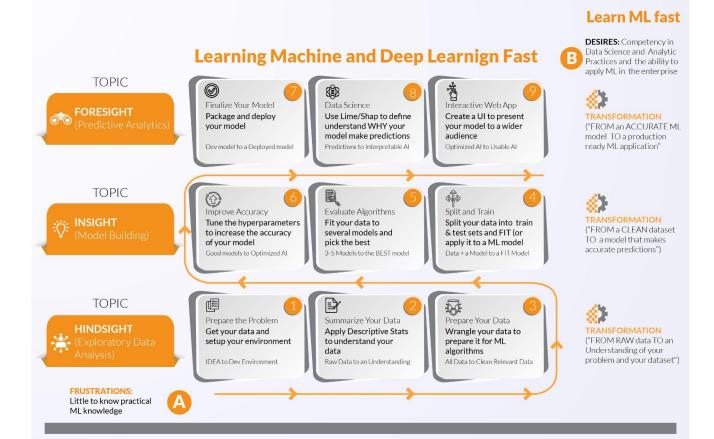
MACHINE LEARNING

We transfer expert Data Science knowledge to intelligent IT professionals, so they can apply Machine and Deep Learning in the enterprise without spending years in college and without over focusing on math



LOAD DATA

CONSIDERATIONS WHEN LOADING DATA

- File Header
- Comments
- Delimiters
- Quotes



LOAD CSV FILES WITH PANDAS

```
from urllib.request import urlopen # Load CSV using Pandas
from pandas import read_csv
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(filename, names=names)
print(data.shape)
```

LOAD CSV FILES FROM A URL INTO PANDAS

Let's do this!

```
# Load CSV using Pandas from URL
from pandas import read_csv
url = 'https://goo.gl/bDdBiA'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(url, names=names)
print(data.shape)
```

UNDERSTAND YOUR DATA WITH DESCRIPTIVE STATISTICS

UNDERSTAND YOUR DATA WITH STATISTICS

- 1. Take a peek at your raw data.
- 2. Review the dimensions of your dataset.
- 3. Review the data types of attributes in your data.
- 4. Summarize the distribution of instances across classes in your dataset.
- 5. Summarize your data using descriptive statistics.
- 6. Understand the relationships in your data using correlations.
- 7. Review the skew of the distributions of each attribute.



PEEK AT YOUR DATA

```
# View first 20 rows
from pandas import read_csv
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(filename, names=names)
peek = data.head(20)
print(peek)
```



GET THE DIMENSIONS OF YOUR DATA

```
# Dimensions of your data
from pandas import read_csv
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(filename, names=names)
shape = data.shape
print(shape)
```



GET THE DATA TYPE FOR EVERY FEATURE

```
# Data Types for Each Attribute
from pandas import read_csv
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(filename, names=names)
types = data.dtypes
print(types)
```

DESCRIPTIVE STATISTICS

- Count.
- ^ Mean.
- [^] Standard Deviation.
- ^ Minimum Value.
- ^{25th Percentile.}
- [^] 50th Percentile (Median).
- ^{75th Percentile.}
- ^ Maximum Value.





STATISTICAL SUMMARY

```
from pandas import read_csv
from pandas import set_option
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age',
'class'l
data = read_csv(filename, names=names)
set_option('display.width', 100)
set_option('precision', 3)
description = data.describe()
print(description)
```



CLASS DISTRIBUTIONS (CLASSIFICATION ONLY)

```
# Class Distribution
from pandas import read_csv
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(filename, names=names)
class_counts = data.groupby('class').size()
print(class counts)
```



CORRELATIONS BETWEEN ATTRIBUTES

```
from pandas import read_csv
from pandas import set_option
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi',
'age', 'class'l
data = read_csv(filename, names=names)
set_option('display.width', 100)
set_option('precision', 3)
correlations = data.corr(method='pearson')
print(correlations)
```



SKEW OF UNIVARIATE DISTRIBUTIONS

```
# Skew for each attribute
from pandas import read_csv
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(filename, names=names)
skew = data.skew()
print(skew)
```

SUMMARY

- Peek At Your Data.
- ^ Dimensions of Your Data.
- Data Types.
- [^] Class Distribution.
- ^ Data Summary.
- ^ Correlations.
- Skewness.



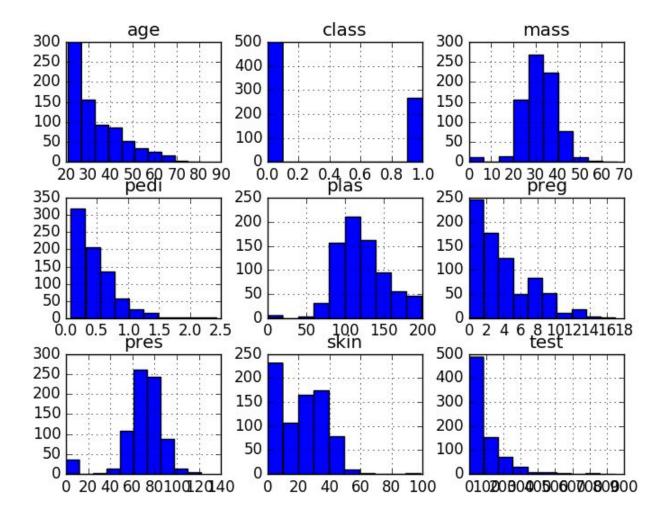
VISUALIZE YOUR DATA

UNIVARIATE PLOTS

- ^ Histograms.
- Density Plots.
- [^] Box and Whisker Plots.

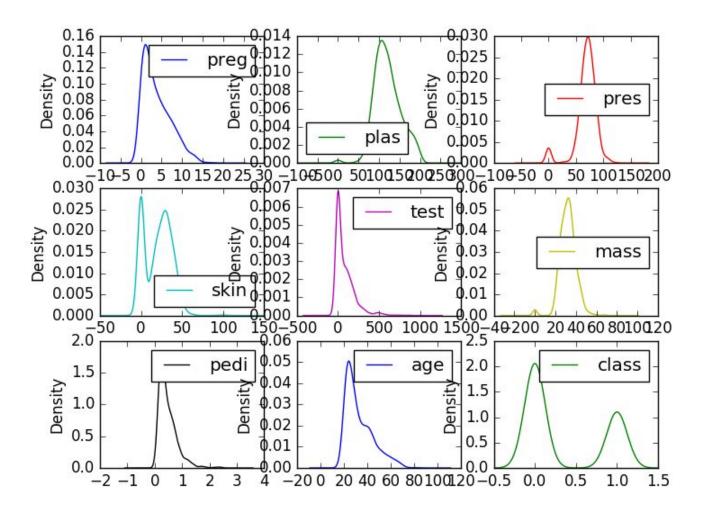
UNIVARIATE HISTOGRAM

```
from matplotlib import pyplot
from pandas import read_csv
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read_csv(filename, names=names)
data.hist()
pyplot.show()
```



