

# Unsupervised Learning

UNSUPERVISED LEARNING IN PYTHON



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# Unsupervised learning

- Unsupervised learning finds patterns in data
- E.g., *clustering* customers by their purchases
- Compressing the data using purchase patterns (*dimension reduction*)

# Supervised vs unsupervised learning

- *Supervised* learning finds patterns for a prediction task
- E.g., classify tumors as benign or cancerous (*labels*)
- Unsupervised learning finds patterns in data
- ... but *without* a specific prediction task in mind

# Iris dataset

- Measurements of many iris plants
- Three species of iris:
  - *setosa*
  - *versicolor*
  - *virginica*
- Petal length, petal width, sepal length, sepal width  
(the *features* of the dataset)



<sup>1</sup> [https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load\\_iris.html](https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_iris.html)

# Arrays, features & samples

- 2D NumPy array
- Columns are measurements (the *features*)
- Rows represent iris plants (the *samples*)

# Iris data is 4-dimensional

- Iris samples are points in 4 dimensional space
- Dimension = number of features
- Dimension too high to visualize!
- ... but unsupervised learning gives insight

# k-means clustering

- Finds clusters of samples
- Number of clusters must be specified
- Implemented in `sklearn` ("scikit-learn")

```
print(samples)
```

```
[[ 5.   3.3  1.4  0.2]
 [ 5.   3.5  1.3  0.3]
 ...
 [ 7.2  3.2  6.   1.8]]
```

```
from sklearn.cluster import KMeans
model = KMeans(n_clusters=3)
model.fit(samples)
```

```
KMeans(n_clusters=3)
```

```
labels = model.predict(samples)
print(labels)
```

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

# Cluster labels for new samples

- New samples can be assigned to existing clusters
- k-means remembers the mean of each cluster (the "centroids")
- Finds the nearest centroid to each new sample

# Cluster labels for new samples

```
print(new_samples)
```

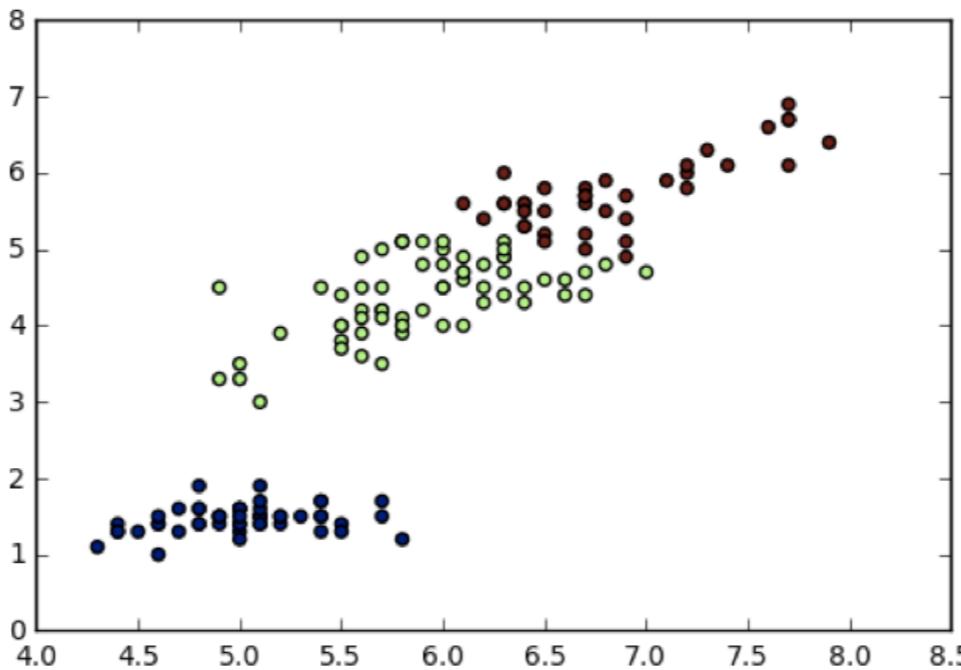
```
[[ 5.7  4.4  1.5  0.4]
 [ 6.5  3.   5.5  1.8]
 [ 5.8  2.7  5.1  1.9]]
```

```
new_labels = model.predict(new_samples)
print(new_labels)
```

```
[0 2 1]
```

