



McCOMBS SCHOOL OF BUSINESS

Salem Center for Policy

Unsupervised learning

David Puelz

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Outline

Clustering

Principal Components Analysis

Clustering



1. Introduction to clustering
2. K-means
3. Implementing K-means: some practical details
4. Hierarchical clustering

Introduction to clustering

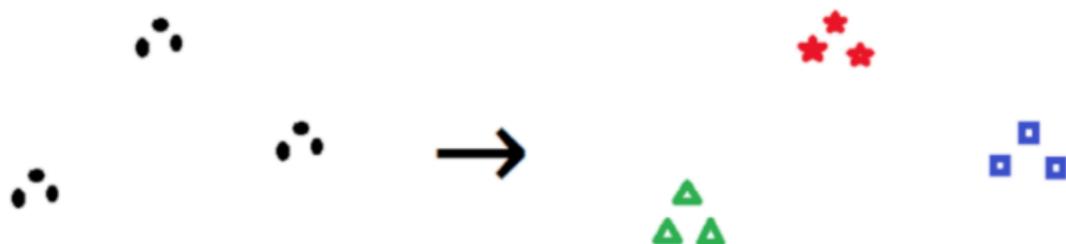


You've seen a lot of models for $p(y | x)$. This is supervised learning (knowing outcomes y = "supervision").

The next few topics are all about models for x alone.

- Clustering means dividing data points into categories which are not defined in advance.
- It's different from classification: dividing data points into categories which are defined in advance, and for which we have explicit labels.

Clustering: Toy example



Three Clusters of Data Points

Associated Cluster Labels

- The horizontal and vertical locations of each point give its location $x_i = (x_{i1}, x_{i2}, \dots, x_{ip})$ in **feature** space.
- From these locations, we impute the cluster labels: $\gamma_i = k$ if point i is in cluster $k \in \{1, \dots, K\}$.

Criteria for clustering



Clusters should partition the data:

- Partition = mutually exclusive, collectively exhaustive set of categories (each data point is in one and only one cluster).
- No “mixed membership.” If you encounter a [Chiweenie](#), you need a new cluster!



Criteria for clustering

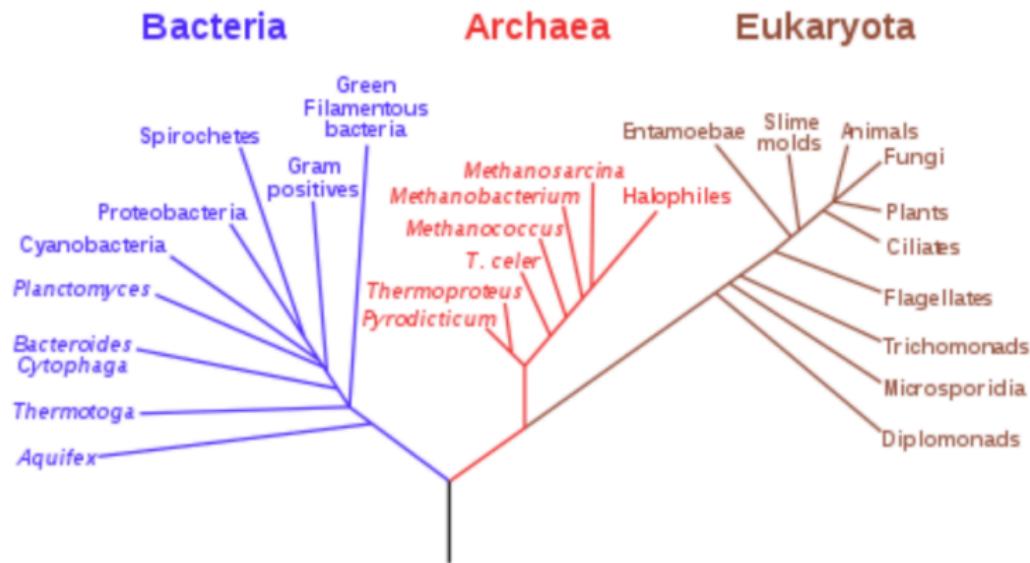


Data points within the same cluster should be close/similar, and data points in different clusters should be far apart/dissimilar.



Criteria for clustering

Clusters should (ideally) be **balanced**. A sensible clustering of living creatures:



Criteria for clustering

A less sensible clustering of living creatures:



1



2

All other living
creatures

3



How can we cluster without labels?

There are many algorithms which do this, i.e. try to find clusters that are homogenous, well separated, balanced, etc.

Key fact: we need to know about **distances** to quantify similarity (within a cluster) and difference (between clusters).

Generically, if x_i and x_j are two data points, we let $d(x_i, x_j)$ denote the distance between them.

Distance functions



Properties of distance functions:

1. $d(x_i, x_j) \geq 0$
2. $d(x_i, x_j) = 0 \iff x_i = x_j$.
3. $d(x_i, x_j) = d(x_j, x_i)$ ([symmetry](#))
4. $d(x_i, x_j) \leq d(x_i, x_k) + d(x_j, x_k)$ ([triangle inequality](#), i.e. “If you want to get from Austin to Houston, don’t go through Dallas!”)

NB: in math, distance functions are called “metrics.”



Distance functions

Euclidean (ℓ^2):

$$d(x_i, x_j) = \left[\sum_{d=1}^D (x_{id} - x_{jd})^2 \right]^{1/2}$$

(just the Pythagorean theorem!)

Manhattan (ℓ^1):

$$d(x_i, x_j) = \sum_{d=1}^D |x_{id} - x_{jd}|$$

(also called “taxicab” distance)

Distance functions



The x points can be arbitrary objects in potentially crazy spaces:

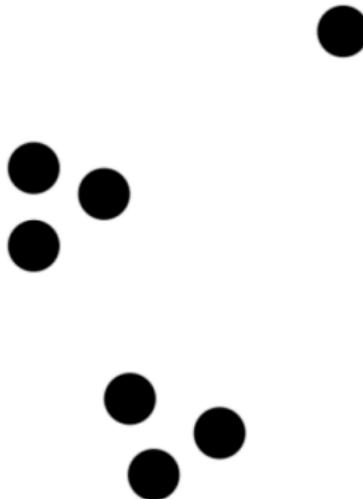
- playlists on Spotify
- phrase counts for books
- economic indicators
- DNA sequences ("Hamming distance")
- etc.

As long as we can measure the distance between any two points, we can cluster them!