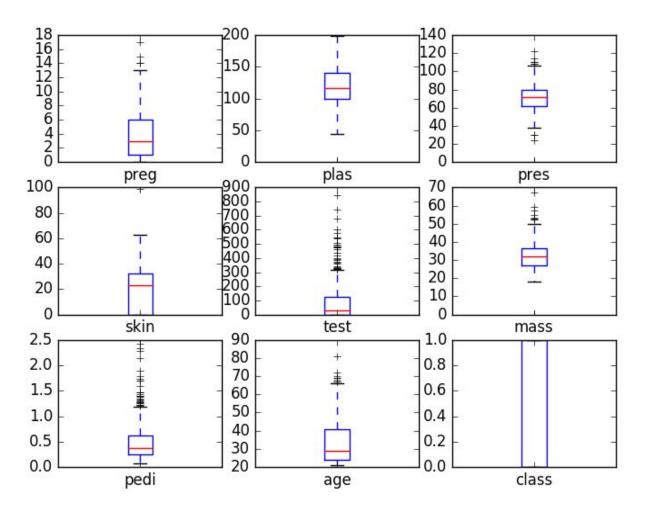
UNIVARIATE DENSITY PLOTS

```
from matplotlib import pyplot
from pandas import read_csv
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi',
'age', 'class'l
data = read_csv(filename, names=names)
data.plot(kind='density', subplots=True, layout=(3,3),
sharex=False)
pyplot.show()
```



BOX AND WHISKER PLOTS

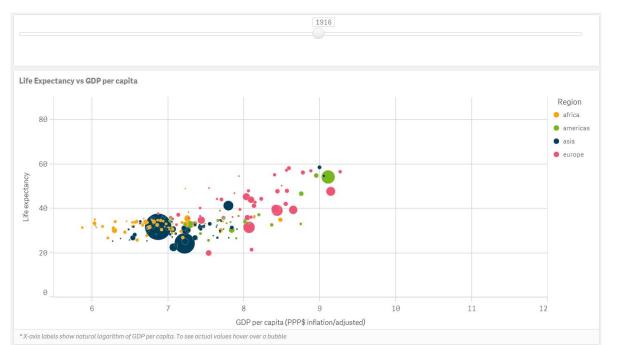
```
from matplotlib import pyplot
from pandas import read_csv
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi',
'age', 'class'l
data = read_csv(filename, names=names)
data.plot(kind='box', subplots=True, layout=(3,3), sharex=False,
sharev=False)
pyplot.show()
```



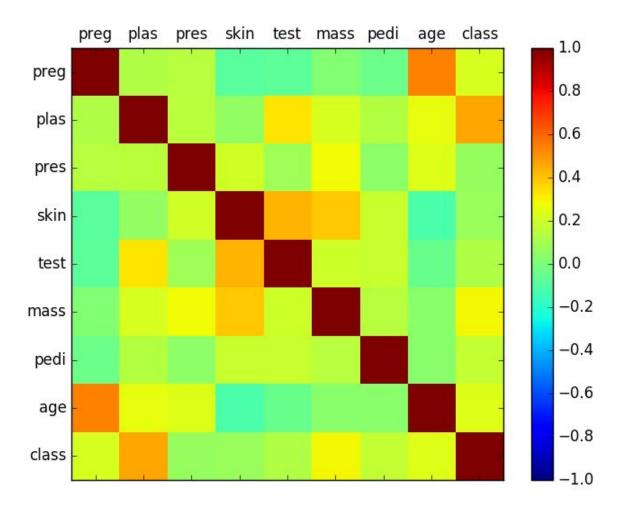
MULTIVARIATE VISUALIZATIONS

MULTIVARIATE VISUALIZATIONS FOR ML

- Correlation Matrix Plot.
- Scatter Plot Matrix.



```
from matplotlib import pyplot
from pandas import read_csv
import numpy
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age', 'class']
data = read_csv('pima-indians-diabetes.csv', names=names)
correlations = data.corr()
fig = pyplot.figure() # plot correlation matrix
ax = fig.add_subplot(111)
cax = ax.matshow(correlations, vmin=-1, vmax=1)
fig.colorbar(cax)
                                         CORRELATION MATRIX:
ticks = numpy.arange(0,9,1)
ax.set_xticks(ticks)
                                         HTTPS://BIT.LY/JPMCML
ax.set_yticks(ticks)
ax.set_xticklabels(names)
ax.set_yticklabels(names)
pyplot.show()
```



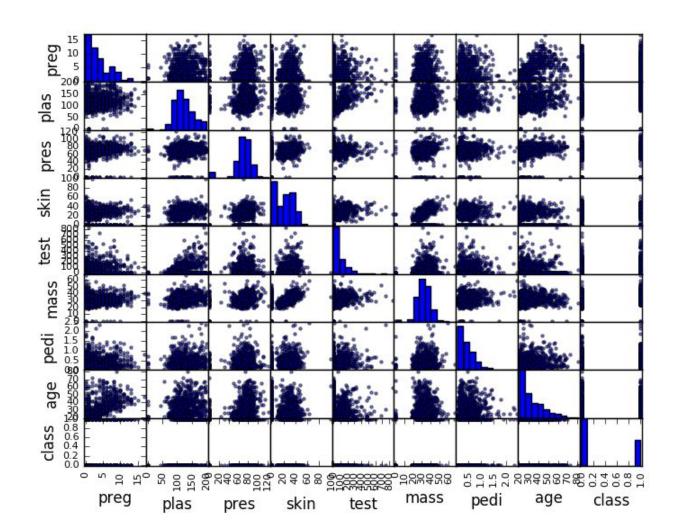
GENERIC CORRELATION MATRIX

pyplot.show()

```
from matplotlib import pyplot
from pandas import read csv
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age',
'class'l
data = read_csv(filename, names=names)
correlations = data.corr()
fig = pyplot.figure() # plot correlation matrix
ax = fig.add_subplot(111)
cax = ax.matshow(correlations, vmin=-1, vmax=1)
fig.colorbar(cax)
```

SCATTER PLOT MATRIX

```
from matplotlib import pyplot
from pandas import read_csv
from pandas.plotting import scatter_matrix
filename = "pima-indians-diabetes.data.csv"
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass',
'pedi', 'age', 'class']
data = read csv(filename, names=names)
scatter_matrix(data)
pyplot.show()
```



SUMMARY

PREPARE YOUR DATA

PREPARE YOUR DATA

- 1. Rescale data.
- 2. Standardize data.
- 3. Normalize data.
- 4. Binarize data.

DATA TRANSFORMS

- Load the dataset
- Split the dataset into the input and output variables for machine learning.
- Apply a pre-processing transform to the input variables.
- Summarize the data to show the change.

Scikit-learn offers two ways to transform data:

- 1. Fit and Multiple Transform.
- 2. Combined Fit-And-Transform.

```
RESCALE DATA (BETWEEN 0 AND 1)
from pandas import read_csv
from numpy import set_printoptions
                                                      NEURAL NETWORKS
from sklearn.preprocessing import MinMaxScaler
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi',
'age', 'class']
dataframe = read_csv(filename, names=names)
array = dataframe.values
X = array[:,0:8] # separate array into input and output components
Y = array[:,8]
scaler = MinMaxScaler(feature_range=(0, 1))
```

rescaledX = scaler.fit_transform(X)

print(rescaledX[0:5,:])

set_printoptions(precision=3) # summarize transformed data

```
from sklearn.preprocessing import StandardScalerSTANDARDIZE YOUR DATA
from pandas import read_csv
                                          LINEAR/LOGISTIC REGRESSION
from numpy import set_printoptions
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi',
'age', 'class']
dataframe = read_csv(filename, names=names)
array = dataframe.values
X = array[:,0:8] # separate array into input and output components
Y = array[:,8]
scaler = StandardScaler().fit(X)
rescaledX = scaler.transform(X)
set_printoptions(precision=3) # summarize transformed data
                                                                         38
print(rescaledX[0:5,:])
```

```
from sklearn.preprocessing import Normalizer
                                                 NORMALIZE YOUR DATA
from pandas import read_csv
from numpy import set_printoptions
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi',
'age', 'class'l
dataframe = read_csv(filename, names=names)
array = dataframe.values
X = array[:,0:8] # separate array into input and output components
Y = array[:,8]
scaler = Normalizer().fit(X)
```

set_printoptions(precision=3) # summarize transformed data

normalizedX = scaler.transform(X)

print(normalizedX[0:5,:])

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FEATURE SELECTION

FEATURE SELECTION

- 1. Univariate Selection.
- 2. Recursive Feature Elimination.
- 3. Principle Component Analysis.
- 4. Feature Importance.

