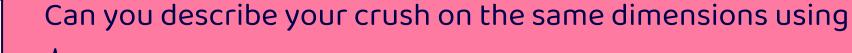


What is data reduction?



Can you describe your crush along the following dimensions: Hair, height, eye colour, smile, personality







♦ fewer words?

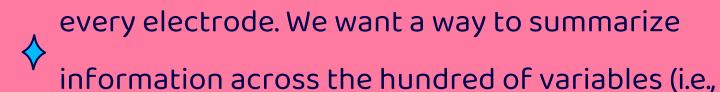






(e.g., EEG recordings from 200+ electrodes). While we are

interested in global patterns we may not be interested in







Data reduction

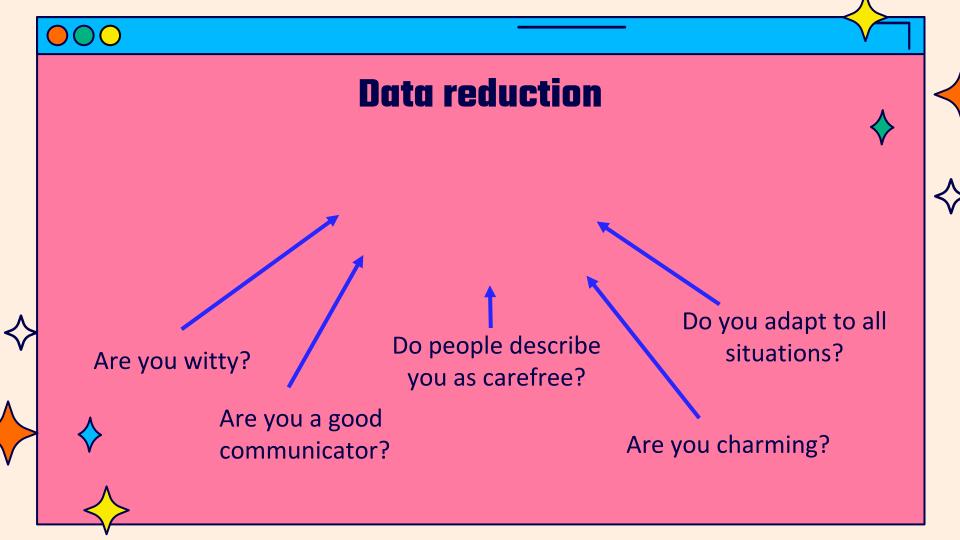


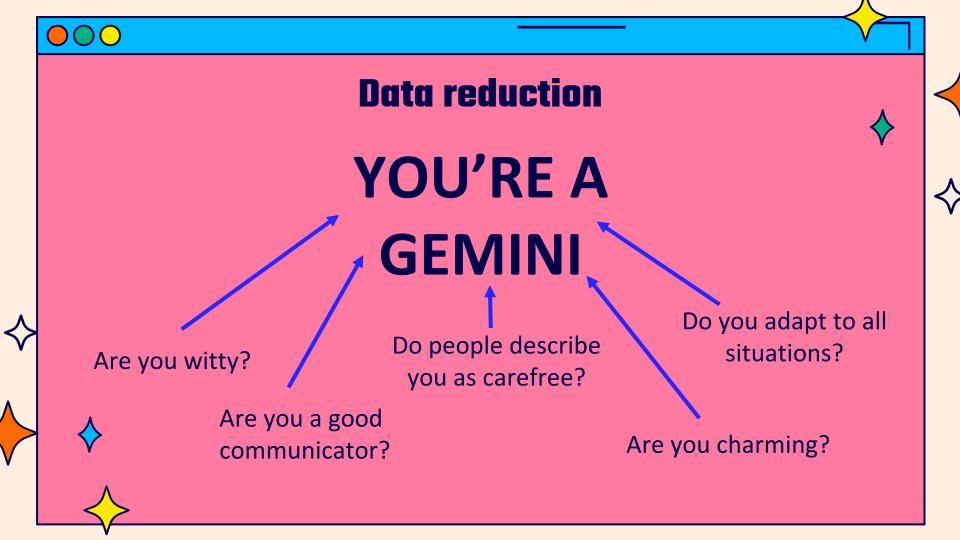
Like a questionnaire in psychology research, observations of all your measures (i.e., questions on a questionnaire) can be described by latent variables that may be of interest to you (i.e., personality)

