Unsupervised Learning

UNSUPERVISED LEARNING IN PYTHON

Benjamin Wilson
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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)

[1] http://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(algorithm='auto', ...)
```

```
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)
```

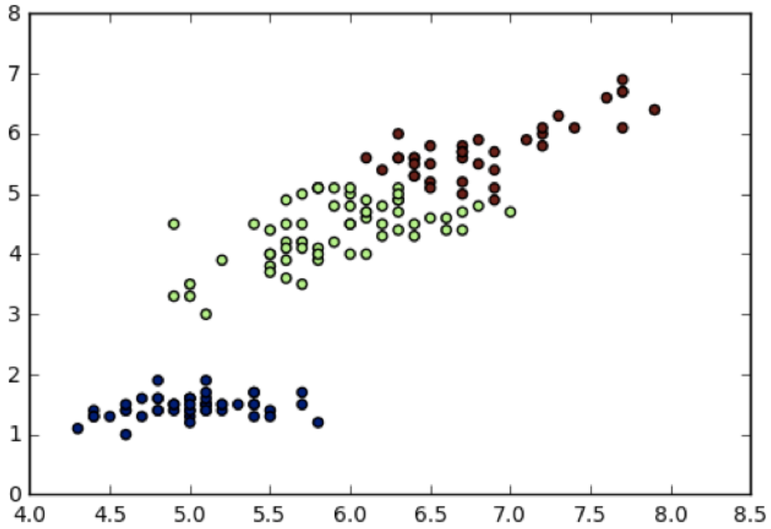
```
[[ 5.7  4.4  1.5  0.4]
 [ 6.5  3.   5.5  1.8]
 [ 5.8  2.7  5.1  1.9]]
```

```
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

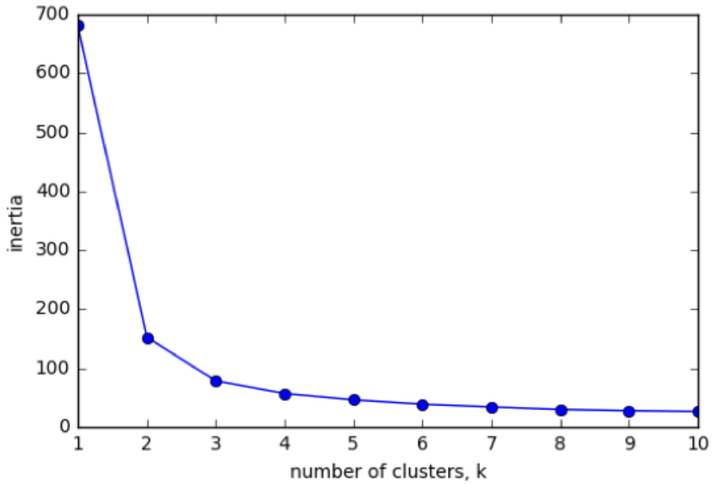
```
from sklearn.cluster import KMeans

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

```
78.9408414261
```

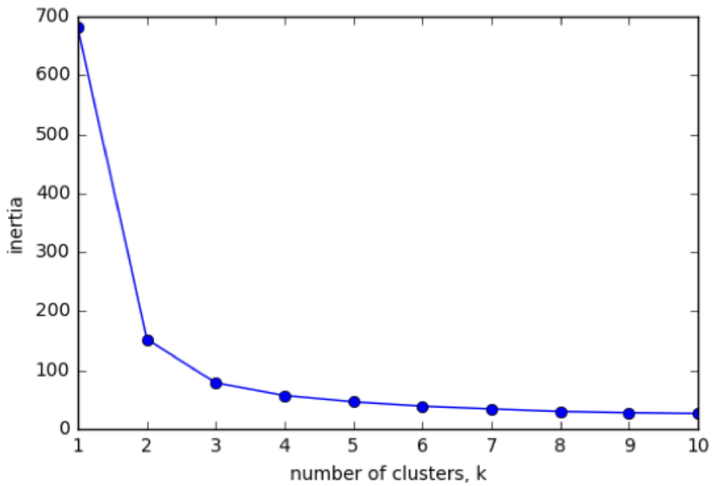
The number of clusters

- 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"

[1] 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)
```

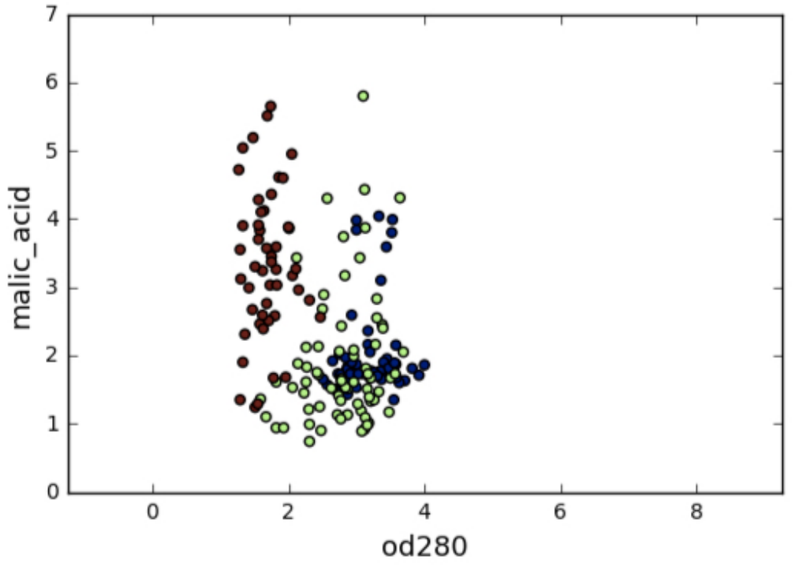
Clusters vs. varieties

```
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

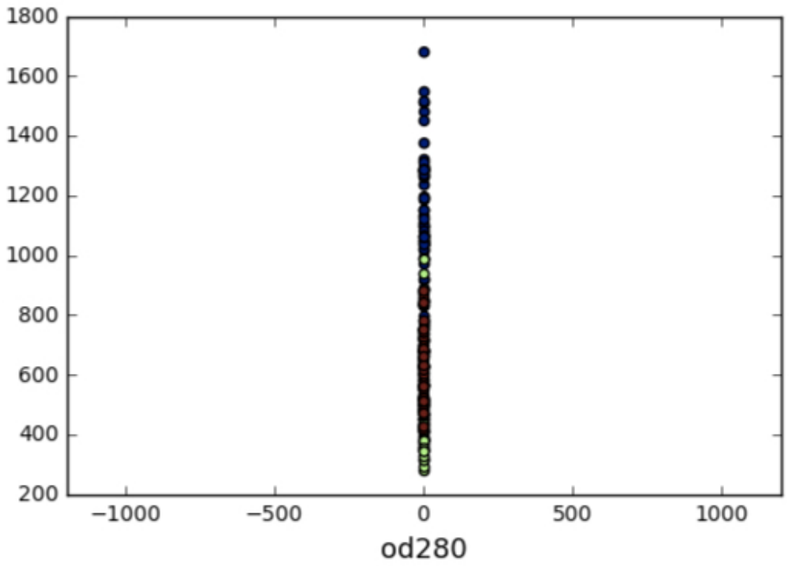
- The wine features have very different variances!
- Variance of a feature measures spread of its values




```
feature      variance
alcohol          0.65
malic_acid       1.24
...
od280            0.50
proline      99166.71
```

Feature variances

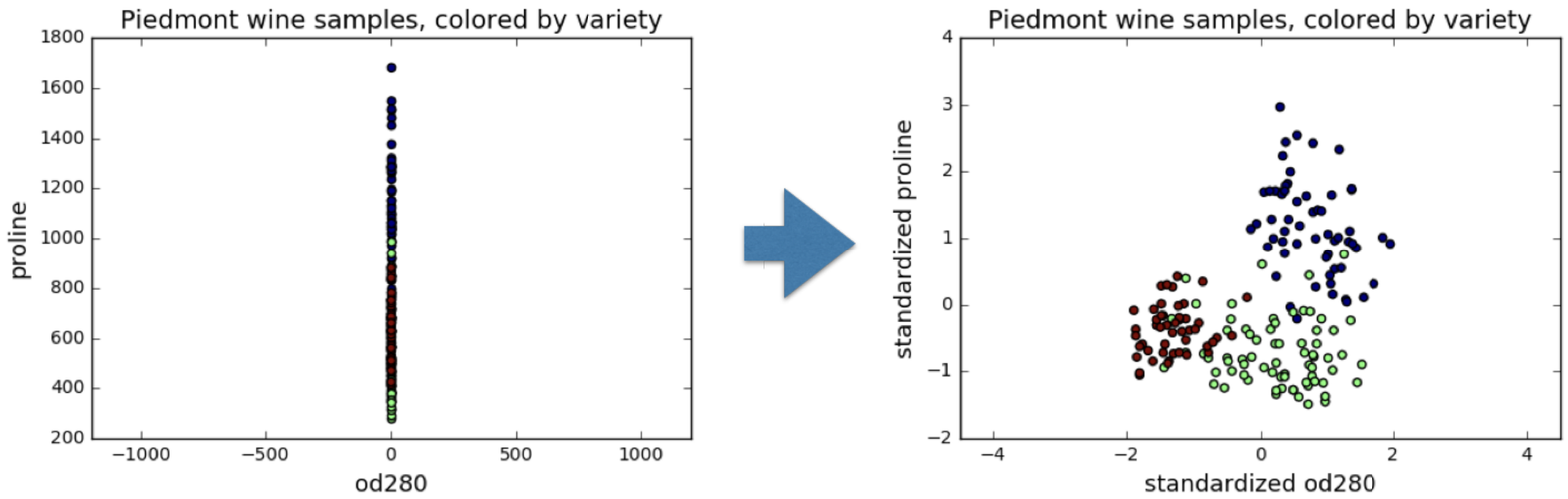
- The wine features have very different variances!
- Variance of a feature measures spread of its values




```
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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Visualizing hierarchies

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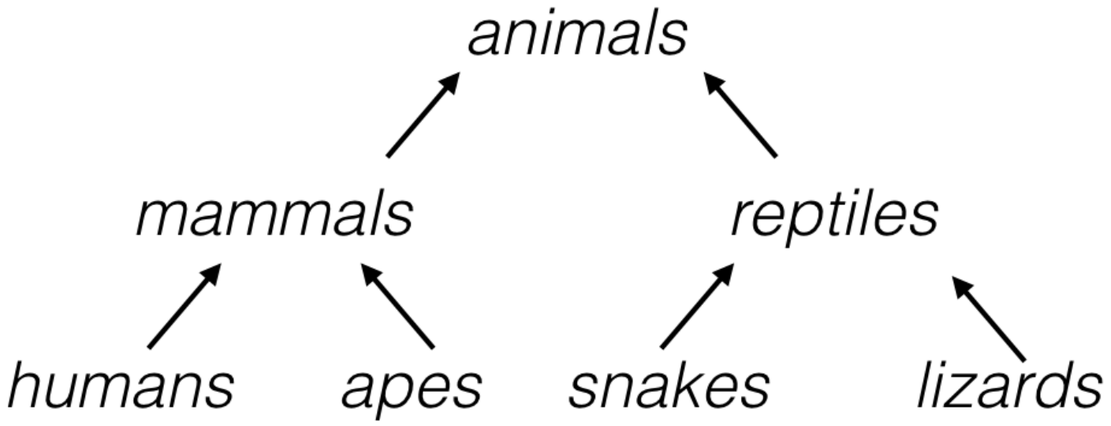
Visualizations communicate insight

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

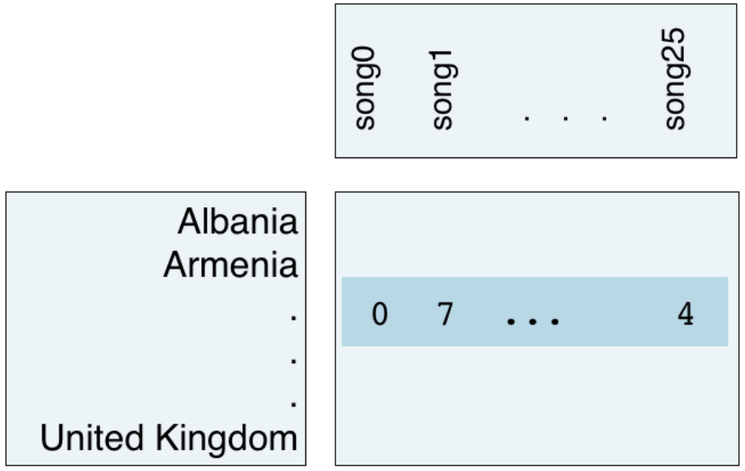
A hierarchy of groups

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



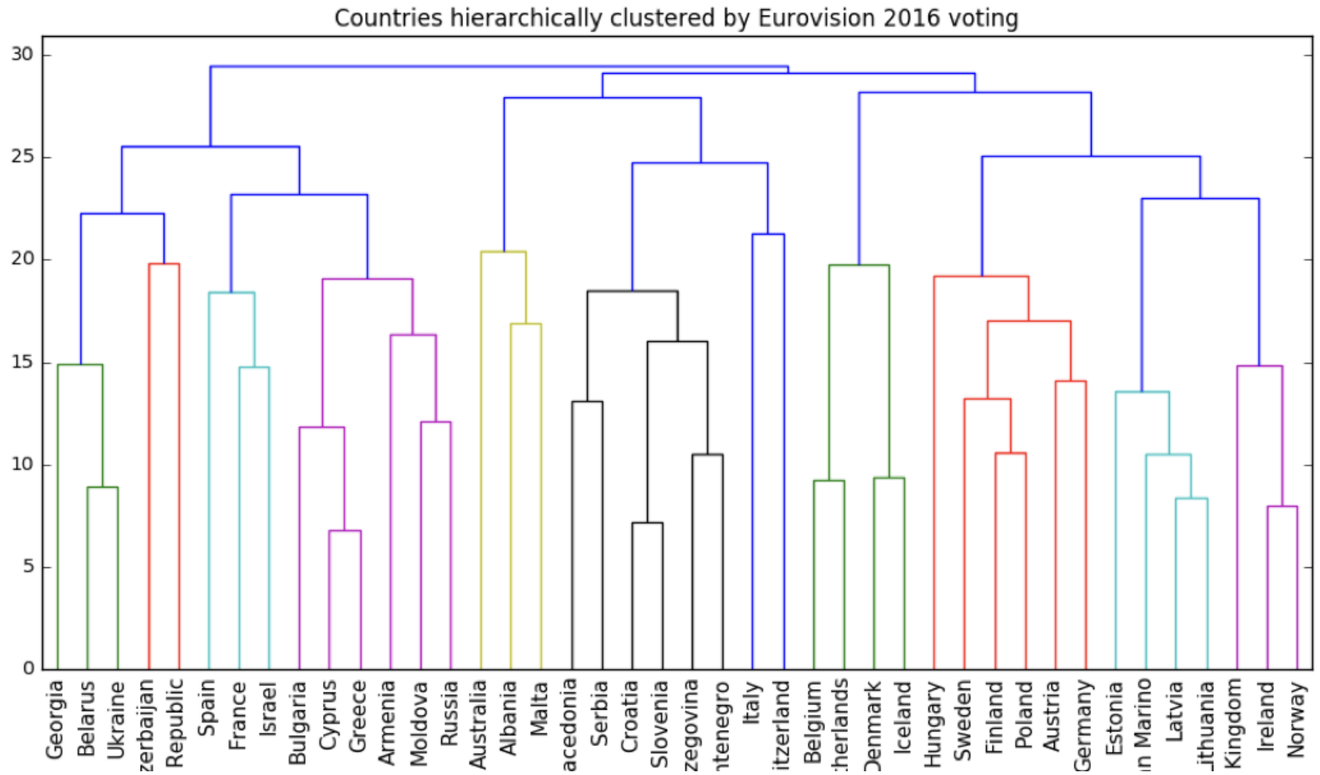
Eurovision scoring dataset

- Countries gave scores to songs performed at the Eurovision 2016
- 2D array of scores
- Rows are countries, columns are songs



[1] http://www.eurovision.tv/page/results

Hierarchical clustering of voting countries

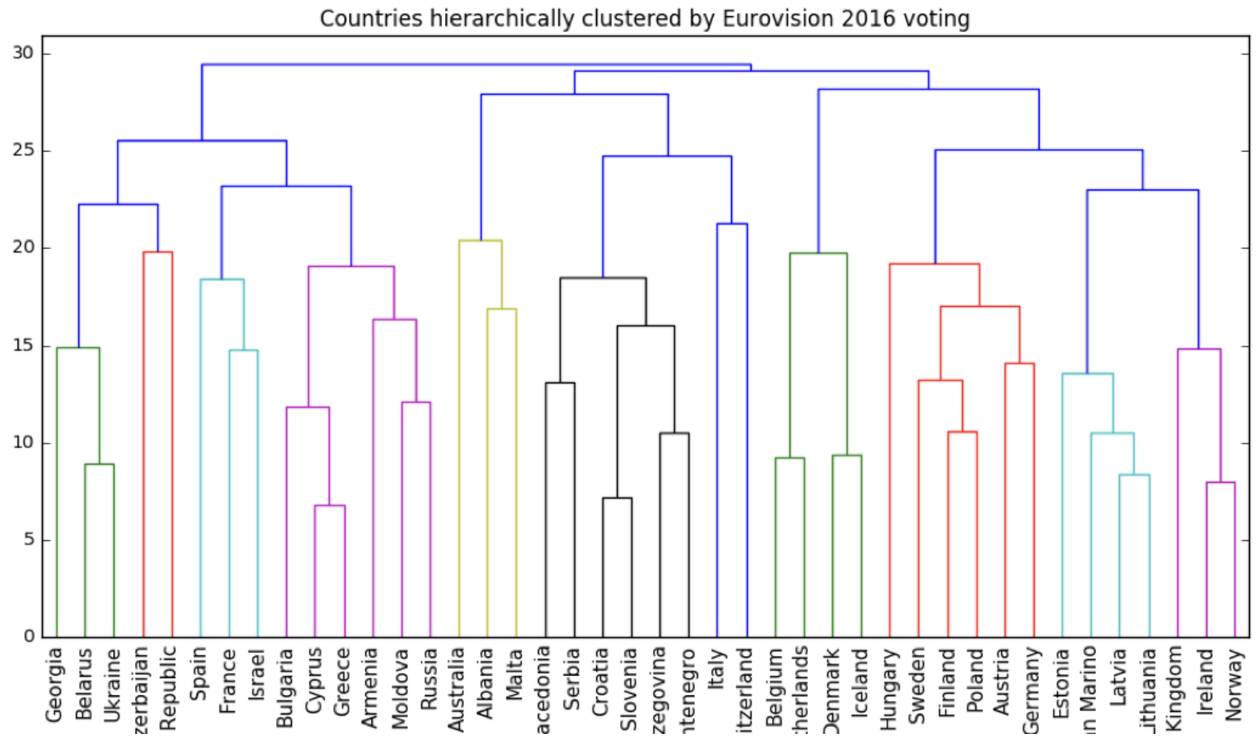


Hierarchical clustering

- 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

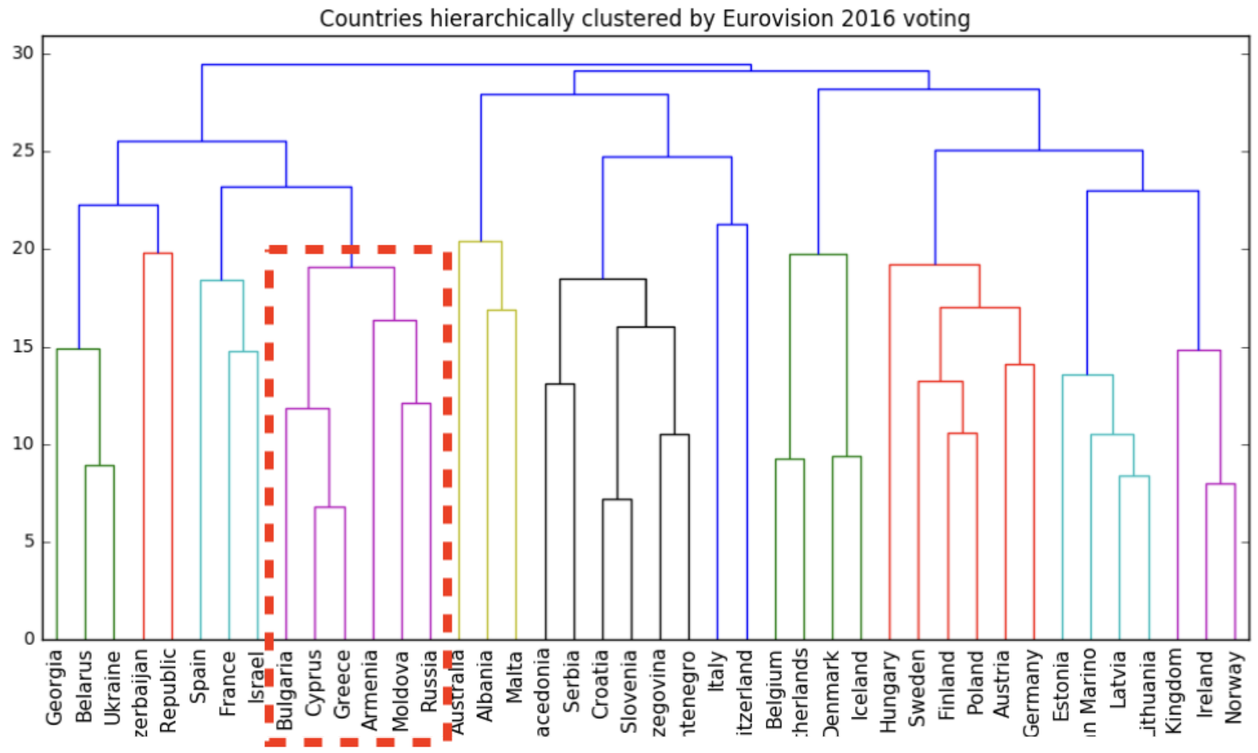
The dendrogram of a hierarchical clustering

- Read from the bottom up
- Vertical lines represent clusters

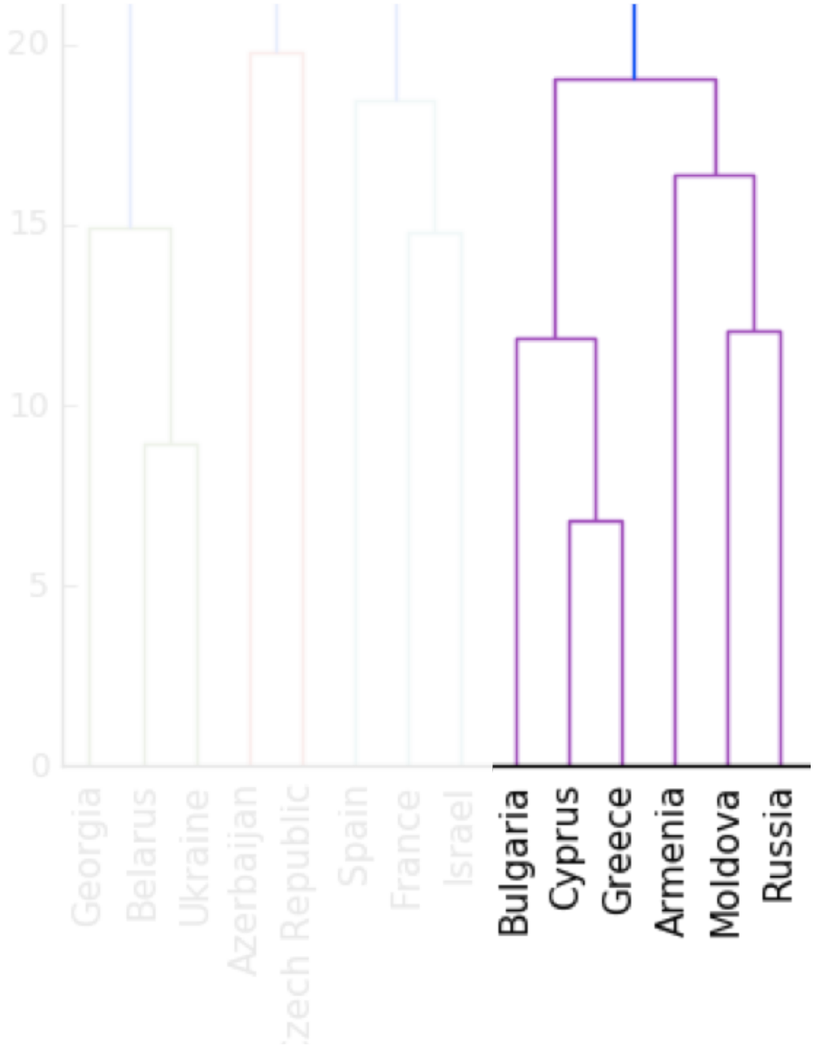


The dendrogram of a hierarchical clustering

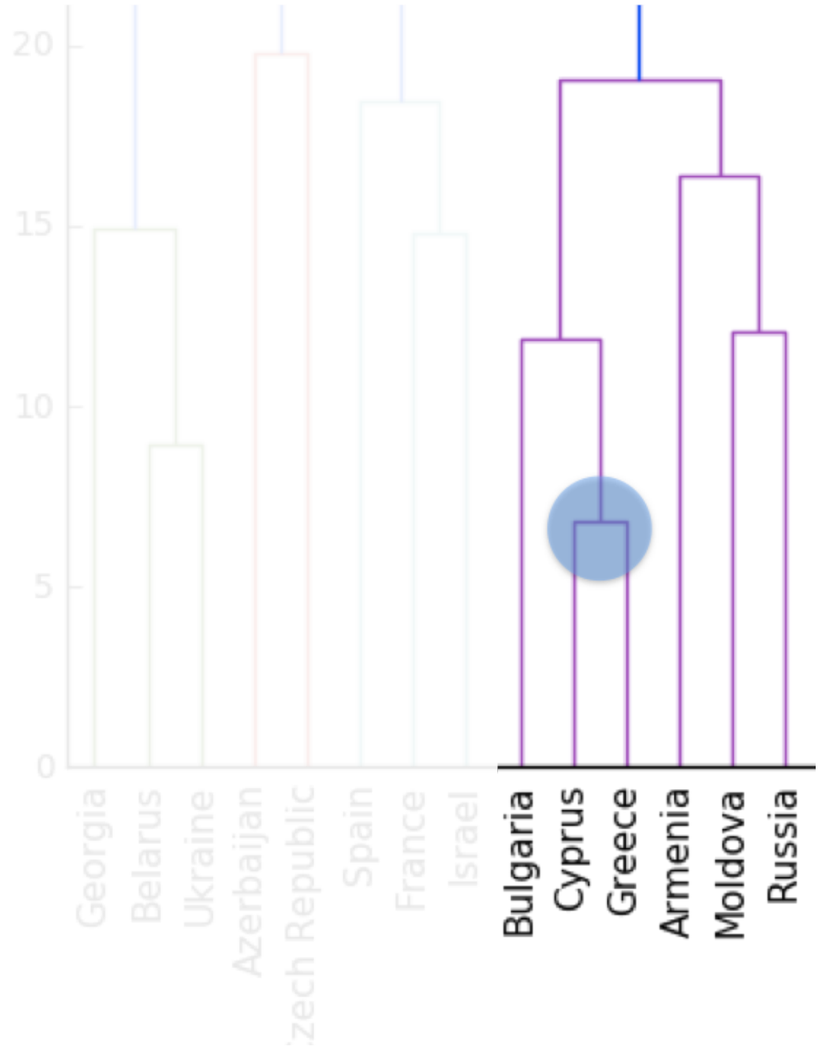
- Read from the bottom up
- Vertical lines represent clusters



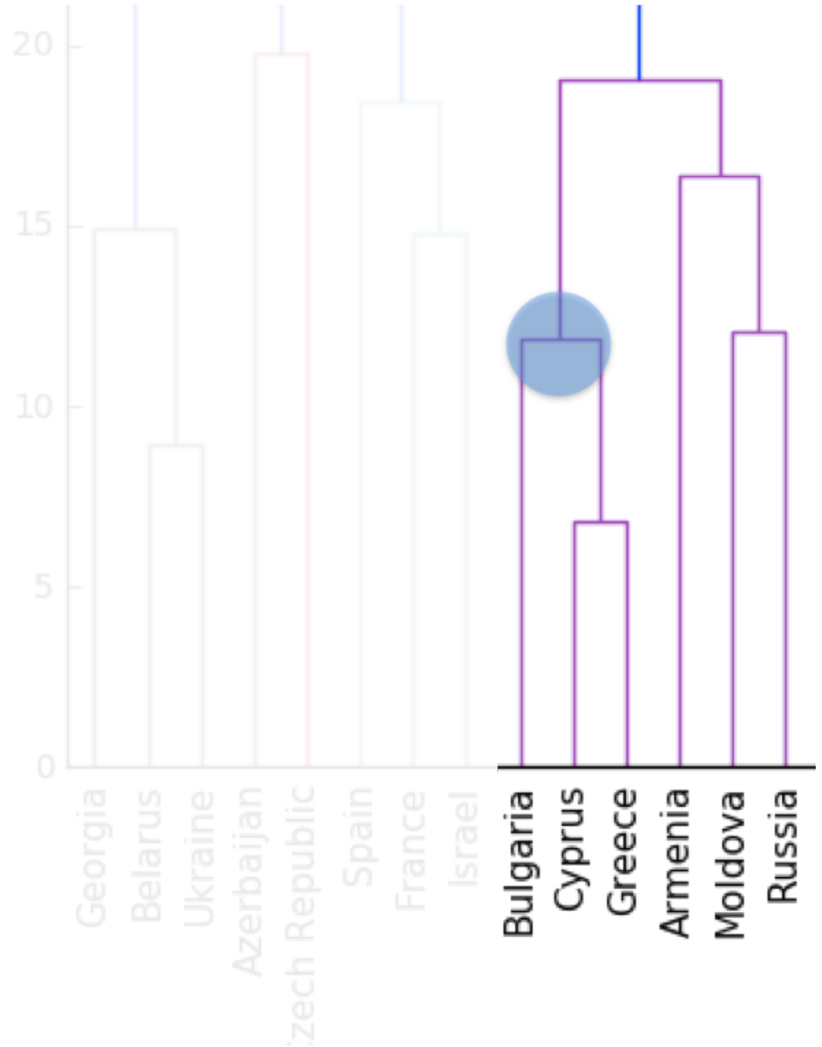
Dendrograms, step-by-step



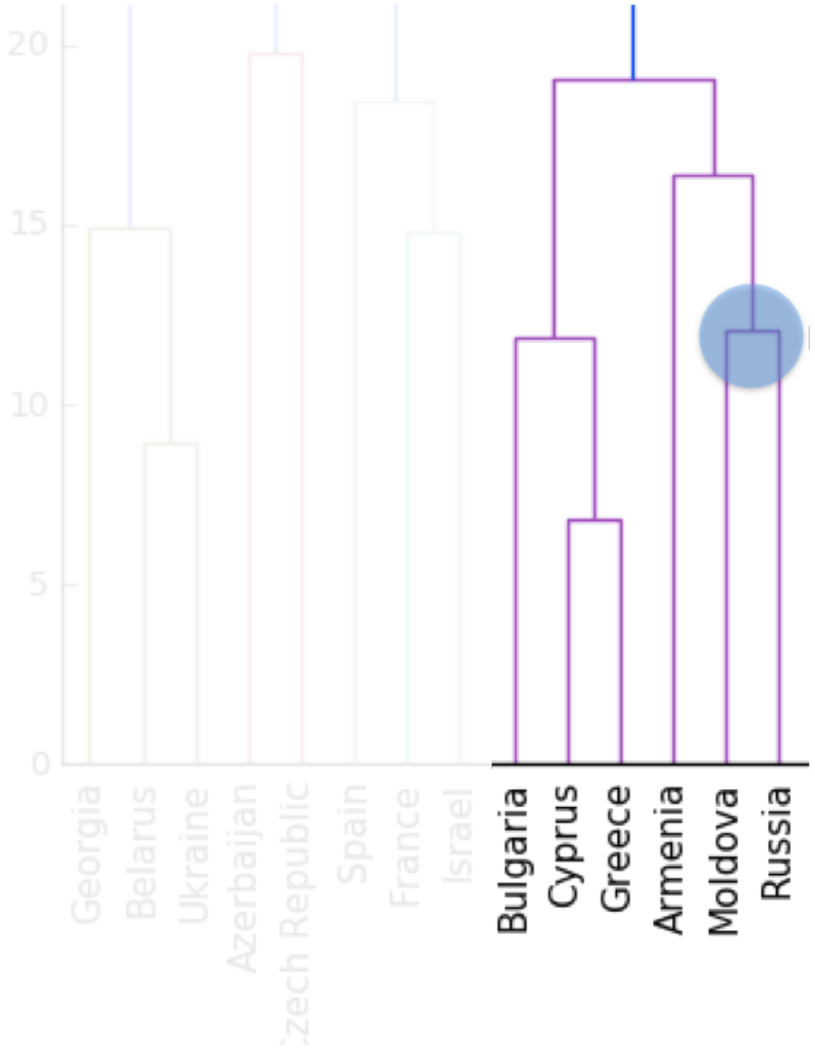
Dendrograms, step-by-step



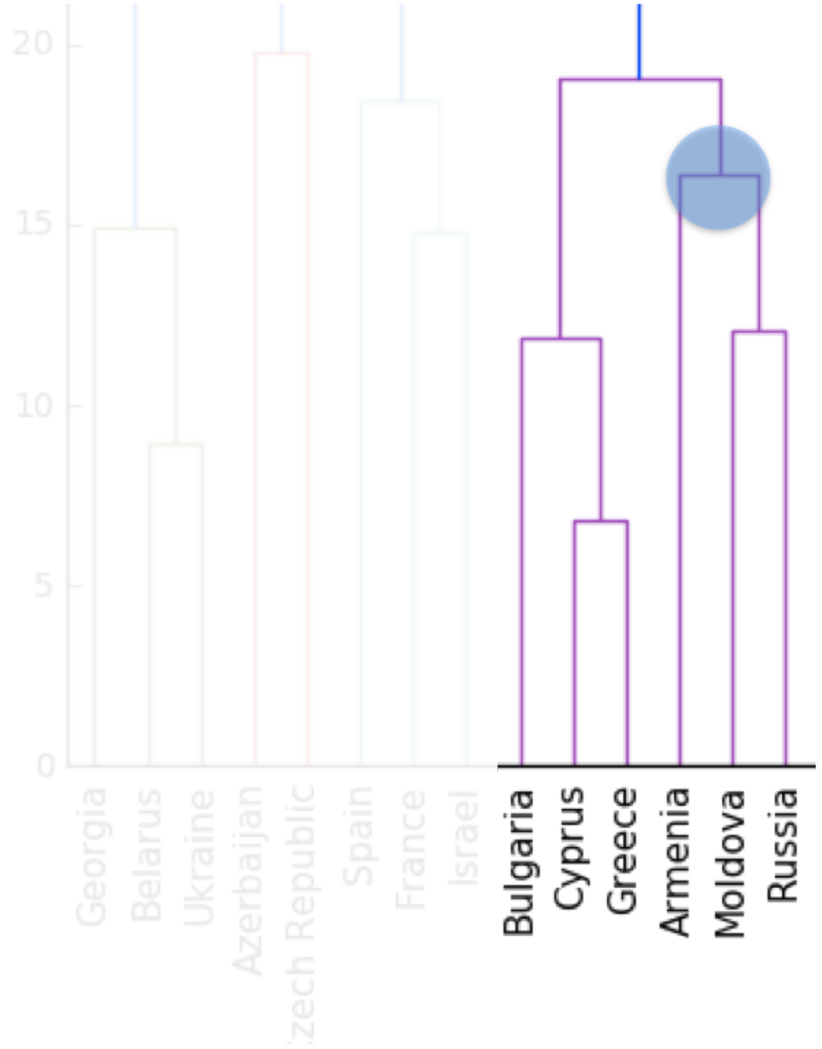
Dendrograms, step-by-step



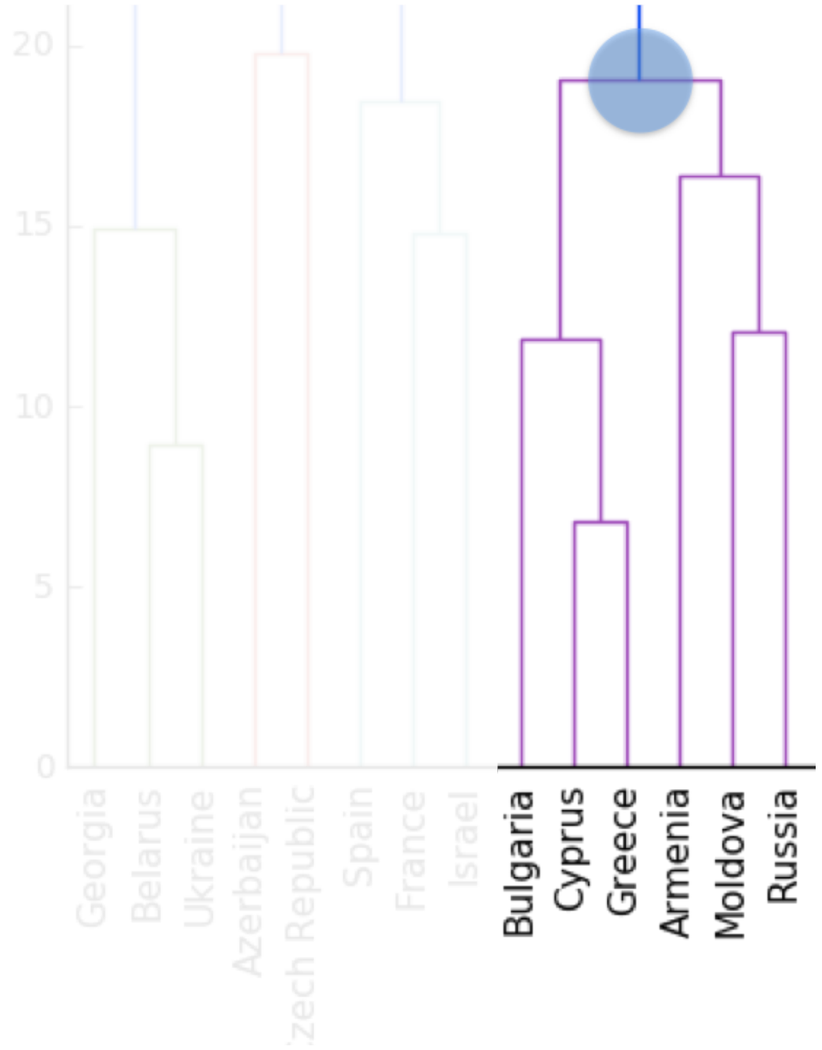
Dendrograms, step-by-step



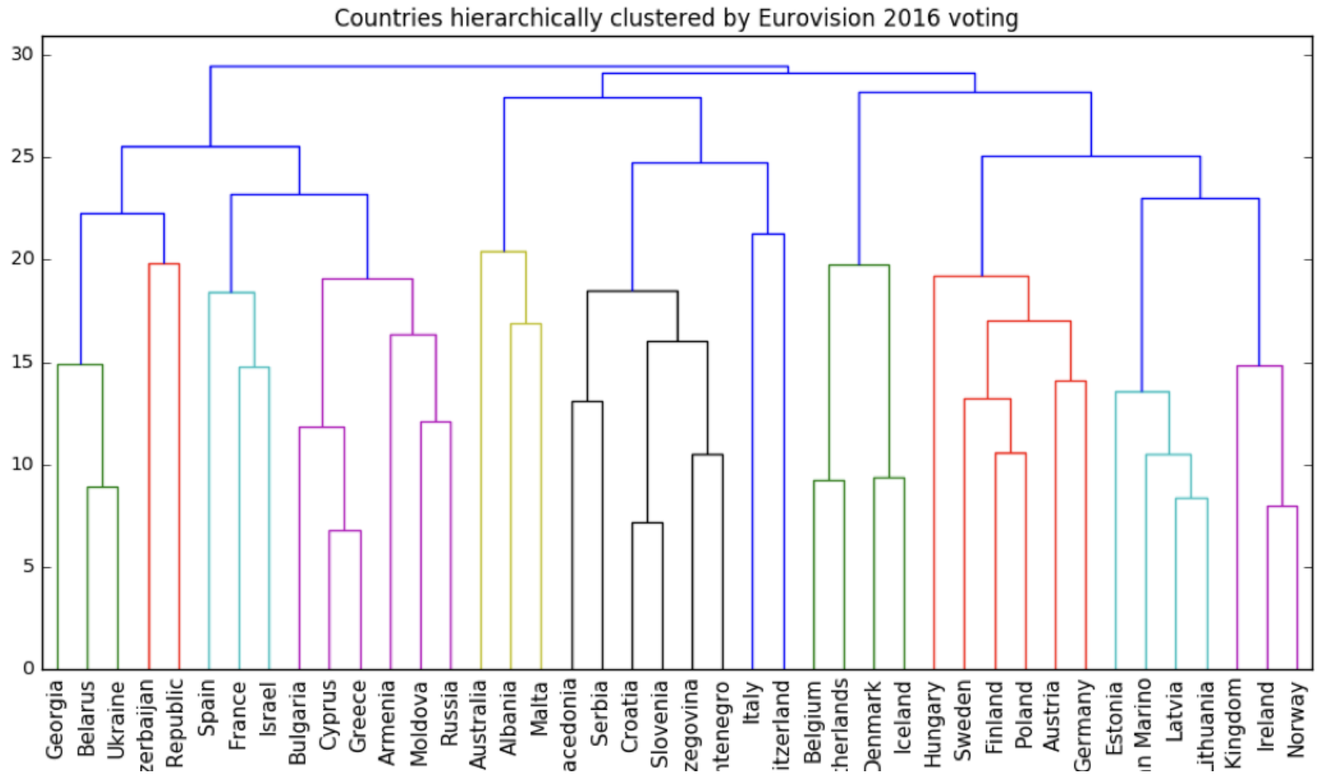
Dendrograms, step-by-step



Dendrograms, step-by-step



Dendrograms, step-by-step



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()
```

Let's practice!

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Cluster labels in hierarchical clustering

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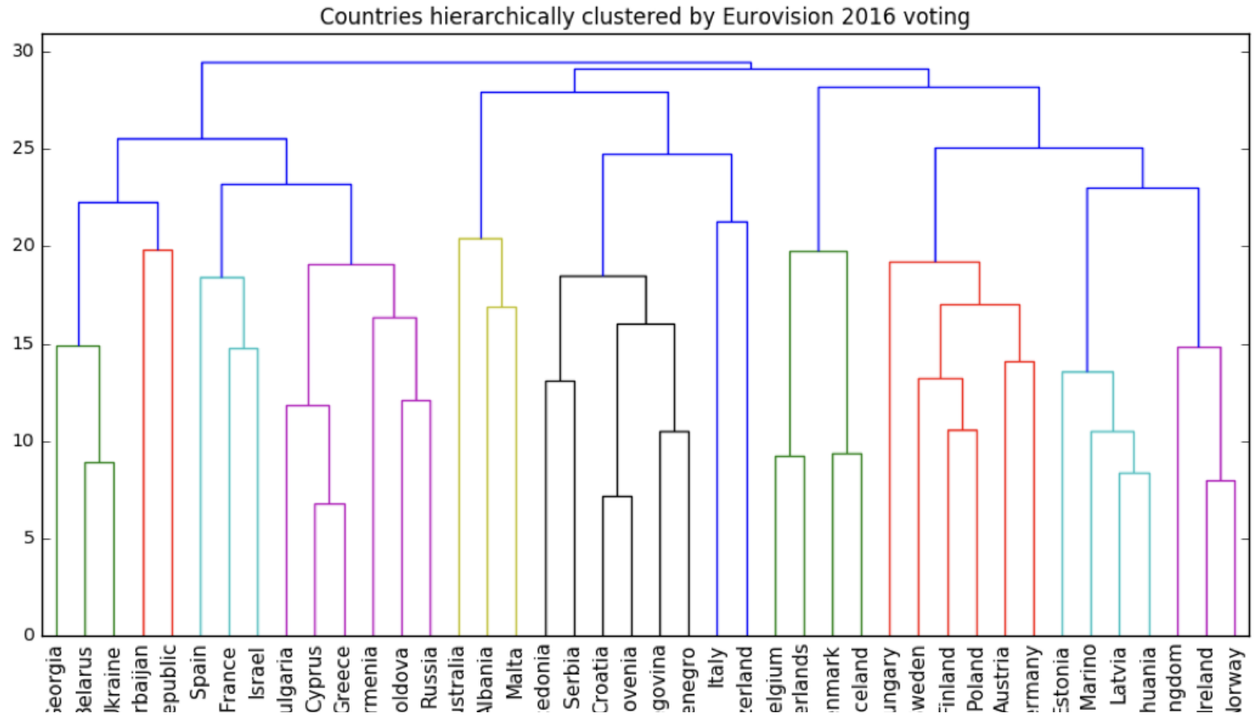
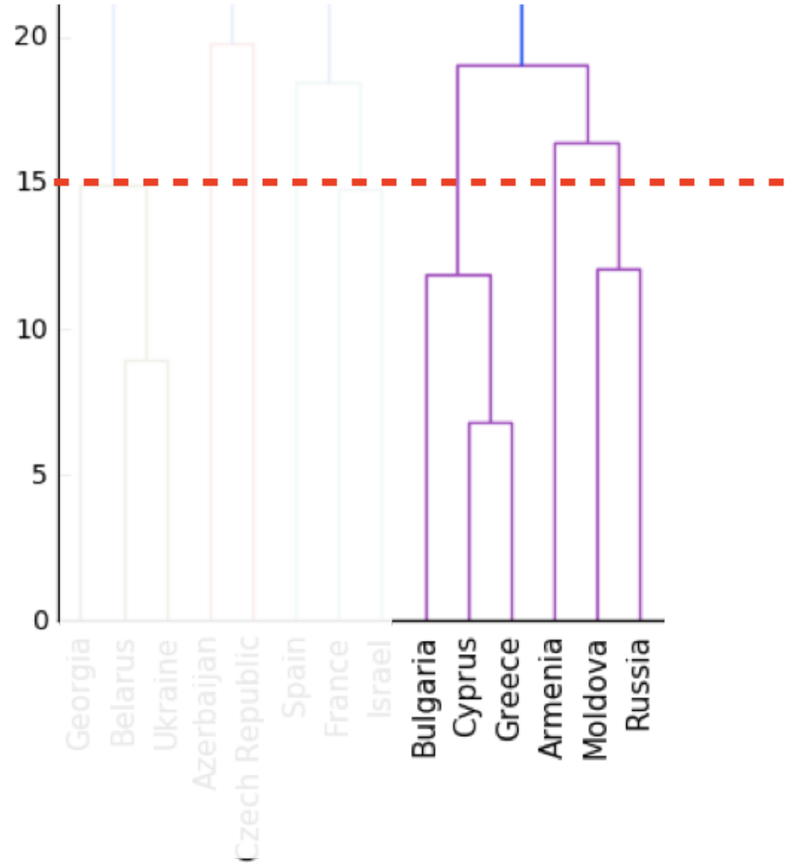
Cluster labels in hierarchical clustering

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



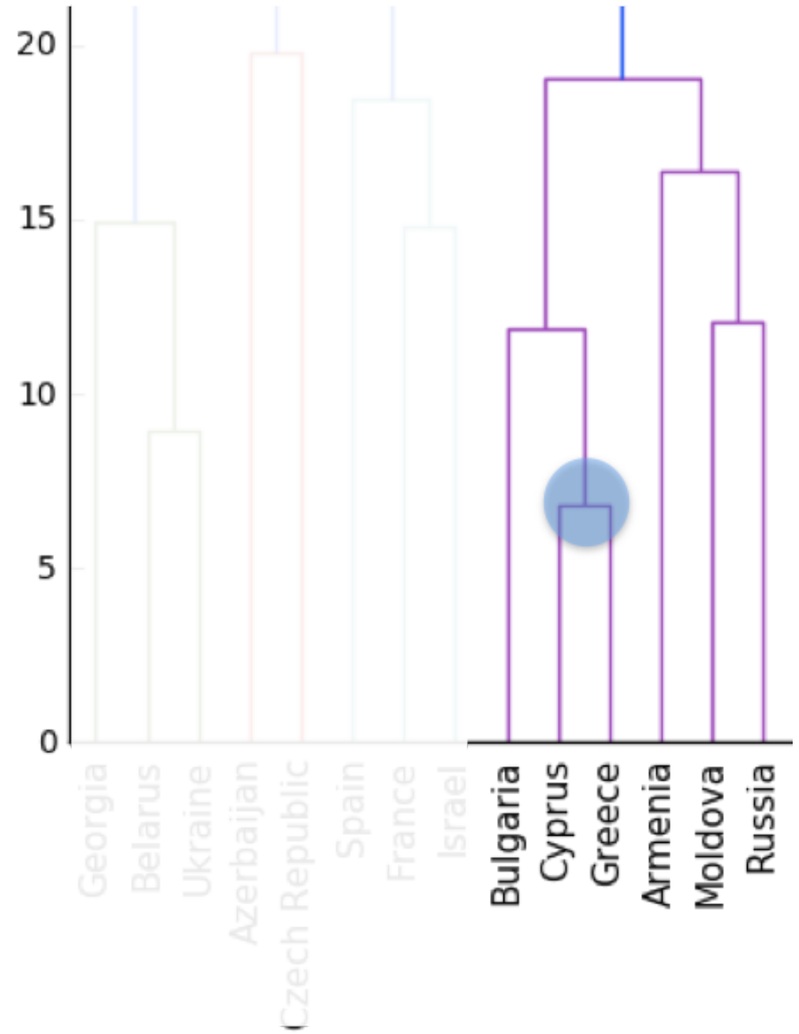
Intermediate clusterings & height on dendrogram

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



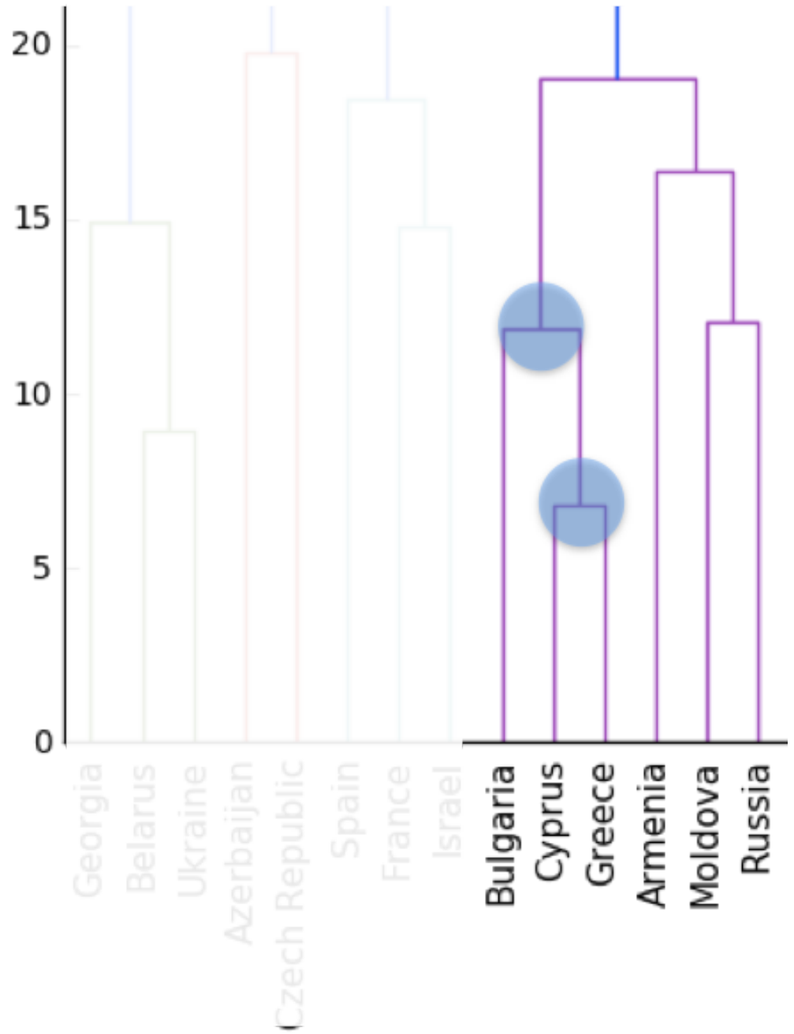
Dendrograms show cluster distances

- Height on dendrogram = distance between merging clusters
- E.g. clusters with only Cyprus and Greece had distance approx. 6



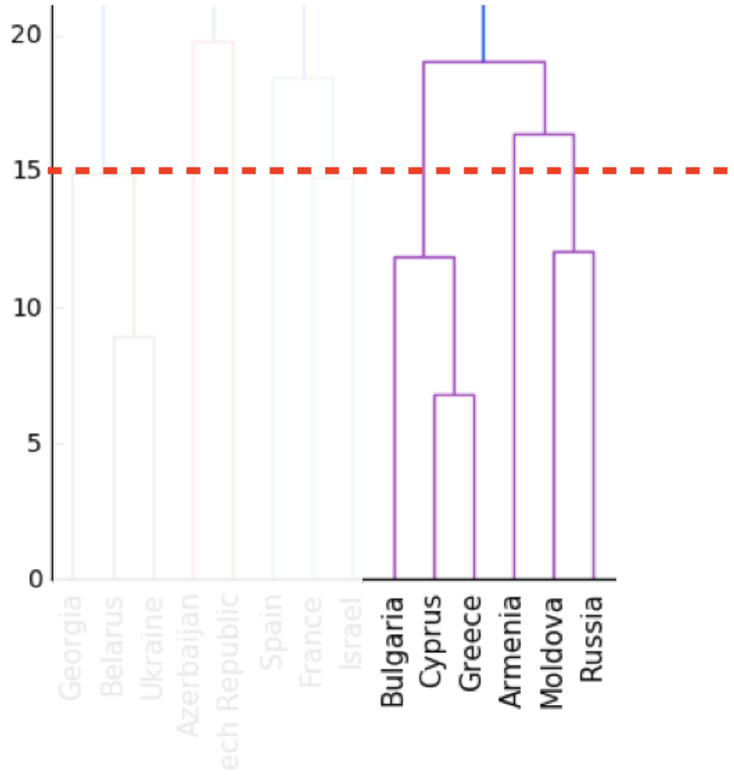
Dendrograms show cluster distances

- 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 dendrogram

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

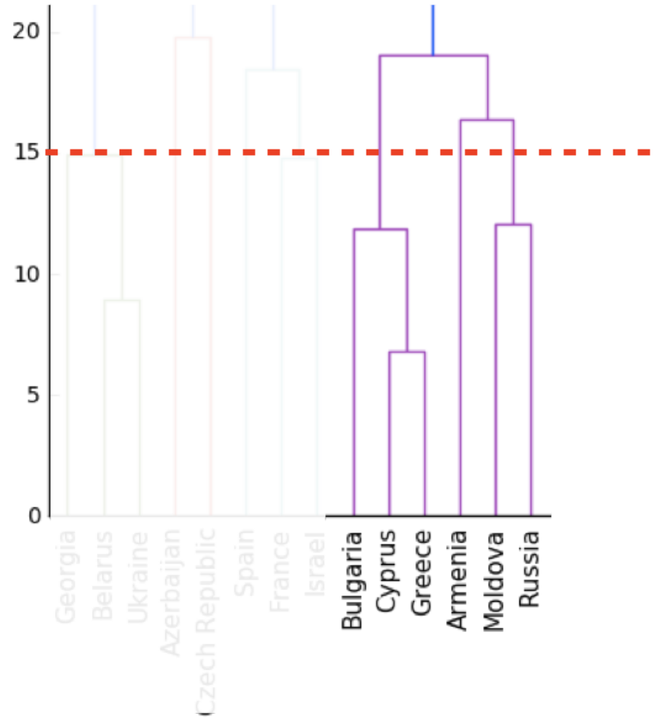


Distance between clusters

- 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
...
```

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t-SNE for 2-dimensional maps

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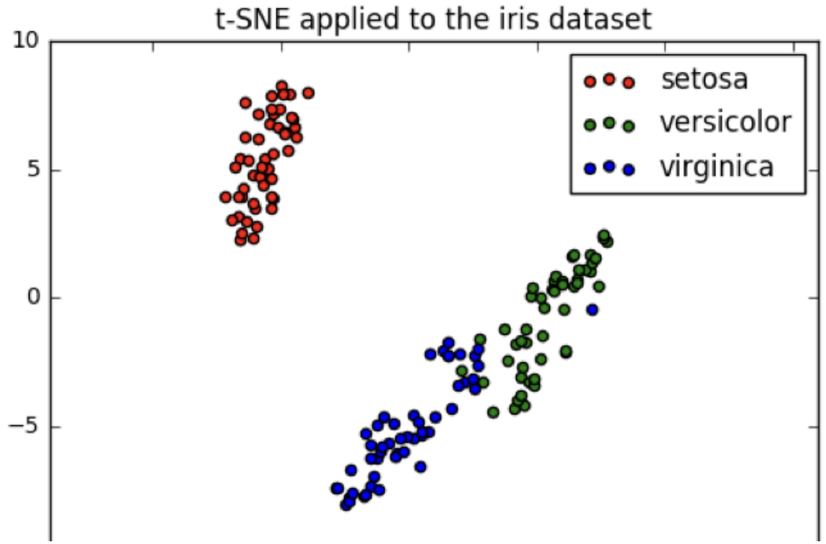
t-SNE for 2-dimensional maps

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

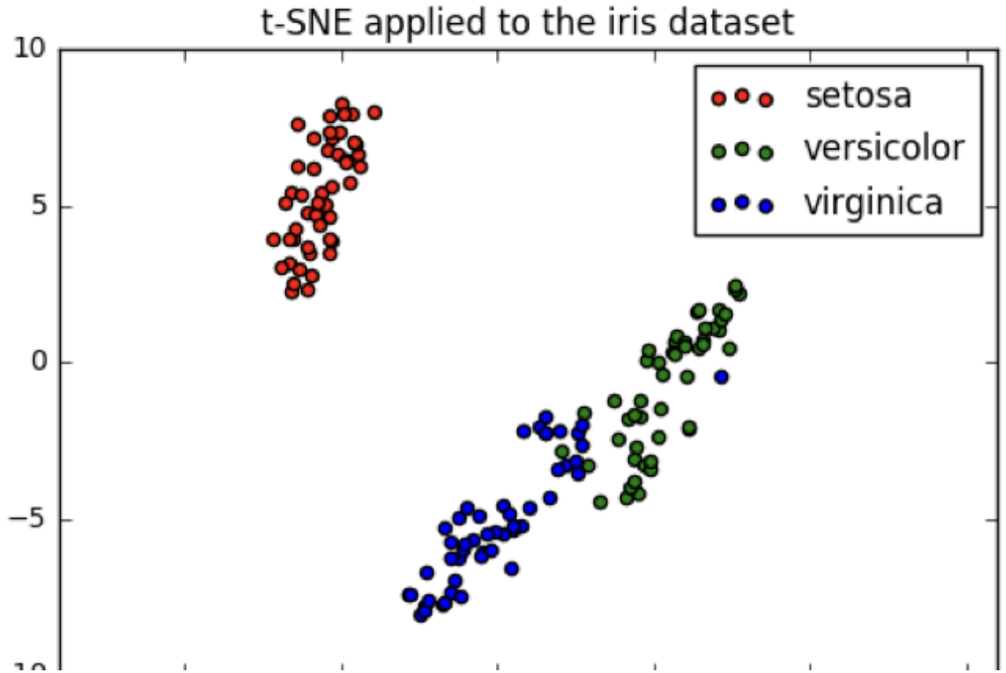
t-SNE on the iris dataset

- 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
- ... yet kept the species mostly separate



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]]
```

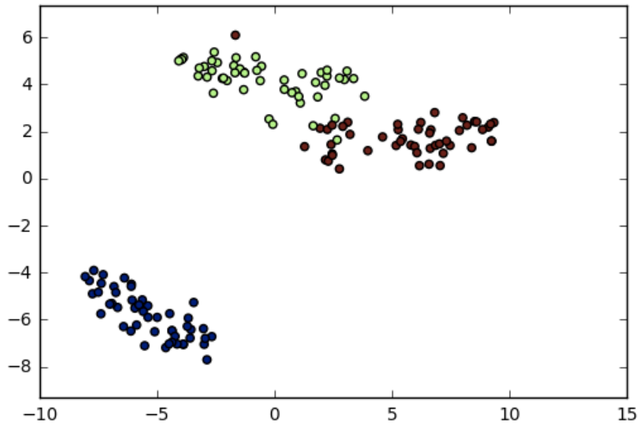
- List `species` giving species of labels as number (0, 1, or 2)

```
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()

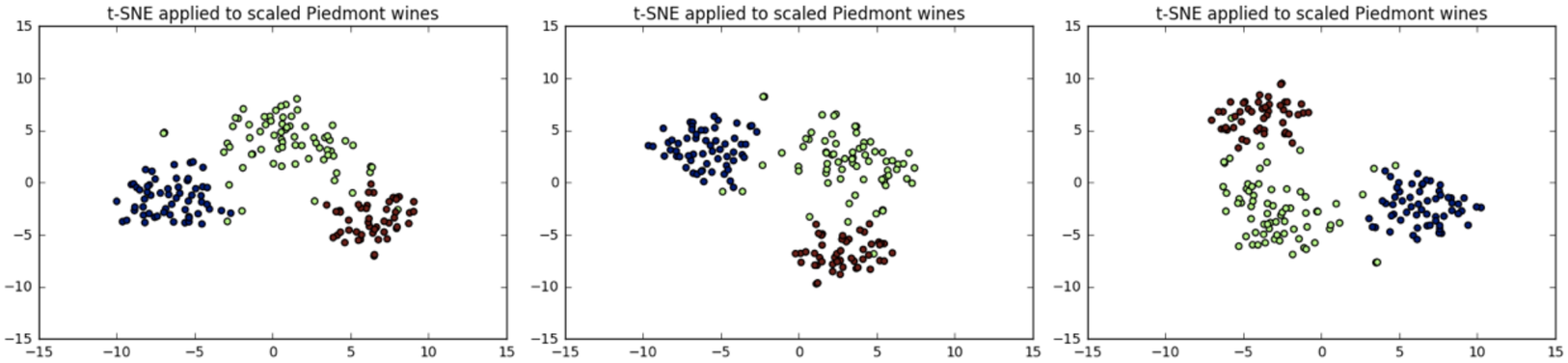
- Has a `fit_transform()` method
- Simultaneously fits the model and transforms the data
- Has no separate `fit()` or `transform()` methods
- Can't extend the map to include new data samples
- Must start over each time!

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



Let's practice!

UNSUPERVISED LEARNING IN PYTHON

Visualizing the PCA transformation

UNSUPERVISED LEARNING IN PYTHON

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Dimension reduction

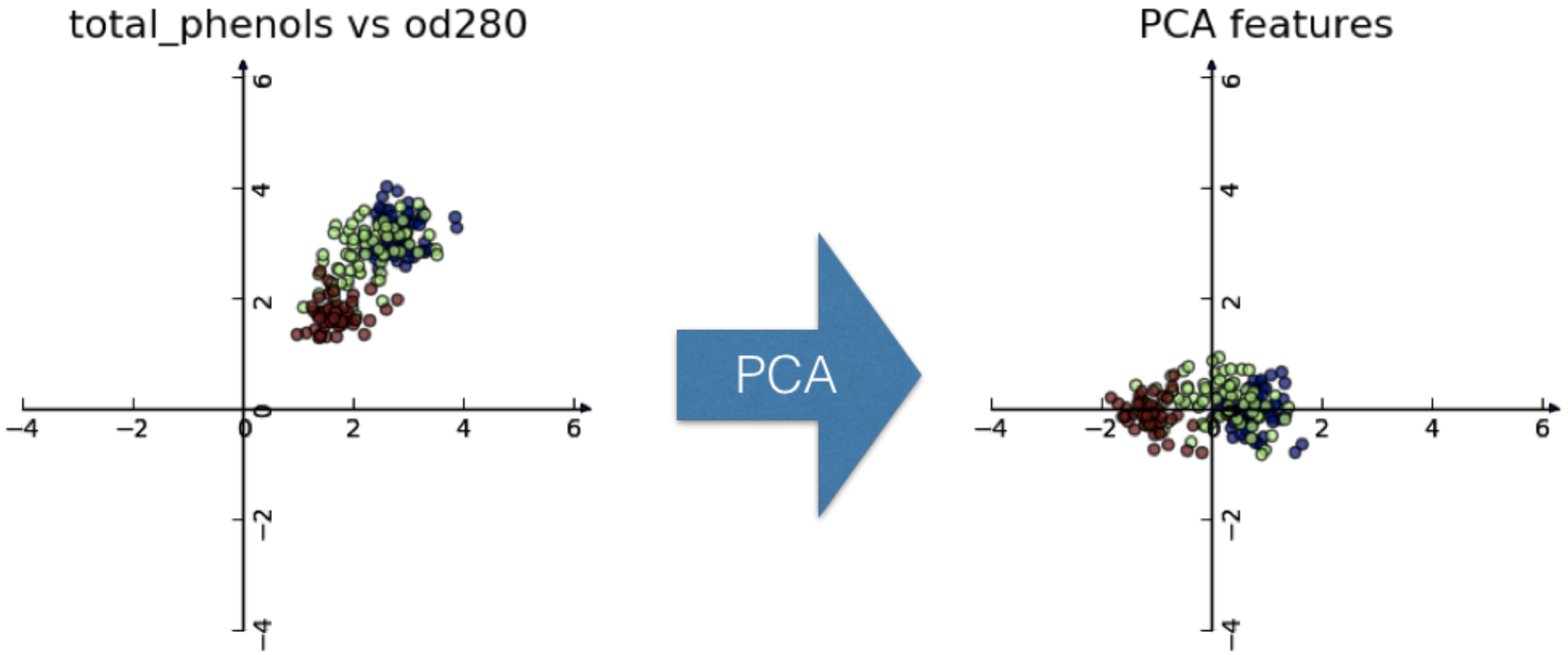
- More efficient storage and computation
- Remove less-informative "noise" features
- ... which cause problems for prediction tasks, e.g. classification, regression

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(copy=True, ...)
```

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

PCA features

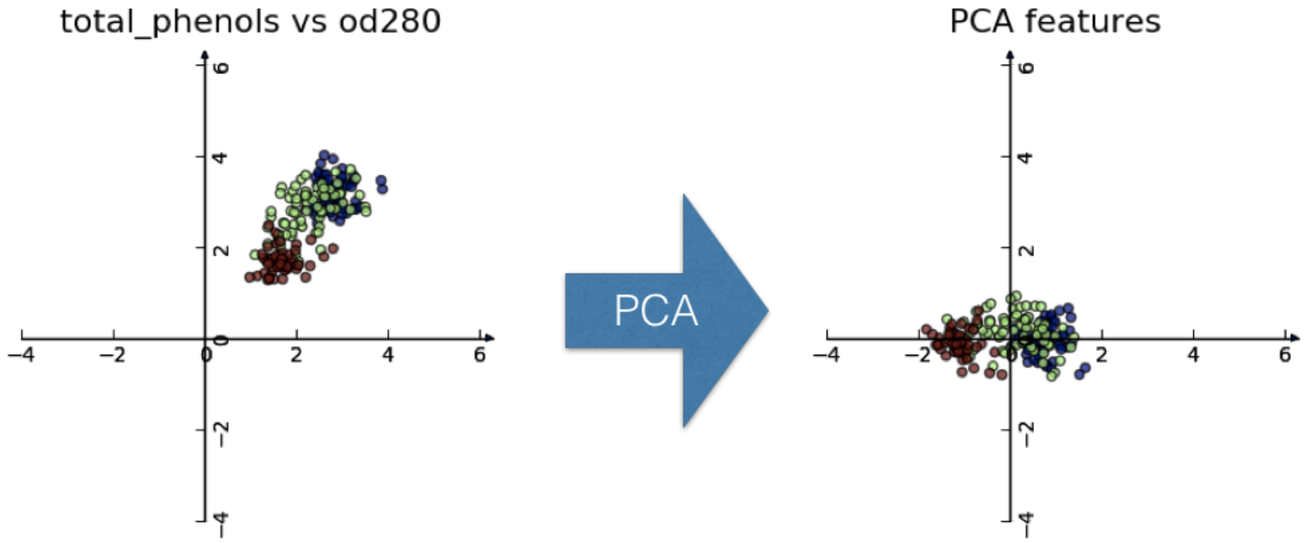
- Rows of transformed correspond to samples
- Columns of transformed are the "PCA features"
- Row gives PCA feature values of corresponding sample

```
print(transformed)
```

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

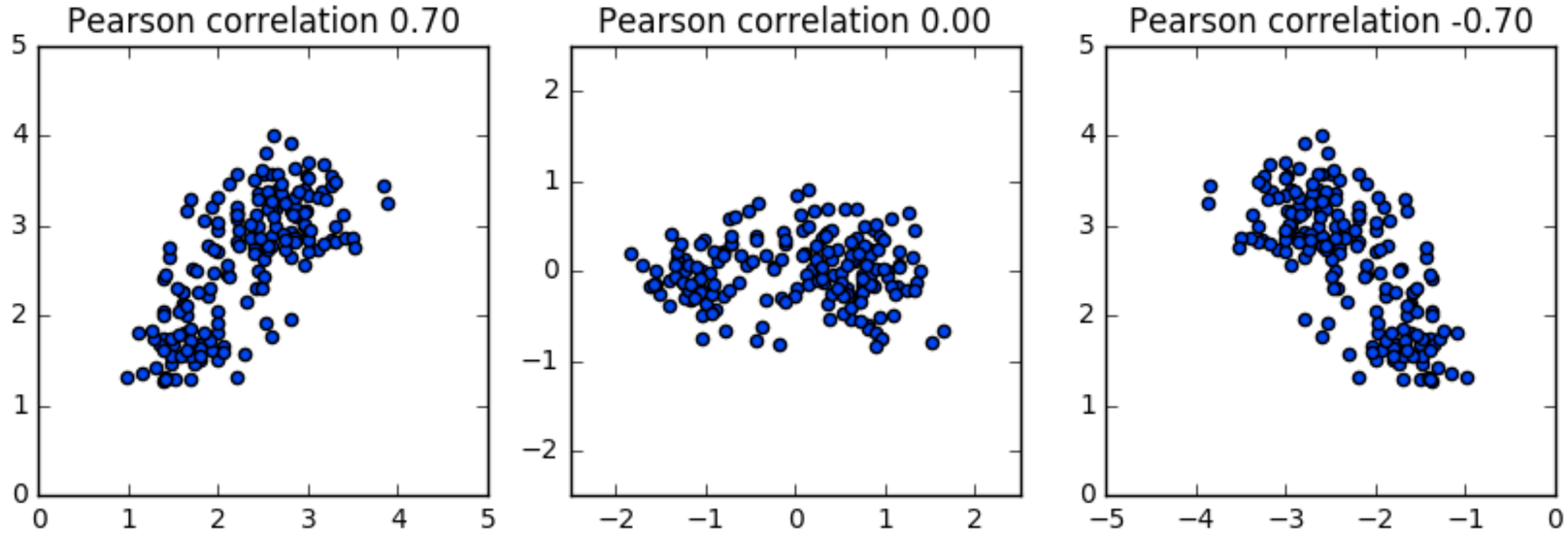
PCA features are not correlated

- 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")



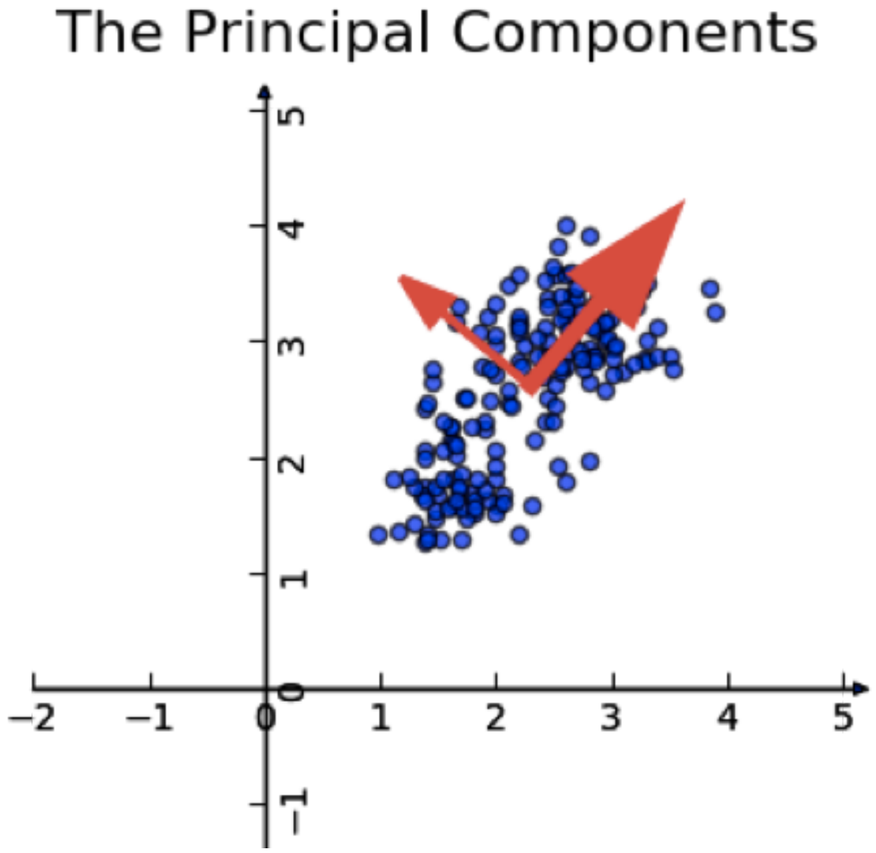
Pearson correlation

- 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



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]]
```

Let's practice!

UNSUPERVISED LEARNING IN PYTHON

Intrinsic dimension

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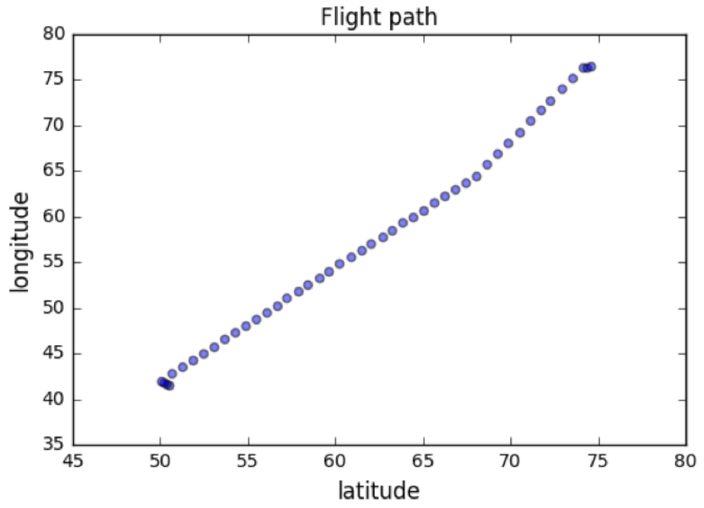
Intrinsic dimension of a flight path

- 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

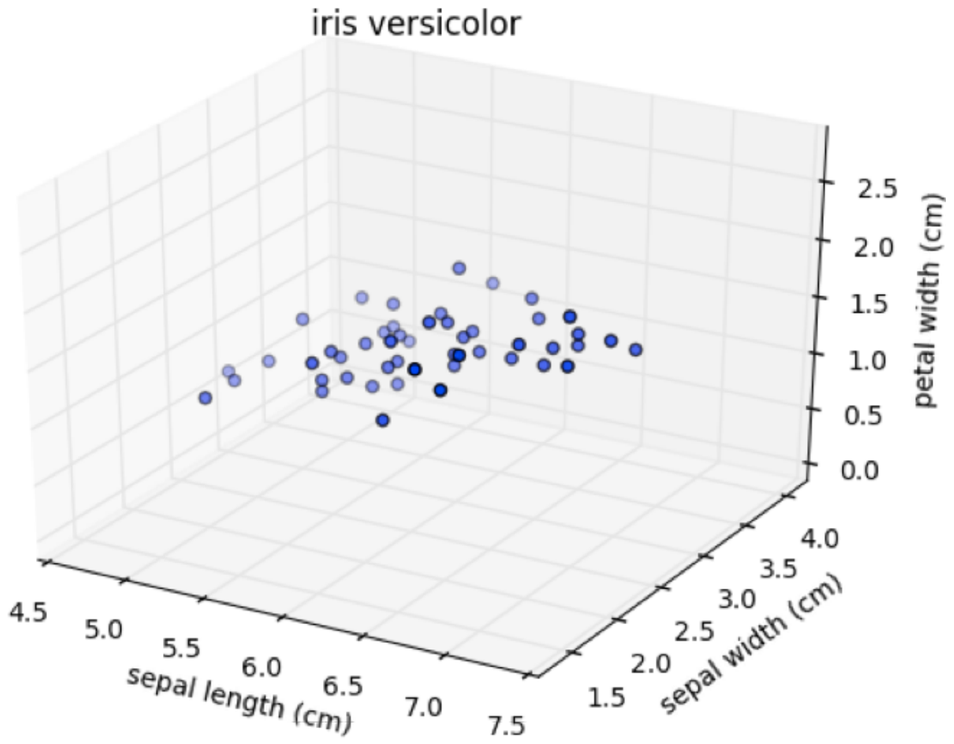
- Intrinsic dimension = number of features needed to approximate the dataset
- Essential idea behind dimension reduction
- What is the most compact representation of the samples?
- Can be detected with PCA

Versicolor dataset

- "versicolor", one of the iris species
- Only 3 features: sepal length, sepal width, and petal width
- Samples are points in 3D space

Versicolor dataset has intrinsic dimension 2

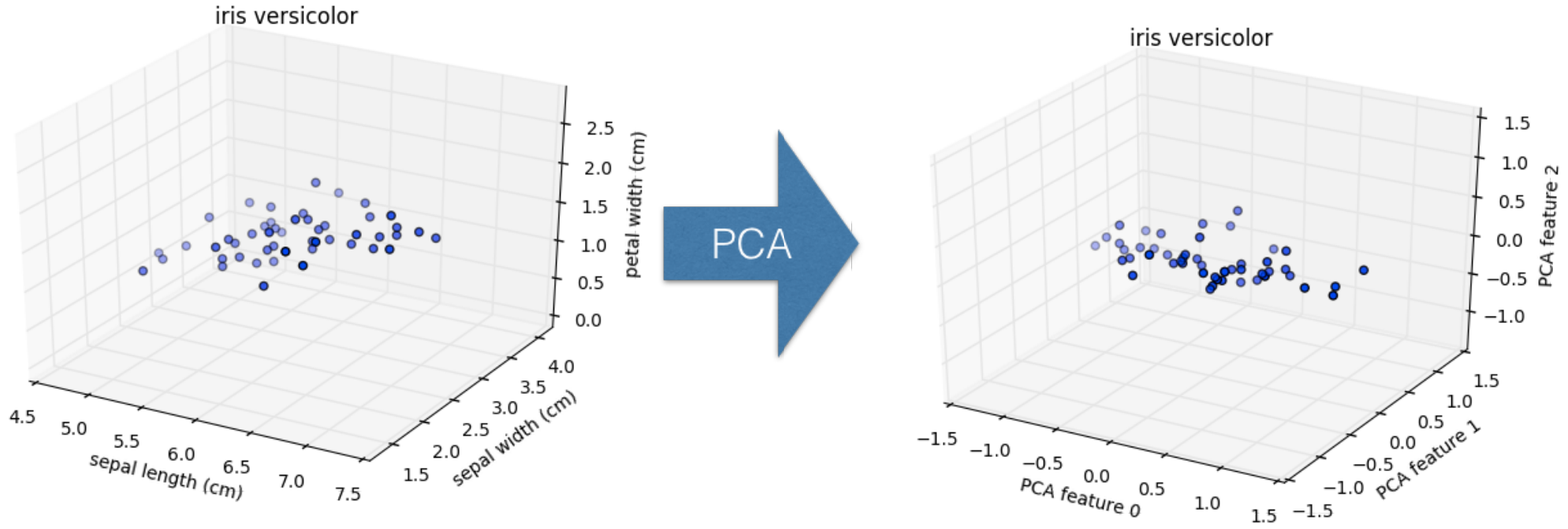
- Samples lie close to a flat 2-dimensional sheet
- So can be approximated using 2 features



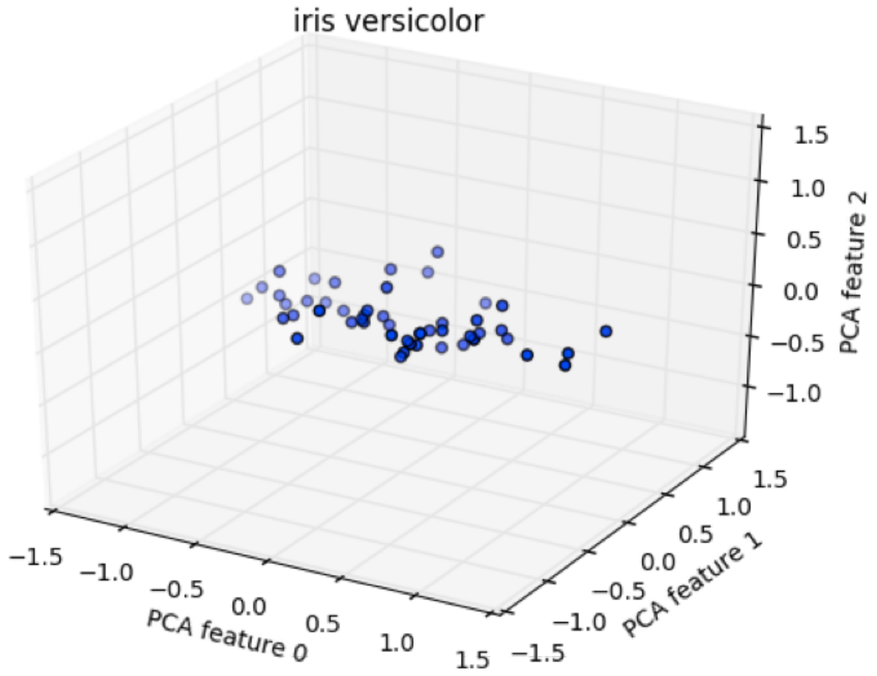
PCA identifies intrinsic dimension

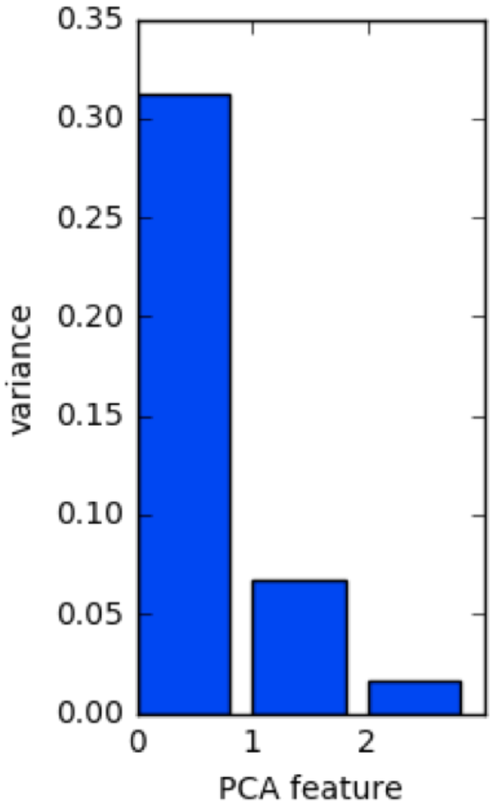
- Scatter plots work only if samples have 2 or 3 features
- PCA identifies intrinsic dimension when samples have any number of features
- Intrinsic dimension = number of PCA features with significant variance

PCA of the versicolor samples



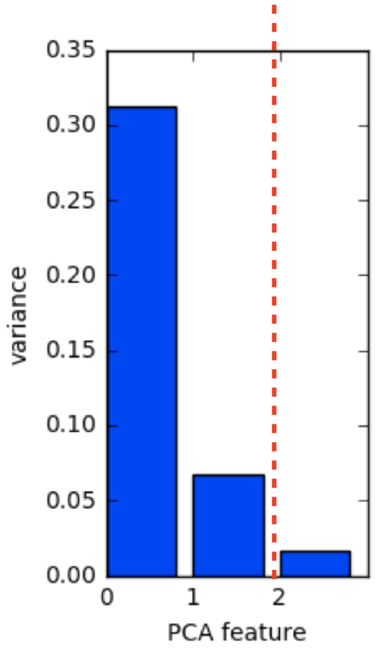
PCA features are ordered by variance descending





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

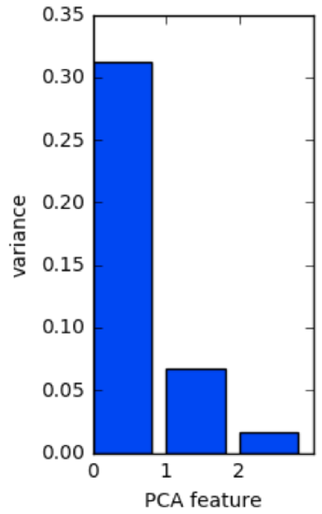
```
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
pca = PCA()
pca.fit(samples)
```

```
PCA(copy=True, ... )
```

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

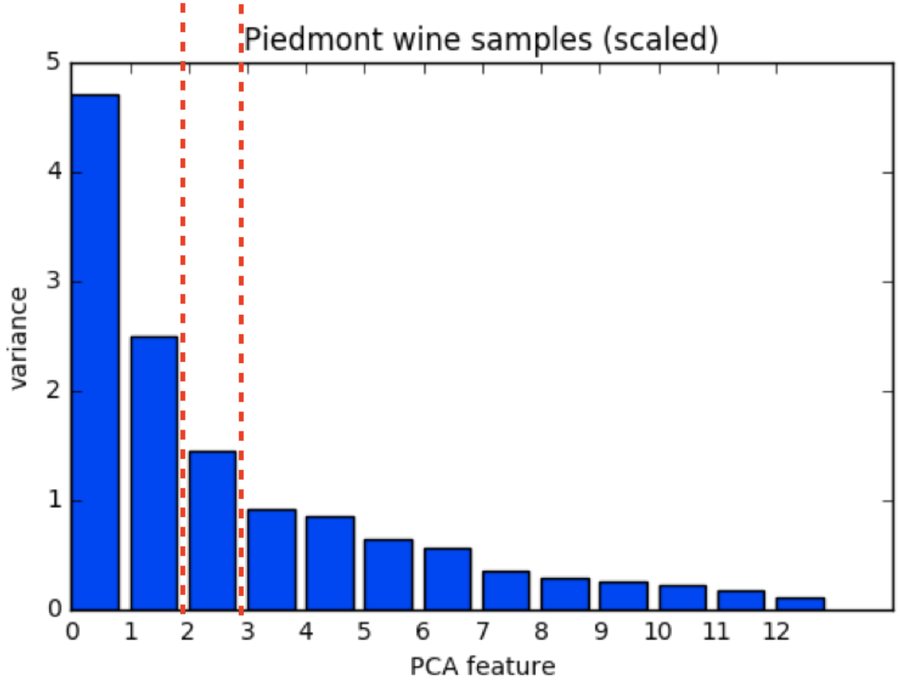
Plotting the variances of PCA features

```
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



Let's practice!

UNSUPERVISED LEARNING IN PYTHON

Dimension reduction with PCA

UNSUPERVISED LEARNING IN PYTHON

Benjamin Wilson
Director of Research at lateral.io

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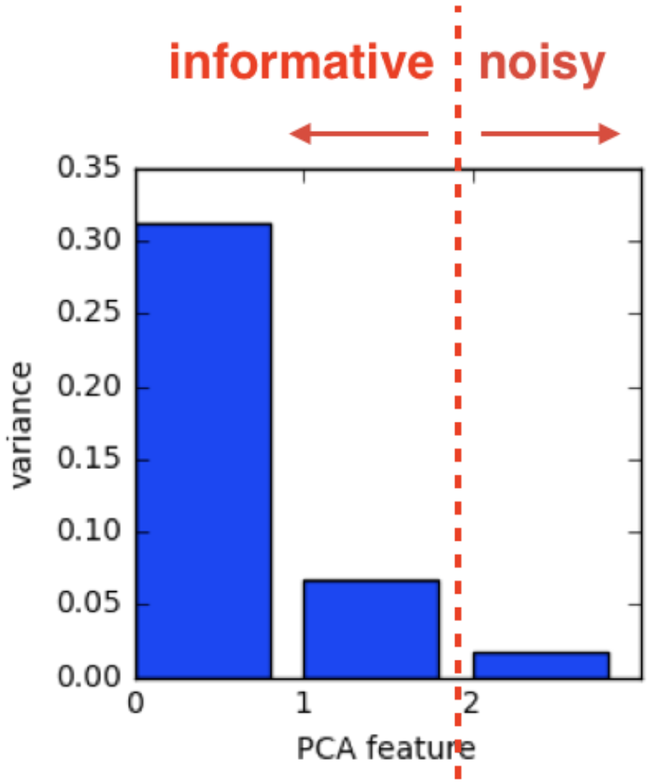
Dimension reduction

- 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(copy=True, ... )
```

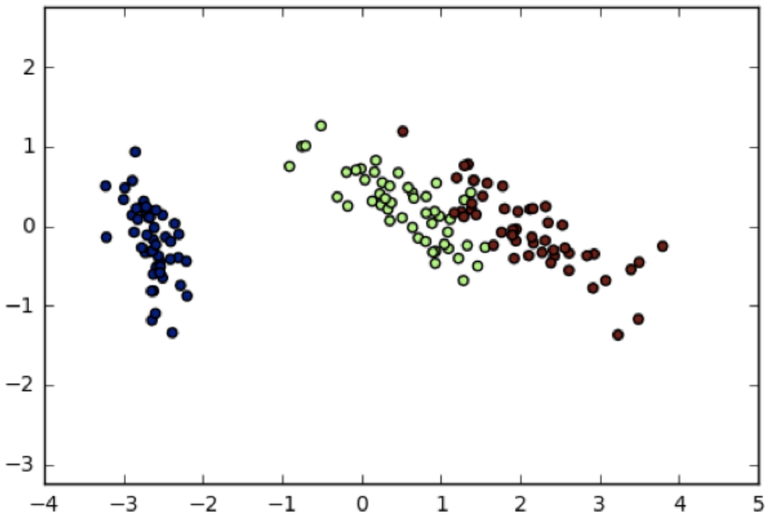
```
transformed = pca.transform(samples)
print(transformed.shape)
```

```
(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()
```

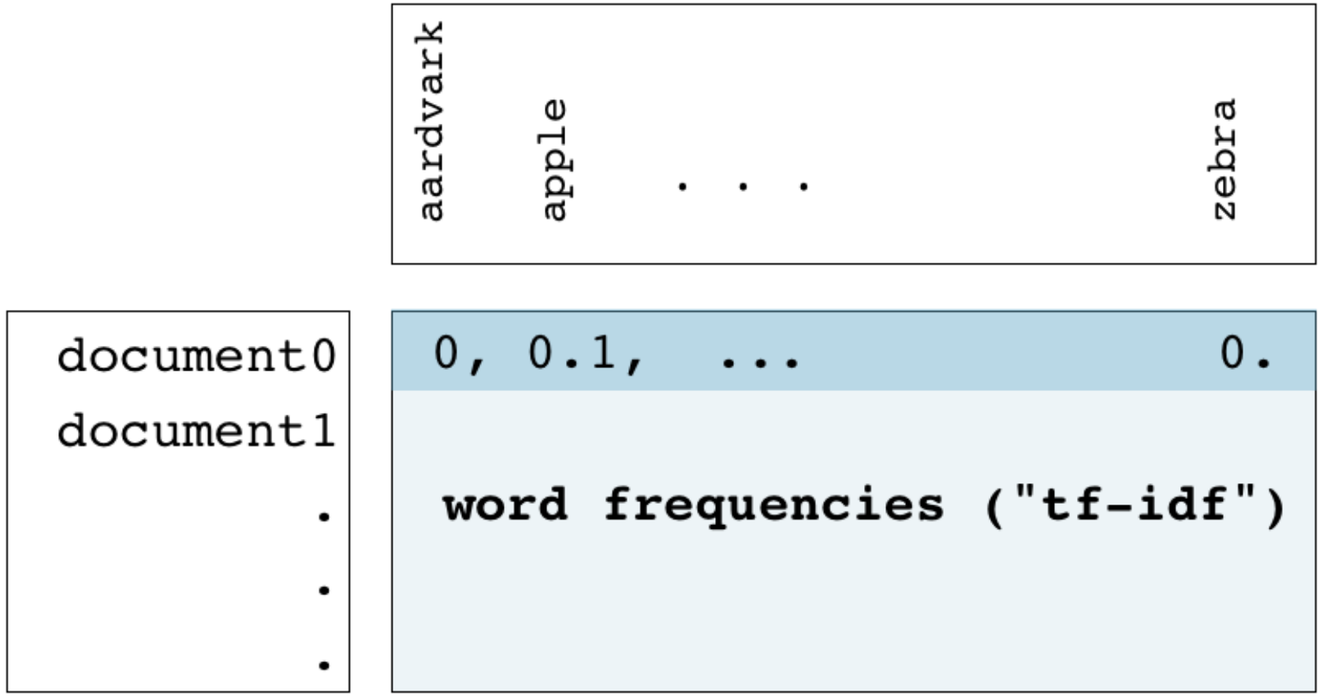


Dimension reduction with PCA

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

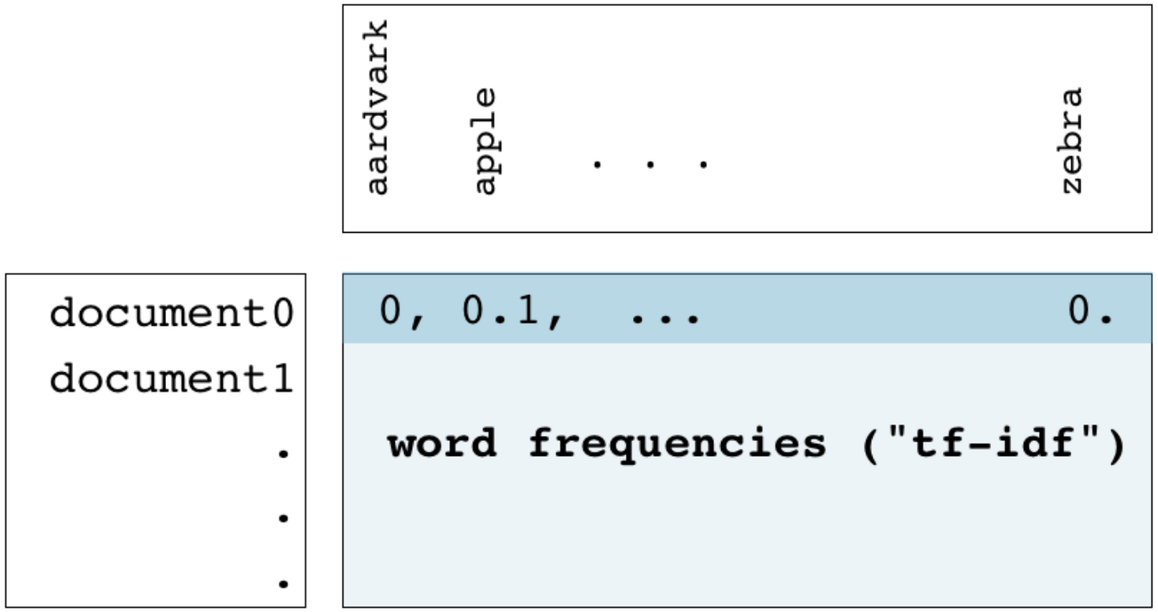
Word frequency arrays

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



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!)



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
TruncatedSVD(algorithm='randomized', ... )
transformed = model.transform(documents)
```

Let's practice!

UNSUPERVISED LEARNING IN PYTHON

Non-negative matrix factorization (NMF)

UNSUPERVISED LEARNING IN PYTHON

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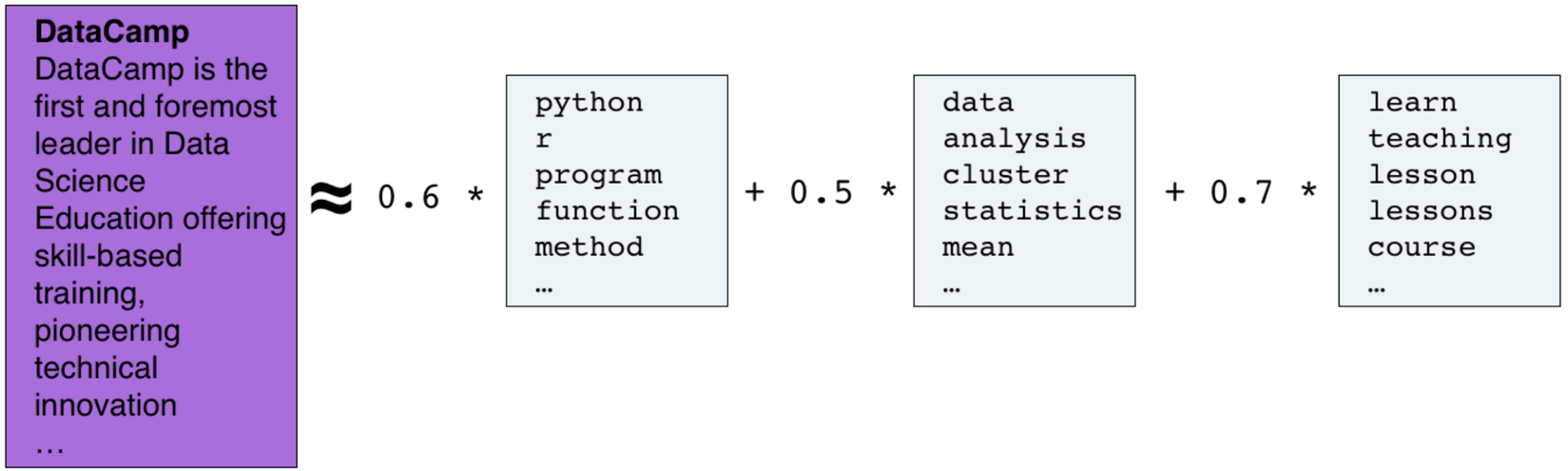
Non-negative matrix factorization

- 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)

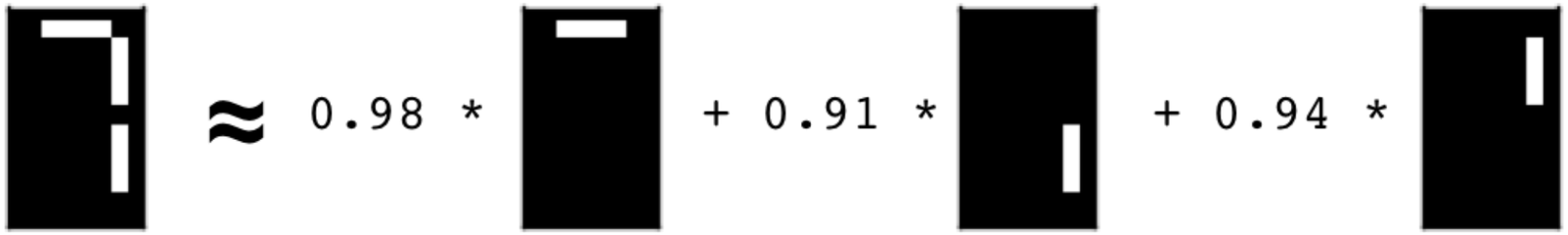
Interpretable parts

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



Interpretable parts

- NMF expresses images as combinations of patterns

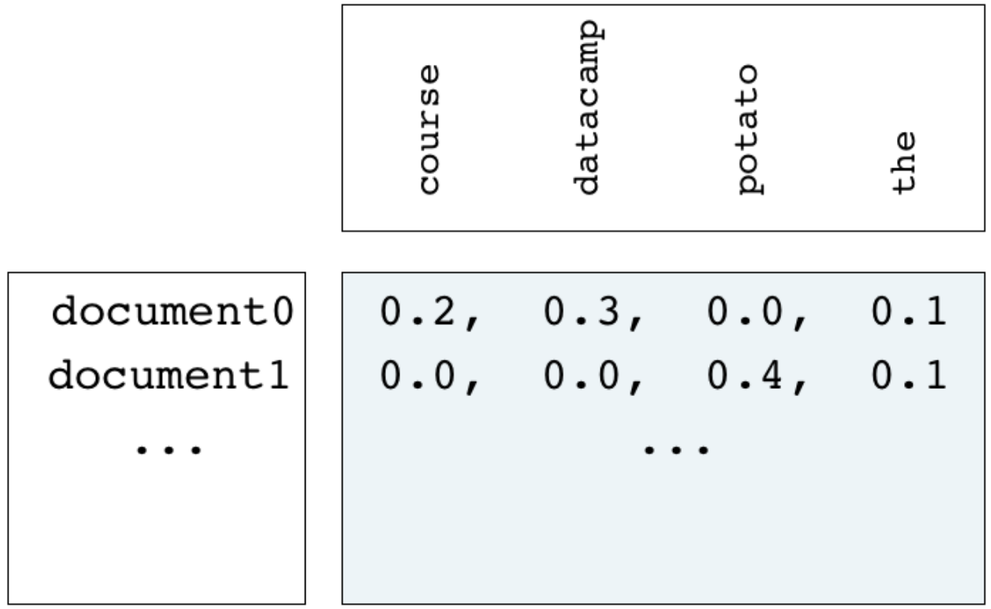


Using scikit-learn NMF

- 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



Example usage of NMF

- `samples` is the word-frequency array

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

```
NMF(alpha=0.0, ... )
```

```
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]]
```

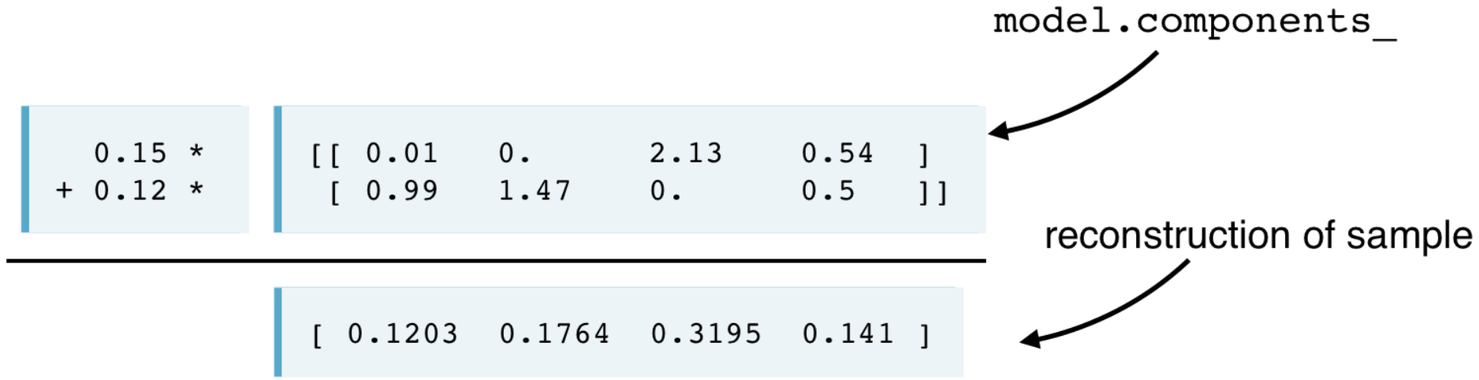
Reconstruction of a sample

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

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

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

```
[ 0.15  0.12]
```



Sample reconstruction

- Multiply components by feature values, and add up
- Can also be expressed as a product of matrices
- This is the "**M**atrix **F**actorization" 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!

Let's practice!

UNSUPERVISED LEARNING IN PYTHON

NMF learns interpretable parts

UNSUPERVISED LEARNING IN PYTHON

Benjamin Wilson
Director of Research at lateral.io

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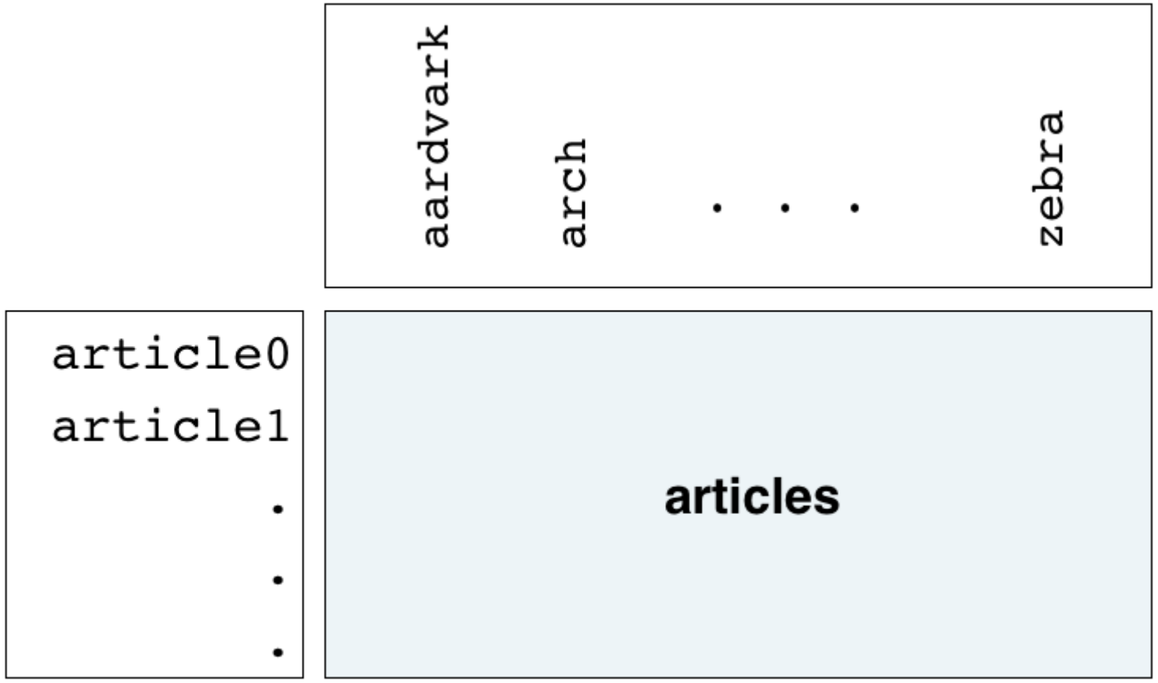
Example: NMF learns interpretable parts

- Word-frequency array articles (tf-idf)
- 20,000 scientific articles (rows)
- 800 words (columns)



Applying NMF to the articles

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

```
(20000, 800)
```

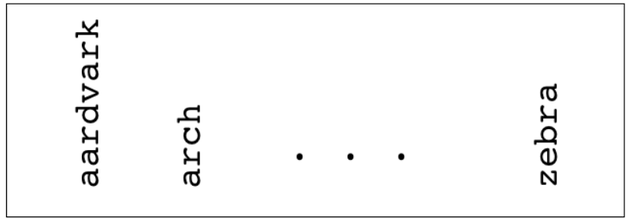
```
from sklearn.decomposition import NMF
nmf = NMF(n_components=10)
nmf.fit(articles)
```

```
NMF(alpha=0.0, ... )
```

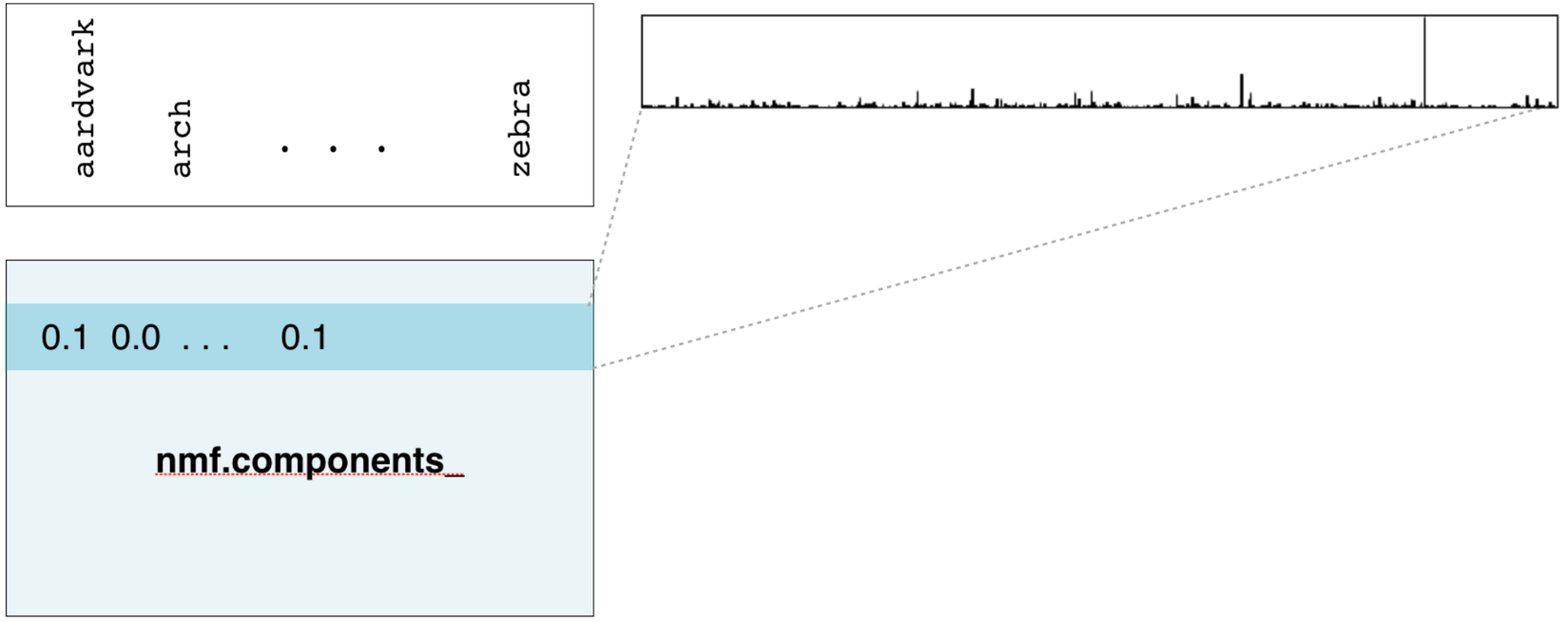
```
print(nmf.components_.shape)
```