WHY FEATURE SELECTION?

- Reduces Overfitting
- Improves Accuracy
- Reduces Training Time

UNIVARIATE SELECTION

See Lesson 8 Univariate Selection in github

```
# Feature Extraction with Univariate Statistical Tests (Chi-squared for classification)
from pandas import read_csv
from numpy import set_printoptions
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import chi2
# load data
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age', 'class']
dataframe = read_csv(filename, names=names)
array = dataframe.values
X = array[:,0:8]
Y = array[:,8]
# feature extraction
test = SelectKBest(score_func=chi2, k=4)
fit = test.fit(X, Y)
# summarize scores
set_printoptions(precision=3)
print(fit.scores_)
features = fit.transform(X)
# summarize selected features
print(features[0:5,:])
```

RECURSIVE FEATURE ELIMINATION

See Lesson 8 Recursive Feature Elimination in github

```
# Feature Extraction with RFE
from pandas import read_csv
from sklearn.feature_selection import RFE
from sklearn.linear_model import LogisticRegression
# load data
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age', 'class']
dataframe = read_csv(filename, names=names)
array = dataframe.values
X = array[:,0:8]
Y = array[:,8]
# feature extraction
model = LogisticRegression(solver='liblinear')
rfe = RFE(model, 3)
fit = rfe.fit(X, Y)
print("Num Features: %d" % fit.n_features_)
print("Selected Features: %s" % fit.support_)
print("Feature Ranking: %s" % fit.ranking_)
```

PRINCIPLE COMPONENT ANALYSIS

```
# Feature Extraction with PCA
from pandas import read_csv
from sklearn.decomposition import PCA
# load data
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age', 'class']
dataframe = read_csv(filename, names=names)
array = dataframe.values
X = array[:,0:8]
Y = array[:,8]
# feature extraction
pca = PCA(n_components=3)
fit = pca.fit(X)
# summarize components
print("Explained Variance: %s" % fit.explained_variance_ratio_)
print(fit.components_)
```

FEATURE IMPORTANCE

```
# Feature Importance with Extra Trees Classifier
from pandas import read_csv
from sklearn.ensemble import ExtraTreesClassifier
# load data
filename = 'pima-indians-diabetes.data.csv'
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age', 'class']
dataframe = read_csv(filename, names=names)
array = dataframe.values
X = array[:,0:8]
Y = array[:.8]
# feature extraction
model = ExtraTreesClassifier(n_estimators=100)
model.fit(X, Y)
print(model.feature_importances_)
```

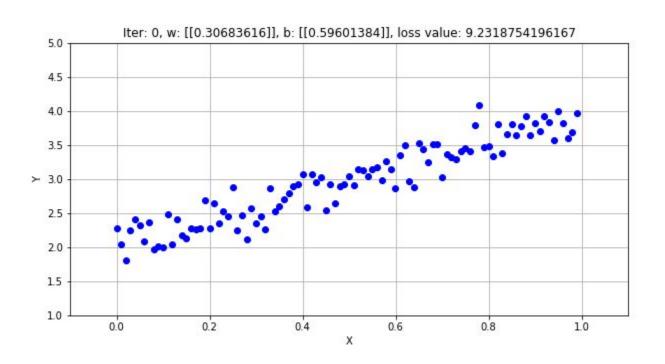
LINEAR REGRESSION

Professor Ernesto Lee

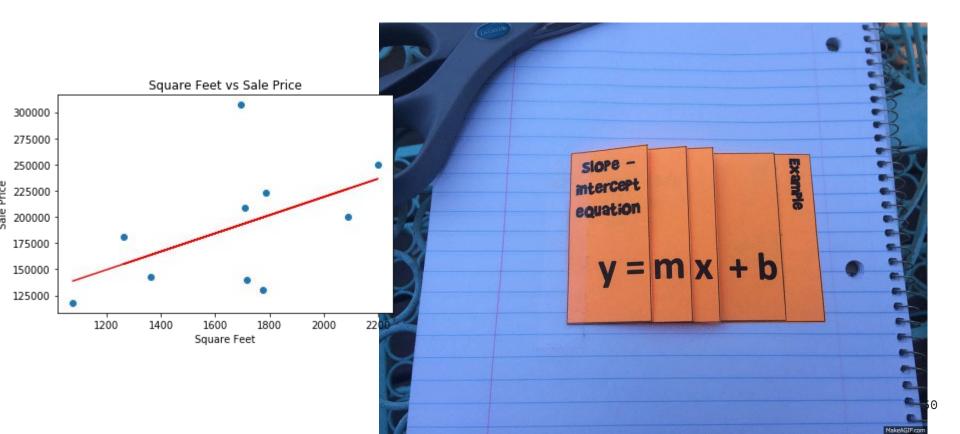
HTTPS://BIT.LY/MLTRAIN

Go here for your LAB ENVIRONMENT

LINEAR RELATIONSHIPS



REGRESSION ALGORITHM



LINEAR REGRESSION WITH SCIKIT-LEARN



IMPORT YOUR LIBRARIES

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn import metrics
```

PULL IN YOUR DATA

```
You can access your data here:
https://bit.ly/21homes
Or here:
https://raw.githubusercontent.com/fenago/pythonml/main/data/HousePrice.
CSV
pd.read_csv('https://raw.githubusercontent.com/fenago/pythonml/
main/data/HousePrice.csv')
```

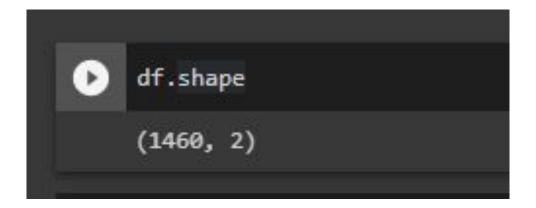
PUTTING THE COLUMNS YOU WANT IN YOUR DATA

df2 = df[["open", "close"]] #open and close are the
columns

Make sure you have the columns you want and need!

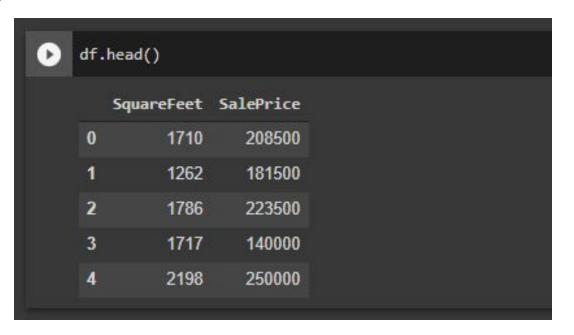
UNDERSTAND YOUR DATA WITH SHAPE

df.shape



UNDERSTAND YOUR DATA: HEAD

df.head()



UNDERSTAND YOUR DATA: DESCRIPTIVE STATISTICS

df.describe()

[8]	df.desc	ribe()	
		SquareFeet	SalePrice
	count	1460.000000	1460.000000
	mean	1515.463699	180921.195890
	std	525.480383	79442.502883
	min	334.000000	34900.000000
	25%	1129.500000	129975.000000
	50%	1464.000000	163000.000000
	75%	1776.750000	214000.000000
	max	5642.000000	755000.000000

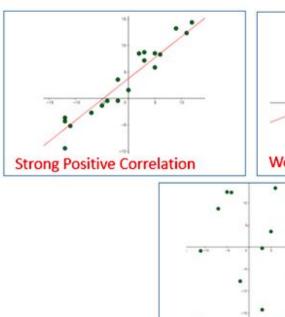
FIND YOUR CORRELATIONS IN YOUR DATASETS

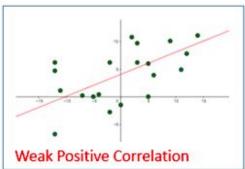
correlation between 2 Specific Columns

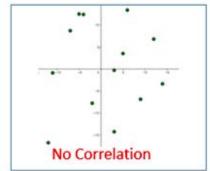
```
print(df['SquareFeet'].corr(df['SalesPrice']))
```

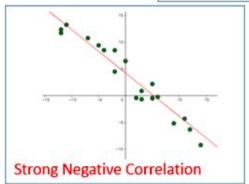
pair-wise correlation between all columns

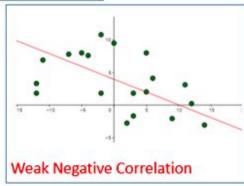
```
print(df.corr())
```











HEATMAP