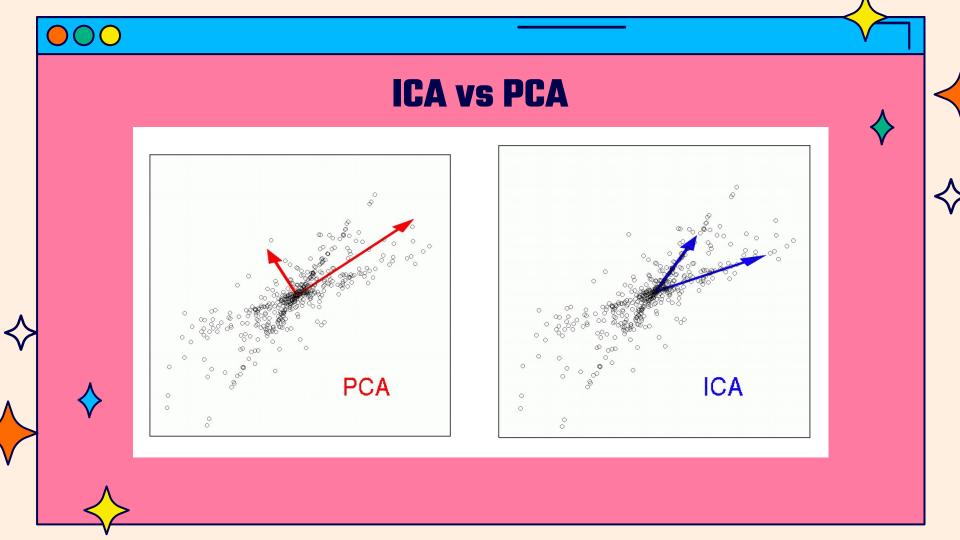














Principal Component Analysis

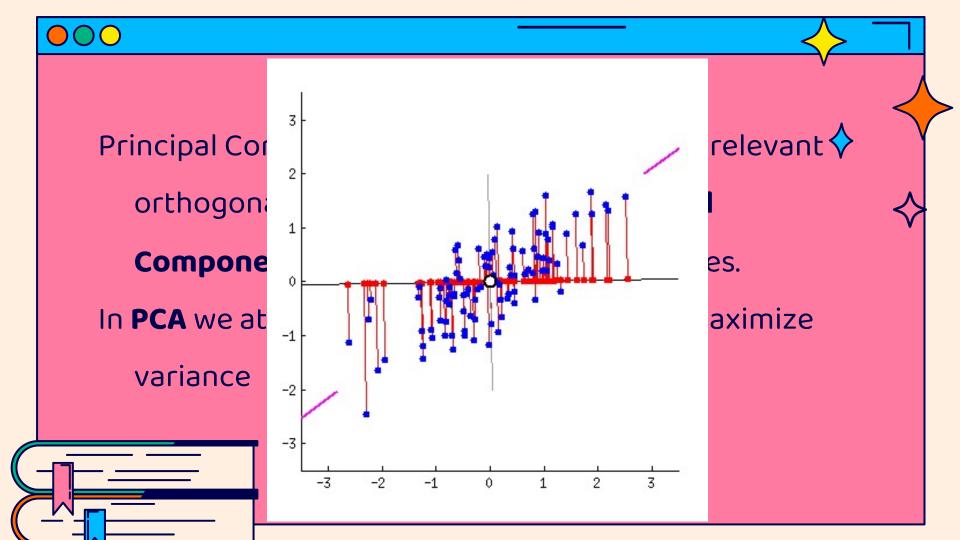
Principal Component Analysis (PCA) extracts relevant 💠



Components, from a large pool of variables.

In **PCA** we attempt to find dimensions that maximize variance









PCA

[coeff, score, latent, tsquared, explained, mu] = pca(X)

X -> data matrix (m by n) to apply PCA (rows observations, col variables)

Coeff -> matrix (n by n) PCA coefficients each col is one PC, rows are weights for your variables

Score -> matrix (m by n) how much a given observation

'scores' or 'loads' onto a PC



PCA

[coeff, score, latent, tsquared, explained, mu] = pca(X)

Latent -> eigenvalues of the covariance matrix of X

Tsquared -> Sum of squares of standardized scores

Explained -> Percent variance explained per component

Mu -> estimated means of each variable



Normalizing data

In Generally, you want to normalize your data **BEFORE** running a PCA both by subtracting the mean of each column and dividing by the standard deviation of each column



















Since PCA is a linear transformation, translating our data into a new space, we can simply rotate it back to where it began:



Where the **score** is the loadings of the components and **coeff** is the weights matrix that was used to rotate your data. Notice how we add back the mean of our Original data.





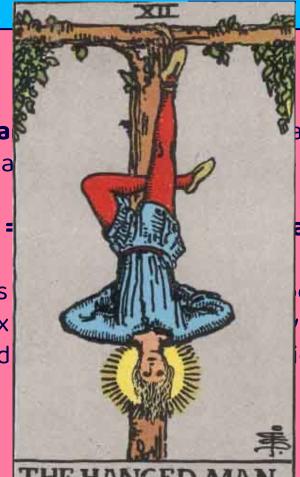


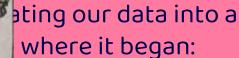


Since PCA is a **linea** new space, we ca

Original_data =

Where the **score** is the weights matrix Notice how we add





ata);

onents and **coeff** is our data. ginal data.