A few miscellaneous notes



Clusters can be ambiguous:



How many clusters do you see?

A few miscellaneous notes



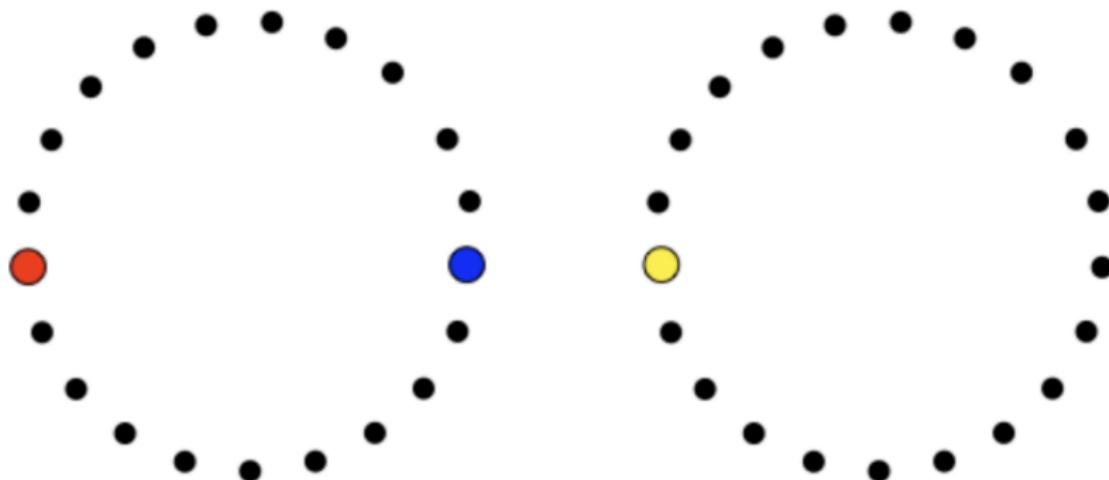
We can organize algorithms into two broad classes:

1. “[hierarchical](#)” clustering methods. Think the tree of life! Mammals and reptiles are both vertebrates. Vertebrates and invertebrates are both animals. Animals and plants are both eukaryotes. Etc.
2. “[partitional](#)” clustering methods. Here there is no tree or hierarchy, just a “flat” set of clusters.

A few miscellaneous notes



Distance-based clustering isn't magic.



Should blue cluster with red or with yellow?

(We can often deal with situations like this by redefining what distance is. The term here is “manifold learning.”)



K-means clustering

K-means clustering



- K-means is a partitional clustering approach. It's the “Least Squares Regression of clustering”
- Each cluster is associated with a centroid (center point). The number of clusters K must be chosen in advance
- Each point is assigned to the cluster with the closest centroid

K-means clustering



The basic algorithm is super simple:

-
- 1: Select K points as the initial centroids.
 - 2: **repeat**
 - 3: Form K clusters by assigning all points to the closest centroid.
 - 4: Recompute the centroid of each cluster.
 - 5: **until** The centroids don't change
-

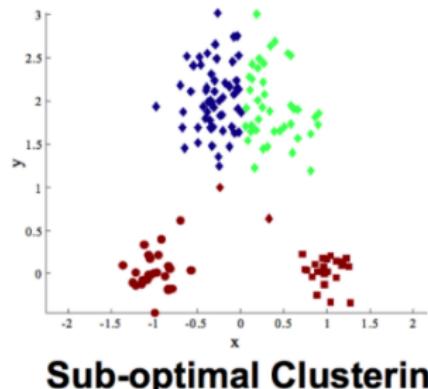
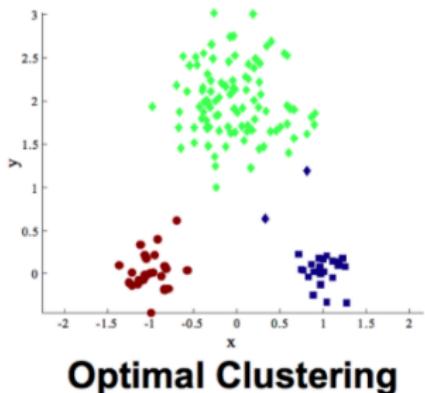
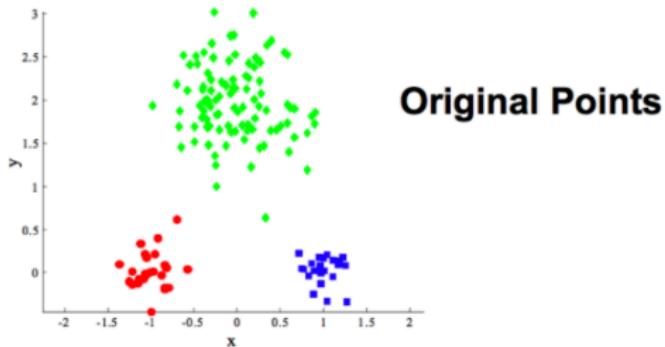
That's it! Algorithms don't get any simpler in machine learning

K-means clustering ([considerations](#))

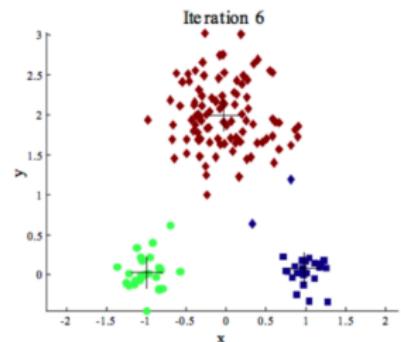
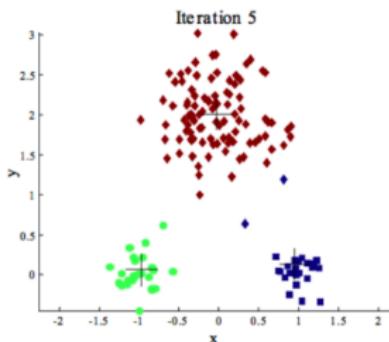
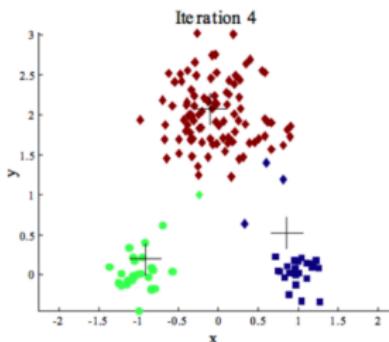
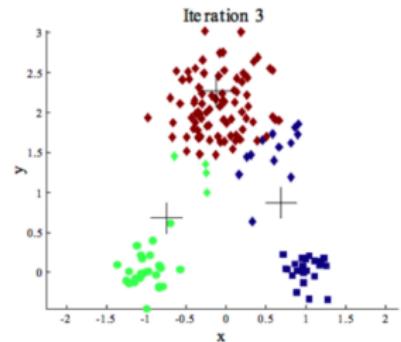
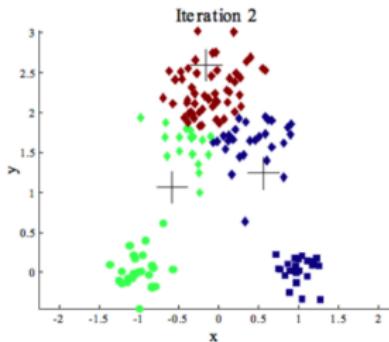
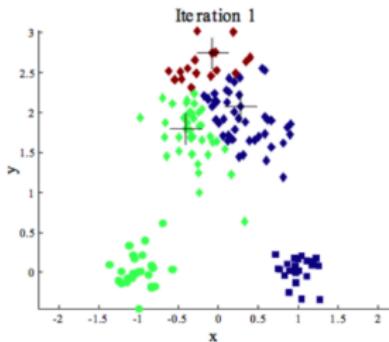


- Initial centroids are often chosen randomly. Thus the clusters produced vary from one run to another
- The centroid is (typically) the mean of the points in the cluster
- Closeness is measured by Euclidean (default) or any valid distance
- K-means will converge pretty rapidly for these common distance measures. Most of the convergence happens in the first few iterations

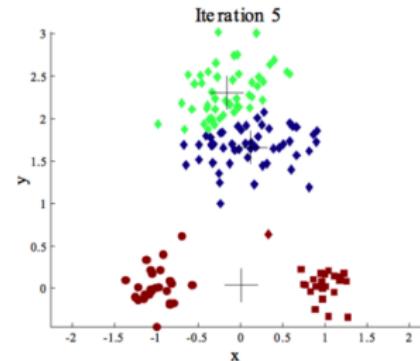
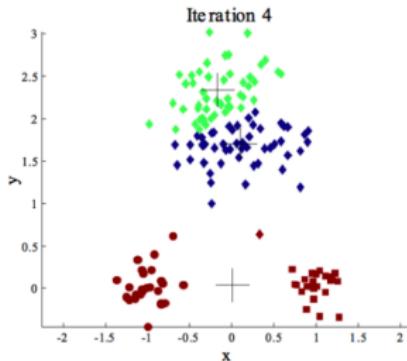
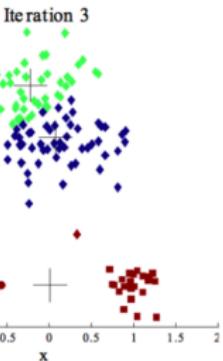
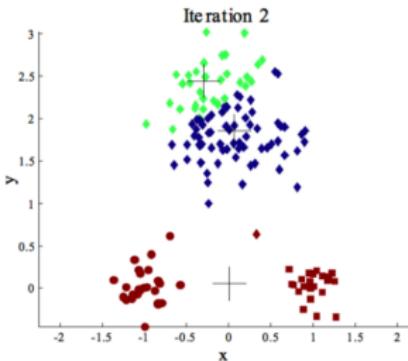
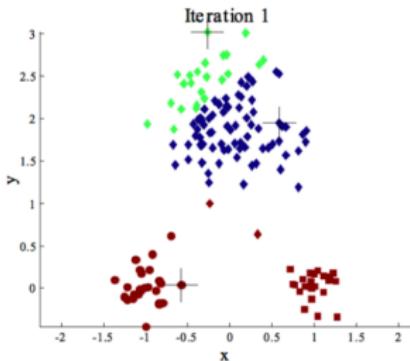
Two different k-means clusterings



From one set of initial centroids

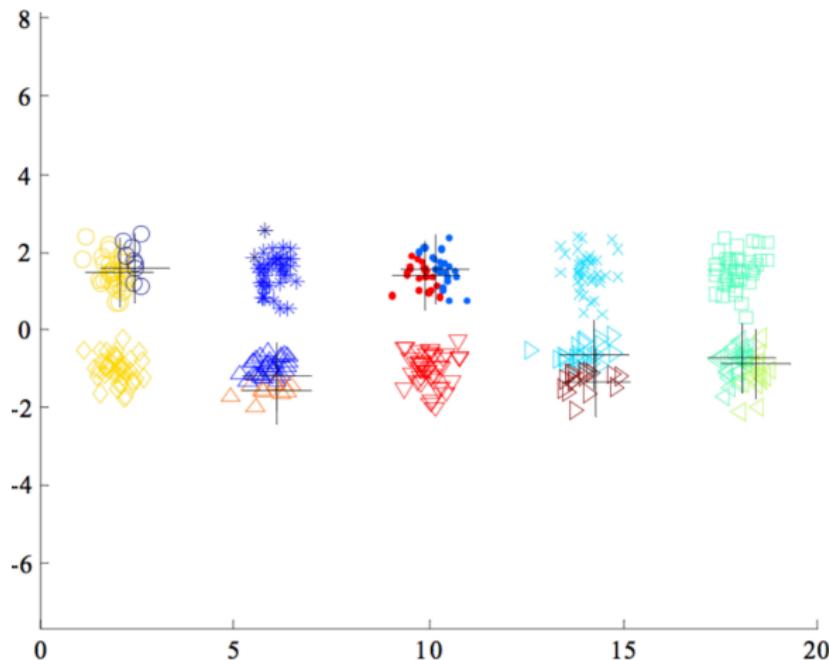


From a different set of initial centroids



Ten initial centroids

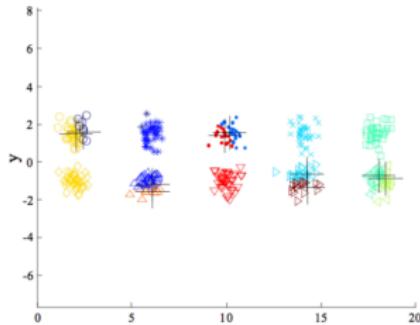
Iteration 1



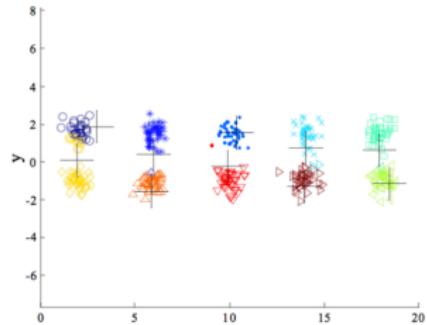
Each pair of clusters has two initial centroids

