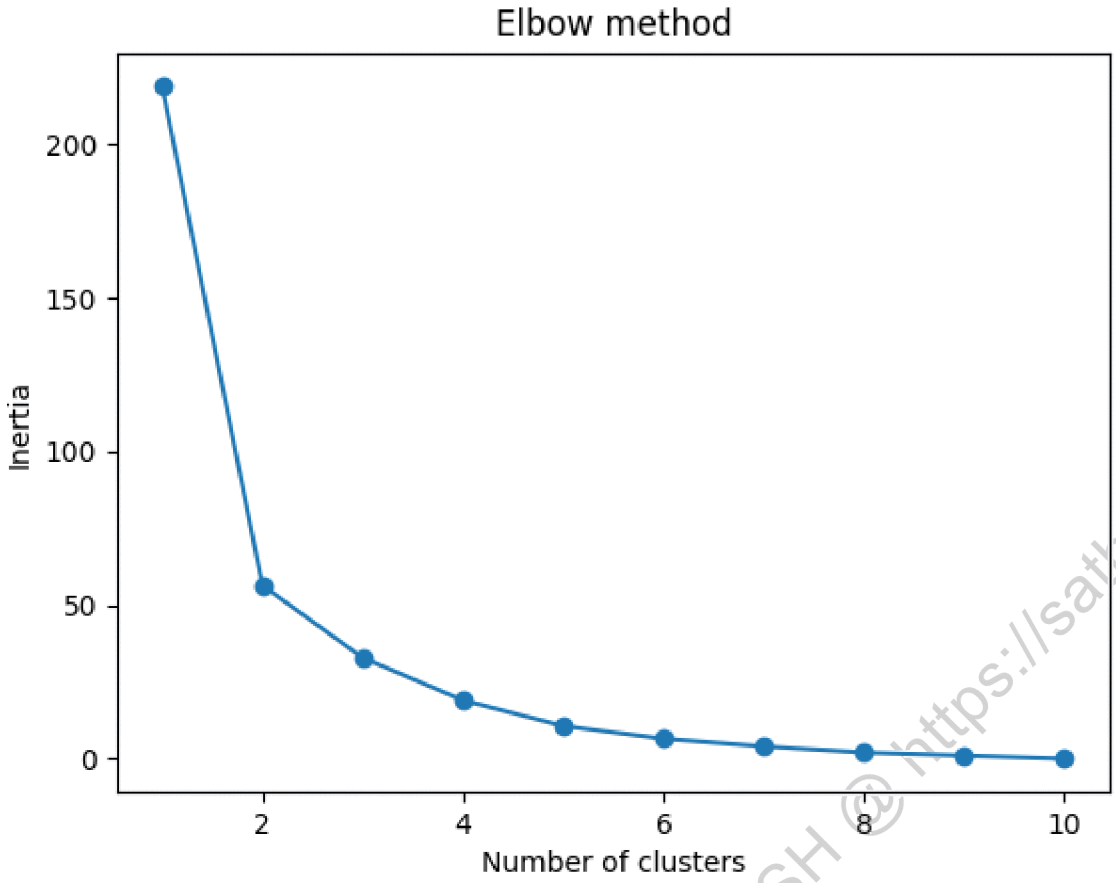
Now we utilize the elbow method to visualize the intertia for different values of K:

Example

```
from sklearn.cluster import KMeans

data = list(zip(x, y))
inertias = []

for i in range(1,11):
    kmeans = KMeans(n_clusters=i)
    kmeans.fit(data)
    inertias.append(kmeans.inertia_)

plt.plot(range(1,11), inertias, marker='o')
plt.title('Elbow method')
plt.xlabel('Number of clusters')
```

```
plt.ylabel('Inertia')
plt.show()
```

Result

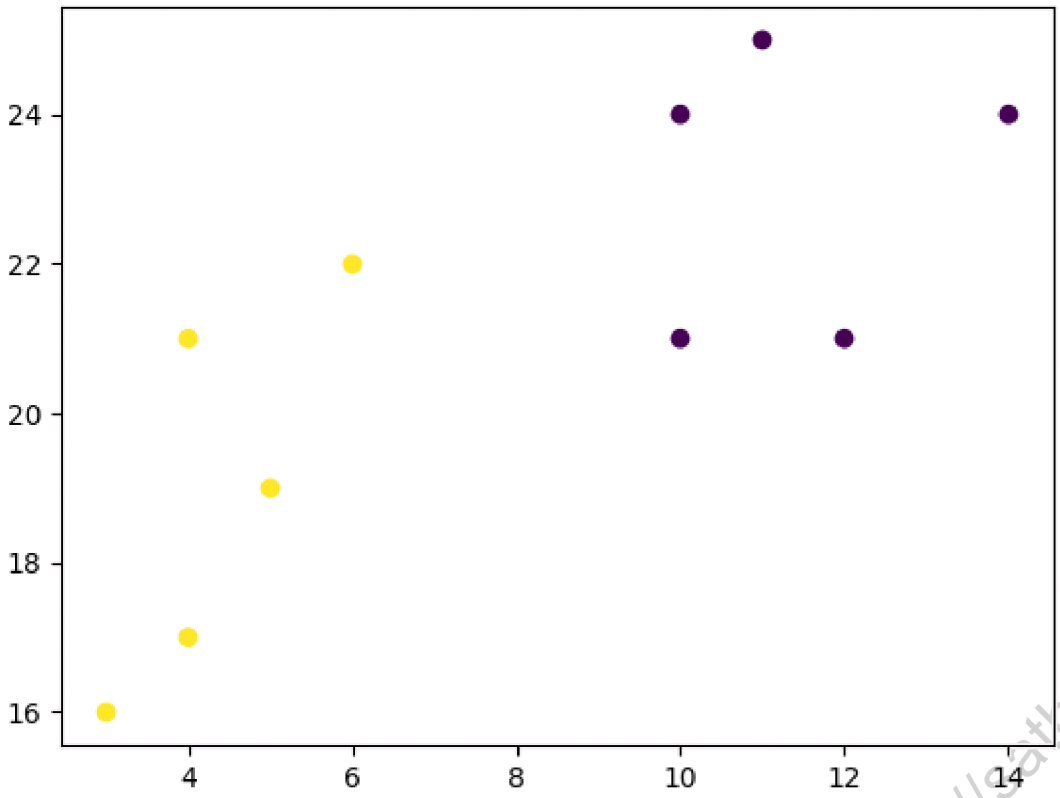


The elbow method shows that 2 is a good value for K, so we retrain and visualize the result:

Example

```
kmeans = KMeans(n_clusters=2)
kmeans.fit(data)

plt.scatter(x, y, c=kmeans.labels_)
plt.show()
```

Result



Example Explained

Import the modules you need.

```
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
```

You can learn about the Matplotlib module in our "Matplotlib

scikit-learn is a popular library for machine learning.

Create arrays that resemble two variables in a dataset. Note that while we only use two variables here, this method will work with any number of variables:

```
x = [4, 5, 10, 4, 3, 11, 14 , 6, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]
```

