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Data Science and Machine Learning for Engineering Applications

Scikit-learn Clustering

Salvatore Greco Andrea Pasini Flavio Giobergia Elena Baralis Tania Cerquitelli

DataBase and Data Mining Group

Introduction to Scikit-learn

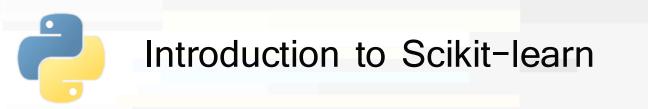
Scikit-learn

- Machine learning library built on NumPy, SciPy and Matplotlib
- What Scikit-learn can do
 - Unsupervised learning
 - Clustering
 - Supervised learning
 - Regression, classification
 - Data preprocessing
 - Feature extraction, feature selection, dimensionality reduction

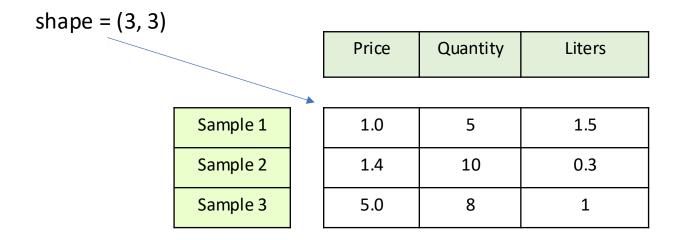


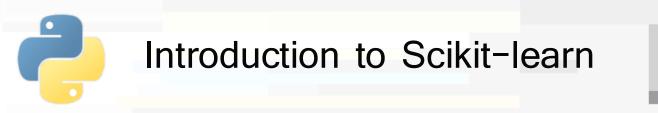
What Scikit-learn cannot do

- Distributed computation on multiple computers
 - Only multi-core optimization
- Deep learning
 - Use Torch, Keras and Tensorflow instead



- Scikit learn models work with structured data
 - Data must be in the form of 2D Numpy arrays
 - Rows represent the samples
 - Columns represent the attributes (or features)
 - This table is called features matrix





- Features can be
 - Real values
 - Integer values to represent categorical data
- If you have strings in your data, you first have to convert them to integers (preprocessing)

Input data

1.0	January	1.5	
1.4	February	0.3	
5.0	March	1	

Features matrix

1.0	0	1.5
1.4	1	0.3
5.0	2	1



Also missing values must be solved before applying any model

With imputation or by removing rows

Input data

1.0	0.5	1.5	
1.4	NaN	0.3	
5.0	0.5	1	

Features matrix

1.0	0.5	1.5
1.4	0.5	0.3
5.0	0.5	1

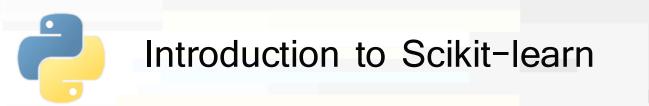
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Input data

1.0	0.5	1.5	
1.4	NaN	0.3	
5.0	0.5	1	

Features matrix

1.0	0.5	1.5
5.0	0.5	1

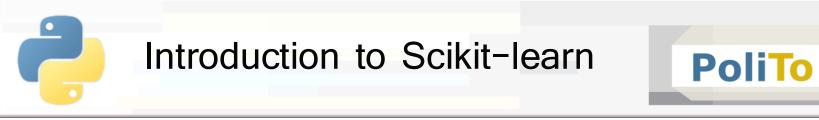


- For **unsupervised** learning you only need the features matrix
- For supervised learning you also need a target array to train the model
 - It is typically one-dimensional, with length n_samples
 - May be 2-dimensional for multi-output models

Features matrix shape = (n_samples, n_features)

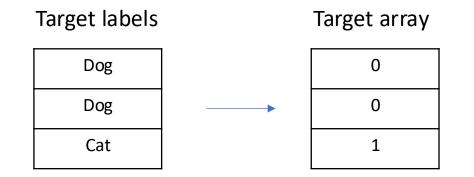
1.0	5	1.5
1.4	10	0.3
5.0	8	1

Target array
shape = (n_samples,)



The target array can contain

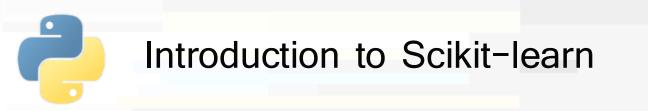
Integer values, each corresponding to a class label