Ten initial centroids

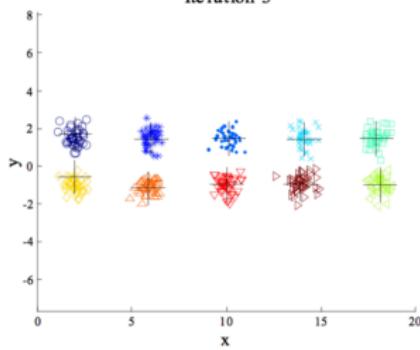
Iteration 1



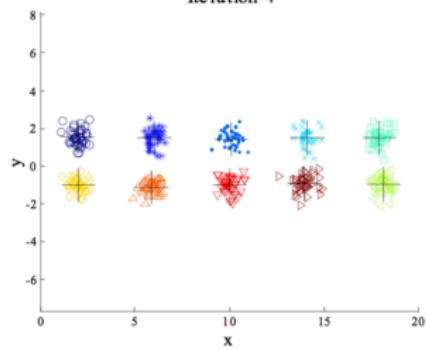
Iteration 2



Iteration 3



Iteration 4

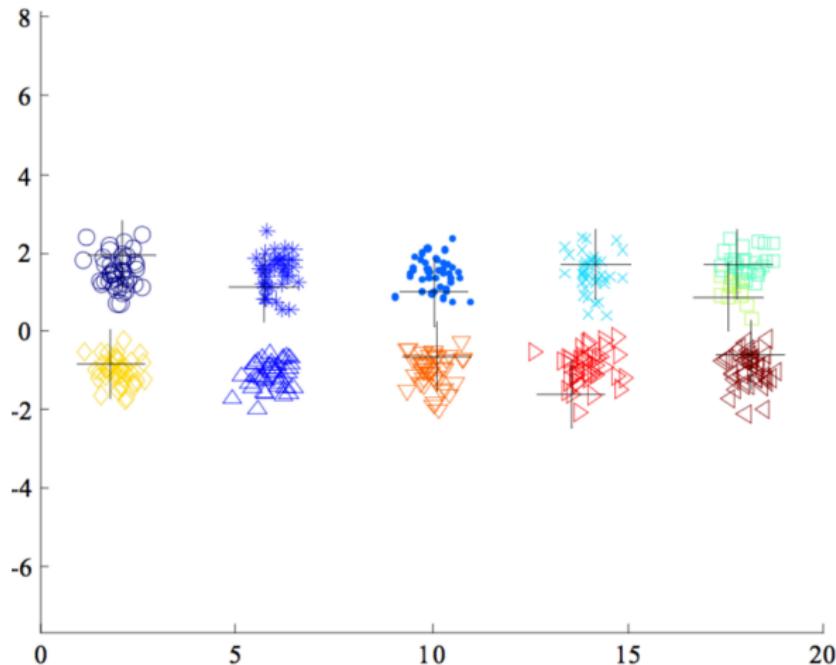


Not bad!

Ten initial centroids: Another try

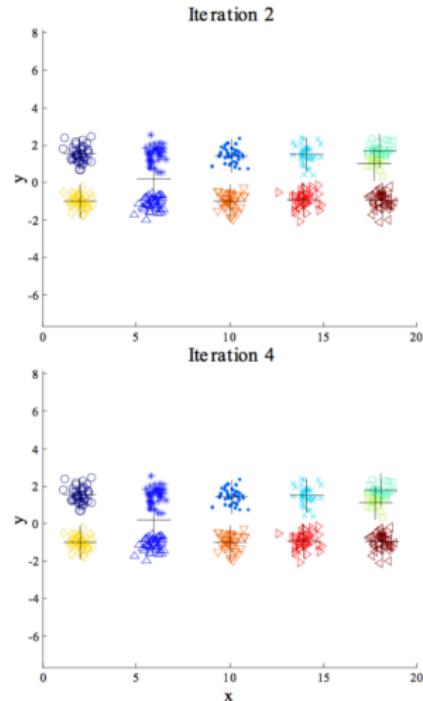
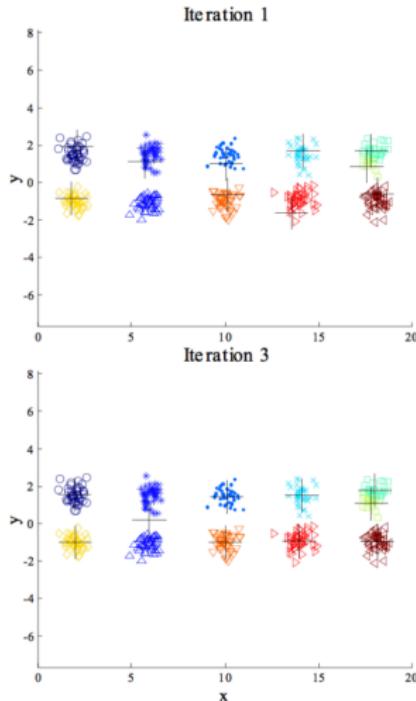


Iteration 1



Now one pair of clusters has one centroid (another pair has three)

Ten initial centroids: Another try



Not as good!

Solutions to the “initial centroid” problem



- Multiple restarts (helps, but probability is not on your side)
- Select more than K initial centroids and then select the most widely separated among these initial centroids
- Postprocessing
- Different initialization strategies (e.g. K-means++)



Initialize by choosing 1 centroid at random, m_1 .

Then for $k = 2, \dots, K$:

- 1) For each point, compute d_i as the minimum distance of x_i to the existing centroids.
- 2) Choose x_i as initial centroid k probability proportional to d_i^2 .
Thus points that are far away from existing cluster centroids are more likely to get chosen.

Note: this is just a different initialization strategy. After initialization, it works the same as K-means

K-means: Evaluating in-sample fit



Let m_k be cluster centroid k , and let C_k be the set of points in cluster k (i.e. for which $\gamma_i = k$).

