

Computational Political Science

Session 7

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Outline for today

1. **Similarity metrics**

- Cosine
- Euclidean
- Jaccard
- Edit distance

2. **Clustering methods**

- k-means clustering
- Hierarchical clustering

3. **Computer exercises**

- Building a movie recommendation engine
- Clustering UK party manifestos

Course schedule

Session	Date	Topic	Assignment	Due date
1	Feb 02	Overview and key concepts	-	-
2	Feb 09	Preprocessing and descriptive statistics	Formative	Feb 22 23:59:59
3	Feb 16	Dictionary methods	-	-
4	Feb 23	Machine learning for texts: Classification I	Summative 1	Mar 08 23:59:59
5	Mar 02	Machine learning for texts: Classification II	-	-
6	Mar 09	Supervised and unsupervised scaling	Summative 2	Mar 22 23:59:59
7	Mar 16	<i>Similarity and clustering</i>	-	-
8	Mar 23	Topic models	Summative 3	Apr 12 23:59:59
-	-	<i>Break</i>	-	-
9	Apr 13	Retrieving data from the web	-	-
10	Apr 20	Published applications	-	-
11	Apr 27	Project Presentations	-	-

Comparing documents

Comparing documents

Idea

The (weighted) features form a vector for each document and these vectors can be judged using metrics of similarity

A document's vector for us is simply (for us) the row of the document-feature matrix containing the (relative) frequency of features

Problem

How do we measure distance or similarity between the vector representation of two (or more) different documents?

Characteristics of similarity measures

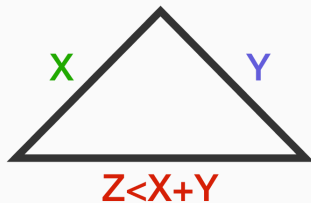
Let A and B be any two documents in a set and $d(A, B)$ be the distance between A and B

- $d(A, B) \geq 0$ (the distance between any two points must be non-negative)
- $d(A, B) = 0$ iff $A = B$ (the distance between two documents must be zero if and only if the objects are identical)
- $d(A, B) = d(B, A)$ (the distance must be symmetric: A to B is the same distance as from B to A)
- $d(A, C) \leq d(A, B) + d(B, C)$ (the measure must satisfy the triangle inequality)

A note on the triangle inequality

The triangle inequality states that the sum of the lengths of any two sides of a triangle is greater than the length of the remaining side.

It follows from the fact that a straight line is the shortest path between two points. The inequality is strict if the triangle is non-degenerate (meaning it has a non-zero area).



Example

Two legs of a triangle have lengths of 7.4 and 17.3 respectively.

What is the *largest possible* length for the third side z ?

$$7.4 + 17.3 = 24.7 \text{ so that } z < 24$$

Euclidian distance

Between document A and B where j indexes their features and y_{ij} is the value for feature j of document i

Euclidean distance is based on the *Pythagorean theorem*

Formula

$$d(A, B) = \sqrt{\sum_{j=1}^j (y_{Aj} - y_{Bj})^2}$$

In vector notation

$$\|\mathbf{y}_A - \mathbf{y}_B\|$$

Can be performed for any number of features J where J is the number of columns of the dfm

y_{Aj} and y_{Bj} can be any representation of features (count, relative frequency, indicator)

Euclidean distance

Let's create a dfm from these two texts

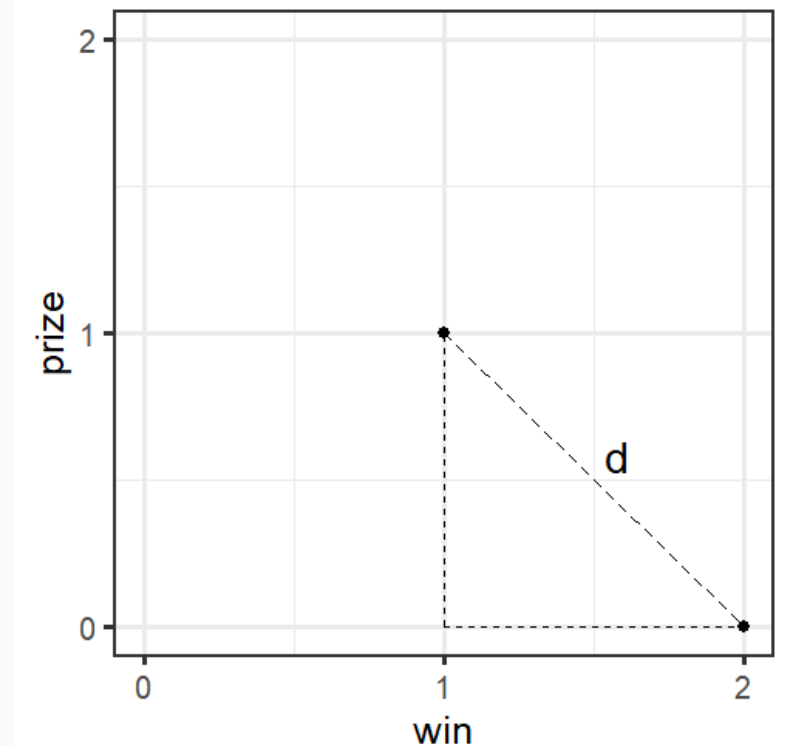
```
# corpus
txt <- c("Win Prize",
        "Win win")

# document-feature-matrix
x <- dfm(txt)
```

	win	prize
text1	1	1
text2	2	0

```
textstat_dist(x, method="euclidean")
```

```
##      text1 text2
## text1  0.00  1.41
## text2  1.41  0.00
```



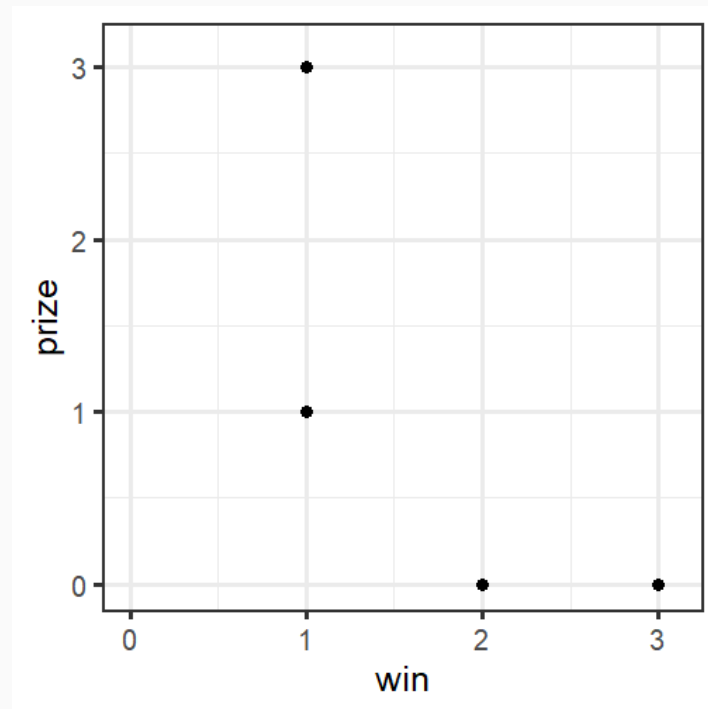
$$\begin{aligned}d(A, B) &= \sqrt{(y_{A1} - y_{B1})^2 + (y_{A2} - y_{B2})^2} \\&= \sqrt{(2 - 1)^2 + (1 - 0)^2} \\&= 1.41\end{aligned}$$