Turn the data into a set of points:

```
data = list(zip(x, y))
print(data)
```

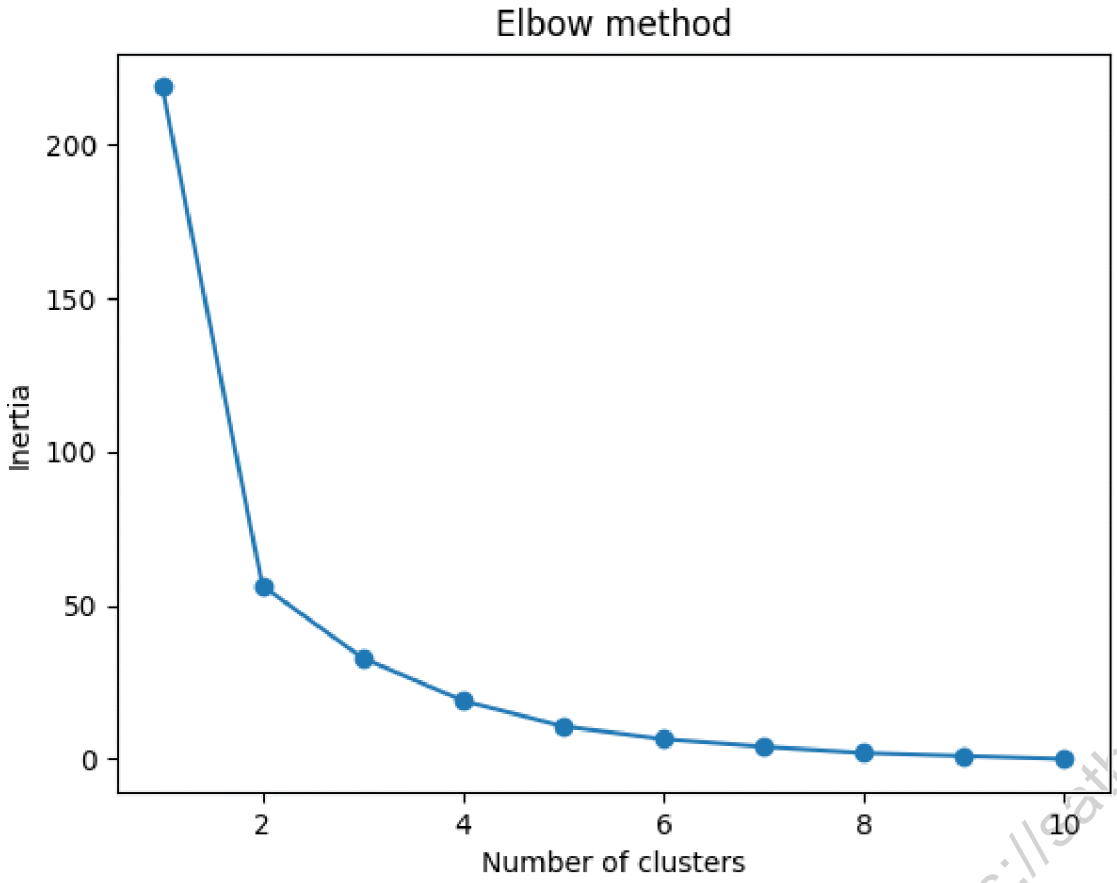
Result:

[(4, 21), (5, 19), (10, 24), (4, 17), (3, 16), (11, 25), (14, 24), (6, 22), (10, 21), (12, 21)]

In order to find the best value for K, we need to run K-means across our data for a range of possible values. We only have 10 data points, so the maximum number of clusters is 10. So for each value K in range(1,11), we train a K-means model and plot the intertia at that number of clusters:

```
inertias = []

for i in range(1,11):
    kmeans = KMeans(n_clusters=i)
    kmeans.fit(data)
    inertias.append(kmeans.inertia_)

plt.plot(range(1,11), inertias, marker='o')
plt.title('Elbow method')
plt.xlabel('Number of clusters')
plt.ylabel('Inertia')
plt.show()
```

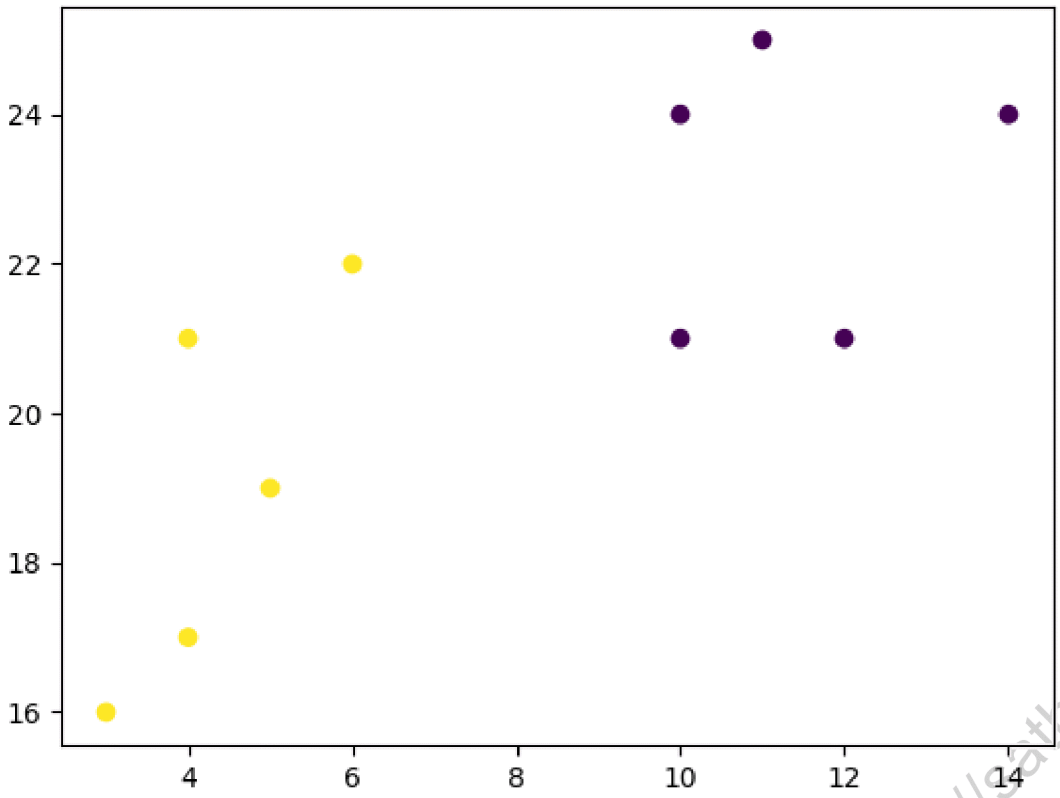
Result:



We can see that the "elbow" on the graph above (where the interia becomes more linear) is at K=2. We can then fit our K-means algorithm one more time and plot the different clusters assigned to the data:

```
kmeans = KMeans(n_clusters=2)
kmeans.fit(data)

plt.scatter(x, y, c=kmeans.labels_)
plt.show()
```

Result:



Machine Learning - Bootstrap Aggregation (Bagging)

Bagging

Methods such as Decision Trees, can be prone to overfitting on the training set which can lead to wrong predictions on new data.

Bootstrap Aggregation (bagging) is aensembling method that attempts to resolve overfitting for classification or regression problems. Bagging aims to improve the accuracy and performance of machine learning algorithms. It does this by taking random subsets of an original dataset, with replacement, and fits either a classifier (for classification) or regressor (for regression) to each subset. The predictions for each subset are then aggregated through majority vote for classification or averaging for regression, increasing prediction accuracy.

Evaluating a Base Classifier of Bagging

To see how bagging can improve model performance, we must start by evaluating how the base classifier performs on the dataset. If you do not know what decision trees are review the lesson on decision trees before moving forward, as bagging is a continuation of the concept.

We will be looking to identify different classes of wines found in Sklearn's wine dataset.

Let's start by importing the necessary modules.

```
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.tree import DecisionTreeClassifier
```

Next we need to load in the data and store it into X (input features) and y (target). The parameter as_frame is set equal to True so we do not lose the feature names when loading the data. (sklearn version older than 0.23 must skip the as_frame argument as it is not supported)

```
data = datasets.load_wine(as_frame = True)
```

```
X = data.data
y = data.target
```

In order to properly evaluate our model on unseen data, we need to split X and y into train and test sets. For information on splitting data, see the Train/Test lesson.

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.25, random_state = 22)
```

With our data prepared, we can now instantiate a base classifier and fit it to the training data.

```
dtree = DecisionTreeClassifier(random_state = 22)
dtree.fit(X_train,y_train)
```

Result:

```
DecisionTreeClassifier(random_state=22)
```

We can now predict the class of wine the unseen test set and evaluate the model performance.

```
y_pred = dtree.predict(X_test)

print("Train data accuracy:",accuracy_score(y_true = y_train, y_pred =
dtree.predict(X_train)))
print("Test data accuracy:",accuracy_score(y_true = y_test, y_pred = y_pred))
```

Result:

```
Train data accuracy: 1.0
Test data accuracy: 0.8222222222222222
```

Example

Import the necessary data and evaluate base classifier performance.

