

```
from sklearn import datasets
import pandas as pd
iris=datasets.load_iris()
print(iris)

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'virginica'], dtype='<U10'), 'DESCR': '.. _iris_dataset:\n\nIris
plants dataset\n-----\n\n**Data Set Characteristics:**\n\n
: Number of Instances: 150 (50 in each of three classes)\n
: Number of Attributes: 4 numeric, predictive attributes and the
class\n
: Attribute Information:\n
- sepal length in cm\n
- sepal width in cm\n
- petal length in cm\n
- petal width in cm\n
- class:\n
- Iris-Setosa\n
- Iris-Versicolour\n
- Iris-Virginica\n
\n
: Summary Statistics:\n\n
=====
Mean    SD    Class Correlation\n
=====
sepal length:  4.3  7.9  5.84  0.83
sepal width:   2.0  4.4  3.05  0.43  -0.4194\n
petal length:  1.0  6.9  3.76  1.76  0.9490 (high!)\n
petal width:   0.1  2.5  1.20  0.76  0.9565 (high!)\n
=====
\n
: Missing Attribute Values: None\n
: Class Distribution: 33.3%
for each of 3 classes.\n
: Creator: R.A. Fisher\n
: Donor: Michael
Marshall (MARSHALL%PLU@io.arc.nasa.gov)\n
: Date: July, 1988\n\n
The famous Iris database, first used by Sir R.A. Fisher. The dataset is
taken\nfrom Fisher\'s paper. Note that it\'s the same as in R, but not
as in the UCI\nMachine Learning Repository, which has two wrong data
points.\n\n
This is perhaps the best known database to be found in the\npattern
recognition literature. Fisher\'s paper is a classic in the
field and\nis referenced frequently to this day. (See Duda & Hart,
for example.) The\ndata set contains 3 classes of 50 instances each,
where each class refers to a\ntype of iris plant. One class is
linearly separable from the other 2; the\nlatter are NOT linearly
separable from each other.\n\n
|details-start|\n**References**\n|

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Convert Data set to data frame

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[150 rows x 4 columns]
```

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print(a.head())
print(a.tail())
print(a.describe())
```

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
0	5.1	3.5	1.4	
0.2				
1	4.9	3.0	1.4	
0.2				
2	4.7	3.2	1.3	
0.2				
3	4.6	3.1	1.5	
0.2				
4	5.0	3.6	1.4	
0.2				
	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
145	6.7	3.0	5.2	
2.3				
146	6.3	2.5	5.0	
1.9				
147	6.5	3.0	5.2	
2.0				
148	6.2	3.4	5.4	
2.3				
149	5.9	3.0	5.1	
1.8				
	sepal length (cm)	sepal width (cm)	petal length (cm)	\
count	150.000000	150.000000	150.000000	
mean	5.843333	3.057333	3.758000	
std	0.828066	0.435866	1.765298	
min	4.300000	2.000000	1.000000	
25%	5.100000	2.800000	1.600000	
50%	5.800000	3.000000	4.350000	
75%	6.400000	3.300000	5.100000	
max	7.900000	4.400000	6.900000	
	petal width (cm)			
count	150.000000			
mean	1.199333			
std	0.762238			
min	0.100000			
25%	0.300000			
50%	1.300000			
75%	1.800000			
max	2.500000			
a.min()				
a.max()				
a.mean()				
a.median()				
a.std()				

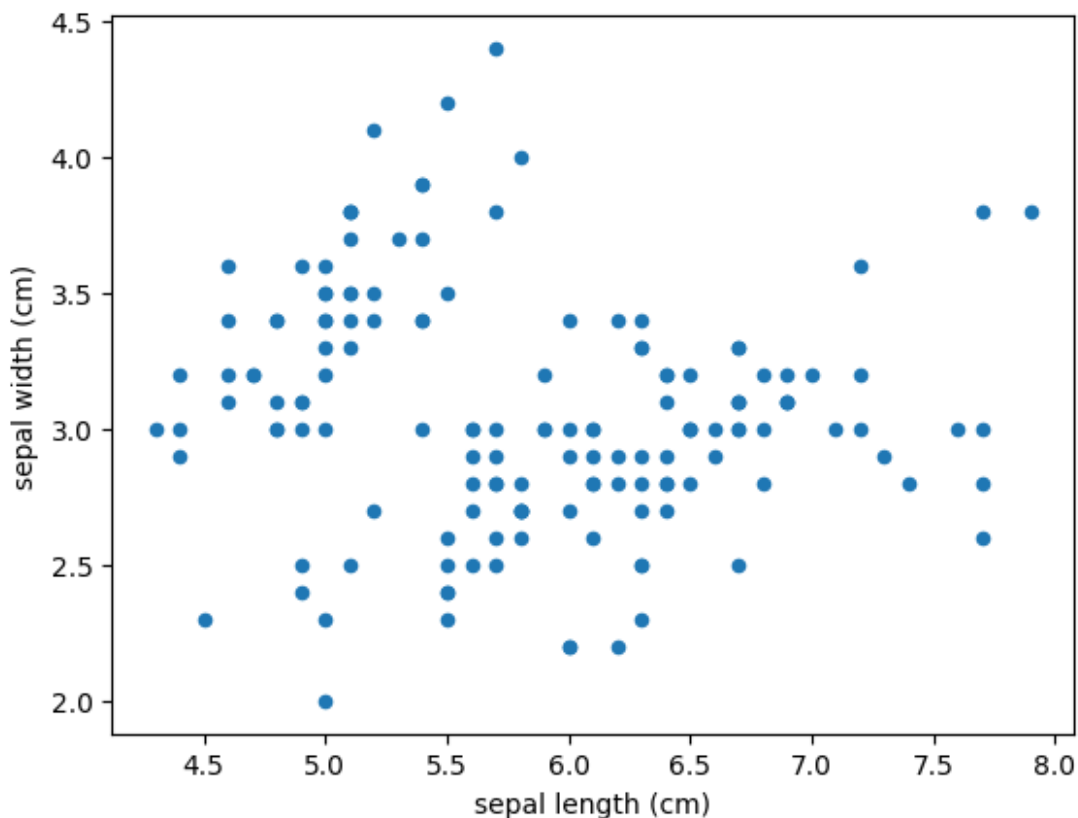
```

sepal length (cm)    0.828066
sepal width (cm)     0.435866
petal length (cm)    1.765298
petal width (cm)     0.762238
dtype: float64

import matplotlib.pyplot as plt
#a.plot(x='sepal length (cm)',y='sepal width (cm)',kind='scatter')