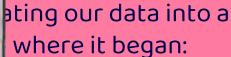


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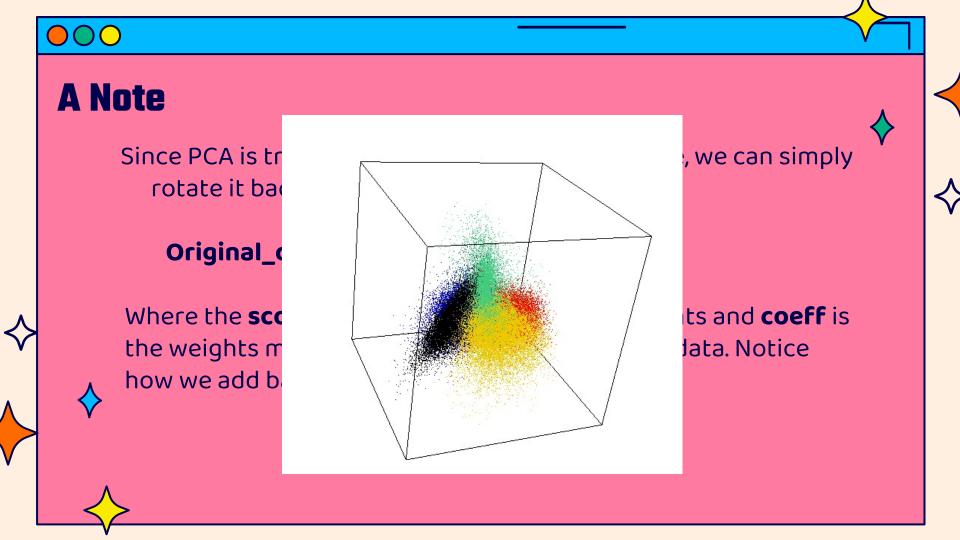


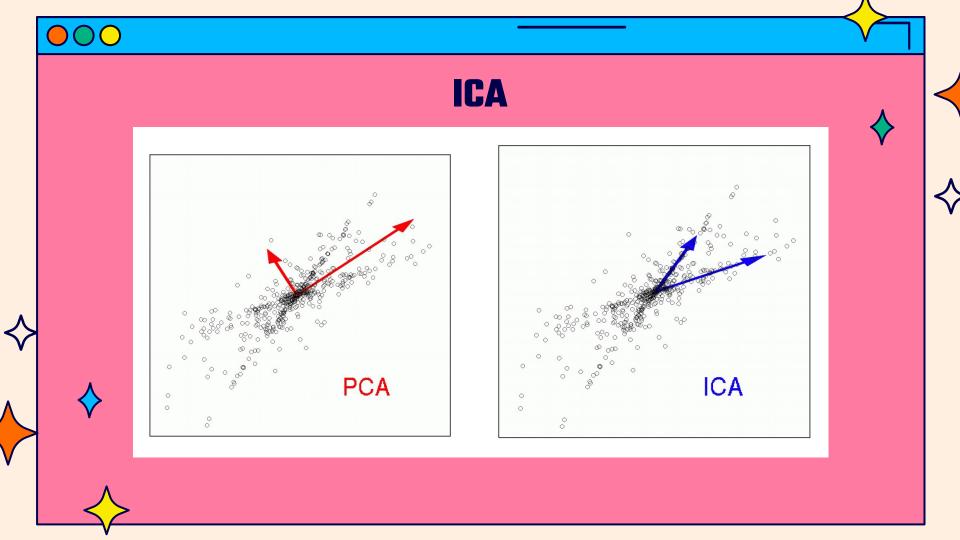


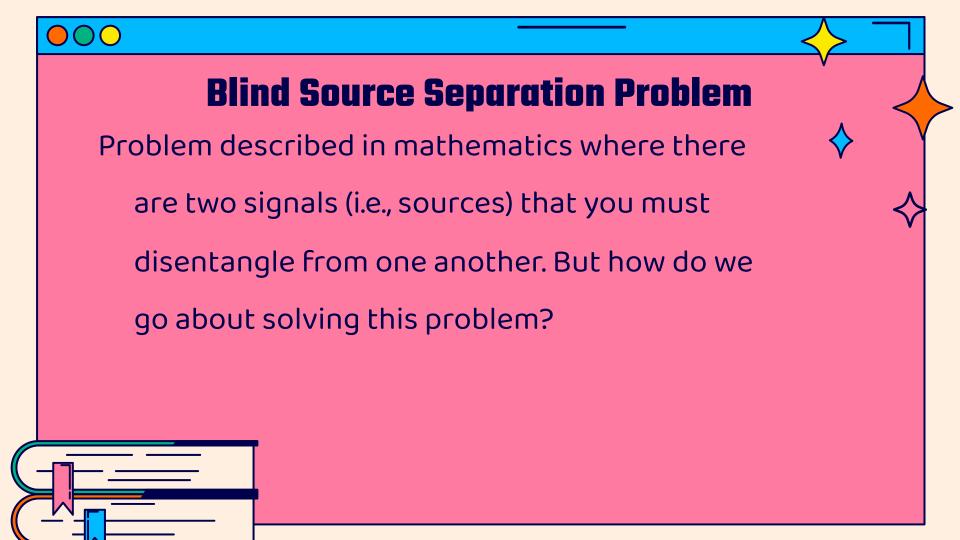


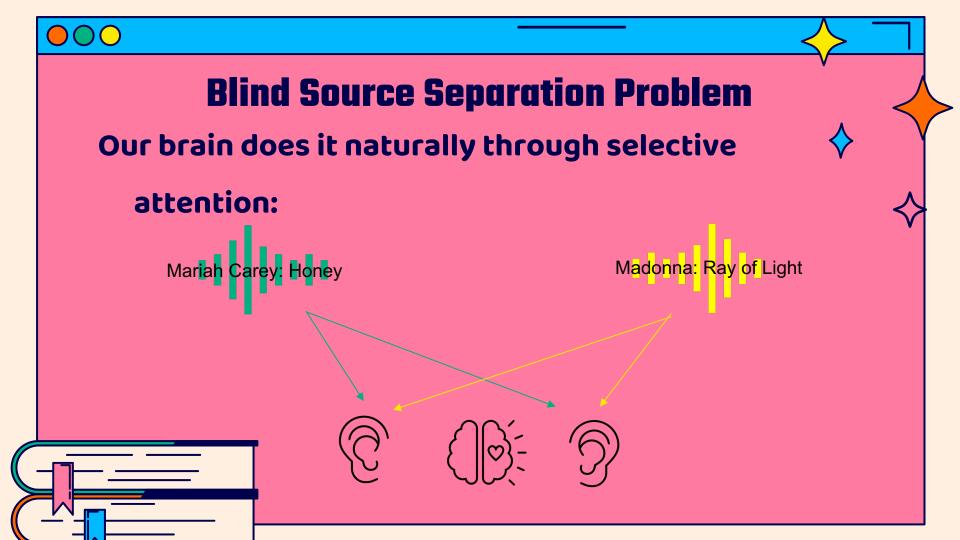


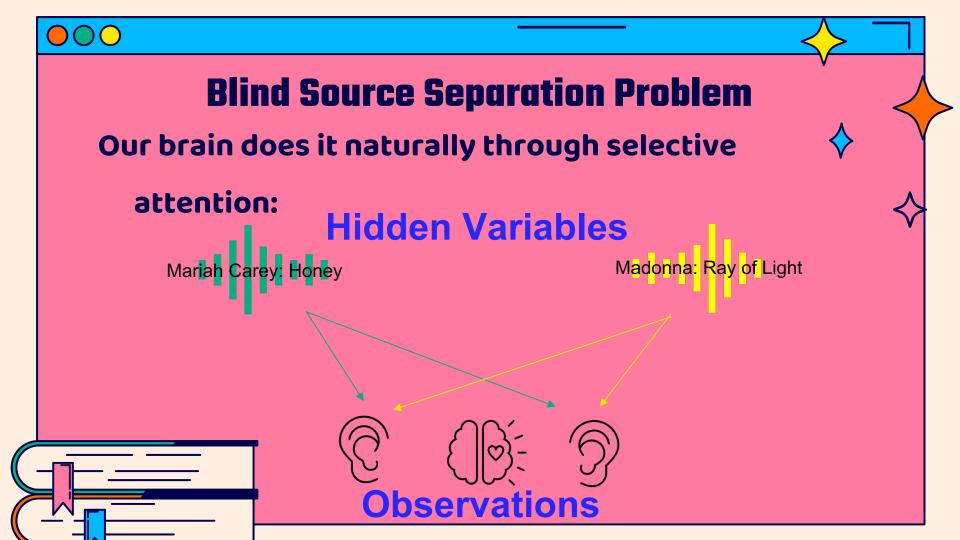


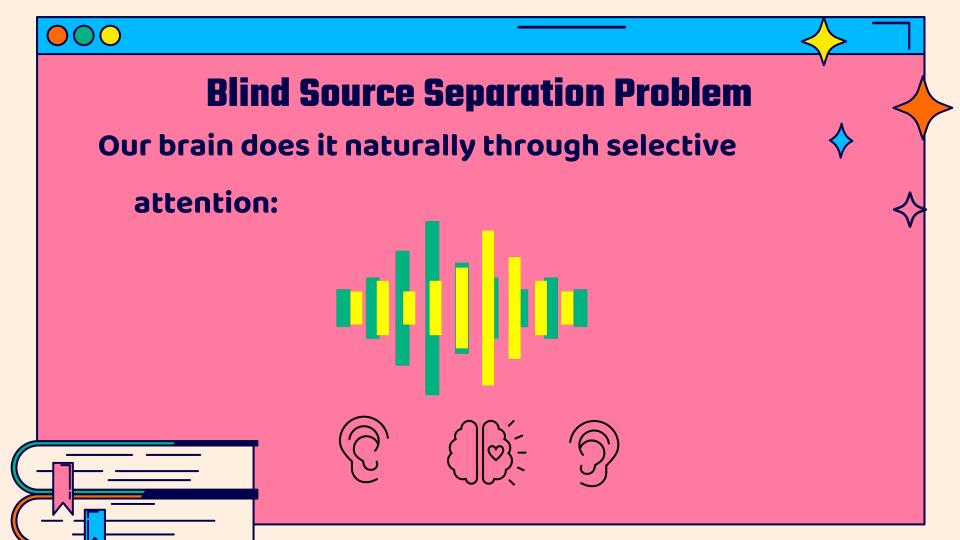


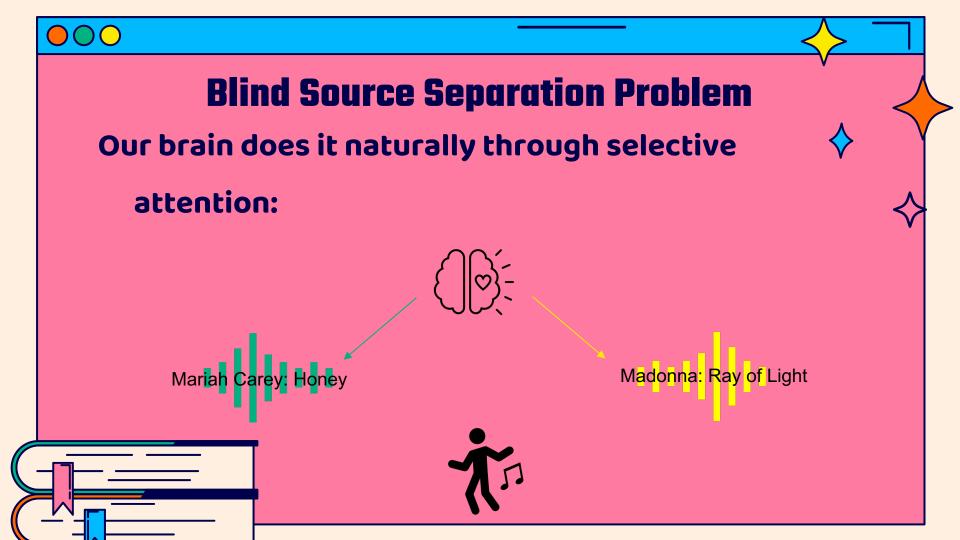








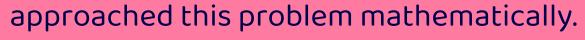






Independent Component Analysis

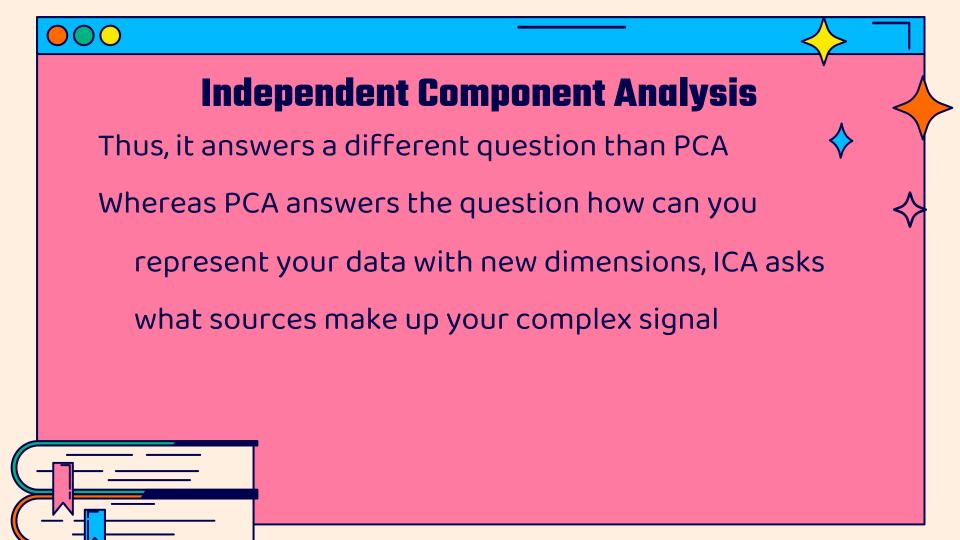
Independent component analysis is one way we have 💠



This algorithm attempts to decompose a complex signal into its many sub-signals or sources

They have different underlying assumptions







Independent Component Analysis

ICA finds components that are statistically independent

from one another (i.e., independent sources)

There are various methods to solve this (e.g., FastICA, infomax etc.) That rely on different strategies like minimizing the **Mutual Information** between

components







ICA

```
[mdl] = rica(X,q)
```

X -> data matrix (m by n) to apply ICA (rows observations, col predictors)

Q -> is the number of features or dimensions you wish to extract

mdl -> struct containing result of ICA



ICA

<u>Mdl</u>

mdl.mu -> mean along dimensions

mdl.TransformationWeights -> matrix used to rotate your data

mdl.NumPredictors -> same as the number of columns of X

mdl.NumLearnedFeatures -> same as the input q



ICA

Use the function transform(MDL, X) to rotate your data X to the new dimensions using the transformation weights

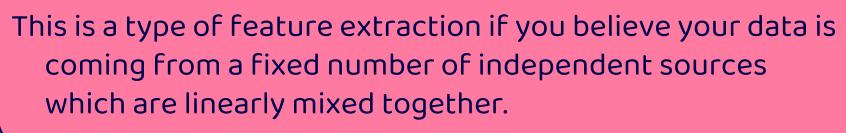
This is the equivalent to the score in PCA

To project back to the original data you need to multiply the scores by the transformation weights



ICA is typically used to remove components or sources from your data (i.e., clean the data of artifacts)

Similarly, ICA is used to extract sources from noisy data









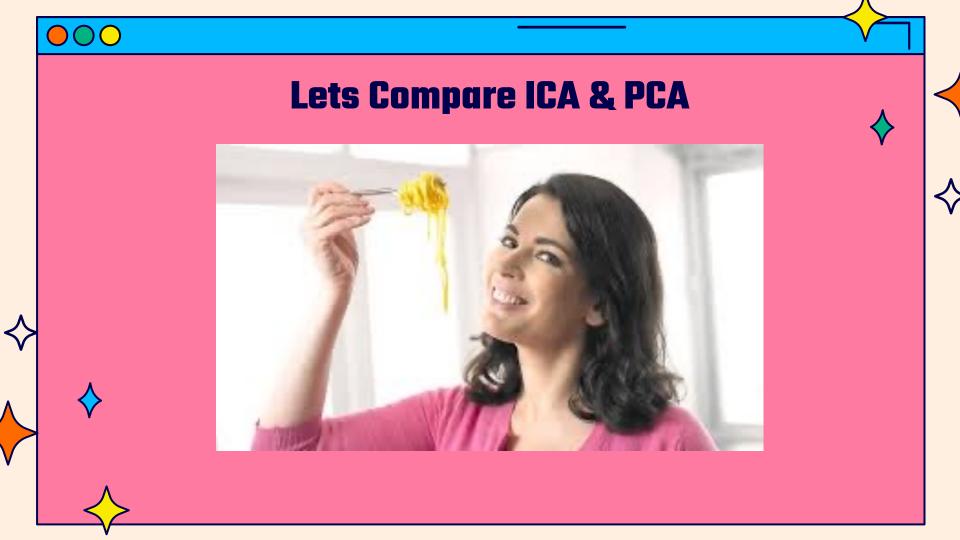


Underdetermined matrices occur when you have less observations than you have sources (i.e., more songs mixed together than microphones to record the songs). This may make finding the sources more difficult.



Sometimes we know how many sources we want to unmix from our data, or the source itself, other times we do not know the number or identity of the source









Lets Compare ICA & PCA





What would PCA do if you fed the algorithm a piece of this delicious cake?









Lets Compare ICA & PCA





What would ICA do if you fed the algorithm a piece of this delicious cake?









Lets Compare ICA & PCA



PCA

Finds orthogonal components Finds components that maximize variance Features ordered in terms of variance explained

ICA

Finds Statistically Independent (MI) components Solution for the blind source separation problem Finds components that

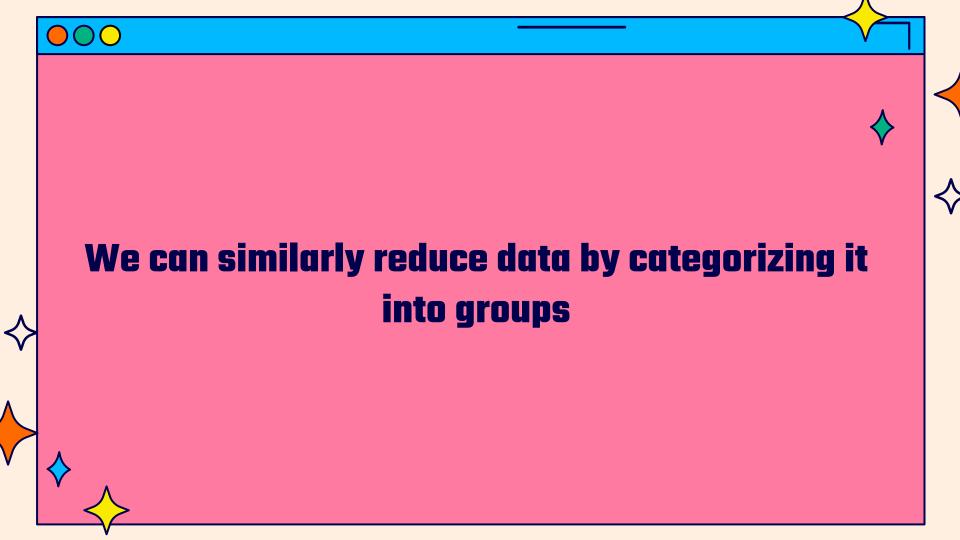
share no Mutual

Information











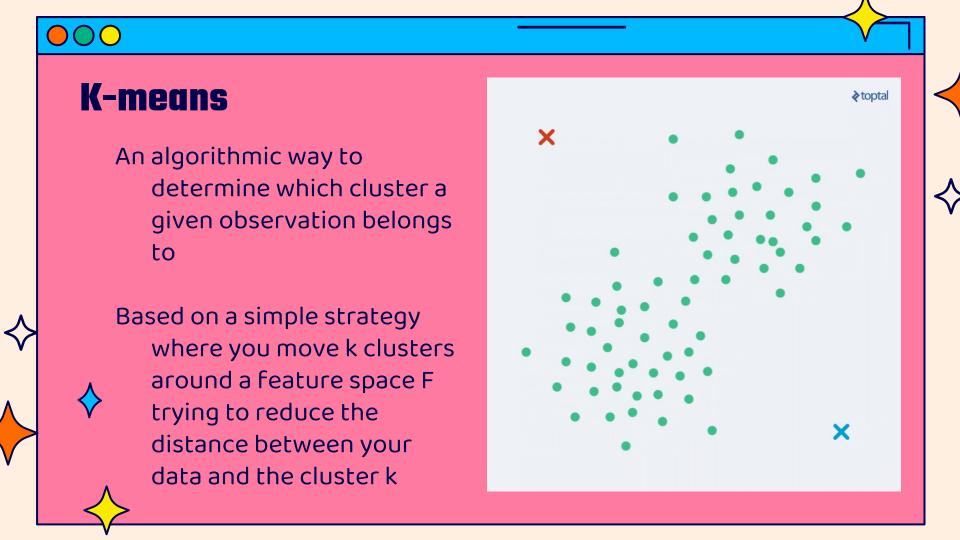
K-means

The previous techniques allow you to reduce data in terms of their dimensions, attempting to describe observations along new dimensions that are more interesting to you We can also reduce data by clustering or grouping them into a smaller number of cliques

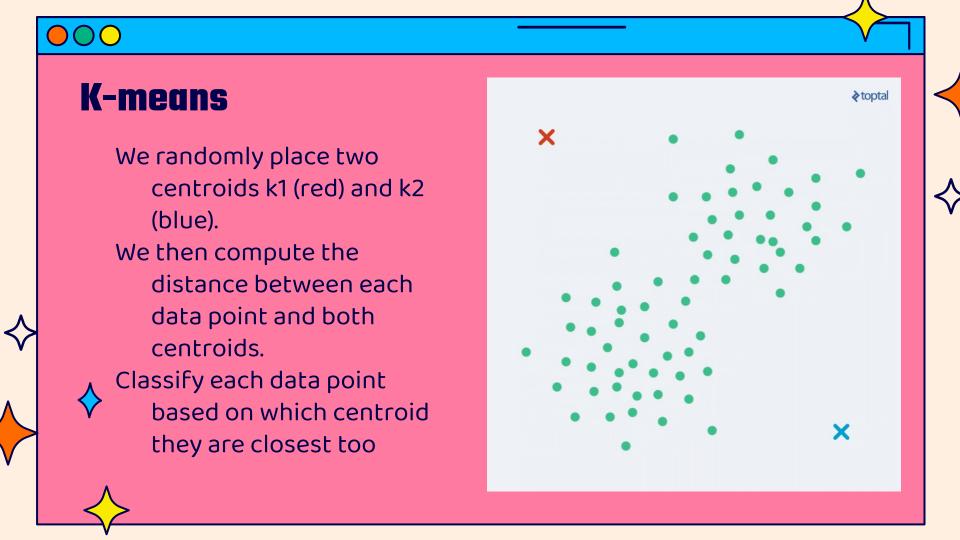


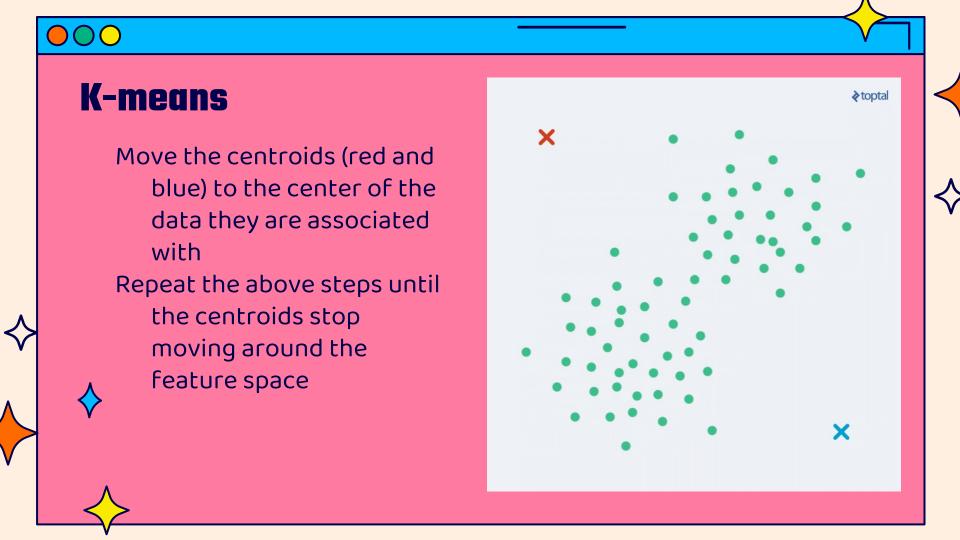
K-means

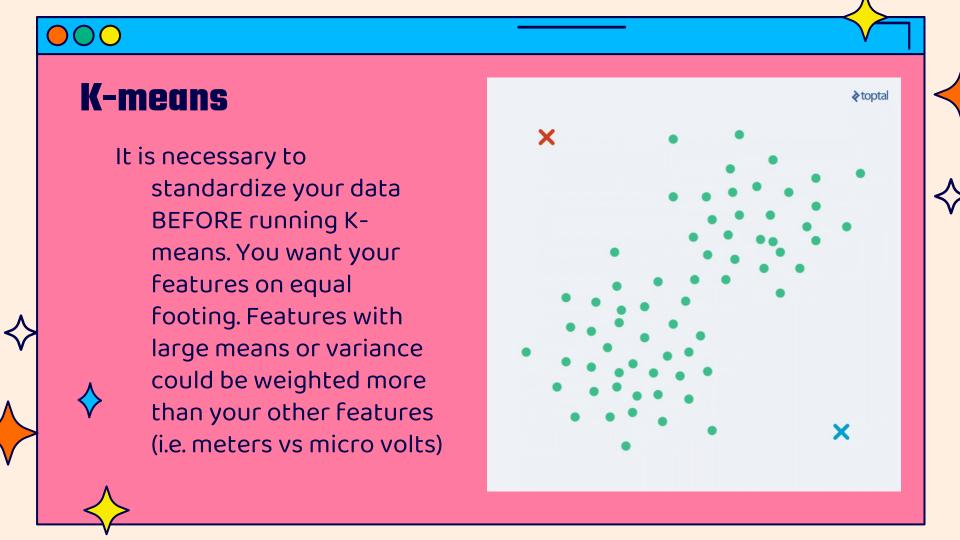














You can do this with a *training* and *testing* set. This is highly recommended as to avoid overfitting (see class 7)

Splitting your data into different subsets is common in machine learning algorithms

Normally you will have a large dataset to **train** on (i.e., teach your algorithm) and a smaller set to **test** if your algorithm works

(i.e., see if it still works with other data)



If you do not know *apriori* how many different classes or categories exist in your data, you need to compute this parameter

The optimal values of k are determined several ways:

Calinski-Harabasz criterion

Silhouette plots

Navies Bouldin index



Calinski-Harabasz criterion

Ratio of between cluster dispersion against within cluster dispersion

Tight-knit clusters that are further apart get better scores, are described as better defined clusters



Silhouette plots

For each point, measures how similar the observation is to its cluster. Values range from -1 to 1, unrelated to very related respectively

When looking at silhouette plots, one should expect to see all positive values that are very high (a 'box' per cluster)



Davies Bouldin index

Compares the distance between clusters against the size of the cluster itself. Favours small clusters that are father apart