```
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.tree import DecisionTreeClassifier

data = datasets.load_wine(as_frame = True)

X = data.data
y = data.target

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.25, random_state = 22)

dtree = DecisionTreeClassifier(random_state = 22)
dtree.fit(X_train,y_train)

y_pred = dtree.predict(X_test)

print("Train data accuracy:",accuracy_score(y_true = y_train, y_pred =
dtree.predict(X_train)))
print("Test data accuracy:",accuracy_score(y_true = y_test, y_pred = y_pred))
```

The base classifier performs reasonably well on the dataset achieving 82% accuracy on the test dataset with the current parameters (Different results may occur if you do not have the random_state parameter set).

Now that we have a baseline accuracy for the test dataset, we can see how the Bagging Classifier out performs a single Decision Tree Classifier.

Creating a Bagging Classifier

For bagging we need to set the parameter n_estimators, this is the number of base classifiers that our model is going to aggregate together.

For this sample dataset the number of estimators is relatively low, it is often the case that much larger ranges are explored. Hyperparameter tuning is usually done with a grid search, but for now we will use a select set of values for the number of estimators.

We start by importing the necessary model.

from sklearn.ensemble import BaggingClassifier

Now lets create a range of values that represent the number of estimators we want to use in each ensemble.

estimator_range = [2,4,6,8,10,12,14,16]

To see how the Bagging Classifier performs with differing values of n_estimators we need a way to iterate over the range of values and store the results from each ensemble. To do this we will create a for loop, storing the models and scores in separate lists for later vizualizations.

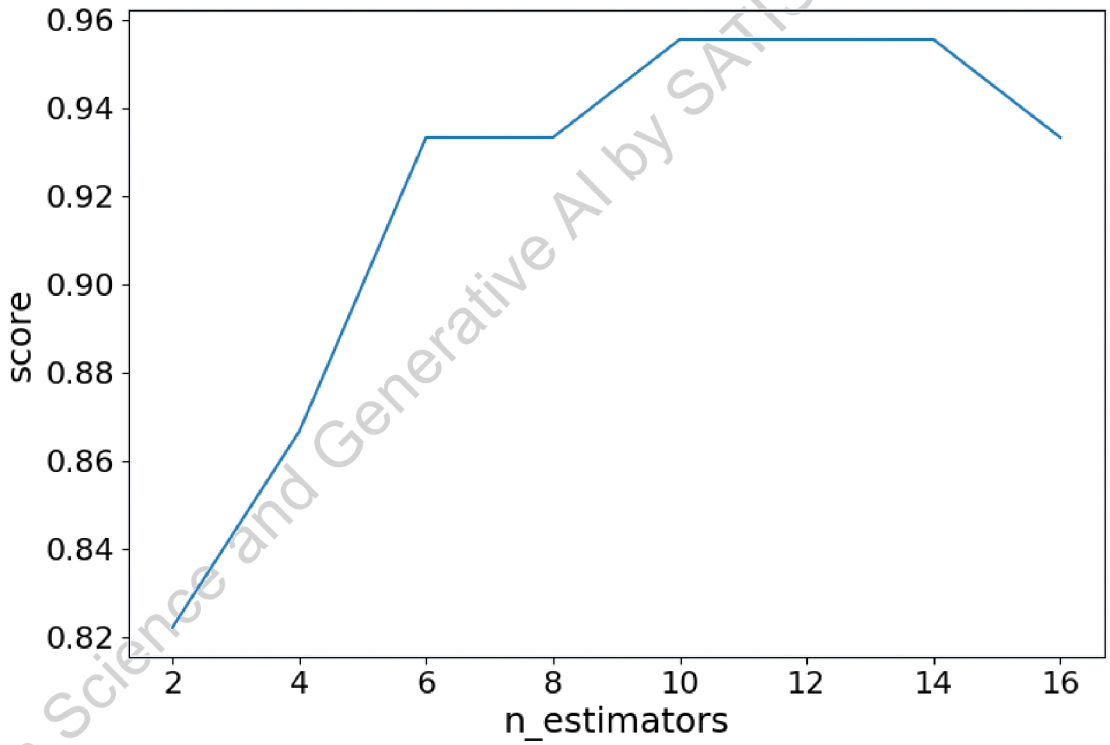
Note: The default parameter for the base classifier in BaggingClassifier is the DicisionTreeClassifier therefore we do not need to set it when instantiating the bagging model.

```
models = []
scores = []

for n_estimators in estimator_range:

    # Create bagging classifier
    clf = BaggingClassifier(n_estimators = n_estimators, random_state = 22)

    # Fit the model
    clf.fit(X_train, y_train)
```

```
# Append the model and score to their respective list
models.append(clf)
scores.append(accuracy_score(y_true = y_test, y_pred = clf.predict(X_test)))
```

With the models and scores stored, we can now visualize the improvement in model performance.

```
import matplotlib.pyplot as plt

# Generate the plot of scores against number of estimators
plt.figure(figsize=(9,6))
plt.plot(estimator_range, scores)

# Adjust labels and font (to make visable)
plt.xlabel("n_estimators", fontsize = 18)
plt.ylabel("score", fontsize = 18)
plt.tick_params(labelsize = 16)

# Visualize plot
plt.show()
```



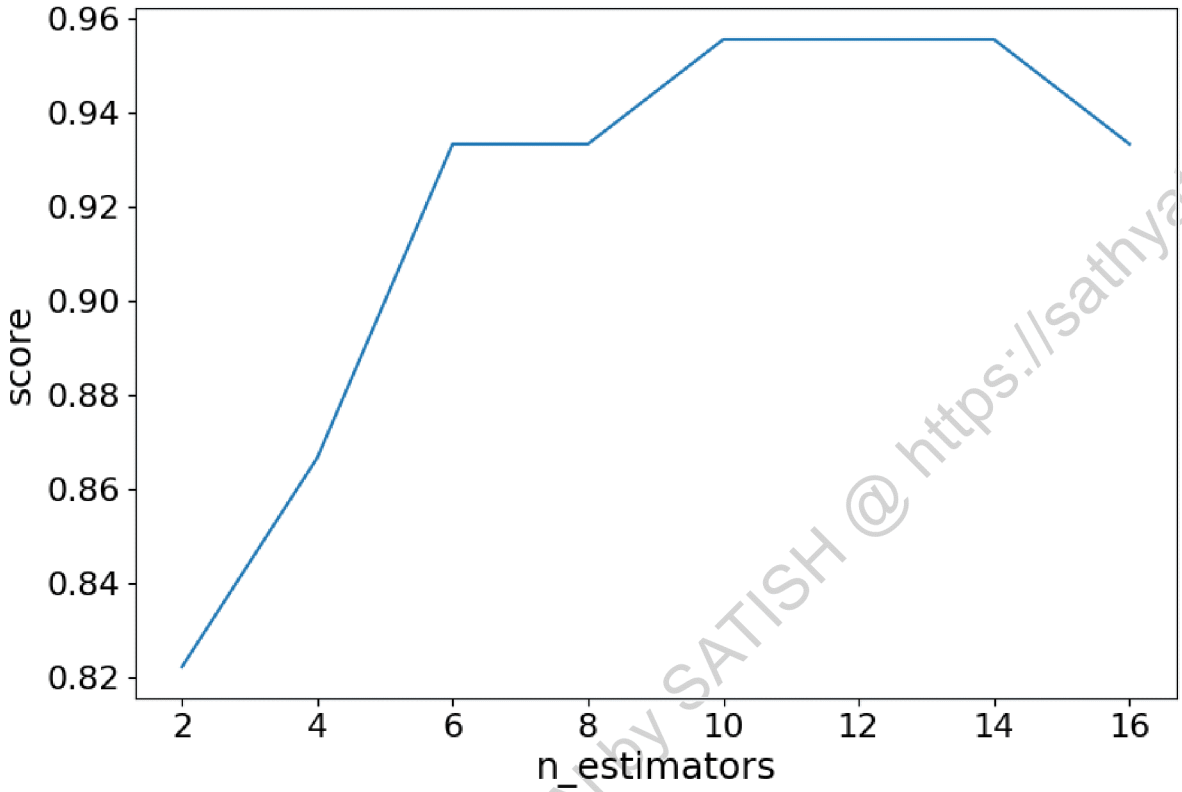
Example

Import the necessary data and evaluate the BaggingClassifier performance.

```
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.ensemble import BaggingClassifier

data = datasets.load_wine(as_frame = True)

X = data.data
y = data.target

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.25, random_state = 22)

estimator_range = [2,4,6,8,10,12,14,16]

models = []
scores = []

for n_estimators in estimator_range:

    # Create bagging classifier
    clf = BaggingClassifier(n_estimators = n_estimators, random_state = 22)

    # Fit the model
    clf.fit(X_train, y_train)

    # Append the model and score to their respective list
    models.append(clf)
    scores.append(accuracy_score(y_true = y_test, y_pred = clf.predict(X_test)))

# Generate the plot of scores against number of estimators
plt.figure(figsize=(9,6))
plt.plot(estimator_range, scores)
```

```
# Adjust labels and font (to make visable)
plt.xlabel("n_estimators", fontsize = 18)
plt.ylabel("score", fontsize = 18)
plt.tick_params(labelsize = 16)

# Visualize plot
plt.show()
```

Result



Results Explained

By iterating through different values for the number of estimators we can see an increase in model performance from 82.2% to 95.5%. After 14 estimators the accuracy begins to drop, again if you set a different random_state the values you see will vary. That is why it is best practice to use cross validation to ensure stable results.

In this case, we see a 13.3% increase in accuracy when it comes to identifying the type of the wine.

Another Form of Evaluation

As bootstrapping chooses random subsets of observations to create classifiers, there are observations that are left out in the selection process. These "out-of-bag" observations can then be used to evaluate the model, similarly to that of a test set. Keep in mind, that out-of-bag estimation can overestimate error in binary classification problems and should only be used as a compliment to other metrics.

We saw in the last exercise that 12 estimators yielded the highest accuracy, so we will use that to create our model. This time setting the parameter oob_score to true to evaluate the model with out-of-bag score.

Example

Create a model with out-of-bag metric.