```
# Correlation between different variables
corr = df.corr()
# Set up the matplotlib plot configuration
f, ax = plt.subplots(figsize=(12, 10))
# Generate a mask for upper traingle
mask = np.triu(np.ones_like(corr, dtype=bool))
# Configure a custom diverging colormap
cmap = sns.diverging_palette(230, 20, as_cmap=True)
# Draw the heatmap
sns.heatmap(corr, annot=True, mask = mask, cmap=cmap)
```

VISUALIZE YOUR DATA: PLOT

```
df.plot(x='SquareFeet', y='SalePrice', style='*')
plt.title('Square Feet vs Sale Price')
plt.xlabel('Square Feet')
plt.ylabel('Sale Price')
plt.show()
```

PREPARE YOUR DATA: SPLIT INTO TRAINING AND TEST SETS

```
X = df.iloc[:, :-1].values
y = df.iloc[:, 1].values
```

TRAIN TEST SPLIT

```
X_train, X_test, y_train, y_test = train_test_split(X,
y, test_size=0.2, random_state=0)
```

RUN THE MODEL

```
def get_cv_scores(model):
    scores = cross_val_score(model, X_train, y_train, cv=10, scoring='r2')
    print('CV Mean: ', np.mean(scores))
    print('STD: ', np.std(scores))
    print('\n')
lr = LinearRegression().fit(X_train, y_train)
get_cv_scores(lr)
```

VIEW THE COEFFICIENTS

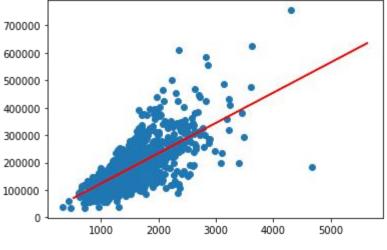
```
print(lr.intercept_)
print(lr.coef_)
```

```
print(lr.intercept_)
print(lr.coef_)

13330.293444921088
[110.26434426]
```

PREDICTIONS

```
y_pred = lr.predict(X_test)
```



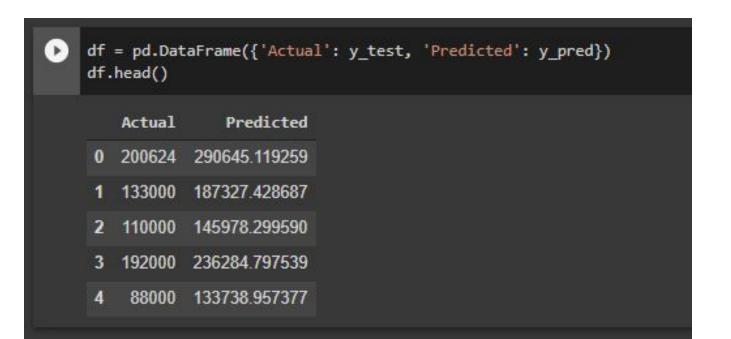
```
plt.scatter(X_train, y_train)
plt.plot(X_test, y_pred, color='red')
plt.show()
```

PREDICT WITH NEW UNSEEN DATA

lr.predict([[2515]])

EVALUATE PREDICTED VALUES FROM ACTUALS

```
df = pd.DataFrame({'Actual': y_test, 'Predicted': y_pred})
df.head()
```



R-SQUARED (R2)

```
df = pd.DataFrame({'Actual': y_test, 'Predicted': y_pred})
df.head()
```

```
print('R-Squared:',metrics.r2_score(df['Actual'],df['Predicted']))
```

Summary Definition

Define R-Squared: Coefficient of determination means a statistical measurement of the correlation between two variables.

https://scikit-learn.org/stable/modules/generated/sklearn.metrics.r2_score.html

EVALUATE YOUR MODEL

```
print('Mean Absolute Error:',
metrics.mean_absolute_error(y_test, y_pred))
print('Mean Squared Error:',
metrics.mean_squared_error(y_test, y_pred))
print('Root Mean Squared Error:',
np.sqrt(metrics.mean_squared_error(y_test, y_pred)))
```

```
print('Mean Absolute Error:', metrics.mean_absolute_error(y_test, y_pred))
print('Mean Squared Error:', metrics.mean_squared_error(y_test, y_pred))
print('Root Mean Squared Error:', np.sqrt(metrics.mean_squared_error(y_test, y_pred)))

Mean Absolute Error: 39364.76724953735
Mean Squared Error: 3913788296.4027987
Root Mean Squared Error: 62560.277304394986
```

https://scikit-learn.org/

https://github.com/scikit-learn/scikit-learn

TUNING HYPERPARAMETERS WITH SIMPLE LINEAR REGRESSION

https://bit.ly/ucidata

Hint: To create a new dataframe with selected columns - do this:

df2 = df[["open", "close"]] #open and close are the
colomns

LAB 1

Read in this DATA:

pd.read_csv('https://raw.githubu
sercontent.com/fenago/pythonml/m
ain/data/poverty.txt',sep="\t")

Apply what you have learned to create Simple Linear Models.

This dataset of size n = 51 are for the 50 states and the District of Columbia in the United States (poverty.txt). The variables are y = year 2002 birth rate per 1000females 15 to 17 years old and x = poverty rate, which is the percent of the state's population living in households with incomes below the federally defined poverty level. (Data source: Mind On *Statistics*, 3rd edition, Utts and Heckard).

LAB 2

Read in this DATA:

pd.read_csv('https://raw.githubu
sercontent.com/fenago/pythonml/m
ain/data/lungfunction.txt',sep="
\t")

Apply what you have learned to create Simple Linear Models.

This dataset of size n = 51 are for the 50 states and the District of Columbia in the United States (poverty.txt). The variables are y = year 2002 birth rate per 1000females 15 to 17 years old and x = povertyrate, which is the percent of the state's population living in households with incomes below the federally defined poverty level. (Data source: Mind On *Statistics*, 3rd edition, Utts and Heckard).

MULTIVARIATE LINEAR REGRESSION

OUR DATASET