Comparing more than two observations

When can look at $\frac{n-1}{2}$ pairwise comparisons between different documents

```
txt2 <- c(A = "Win Prize",  
          B = "Win Prize Prize Prize",  
          C = "Win Win",  
          D = "Win Win Win")  
x2 <- dfm(txt2)
```

	win	prize
A	1	1
B	1	3
C	2	0
D	3	0

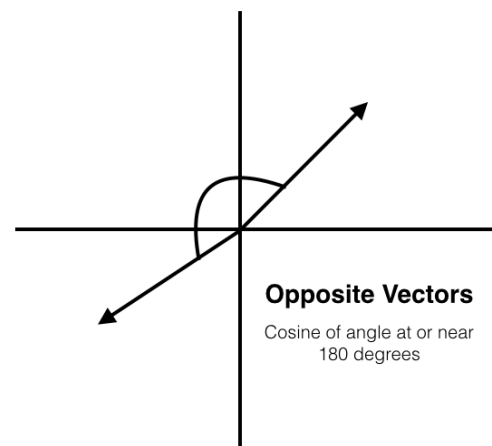
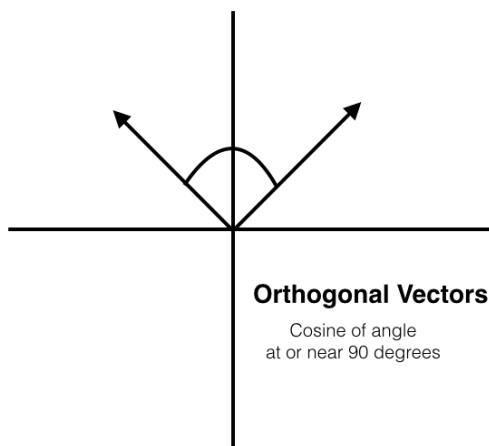
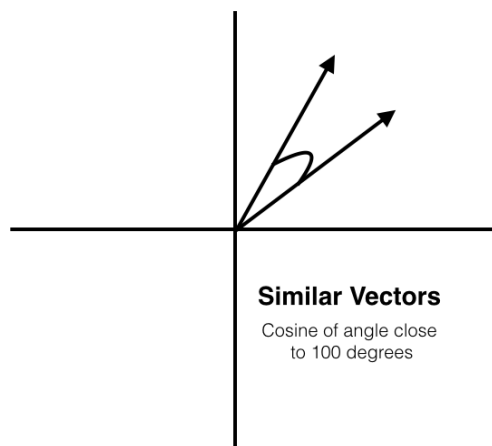


```
textstat_dist(x2, method="euclidean")
```

```
##      A      B      C      D  
## A 0.00 2.00 1.41 2.24  
## B 2.00 0.00 3.16 3.61  
## C 1.41 3.16 0.00 1.00  
## D 2.24 3.61 1.00 0.00
```

Cosine similarity

Cosine similarity is based on the size of the angle between vectors. Perfect similarity yields a score of 1, no relation will yield 0, and -1 means the vectors are opposites.



Properties

- cosine similarity between frequency vectors of (relative) frequencies cannot be negative as word-counts cannot be negative
- the measure is independent of document length because it deals only with the angle of the vectors

Cosine similarity

Formula

$$\frac{\mathbf{y}_A \cdot \mathbf{y}_B}{\|\mathbf{y}_A\| \|\mathbf{y}_B\|} = \frac{\sum_j y_{Aj} y_{Bj}}{\sqrt{\sum_j y_{Aj}^2} \sqrt{\sum_j y_{Bj}^2}}$$

The \cdot operator is the dot product, or $\sum_j y_{Aj} y_{Bj}$

$\|\mathbf{y}_A\|$ is the norm of the feature vector \mathbf{y} for document A , such that $\|\mathbf{y}_A\| = \sqrt{\sum_j y_{Aj}^2}$

Euclidean distance measures how *different* documents are, whereas cosine similarity measures how *similar* documents are. Of course, it's easy to reverse them; generally, we can say $(1 - \text{distance}) = \text{similarity}$.

Norm of a vector

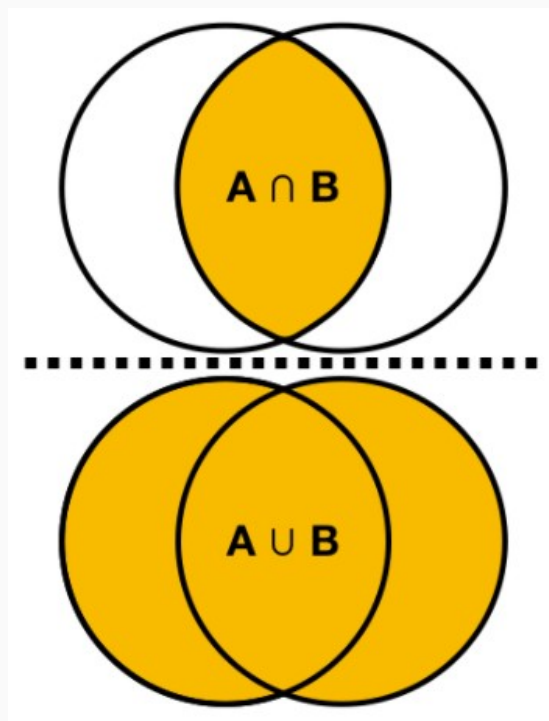
If $\vec{u} \in \mathbb{R}^n$, then the Norm or Magnitude of \vec{u} denoted $\|\vec{u}\|$ is defined as the length or magnitude of the vector and can be calculated using the formula:

$$\|\vec{u}\| = \sqrt{u_1^2 + u_2^2 + \dots + u_J^2} = \sqrt{\sum_{j=1}^J u_j^2}$$

Jaccard coefficient

The Jaccard coefficient is similar to the Cosine similarity measure and ranges from 0 to 1

$$\frac{\text{doc}_A \cap \text{doc}_B}{\text{doc}_A \cup \text{doc}_B} = \frac{\mathbf{y}_A \cdot \mathbf{y}_B}{\|\mathbf{y}_A\| + \|\mathbf{y}_B\| - \mathbf{y}_A \cdot \mathbf{y}_B}$$



Using set notation, the coefficient is

$$\frac{\{\text{win, prize}\} \cap \{\text{win, win}\}}{\{\text{win, prize}\} \cup \{\text{win, win}\}} = \frac{\{\text{win}\}}{\{\text{win, prize}\}} = \frac{1}{2}$$

In R we calculate the measure on the dfm

```
textstat_simil(x, method="jaccard")
```

```
##           text1 text2
## text1      1.0   0.5
## text2      0.5   1.0
```

Edit distances

Edit distance refers to the number of operations required to transform one string into another for strings of equal length

Levenshtein distance

Example: the Levenshtein distance between "kitten" and "sitting" is 3

1. kitten ! sitten (substitution of "s" for "k")
2. sitten ! sittin (substitution of "i" for "e")
3. sittin ! sitting (insertion of "g" at the end).