```
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.ensemble import BaggingClassifier

data = datasets.load_wine(as_frame = True)

X = data.data
y = data.target

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.25, random_state = 22)

oob_model = BaggingClassifier(n_estimators = 12, oob_score = True,random_state = 22)

oob_model.fit(X_train, y_train)

print(oob_model.oob_score_)
```

Since the samples used in OOB and the test set are different, and the dataset is relatively small, there is a difference in the accuracy. It is rare that they would be exactly the same, again OOB should be used quick means for estimating error, but is not the only evaluation metric.

Generating Decision Trees from Bagging Classifier

it is possible to graph the decision tree the model created. It is also possible to see the individual decision trees that went into the aggregated classifier. This helps us to gain a more intuitive understanding on how the bagging model arrives at its predictions.

Note: This is only functional with smaller datasets, where the trees are relatively shallow and narrow making them easy to visualize.

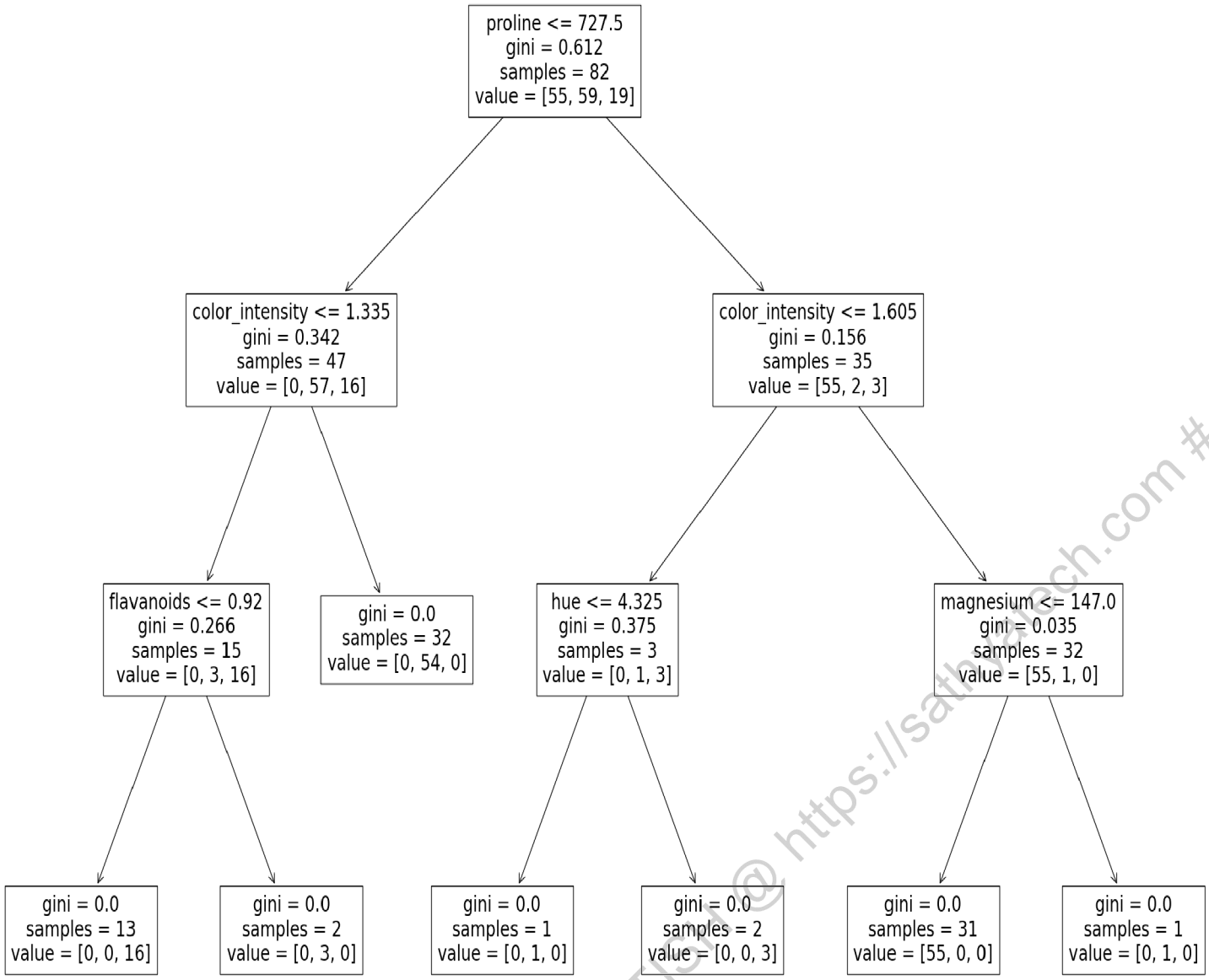
We will need to import plot_tree function from sklearn.tree. The different trees can be graphed by changing the estimator you wish to visualize.

Example

Generate Decision Trees from Bagging Classifier

```
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.ensemble import BaggingClassifier
from sklearn.tree import plot_tree

X = data.data
y = data.target

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.25, random_state = 22)

clf = BaggingClassifier(n_estimators = 12, oob_score = True,random_state = 22)

clf.fit(X_train, y_train)

plt.figure(figsize=(30, 20))

plot_tree(clf.estimators_[0], feature_names = X.columns)
```

Result



Here we can see just the first decision tree that was used to vote on the final prediction. Again, by changing the index of the classifier you can see each of the trees that have been aggregated.

Machine Learning - Cross Validation

Cross Validation

When adjusting models we are aiming to increase overall model performance on unseen data. Hyperparameter tuning can lead to much better performance on test sets. However, optimizing parameters to the test set can lead information leakage causing the model to preform worse on unseen data. To correct for this we can perform cross validation.

To better understand CV, we will be performing different methods on the iris dataset. Let us first load in and separate the data.

```
from sklearn import datasets

X, y = datasets.load_iris(return_X_y=True)
```

There are many methods to cross validation, we will start by looking at k-fold cross validation.

K-Fold

The training data used in the model is split, into k number of smaller sets, to be used to validate the model. The model is then trained on k-1 folds of training set. The remaining fold is then used as a validation set to evaluate the model.

As we will be trying to classify different species of iris flowers we will need to import a classifier model, for this exercise we will be using a DecisionTreeClassifier. We will also need to import CV modules from sklearn.

```
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import KFold, cross_val_score
```

With the data loaded we can now create and fit a model for evaluation.

```
clf = DecisionTreeClassifier(random_state=42)
```

Now let's evaluate our model and see how it performs on each *k*-fold.

```
k_folds = KFold(n_splits = 10)

scores = cross_val_score(clf, X, y, cv = k_folds)
```

It is also good pratice to see how CV performed overall by averaging the scores for all folds.

Example

Run k-fold CV:

```
from sklearn import datasets
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import KFold, cross_val_score
```

```
X, y = datasets.load_iris(return_X_y=True)

clf = DecisionTreeClassifier(random_state=42)

k_folds = KFold(n_splits = 5)

scores = cross_val_score(clf, X, y, cv = k_folds)

print("Cross Validation Scores: ", scores)
print("Average CV Score: ", scores.mean())
print("Number of CV Scores used in Average: ", len(scores))
```

Stratified K-Fold

In cases where classes are imbalanced we need a way to account for the imbalance in both the train and validation sets. To do so we can stratify the target classes, meaning that both sets will have an equal proportion of all classes.

Example

```
from sklearn import datasets
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import StratifiedKFold, cross_val_score

X, y = datasets.load_iris(return_X_y=True)

clf = DecisionTreeClassifier(random_state=42)
sk_folds = StratifiedKFold(n_splits = 5)
scores = cross_val_score(clf, X, y, cv = sk_folds)

print("Cross Validation Scores: ", scores)
print("Average CV Score: ", scores.mean())
print("Number of CV Scores used in Average: ", len(scores))
```

While the number of folds is the same, the average CV increases from the basic k-fold when making sure there is stratified classes.

Leave-One-Out (LOO)

Instead of selecting the number of splits in the training data set like k-fold LeaveOneOut, utilize 1 observation to validate and n-1 observations to train. This method is an exaustive technique.

Example

Run LOO CV:

```
from sklearn import datasets
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import LeaveOneOut, cross_val_score

X, y = datasets.load_iris(return_X_y=True)

clf = DecisionTreeClassifier(random_state=42)

loo = LeaveOneOut()

scores = cross_val_score(clf, X, y, cv = loo)

print("Cross Validation Scores: ", scores)
print("Average CV Score: ", scores.mean())
print("Number of CV Scores used in Average: ", len(scores))
```

We can observe that the number of cross validation scores performed is equal to the number of observations in the dataset. In this case there are 150 observations in the iris dataset.

The average CV score is 94%.

Leave-P-Out (LPO)

Leave-P-Out is simply anuanced diffence to the Leave-One-Out idea, in that we can select the number of p to use in our validation set.

Example

Run LPO CV:

```
from sklearn import datasets
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import LeavePOut, cross_val_score

X, y = datasets.load_iris(return_X_y=True)

clf = DecisionTreeClassifier(random_state=42)

lpo = LeavePOut(p=2)

scores = cross_val_score(clf, X, y, cv = lpo)

print("Cross Validation Scores: ", scores)
print("Average CV Score: ", scores.mean())
print("Number of CV Scores used in Average: ", len(scores))
```

As we can see this is an exhaustive method we many more scores being calculated than Leave-One-Out, even with a p = 2, yet it achieves roughly the same average CV score.

Shuffle Split

Unlike KFold, ShuffleSplit leaves out a percentage of the data, not to be used in the train or validation sets. To do so we must decide what the train and test sizes are, as well as the number of splits.

Example

Run Shuffle Split CV:

```
from sklearn import datasets
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import ShuffleSplit, cross_val_score

X, y = datasets.load_iris(return_X_y=True)

clf = DecisionTreeClassifier(random_state=42)

ss = ShuffleSplit(train_size=0.6, test_size=0.3, n_splits = 5)
```

```
scores = cross_val_score(clf, X, y, cv = ss)

print("Cross Validation Scores: ", scores)
print("Average CV Score: ", scores.mean())
print("Number of CV Scores used in Average: ", len(scores))
```

Ending Notes

These are just a few of the CV methods that can be applied to models. There are many more cross validation classes, with most models having their own class. Check out sklearns cross validation for more CV options.

Machine Learning - AUC - ROC Curve

AUC - ROC Curve

In classification, there are many different evaluation metrics. The most popular is **accuracy**, which measures how often the model is correct. This is a great metric because it is easy to understand and getting the most correct guesses is often desired. There are some cases where you might consider using another evaluation metric.

Another common metric is AUC, area under the receiver operating characteristic (ROC) curve. The Reciever operating characteristic curve plots the true positive (TP) rate versus the false positive (FP) rate at different classification thresholds. The thresholds are different probability cutoffs that separate the two classes in binary classification. It uses probability to tell us how well a model separates the classes.

Imbalanced Data

Suppose we have an imbalanced data set where the majority of our data is of one value. We can obtain high accuracy for the model by predicting the majority class.

Example

```
import numpy as np
from sklearn.metrics import accuracy_score, confusion_matrix, roc_auc_score, roc_curve

n = 10000
```

```
ratio = .95
n_0 = int((1-ratio) * n)
n_1 = int(ratio * n)

y = np.array([0] * n_0 + [1] * n_1)
# below are the probabilities obtained from a hypothetical model that always predicts the majority class
# probability of predicting class 1 is going to be 100%
y_proba = np.array([1]*n)
y_pred = y_proba> .5

print(f'accuracy score: {accuracy_score(y, y_pred)}')
cf_mat = confusion_matrix(y, y_pred)
print('Confusion matrix')
print(cf_mat)
print(f'class 0 accuracy: {cf_mat[0][0]/n_0}')
print(f'class 1 accuracy: {cf_mat[1][1]/n_1}')
```

Although we obtain a very high accuracy, the model provided no information about the data so it's not useful. We accurately predict class 1 100% of the time while inaccurately predict class 0 0% of the time. At the expense of accuracy, it might be better to have a model that can somewhat separate the two classes.

Example

```
# below are the probabilities obtained from a hypothetical model that doesn't always predict the mode
y_proba_2 = np.array(
   np.random.uniform(0, .7, n_0).tolist() +
   np.random.uniform(.3, 1, n_1).tolist()
)
y_pred_2 = y_proba_2 > .5

print(f'accuracy score: {accuracy_score(y, y_pred_2)}')
cf_mat = confusion_matrix(y, y_pred_2)
print('Confusion matrix')
print(cf_mat)
```

```
print(f'class 0 accuracy: {cf_mat[0][0]/n_0}')
print(f'class 1 accuracy: {cf_mat[1][1]/n_1}')
```

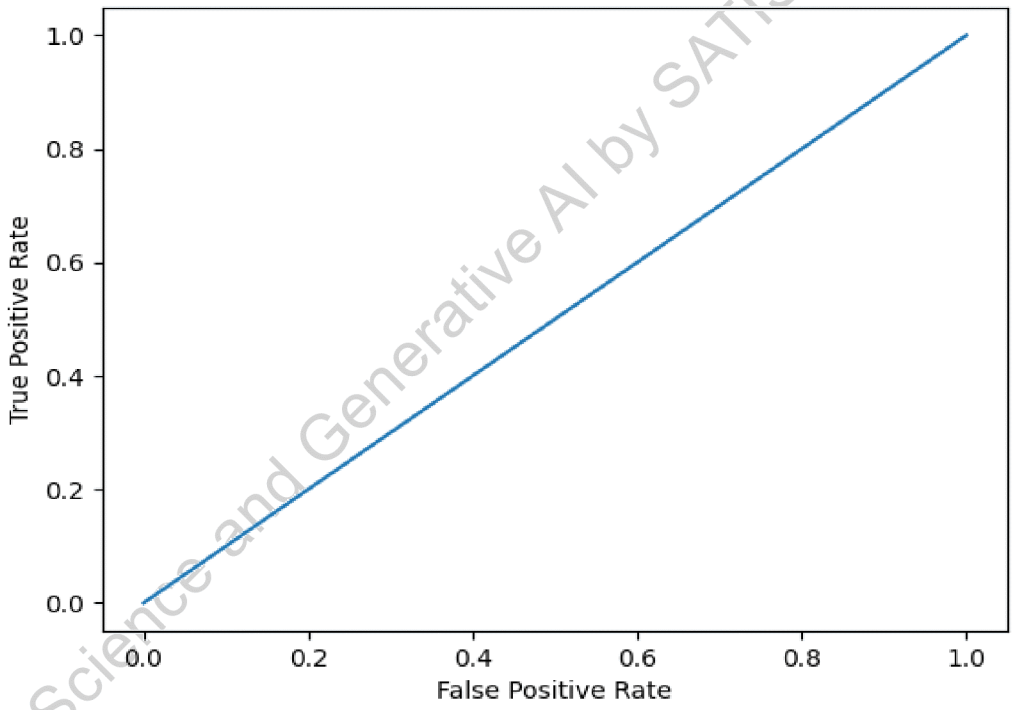
For the second set of predictions, we do not have as high of an accuracy score as the first but the accuracy for each class is more balanced. Using accuracy as an evaluation metric we would rate the first model higher than the second even though it doesn't tell us anything about the data.