# Scatter plots

- Scatter plot of sepal length vs. petal length
- Each point represents an iris sample
- Color points by cluster labels
- PyPlot (`matplotlib.pyplot`)



# Scatter plots

```
import matplotlib.pyplot as plt  
  
xs = samples[:,0]  
ys = samples[:,2]  
plt.scatter(xs, ys, c=labels)  
plt.show()
```

# **Let's practice!**

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# Evaluating a clustering

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# Evaluating a clustering

- Can check correspondence with e.g. iris species
- ... but what if there are no species to check against?
- Measure quality of a clustering
- Informs choice of how many clusters to look for

# Iris: clusters vs species

- k-means found 3 clusters amongst the iris samples
- Do the clusters correspond to the species?

| species | setosa | versicolor | virginica |
|---------|--------|------------|-----------|
| labels  |        |            |           |
| 0       | 0      | 2          | 36        |
| 1       | 50     | 0          | 0         |
| 2       | 0      | 48         | 14        |

# Cross tabulation with pandas

- Clusters vs species is a "cross-tabulation"
- Use the `pandas` library
- Given the species of each sample as a list `species`

```
print(species)
```

```
['setosa', 'setosa', 'versicolor', 'virginica', ... ]
```

# Aligning labels and species

```
import pandas as pd  
df = pd.DataFrame({'Labels': labels, 'species': species})  
print(df)
```

|     | labels | species    |
|-----|--------|------------|
| 0   | 1      | setosa     |
| 1   | 1      | setosa     |
| 2   | 2      | versicolor |
| 3   | 2      | virginica  |
| 4   | 1      | setosa     |
| ... |        |            |

# Crosstab of labels and species

```
ct = pd.crosstab(df['labels'], df['species'])  
print(ct)
```

| species | setosa | versicolor | virginica |
|---------|--------|------------|-----------|
| labels  |        |            |           |
| 0       | 0      | 2          | 36        |
| 1       | 50     | 0          | 0         |
| 2       | 0      | 48         | 14        |

How to evaluate a clustering, if there were no species information?

# Measuring clustering quality

- Using only samples and their cluster labels
- A good clustering has tight clusters
- Samples in each cluster bunched together

# Inertia measures clustering quality

- Measures how spread out the clusters are (*lower* is better)
- Distance from each sample to centroid of its cluster
- After `fit()`, available as attribute `inertia_`
- k-means attempts to minimize the inertia when choosing clusters

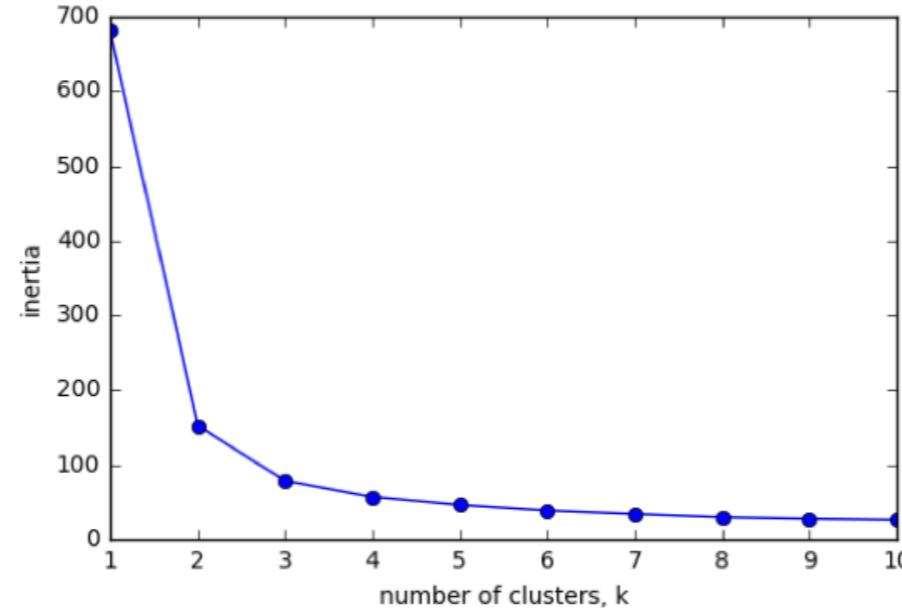
```
from sklearn.cluster import KMeans
```

```
model = KMeans(n_clusters=3)  
model.fit(samples)  
print(model.inertia_)
```

```
78.9408414261
```

