

PYTHON BASICS

Python for data science

WORKING WITH ARRAYS

Numpy

DATA ENGINEERING

pandas

DATA SCIENCE 2 DATA & A.I. 3

IV

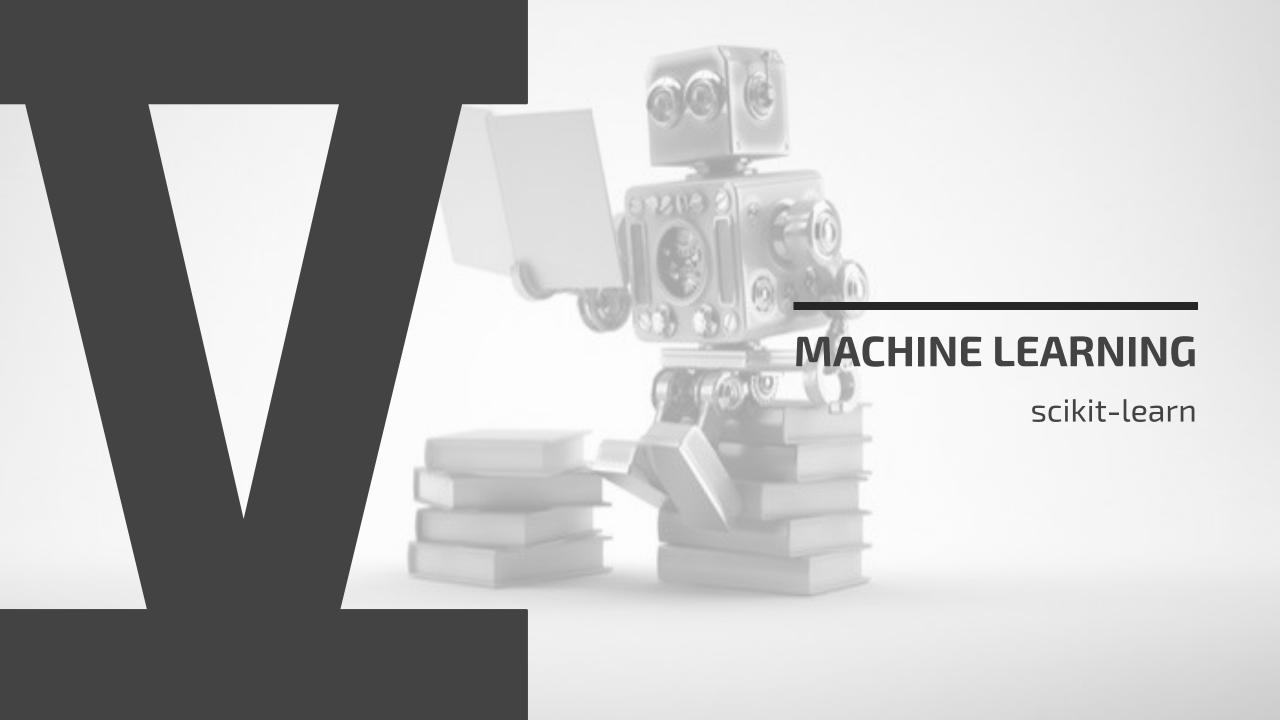
DATA VISUALISATION

Matplotlib

V

MACHINE LEARNING

Automatically find patterns



WHAT IS MACHINE LEARNING

Automatically find patterns

01

INTRODUCING SCIKIT-LEARN

Machine learning with Python

02

HYPERPARAMETERS AND CROSS VALIDATION

Holdout samples and cross-validation

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DECISION TREES

Best separating lines

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MACHINE

LEARNING

K-MEANS CLUSTERING

Object grouping

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Frequent itemsets

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ARTIFICIAL NEURAL NETWORK

Imitate the human brain

REGRESSION

Best fitting line

SUPERVISED LEARNING: REGRESSION

Linear and Polynomial Regression



REGRESSION (SUPERVISED LEARNING)

What?

prediction of numerical outcomes

How?

Fit a mathematical function to the data to model the relationship between features and the target.

Linear Regression: Fits a linear function to predict a numerical outcome.

Polynomial Regression: Fits a polynomial function (with varying degrees) to capture non-linear relationships in the data.