Hamming distance

- For two strings of equal length, the Hamming distance is the number of positions at which the corresponding characters are different
- Not common, as at a textual level this is hard to implement and possibly meaningless

Other uses and extensions

Used extensively in information retrieval (search engines, library searches, ...)

- Summary measures of how far apart two texts are – but be careful exactly how you define "features"
- Some but not many applications in social sciences to measure substantive similarity — scaling models are generally preferred
- Can be used to generalize or represent features in machine learning, by computing similarities between textual (sub)sequences without extracting the features explicitly

Clustering

Clustering

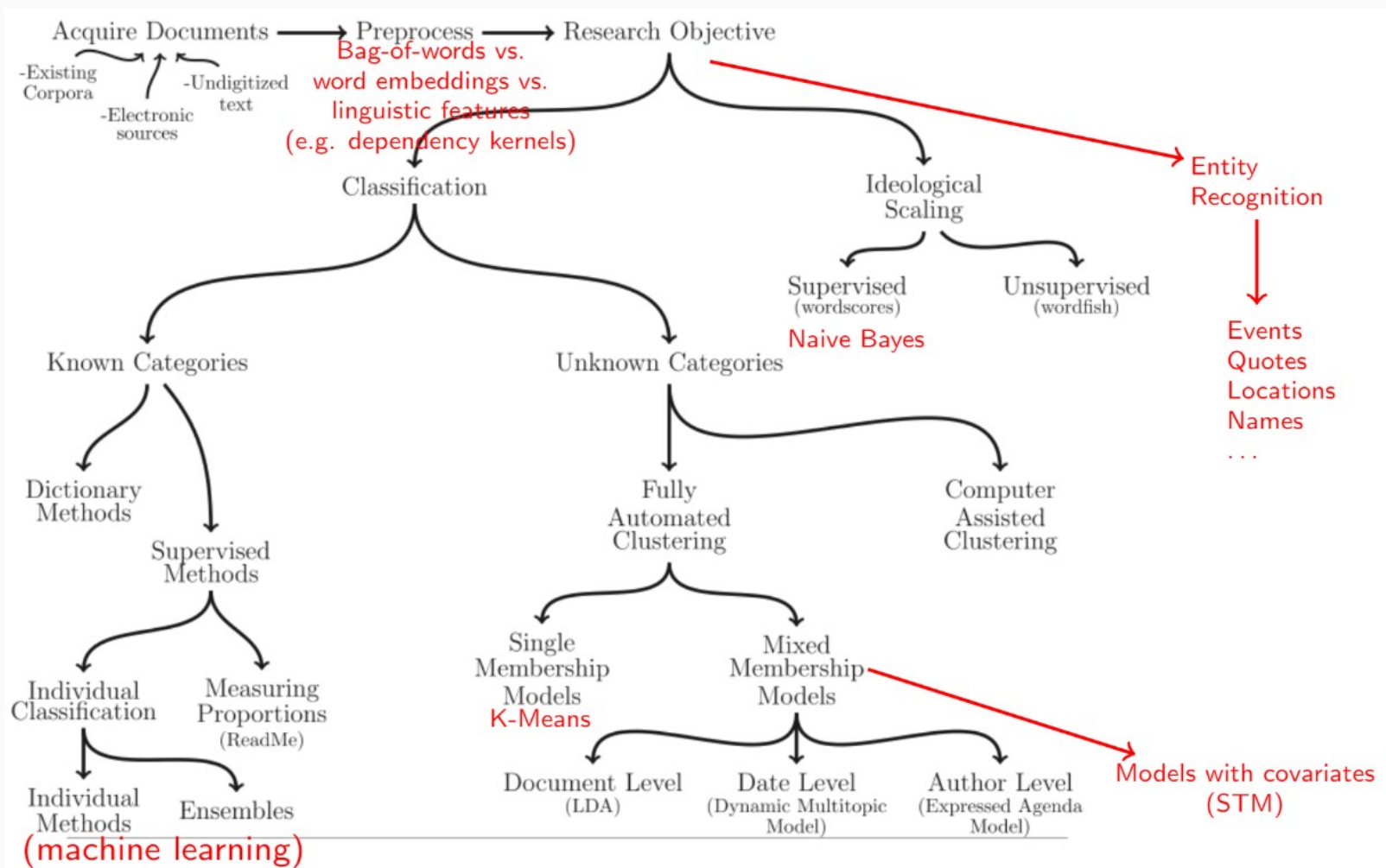


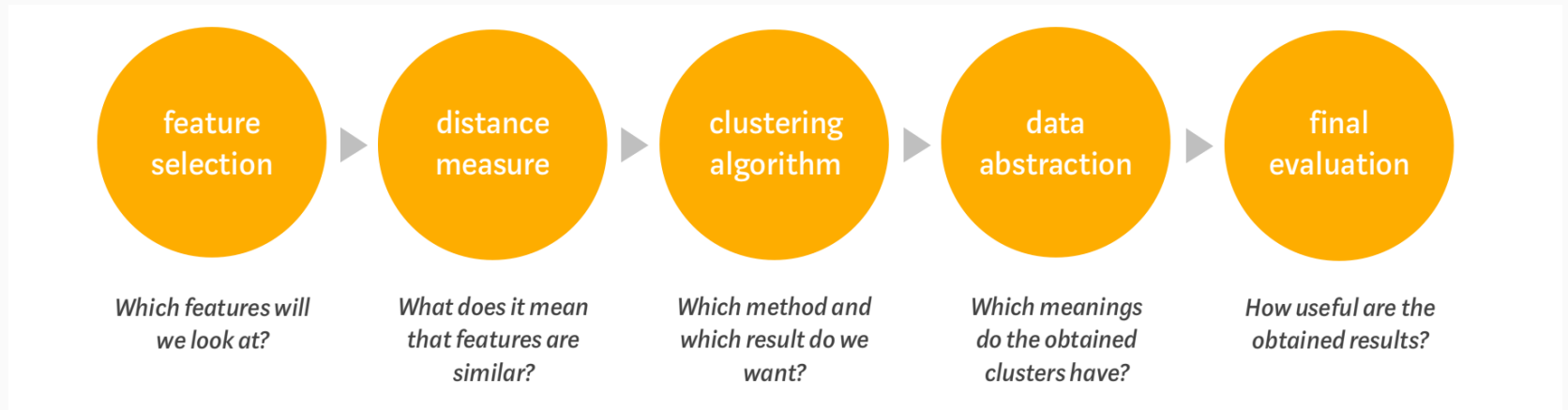
Fig. 1 in Grimmer and Stuart (2013)

The idea of "clusters"

Groups of items such that inside a cluster they are very similar to each other, but very different from those outside the cluster

- Unsupervised classification: cluster is not to relate features to classes or latent traits, but rather to estimate membership of distinct groups
- Groups are given labels through post-estimation interpretation of their elements
- Typically used when we do not and never will know the "true" class labels
- Issues:
 - How many clusters?
 - How to compute distance is arbitrary
 - Which features to include? Cluster might be sensitive to pre-processing (feature selection)

Clustering



Note that this process may require reiteration until you arrive at meaningful groupings of your data!

Figure by Koch (2020)

Hierarchical clustering

1. Start by considering each item as its own cluster, for n clusters
2. Calculate the $\frac{n(n-1)}{2}$ pairwise distances between each of the n clusters, store in a matrix D
3. Find smallest (off-diagonal) distance in D , and merge the items corresponding to the i, j indexes in D into a new "cluster"
4. Recalculate distance matrix D_1 with new cluster(s). Options for determining the location of a cluster include:
 - The furthest point in each cluster (complete-linkage)
 - The closest point in each cluster (single-linkage)
 - The average of each cluster (centroid)
5. Repeat 3-4 until a stopping condition is reached
 - i.e. all items have been merged into a single cluster
6. To plot the dendrograms, need decisions on ordering, since there are $2^{(n-1)}$ possible orderings

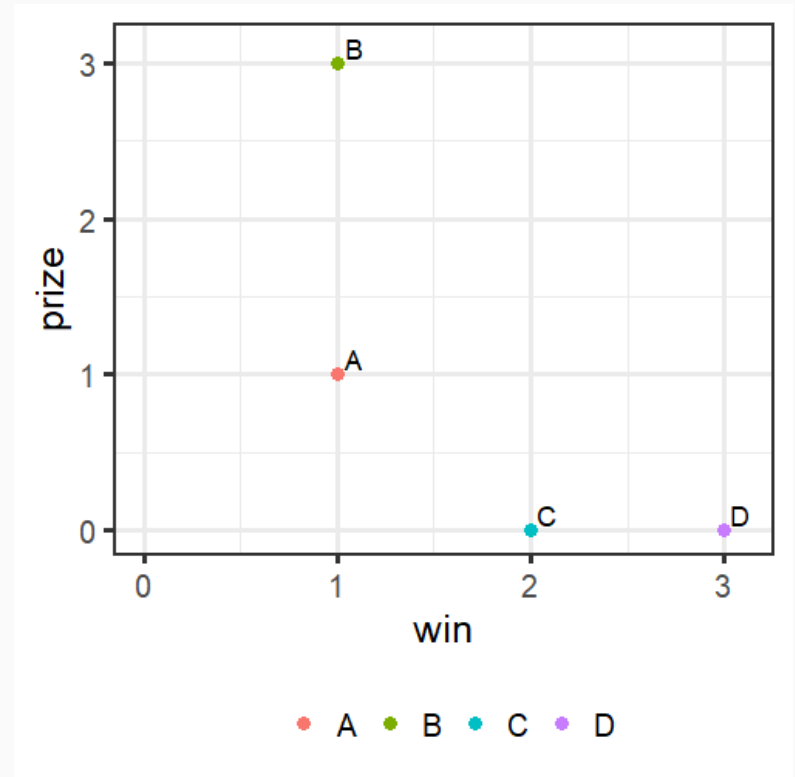
Hierarchical clustering I

Recall the previous example corpus

```
txt2 <- c(A = "Win Prize",  
          B = "Win Prize Prize Prize",  
          C = "Win win",  
          D = "Win win win")
```

... and its document-feature-matrix

	win	prize
A	1	1
B	1	3
C	2	0
D	3	0



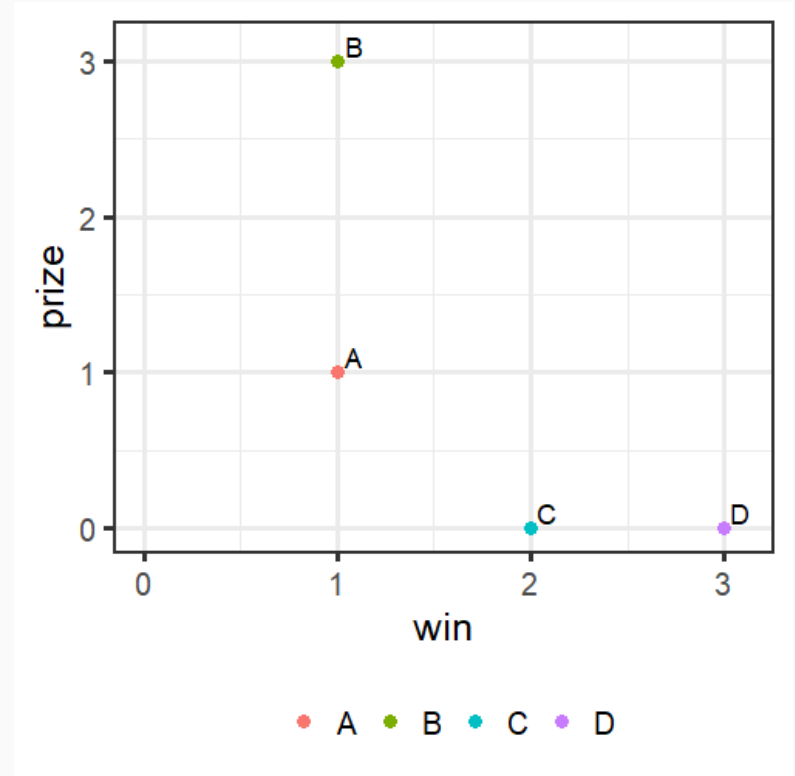
We start by considering each item as its own cluster, for $n=4$ clusters

Hierarchical clustering II

Using euclidean distance, we calculate the $\frac{n(n-1)}{2}$ pairwise distances between each of the n clusters and store them in matrix D

	A	B	C	D
A	0	2	1.41	2.24
B		0	3.16	3.61
C			0.00	1.00
D				0.00

Note we could use any other metric for distance/similarity

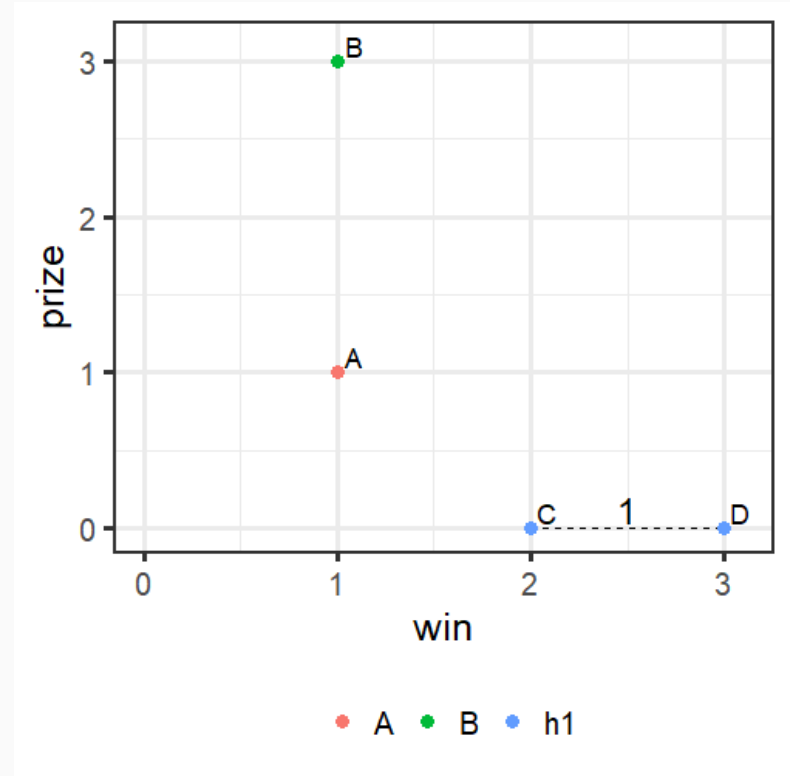


Hierarchical clustering III

Find smallest (off-diagonal) distance in D , and merge the items into a new "cluster"

	A	B	C	D
A	0	2	1.41	2.24
B		0	3.16	3.61
C			0.00	1.00
D				0.00

Based on euclidean distance, C and D are closest to each other so we merge them into a new set!



We are now left with 3 options to connect the sets: $A \leftrightarrow B$, $A \leftrightarrow h1$, and $B \leftrightarrow h1$

Hierarchical clustering IV

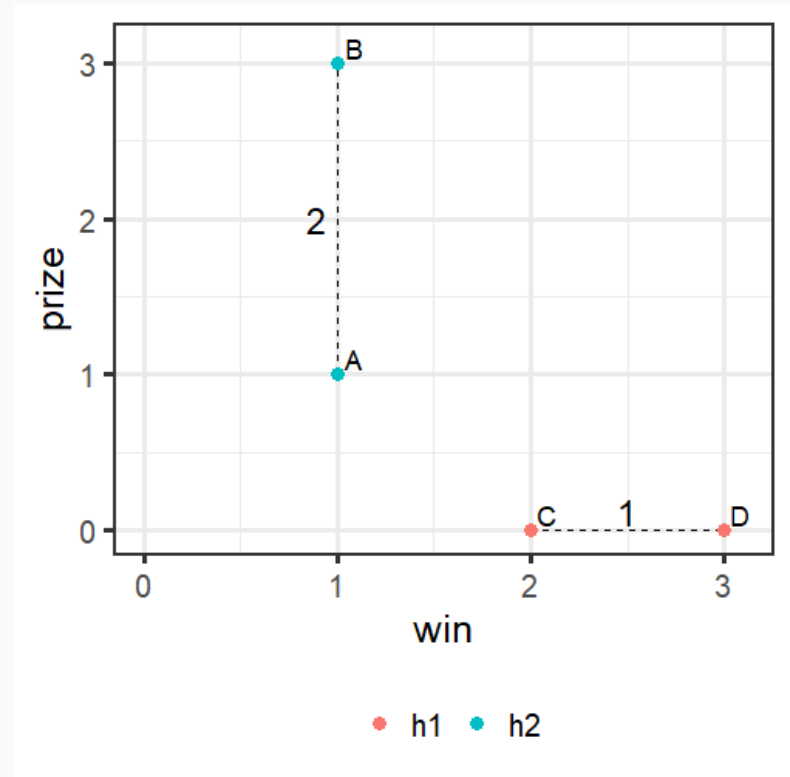
The distance between A and B remains the same $d(A,B) = 2$ but we need to recalculate distances involving the new h1

	A	B	C	D
A	0	2	1.41	2.24
B		0	3.16	3.61
C			0.00	1.00
D				0.00

Complete-linkage: What is the *maximum* distance from A to h1? And from B to h1?

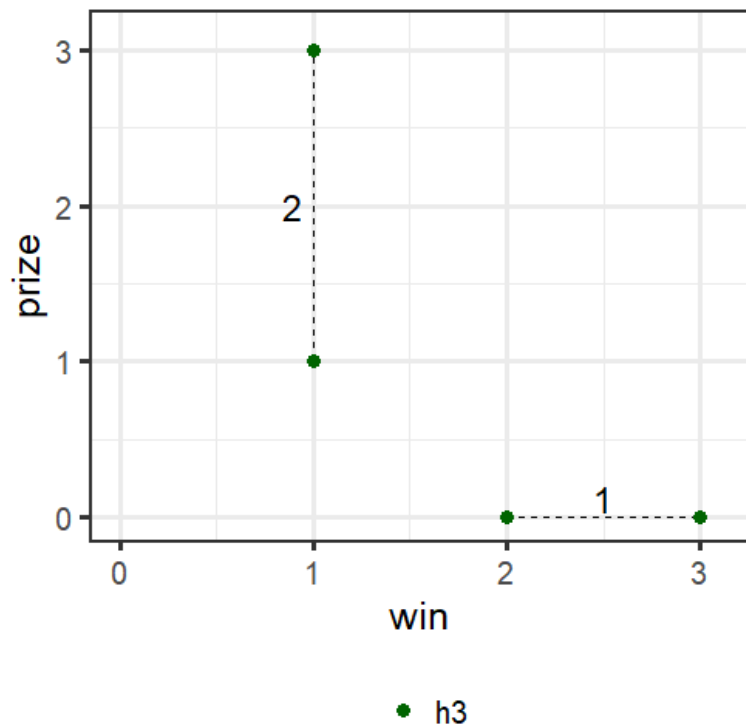
$$\begin{aligned}d(A, h1) &= \max(d(A, C), d(A, D)) \\ &= \max(1.41, 2.24) = 2.24\end{aligned}$$

$$\begin{aligned}d(B, h1) &= \max(d(B, C), d(B, D)) \\ &= \max(3.16, 3.61) = 3.61\end{aligned}$$



With a distance of 2, A and B are closest!

Hierarchical clustering VI



Usually, we would continue until all items have been merged into a single cluster by the same procedure as above.

However, there were only two clusters left which we can merge into a single one without calculations.

So we are done!

Dendrogram (complete-linkage)

Dendrograms indicate both the similarity and the order that the clusters were formed

```
# compute distance matrix with quantda  
d<-textstat_dist(x2,method="euclidean")
```

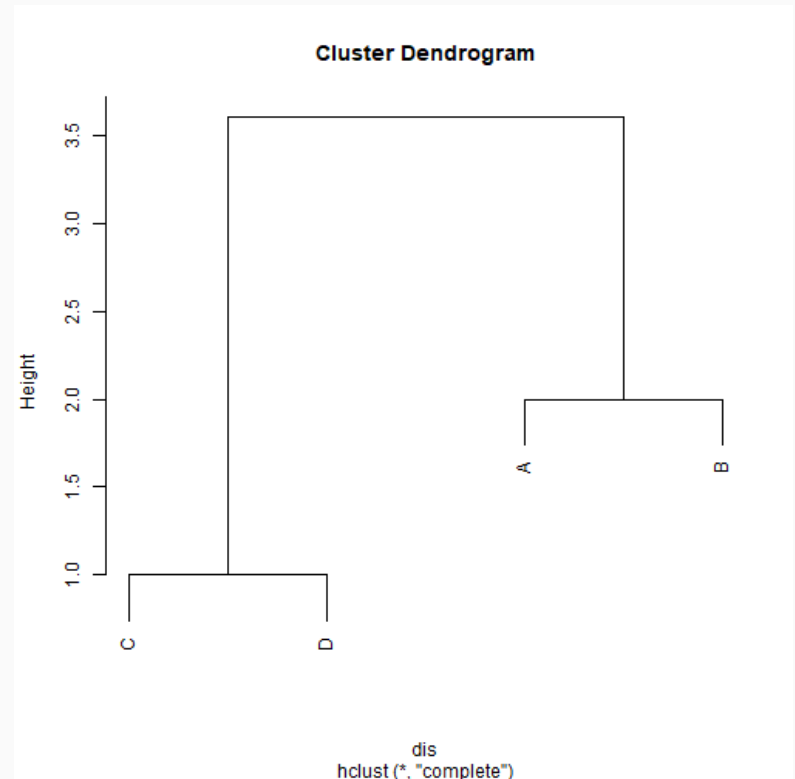
```
# make it compatible  
( dis <- as.dist(d) )
```

```
##           A      B      C      D  
## A 0.00  2.00  1.41  2.24  
## B 2.00  0.00  3.16  3.61  
## C 1.41  3.16  0.00  1.00  
## D 2.24  3.61  1.00  0.00
```

```
# run hierarchical clustering  
( hcc <- hclust(dis,method="complete"))
```

```
##  
## call:  
## hclust(d = dis, method = "complete")  
##  
## Cluster method      : complete  
## Number of objects: 4
```

```
# plot complete linkage dendrogram  
plot(hcc)
```



Dendrogram (single-linkage)

Single-linkage: compute the distance between a point and the closest point in each cluster

```
# compute distance matrix with quantda  
d<-textstat_dist(x2,method="euclidean")
```

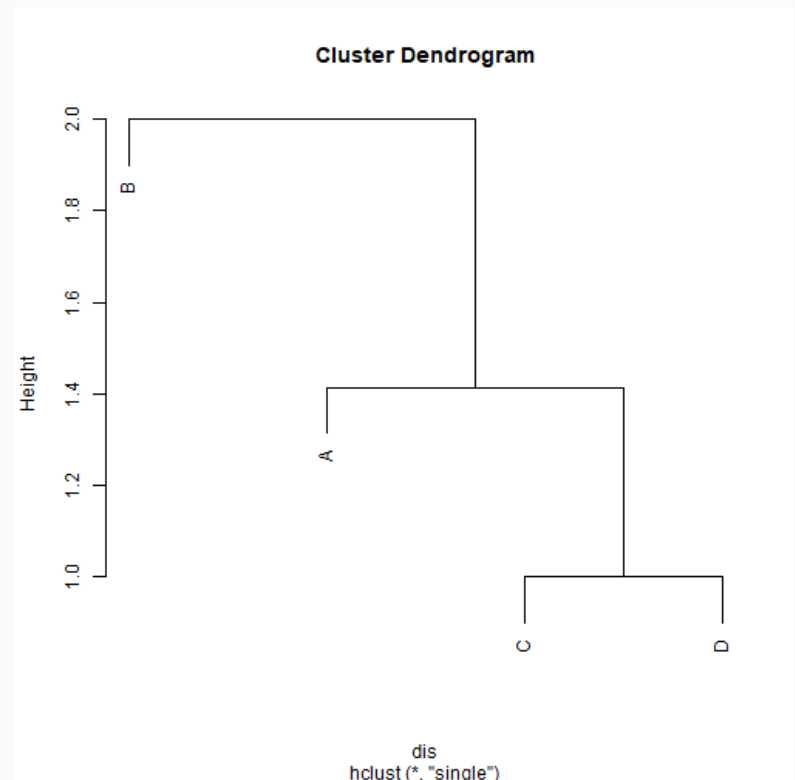
```
# make it compatible  
( dis <- as.dist(d) )
```

```
##           A      B      C      D  
## A 0.00  2.00  1.41  2.24  
## B 2.00  0.00  3.16  3.61  
## C 1.41  3.16  0.00  1.00  
## D 2.24  3.61  1.00  0.00
```

```
# run hierarchical clustering  
( hcs <- hclust(dis,method = "single"))
```

```
##  
## call:  
## hclust(d = dis, method = "single")  
##  
## Cluster method      : single  
## Number of objects: 4
```

```
# plot single linkage dendrogram  
plot(hcs)
```



Dendrogram (centroid)

Centroid: compute the distance between a point and the average distance to a cluster

```
# compute distance matrix with quanteda  
d<-textstat_dist(x2,method="euclidean")
```

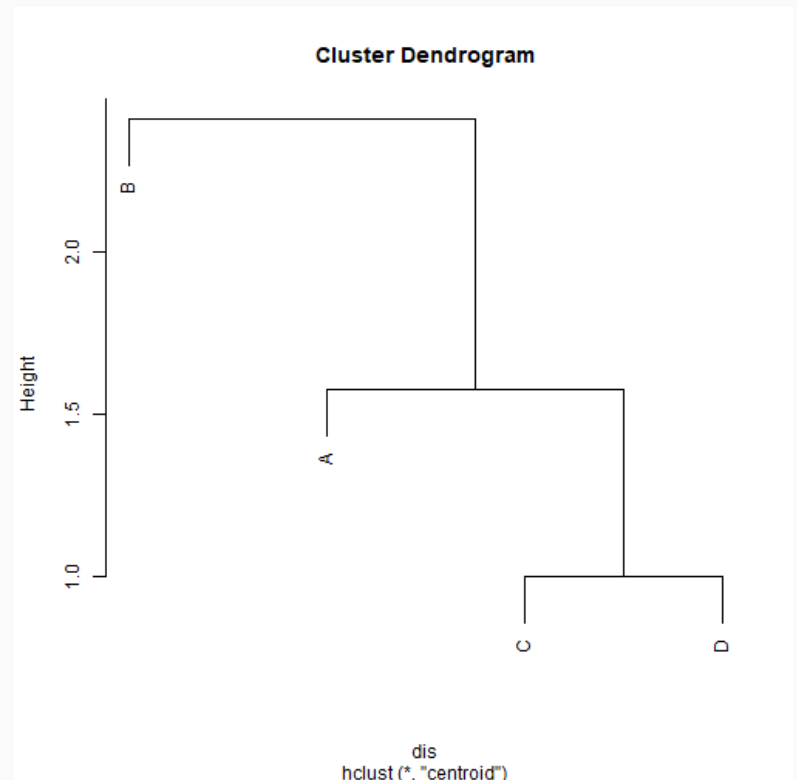
```
# make it compatible  
( dis <- as.dist(d) )
```

```
##           A      B      C      D  
## A 0.00  2.00  1.41  2.24  
## B 2.00  0.00  3.16  3.61  
## C 1.41  3.16  0.00  1.00  
## D 2.24  3.61  1.00  0.00
```

```
# run hierarchical clustering  
( hca <- hclust(dis,method="centroid"))
```