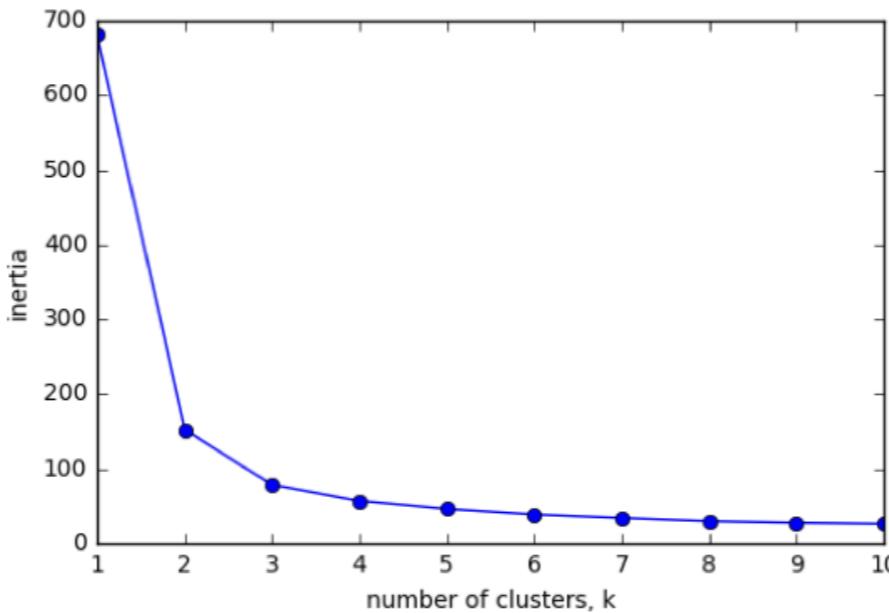
# The number of clusters

- Clusterings of the iris dataset with different numbers of clusters
- More clusters means lower inertia
- What is the best number of clusters?



# How many clusters to choose?

- A good clustering has tight clusters (so low inertia)
- ... but not too many clusters!
- Choose an "elbow" in the inertia plot
- Where inertia begins to decrease more slowly
- E.g., for iris dataset, 3 is a good choice



# **Let's practice!**

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# Transforming features for better clusterings

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# Piedmont wines dataset

- 178 samples from 3 distinct varieties of red wine: Barolo, Grignolino and Barbera
- Features measure chemical composition e.g. alcohol content
- Visual properties like "color intensity"

<sup>1</sup> Source: <https://archive.ics.uci.edu/ml/datasets/Wine>

# Clustering the wines

```
from sklearn.cluster import KMeans  
model = KMeans(n_clusters=3)  
labels = model.fit_predict(samples)
```

# Clusters vs. varieties

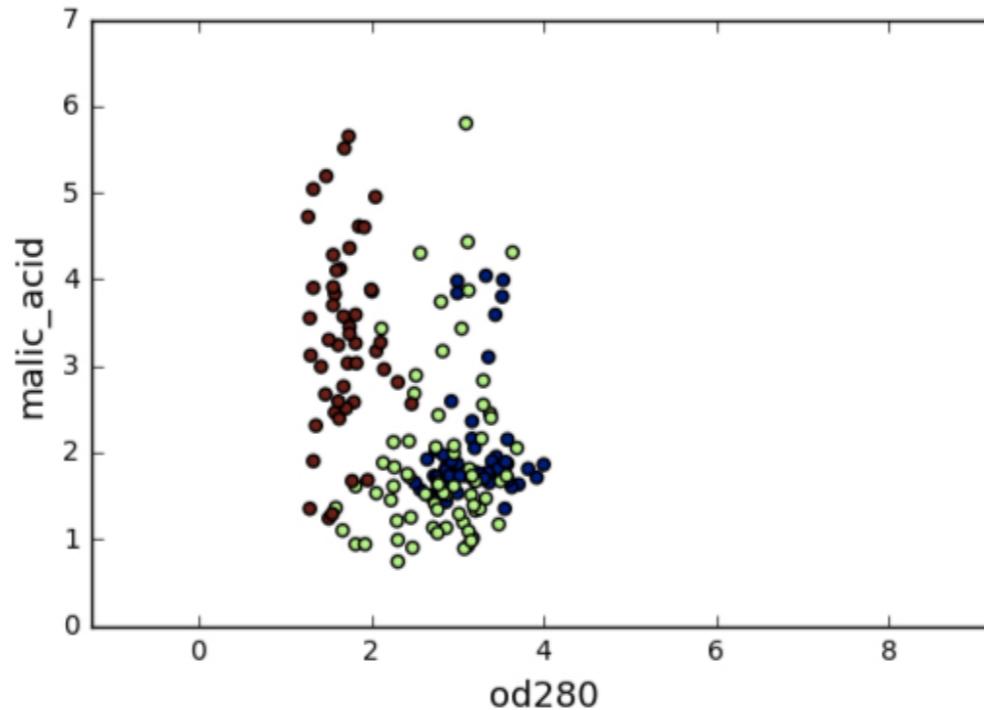
```
df = pd.DataFrame({'labels': labels,  
                   'varieties': varieties})  
ct = pd.crosstab(df['labels'], df['varieties'])  
print(ct)
```