REGRESSION (SUPERVISED LEARNING)

Basic code framework:

```
from sklearn.model_family import ModelAlgo
mymodel = ModelAlgo(param1,param2)
mymodel.fit(X_train,y_train)
predictions = mymodel.predict(X_test)

from sklearn.metrics import error_metric
performance = error_metric(y_test,predictions)
```

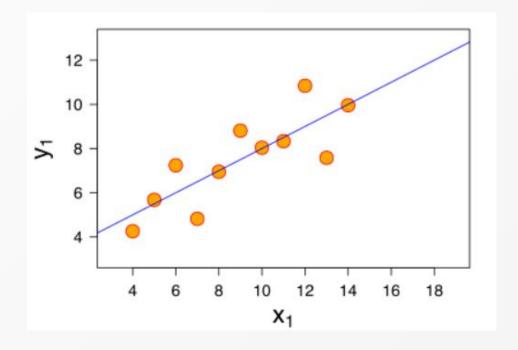
This framework will be similar for any supervised machine learning algorithm. Let's begin exploring it further with Linear Regression!

LINEAR REGRESSION

prediction of numerical features

Try to fit a line (y = ax + b) to the data in the best possible way

See Data & A.I. 2



```
from sklearn.linear_model import LinearRegression
model = LinearRegression(fit intercept=True)
```

Hyperparameters:

fit_intercept

- **Type**: boolean, default = True
- **Description**: Determines whether or not the model should calculate the intercept (also called the bias term). If True, the model calculates the intercept. If False, the model assumes the data is already centered around the origin (i.e., the intercept is 0).
- **Usage**: fit_intercept=False may be useful if you know the data is already centered or you want a model without an intercept.

copy_X

- Type: boolean, default = True
- **Description**: If True, X will be copied before fitting the model. If False, changes to the original data (such as scaling) will affect the original dataset. It's usually safer to leave this as True.

n_jobs

- **Type**: int, default = None
- **Description**: This specifies the number of CPU cores to use when fitting the model. If n_jobs=-1, all available cores will be used. This can help speed up the model fitting when working with large datasets.

```
# DATA PREPARATION
import pandas as pd
pd.options.display.max rows = None
import seaborn as sns
iris = sns.load dataset('iris')
X = iris[['sepal_width', 'sepal_length', 'petal_width']] # Predictors
y = iris['petal_length'] # Target feature to predict
# MODEL SELECTION AND HYPERPARAMETER SELECTION (MODEL SPECIFIC)
from sklearn.linear model import LinearRegression
model = LinearRegression(fit intercept=True)
print(model)
# List all selected hyperparameters
print(model.get params(deep=True))
# DERIVE MODEL FROM LABELED DATA (TRAIN MODEL/FIT MODEL)
model.fit(X,y)
```

```
# DISPLAY COEFFICIENTS (slope and intercept)
print(f"Intercept: { model.intercept_}")
print(f"Coefficients: { model.coef_}")

# SHOW REGRESSION LINE IN SCATTERPLOT
plt.figure(figsize=(8,6))
sns.regplot(x='X_test',y='y_test',data=iris,scatter_kws={"color":"blue"}, line_kws={"color":"red"})
plt.title("Linear Regression: Actual vs Predicted")
plt.xlabel("X values")
plt.ylabel("y values")
plt.show()
```

VALIDATE MODEL USING LABELED DATA

```
from sklearn.metrics import mean absolute error, mean absolute percentage error,
root mean squared error, r2 score
# Predict target feature for the labeled data
y pred = pd.Series(model.predict(X), name='y pred')
# Calculate the difference between predicted and real values for the labeled data
err = pd.Series(y pred-y, name='err')
display(pd.concat([y, y pred, err], axis=1))
# Metrics
mae = mean absolute error (y true=y, y pred=y pred)
mape = mean absolute percentage error (y true=y, y pred=y pred)
rmse = root mean squared error (y true=y, y pred=y pred)
r2 = r2 \text{ score}(y \text{ test, } y \text{ pred})
print(f'MAE : {mae:.3f} - MAPE : {mape:.3f} - RMSE : {rmse:.3f} - R^2 : {r2:.3f}')
```

