Visualizing the PCA transformation

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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

Find the pattern in the data then use these pattern to express the data in the more compressed form

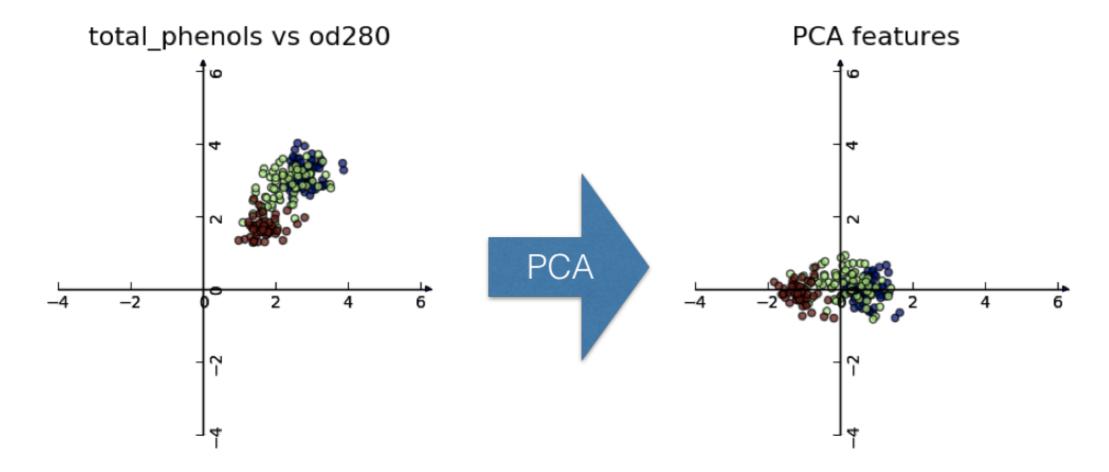


Principal Component Analysis

- 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, ...)
```

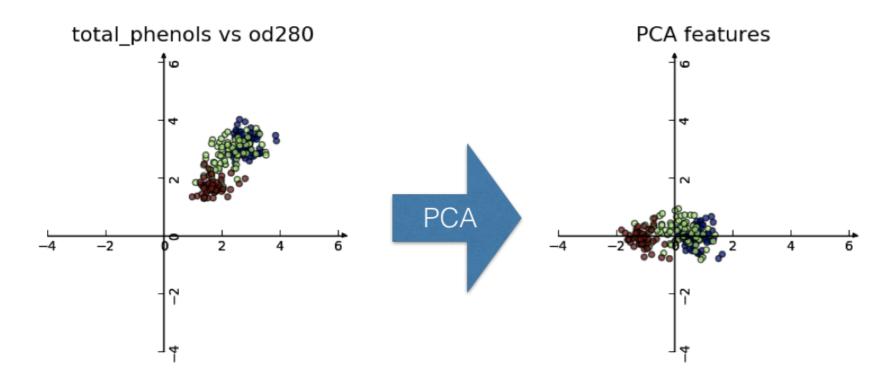
```
transformed = model.transform(samples)
```

PCA features

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

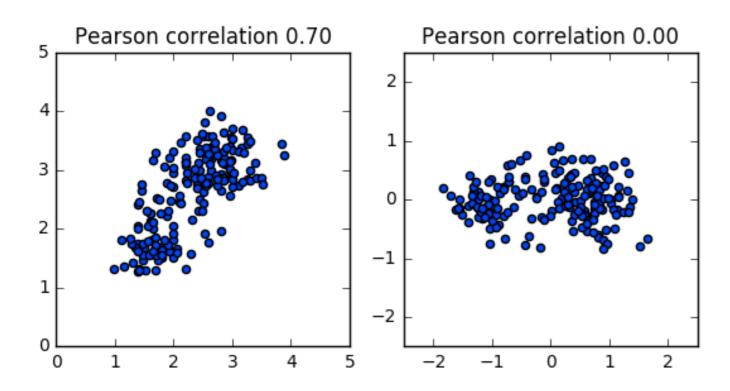
PCA features are not correlated

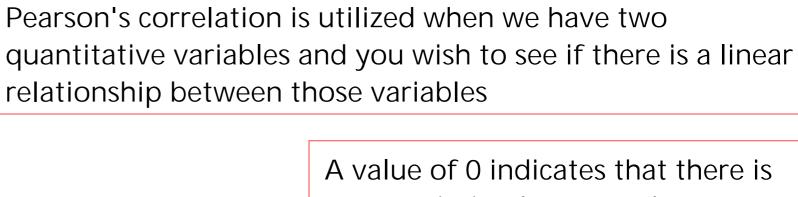
- Features of dataset are often correlated, e.g. total_phenols and od280
- PCA aligns the data with axes
- Resulting PCA features are not linearly correlated ("decorrelation")



Pearson correlation

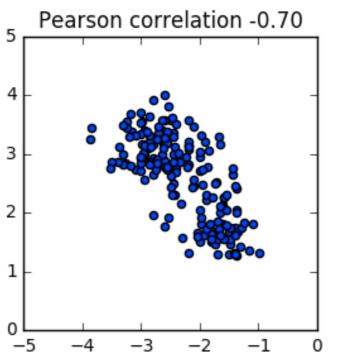
- Measures linear correlation of features
- Value between -1 and 1
- Value of O means no linear correlation





A Pearson correlation is a number between -1 and +1 that