<Axes: xlabel='sepal length (cm)', ylabel='sepal width (cm)'>

```



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d=datasets.load_diabetes()
print(d)

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                0.00286131, -0.02593034],
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                -0.04688253,  0.01549073],

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258., 219., 72., 201., 110., 51., 277., 63., 118., 69., 273.,
72., 43., 198., 242., 232., 175., 93., 168., 275., 293., 281.,
55., 140., 189., 181., 209., 136., 261., 113., 131., 174., 257.,
310., 84., 42., 146., 212., 233., 91., 111., 152., 120., 67.,
132., 94., 183., 66., 173., 72., 49., 64., 48., 178., 104.,

```

```

220., 57.])), 'frame': None, 'DESCR': '.._diabetes_dataset:\n\
nDiabetes dataset\n-----\n\nTen baseline variables, age,
sex, body mass index, average blood\npressure, and six blood serum
measurements were obtained for each of n =\n442 diabetes patients, as
well as the response of interest, a\nquantitative measure of disease
progression one year after baseline.\n\n**Data Set Characteristics:**\
\n\n :Number of Instances: 442\n\n :Number of Attributes: First 10
columns are numeric predictive values\n\n :Target: Column 11 is a
quantitative measure of disease progression one year after baseline\n\
n :Attribute Information:\n      - age      age in years\n      - sex\n      - bmi      body mass index\n      - bp      average blood
pressure\n      - s1      tc, total serum cholesterol\n      - s2
ldl, low-density lipoproteins\n      - s3      hdl, high-density
lipoproteins\n      - s4      tch, total cholesterol / HDL\n      - s5
ltg, possibly log of serum triglycerides level\n      - s6      glu,

```

blood sugar level\n\nNote: Each of these 10 feature variables have been mean centered and scaled by the standard deviation times the square root of `n_samples` (i.e. the sum of squares of each column totals 1).\n\nSource
URL:\n<https://www4.stat.ncsu.edu/~boos/var.select/diabetes.html>\n\nFor more information see:\nBradley Efron, Trevor Hastie, Iain Johnstone and Robert Tibshirani (2004) "Least Angle Regression," Annals of Statistics (with discussion), 407-499.\n(https://web.stanford.edu/~hastie/Papers/LARS/LeastAngle_2002.pdf)\n', 'feature_names': ['age', 'sex', 'bmi', 'bp', 's1', 's2', 's3', 's4', 's5', 's6'], 'data_filename': 'diabetes_data_raw.csv.gz', 'target_filename': 'diabetes_target.csv.gz', 'data_module': 'sklearn.datasets.data'}

MATRIX

```
import numpy as np
a=np.array([[12,45],[23,98]])
print(a)
b=np.array([[35,78],[34,65]])
print(b)
print("ADDITION")
print(np.add(a,b))
print("SUBTRACTION")
print(np.subtract(a,b))
print("MULTIPLICATION")
print(np.multiply(a,b))
print("DIVISION")
print(np.divide(a,b))
```

```
[[12 45]
 [23 98]]
[[35 78]
 [34 65]]
ADDITION
[[ 47 123]
 [ 57 163]]
SUBTRACTION
[[-23 -33]
 [-11  33]]
MULTIPLICATION
[[ 420 3510]
 [ 782 6370]]
DIVISION
[[0.34285714 0.57692308]
 [0.67647059 1.50769231]]
```

```
import pandas as pd
df=pd.DataFrame([[101,'Aliya',59,90,89],[102,'Berna',90,87,67],
```

```
[103,'Celina',90,87,45],[104,'Dalini',90,56,78],
[105,'Elisa',89,78,68]],columns=['Roll
No','Name','Mark1','Mark2','Mark3'])
print(df)
```

	Roll No	Name	Mark1	Mark2	Mark3
0	101	Aliya	59	90	89
1	102	Berna	90	87	67
2	103	Celina	90	87	45
3	104	Dalini	90	56	78
4	105	Elisa	89	78	68

```
print(df.loc[0:3])
print(df.iloc[0:3,1:3])
print(df.iloc[0:3])
```

	Roll No	Name	Mark1	Mark2	Mark3
0	101	Aliya	59	90	89
1	102	Berna	90	87	67
2	103	Celina	90	87	45
3	104	Dalini	90	56	78

	Name	Mark1
0	Aliya	59
1	Berna	90
2	Celina	90

	Roll No	Name	Mark1	Mark2	Mark3
0	101	Aliya	59	90	89
1	102	Berna	90	87	67
2	103	Celina	90	87	45

LINEAR EQUATION

```
import pandas as pd
import numpy as np
a=np.array([[1,1],[1,-1]])
print(a)
b=np.array([2,0])
print(b)
r=np.linalg.solve(a,b)
print(r)

[[ 1  1]
 [ 1 -1]]
[2 0]
[1. 1.]

import pandas as pd
import numpy as np
a=np.array([[1,1,1],[1,-1,1],[-1,-1,1]])
print(a)
```

```

b=np.array([6,2,3])
print(b)
r=np.linalg.solve(a,b)
print(r)

[[ 1  1  1]
 [ 1 -1  1]
 [-1 -1  1]]
[6 2 3]
[-0.5  2.  4.5]

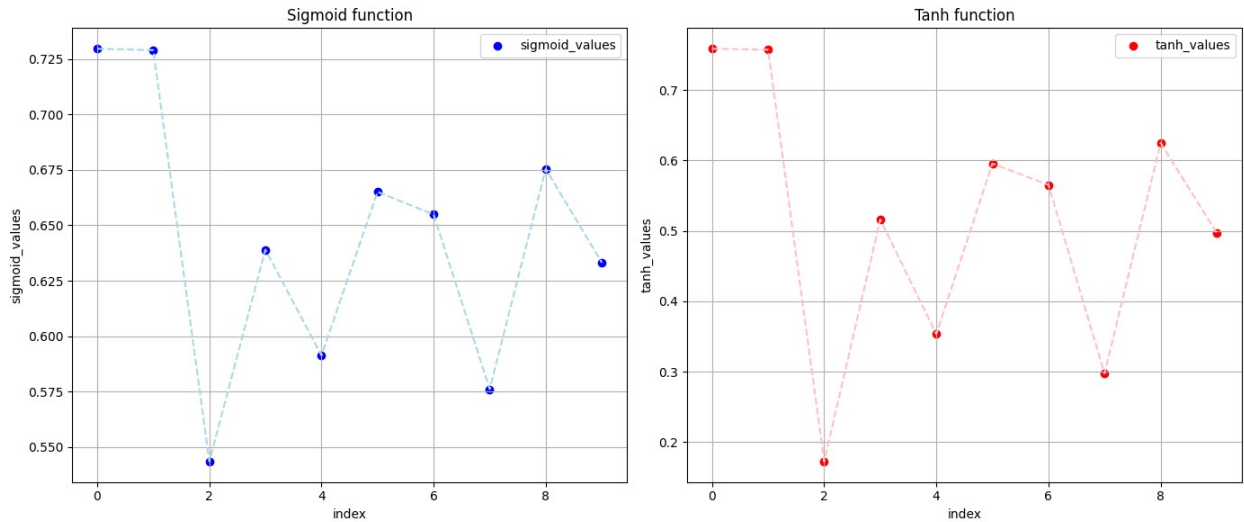
```