```
import matplotlib.pyplot as plt
def plot_roc_curve(true_y, y_prob):
    """
    plots the roc curve based of the probabilities
    """
    fpr, tpr, thresholds = roc_curve(true_y, y_prob)
    plt.plot(fpr, tpr)
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
```

Example

```
plot_roc_curve(y, y_proba)
print(f'model 1 AUC score: {roc_auc_score(y, y_proba)}')
```

Result



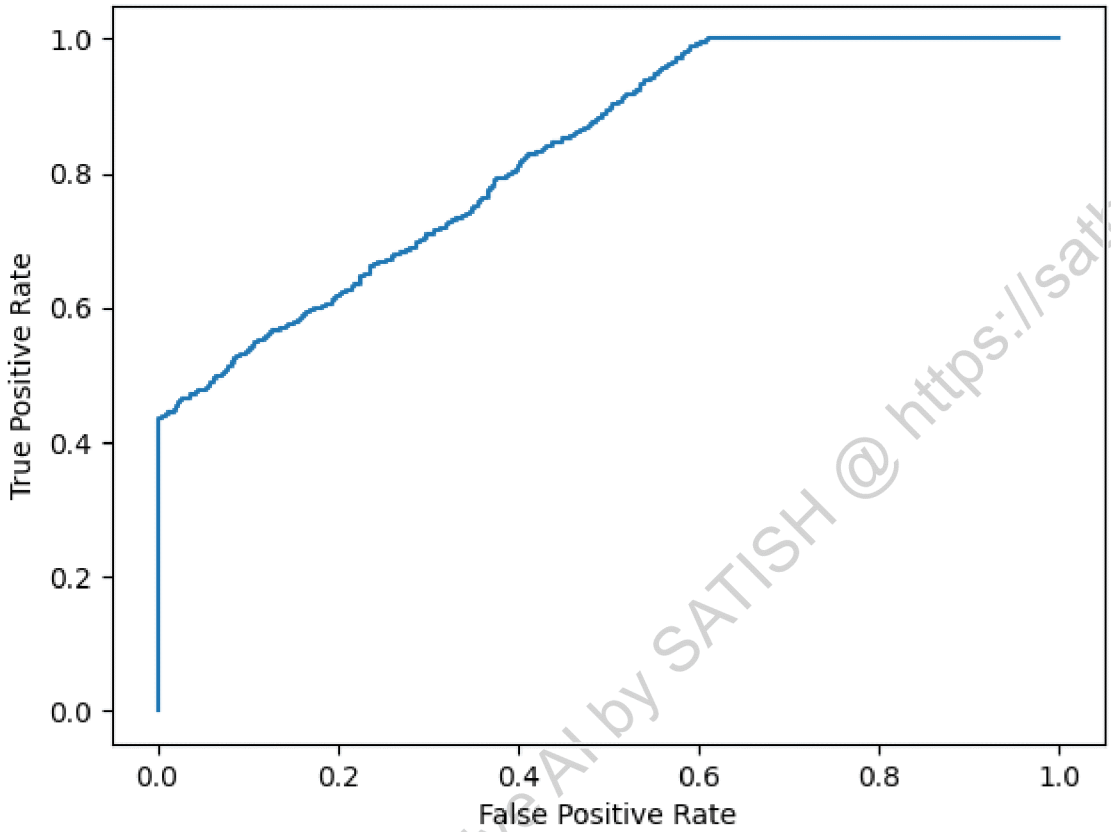
model 1 AUC score: 0.5

Example

Model 2:

```
plot_roc_curve(y, y_proba_2)
print(f'model 2 AUC score: {roc_auc_score(y, y_proba_2)}')
```

Result



model 2 AUC score: 0.8270551578947367

An AUC score of around .5 would mean that the model is unable to make a distinction between the two classes and the curve would look like a line with a slope of 1. An AUC score closer to 1 means that the model has the ability to separate the two classes and the curve would come closer to the top left corner of the graph.

Probabilities

Because AUC is a metric that utilizes probabilities of the class predictions, we can be more confident in a model that has a higher AUC score than one with a lower score even if they have similar accuracies.

In the data below, we have two sets of probabilites from hypothetical models. The first has probabilities that are not as "confident" when predicting the two classes (the probabilities are close to .5). The second has probabilities that are more "confident" when predicting the two classes (the probabilities are close to the extremes of 0 or 1).

Example

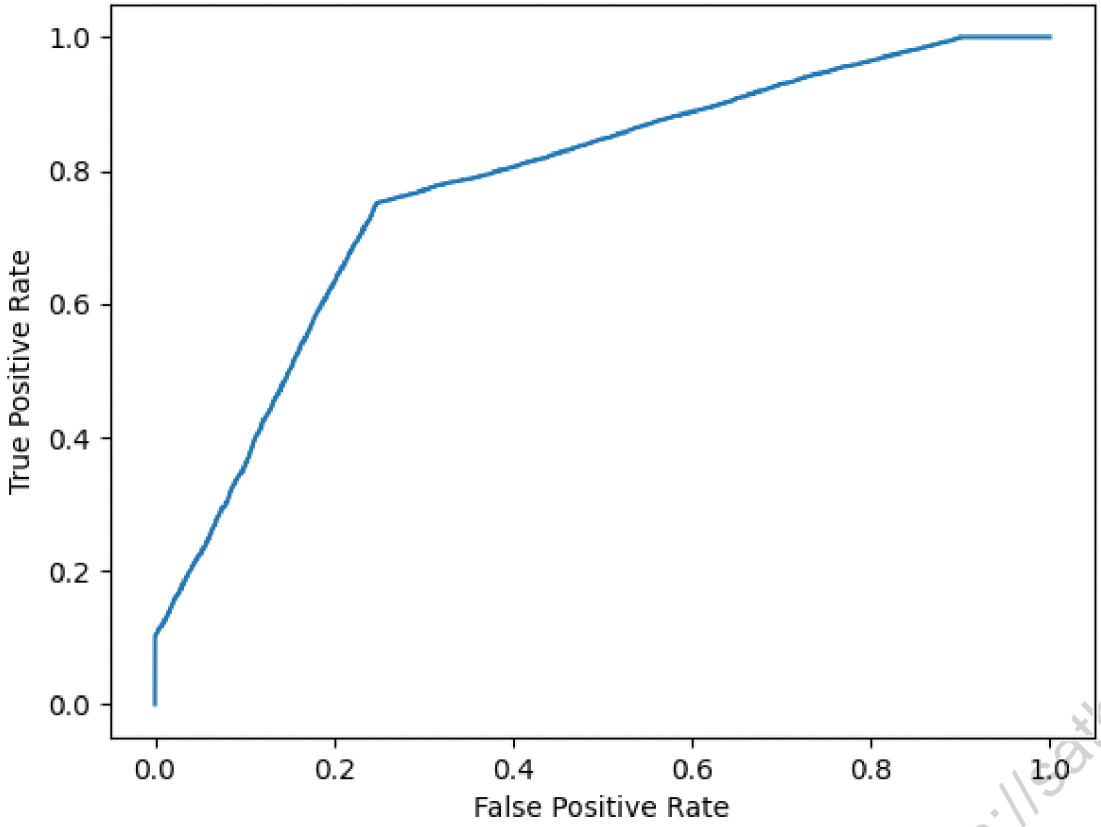
```
import numpy as np

n = 10000
y = np.array([0] * n + [1] * n)
#
y_prob_1 = np.array(
   np.random.uniform(.25, .5, n//2).tolist() +
   np.random.uniform(.3, .7, n).tolist() +
   np.random.uniform(.5, .75, n//2).tolist()
)
y_prob_2 = np.array(
   np.random.uniform(0, .4, n//2).tolist() +
   np.random.uniform(.3, .7, n).tolist() +
   np.random.uniform(.6, 1, n//2).tolist()
)

print(f'model 1 accuracy score: {accuracy_score(y, y_prob_1>.5)}')
print(f'model 2 accuracy score: {accuracy_score(y, y_prob_2>.5)}')

print(f'model 1 AUC score: {roc_auc_score(y, y_prob_1)}')
print(f'model 2 AUC score: {roc_auc_score(y, y_prob_2)}')
```

Example

Plot model 1:

```
plot_roc_curve(y, y_prob_1)
```

Result

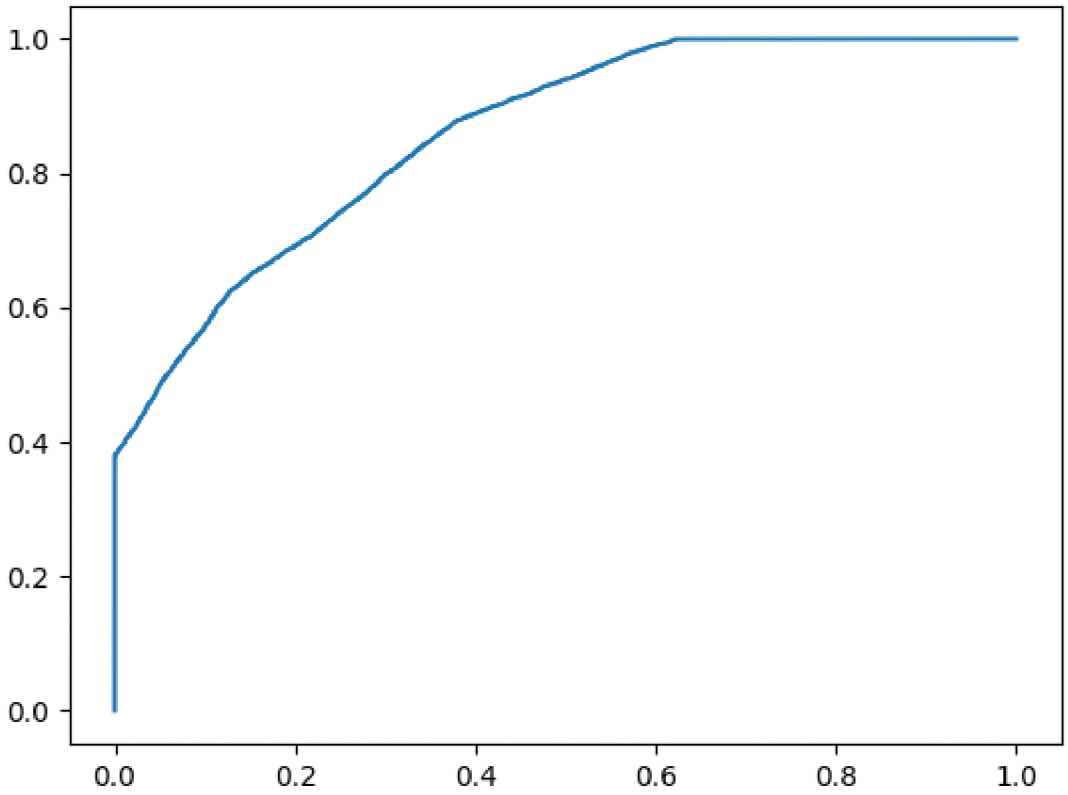


Example

Plot model 2:

```
fpr, tpr, thresholds = roc_curve(y, y_prob_2)
plt.plot(fpr, tpr)
```

Result



Even though the accuracies for the two models are similar, the model with the higher AUC score will be more reliable because it takes into account the predicted probability. It is more likely to give you higher accuracy when predicting future data.

Machine Learning - K-nearest neighbors (KNN)

KNN

KNN is a simple, supervised machine learning (ML) algorithm that can be used for classification or regression tasks - and is also frequently used in missing value imputation. It is based on the idea that the observations closest to a given data point are the most "similar" observations in a data set, and we can therefore classify unforeseen points based on the values of the closest existing points. By choosing *K*, the user can select the number of nearby observations to use in the algorithm.

Here, we will show you how to implement the KNN algorithm for classification, and show how different values of *K* affect the results.

How does it work?

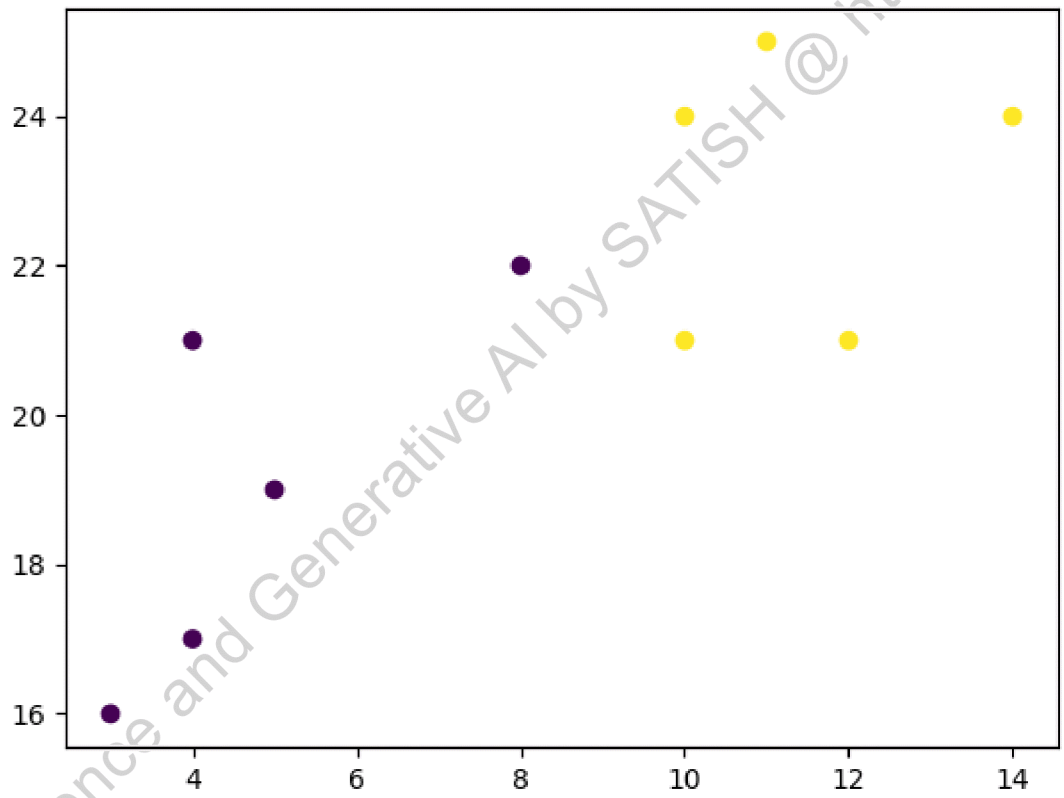
K is the number of nearest neighbors to use. For classification, a majority vote is used to determined which class a new observation should fall into. Larger values of *K* are often more robust to outliers and produce more stable decision boundaries than very small values (*K=3* would be better than *K=1*, which might produce undesirable results.

Example

Start by visualizing some data points:

```
import matplotlib.pyplot as plt

x = [4, 5, 10, 4, 3, 11, 14 , 8, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]
classes = [0, 0, 1, 0, 0, 1, 1, 0, 1, 1]

plt.scatter(x, y, c=classes)
plt.show()
```

Result



Now we fit the KNN algorithm with K=1:

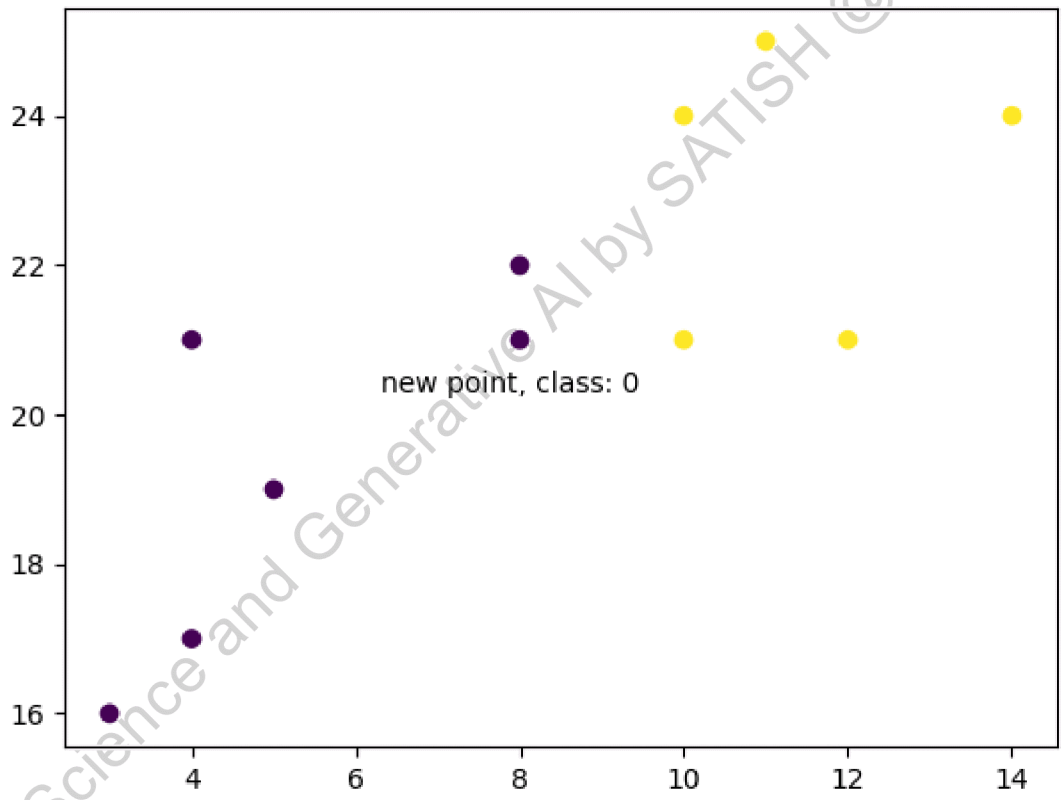
```
from sklearn.neighbors import KNeighborsClassifier

data = list(zip(x, y))
knn = KNeighborsClassifier(n_neighbors=1)
knn.fit(data, classes)
```

And use it to classify a new data point:

Example