APPLY MODEL ON NEW DATA

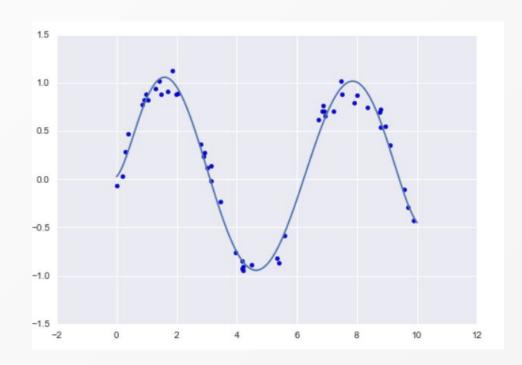
X_pred = (new feature data to predict the target feature for)
y_pred = model.predict(X_pred)

POLYNOMIAL REGRESSION

prediction of numerical features

Try to fit a polynomial function $(y = ax^2 + bx + c)$ to the data in the best possible way

See Data & A.I. 2



POLYNOMIAL REGRESSION WITH SCIKIT-LEARN

- 1. Import necessary libraries: No major change here, still using numpy, pandas, and scikit-learn like with linear regression.
- 2. Transform features for Polynomial Regression: We need to add polynomial features (e.g., squared, cubic terms) to capture non-linear relationships:

```
from sklearn.preprocessing import PolynomialFeatures
poly = PolynomialFeatures(degree=2) # Choose the degree (2 for quadratic, 3 for cubic, etc.)
X_poly = poly.fit_transform(X)
```

3. Fit the Polynomial Regression model: Same as with linear regression, but now using the transformed polynomial features:

```
from sklearn.linear_model import LinearRegression
model = LinearRegression()
model.fit(X_poly, y)
```

4. Make Predictions: Use the polynomial-transformed features for predictions:

```
y_pred = model.predict(poly.transform(X_test))
```

5. Evaluate the model: Same steps as with linear regression

Notebook:

See 05.06-Linear-Regression.ipynb

Exercises: 05.07-EX.ipynb

SUPERVISED LEARNING: DECISION TREES

Decision Trees and Random Forests

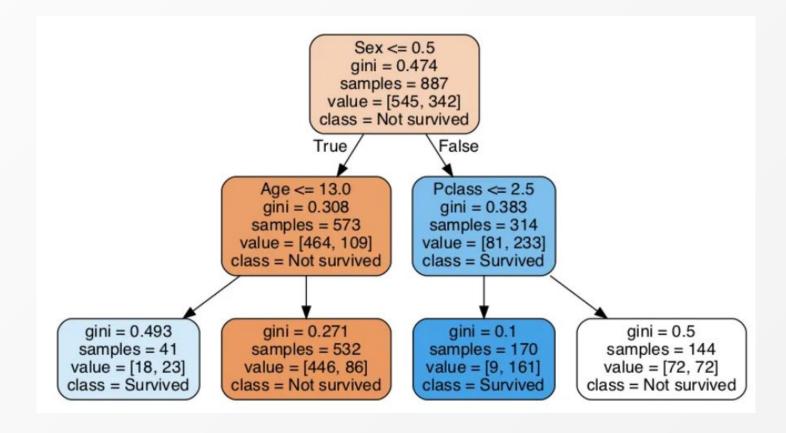


DECISION TREES

Decision trees:

A supervised learning algorithm used for **classification** and **regression** tasks creating a tree-like model of decisions based on input features

See Data & A.I. 2



DECISION TREES WITH SCIKIT-LEARN

```
from sklearn.tree import DecisionTreeClassifier
model = DecisionTreeClassifier(criterion='gini')
```

Hyperparameters:

criterion

- Type: string, default='gini'
- **Description**: This function measures the quality of a split. Supported criteria are 'gini' for the Gini impurity and 'entropy' for the information gain.
- Usage: Choose 'gini' for the Gini impurity (default) or 'entropy' for information gain when building the decision tree.

max_depth

- **Type**: int, default=None
- **Description**: The maximum depth of the tree. If None, nodes are expanded until all leaves are pure or contain fewer samples than the min_samples_split.
- **Usage**: Set this to limit the depth of the tree and avoid overfitting.

min_samples_split

- **Type**: int or float, default=2
- **Description**: The minimum number of samples required to split an internal node. If an integer, it's the minimum number. If a float, it's the fraction of the total number of samples.
- **Usage**: Increase this value to reduce overfitting by making the tree more generalized.

DECISION TREES WITH SCIKIT-LEARN

```
from sklearn.tree import DecisionTreeClassifier
model = DecisionTreeClassifier(criterion='gini')
```

Hyperparameters:

min_samples_leaf

- Type: int or float, default=1
- **Description**: The minimum number of samples required to be at a leaf node. A smaller value allows smaller leaves and may lead to overfitting.
- Usage: A higher value can make the model more conservative and less prone to overfitting.

max_features

- **Type**: int, float, string or None, default=None
- **Description**: The number of features to consider when looking for the best split. If None, all features are considered.
- **Usage**: Restricting the number of features can lead to a more generalized model.

```
# DATA PREPARATION
import pandas as pd
pd.options.display.max rows = None
import seaborn as sns
iris = sns.load dataset('iris')
y = iris['species'] # Target feature to predict
X = iris.copy().drop('species', axis=1) # Predictors
# MODEL SELECTION AND HYPERPARAMETER SELECTION (MODEL SPECIFIC)
from sklearn.tree import DecisionTreeClassifier
model = DecisionTreeClassifier(max depth=1)
print(model)
# List all selected hyperparameters
print(model.get params(deep=True))
# DERIVE MODEL FROM LABELED DATA (TRAIN MODEL/FIT MODEL)
model.fit(X,y)
```

DISPLAY MODEL (MODEL SPECIFIC) from sklearn.tree import plot tree plot tree(model) # VALIDATE MODEL USING LABELED DATA from sklearn.metrics import confusion matrix, accuracy score, precision score, recall score, fl score, precision recall fscore support, classification report import matplotlib.pyplot as plt # Predict target feature for the labeled data y pred = pd.Seeries(model.predict(X), name='y pred') # Calculate the difference between predicted and real values for the labeled data err = pd.Series(y tst pred.reset index(drop=True)!=y tst.reset index(drop=True), name='err').astype(int)

display(pd.concat([y tst.reset index(drop=True), y tst pred.reset index(drop=True), err],

axis=1))

```
# Confusion matrix
# Display as text (console output)
class labels = sorted(list(pd.concat([y tst,y tst_pred], axis=0).unique()))
# Alternative : model.classes
cm = confusion matrix(y true = y tst, y pred = y tst pred)
print('Predicted label')
print(class labels)
print(cm)
# Display as heatmap (nicer output in Jupyter)
disp = sns.heatmap(cm, square=True, annot=True, cbar=True, cmap='Greys',
xticklabels=class labels, yticklabels=class labels)
plt.xlabel('Predicted label')
plt.ylabel('True label')
disp.xaxis.tick top() # Put x-axis tickers on top
disp.xaxis.set label position('top') # Put x-axis label on top
```

```
# Metrics
acc = accuracy score(y true=y, y pred=y pred)
prec = precision score(y true=y, y pred=y pred, average='weighted')
rec = recall score(y true=y, y pred=y pred, average='weighted')
f1 = f1 score(y true=y, y pred=y pred, average='weighted')
# Mind this is a multiclass classification problem, so precision, recall and F1
# are calculated by class and averaged.
print(f'ACC : {acc:.3f} - PREC : {prec:.3f} - REC : {rec:.3f} - F1 : {f1:.3f}')
# The easiest way to get results by class is to use precision recall fscore support
class labels = sorted(list(pd.concat([y tst,y tst pred], axis=0).unique()))
# Display precision/recall/fscore/support table as text (consule output)
print(class labels)
display(precision recall fscore support(y true=y tst, y pred=y tst pred))
# Display precision/recall/fscore/support as pandas dataframe (nicer outputin Jupyter)
display(pd.DataFrame(precision recall fscore support(y true=y tst, y pred=y tst pred),
index=['prec','rec','fscore','sup'], columns=class labels))
# Or use classification report
print(classification report(y true=y tst, y pred=y tst pred,
target names=class lahels))
```