indicates. to which extent 2 variables are linearly related.

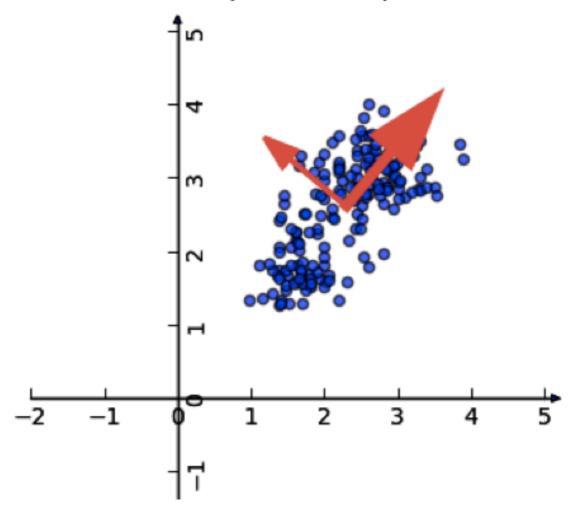


A value of 0 indicates that there is no association between the two variables. A value greater than 0 indicates a positive association; that is, as the value of one variable increases, so does the value of the other variable.

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]]
```

Let's practice!

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Intrinsic dimension

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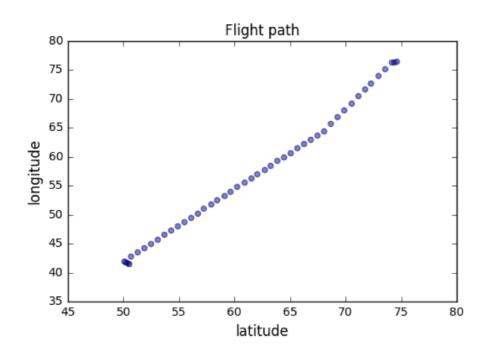
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Intrinsic dimension of a flight path

- 2 features: longitude and latitude at points along a flight path
- Dataset appears to be 2dimensional
- 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

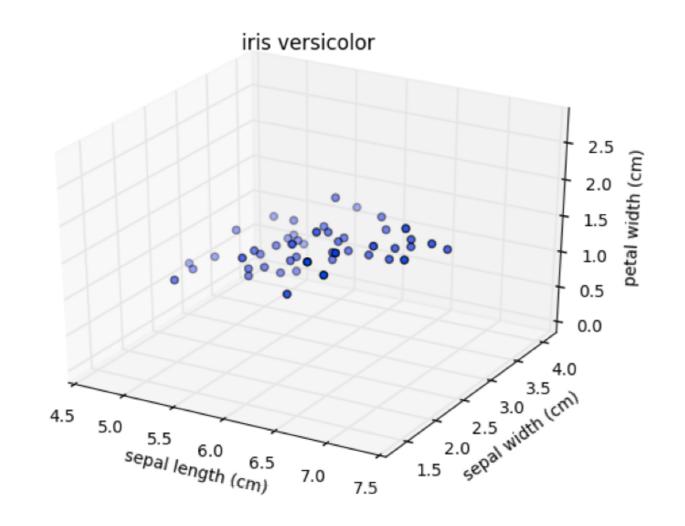
- Intrinsic dimension = number of features needed to approximate the dataset
- Essential idea behind dimension reduction
- What is the most compact representation of the samples?
- Can be detected with PCA