```
new_x = 8
new_y = 21
new_point = [(new_x, new_y)]

prediction = knn.predict(new_point)
plt.scatter(x + [new_x], y + [new_y], c=classes + [prediction[0]])
plt.text(x=new_x-1.7, y=new_y-0.7, s=f"new point, class: {prediction[0]}")
plt.show()
```

Result

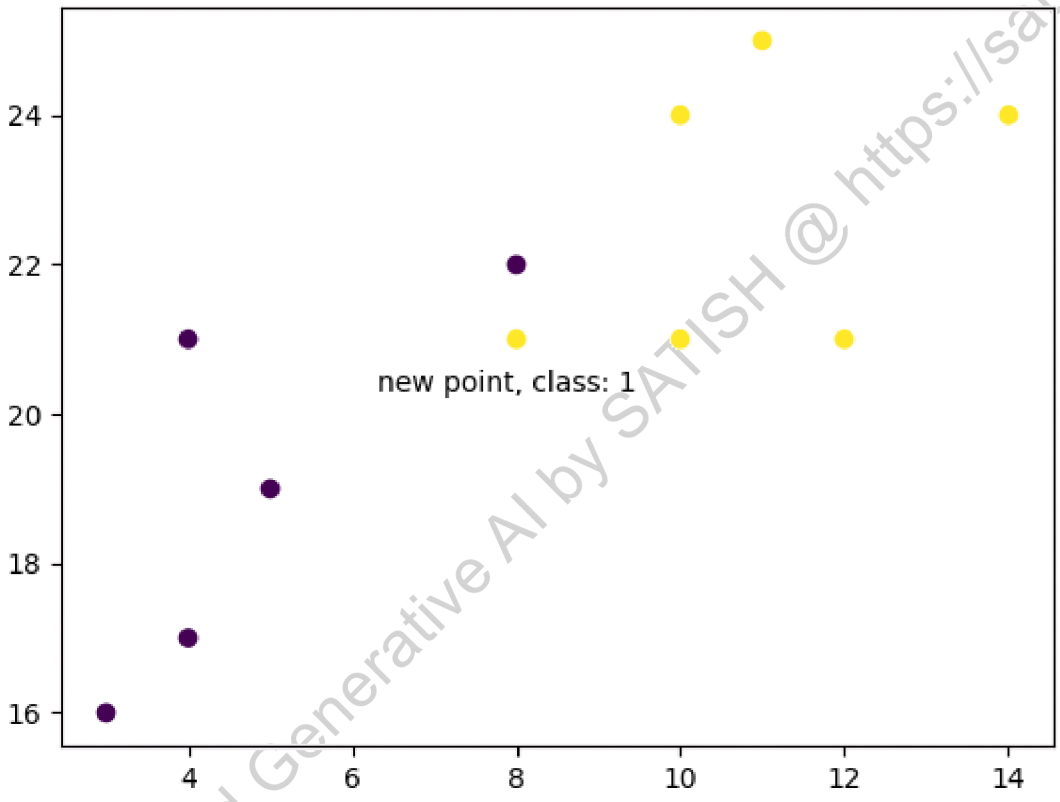


Now we do the same thing, but with a higher K value which changes the prediction:

Example

```
knn = KNeighborsClassifier(n_neighbors=5)

knn.fit(data, classes)

prediction = knn.predict(new_point)

plt.scatter(x + [new_x], y + [new_y], c=classes + [prediction[0]])
plt.text(x=new_x-1.7, y=new_y-0.7, s=f"new point, class: {prediction[0]}")
plt.show()
```

Result



Example Explained

Import the modules you need.

scikit-learn is a popular library for machine learning in Python.

```
import matplotlib.pyplot as plt
from sklearn.neighbors import KNeighborsClassifier
```

Create arrays that resemble variables in a dataset. We have two input features (x and y) and then a target class (class). The input features that are pre-labeled with our target class will be used to predict the class of new data. Note that while we only use two input features here, this method will work with any number of variables:

```
x = [4, 5, 10, 4, 3, 11, 14 , 8, 10, 12]
y = [21, 19, 24, 17, 16, 25, 24, 22, 21, 21]
classes = [0, 0, 1, 0, 0, 1, 1, 0, 1, 1]
```

Turn the input features into a set of points:

```
data = list(zip(x, y))
print(data)
```

Result:

```
[(4, 21), (5, 19), (10, 24), (4, 17), (3, 16), (11, 25), (14, 24), (8, 22), (10, 21), (12, 21)]
```

Using the input features and target class, we fit a KNN model on the model using 1 nearest neighbor:

```
knn = KNeighborsClassifier(n_neighbors=1)
knn.fit(data, classes)
```

Then, we can use the same KNN object to predict the class of new, unforeseen data points. First we create new x and y features, and then call knn.predict() on the new data point to get a class of 0 or 1:

```
new_x = 8
new_y = 21
new_point = [(new_x, new_y)]
prediction = knn.predict(new_point)
print(prediction)
```

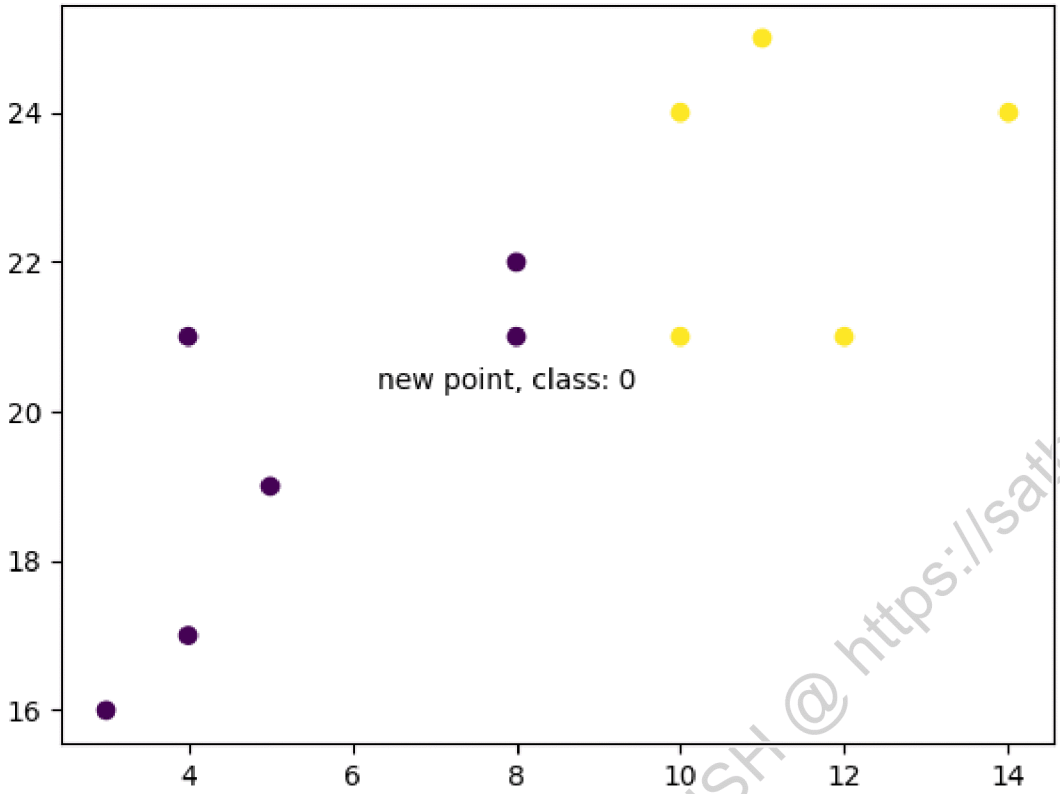
Result:

```
[0]
```

When we plot all the data along with the new point and class, we can see it's been labeled blue with the 1 class. The text annotation is just to highlight the location of the new point:

```
plt.scatter(x + [new_x], y + [new_y], c=classes + [prediction[0]])
plt.text(x=new_x-1.7, y=new_y-0.7, s=f"new point, class: {prediction[0]}")
plt.show()
```

Result:



However, when we changes the number of neighbors to 5, the number of points used to classify our new point changes. As a result, so does the classification of the new point:

```
knn = KNeighborsClassifier(n_neighbors=5)
knn.fit(data, classes)
prediction = knn.predict(new_point)
print(prediction)
```

Result:

[1]

When we plot the class of the new point along with the older points, we note that the color has changed based on the associated class label:

```
plt.scatter(x + [new_x], y + [new_y], c=classes + [prediction[0]])
plt.text(x=new_x-1.7, y=new_y-0.7, s=f"new point, class: {prediction[0]}")
plt.show()
```

Result: