

Unsupervised Learning

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 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")

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

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

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

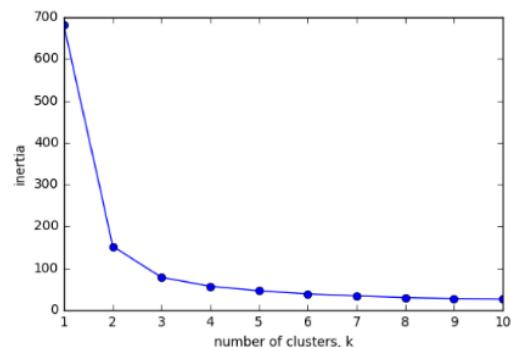
```
from sklearn.cluster import KMeans

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

78.9408414261

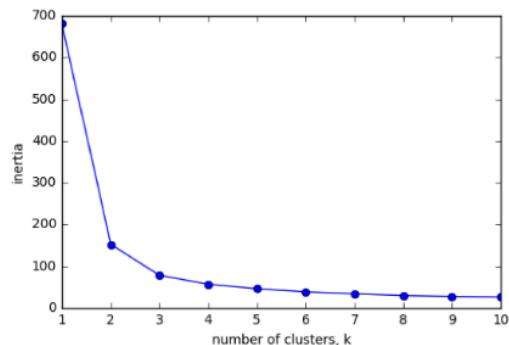
The number of clusters

- 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

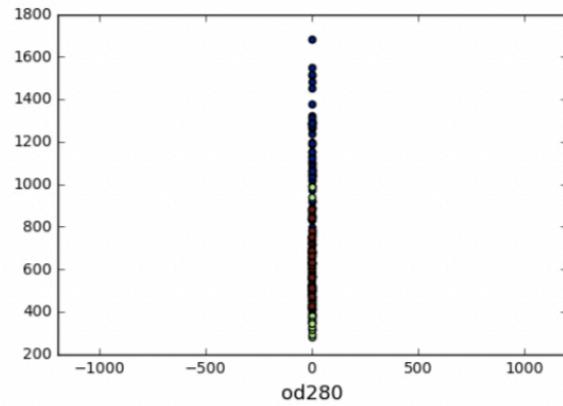


Transforming features for better clusterings

Feature variances

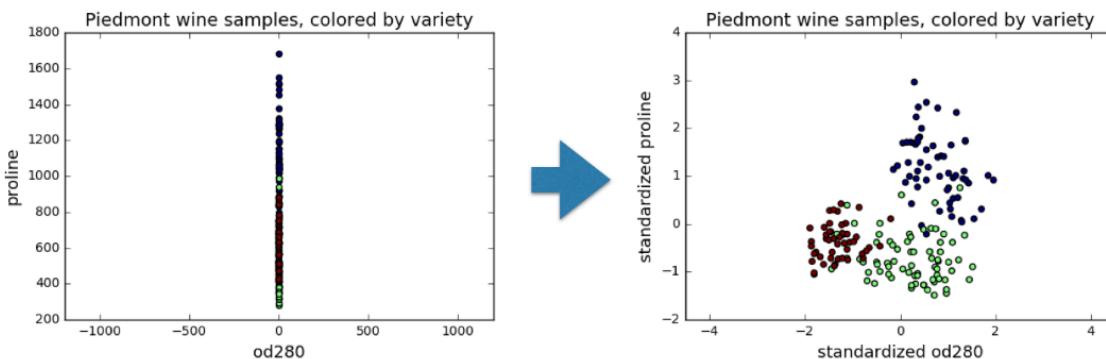
- The wine features have very different variances!
- Variance of a feature measures spread of its values

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

```
# Perform the necessary imports
from sklearn.pipeline import make_pipeline
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
```

```
# Create scaler: scaler
scaler = StandardScaler()
```

```
# Create KMeans instance: kmeans
kmeans = KMeans(n_clusters = 4)
```

```
# Create pipeline: pipeline
pipeline = make_pipeline(scaler, kmeans)
```

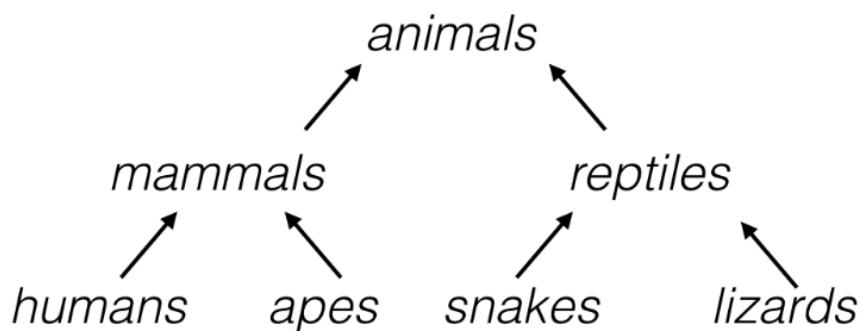
Visualizing hierarchies

Visualizations communicate insight

- "t-SNE" : Creates a 2D map of a dataset (later)
- "Hierarchical clustering" (this video)

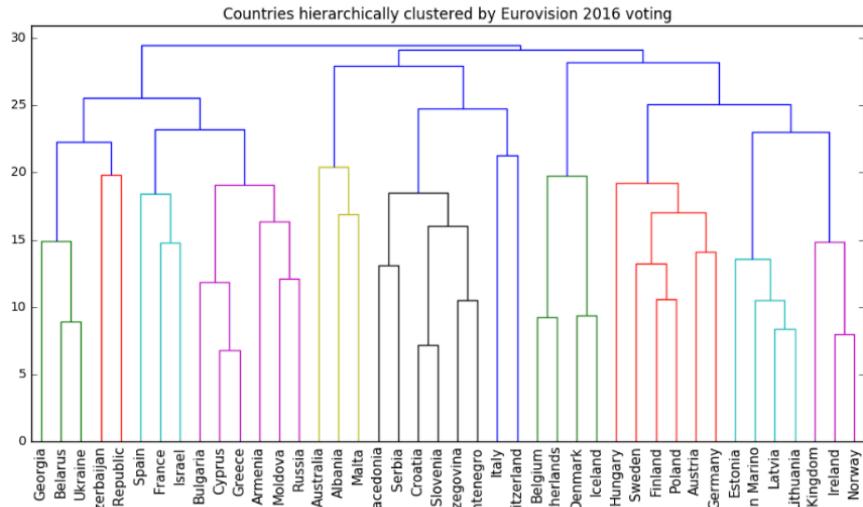
A hierarchy of groups

- Groups of living things can form a hierarchy
- Clusters are contained in one another



Hierarchical Clustering arranges the samples into a hierarchy of clusters.

Hierarchical clustering of voting countries



- Using this we can identify countries that are located near one another geographically, or other relations

Hierarchical clustering

- Every country begins in a separate cluster
- At each step, the two closest clusters are merged
- Continue until all countries in a single cluster
- This is "agglomerative" hierarchical clustering

Hierarchical clustering with SciPy

- Given `samples` (the array of scores), and `country_names`

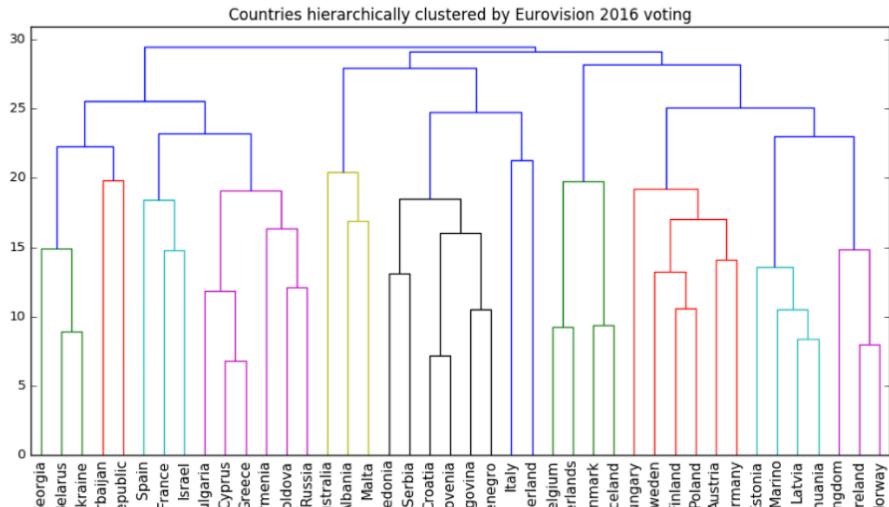
```
import matplotlib.pyplot as plt
from scipy.cluster.hierarchy import linkage, dendrogram
mergings = linkage(samples, method='complete')
dendrogram(mergings,
           labels=country_names,
           leaf_rotation=90,
           leaf_font_size=6)
plt.show()
```

linkage function performs the hierarchical clustering

We pass the output of the linkage function to the dendrogram function with the list of country names as the labels parameter.

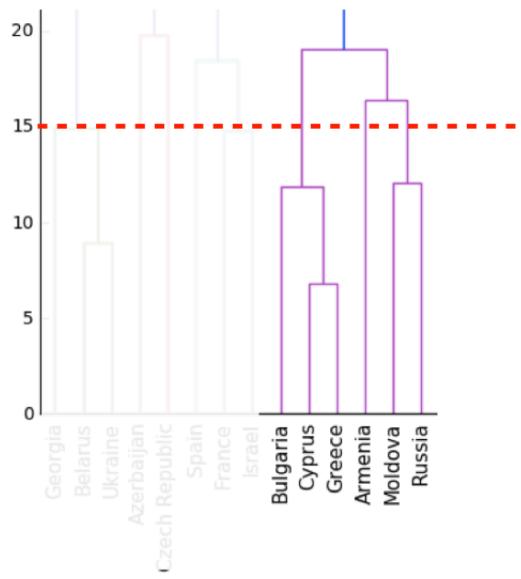
Cluster labels in hierarchical clustering

- Not only a visualization tool!
- Cluster labels at any intermediate stage can be recovered
- For use in e.g. cross-tabulations



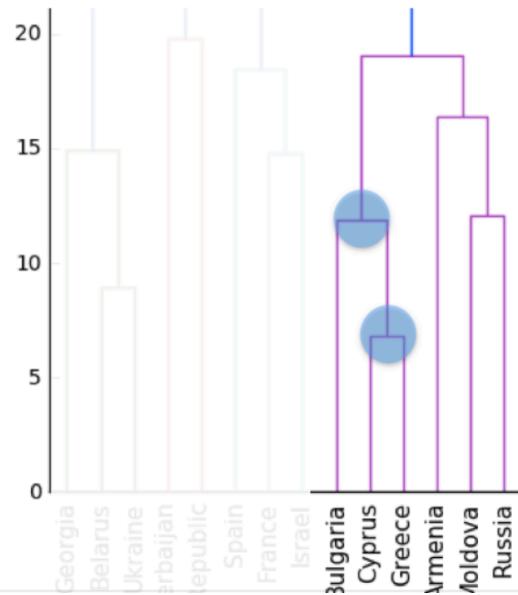
Intermediate clusterings & height on dendrogram

- E.g. at height 15:
 - Bulgaria, Cyprus, Greece are one cluster
 - Russia and Moldova are another
 - Armenia in a cluster on its own



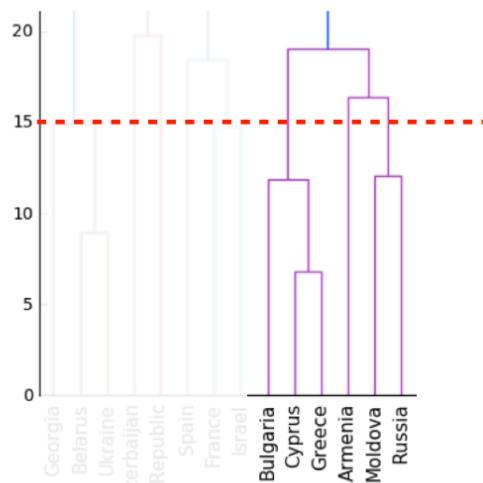
Dendograms show cluster distances

- Height on dendrogram = distance between merging clusters
- E.g. clusters with only Cyprus and Greece had distance approx. 6
- This new cluster distance approx. 12 from cluster with only Bulgaria



Intermediate clusterings & height on den

- Height on dendrogram specifies max. distance between merging clusters
- Don't merge clusters further apart than this (e.g. 15)

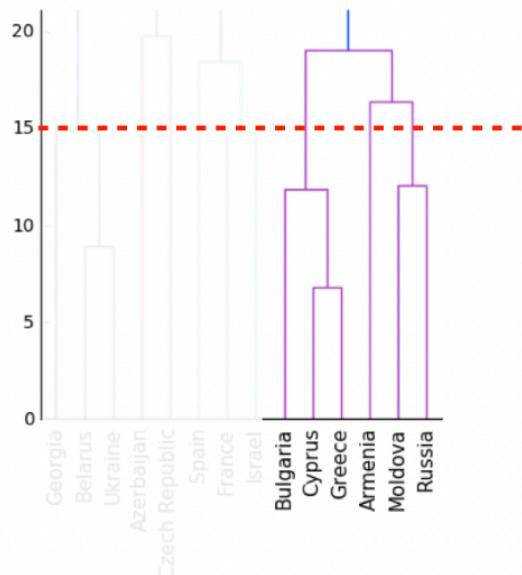


Distance between clusters

- Defined by a "linkage method"
- In "complete" linkage: distance between clusters is max. distance between their samples
- Specified via method parameter, e.g. `linkage(samples, method="complete")`
- Different linkage method, different hierarchical clustering!

Extracting cluster labels

- Use the `fcluster()` function
- Returns a NumPy array of cluster labels



Extracting cluster labels using `fcluster`

```
from scipy.cluster.hierarchy import linkage
mergings = linkage(samples, method='complete')
from scipy.cluster.hierarchy import fcluster
labels = fcluster(mergings, 15, criterion='distance')
print(labels)
```

```
[ 9  8 11 20  2  1 17 14 ... ]
```

Aligning cluster labels with country names

Given a list of strings `country_names` :

```
import pandas as pd
pairs = pd.DataFrame({'labels': labels, 'countries': country_names})
print(pairs.sort_values('labels'))
```

	countries	labels
5	Belarus	1
40	Ukraine	1
...		
36	Spain	5
8	Bulgaria	6
19	Greece	6
10	Cyprus	6
28	Moldova	7
...		

1. Form clusters using linkage method with complete method to perform agglomerative clustering
2. to visualize the clusters make use of the dendrogram method
3. to get cluster labels at a particular height we can make use of the fcluster method.

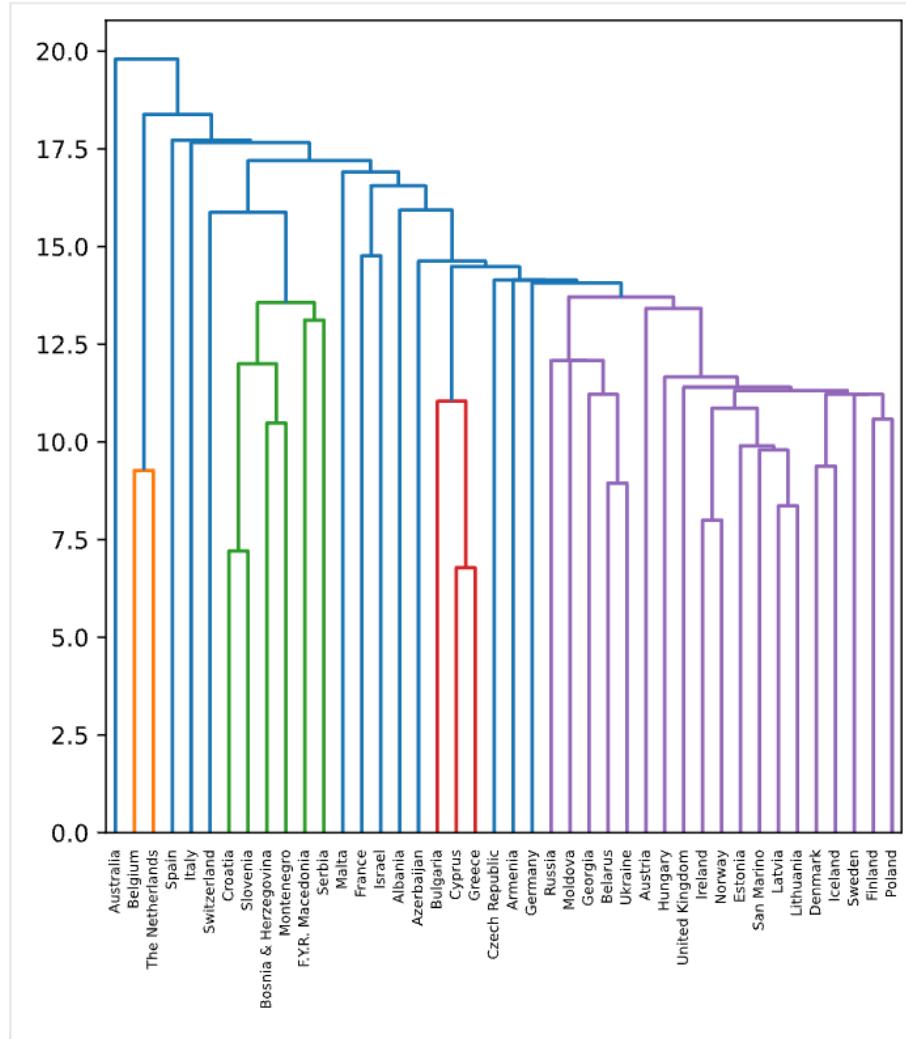
Linkage method defines how the distance between clusters is measured.

In *complete* linkage, the distance between clusters is the distance between the *furthest* points of the clusters. In *single* linkage, the distance between clusters is the distance between the *closest* points of the clusters.

```
# Perform the necessary imports
import matplotlib.pyplot as plt
from scipy.cluster.hierarchy import linkage, dendrogram

# Calculate the linkage: mergings
mergings = linkage(samples, method = 'single')

# Plot the dendrogram
dendrogram(mergings, labels = country_names, leaf_rotation = 90, leaf_font_size
= 6)
plt.show()
```



t-SNE for 2-dimensional maps

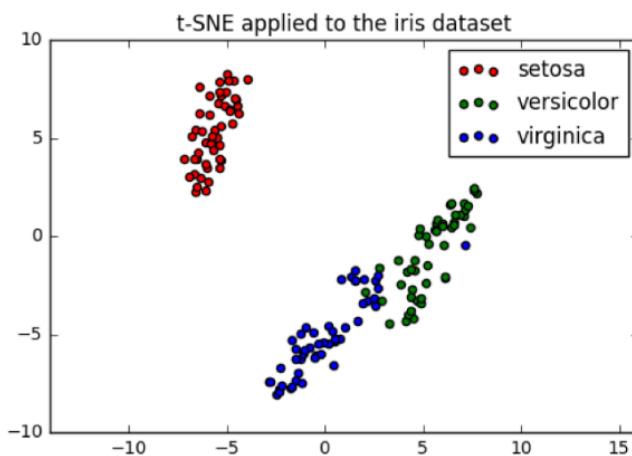
- # t-SNE for 2-dimensional maps
- t-SNE = "t-distributed stochastic neighbor embedding"
 - Maps samples to 2D space (or 3D)
 - Map approximately preserves nearness of samples
 - Great for inspecting datasets

t-SNE on the iris dataset

- Iris dataset has 4 measurements, so samples are 4-dimensional
- t-SNE maps samples to 2D space
- t-SNE didn't know that there were different species

Interpreting t-SNE scatter plots

- "versicolor" and "virginica" harder to distinguish from one another
- Consistent with k-means inertia plot: could argue for 2 clusters, or for 3



t-SNE in sklearn

- 2D NumPy array `samples`

```
print(samples)
```

```
[[ 5.   3.3  1.4  0.2]
 [ 5.   3.5  1.3  0.3]
 [ 4.9  2.4  3.3  1. ]
 [ 6.3  2.8  5.1  1.5]
 ...
 [ 4.9  3.1  1.5  0.1]]
```

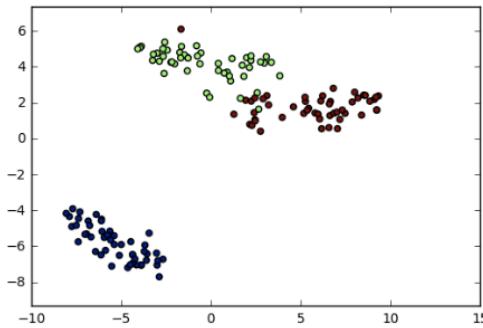
- List `species` giving species of labels as number (0, 1, or 2)

```
print(species)
```

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

t-SNE in sklearn

```
import matplotlib.pyplot as plt
from sklearn.manifold import TSNE
model = TSNE(learning_rate=100)
transformed = model.fit_transform(samples)
xs = transformed[:,0]
ys = transformed[:,1]
plt.scatter(xs, ys, c=species)
plt.show()
```



t-SNE has only fit_transform()

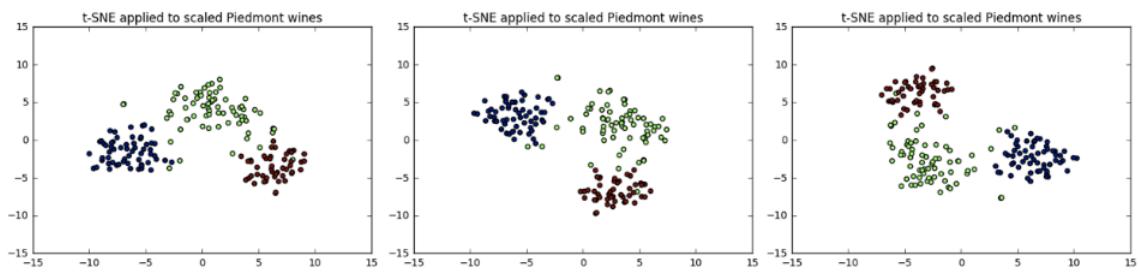
- Has a `fit_transform()` method
- Simultaneously fits the model and transforms the data
- Has no separate `fit()` or `transform()` methods
- Can't extend the map to include new data samples
- Must start over each time!

t-SNE learning rate

- Choose learning rate for the dataset
- Wrong choice: points bunch together
- Try values between 50 and 200

Different every time

- t-SNE features are different every time
- Piedmont wines, 3 runs, 3 different scatter plots!
- ... however: The wine varieties (=colors) have same position relative to one another



PCA transformation

Dimension reduction

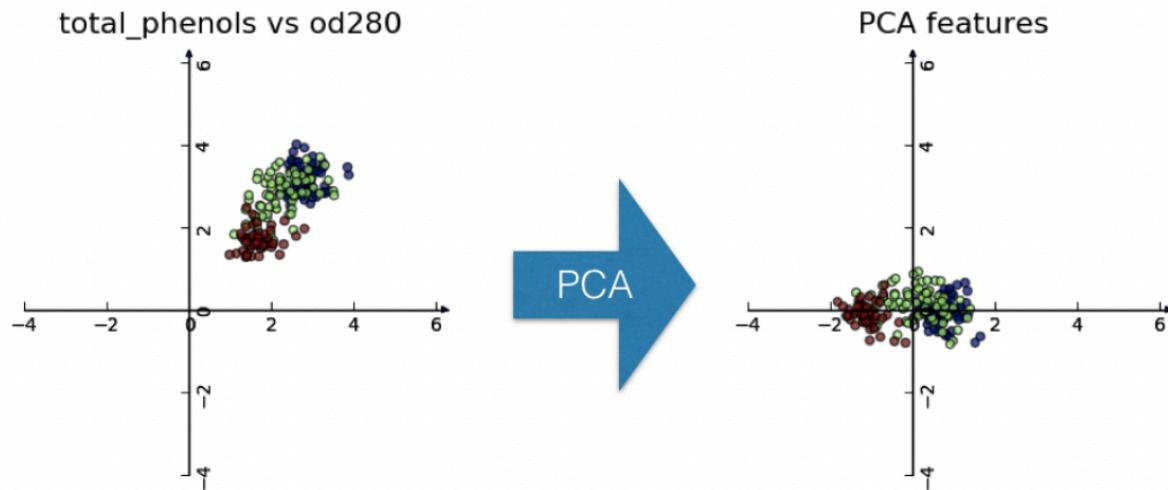
- More efficient storage and computation
- Remove less-informative "noise" features
- ... which cause problems for prediction tasks, e.g. classification, regression

Principal Component Analysis

- PCA = "Principal Component Analysis"
- Fundamental dimension reduction technique
- First step "decorrelation" (considered here)
- Second step reduces dimension (considered later)

PCA aligns data with axes

- Rotates data samples to be aligned with axes
- Shifts data samples so they have mean 0
- No information is lost



PCA follows the fit/transform pattern

- `PCA` is a scikit-learn component like `KMeans` or `StandardScaler`
- `fit()` learns the transformation from given data
- `transform()` applies the learned transformation
- `transform()` can also be applied to new data

Using scikit-learn PCA

- `samples` = array of two features (`total_phenols` & `od280`)