```
Data Dictionary:
http://people.sc.fsu.edu/~jburkardt/datasets/regression/x16.txt
Dataset:
pd.read_csv("https://raw.githubusercontent.com/fenago/pythonml/main/data/petrol_consumption.csv")
```

LOAD THE LIBRARIES

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
```

LOAD THE DATA

```
df =
pd.read_csv("https://raw.githubusercontent.com/fenago/python
ml/main/data/petrol consumption.csv")

df.head()

df.describe()
```

FIND YOUR CORRELATIONS IN YOUR DATASETS

```
# correlation between 2 Specific Columns
print(df['Petrol_tax'].corr(df['Petrol_Consumption']))
# pair-wise correlation between all columns
print(df.corr())
```

PREPARE THE DATA

```
X = dataset[['Petrol_tax', 'Average_income',
'Paved Highways', 'Population Driver licence(%)']]
y = dataset['Petrol Consumption']
#Execute below to divide into train/test sets
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y,
test size=0.2, random state=0)
```

TRAIN THE ALGORITHM AS BEFORE

```
from sklearn.linear_model import LinearRegression
regressor = LinearRegression()
regressor.fit(X_train, y_train)
```

WHAT COEFFICIENTS DID IT FIND?

```
coeff_df = pd.DataFrame(regressor.coef_, X.columns,
columns=['Coefficient'])
```

coeff_df

	Coefficient
Petrol_tax	-24.196784
Average_income	-0.81680
Paved_Highways	-0.000522
Population_Driver_license(%)	1324.675464

PREDICTIONS

```
y_pred = regressor.predict(X_test)

df = pd.DataFrame({'Actual': y_test, 'Predicted': y_pred})

df
```

	Actual	Predicted
36	640	643.176639
22	464	411.950913
20	649	683.712762
38	648	728.049522
18	865	755.473801

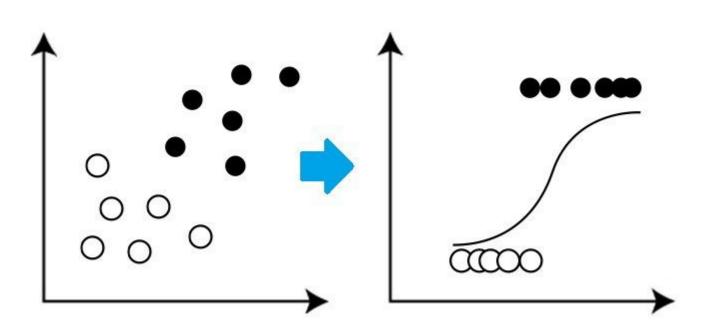
EVALUATE THE ALGORITHM

```
from sklearn import metrics
print('Mean Absolute Error:',
metrics.mean_absolute_error(y_test, y_pred))
print('Mean Squared Error:',
metrics.mean_squared_error(y_test, y_pred))
print('Root Mean Squared Error:',
np.sqrt(metrics.mean_squared_error(y_test, y_pred)))
print('R-Squared:',metrics.r2_score(df['Actual'],
df['Predicted']))
```

LOGISTIC REGRESSION

LOGISTIC REGRESSION

LOGISTIC REGRESSION

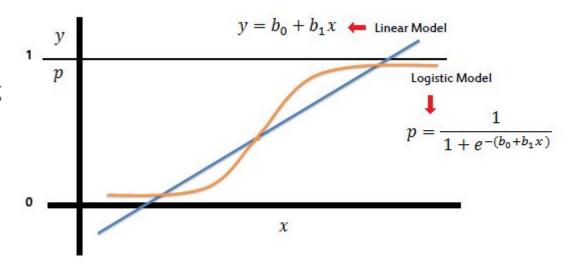


LOGISTIC REGRESSION

when b0+b1X == 0, then the p will be 0.5,

similarly,b0+b1X > 0,
then the p will be going
towards 1 and

b0+b1X < 0, then the p will be going towards 0.



LOADING THE DATA

```
from sklearn.datasets import load_digits
digits = load_digits()
```

SHOWING THE IMAGES AND LABELS

```
import numpy as np
import matplotlib.pyplot as plt
                                       Training: 0
                                                    Training: 1
                                                                 Training: 2
                                                                               Training: 3
                                                                                            Training: 4
plt.figure(figsize=(20,4))
for index, (image, label) in enumerate(zip(digits.data[0:5], digits.target[0:5])):
  plt.subplot(1, 5, index + 1)
  plt.imshow(np.reshape(image, (8,8)), cmap=plt.cm.gray)
  plt.title('Training: %i\n' % label, fontsize = 20)
```

SPLIT THE DATA INTO TRAINING AND TEST SETS

```
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test =
train_test_split(digits.data, digits.target, test_size=0.25,
random_state=0)
```

MODELING

```
from sklearn.linear_model import LogisticRegression
logisticRegr = LogisticRegression()
logisticRegr.fit(x_train, y_train)
```

```
#predict for one image
logisticRegr.predict(x_test[0].reshape(1,-1))
#predict for multiple images
logisticRegr.predict(x_test[0:10])
#for the entire dataset
predictions = logisticRegr.predict(x_test)
```

```
[14] #predict for one image
     logisticRegr.predict(x test[0].reshape(1,-1))
     array([2])
[15] #predict for multiple images
     logisticRegr.predict(x test[0:10])
     array([2, 8, 2, 6, 6, 7, 1, 9, 8, 5])
[16] #for the entire dataset
     predictions = logisticRegr.predict(x test)
[17] predictions
     array([2, 8, 2, 6, 6, 7, 1, 9, 8, 5, 2, 8, 6, 6, 6, 6, 6, 1, 0, 5, 8, 8, 7,
            8, 4, 7, 5, 4, 9, 2, 9, 4, 7, 6, 8, 9, 4, 3, 1, 0, 1, 8, 6, 7, 7,
            1, 0, 7, 6, 2, 1, 9, 6, 7, 9, 0, 0, 9, 1, 6, 3, 0, 2, 3, 4, 1, 9,
            2, 6, 9, 1, 8, 3, 5, 1, 2, 8, 2, 2, 9, 7, 2, 3, 6, 0, 5, 3, 7, 5,
            1, 2, 9, 9, 3, 1, 4, 7, 4, 8, 5, 8, 5, 5, 2, 5, 9, 0, 7, 1, 4, 7,
            3, 4, 8, 9, 7, 9, 8, 2, 1, 5, 2, 5, 8, 4, 1, 7, 0, 6, 1, 5, 5, 9,
            9, 5, 9, 9, 5, 7, 5, 6, 2, 8, 6, 9, 6, 1, 5, 1, 5, 9, 9, 1, 5, 3,
            6, 1, 8, 9, 8, 7, 6, 7, 6, 5, 6, 0, 8, 8, 9, 9, 6, 1, 0, 4, 1, 6,
            3, 8, 6, 7, 4, 9, 6, 3, 0, 3, 3, 3, 0, 7, 7, 5, 7, 8, 0, 7, 1, 9,
            6, 4, 5, 0, 1, 4, 6, 4, 3, 3, 0, 9, 5, 9, 2, 8, 4, 2, 1, 6, 8, 9,
            2, 4, 9, 3, 7, 6, 2, 3, 3, 1, 6, 9, 3, 6, 3, 3, 2, 0, 7, 6, 1, 1,
            9, 7, 2, 7, 8, 5, 5, 7, 5, 3, 3, 7, 2, 7, 5, 5, 7, 0, 9, 1, 6, 5,
            9, 7, 4, 3, 8, 0, 3, 6, 4, 6, 3, 2, 6, 8, 8, 8, 4, 6, 7, 5, 2, 4,
            5, 3, 2, 4, 6, 9, 4, 5, 4, 3, 4, 6, 2, 9, 0, 1, 7, 2, 0, 9, 6, 0,
            4, 2, 0, 7, 9, 8, 5, 7, 8, 2, 8, 4, 3, 7, 2, 6, 9, 9, 5, 1, 0, 8,
            2, 8, 9, 5, 6, 2, 2, 7, 2, 1, 5, 1, 6, 4, 5, 0, 9, 4, 1, 1, 7, 0,
            8, 9, 0, 5, 4, 3, 8, 8, 6, 5, 3, 4, 4, 4, 8, 8, 7, 0, 9, 6, 3, 5,
            2, 3, 0, 8, 8, 3, 1, 3, 3, 0, 0, 4, 6, 0, 7, 7, 6, 2, 0, 4, 4, 2,
            3, 7, 1, 9, 8, 6, 8, 5, 6, 2, 2, 3, 1, 7, 7, 8, 0, 3, 3, 1, 1, 5,
            5, 9, 1, 3, 7, 0, 0, 3, 0, 4, 5, 8, 9, 3, 4, 3, 1, 8, 9, 8, 3, 6,
            3, 1, 6, 2, 1, 7, 5, 5, 1, 9])
```

