

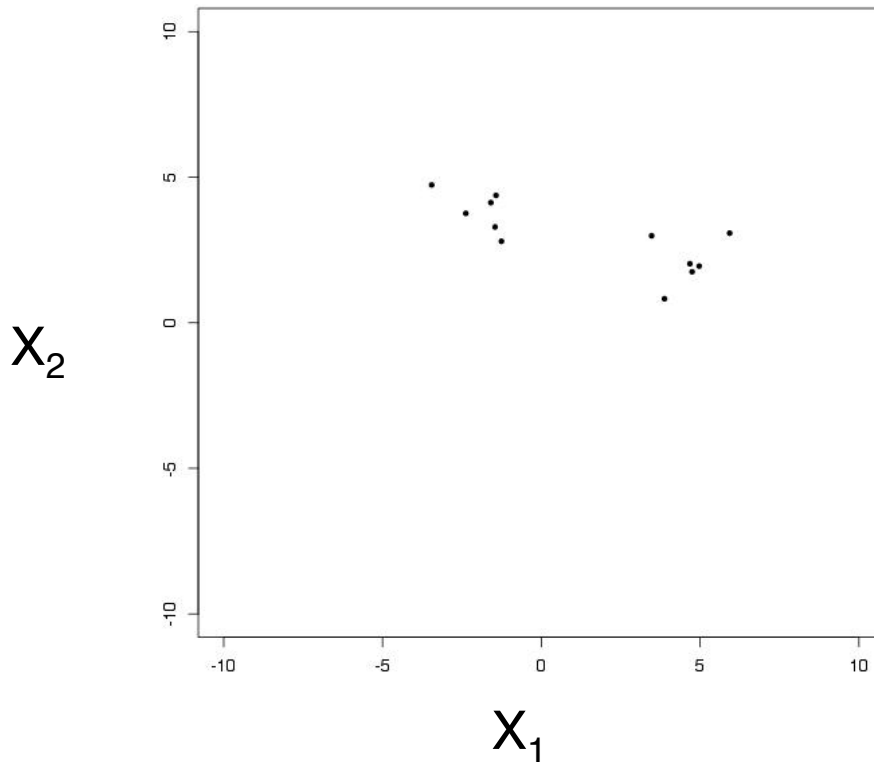
Unsupervised Learning with Clustering

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Clustering Idea

- Given a set of data can we find a natural grouping?



Essential R commands:

```
D =rnorm(12,0,1) #generate 12
```

```
#random normal
```

```
X1 =matrix(D,6,2) #put into 6x2 matrix
```

```
X1[,1]=X1[,1]+4; #shift center
```

```
X1[,2]=X1[,2]+2;
```

```
#repeat for another set of points
```

```
#bind data points and plot
```

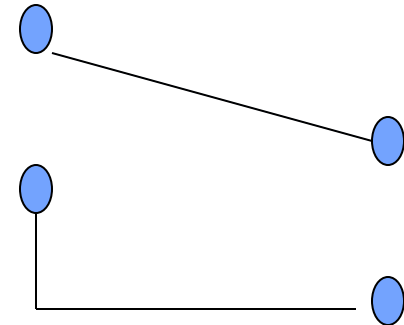
```
plot(rbind(X1,X2),  
      xlim=c(-10,10),ylim=c(-10,10));
```

Why Clustering

- **A good grouping implies some structure**
- **In other words, given a good grouping, we can then:**
 - Interpret and label clusters
 - Identify important features
 - Characterize new points by the closest cluster (or nearest neighbors)
 - Use the cluster assignments as a compression or summary of the data

Clustering Objective

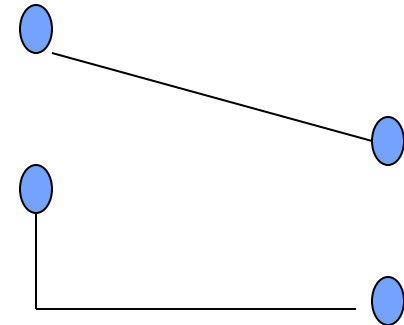
- **Objective:** find subsets that are similar within cluster and dissimilar between clusters
- **Similarity defined by distance measures**
 - Euclidean distance
 - Manhattan distance



Clustering Objective

- **Objective:** find subsets that are similar within cluster and dissimilar between clusters
- **Similarity defined by distance measures**

- Euclidean distance =
 $\text{sqrt}[(a_1 - b_1)^2 + (a_2 - b_2)^2 + \dots]$
- Manhattan distance
 $[|a_1 - b_1| + |a_2 - b_2| + \dots]$



Kmeans Clustering

- **A simple, effective, and standard method**

Start with K initial cluster centers

Loop:

Assign each data point to nearest cluster center

Calculate mean of cluster for new center

Stop when assignments don't change

- **Issues:**

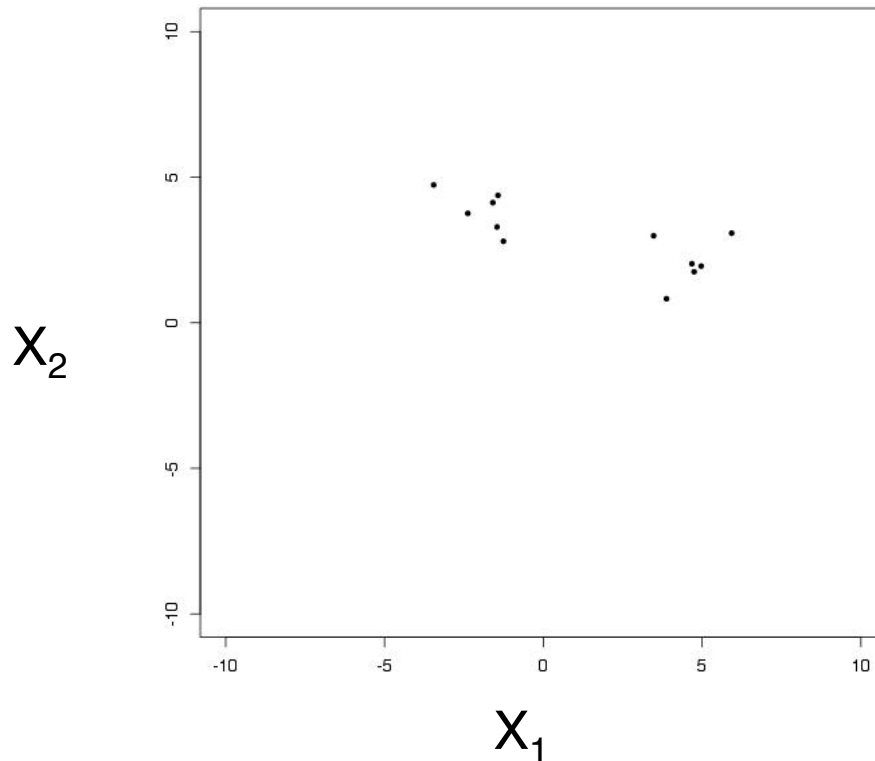
How to choose K ?