Within-cluster sum of squares should be low:

$$\text{SSE}_W = \sum_{k=1}^K \sum_{x_i \in C_k} d(m_k, x_i)^2$$

Between-cluster sum of squares should be high:

$$\text{SSE}_B = \sum_{k=1}^K d(m_k, \bar{x})^2$$

where \bar{x} is the overall sample mean.

K-means: Example



Let's go to cars.R!



K-means only finds a local optimum

K-means tries to minimize within-cluster SSE. But:

- It basically never finds a global optimizer, except in simple problems.
- There are too many possible clusterings to check them all!

$$A(N, K) = \# \text{ of assignments of } N \text{ points to } K \text{ groups}$$

$$= \frac{1}{K!} \sum_{j=1}^K (-1)^{K-j} \cdot \binom{K}{j} \cdot j^N$$

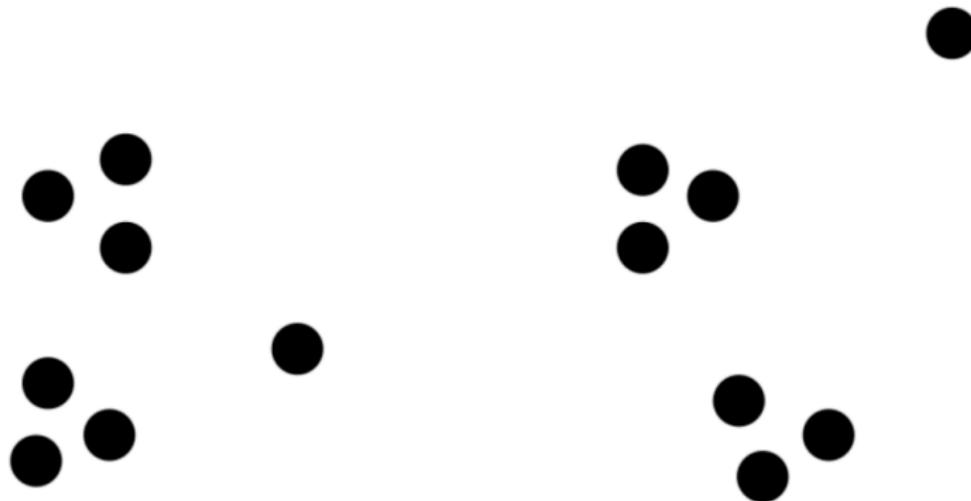
$$A(10, 4) = 34,105$$

$$A(25, 4) \approx 5 \times 10^{13} \quad (\text{ouch!})$$

Choosing K



Remember: K is an *input* to K-means, not an estimated parameter.
There is no generally accepted “best” method for choosing K, and
there never will be. Recall this example:



Choosing K



Some heuristics that people use in practice:

- choose it in advance based on prior knowledge or prior utility
- find the **elbow** on a plot of SSE_W versus K.
- optimize one of many quantitative model-selection criteria (CH index, AIC, BIC, gap statistic...)

Choosing K



But probably the most popular principle is this:

- **satisfice**, don't optimize: pick a value of K that gives clusters you and your stakeholders can interpret, and call it a day.
- There is absolutely no shame in this, and smart people do it all the time.

Choosing K



Let's try many values of K for the cars data ...

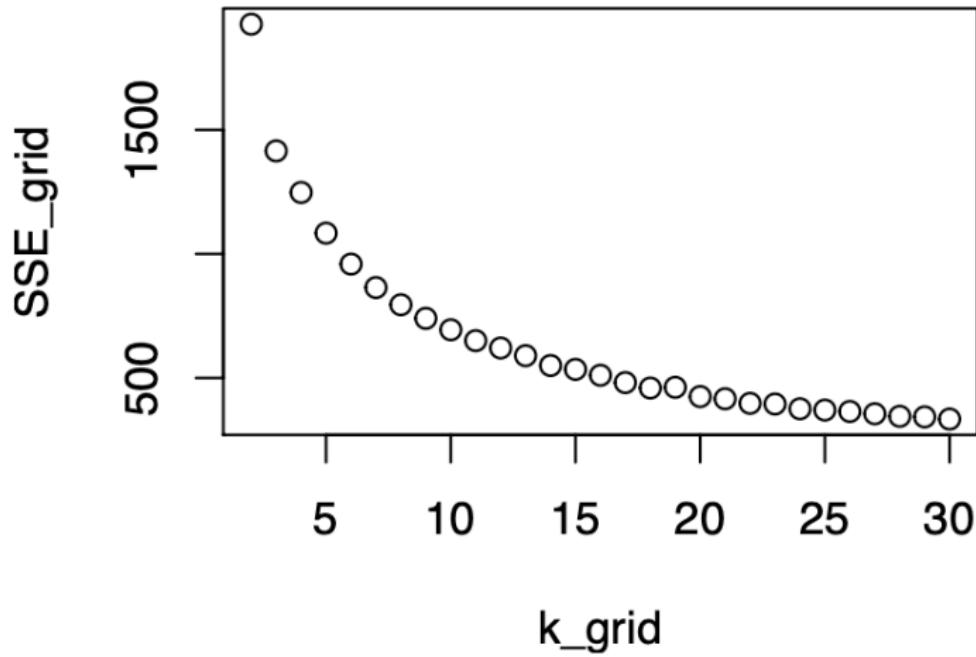
```
library(foreach)
cars = read.csv('data/cars.csv')
cars = scale(cars[,10:18]) # cluster on measurables
k_grid = seq(2, 30, by=1)
SSE_grid = foreach(k = k_grid, .combine='c') %do% {
  cluster_k = kmeans(cars, k, nstart=50)
  cluster_k$tot.withinss
}
```



What do we expect this plot to look like?

To the board!

What does the plot actually look like?



Do you see an elbow?

Elbow plots: Reality



A lot of elbow plots I've seen look something like this. It depends on the data whether or not they will be useful.