Sigmoid and tanh

```

import numpy as np
import matplotlib.pyplot as plt
def sigmoid(x):
    return 1/(1+np.exp(-x))
def tanh(x):
    return np.tanh(x)
random_values=np.random.rand(10)
sigmoid_values=sigmoid(random_values)
tanh_values=tanh(random_values)
indices=np.arange(len(random_values))
plt.figure(figsize=(14,6))
plt.subplot(1,2,1)
plt.scatter(indices,sigmoid_values,color='blue',label='sigmoid_values')
plt.plot(indices,sigmoid_values,color='lightblue',linestyle='--')
plt.title('Sigmoid function')
plt.xlabel('index')
plt.ylabel('sigmoid_values')
plt.grid(True)
plt.legend()
plt.subplot(1,2,2)
plt.scatter(indices,tanh_values,color='red',label='tanh_values')
plt.plot(indices,tanh_values,color='pink',linestyle='--')
plt.title('Tanh function')
plt.xlabel('index')
plt.ylabel('tanh_values')
plt.grid(True)
plt.legend()
plt.tight_layout()
plt.show()

```

Build in data set

```
from sklearn import datasets
import pandas as pd
iris=datasets.load_iris()
print(iris)
print("\ntype:\n",type(iris))
print("\nkeys:\n",iris.keys())
print("\ntype of data and target:\n",type(iris.data), type
(iris.target))
print("\ndata shape:\n",iris.data.shape)
print("\ntarget names:\n",iris.target_names)
X = iris.data
Y = iris.target
df = pd.DataFrame(X, columns=iris.feature_names)
print("\nIris dataframe:\n", df.head())
print("-----\n")
diabetes = datasets.load_diabetes()
print("\ndiabetes dataset:\n", diabetes);
X = diabetes.data
Y = diabetes.target
df = pd.DataFrame(X, columns=diabetes.feature_names)
print("\nDiabetes dataframe:\n",df.head())
print("-----\n")
data = datasets.load_breast_cancer()
label_names = data['target_names']
labels = data['target']
feature_names = data['feature_names']
features= data['data']
print("Breast Cancer data:\n", data);
print("\nLabel names:\n", label_names)
print("\nLabels:\n", labels)
```

```
print("\nFeature names:\n", feature_names)
print("\nFeatures:\n", features)
```

```
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'frame': None, 'target_names': array(['setosa', 'versicolor',
'virginica'], dtype='<U10'), 'DESCR': '.. _iris_dataset:\n\nIris
plants dataset\n-----\n\n**Data Set Characteristics:**\n\n:
Number of Instances: 150 (50 in each of three classes)\n:
Number of Attributes: 4 numeric, predictive attributes and the class\n:
Attribute Information:\n    - sepal length in cm\n    - sepal width in cm\n    -
petal length in cm\n    - petal width in cm\n    - class:\n    - Iris-Setosa\n    - Iris-Versicolour\n    - Iris-Virginica\n\n:
Summary Statistics:\n\n=====
=====
=====
=====
Min    Max    Mean    SD
Class Correlation\n=====
=====
=====
=====
\nsepal length:    4.3  7.9    5.84    0.83
0.7826\nsepal width:    2.0  4.4    3.05    0.43    -0.4194\npetal
length:    1.0  6.9    3.76    1.76    0.9490 (high!)\npetal width:
0.1  2.5    1.20    0.76    0.9565 (high!)\n=====
=====
=====
=====
\n\n:Missing Attribute Values: None\n\n:
Class Distribution: 33.3% for each of 3 classes.\n:
Creator: R.A. Fisher\n:
Donor: Michael Marshall (MARSHALL%PLU@io.arc.nasa.gov)\n\n:
Date: July, 1988\n\nThe famous Iris database, first used by Sir R.A.
Fisher. The dataset is taken\nfrom Fisher\'s paper. Note that it\'s
the same as in R, but not as in the UCI\nMachine Learning Repository,
which has two wrong data points.\n\nThis is perhaps the best known
database to be found in the\npattern recognition literature.
Fisher\'s paper is a classic in the field and\nis referenced
frequently to this day. (See Duda & Hart, for example.) The\ndata
set contains 3 classes of 50 instances each, where each class refers
to a\ntype of iris plant. One class is linearly separable from the
other 2; the\nlatter are NOT linearly separable from each other.\n\n..
dropdown:: References\n\n    - Fisher, R.A. "The use of multiple
measurements in taxonomic problems"\n        Annual Eugenics, 7, Part II,
179-188 (1936); also in "Contributions to\n        Mathematical
Statistics" (John Wiley, NY, 1950).\n    - Duda, R.O., & Hart, P.E.
(1973) Pattern Classification and Scene Analysis.\n        (Q327.D83) John
Wiley & Sons. ISBN 0-471-22361-1. See page 218.\n    - Dasarthy, B.V.
(1980) "Nosing Around the Neighborhood: A New System\n        Structure