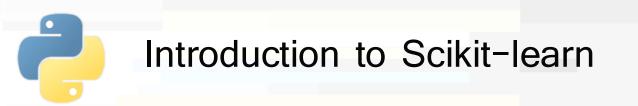
Real values for regression

Target array

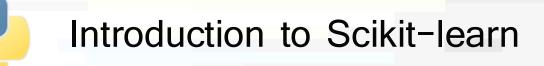
0.4	
1.8	
-6.9	



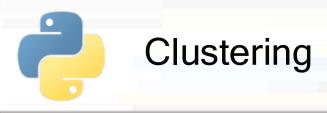
- Scikit-learn estimator API
 - All models are represented with Python classes
 - Their classes include
 - The values of the hyperparameters used to configure the model
 - The values of the parameters learned after training
 - By convention these attributes end with an underscore
 - The methods to train the model and make inference
 - Scikit-learn models are provided with sensible defaults for the hyperparameters



- Scikit learn models follow a simple, shared pattern
 - 1. Import the model that you need to use
 - 2. Build the model, setting its hyperparameters
 - 3. Train model parameters on your data
 - Using the fit() method
 - 4. Use the model to make predictions
 - Using the predict()/transform() methods
- Sometimes fit and predict/transform are implemented within the same class method

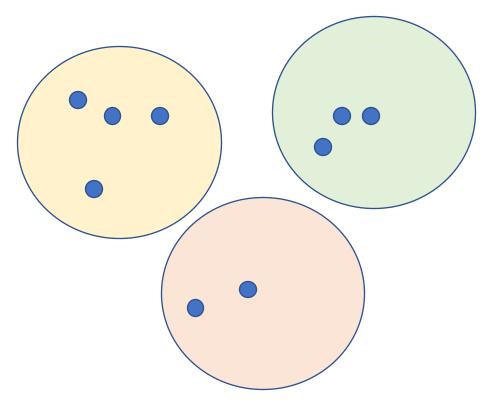


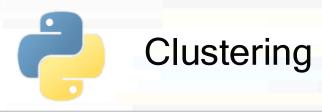
- **fit():** learn model parameters from input data
 - E.g. train a classifier
- predict(): apply model parameters to make predictions on data
 - E.g. predict class labels
- transform(): transform data into a different representation
 - E.g. normalize test data
- fit_predict(): fit model and make predictions
 - E.g. apply clustering to data
- fit_transform(): fit model and transform data
 - E.g. apply PCA to transform data





- Unsupervised technique that analyzes the data distribution to generate N partitions
 - Unsupervised = it only requires a features matrix







Import a model

from sklearn.cluster import KMeans

Build model object

km = KMeans(n_clusters = 5)

- The hyperparameter n_clusters specifies the number of centroids (= number of clusters)
 - Default is 8 (buy may change across different library versions)

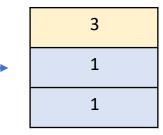


Apply clustering to input data (Numpy)

Out[1]: | [3, 1, 1, 1, 2, 2, 0]

- This operation assigns data to their respective cluster
 - X is the 2D NumPy array with input features (features matrix)
 - y pred is a 1D array with cluster labels

1.0	5	1.5
1.4	10	0.3

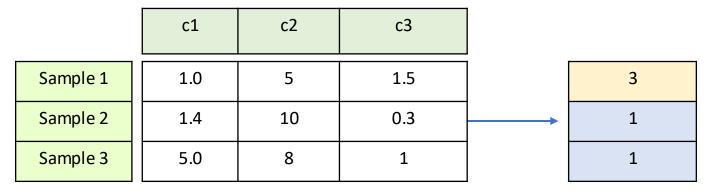




Apply clustering to input data (Pandas)

Out[1]: [3, 1, 1, 1, 2, 2, 0]

- This operation assigns data to their respective cluster
 - df is the 2D DataFrame with input features (features matrix)
 - y pred is a 1D array with cluster labels



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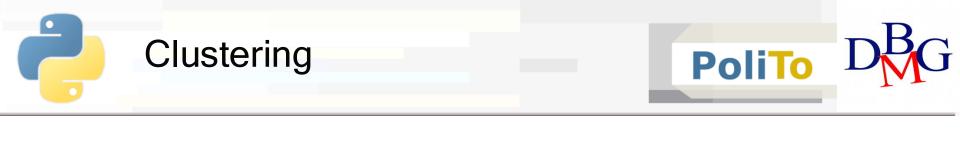
Example: DBSCAN

from sklearn.cluster import DBSCAN

```
cl_alg = DBSCAN(eps=3, min_samples=2)
```

 Example: Hierarchical clustering, n_clusters=5, average linkage

```
from sklearn.cluster import AgglomerativeClustering
cl_alg = AgglomerativeClustering(5, linkage='average')
```