How to choose initial centers?

Will it always stop?

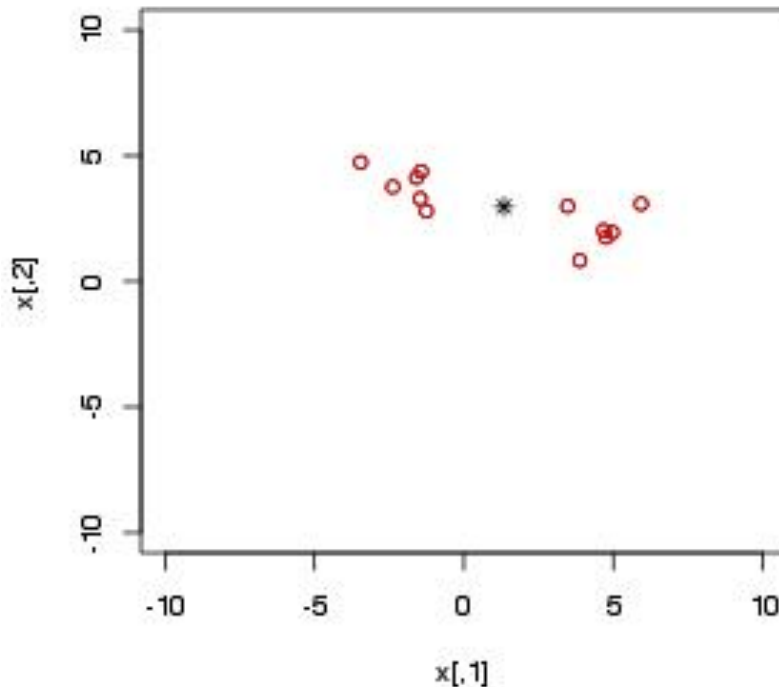
Kmeans Example

- For $K=1$, using Euclidean distance, where will the cluster center be?



Kmeans Example

- For $K=1$, the overall mean minimizes Sum Squared Error (SSE), aka Euclidean distance

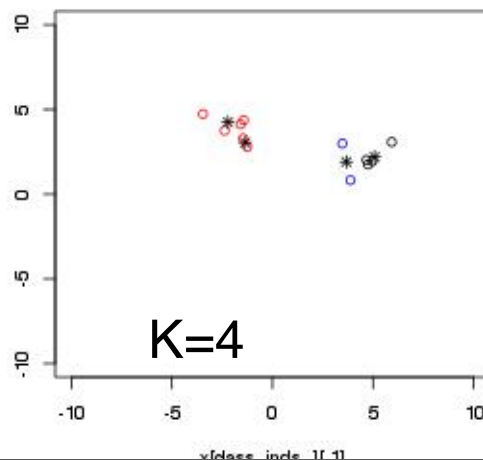
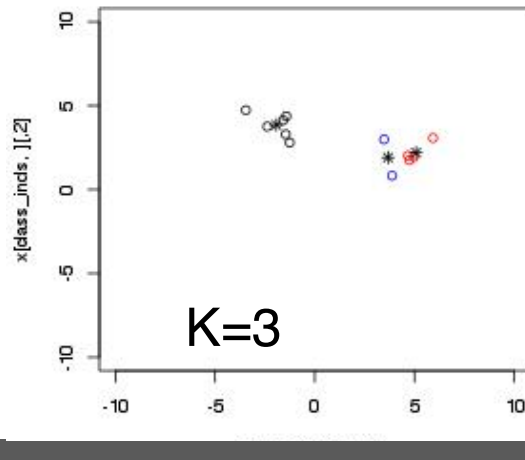
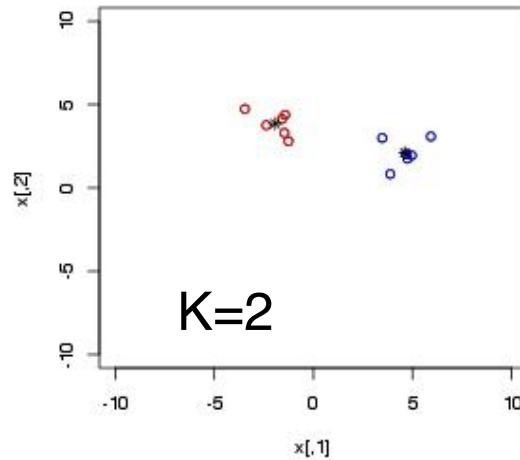
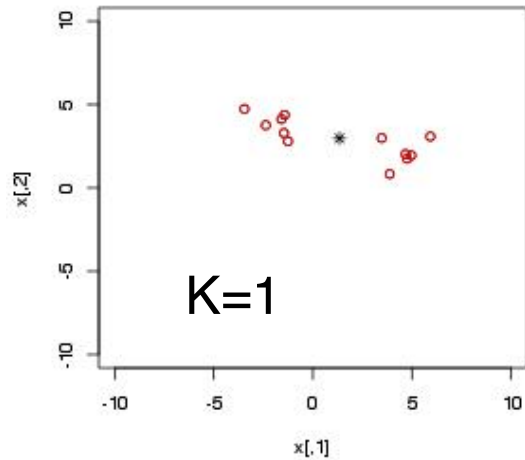


Essential R commands:
`Kresult = kmeans(X,1,10,1)`

#choose 1 data point as initial K centers
#10 is max loop iterations
#1 is number of initial sets to try

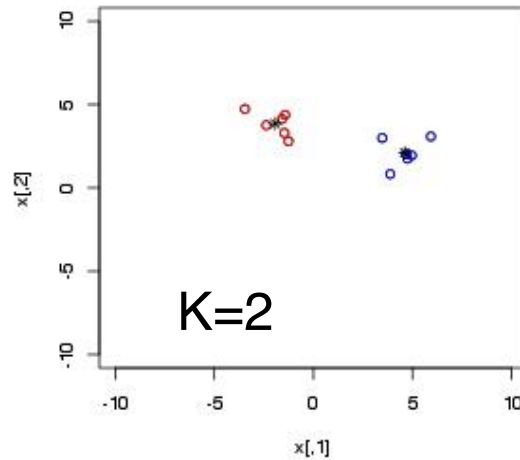
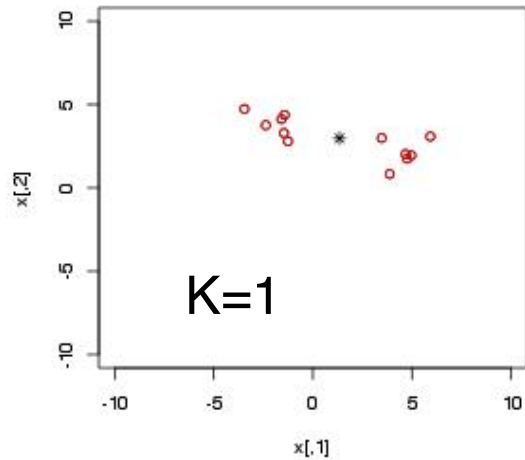
#Kresult is an R object with subfields
`Kresult$cluster` #cluster assignments
`Kresult$tot.withinss` # tot within SSE

Kmeans Example



Essential R commands:
`inds=which(Kresult$cluster==K)`
`plot(X[inds,],col2use="red");`
...

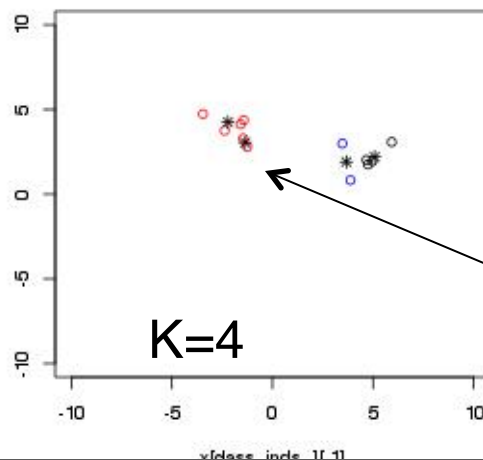
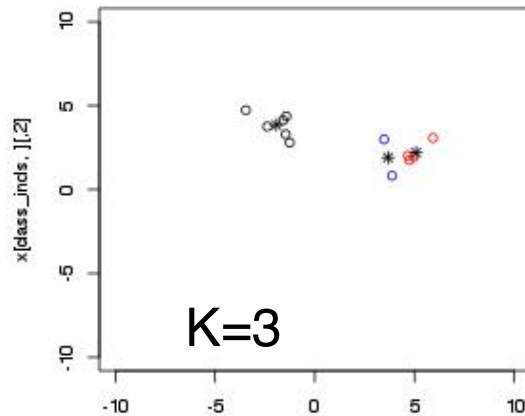
Kmeans Example



Essential R commands:
`inds=which(Kresult$cluster==K)`

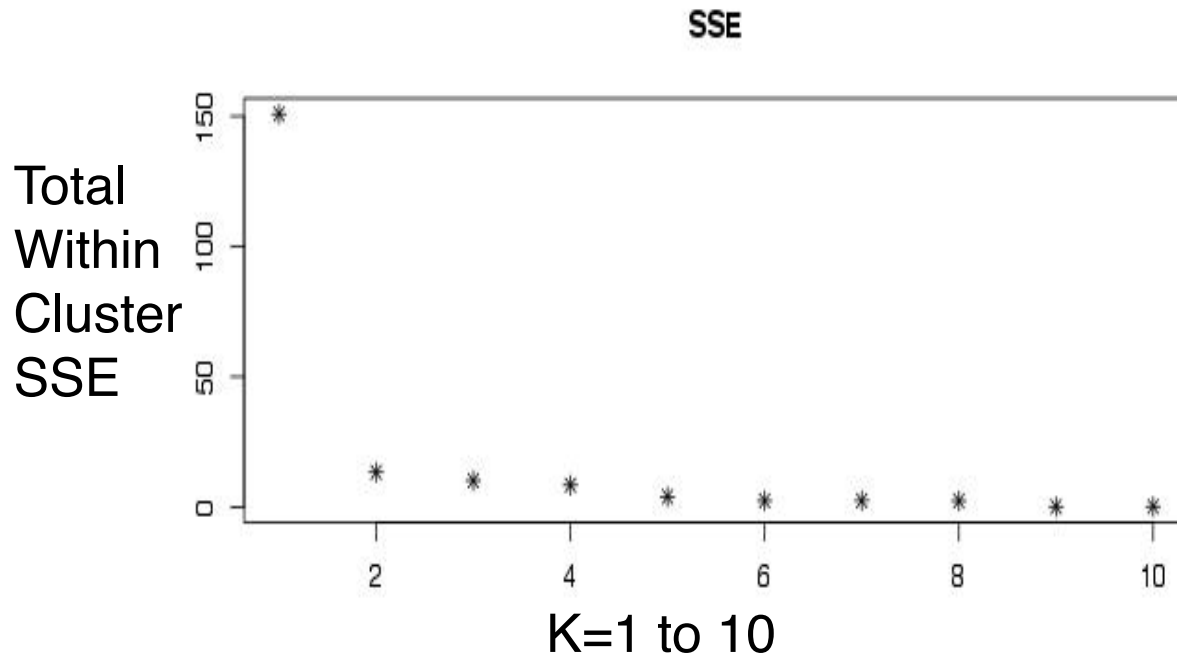
`plot(X[inds,],col2use="red");`

...