APPLY MODEL ON NEW DATA

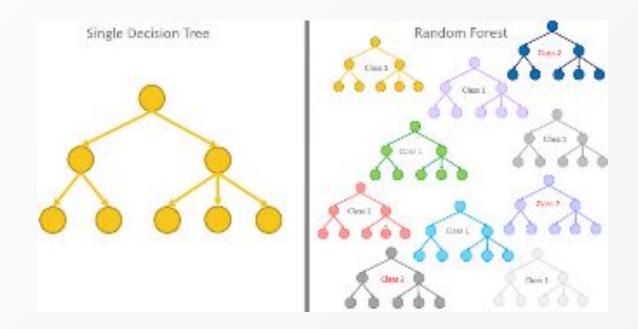
X_pred = (new feature data to predict the target feature for)
y pred = model.predict(X pred)

RANDOM FORESTS

Random forests:

An ensemble method that builds multiple decision trees and aggregates their results for improved accuracy in classification and regression tasks.

See Data & A.I. 2



RANDOM FORESTS WITH SCIKIT-LEARN

```
from sklearn.ensemble import RandomForestClassifier
model = RandomForestClassifier(n_estimators=100)
```

Hyperparameters:

n estimators

- Type: int, default=100
- **Description**: The number of trees in the forest. More trees usually lead to better performance but increase computation time.
- Usage: Use higher values (e.g., 500, 1000) for larger datasets to improve performance.

max_depth

- **Type**: int, default=None
- **Description**: The maximum depth of each tree in the forest. If None, nodes are expanded until all leaves are pure.
- **Usage**: Restrict this to prevent overfitting, especially when building deep trees.

max_features

- Type: int, float, string or None, default='auto'
- **Description**: The number of features to consider when looking for the best split. 'auto' uses the square root of the number of features.
- **Usage**: Try different values such as 'sqrt' (square root) or 'log2' to tune the model for better performance.

min_samples_split

- Type: int or float, default=2
- **Description**: The minimum number of samples required to split an internal node in each tree.
- **Usage**: Adjust this to balance between underfitting and overfitting.

RANDOM FORESTS WITH SCIKIT-LEARN: EXAMPLE

Import necessary libraries

```
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
```

Create some example data

```
# For illustration, we generate a synthetic dataset from sklearn.datasets import make classification
```

```
X, y = make_classification(n_samples=1000, n_features=10, n_classes=2,
random state=42)
```

Split the data into training and test sets

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,
random state=42)
```

Initialize and train the Random Forest Classifier

```
model = RandomForestClassifier(n_estimators=100, max_depth=5, random_state=42)
model.fit(X train, y train)
```

RANDOM FORESTS WITH SCIKIT-LEARN: EXAMPLE

Make predictions

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

Evaluate the model

```
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")
print("Confusion Matrix:")
print(conf_matrix)
print("Classification Report:")
print(class report)
```

DECISION TREES AND RANDOM FORESTS

Notebook:

See 05.08-Random-Forests.ipynb

Exercises: 05.08and11_EX.ipynb

UNSUPERVISED LEARNING: CLUSTERING

K-Means

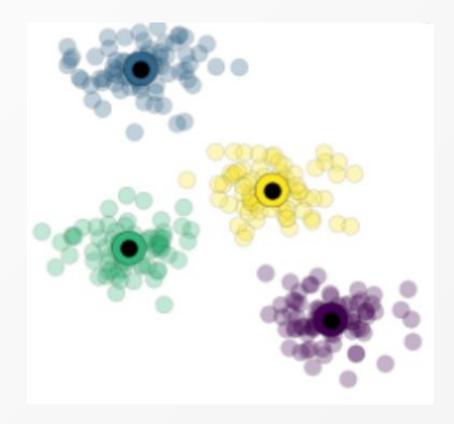


K-MEANS CLUSTERING

K-Means Clustering:

An unsupervised machine learning algorithm used to group similar data points into a predefined number of clusters based on their feature similarities.

See Data & A.I. 2



K-MEANS CLUSTERING WITH SCIKIT-LEARN