```

and Classification Rule for Recognition in Partially Exposed\n
 Environments". IEEE Transactions on Pattern Analysis and Machine\n
 Intelligence, Vol. PAMI-2, No. 1, 67-71.\n - Gates, G.W. (1972) "The
 Reduced Nearest Neighbor Rule". IEEE Transactions\n on Information
 Theory, May 1972, 431-433.\n - See also: 1988 MLC Proceedings, 54-64.
 Cheeseman et al"s AUTOCLASS II\n conceptual clustering system finds
 3 classes in the data.\n - Many, many more ...'\n', 'feature_names':
 ['sepal length (cm)', 'sepal width (cm)', 'petal length (cm)', 'petal
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 'sklearn.datasets.data'}

type:
 <class 'sklearn.utils._bunch.Bunch'>

keys:
 dict_keys(['data', 'target', 'frame', 'target_names', 'DESCR',
 'feature_names', 'filename', 'data_module'])

type of data and target:
 <class 'numpy.ndarray'> <class 'numpy.ndarray'>

data shape:
 (150, 4)

target names:
 ['setosa' 'versicolor' 'virginica']

Iris dataframe:

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
0	5.1	3.5	1.4	
0.2				
1	4.9	3.0	1.4	
0.2				
2	4.7	3.2	1.3	
0.2				
3	4.6	3.1	1.5	
0.2				
4	5.0	3.6	1.4	
0.2				

diabetes dataset:
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 -0.06833155, -0.09220405],
 [0.08529891, 0.05068012, 0.04445121, ..., -0.00259226,

```
0.00286131, -0.02593034],
...,
[ 0.04170844,  0.05068012, -0.01590626, ..., -0.01107952,
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    94., 283., 64., 102., 200., 265., 94., 230., 181., 156.,
233.,
    60., 219., 80., 68., 332., 248., 84., 200., 55., 85.,
89.,
    31., 129., 83., 275., 65., 198., 236., 253., 124., 44.,
172.,
    114., 142., 109., 180., 144., 163., 147., 97., 220., 190.,
109.,
    191., 122., 230., 242., 248., 249., 192., 131., 237., 78.,
135.,
    244., 199., 270., 164., 72., 96., 306., 91., 214., 95.,
216.,
    263., 178., 113., 200., 139., 139., 88., 148., 88., 243.,
71.,
    77., 109., 272., 60., 54., 221., 90., 311., 281., 182.,
321.,
    58., 262., 206., 233., 242., 123., 167., 63., 197., 71.,
168.,
    140., 217., 121., 235., 245., 40., 52., 104., 132., 88.,
69.,
    219., 72., 201., 110., 51., 277., 63., 118., 69., 273.,
258.,
    43., 198., 242., 232., 175., 93., 168., 275., 293., 281.,
72.,
    140., 189., 181., 209., 136., 261., 113., 131., 174., 257.,
55.,
    84., 42., 146., 212., 233., 91., 111., 152., 120., 67.,
310.,
    94., 183., 66., 173., 72., 49., 64., 48., 178., 104.,
132.,
    220., 57.] ), 'frame': None, 'DESCR': '.._diabetes_dataset:\n
nDiabetes dataset\n-----\n\nTen baseline variables, age,
sex, body mass index, average blood\npressure, and six blood serum
measurements were obtained for each of n =\n442 diabetes patients, as
well as the response of interest, a\nquantitative measure of disease
progression one year after baseline.\n\n**Data Set Characteristics:**\n
n\nNumber of Instances: 442\n\nNumber of Attributes: First 10
columns are numeric predictive values\n\nTarget: Column 11 is a
quantitative measure of disease progression one year after baseline\n
n\nAttribute Information:\n    - age      age in years\n    - sex\n    - bmi      body mass index\n    - bp      average blood pressure\n    - s1      tc, total serum cholesterol\n    - s2      ldl, low-density
lipoproteins\n    - s3      hdl, high-density lipoproteins\n    - s4

```


tch, total cholesterol / HDL\n - s5 ltg, possibly log of serum triglycerides level\n - s6 glu, blood sugar level\n\nNote: Each of these 10 feature variables have been mean centered and scaled by the standard deviation times the square root of `n_samples` (i.e. the sum of squares of each column totals 1).\n\nSource URL:\n<https://www4.stat.ncsu.edu/~boos/var.select/diabetes.html>\n\nFor more information see:\nBradley Efron, Trevor Hastie, Iain Johnstone and Robert Tibshirani (2004) "Least Angle Regression," Annals of Statistics (with discussion), 407-499.\n(https://web.stanford.edu/~hastie/Papers/LARS/LeastAngle_2002.pdf)\n', 'feature_names': ['age', 'sex', 'bmi', 'bp', 's1', 's2', 's3', 's4', 's5', 's6'], 'data_filename': 'diabetes_data_raw.csv.gz', 'target_filename': 'diabetes_target.csv.gz', 'data_module': 'sklearn.datasets.data'}

Diabetes dataframe:

	age	sex	bmi	bp	s1	s2
s3 \						
0	0.038076	0.050680	0.061696	0.021872	-0.044223	-0.034821
0.043401						
1	-0.001882	-0.044642	-0.051474	-0.026328	-0.008449	-0.019163
0.074412						
2	0.085299	0.050680	0.044451	-0.005670	-0.045599	-0.034194
0.032356						
3	-0.089063	-0.044642	-0.011595	-0.036656	0.012191	0.024991
0.036038						
4	0.005383	-0.044642	-0.036385	0.021872	0.003935	0.015596
0.008142						

	s4	s5	s6
0	-0.002592	0.019907	-0.017646
1	-0.039493	-0.068332	-0.092204
2	-0.002592	0.002861	-0.025930
3	0.034309	0.022688	-0.009362
4	-0.002592	-0.031988	-0.046641