EVALUATION

```
#Accuracy = correct predictions / total number of data points
#Use score method to get accuracy of model
score = logisticRegr.score(x_test, y_test)
print(score)
```

```
[18] #Use score method to get accuracy of model
    score = logisticRegr.score(x_test, y_test)
    print(score)

0.951111111111111
```

CONFUSION MATRIX

from sklearn import metrics

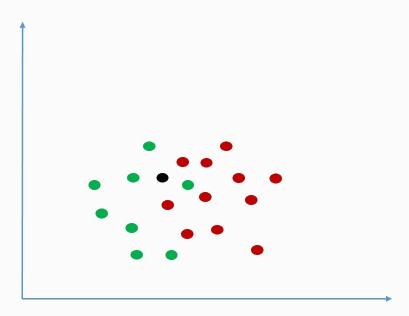
cm = metrics.confusion_matrix(y_test, predictions)

print(cm)

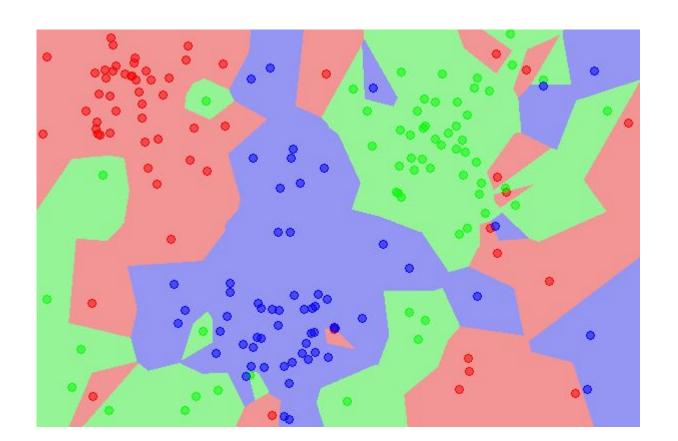
KNN



Choice of value of K

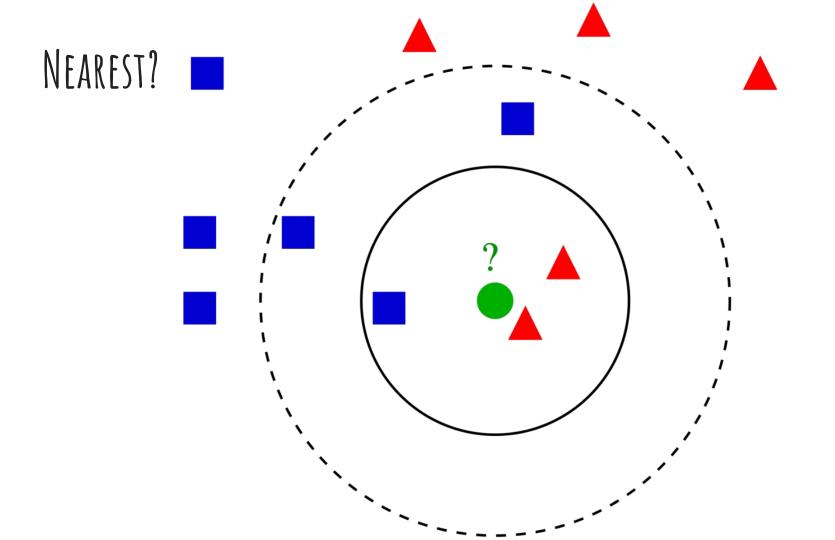


HOW DOES KNN WORK?



DISTANCE IN KNN

$$egin{split} d(\mathbf{p},\mathbf{q}) &= d(\mathbf{q},\mathbf{p}) = \sqrt{(q_1-p_1)^2 + (q_2-p_2)^2 + \dots + (q_n-p_n)^2} \ &= \sqrt{\sum_{i=1}^n (q_i-p_i)^2}. \end{split}$$



STEPS TO SOLVE A KNN PROBLEM

- 1. Load and store the data.
- 2. Calculate the distance from x (new data point) to all other data points.
- 3. Sort all the distances from your data in ascending order.
- 4. Initialize the K value for the nearest data points.
- 5. Make a prediction based on the majority of data points with the same label within the K value.
- 6. Evaluate your machine learning model.

THE USE CASE...

we want to create a machine model that will allow botanists to classify different species of iris flowers.



LET'S BUILD THE MODEL

IMPORTS

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib
```

DATA PREPARATION

```
from sklearn.datasets import load_iris
iris dataset = load iris()
print("Keys of iris_dataset:\n", iris_dataset.keys())
OUTPUT
Keys of iris_dataset:
dict_keys(['data', 'target', 'target_names', 'DESCR',
'feature_names', 'filename'])
```

DATA TYPE

```
print("Data Type:", type(iris_dataset['data']))
OUTPUT:
Data Type: <class 'numpy.ndarray'>
```

SHAPE

```
print("Shape of Data:", iris_dataset['data'].shape)
```

FEATURES

```
print("First 10 Samples and Their Features:\n",
iris_dataset['data'][:10])
```

TARGET

```
print("Type of Target:", type(iris_dataset['target']))
print("Shape of Target:", iris_dataset['target'].shape)
print(iris_dataset['target'])
```

TARGET NAMES

```
print("Target names:", iris_dataset['target_names'])
```

DESCRIPTION

```
print(iris_dataset['DESCR'])

OR
print(iris_dataset['DESCR'][:500] + "\n...")
```

FEATURE NAMES

```
print("Feature Names:", iris_dataset['feature_names'])
```

TRAINING AND TESTING DATA

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(
    iris_dataset['data'], iris_dataset['target'],
random_state=0)
```

VALIDATE THE SHAPE OF THE DATA AND TEST THE DATASET

```
print("X_train Shape:", X_train.shape)
print("y_train Shape:", y_train.shape)
print("X_test Shape:", X_test.shape)
print("y_test Shape:", y_test.shape)
```

VISUALIZE YOUR DATA

CREATE THE DF FOR VISUALIZING

```
df = pd.DataFrame(X_train,
  columns=iris_dataset.feature_names)
df.head()
```