```
from sklearn.cluster import KMeans
model = KMeans(n_clusters=4)
```

Hyperparameters:

n_clusters

- **Type**: int, default=8
- Description: The number of clusters to form, and the number of centroids to generate.
- **Usage**: Set this to specify how many groups you want the data divided into.

init

- Type: {'k-means++', 'random'}, default='k-means++'
- **Description**: Method for initializing the cluster centroids. k-means++ chooses centroids to speed up convergence, while random selects random points.
- **Usage**: k-means++ is typically preferred, but random can be used for experimentation.

max_iter

- **Type**: int, default=300
- **Description**: The maximum number of iterations allowed for the algorithm to run until it converges.
- **Usage**: Increase this if your model is not converging, but usually the default works well.

K-MEANS CLUSTERING WITH SCIKIT-LEARN

Hyperparameters:

tol

- Type: float, default=1e-4
- **Description**: The tolerance for the convergence criterion. The algorithm stops when the difference in the cluster centers falls below this threshold.
- Usage: Decrease this value to make the algorithm more precise at the cost of computation time.

n init

- **Type**: int, default=10
- **Description**: The number of times the algorithm will be run with different centroid seeds. The final result will be the best output of these runs.
- Usage: Increase this to get a more stable result by running the algorithm multiple times with different initializations.

algorithm

- Type: {'auto', 'full', 'elkan'}, default='llkan'
- **Description**: The algorithm to use for clustering. elkan is faster with sparse data, while full uses the standard EM-style algorithm.
- Usage: elkan is recommended for efficiency, especially when handling large datasets.

random_state

- **Type**: int, default=None
- **Description**: The seed used by the random number generator. Setting this ensures the same results each time the algorithm is run.
- Usage: Useful when you want reproducible results.

K-MEANS CLUSTERING WITH SCIKIT-LEARN EXAMPLE

Import necessary libraries

```
import numpy as np
import pandas as pd
from sklearn.cluster import KMeans
import seaborn as sns
import matplotlib.pyplot as plt
```

Create or load some example data

```
# For illustration, we generate a synthetic dataset from sklearn.datasets import make_blobs
```

```
# Generate synthetic data with 4 clusters
X, y_true = make_blobs(n_samples=300, centers=4, cluster_std=0.60, random_state=42)
```

Initialize and fit the KMeans model

```
kmeans = KMeans(n_clusters=4, init='k-means++', max_iter=300, random_state=42)
kmeans.fit(X)
```

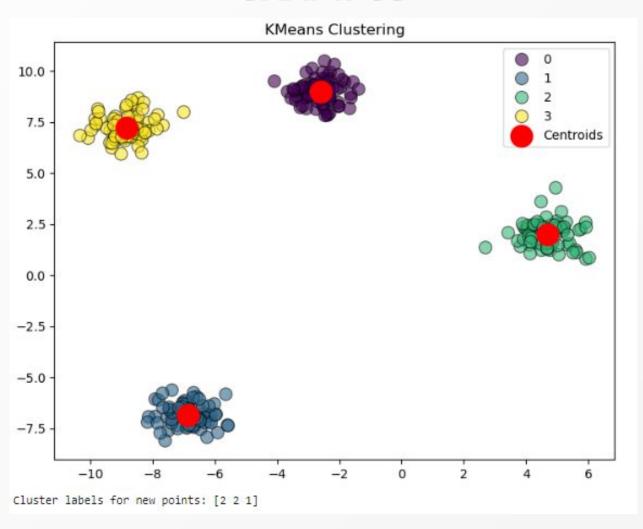
Get the cluster centers and labels

```
centroids = kmeans.cluster_centers_
labels = kmeans.labels_
```

K-MEANS CLUSTERING WITH SCIKIT-LEARN centers and labels EXAMPLE