Breast Cancer data:

```
{'data': array([[1.799e+01, 1.038e+01, 1.228e+02, ..., 2.654e-01,
4.601e-01,
1.189e-01],
[2.057e+01, 1.777e+01, 1.329e+02, ..., 1.860e-01, 2.750e-01,
8.902e-02],
[1.969e+01, 2.125e+01, 1.300e+02, ..., 2.430e-01, 3.613e-01,
8.758e-02],
...,
[1.660e+01, 2.808e+01, 1.083e+02, ..., 1.418e-01, 2.218e-01,
7.820e-02],
[2.060e+01, 2.933e+01, 1.401e+02, ..., 2.650e-01, 4.087e-01,
1.240e-01],
```



```

1,
    1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1]),
'frame': None, 'target_names': array(['malignant', 'benign'],
dtype='<U9'), 'DESCR': '.. _breast_cancer_dataset:\n\nBreast cancer
wisconsin (diagnostic) dataset\
n-----\n\n**Data Set
Characteristics:**\n\n: Number of Instances: 569\n\n: Number of
Attributes: 30 numeric, predictive attributes and the class\n\n
: Attribute Information:\n    - radius (mean of distances from center
to points on the perimeter)\n    - texture (standard deviation of
gray-scale values)\n    - perimeter\n    - area\n    - smoothness
(local variation in radius lengths)\n    - compactness (perimeter^2 /
area - 1.0)\n    - concavity (severity of concave portions of the
contour)\n    - concave points (number of concave portions of the
contour)\n    - symmetry\n    - fractal dimension ("coastline
approximation" - 1)\n\n    The mean, standard error, and "worst" or
largest (mean of the three\n    worst/largest values) of these
features were computed for each image,\n    resulting in 30 features.
For instance, field 0 is Mean Radius, field\n    10 is Radius SE,
field 20 is Worst Radius.\n\n    - class:\n    - WDBC-
Malignant\n    - WDBC-Benign\n\n: Summary Statistics:\n
n===== \n
Min    Max\n===== \n
nradius (mean):                6.981  28.11\ntexture (mean):
9.71  39.28\nnperimeter (mean):                43.79  188.5\nnarea
(mean):                143.5  2501.0\nnsmoothness (mean):
0.053  0.163\nncompactness (mean):                0.019  0.345\
nconcavity (mean):                0.0  0.427\nnconcave points
(mean):                0.0  0.201\nnsymmetry (mean):
0.106  0.304\nnfractal dimension (mean):                0.05  0.097\
nradius (standard error):                0.112  2.873\ntexture (standard
error):                0.36  4.885\nnperimeter (standard error):
0.757  21.98\nnarea (standard error):                6.802  542.2\
nsmoothness (standard error):                0.002  0.031\nncompactness
(standard error):                0.002  0.135\nnconcavity (standard error):
0.0  0.396\nnconcave points (standard error):                0.0  0.053\
nsymmetry (standard error):                0.008  0.079\nnfractal dimension
(standard error):                0.001  0.03\nnradius (worst):
7.93  36.04\ntexture (worst):                12.02  49.54\
nperimeter (worst):                50.41  251.2\nnarea (worst):
185.2  4254.0\nnsmoothness (worst):                0.071  0.223\
ncompactness (worst):                0.027  1.058\nnconcavity
(worst):                0.0  1.252\nnconcave points (worst):
0.0  0.291\nnsymmetry (worst):                0.156  0.664\
nfractal dimension (worst):                0.055  0.208\
n===== \n\n: Missing
Attribute Values: None\n\n: Class Distribution: 212 - Malignant, 357 -
Benign\n\n: Creator: Dr. William H. Wolberg, W. Nick Street, Olvi L.
Mangasarian\n\n: Donor: Nick Street\n\n: Date: November, 1995\n\n\nThis is
a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.\

```

<https://goo.gl/U2Uwz2>

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

Separating plane described above was obtained using Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree Construction Via Linear Programming." Proceedings of the 4th Midwest Artificial Intelligence and Cognitive Science Society, pp. 97-101, 1992], a classification method which uses linear programming to construct a decision tree. Relevant features were selected using an exhaustive search in the space of 1-4 features and 1-3 separating planes.

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

This database is also available through the UW CS ftp server: <ftp://ftp.cs.wisc.edu/ncd/math-prog/cpo-dataset/machine-learning/WDBC/>

References:

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

```

'feature_names': array(['mean radius', 'mean texture', 'mean
perimeter', 'mean area',
                        'mean smoothness', 'mean compactness', 'mean concavity',
                        'mean concave points', 'mean symmetry', 'mean fractal
dimension',
                        'radius error', 'texture error', 'perimeter error', 'area
error',
                        'smoothness error', 'compactness error', 'concavity error',
                        'concave points error', 'symmetry error',
                        'fractal dimension error', 'worst radius', 'worst texture',
                        'worst perimeter', 'worst area', 'worst smoothness',
                        'worst compactness', 'worst concavity', 'worst concave points',
                        'worst symmetry', 'worst fractal dimension'], dtype='<U23'),
'filename': 'breast_cancer.csv', 'data_module':
'sklearn.datasets.data'}
  
```

Label names:
 ['malignant' 'benign']

Labels:

```

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

```

1 0 1 0 0 1 1 1 0 0 1 0 0 0 1 1 1 0 1 1 0 0 1 1 1 0 0 1 1 1 1 0 1 1 0
1 1
1 1 1 1 1 1 0 0 0 1 0 0 1 1 1 0 0 1 0 1 0 0 1 0 0 1 1 0 1 1 0 1 1 1 1
0 1
1 1 1 1 1 1 1 1 0 1 1 1 1 0 0 1 0 1 1 0 0 1 1 0 0 1 1 1 1 0 1 1 0 0 0
1 0
1 0 1 1 1 0 1 1 0 0 1 0 0 0 0 1 0 0 0 1 0 1 0 1 1 0 1 0 0 0 0 1 1 0 0
1 1
1 0 1 1 1 1 1 0 0 1 1 0 1 1 0 0 1 0 1 1 1 1 0 1 1 1 1 1 0 1 0 0 0 0 0
0 0
0 0 0 0 0 0 0 1 1 1 1 1 1 0 1 0 1 1 0 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1
1 1
1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 0 1 0 1 1 1 1 0 0 0
1 1
1 1 0 1 0 1 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 0 0 1
0 0
0 1 0 0 1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 0 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1
1 1
1 0 1 1 1 1 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 1 1 1 1 0
1 1
0 1 0 1 1 0 1 0 1 1 1 1 1 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1
0 1
1 1 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 0 0 1 0 1 0 1 1 1 1 1 0 1 1 0 1 0 1
0 0
1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1
1 1 1 1 1 1 1 0 0 0 0 0 0 1]

```

Feature names:

```

['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
 'worst smoothness' 'worst compactness' 'worst concavity'
 'worst concave points' 'worst symmetry' 'worst fractal dimension']

```

Features:

```

[[1.799e+01 1.038e+01 1.228e+02 ... 2.654e-01 4.601e-01 1.189e-01]
 [2.057e+01 1.777e+01 1.329e+02 ... 1.860e-01 2.750e-01 8.902e-02]
 [1.969e+01 2.125e+01 1.300e+02 ... 2.430e-01 3.613e-01 8.758e-02]
 ...
 [1.660e+01 2.808e+01 1.083e+02 ... 1.418e-01 2.218e-01 7.820e-02]
 [2.060e+01 2.933e+01 1.401e+02 ... 2.650e-01 4.087e-01 1.240e-01]
 [7.760e+00 2.454e+01 4.792e+01 ... 0.000e+00 2.871e-01 7.039e-02]]

```

Decision tree

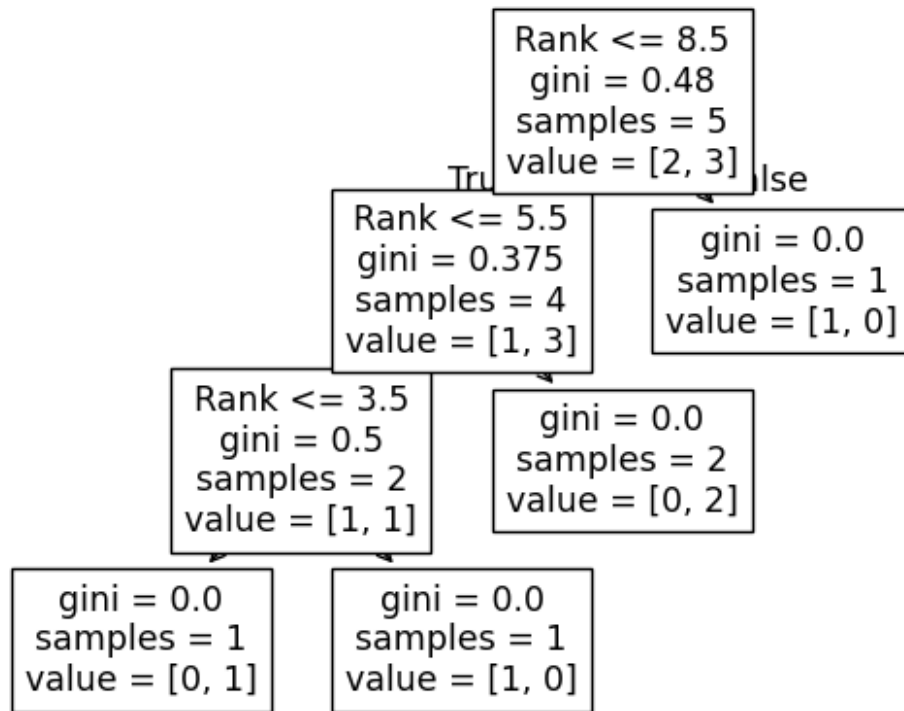
```

import pandas as pd
data = {
    'Age': [25, 30, 35, 40, 45],
    'Experience': [1, 3, 5, 10, 15],
    'Rank': [3, 4, 7, 9, 8],
    'Nationality': ['UK', 'USA', 'N', 'UK', 'USA'],
    'Go': ['YES', 'NO', 'YES', 'NO', 'YES']
}
df = pd.DataFrame(data)
df.to_csv('decision_tree.csv', index=False)

import matplotlib.pyplot as plt
import pandas
from sklearn import tree
from sklearn.tree import DecisionTreeClassifier
import matplotlib.pyplot as plt
df = pandas.read_csv("decision_tree.csv")
print(df)
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)
plt.show()

```

	Age	Experience	Rank	Nationality	Go
0	25	1	3	UK	YES
1	30	3	4	USA	NO
2	35	5	7	N	YES
3	40	10	9	UK	NO
4	45	15	8	USA	YES

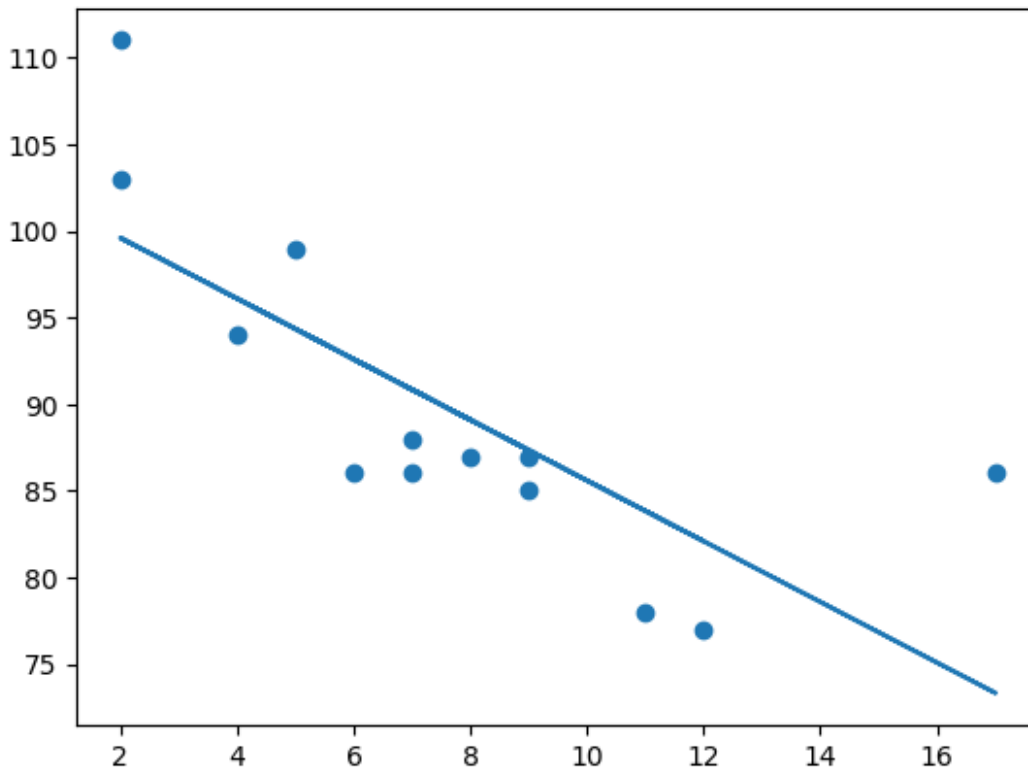


Linear Regression