Elbow plots and other statistics



There are a couple other statistics one can look at to discern a reasonable value for K:

- CH statistic
- Gap statistic

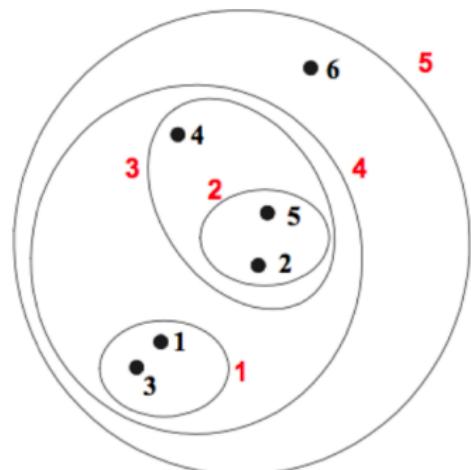
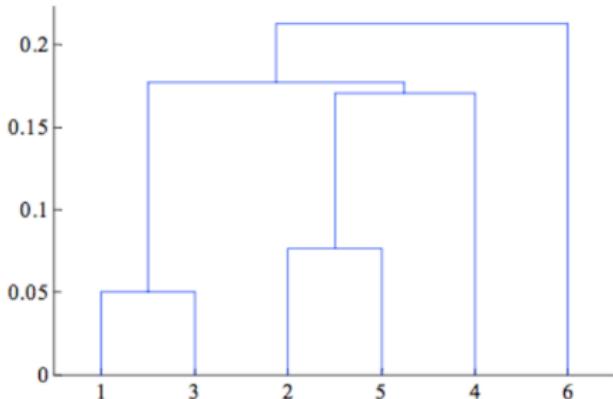
Both of these are potentially useful. If you're interested, you can read more about them in the R documentation. I just want you to know that they exist!



Hierarchical clustering

Hierarchical clustering

- Produces a set of nested clusters organized hierarchically
- Can be visualized as a “dendrogram,” a tree like diagram that records the sequences of merges or splits:



Strengths of hierarchical clustering



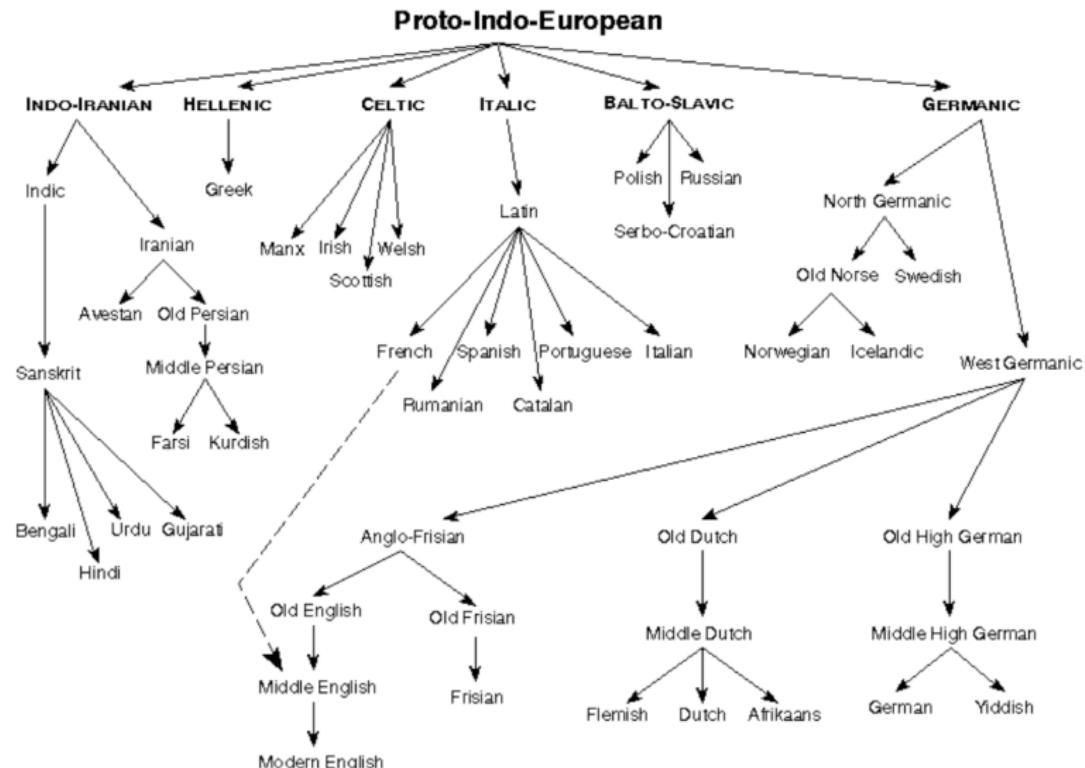
You don't have to assume any particular number of clusters.

- Any desired number of clusters can be obtained from a dendrogram.
- Just “cut” the tree at the proper level.

The hierarchy itself may correspond to meaningful taxonomies:

- the tree of life
- languages

Example



Prepared by Jack Lynch, jlynch@midromeda.nj.gov.edu

Hierarchical clustering



Two main types:

Agglomerative (bottom up):

1. Start with the points as individual clusters
2. At each step, merge the closest pair of clusters until only one cluster (or k clusters) left

Divisive (top down):

1. Start with one, all-inclusive cluster
2. At each step, split a cluster until each cluster contains a point (or there are k clusters)

Agglomerative clustering



The basic algorithm is straightforward: start with every point in its own cluster and compute a **proximity matrix** $D(i,j)$ between every pair of points i and j .

Then repeat:

1. Merge the two closest clusters.
2. Update the proximity matrix.

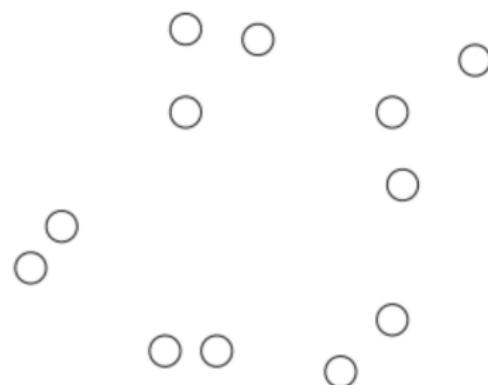
Until only a single cluster remains.

Key operation is the computation of the **proximity** of two clusters. Different approaches to defining the distance between clusters distinguish the different algorithms.

Agglomerative clustering



Start with a bunch of points and a proximity matrix:

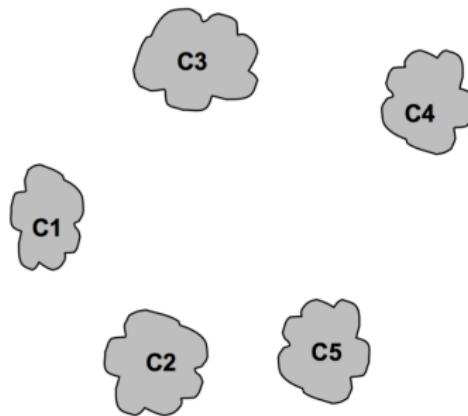


	p1	p2	p3	p4	p5	...
p1						
p2						
p3						
p4						
p5						
.						
.						
.						
Proximity Matrix						

p1 p2 p3 p4 ... p9 p10 p11 p12

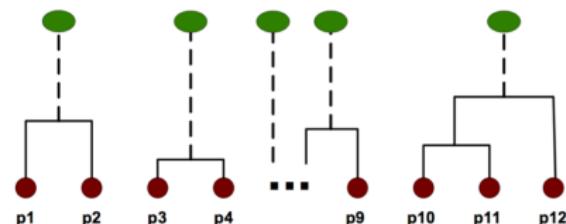
Agglomerative clustering

After some merging steps, we have a handful of clusters:



	C1	C2	C3	C4	C5
C1					
C2					
C3					
C4					
C5					

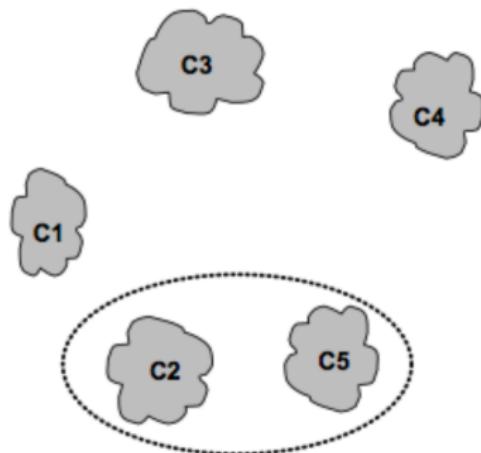
Proximity Matrix



Agglomerative clustering

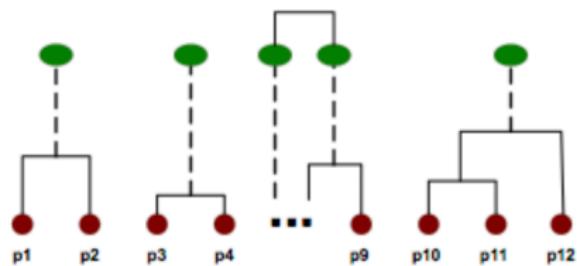


We want to merge C2 and C5 and update the proximity matrix:



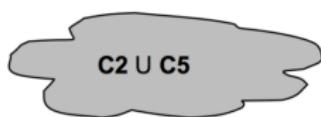
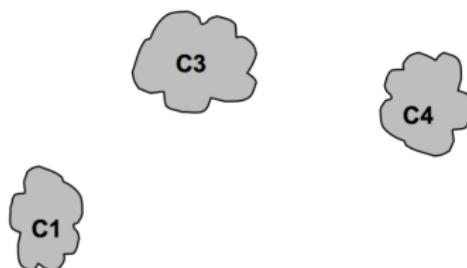
	C1	C2	C3	C4	C5
C1					
C2					
C3					
C4					
C5					

Proximity Matrix



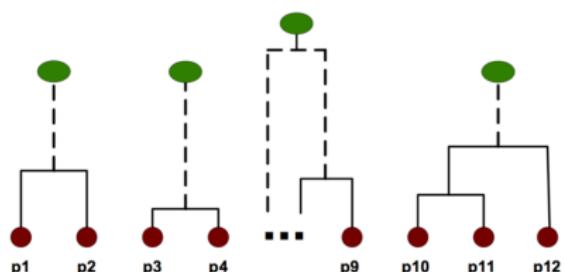
Agglomerative clustering

How do we do this?



		C2 U C5			
		C1	C5	C3	C4
C1	C1	?			
	C2 U C5	?	?	?	?
C3		?			
C4		?			

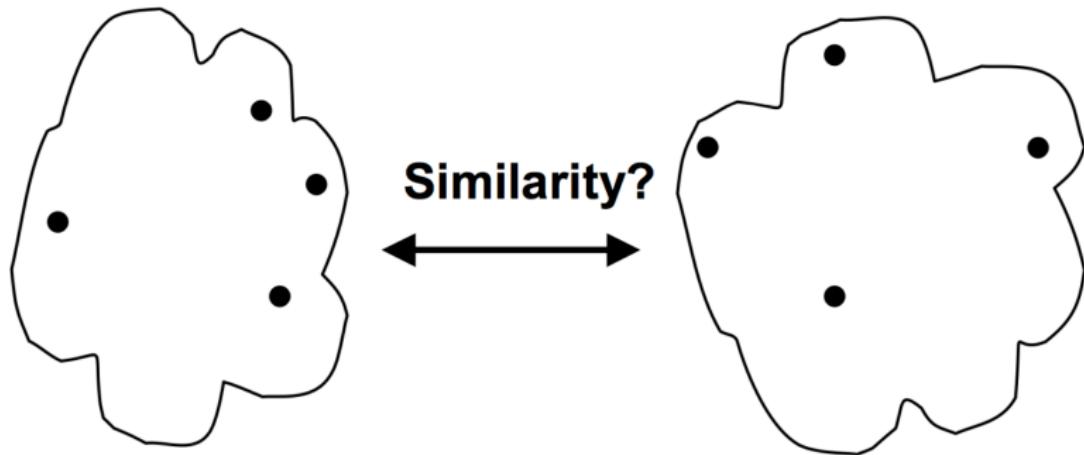
Proximity Matrix



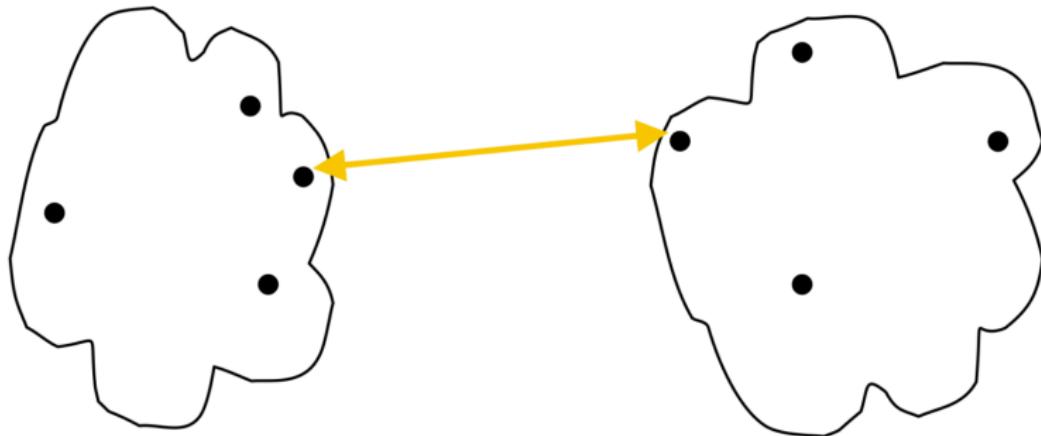
Agglomerative clustering



To frame the question very precisely, how do we measure the similarity/distance between two clusters of points?