```
# Get the cluster centers and labels
centroids = kmeans.cluster centers
labels = kmeans.labels
# Visualize the clusters
plt.figure(figsize=(8, 6))
# Plot the points and color by cluster
sns.scatterplot(x=X[:, 0], y=X[:, 1], hue=labels, palette="viridis", s=100, alpha=0.6,
edgecolor="k")
# Plot the centroids
plt.scatter(centroids[:, 0], centroids[:, 1], s=300, c='red', label='Centroids')
plt.title('KMeans Clustering')
plt.legend()
plt.show()
# Predicting new points
new points = np.array([[0, 0], [5, 5], [-5, -5]])
predictions = kmeans.predict(new points)
print(f"Cluster labels for new points: {predictions}")
```

K-MEANS CLUSTERING WITH SCIKIT-LEARN EXAMPLE



K-MEANS CLUSTERING

Notebook:

See 05.11-K-Means.ipynb

Exercises: 05.08and11_EX.ipynb

TEMPLATE

Dark colour: RGB 67 67 67 (HEX #434343)

Dark colour greyed out: RGB 191 191 191 (HEX #BFBFBF)

Light colour : RGB 242 242 242 (HEX #F2F2F2)

Light colour greyed out: RGB 191 191 191 (HEX #BFBFBF)

Base font: Roboto Condensed (size 16 / 14)

Alternative font: Exo 2 (bold, size 28 / 20 / 16 / 14) or Proxima Nova or Verdana

Dark gradient fill Linear 45° RGB 35 35 35 - RGB 67 67 67

Light gradient fill Linear 45° RGB 255 255 255 - RGB 242 242 242

WHAT IS DATA **ANALYTICS**

Data driven decision support

WHY IS THIS RELEVANT

Radical innovation

HOW DOES IT WORK

Variation, correlation & coincidence



HOW DOES IT WORK

Variation, correlation & coincidence



OVERVIEW OF THE FIELD

Descriptive, exploratory, confirmatory, predictive & prescriptive analysis

WHAT IS THIS

ALL ABOUT

OVERVIEW OF THE FIELD

Descriptive, exploratory, confirmatory, predictive & prescriptive analysis

THE BROADER PICTURE

The data analytics cycle

WHAT'S IN IT FOR YOU

User, integrator, enabler, data engineer, data scientist, data analyst

INTRODUCTION TO EXPLORATIVE DATA ANALYSIS

Why is this happening

UNIVARIATE

One variable at a time

MULTIVARIATE Multiple variables at the same time



SECTION 4

Whatever



SECTION 5

Whatever

WHAT IS DATA **ANALYTICS**

01

Data driven decision support

WHY IS THIS RELEVANT

Radical innovation

02

HOW DOES IT WORK

Variation, correlation & coincidence

HOW DOES IT WORK

Variation, correlation & coincidence 03

04

WHAT IS THIS

ALL ABOUT

05

OVERVIEW OF THE FIELD

Descriptive, exploratory, confirmatory, predictive & prescriptive analysis

OVERVIEW OF THE 06 **FIELD**

Descriptive, exploratory, confirmatory, predictive & prescriptive analysis

07

THE BROADER PICTURE

The data analytics cycle

08

WHAT'S IN IT FOR YOU

User, integrator, enabler, data engineer, data scientist, data analyst

WHAT IS DATA ANALYTICS

Data driven decision support











SUMMARY

WAARDECREATIE

- Data analytics gaat over het creëren van waarde;
- Maatschappelijke waarde en bedrijfswaarde;
- Door allerlei producten en diensten te verbeteren;
- In alle mogelijke afdelingen;
- In alle mogelijke sectoren.

3 MANIEREN VAN WAARDECREATIE

- Kostreductie: doe bestaande dingen goedkoper;
- Snellere en betere beslissingen: doe bestaande dingen beter;
- Nieuwe producten en diensten: doe nieuwe dingen.

WAT IS NIEUW?

- Niet nieuw, statistiiek bestaat al meer dan 200 jaar;
- Maar groeit en evolueert snel, omwille van:
 - massieve beschikbaarheid van data,
 - massive computerkracht,
 - geavanceerde technieken en gereedschappen.

DATA DRIVEN COMPETITION

- De huidige boom is geen hype;
- Technologische factoren (beschikbaarheid van data en computerkracht, technieken en gereedschappen) zijn enkel maar faciliterende factoren;
- De echte drijvende factor is innovatie;
- Niet de traditionele incrementele innovatie (alles wordt elk jaar een beetje beter);
- Maar radicale innovatie (radicaal nieuwe of betere producten);
- Daar zit het geld;
- De kracht van data analytics zit in het potentieel voor radicale innovatie;
- Resulteert in data driven competitiie: je verwerft een competitief voordeel dat niet genegeerd kan worden.

RADICALE INNOVATIE

- Procesinnovatie: maak bestaande producten en diensten goedkoper;
- Productinnovatie: maak bestaande producten en diensten beter of creëer nieuwe producten en diensten;
- Marktinnovatie: herschrijf de regels;