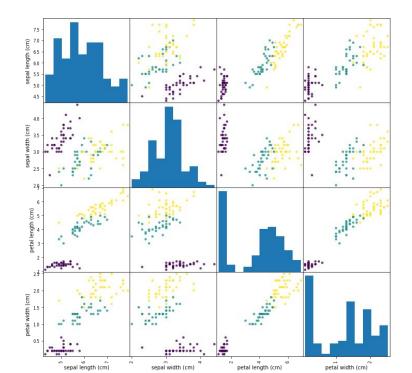
	sepal	length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
0		5.9	3.0	4.2	1.5
1		5.8	2.6	4.0	1.2
2		6.8	3.0	5.5	2.1
3		4.7	3.2	1.3	0.2
4		6.9	3.1	5.1	2.3

SHOW THE VISUALIZATION

pd.plotting.scatter_matrix(df,c=y_train,figsize=(12,12),

marker='o',s=20,alpha=.8)

plt.show()

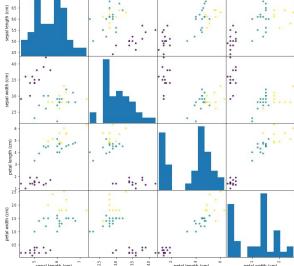


DO THE SAME WITH X

```
df = pd.DataFrame(X_test,
  columns=iris_dataset.feature_names)

pd.plotting.scatter_matrix(df,c=y_test,figsize=(12,12),
  marker='o',s=20,alpha=.8)
```

plt.show()



CREATE THE MODEL

from sklearn.neighbors import KNeighborsClassifier
knnObject = KNeighborsClassifier(n_neighbors=1)
knnObject.fit(X_train, y_train)

MAKING PREDICTIONS

PREDICTIONS ON NEW DATA

Imagine you are a machine learning engineer for a company. A client of yours reached out to you to verify an iris species they found in the wild. They only gave us the following information:

- Sepal length: 40 cm
- Sepal width: 10 cm
- Petal length: 5 cm
- Petal width: 2 cm

```
newIris = np.array([[40, 10, 5, 2]])
print("newIris Shape:", newIris.shape)
```

PREDICT

MODEL EVALUATION

SEE YOUR TEST PREDICTIONS

```
testSetPredictions = knnObject.predict(X_test)
print("Test Set Predictions:", testSetPredictions)
```

CHECK FOR ACCURACY

```
accuaracy = round(knn0bject.score(X_test, y_test),2)
print("The Test Set Accuracy is:",accuracy)
```

BREAST CANCER USE CASE -KNN

INITIALIZE THE LIBRARIES

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
```

IMPORT THE DATA SET

It is in the data folder and named dataR2.csv

data=pd.read_csv("./data/dataR2.csv")

UNDERSTAND YOUR DATA

data.shape

	Age	ВМІ	Glucose	Insulin	HOMA	Leptin	Adiponectin	Resistin	MCP.1	Classification
0	48	23.500000	70	2.707	0.467409	8.8071	9.702400	7.99585	417.114	*1
1	83	20.690495	92	3.115	0.706897	8.8438	5.429285	4.06405	468.786	a.
2	82	23.124670	91	4.498	1.009651	17.9393	22.432040	9.27715	554.697	3
3	68	21.367521	77	3.226	0.612725	9.8827	7.169560	12.76600	928.220	0.
4	86	21.111111	92	3.549	0.805386	6.6994	4.819240	10.57635	773.920	8
	***	***	***	1992	***		***	***	2221	
111	45	26.850000	92	3.330	0.755688	54.6800	12.100000	10.96000	268.230	3
112	62	26.840000	100	4.530	1.117400	12.4500	21.420000	7.32000	330.160	
113	65	32.050000	97	5.730	1.370998	61.4800	22.540000	10.33000	314.050	
114	72	25.590000	82	2.820	0.570392	24.9600	33.750000	3.27000	392.460	
115	86	27.180000	138	19.910	6.777364	90.2800	14.110000	4.35000	90.090	

FIND MISSING VALUES

data.isna().sum()

Age	0
BMI	0
Glucose	0
Insulin	0
HOMA	0
Leptin	0
Adiponectin	0
Resistin	0
MCP.1	0
Classification	0
dtype: int64	

EXPLORATORY DATA ANALYSIS

data.info()

<pre><class 'pandas.core.frame.dataframe'=""> RangeIndex: 116 entries, 0 to 115 Data columns (total 10 columns):</class></pre>						
	Column	Non-Null Count	Dtype			
0	Age	116 non-null	int64			
1	BMI	116 non-null	float64			
2	Glucose	116 non-null	int64			
3	Insulin	116 non-null	float64			
4	HOMA	116 non-null	float64			
5	Leptin	116 non-null	float64			
6	Adiponectin	116 non-null	float64			
7	Resistin	116 non-null	float64			
	MCP.1	116 non-null	float64			
9	Classification	116 non-null	int64			
dtypes: float64(7), int64(3) memory usage: 9.2 KB						

HEATMAPS AND CORRELATION

```
#Heatmap to find correlation
plt.subplots(figsize=(20,20))
sns.heatmap(data.corr(),cmap='RdYlGn',annot=True)
```

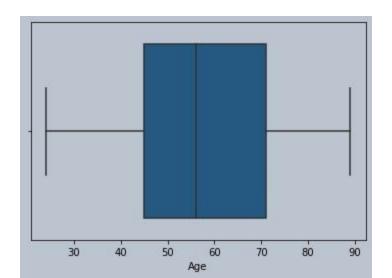
COLUMNS

data.columns

KNN IS SENSITIVE TO OUTLIERS

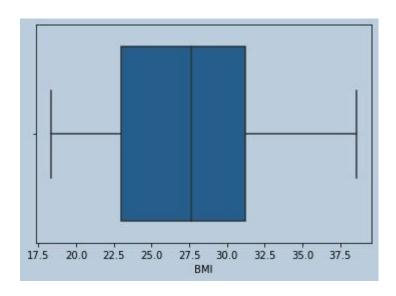
OUTLIERS FOR AGE?

```
#No outliers for age
sns.boxplot(data['Age'])
```



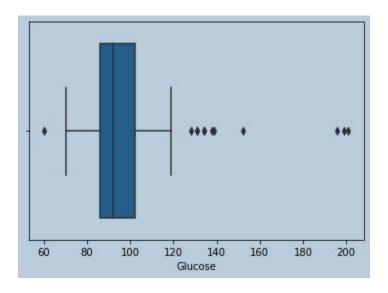
OUTLIERS FOR BMI?