| varieties | Barbera | Barolo | Grignolino |
|-----------|---------|--------|------------|
| labels    |         |        |            |
| 0         | 29      | 13     | 20         |
| 1         | 0       | 46     | 1          |
| 2         | 19      | 0      | 50         |

# Feature variances

- The wine features have very different variances!
- Variance of a feature measures spread of its values

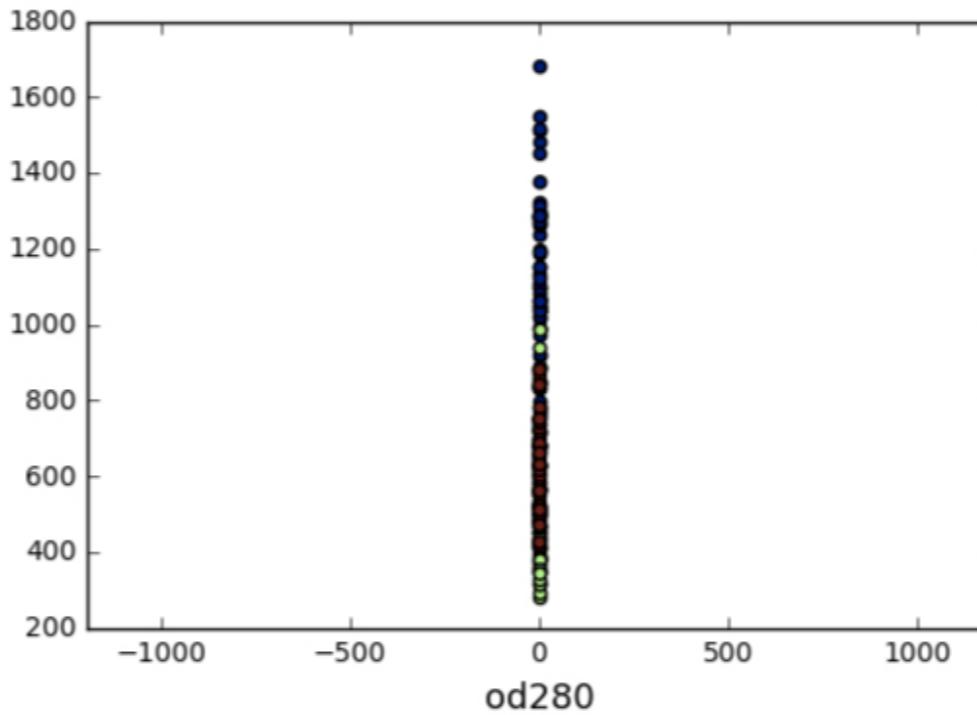
| feature    | variance |
|------------|----------|
| alcohol    | 0.65     |
| malic_acid | 1.24     |
| ...        |          |
| od280      | 0.50     |
| proline    | 99166.71 |