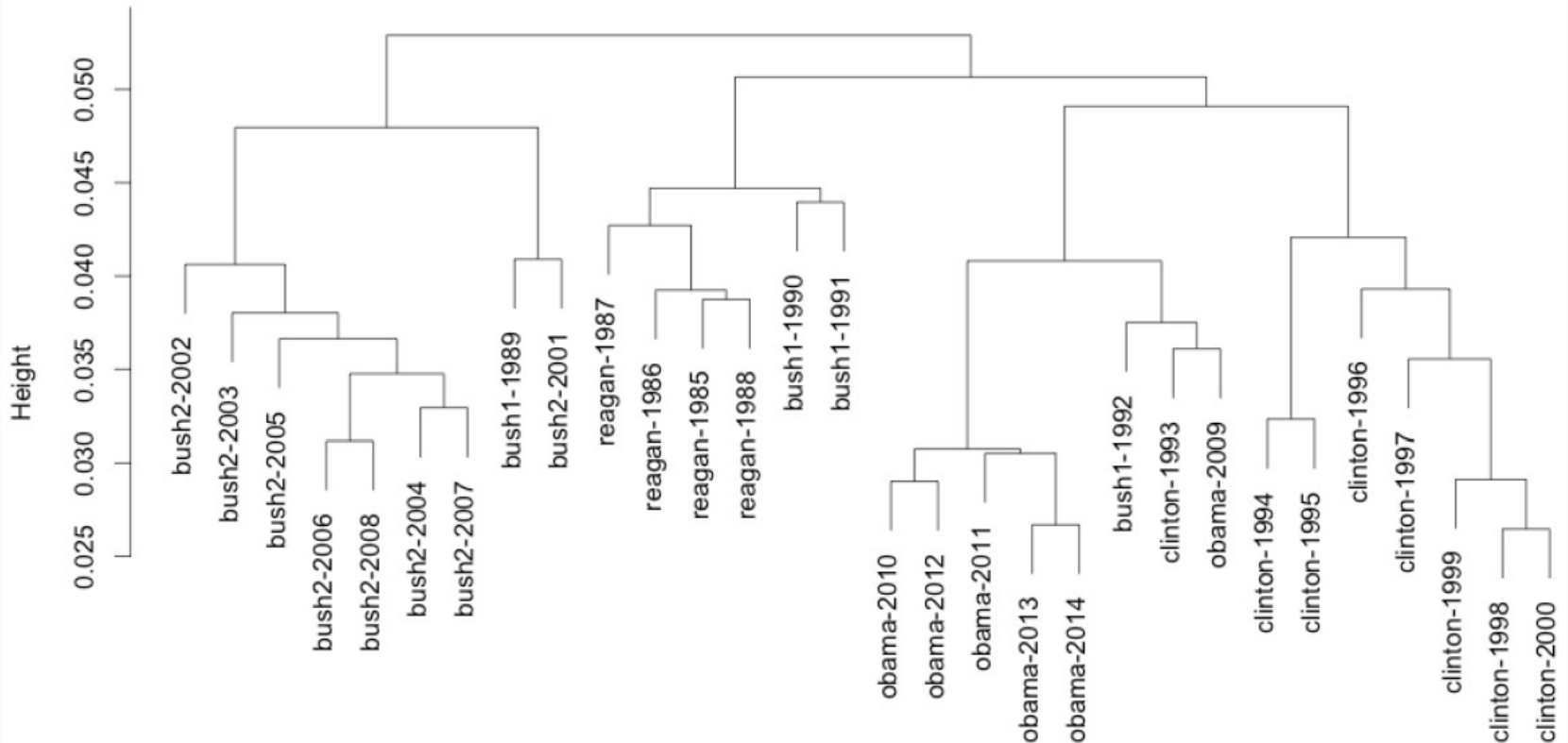
```
##  
## call:  
## hclust(d = dis, method = "centroid")  
##  
## Cluster method      : centroid  
## Number of objects: 4
```

```
# plot dendrogram centroid linkage  
plot(hca)
```



Dendrogram

Dendrograms indicate both the similarity and the order that the clusters were formed



Data: Presidential State of the Union addresses

Pros and Cons of hierarchical clustering

Advantages

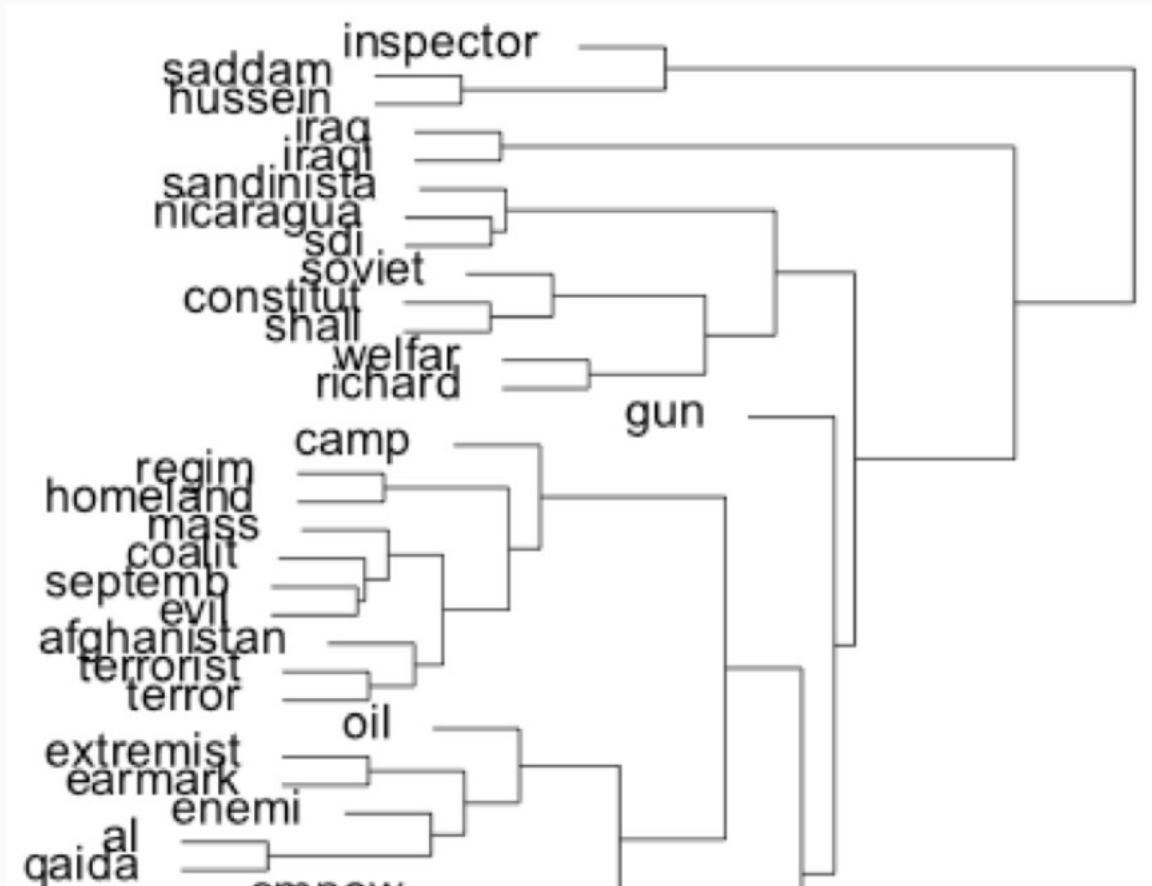
- deterministic, unlike k-means
- no need to decide on k in advance (although can specify as a stopping condition)
- allows hierarchical relations to be examined (usually through dendrograms)

Disadvantages

- more complex to compute: quadratic in complexity: $O(n^2)$ - whereas k-means has complexity that is $O(n)$
- the decision about where to create branches and in what order can be somewhat arbitrary, determined by method of declaring the "distance" to already formed clusters
- for words, tends to identify collocations as base-level clusters (e.g. "saddam" and "hussein")