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

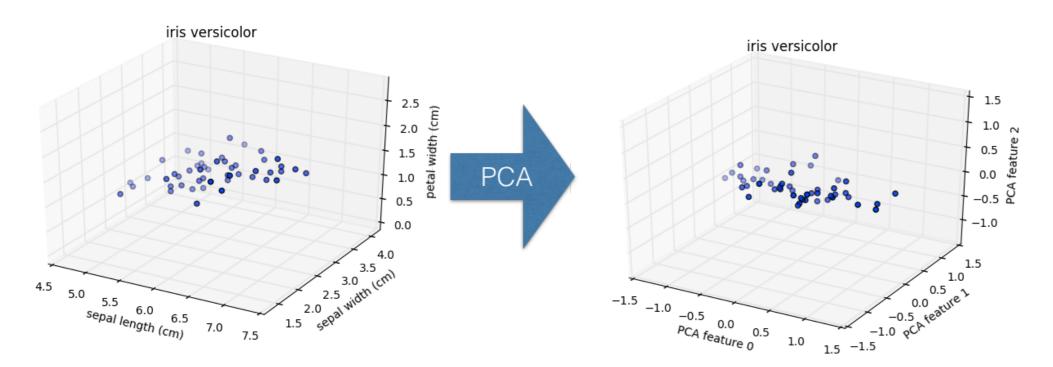
- Samples lie close to a flat 2-dimensional sheet
- So can be approximated using 2 features



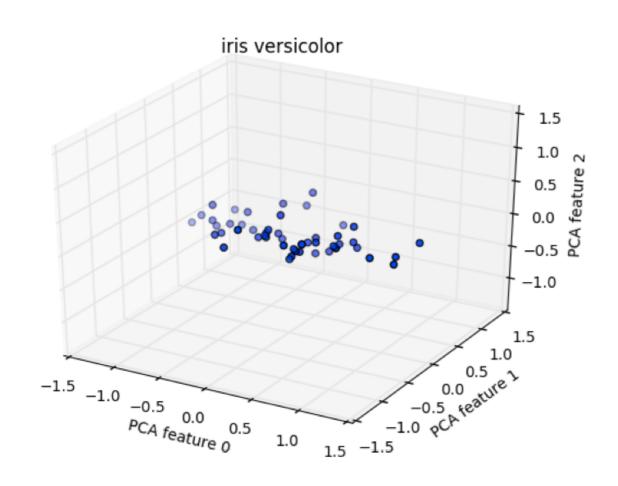
PCA identifies intrinsic dimension

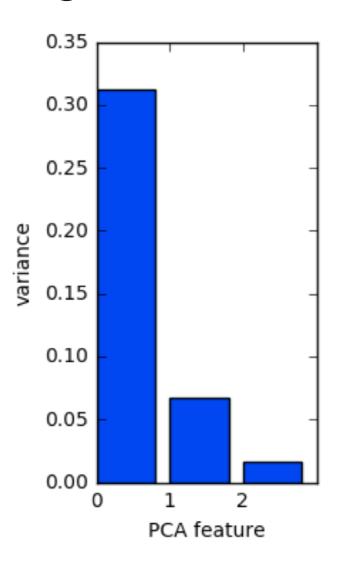
- Scatter plots work only if samples have 2 or 3 features
- PCA identifies intrinsic dimension when samples have any number of features
- Intrinsic dimension = number of PCA features with significant variance