```

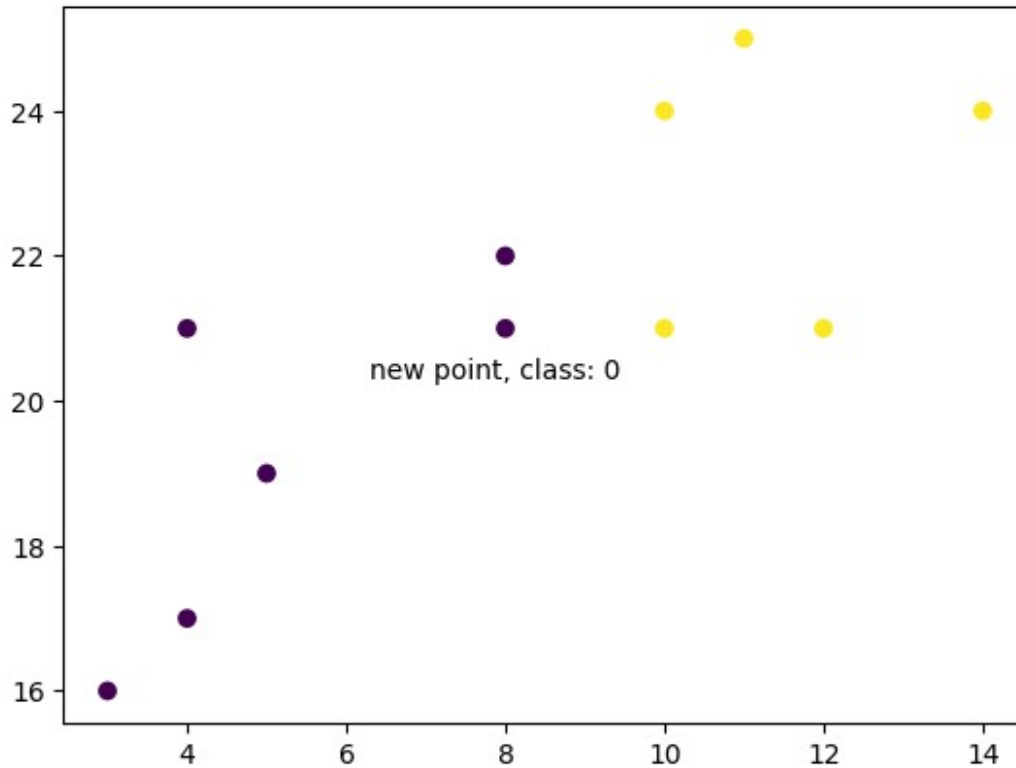
import matplotlib.pyplot as plt
from scipy import stats
x= [5,7,8,7,2,17,2,9,4,11,12,9,6]
y = [99,86,87,88,111,86,103,87,94,78,77,85,86]
slope, intercept, r, p, std_err = stats.linregress(x, y)
def myfunc(x):
    return slope *x + intercept
mymodel = list(map(myfunc, x))
plt.scatter(x, y)
plt.plot(x, mymodel)
plt.show()

```



K Nearest Neighbour

```
import matplotlib.pyplot as plt
from sklearn.neighbors import KNeighborsClassifier
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]
data = list(zip(x, y))
knn = KNeighborsClassifier(n_neighbors=1)
knn.fit(data, classes)
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()
```

Unsupervised Learning

Clustering

```
#Importing Modules
from sklearn import datasets
import matplotlib.pyplot as plt
# Loading dataset
iris_df = datasets.load_iris()
# Available methods on dataset
print("Methods:\n",dir(iris_df))
# Features
print("\nFeatures:\n",iris_df.feature_names)
# Targets
print("\nTargets: \n", iris_df.target)
#Target Names
print("\nTarget names:\n",iris_df.target_names)
label = {0: 'red', 1: 'blue', 2: 'green'}
# Dataset Slicing
x_axis = iris_df.data[:, 0] # Sepal Length
y_axis = iris_df.data[:, 2] # Sepal Width
# Plotting
plt.scatter(x_axis, y_axis, c=iris_df.target)
plt.show()
```

Methods:

```
['DESCR', 'data', 'data_module', 'feature_names', 'filename',  
'frame', 'target', 'target_names']
```

Features:

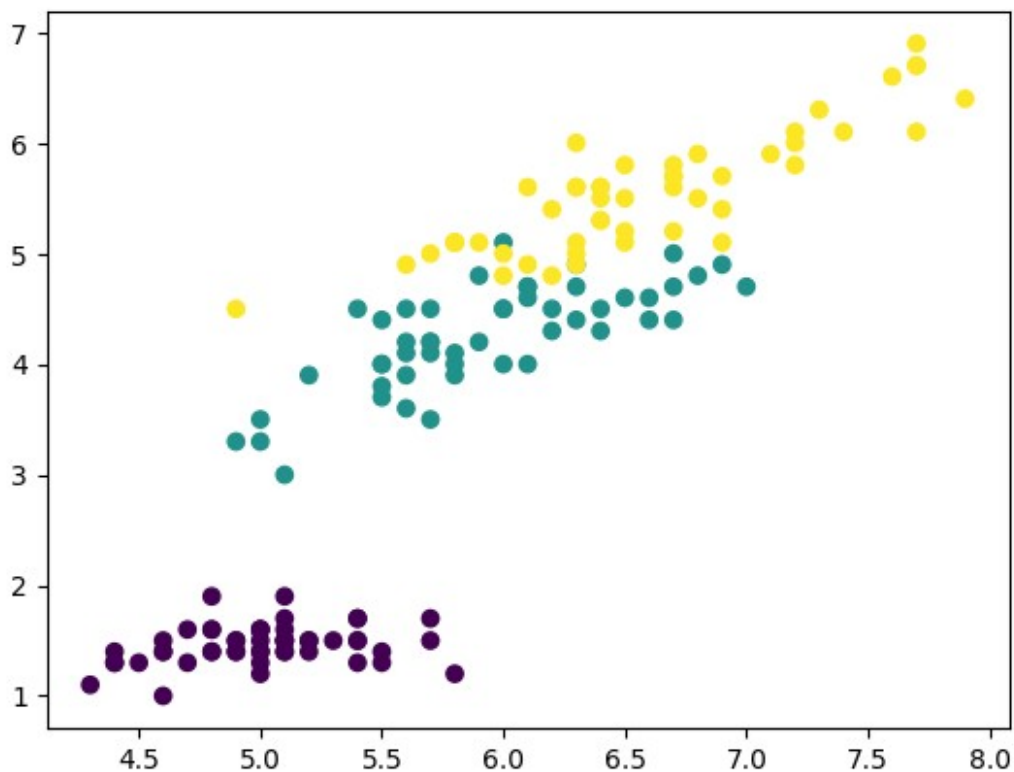
```
['sepal length (cm)', 'sepal width (cm)', 'petal length (cm)', 'petal  
width (cm)']
```

Targets:

```
[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  
0 0 0  
0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  
1 1  
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2  
2 2  
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2  
2 2  
2 2]
```

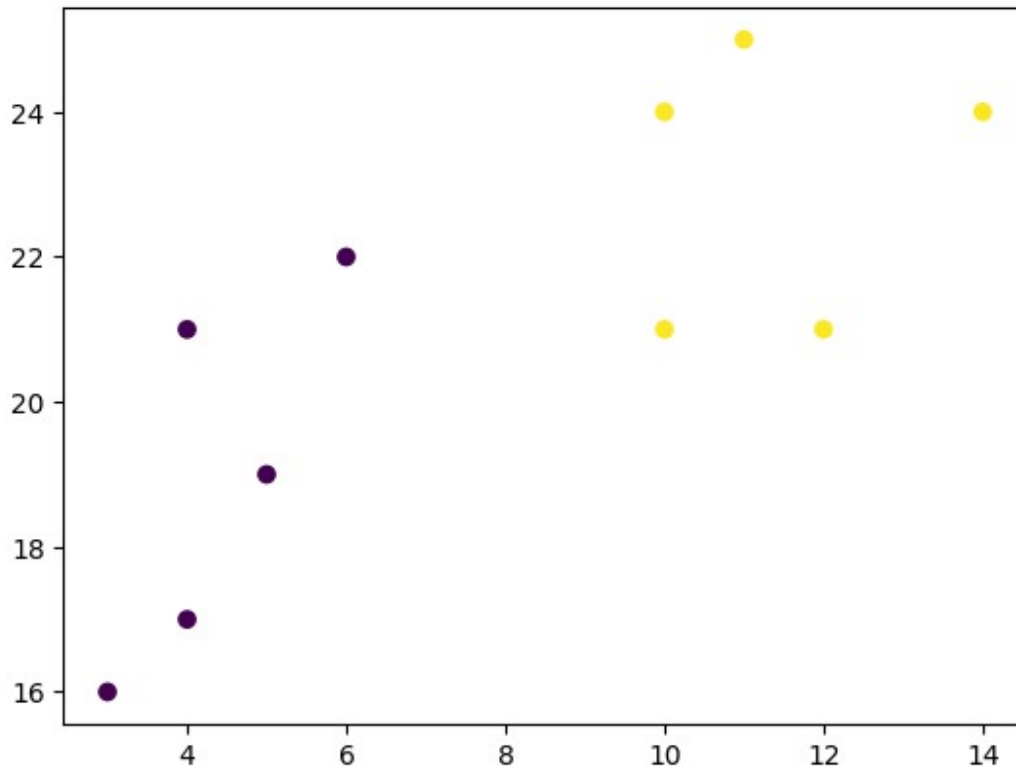
Target names:

```
['setosa' 'versicolor' 'virginica']
```



K-Means

```
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
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))
kmeans = KMeans(n_clusters=2)
kmeans.fit(data)
plt.scatter(x, y, c=kmeans.labels_)
plt.show()
```



Model Evaluation

```
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.datasets import make_blobs
X, y = make_blobs(random_state=0)
X_train, X_test, y_train, y_test = train_test_split(X, y,
random_state=0)
logreg = LogisticRegression().fit(X_train, y_train)
print("Test set score: {:.2f}".format(logreg.score(X_test, y_test)))
```

Test set score: 0.88

```
from sklearn.model_selection import train_test_split
from sklearn.datasets import make_blobs
```

```

from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
X, y = make_blobs(random_state=0)
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.33, random_state=42)
clf_model=LogisticRegression()
clf_model.fit(X_train, y_train)
y_pred = clf_model.predict(X_test)
print("Accuracy: ", accuracy_score(y_test, y_pred))

```

Accuracy: 0.9393939393939394

Engineering Features

```

import pandas as pd
import numpy as np
df = pd.DataFrame({'Age': [42, 15, 67, 55, 1, 29, 75, 89, 4,
10, 15, 38, 22, 77]})
print("Before: \n")
print(df)
df['Label'] = pd.cut(x=df['Age'], bins=[0, 3, 17, 63, 99],
labels=['Baby/Toddler', 'Child', 'Adult',
'Elderly'])
print("After: \n")
print(df)
print("Categories: \n")
print(df['Label'].value_counts())

```

Before:

	Age
0	42
1	15
2	67
3	55
4	1
5	29
6	75
7	89
8	4
9	10
10	15
11	38
12	22
13	77

After:

	Age	Label
0	42	Adult
1	15	Child

2	67	Elderly
3	55	Adult
4	1	Baby/Toddler
5	29	Adult
6	75	Elderly
7	89	Elderly
8	4	Child
9	10	Child
10	15	Child
11	38	Adult
12	22	Adult
13	77	Elderly

Categories:

Label

Adult	5
-------	---

Child	4
-------	---

Elderly	4
---------	---

Baby/Toddler	1
--------------	---

Name: count, dtype: int64

Importing pandas and numpy libraries

```
import pandas as pd
```

```
import numpy as np
```

Creating a dummy DataFrame of 12 numbers randomly

ranging from 150-180 for height

```
df = pd.DataFrame({'Height': [150.4, 157.6, 170, 176, 164.2, 155, 159.2, 175, 162.4, 176, 153, 170.9]})
```

Printing DataFrame Before Sorting Continuous to Categories

```
print("Before: ")
```

```
print(df)
```

A column of name 'Label' is created in DataFrame

Categorizing Height into 3 Categories

Short: (150,157], 150 is excluded & 157 is included

Average: (157,169], 157 is excluded & 169 is included

Tall: (169,180], 169 is excluded & 180 is included.

```
df['Label'] = pd.cut(x=df['Height'],
```

```
bins=[150, 157, 169, 180],
```

```
labels=['Short', 'Average', 'Tall'])
```

Printing Data Frame After Sorting Continuous to Categories

```
print("After: ")
```

```
print(df)
```

Check the number of values in each bin

```
print("Categories: ")
```

```
print(df['Label'].value_counts())
```

Before:

	Height
0	150.4
1	157.6

```
2    170.0
3    176.0
4    164.2
5    155.0
6    159.2
7    175.0
8    162.4
9    176.0
10   153.0
11   170.9
```

After:

	Height	Label
0	150.4	Short
1	157.6	Average
2	170.0	Tall
3	176.0	Tall
4	164.2	Average
5	155.0	Short
6	159.2	Average
7	175.0	Tall
8	162.4	Average
9	176.0	Tall
10	153.0	Short
11	170.9	Tall

Categories:

Label

Tall 5

Average 4

Short 3

Name: count, dtype: int64