Dendrogram at word level

Hierarchical clustering tends to create word collocations as base-level clusters



Data: Presidential State of the Union addresses

k-means clustering

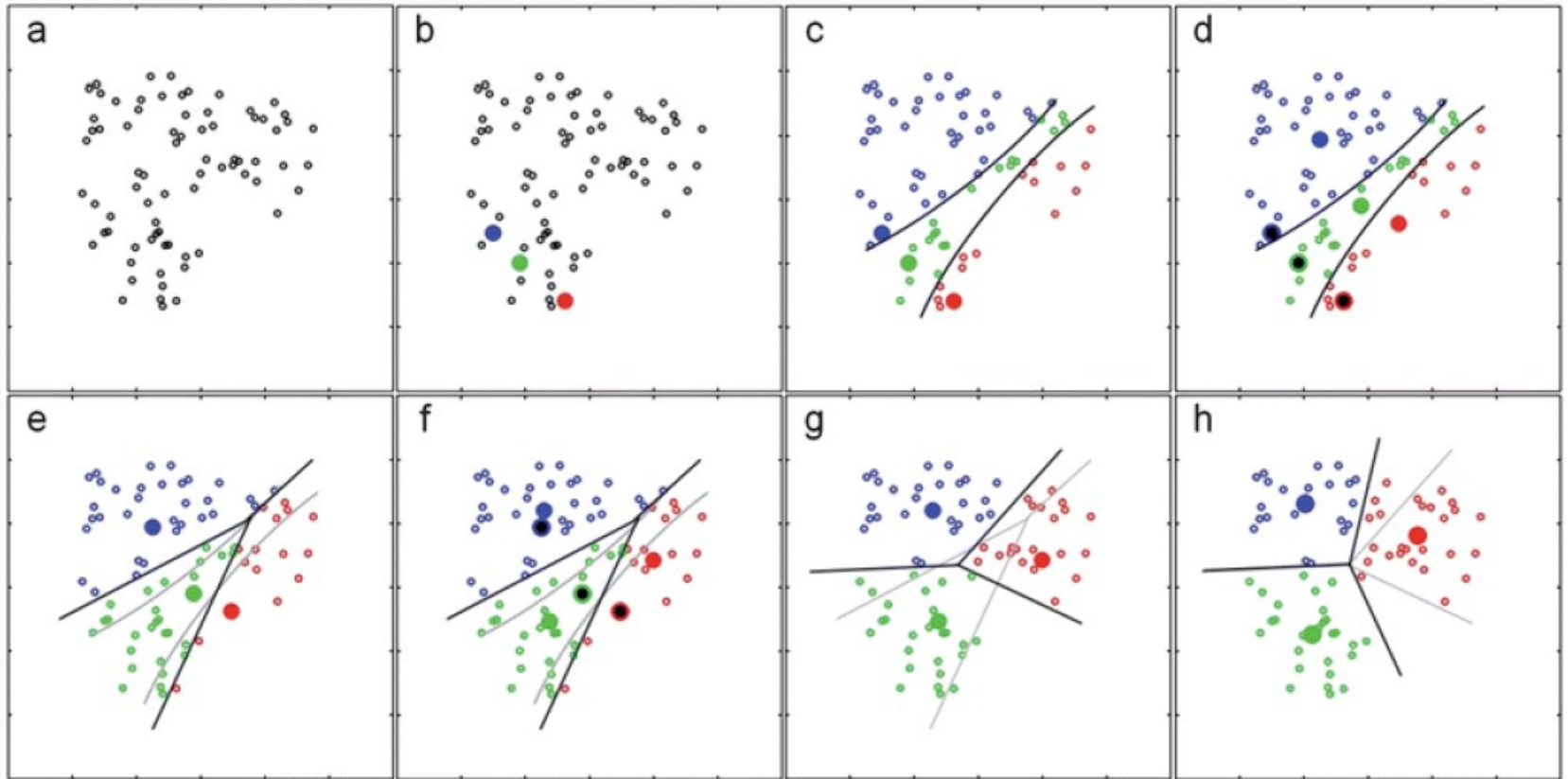
Assign each item to one of k clusters, where the goal is to minimise within-cluster difference and maximize between-cluster differences

- Uses random starting positions and iterates until stable. Hence, results can be different when running the algorithm again!
- k-means clustering treats feature values as coordinates in a multi-dimensional space
- Advantages
 - simplicity
 - highly flexible
 - efficient
- Disadvantages
 - no fixed rules for determining k
 - uses an element of randomness for starting values

Algorithm details

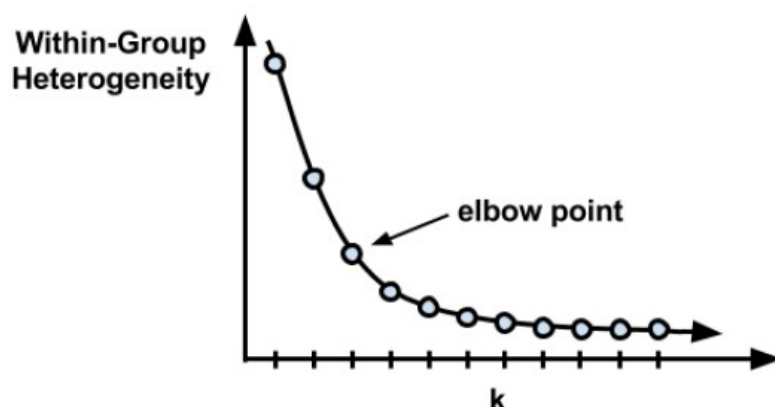
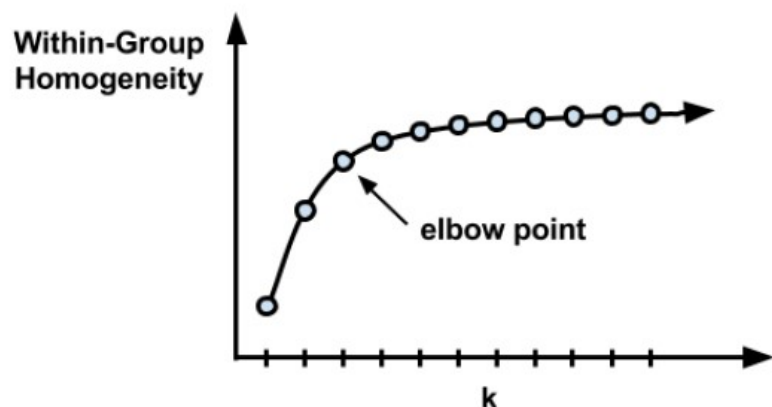
1. Choose starting values
 - assign random positions to k starting values that will serve as the "cluster centres", known as "centroids" ; or,
 - assign each feature randomly to one of k classes
2. assign each item to the class of the centroid that is "closest"
 - Euclidean distance is most common
 - any others may also be used (Manhattan, Minkowski, Mahalanobis, etc.)
 - (assumes feature vectors are normalized within document)
3. update: recompute the cluster centroids as the mean value of the points assigned to that cluster
4. repeat reassignment of points and updating centroids
5. repeat 2-4 until some stopping condition is satisfied
 - e.g. when no items are reclassified following update of centroids

k-means clustering



Appropriate number of clusters

- very often based on prior information about the number of categories sought
- for example, you need to cluster people in a class into a fixed number of (like-minded) tutorial groups
- a (rough!) guideline: set k equal to $\sqrt{\frac{N}{2}}$ where N is the number of items to be classified
- usually too big: setting k to large values will improve within-cluster similarity, but risks overfitting
- "elbow plots": fit multiple clusters with different k values, and choose k beyond which are diminishing gains



Computer exercises