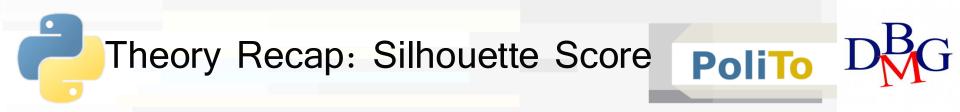


Assessing clustering results

- Internal metrics: use only the information of the features matrix
 - E.g. Silhouette, SSE

```
from sklearn.metrics import silhouette_score, silhouette_samples
silh_avg = silhouette_score(X, clusters)
silh_i = silhouette_samples(X, clusters)
```

- Silhouette is a number in the range [-1, 1]
- Higher values mean higher cluster quality
 - Clusters are well separated and cohesive
- Expensive computation! O(n²)

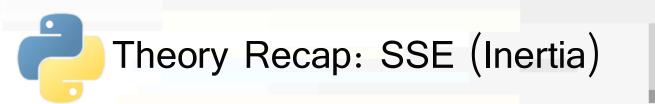


a(i): Average distance to points in the same cluster.b(i): Smallest average distance to another cluster.Formula:

$$s(i) = \frac{b(i) - a(i)}{max(b(i), a(i))}$$

Average s(i):

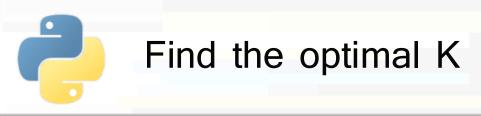
- Per cluster \rightarrow cohesion.
- Whole dataset \rightarrow clustering quality (close to 1).

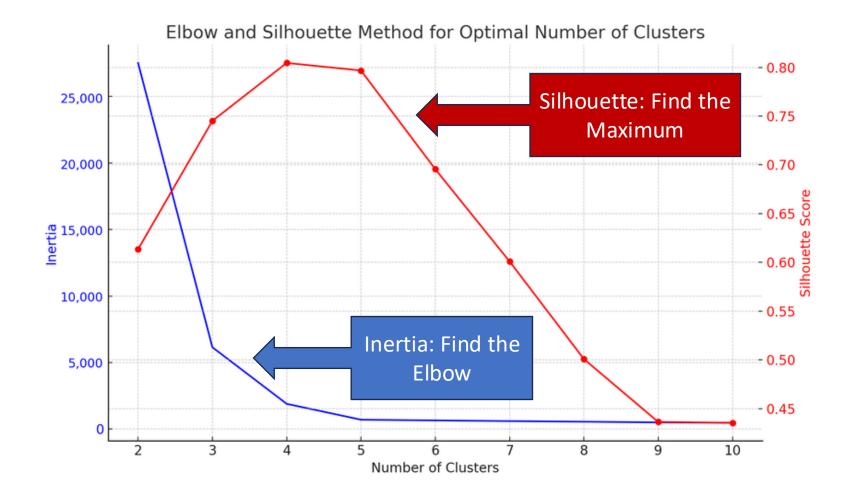


- SSE (Sum of Squared Errors): Sum of the squared distances between each point x_i and its cluster center $C(x_i)$.
- Also called <u>Inertia</u>
- Formula:

$$SSE = \sum_{i}^{N} \left| |x_i - C(x_i)| \right|^2$$

- Meaning:
 - Lower **SSE** \rightarrow points are closer to their cluster center.
 - Used to evaluate clustering compactness.





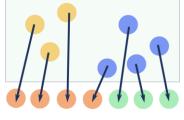


- Assessing clustering results
 - External metrics: compare a clustering result with some ground-truth labels
 - E.g. Adjusted Rand Score, Fowlkes-Mallows index

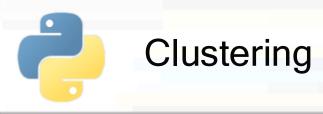
from sklearn.metrics import adjusted_rand_score

ars = adjusted_rand_score(c_truth, c_pred)

- The ARS score ranges* in [0, 1]
 - • 0: randomly assigned clusters
 - 1: perfect agreement
 - [!] Values < 0 may occur if cluster assignments are worse than random
- It is close to 1 when data in the predicted clusters is grouped in a similar way compared with ground truth



ground truth



- Adjusted Rand Score (ARS)
 - Does not check for equality of target and predictions
 - It checks whether data are clustered in the same way
 - Example:
 - c_truth = [1, 1, 2, 2, 2, 1]
 c_pred = [2, 2, 1, 1, 1, 2]
 - ARS(c_truth, c_pred) is 1