```
[[ 2.8   3.92]  
 ...  
 [ 2.05  1.6 ]]
```

```
from sklearn.decomposition import PCA  
model = PCA()  
model.fit(samples)
```

```
PCA()
```

```
transformed = model.transform(samples)
```

PCA features

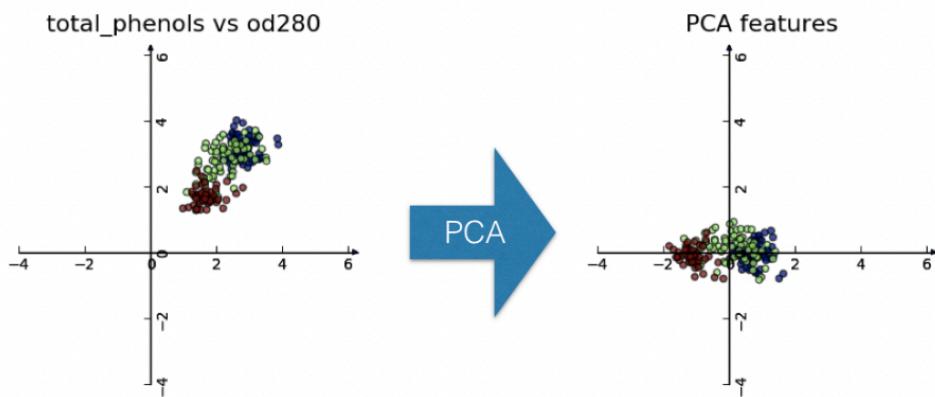
- Rows of transformed correspond to samples
- Columns of transformed are the "PCA features"
- Row gives PCA feature values of corresponding sample

```
print(transformed)
```

```
[[ 1.32771994e+00   4.51396070e-01]  
 [ 8.32496068e-01   2.33099664e-01]  
 ...  
 [ -9.33526935e-01  -4.60559297e-01]]
```

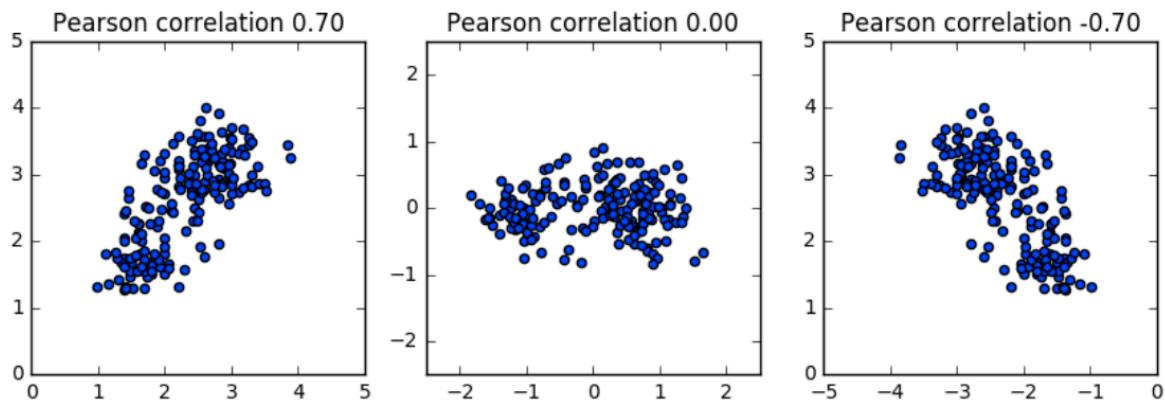
PCA features are not correlated

- Features of dataset are often correlated, e.g. `total_phenols` and `od280`
- PCA aligns the data with axes
- Resulting PCA features are not linearly correlated ("decorrelation")



Pearson correlation

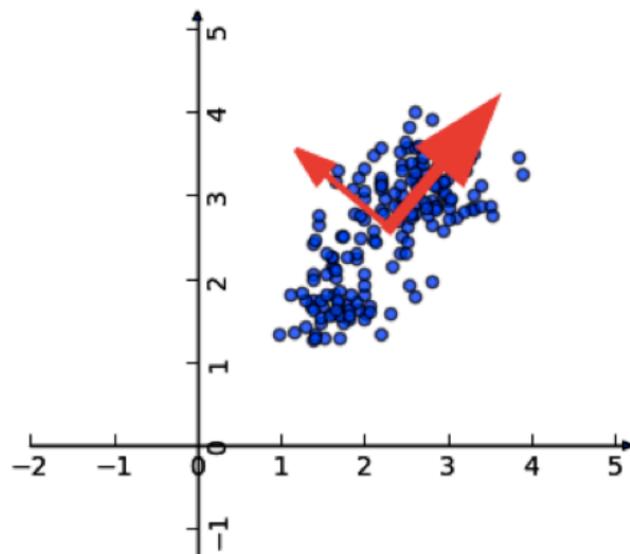
- Measures linear correlation of features
- Value between -1 and 1
- Value of 0 means no linear correlation



Principal components

- "Principal components" = directions of variance
- PCA aligns principal components with the axes

The Principal Components



Principal components

- Available as `components_` attribute of PCA object
- Each row defines displacement from mean

```
print(model.components_)
```

```
[[ 0.64116665  0.76740167]
 [-0.76740167  0.64116665]]
```

```
# Import PCA
from sklearn.decomposition import PCA
```

```
# Create PCA instance: model
model = PCA()
```

```
# Apply the fit_transform method of model to grains: pca_features
```

```

pca_features = model.fit_transform(grains)

# Assign 0th column of pca_features: xs
xs = pca_features[:,0]

# Assign 1st column of pca_features: ys
ys = pca_features[:,1]

# Scatter plot xs vs ys
plt.scatter(xs, ys)
plt.axis('equal')
plt.show()

# Calculate the Pearson correlation of xs and ys
correlation, pvalue = pearsonr(xs, ys)

# Display the correlation
print(correlation)

```

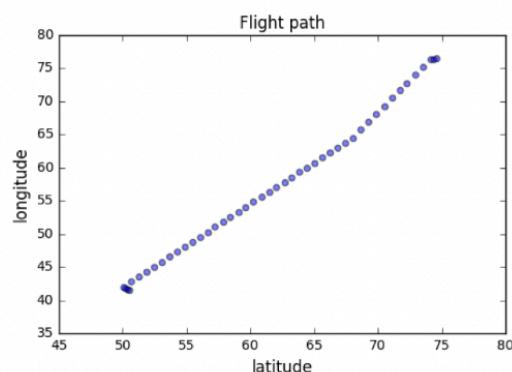
Intrinsic dimension

- number of features needed to approximate the dataset.

Intrinsic dimension of a flight path

- 2 features: longitude and latitude at points along a flight path
- Dataset *appears* to be 2-dimensional
- But can approximate using one feature: displacement along flight path
- Is intrinsically 1-dimensional

latitude	longitude
50.529	41.513
50.360	41.672
50.196	41.835
...	

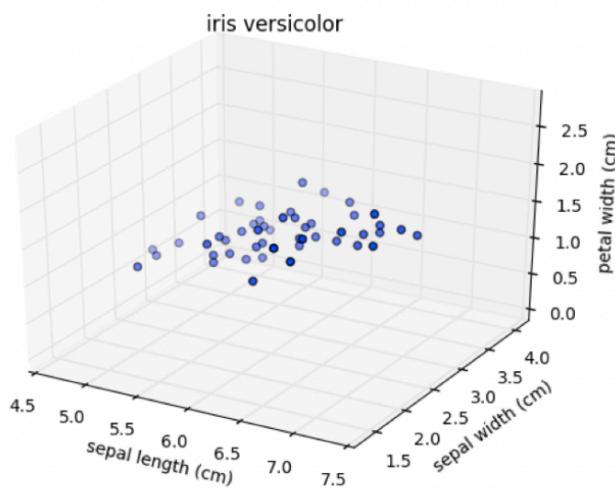


Intrinsic dimension

- Intrinsic dimension = number of features needed to approximate the dataset
- Essential idea behind dimension reduction
- What is the most compact representation of the samples?
- Can be detected with PCA

Versicolor dataset has intrinsic dimension 2

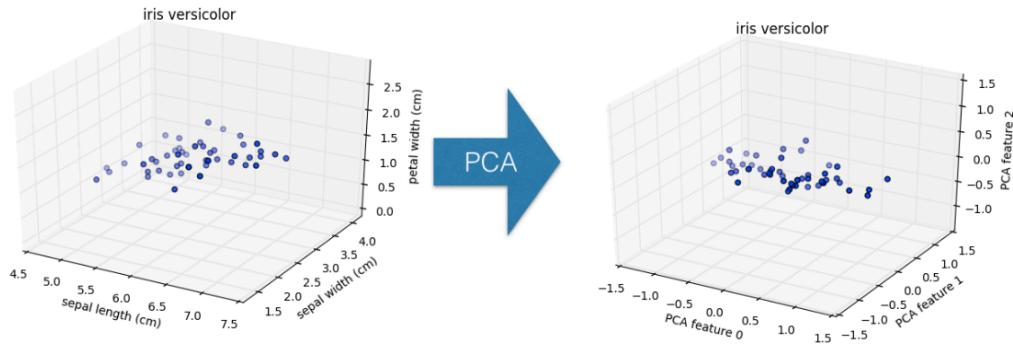
- Samples lie close to a flat 2-dimensional sheet
- So can be approximated using 2 features



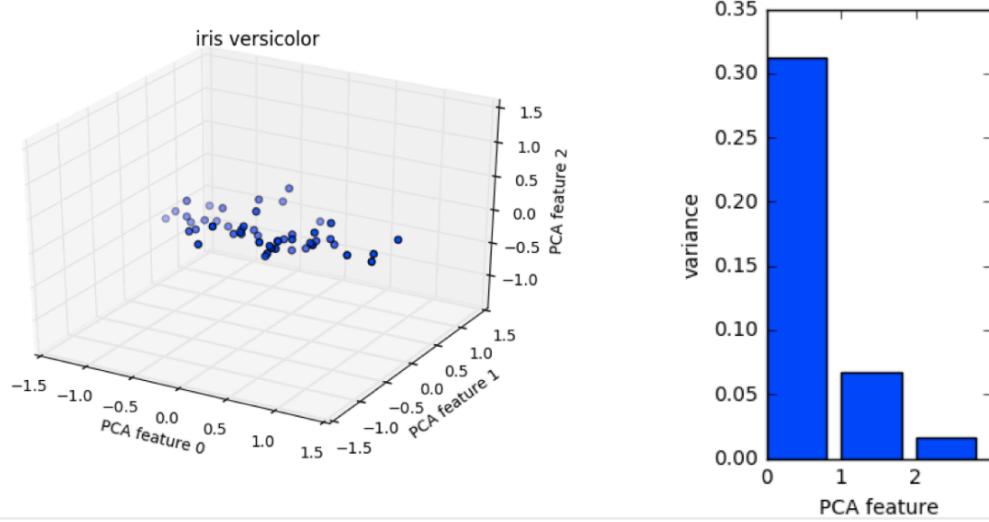
PCA identifies intrinsic dimension

- Scatter plots work only if samples have 2 or 3 features
- PCA identifies intrinsic dimension when samples have any number of features
- Intrinsic dimension = number of PCA features with significant variance

PCA of the versicolor samples

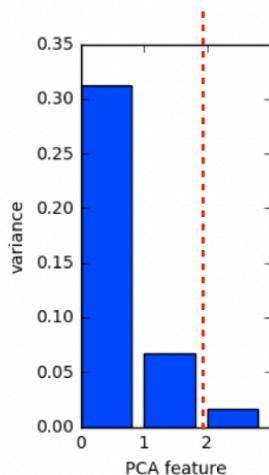


PCA features are ordered by variance desc



Variance and intrinsic dimension

- Intrinsic dimension is number of PCA features with significant variance
- In our example: the first two PCA features
- So intrinsic dimension is 2



Plotting the variances of PCA features

- `samples` = array of versicolor samples

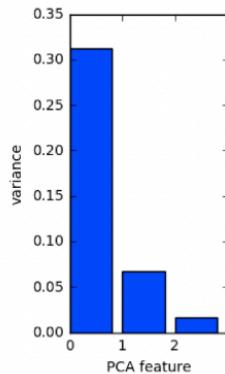
```
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
pca = PCA()
pca.fit(samples)
```

PCA()

```
features = range(pca.n_components_)
```

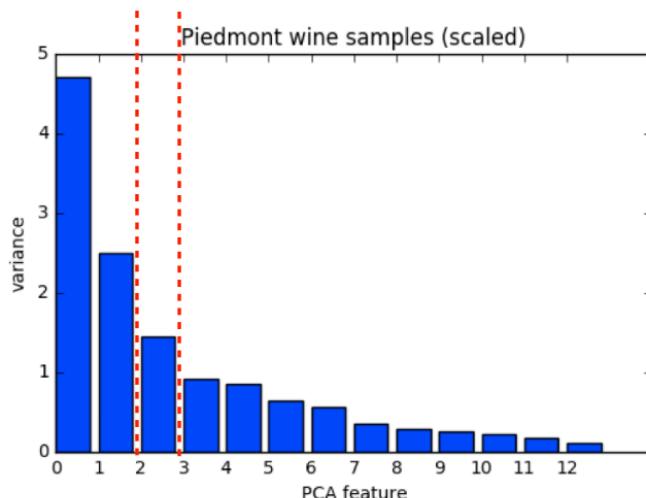
Plotting the variances of PCA features

```
plt.bar(features, pca.explained_variance_)
plt.xticks(features)
plt.ylabel('variance')
plt.xlabel('PCA feature')
plt.show()
```



Intrinsic dimension can be ambiguous

- Intrinsic dimension is an idealization
- ... there is not always one correct answer!
- Piedmont wines: could argue for 2, or for 3, or more



The first principal component of the data is the direction in which the data varies

the most.

```
# Make a scatter plot of the untransformed points  
plt.scatter(grains[:,0], grains[:,1])
```

```
# Create a PCA instance: model  
model = PCA()
```

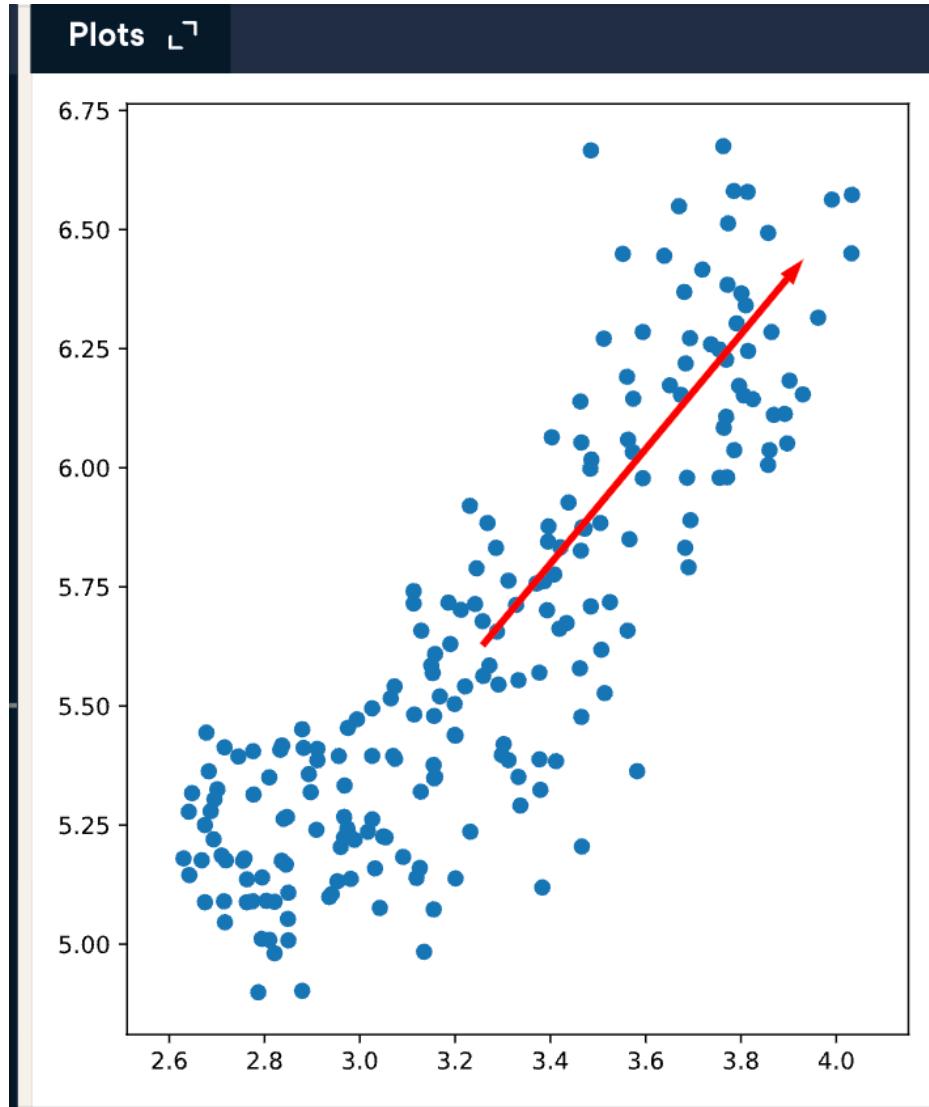
```
# Fit model to points  
model.fit(grains)
```

```
# Get the mean of the grain samples: mean  
mean = model.mean_
```

```
# Get the first principal component: first_pc  
first_pc = model.components_[0,:]
```

```
# Plot first_pc as an arrow, starting at mean  
plt.arrow(mean[0], mean[1], first_pc[0], first_pc[1], color='red', width=0.01)
```

```
# Keep axes on same scale  
plt.axis('equal')  
plt.show()
```



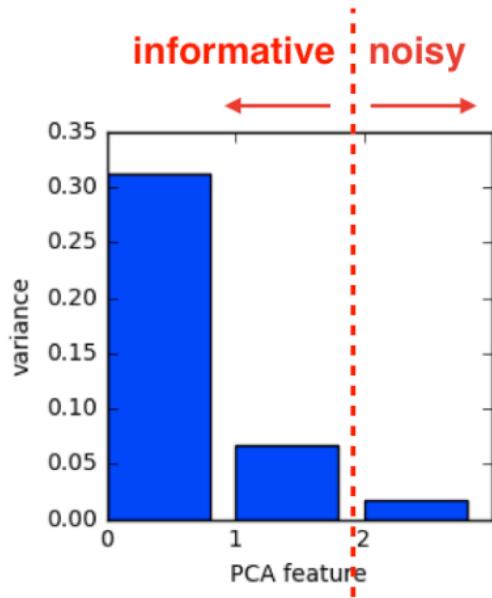
Dimension reduction with PCA

Dimension reduction

- Represents same data, using less features
- Important part of machine-learning pipelines
- Can be performed using PCA

Dimension reduction with PCA

- PCA features are in decreasing order of variance
- Assumes the low variance features are "noise"
- ... and high variance features are informative



Dimension reduction with PCA

- Specify how many features to keep
- E.g. `PCA(n_components=2)`
- Keeps the first 2 PCA features
- Intrinsic dimension is a good choice

Dimension reduction of iris dataset

- `samples` = array of iris measurements (4 features)
- `species` = list of iris species numbers

```
from sklearn.decomposition import PCA  
pca = PCA(n_components=2)  
pca.fit(samples)
```

```
PCA(n_components=2)
```

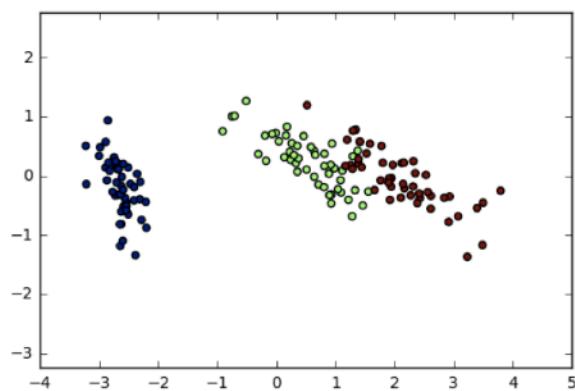
```
transformed = pca.transform(samples)  
print(transformed.shape)
```

```
(150, 2)
```

Iris dataset in 2 dimensions

- PCA has reduced the dimension to 2
- Retained the 2 PCA features with highest variance
- Important information preserved: species remain distinct

```
import matplotlib.pyplot as plt
xs = transformed[:,0]
ys = transformed[:,1]
plt.scatter(xs, ys, c=species)
plt.show()
```



Dimension reduction with PCA

- Discards low variance PCA features
- Assumes the high variance features are informative
- Assumption typically holds in practice (e.g. for iris)

Word frequency arrays

- Rows represent documents, columns represent words
- Entries measure presence of each word in each document
- ... measure using "tf-idf" (more later)

	aardvark	apple	...	zebra
document0		0, 0.1, ...		0.
document1				
.				
.				
.				
		word frequencies ("tf-idf")		

Sparse arrays and csr_matrix

- "Sparse": most entries are zero
- Can use `scipy.sparse.csr_matrix` instead of NumPy array
- `csr_matrix` remembers only the non-zero entries (saves space!)

aardvark	apple	...	zebra
document0	0, 0.1,	0.
document1			
.			
.			
.			
		word frequencies ("tf-idf")	

TruncatedSVD and csr_matrix

- scikit-learn `PCA` doesn't support `csr_matrix`
- Use scikit-learn `TruncatedSVD` instead
- Performs same transformation

```
from sklearn.decomposition import TruncatedSVD
model = TruncatedSVD(n_components=3)
model.fit(documents) # documents is csr_matrix
transformed = model.transform(documents)
```

Non-negative matrix factorization (NMF)

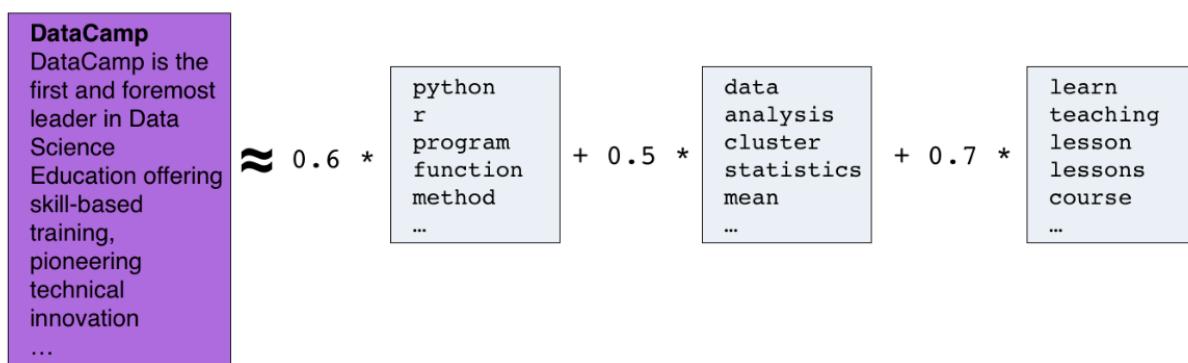
- Dimension Reduction Technique
- Easier to interpret than PCA but this requires all the input features to be non-negative

Non-negative matrix factorization

- NMF = "non-negative matrix factorization"
- Dimension reduction technique
- NMF models are interpretable (unlike PCA)
- Easy to interpret means easy to explain!
- However, all sample features must be non-negative (≥ 0)

Interpretable parts

- NMF expresses documents as combinations of topics (or "themes")



Interpretable parts

- NMF expresses images as combinations of patterns

$$\begin{matrix} \text{[Image]} \\ \approx 0.98 * \end{matrix} \quad \begin{matrix} \text{[Image]} \\ + 0.91 * \end{matrix} \quad \begin{matrix} \text{[Image]} \\ + 0.94 * \end{matrix} \quad \begin{matrix} \text{[Image]} \end{matrix}$$

Using scikit-learn NMF

- Follows `fit()` / `transform()` pattern
- Must specify number of components e.g.
`NMF(n_components=2)`
- Works with NumPy arrays and with `csr_matrix`

Example word-frequency array

- Word frequency array, 4 words, many documents
- Measure presence of words in each document using "tf-idf"
 - "tf" = frequency of word in document
 - "idf" reduces influence of frequent words

	course	datacamp	potato	the
document0	0.2,	0.3,	0.0,	0.1
document1	0.0,	0.0,	0.4,	0.1
...			...	

Example usage of NMF

- `samples` is the word-frequency array

```
from sklearn.decomposition import NMF  
model = NMF(n_components=2)  
model.fit(samples)
```

```
NMF(n_components=2)
```

```
nmf_features = model.transform(samples)
```

NMF components

- NMF has components
- ... just like PCA has principal components
- Dimension of components = dimension of samples
- Entries are non-negative

```
print(model.components_)
```

```
[[ 0.01  0.      2.13  0.54]
 [ 0.99  1.47   0.     0.5 ]]
```

NMF features

- NMF feature values are non-negative
- Can be used to reconstruct the samples
- ... combine feature values with components

```
print(nmf_features)
```

```
[[ 0.      0.2 ]
 [ 0.19   0.   ]
 ...
 [ 0.15   0.12]]
```

Reconstruction of a sample

```
print(samples[i,:])
```

```
[ 0.12  0.18  0.32  0.14]
```

```
print(nmf_features[i,:])
```

```
[ 0.15  0.12]
```

$$\begin{array}{r} 0.15 * \\ + 0.12 * \\ \hline [0.01 \quad 0. \quad 2.13 \quad 0.54] \\ [0.99 \quad 1.47 \quad 0. \quad 0.5] \end{array}$$

model.components_

reconstruction of sample

$$[0.1203 \quad 0.1764 \quad 0.3195 \quad 0.141]$$

Sample reconstruction

- Multiply components by feature values, and add up
- Can also be expressed as a product of matrices
- This is the "**Matrix Factorization**" in "NMF"

NMF fits to non-negative data only

- Word frequencies in each document
- Images encoded as arrays
- Audio spectrograms
- Purchase histories on e-commerce sites
- ... and many more!

NMF learns interpretable parts

Applying NMF to the articles

```
print(articles.shape)
```

```
(20000, 800)
```

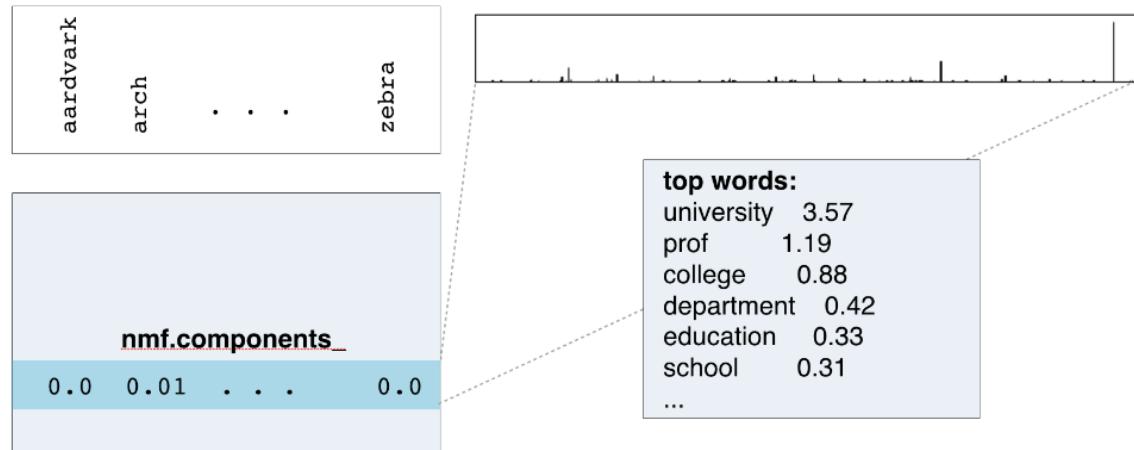
```
from sklearn.decomposition import NMF  
nmf = NMF(n_components=10)  
nmf.fit(articles)
```