# Feature variances

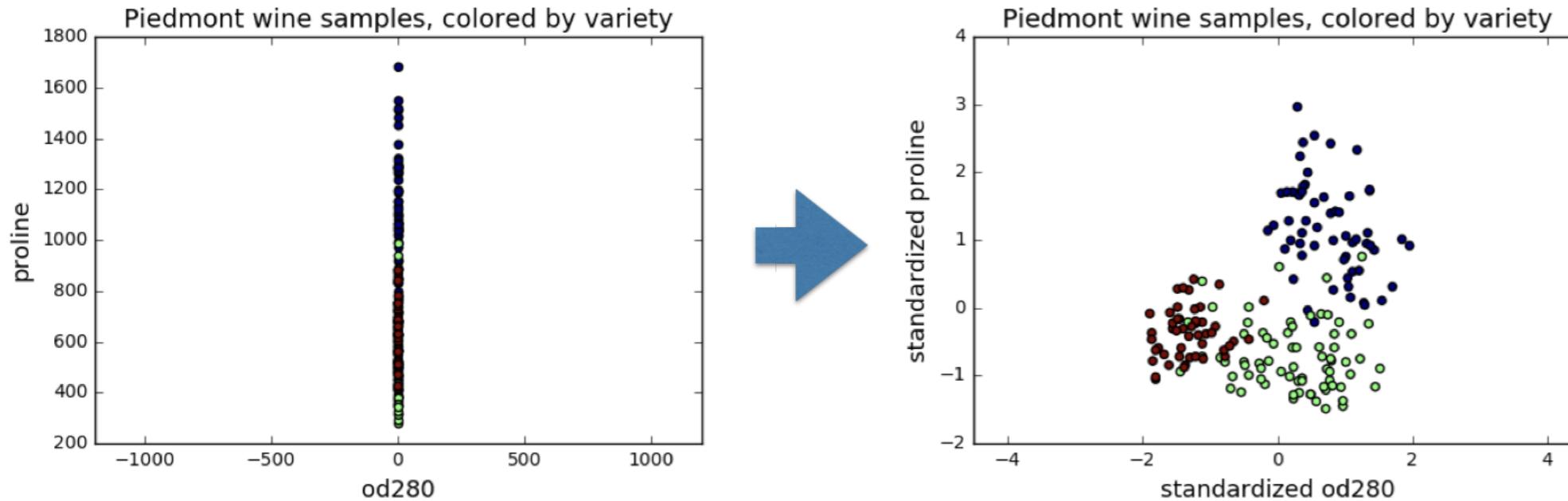
- The wine features have very different variances!
- Variance of a feature measures spread of its values

| feature    | variance |
|------------|----------|
| alcohol    | 0.65     |
| malic_acid | 1.24     |
| ...        |          |
| od280      | 0.50     |
| proline    | 99166.71 |



# StandardScaler

- In kmeans: feature variance = feature influence
- StandardScaler transforms each feature to have mean 0 and variance 1
- Features are said to be "standardized"



# sklearn StandardScaler

```
from sklearn.preprocessing import StandardScaler  
scaler = StandardScaler()  
scaler.fit(samples)  
StandardScaler(copy=True, with_mean=True, with_std=True)  
samples_scaled = scaler.transform(samples)
```

# Similar methods

- `StandardScaler` and `KMeans` have similar methods
- Use `fit()` / `transform()` with `StandardScaler`
- Use `fit()` / `predict()` with `KMeans`

# StandardScaler, then KMeans

- Need to perform two steps: StandardScaler , then KMeans
- Use sklearn pipeline to combine multiple steps
- Data flows from one step into the next

# Pipelines combine multiple steps

```
from sklearn.preprocessing import StandardScaler  
from sklearn.cluster import KMeans  
scaler = StandardScaler()  
kmeans = KMeans(n_clusters=3)  
from sklearn.pipeline import make_pipeline  
pipeline = make_pipeline(scaler, kmeans)  
pipeline.fit(samples)
```

```
Pipeline(steps=...)
```

```
labels = pipeline.predict(samples)
```

# Feature standardization improves clustering

*With feature standardization:*

| varieties | Barbera | Barolo | Grignolino |
|-----------|---------|--------|------------|
| labels    |         |        |            |
| 0         | 0       | 59     | 3          |
| 1         | 48      | 0      | 3          |
| 2         | 0       | 0      | 65         |

*Without feature standardization was very bad:*

| varieties | Barbera | Barolo | Grignolino |
|-----------|---------|--------|------------|
| labels    |         |        |            |
| 0         | 29      | 13     | 20         |
| 1         | 0       | 46     | 1          |
| 2         | 19      | 0      | 50         |

# sklearn preprocessing steps

- `StandardScaler` is a "preprocessing" step
- `MaxAbsScaler` and `Normalizer` are other examples

# **Let's practice!**

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