PCA of the versicolor samples



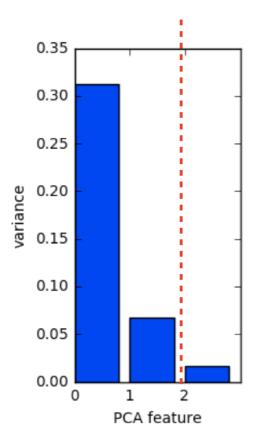
PCA features are ordered by variance descending





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

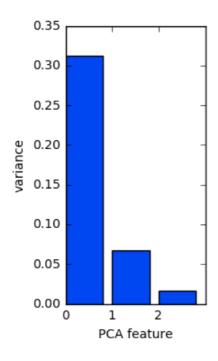
```
import matplotlib.pyplot as plt
from sklearn.decomposition import PCA
pca = PCA()
pca.fit(samples)
```

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

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

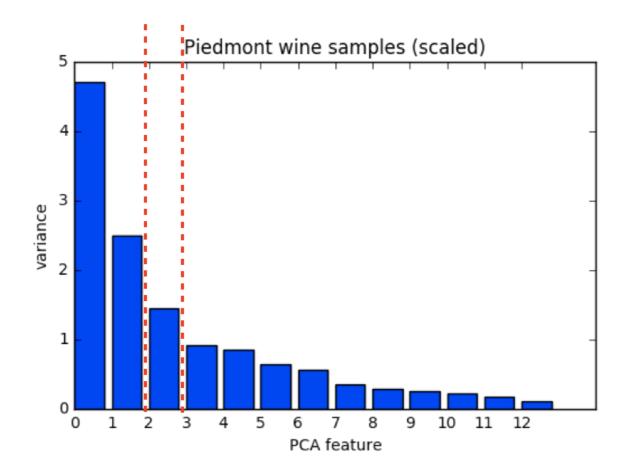
Plotting the variances of PCA features

```
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



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Dimension reduction with PCA

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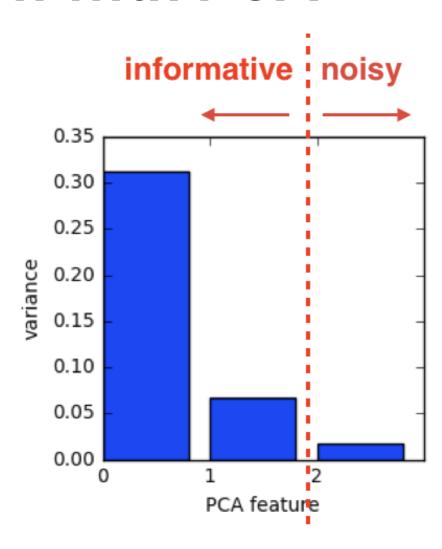


Dimension reduction

- 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, ...)
```

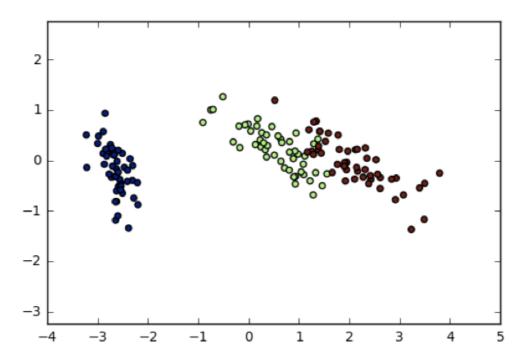
```
transformed = pca.transform(samples)
print(transformed.shape)
```

```
(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()
```

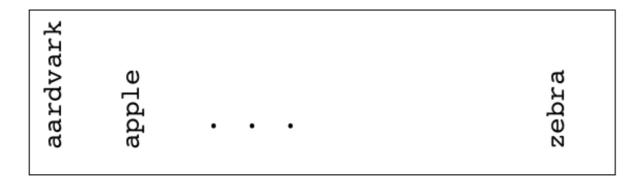


Dimension reduction with PCA

- 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)



document0
document1
.

```
0, 0.1, ... 0.

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
.
```

```
document0
document1
.
```

```
0, 0.1, ... 0.

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

Let's practice!

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