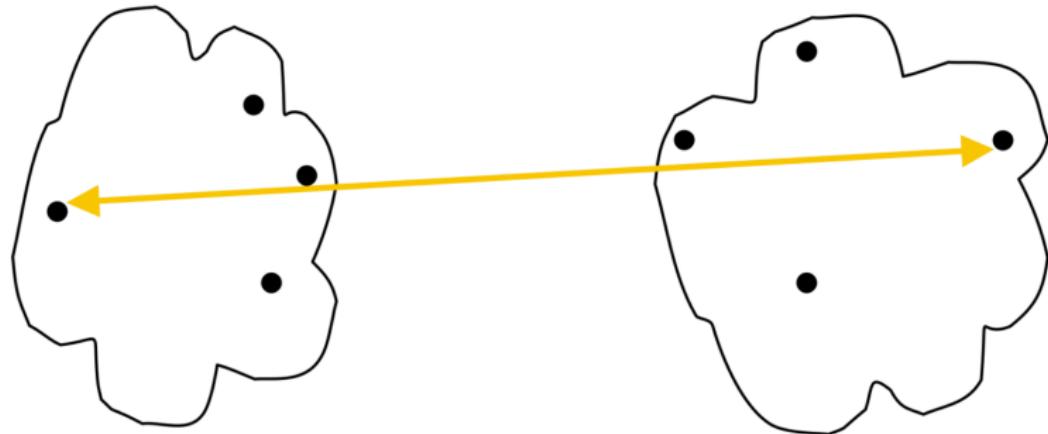


Min linkage (“single” in R)



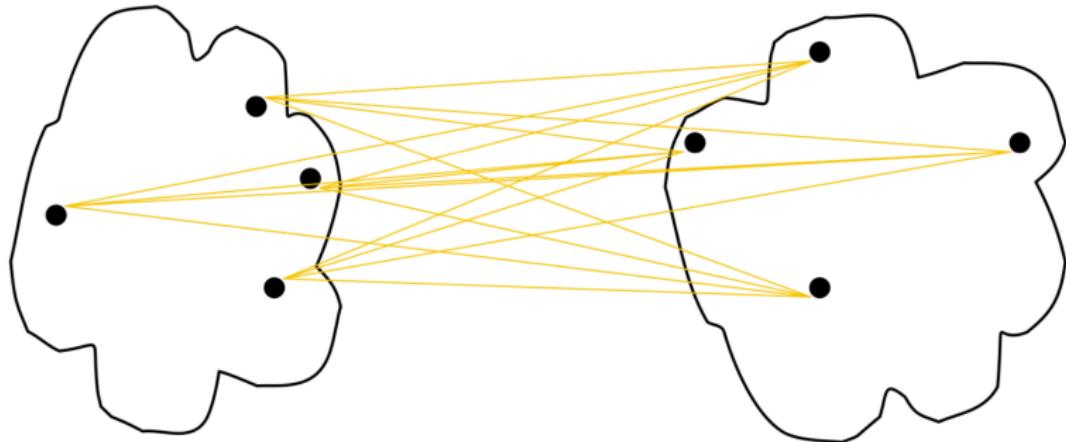
The minimum distance between two points, one in each cluster.

Max linkage (“complete” in R)



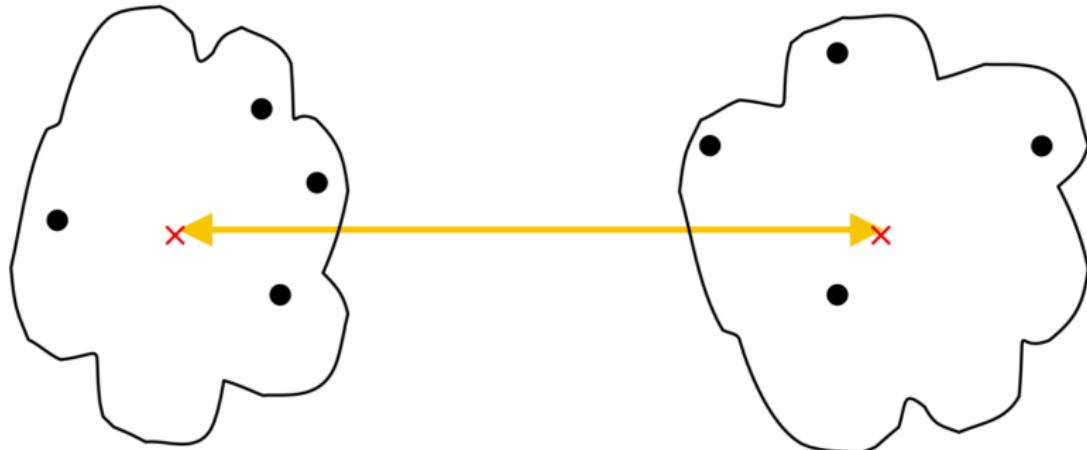
The maximum distance between two points, one in each cluster.

Average linkage (“average” in R)



The average distance between all pairs of points, one in each cluster.

Centroid linkage (“centroid” in R)



The distance between the centroids of each cluster.



Choice of linkage function

Each has its own pros and cons:

- **Min**: more sensitive to noise and outliers, but will leave large, obvious clusters mostly intact
- **Max**: more robust to noise and outliers, but tends to break up large clusters
- **Average** and **centroid**: kind of a compromise between the two

See `linkage_minmax.R` and `hclust_examples.R`, where we'll see these ideas in action and getting the desired number of clusters by cutting the dendrogram.