```
(10, 800)
```

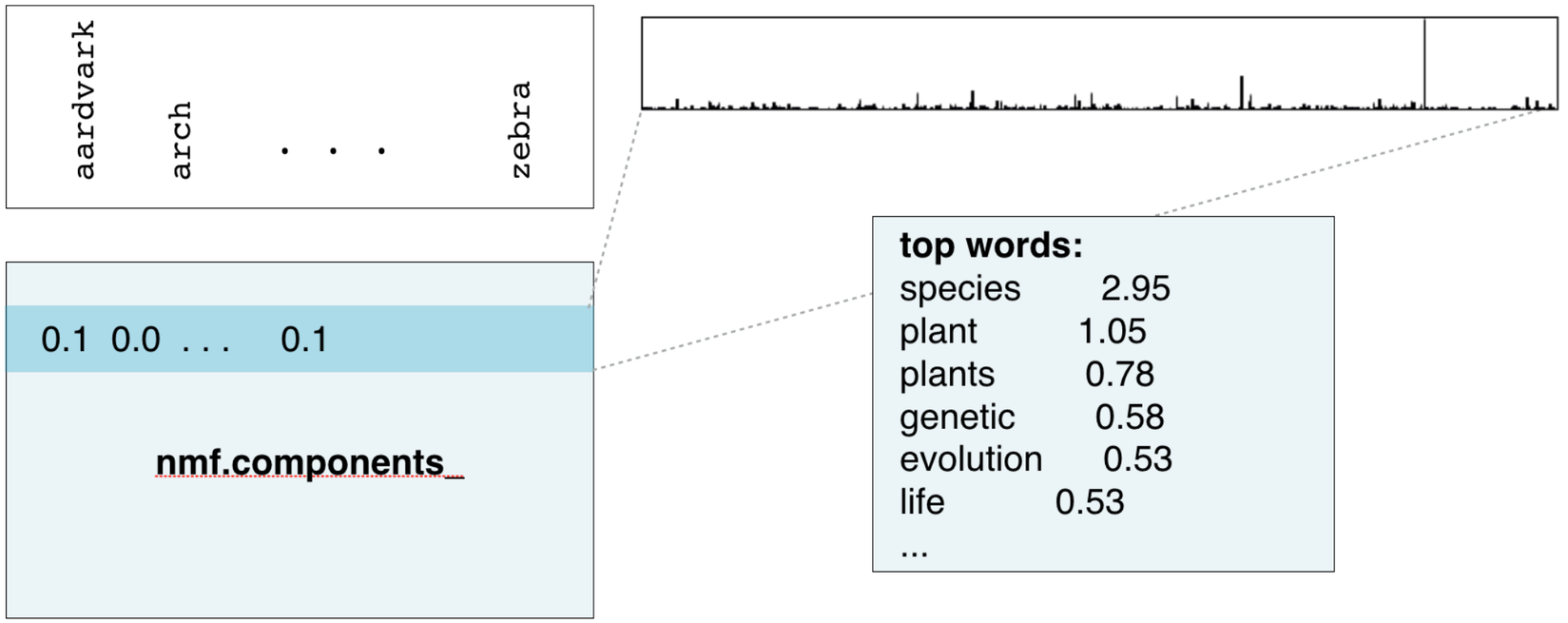
NMF components are topics



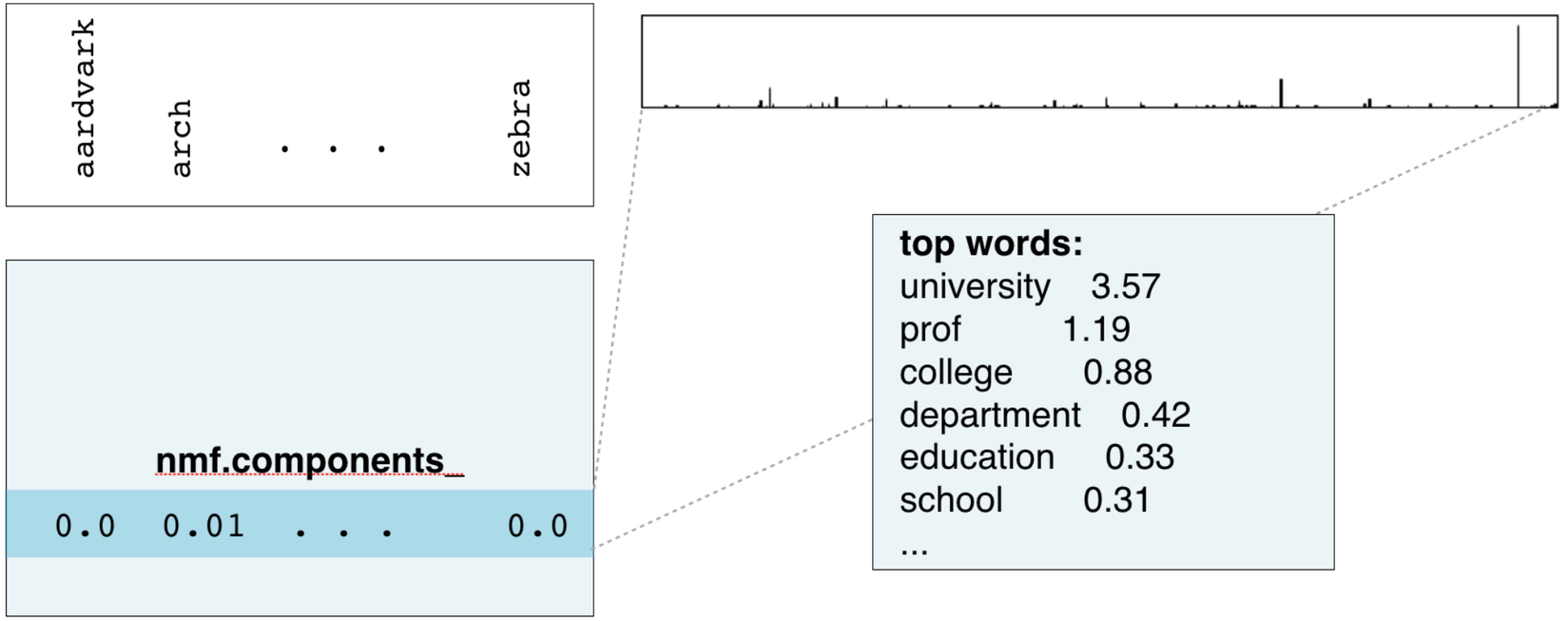
NMF components are topics



NMF components are topics

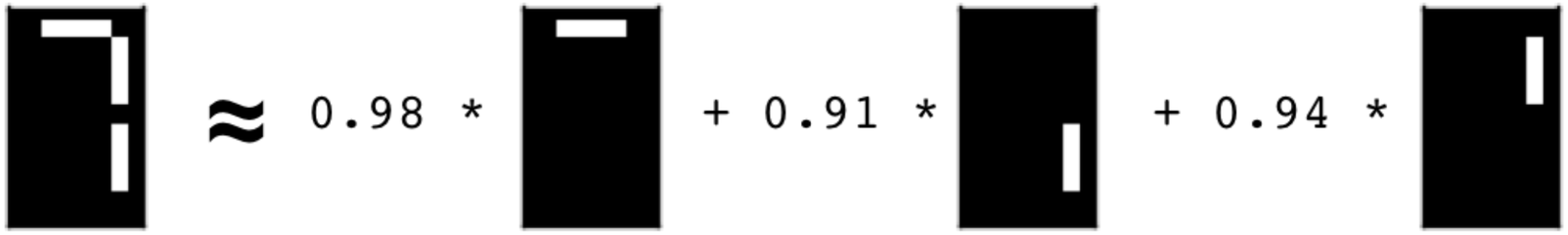


NMF components are topics



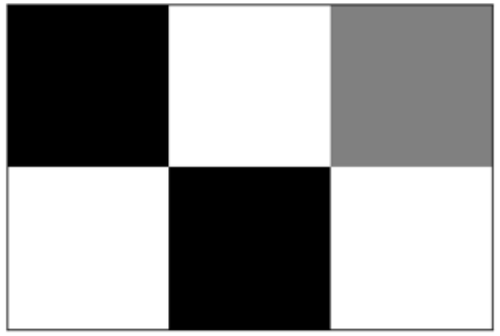
NMF components

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



Grayscale images

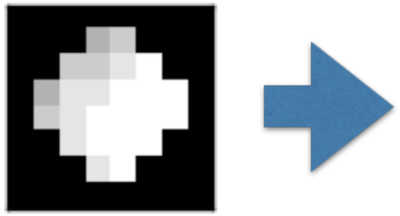
- "Grayscale" image = no colors, only shades of gray
- Measure pixel brightness
- Represent with value between 0 and 1 (0 is black)
- Convert to 2D array



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

Grayscale image example

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

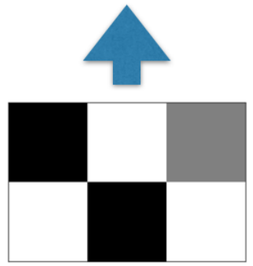


```
[[ 0.   0.   0.   0.   0.   0.   0.   0. ]
 [ 0.   0.   0.   0.7  0.8  0.   0.   0. ]
 [ 0.   0.   0.8  0.8  0.9  1.   0.   0. ]
 [ 0.   0.7  0.9  0.9  1.   1.   1.   0. ]
 [ 0.   0.8  0.9  1.   1.   1.   1.   0. ]
 [ 0.   0.   0.9  1.   1.   1.   0.   0. ]
 [ 0.   0.   0.   0.9  1.   0.   0.   0. ]
 [ 0.   0.   0.   0.   0.   0.   0.   0. ]]
```

Grayscale images as flat arrays

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

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



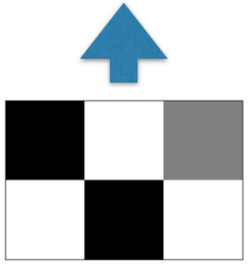
Grayscale images as flat arrays

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

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

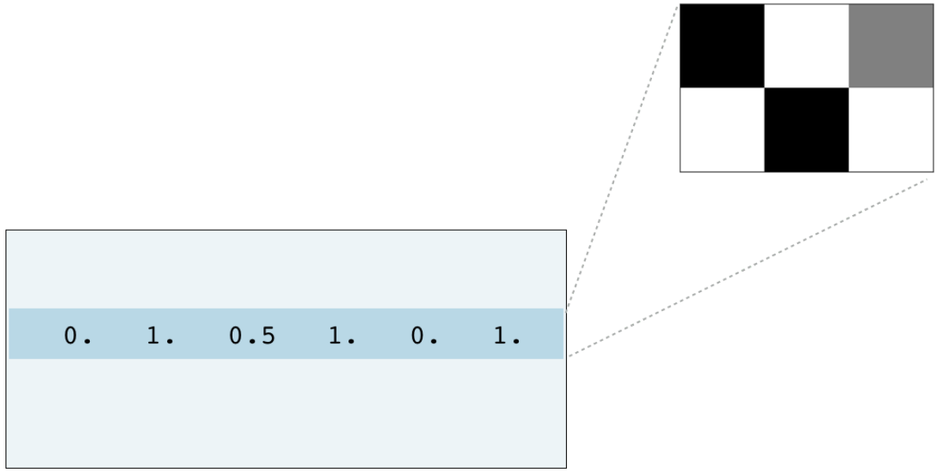


```
[ 0.   1.   0.5   1.   0.   1. ]
```



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()
```

Let's practice!

UNSUPERVISED LEARNING IN PYTHON

Building recommender systems using NMF

UNSUPERVISED LEARNING IN PYTHON

Benjamin Wilson
Director of Research at lateral.io

datacamp

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)
```

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?

Versions of articles

- Different versions of the same document have same topic proportions
- ... exact feature values may be different!
-
-

strong version

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

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
-

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 ...

Versions of articles

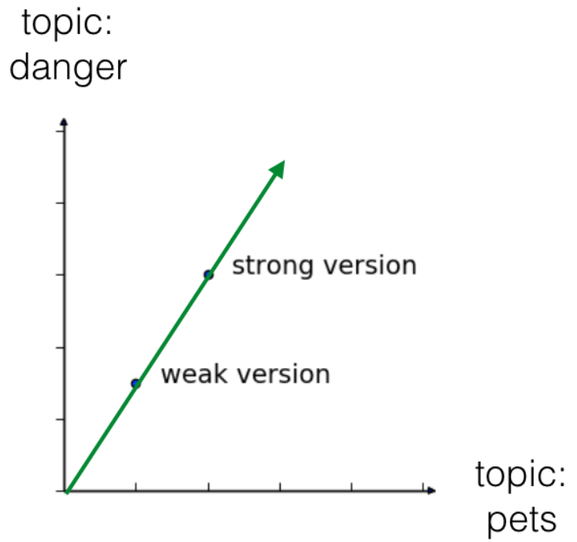
- Different versions of the same document have same topic proportions
- ... exact feature values may be different!
- E.g. because one version uses many meaningless words
- But all versions lie on the same line through the origin

strong version

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

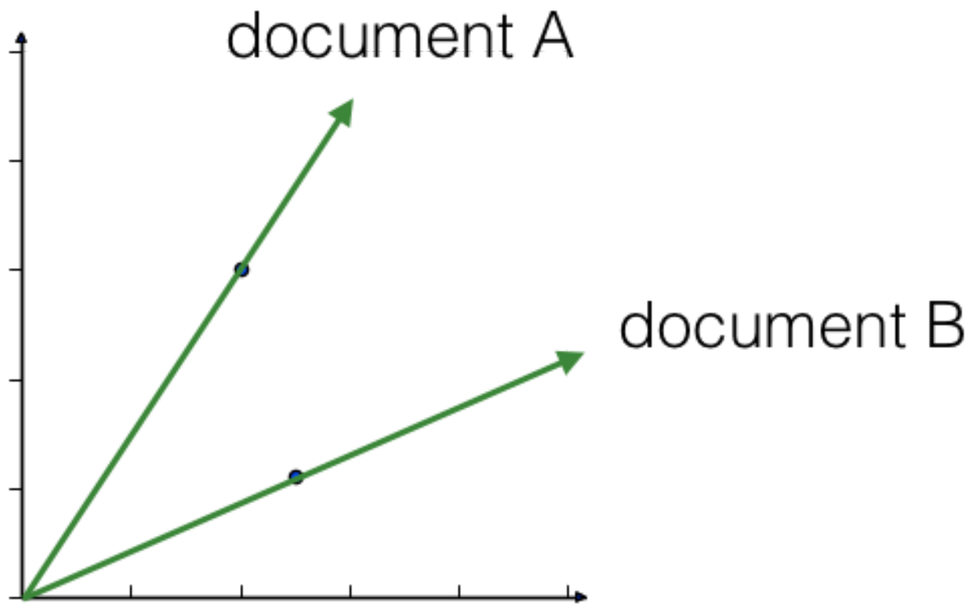
weak version

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



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
```

Let's practice!

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Final thoughts

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Congratulations!

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