As K increases
individual points
get a cluster

Choosing K for Kmeans



Essential R commands:

```
for (num_k in 1:10) {  
  Kres=kmeans(X,num_k,10,1);
```

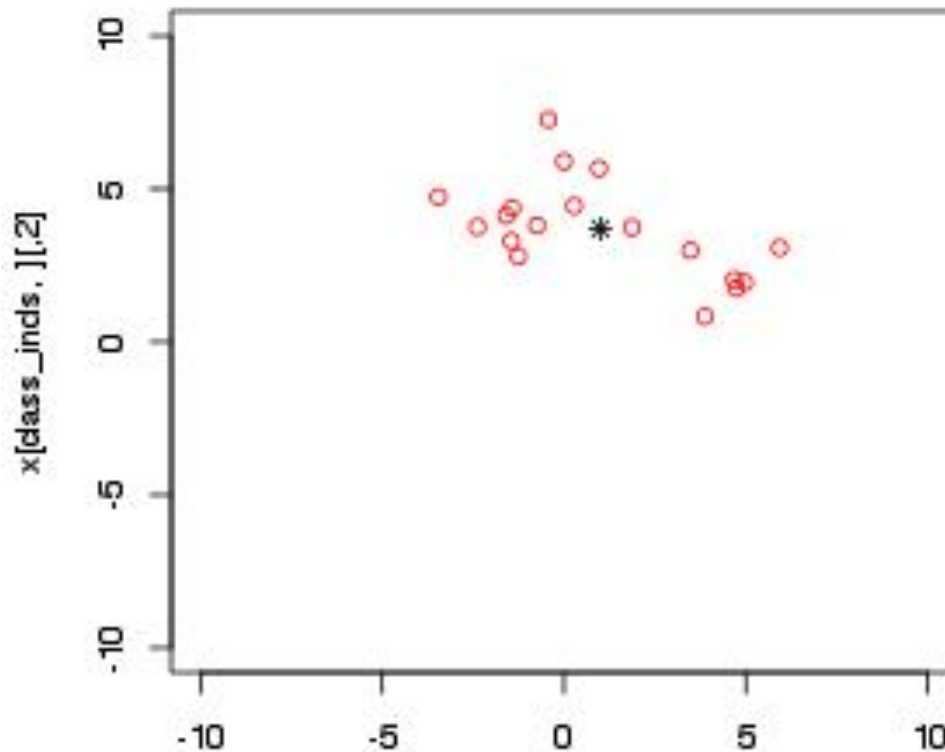
Save and then plot
Kres\$tot.withinss

...

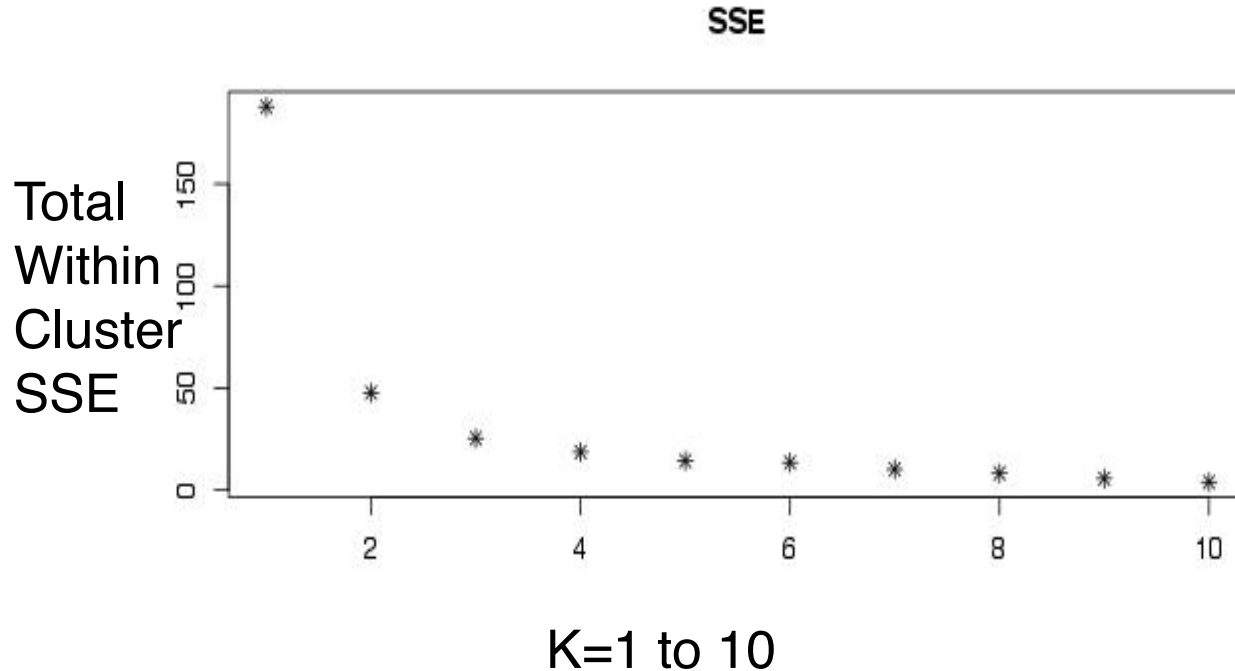
- Not much improvement after K=2 (“elbow”)

Kmeans Example – more points

How many clusters should there be?



Choosing K for Kmeans

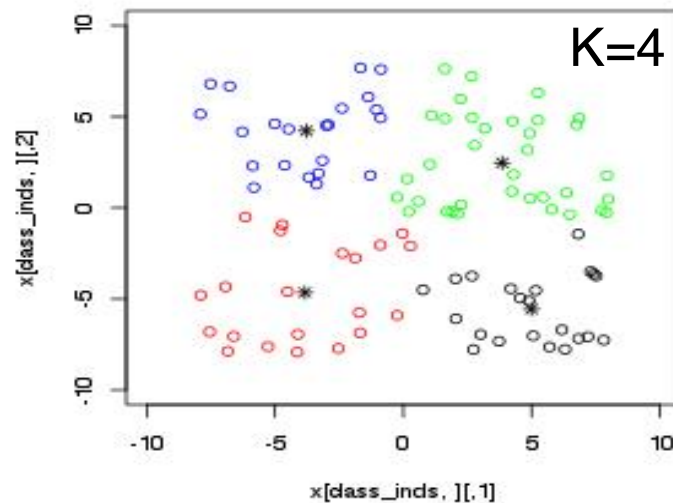
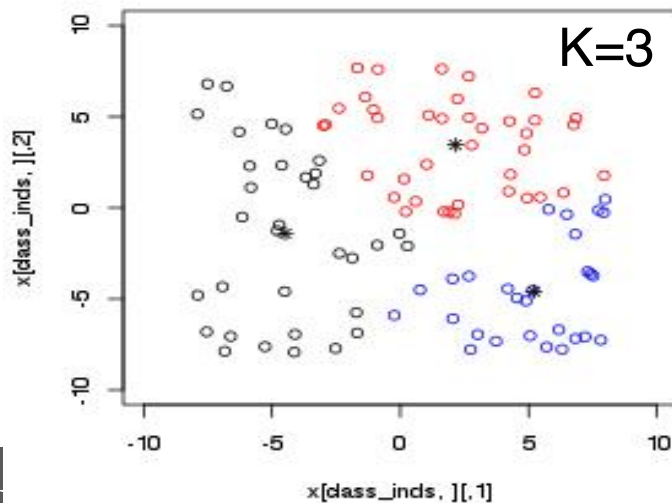
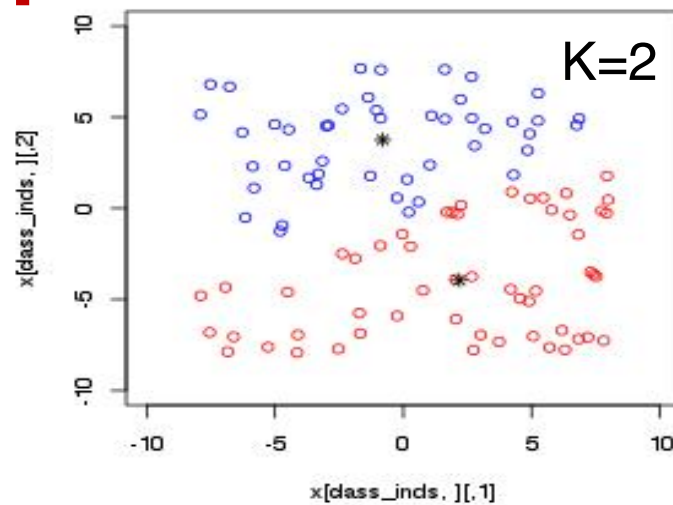
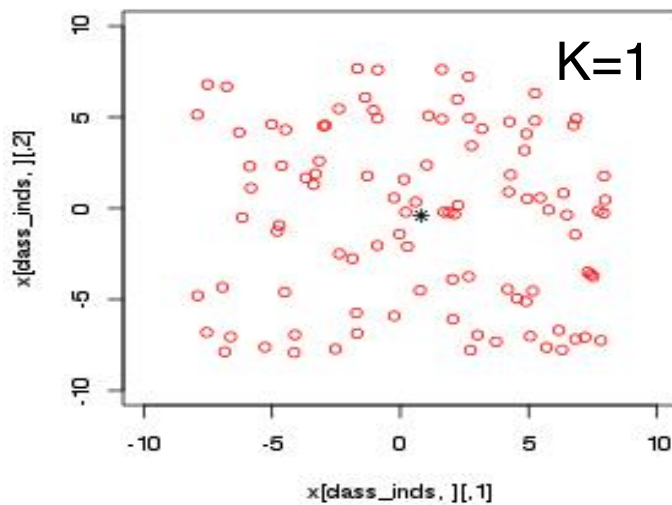


- Smooth decrease at $K \geq 2$, harder to choose
- In general, smoother decrease \Rightarrow less structure

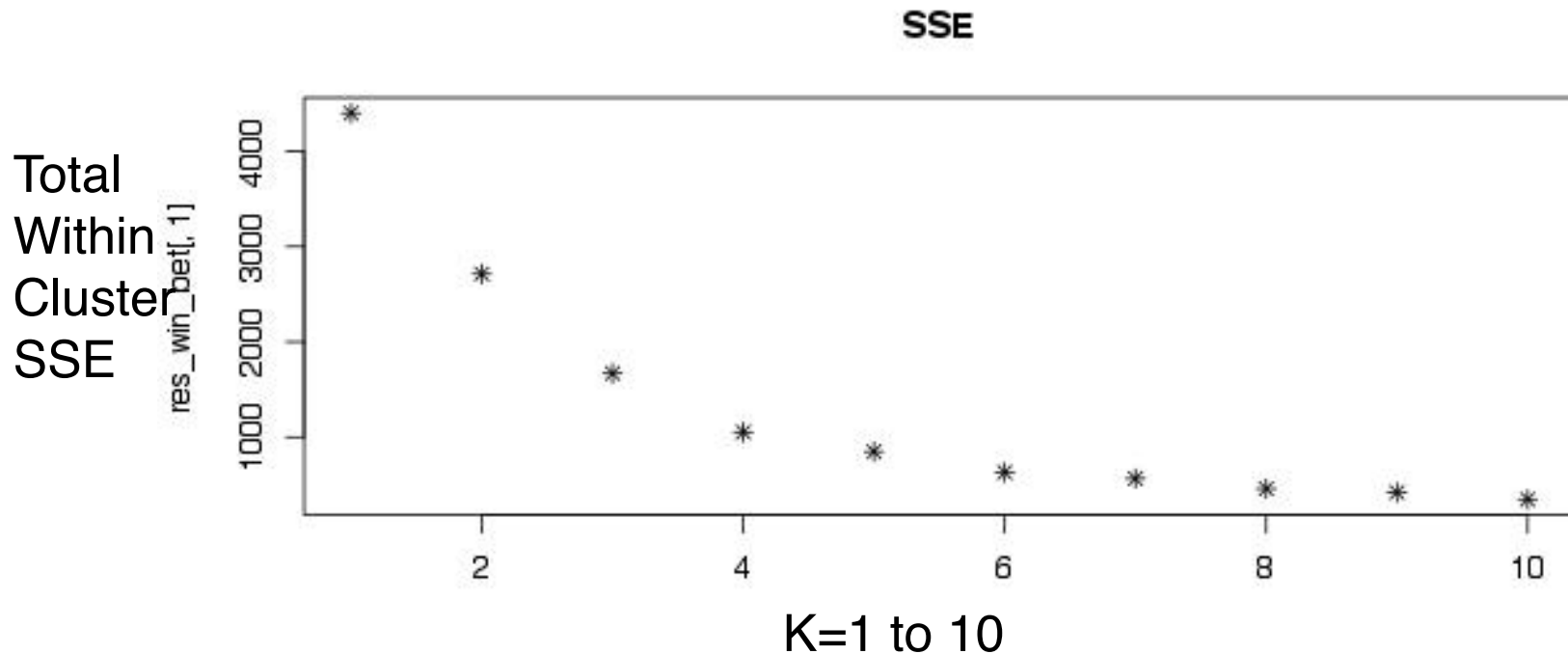
Kmeans Guidelines

- **Choosing K:**
 - “Elbow” in total-within-cluster SSE as $K=1\dots N$
 - Cross-validation: hold out points, compare fit as $K=1\dots N$
- **Choosing initial starting points:**
 - take K random data points, do several Kmeans, take best fit
- **Stopping:**
 - may converge to sub-optimal clusters
 - may get stuck or have slow convergence (point assignments bounce around), 10 iterations is often good

Kmeans Example: uniform dist.



Choosing K - uniform



- Smooth decrease across K => less structure

Kmeans Clustering Issues

- **Scale:**
 - Dimensions with large numbers may dominate distance metrics (so can be good to normalize or scale data)
- **Outliers:**
 - Outliers can pull cluster mean
(K-mediods uses median instead of mean)

Soft Clustering Methods

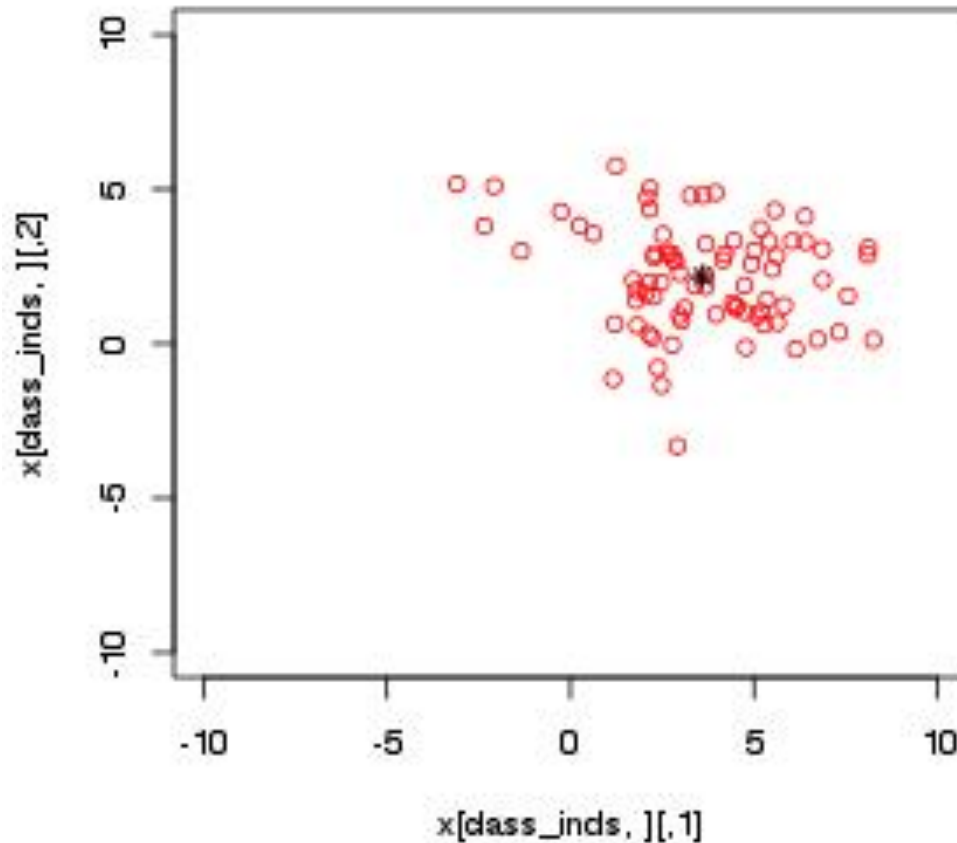
- **Fuzzy Clustering**

- Kmeans with weighted assignments to all clusters
- Weights depend on relative distance
- Find min weighted SSE

- **Expectation-Maximization:**

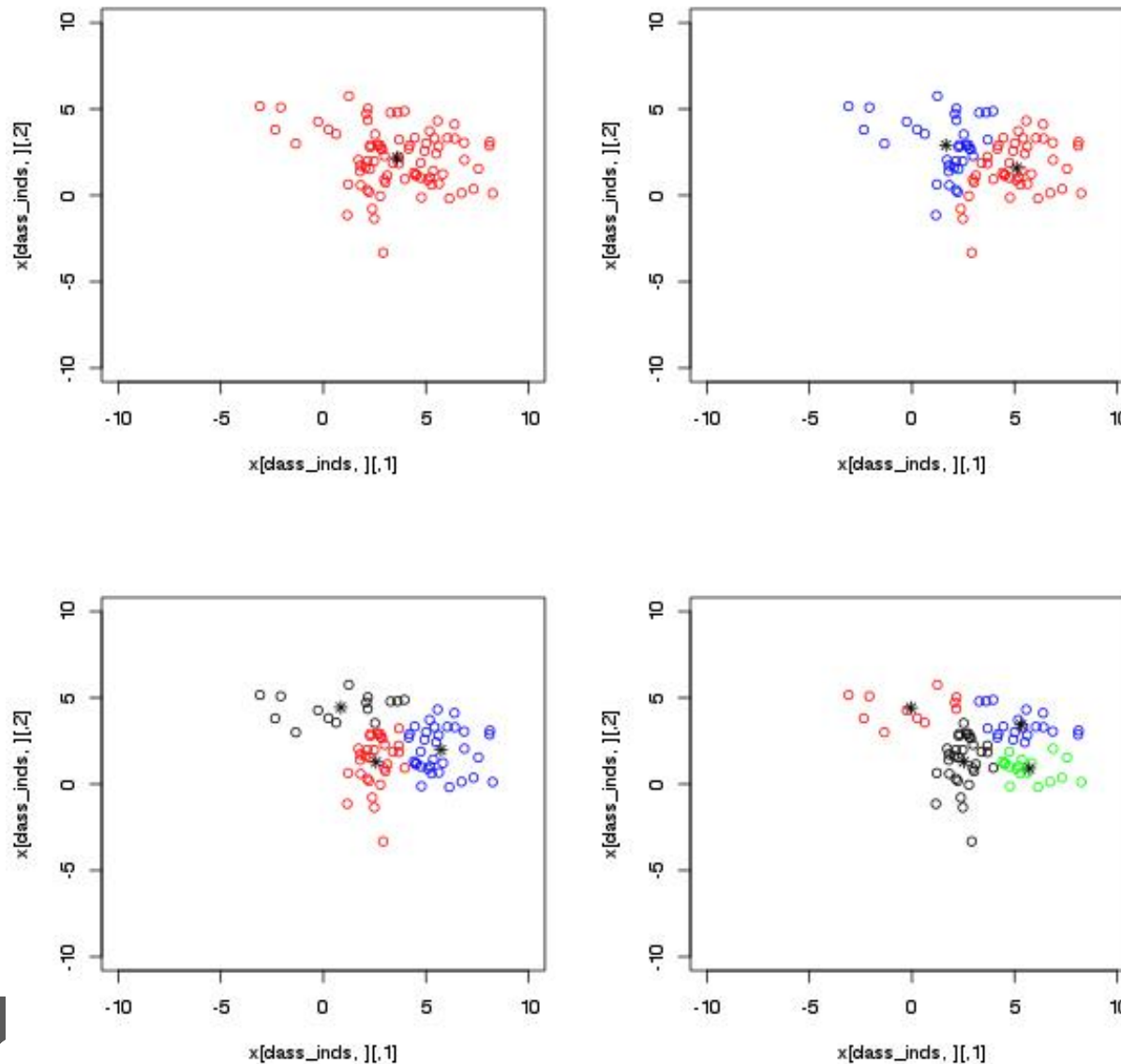
- Initialize a mixture of multivariate Gaussian distributions
- Find means, variances, and mixture weights that maximize probability of data

Kmeans with unequal cluster variance and/or size

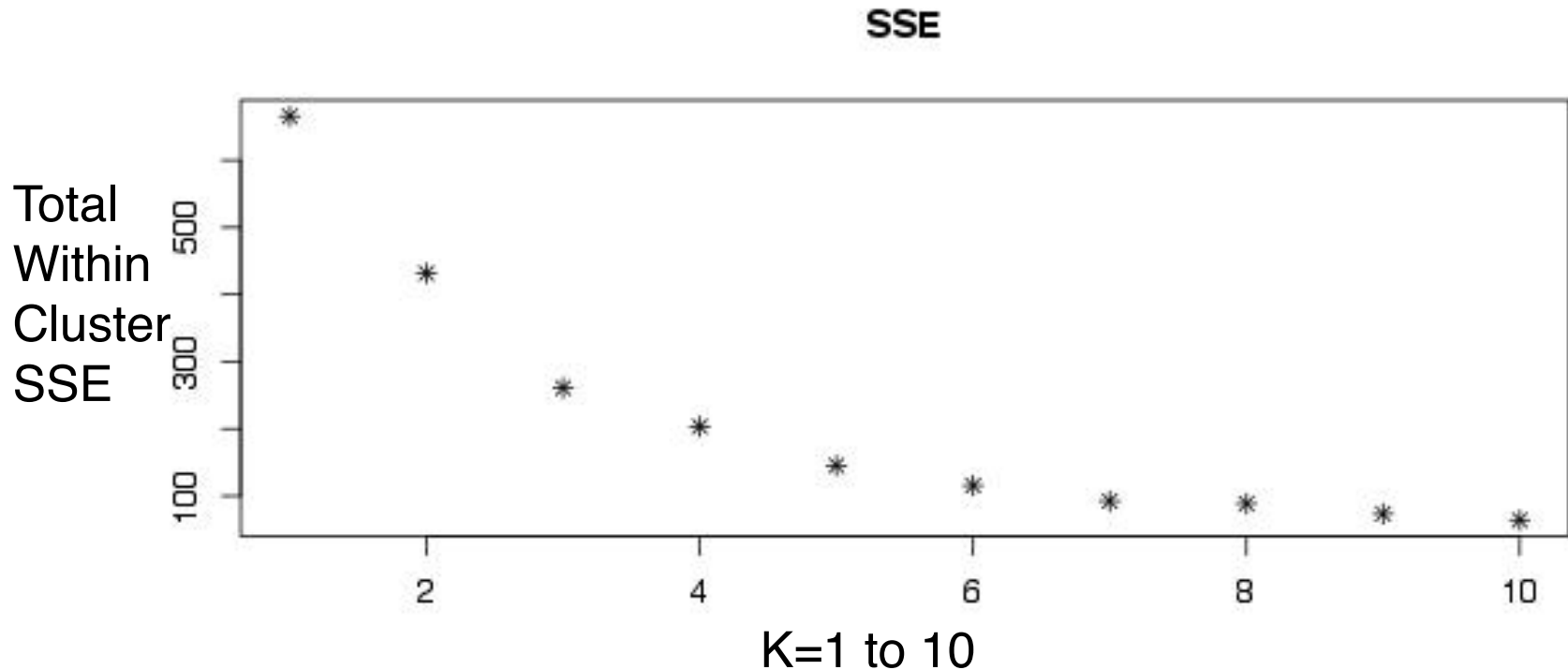


Can you guess K?

Kmeans – unequal cluster variance

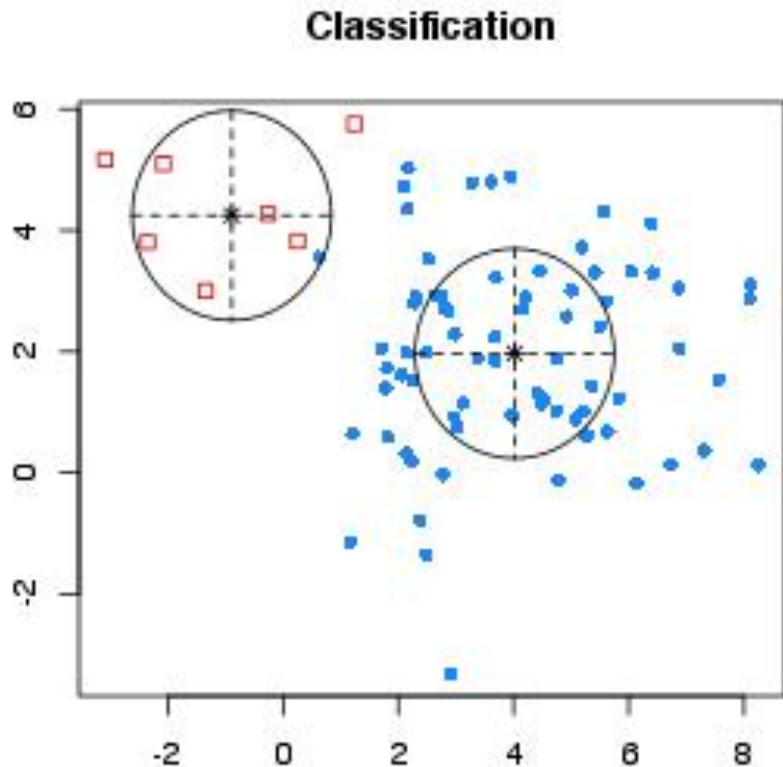


Choosing K – unequal distributions



- Smooth decrease across K => less structure

EM clustering



- Selects $K=2$
(either by Information Criterion=
min of $SSE + K \cdot \log N$,
Or by cross-validation)
- Handles unequal variance
and/or size