```
#NO outliers for BMI
sns.boxplot(data['BMI'])
```



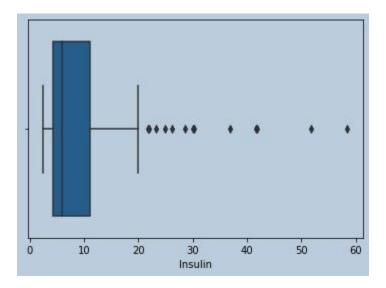
OUTLIERS FOR GLUCOSE

#Some outliers are there for Glucose and data is Skewed
sns.boxplot(data['Glucose'])



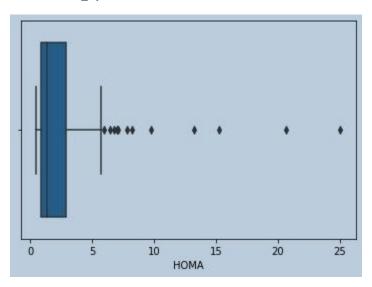
OUTLIERS FOR INSULIN?

#Outliers are present in Insulin
sns.boxplot(data['Insulin'])



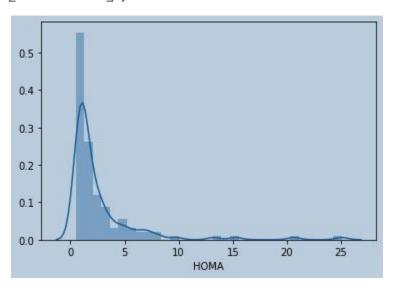
OUTLIERS FOR HOMA

#lots of Outliers in Homa
sns.boxplot(data['HOMA'])



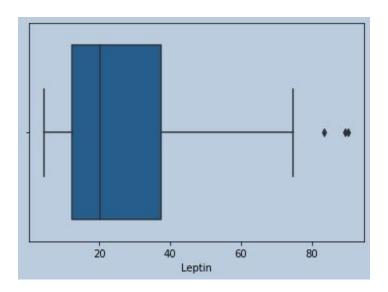
DISTRIBUTION OF HOMA

#Distribution plot of HOMA
sns.distplot(data['HOMA'])

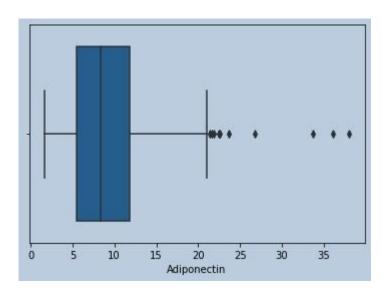


OUTLIERS FOR LEPTIN

```
#Outliers present for Leptin
sns.boxplot(data['Leptin'])
```

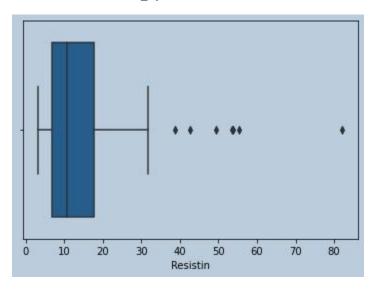


#Outliers present for Adiponectin
sns.boxplot(data['Adiponectin'])



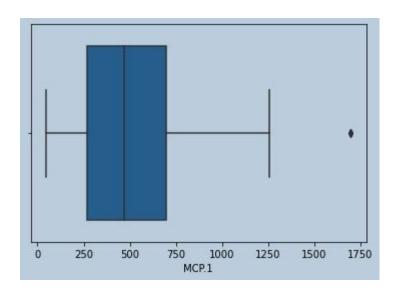
OUTLIERS FOR RESISTIN

#Ouliers present for Resistin
sns.boxplot(data['Resistin'])



OUTLIERS FOR MCP. 1?

```
#Outliers present for MCP.1
sns.boxplot(data['MCP.1'])
```



REMOVE OUTLIERS

```
#Removing Outliers Since they may affect prediction for KNN (quantile method)
   cancer=data.copy()
   insulinQ1=cancer['Insulin'].quantile(0.25)
   insulinQ3=cancer['Insulin'].quantile(0.75)
    insulinIQR=insulinQ3-insulinQ1
    lowerliminsulin=insulinQ1-1.5*insulinIQR
   upperliminsulin=insulinQ3+1.5*insulinIQR
   insulrem=cancer[(cancer['Insulin']>lowerliminsulin)&(upperliminsulin >
cancer['Insulin'])]
```

```
sns.boxplot(insulrem['Glucose'])
glucoseQ1=insulrem['Glucose'].quantile(0.25)
glucoseQ3=insulrem['Glucose'].quantile(0.75)
glucoseIQR=glucoseQ3-glucoseQ1
upperlimglucose=glucoseQ3+1.5*glucoseIQR
lowerlimglucose=glucoseQ1-1.5*glucoseIQR
glucoserem=insulrem[(insulrem['Glucose'] >
lowerlimglucose)&(upperlimglucose > insulrem['Glucose'])]
```

```
sns.boxplot(glucoserem['HOMA'])
homaQ1=glucoserem['HOMA'].quantile(0.25)
homaQ3=glucoserem['HOMA'].quantile(0.75)
homaIQR=homaQ3-homaQ1
upperlimhoma=homaQ3+1.5*homaIQR
lowerlimhoma=homaQ1-1.5*homaIQR
homarem=glucoserem[(glucoserem['HOMA'] >
lowerlimhoma)&(upperlimhoma > glucoserem['HOMA'])
```

```
sns.boxplot(homarem['Adiponectin'])
AdiponectinQ1=homarem['Adiponectin'].quantile(0.25)
AdiponectinQ3=homarem['Adiponectin'].quantile(0.75)
AdiponectinIOR=AdiponectinO3-AdiponectinO1
upperlimAdiponectin=AdiponectinQ3+1.5*AdiponectinIQR
lowerlimAdiponectin=AdiponectinQ1-1.5*AdiponectinIQR
adirem=homarem[(homarem['Adiponectin'] >
lowerlimAdiponectin)&(upperlimAdiponectin >
homarem['Adiponectin'])]
```

sns.boxplot(adirem['Resistin'])

sns.boxplot(adirem['Leptin'])

sns.boxplot(adirem['MCP.1'])

create the features from data
X=mcprem.iloc[:,0:9]

create the target variable from data
Y=mcprem.iloc[:,9]

STANDARDIZE

STANDARDIZE TO BRING ALL TO THE SAME SCALE

```
from sklearn.preprocessing import StandardScaler
ss=StandardScaler()
X=ss.fit_transform(X)
X=pd.DataFrame(X)
```

SPLIT DATA

from sklearn.model_selection import train_test_split

xtrain,xtest,ytrain,ytest=train_test_split(X,Y,test_size=0.3)

BUILD THE CLASSIFIER

BUILD THE MODEL

```
#Finding accuracies on TrainData and Test data with euclidean distance(by default
p=2
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score
for x in range(5,10,2):
        knn=KNeighborsClassifier(n_neighbors=x,metric='minkowski',weights='distance')
        knn.fit(xtrain,ytrain)
        train_ypred=knn.predict(xtrain)
        acc_train_score=accuracy_score(train_ypred,ytrain)
        test_ypred=knn.predict(xtest)
        acc_test_score=accuracy_score(test_ypred,ytest)
        print(f'Accuracy score for train data and test data is {acc_train_score} and
{acc_test_score} respectively for {x} neighbours')
```

BUILD THE MODEL WITH EUCLIDEAN DISTANCE

```
knn=KNeighborsClassifier(n_neighbors=7,metric='minkowski',we
ights='distance')
knn.fit(xtrain,ytrain)
trainypred=knn.predict(xtrain)
```

RUN A METRIC REPORT

```
from sklearn.metrics import classification_report
print(classification_report(trainypred,ytrain))
accuracy_score(trainypred,ytrain)
testypredicted=knn.predict(xtest)
from sklearn.metrics import accuracy_score
```

<pre>accuracy_score(testypredicted,ytest)</pre>		precision	recall	f1-score	support
	1	0.92	0.71	0.80	31
	2	0.64	0.89	0.74	18
	accuracy			0.78	49
	macro avg	0.78	0.80	0.77	49
	weighted avg	0.82	0.78	0.78	49

PICKLES

```
import pickle
#Save our model as a pickle to a file
pickle.dump(knn, open("my_knn_model.pickle.dat", "wb"))
# delete the existing knn model from the environment
del knn
#Load the pickled object from the file
load knn=pickle.load(open("my knn model.pickle.dat", "rb"))
# Use the loaded model to make predictions
load knn.predict(xtest)
```

SUMMARY