```
NMF(n_components=10)
```

```
print(nmf.components_.shape)
```

```
(10, 800)
```

NMF components are topics



NMF components

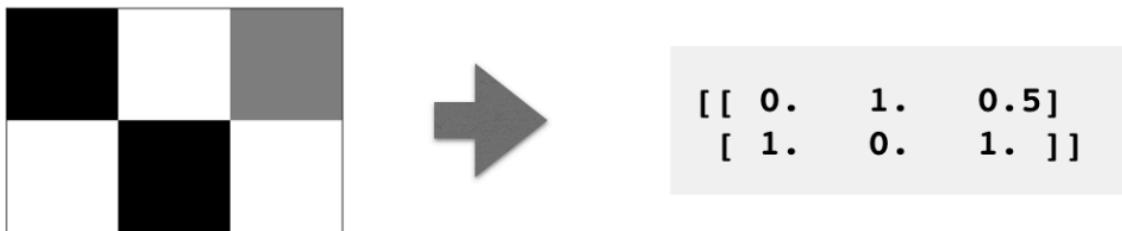
- For documents:
 - NMF components represent topics
 - NMF features combine topics into documents
- For images, NMF components are parts of images

The diagram illustrates the decomposition of a complex image into simpler components. On the left is a complex image of a person's face. To its right is an approximation symbol (\approx) followed by a weighted sum of three simpler images. The weights are 0.98, 0.91, and 0.94 respectively.

$$\text{Complex Image} \approx 0.98 * \text{Component 1} + 0.91 * \text{Component 2} + 0.94 * \text{Component 3}$$

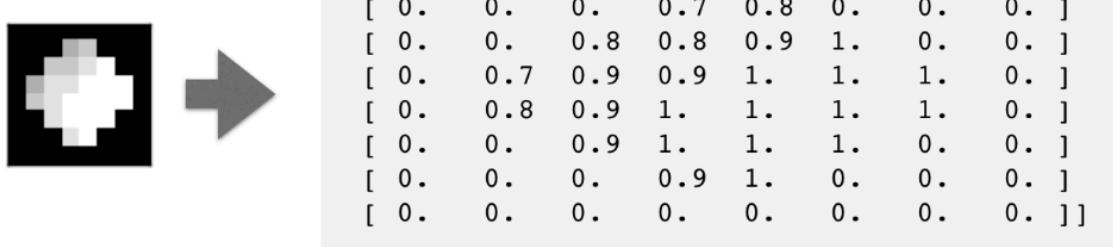
Grayscale images

- "Grayscale" image = no colors, only shades of gray
- Measure pixel brightness
- Represent with value between 0 and 1 (0 is black)
- Convert to 2D array



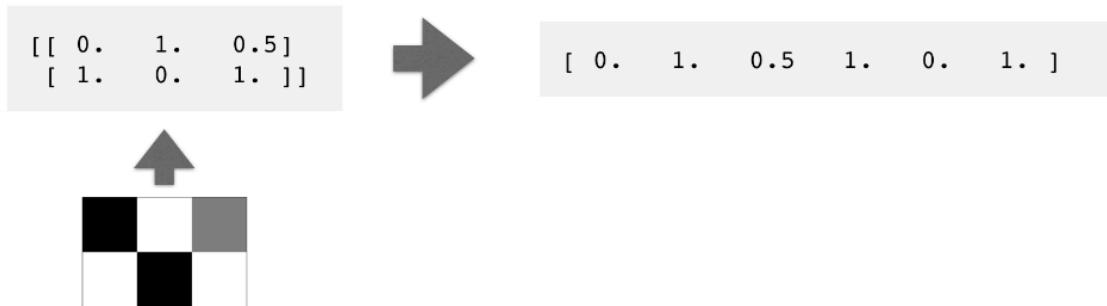
Grayscale image example

- An 8x8 grayscale image of the moon, written as an array



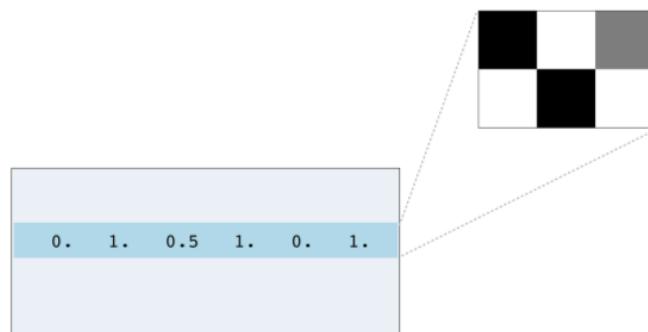
Grayscale images as flat arrays

- Enumerate the entries
- Row-by-row
- From left to right, top to bottom



Encoding a collection of images

- Collection of images of the same size
- Encode as 2D array
- Each row corresponds to an image
- Each column corresponds to a pixel
- ... can apply NMF!



Visualizing samples

```
print(sample)
```

```
[ 0.  1.  0.5 1.  0.  1. ]
```

```
bitmap = sample.reshape((2, 3))
print(bitmap)
```

```
[[ 0.  1.  0.5]
 [ 1.  0.  1. ]]
```

```
from matplotlib import pyplot as plt
plt.imshow(bitmap, cmap='gray', interpolation='nearest')
plt.show()
```

Building recommender systems using NMF

Finding similar articles

- Engineer at a large online newspaper
- Task: recommend articles similar to article being read by customer
- Similar articles should have similar topics

Strategy

- Apply NMF to the word-frequency array
- NMF feature values describe the topics
 - ... so similar documents have similar NMF feature values
- Compare NMF feature values?

Apply NMF to the word-frequency array

- `articles` is a word frequency array

```
from sklearn.decomposition import NMF
nmf = NMF(n_components=6)
nmf_features = nmf.fit_transform(articles)
```

Versions of articles

- Different versions of the same document have same topic proportions
- ... exact feature values may be different!
- E.g. because one version uses many meaningless words
- But all versions lie on the same line through the origin

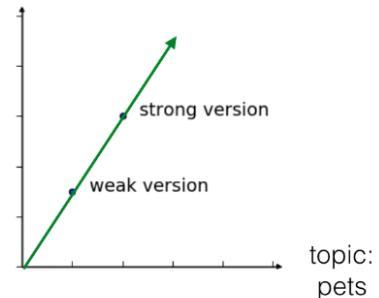
strong version

Dog bites man!
Attack by terrible
canine leaves man
paralyzed...

weak version

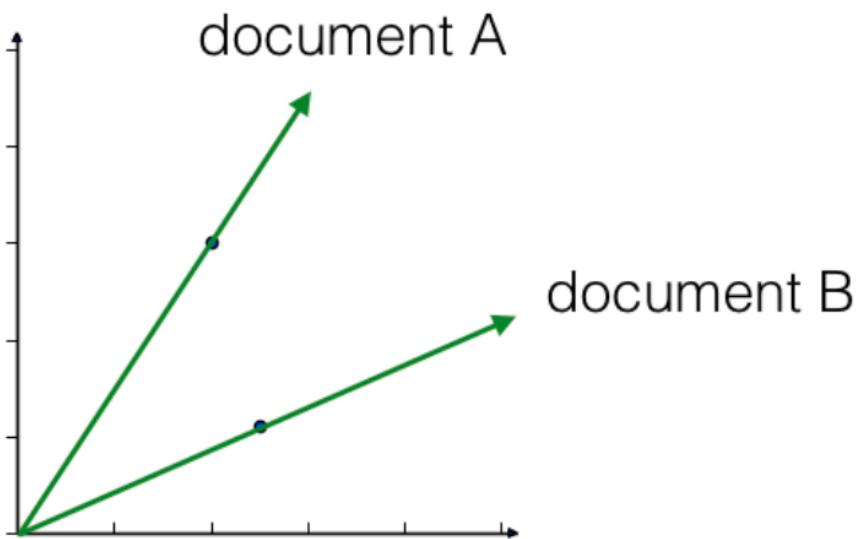
You may have heard,
unfortunately it seems
that a dog has perhaps
bitten a man ...

topic:
danger



Cosine similarity

- Uses the angle between the lines
- Higher values means more similar
- Maximum value is 1, when angle is 0 degrees



Calculating the cosine similarities

```
from sklearn.preprocessing import normalize
norm_features = normalize(nmf_features)
# if has index 23
current_article = norm_features[23,:]
similarities = norm_features.dot(current_article)
print(similarities)
```

```
[ 0.7150569  0.26349967 ...,  0.20323616  0.05047817]
```

DataFrames and labels

- Label similarities with the article titles, using a DataFrame
- Titles given as a list: `titles`

```
import pandas as pd
norm_features = normalize(nmf_features)
df = pd.DataFrame(norm_features, index=titles)
current_article = df.loc['Dog bites man']
similarities = df.dot(current_article)
```

DataFrames and labels

```
print(similarities.nlargest())
```

```
Dog bites man                1.000000
Hound mauls cat              0.979946
Pets go wild!                 0.979708
Dachshunds are dangerous      0.949641
Our streets are no longer safe 0.900474
dtype: float64
```