R:
`library('mclust')`
`em_fit=Mclust(x);`
`plot(em_fit);`

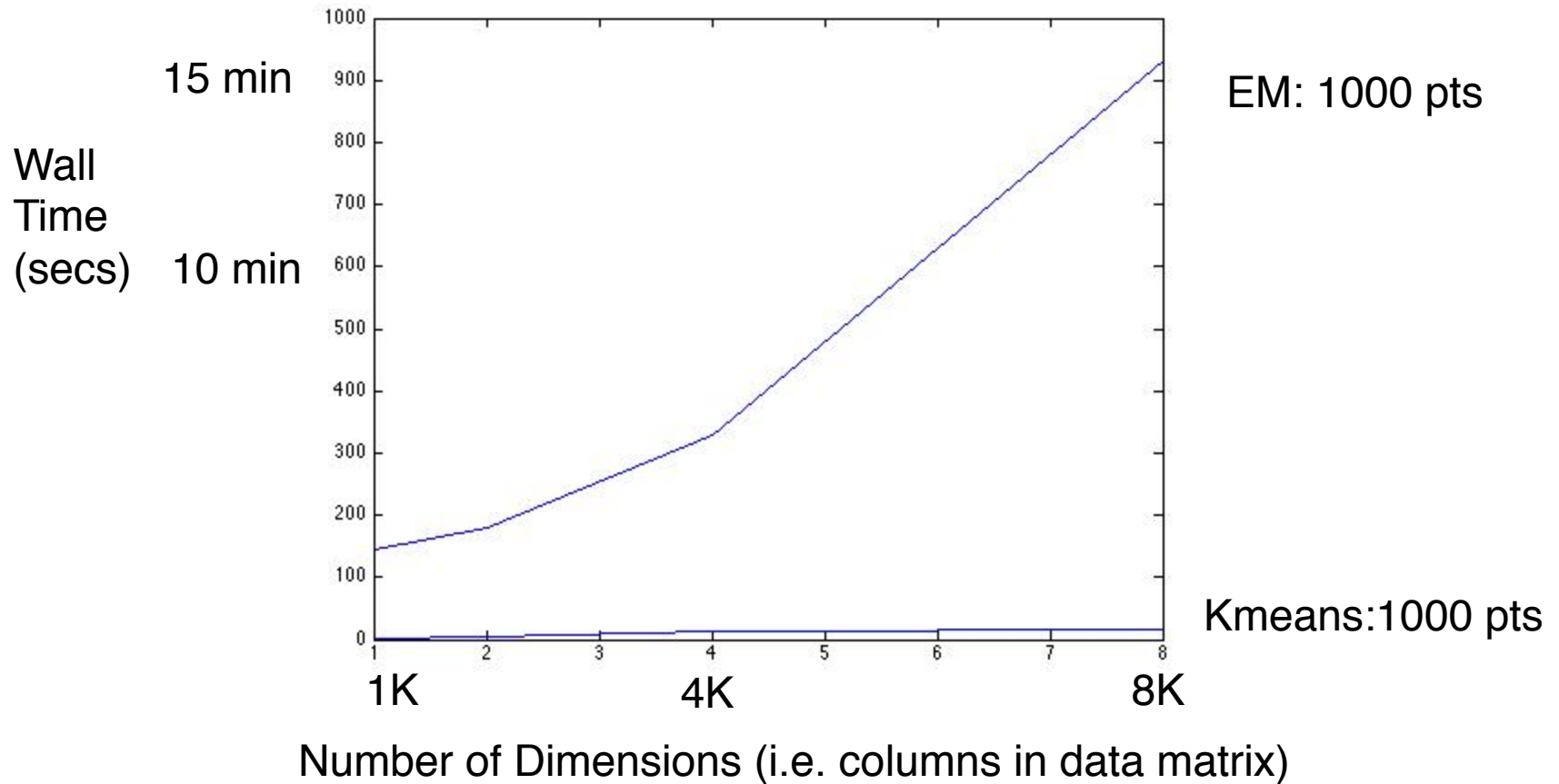
Kmeans computations

- **Distance of each point to each cluster center**
 - For N points, D dimensions: each loop requires $N*D*K$ operations
- **Update Cluster centers**
 - only track points that change, get change in cluster center
- **But for EM errors to each cluster center update a probability function**

Kmeans vs EM performance

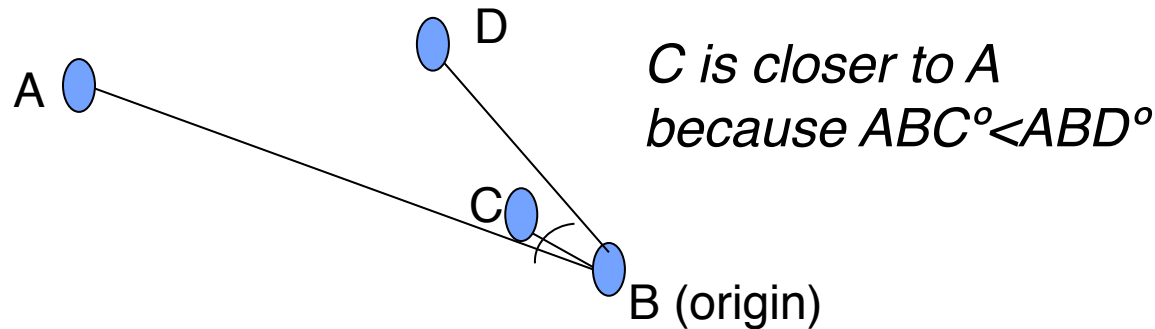
1 Gordon compute node, normal random matrices

R: `system.time(Mclust())`



Other distance measures

- Cosine: take angle difference (good for sparse vectors)



- Mahalanobis: dimensions rescaled by variance
- Jaccard (over sets A,B): $1 - (|A \cap B| / |A \cup B|)$

Other distance measures

- Hamming distance: count 1 if values different
e.g. appropriate for binary strings

010100110
000100010



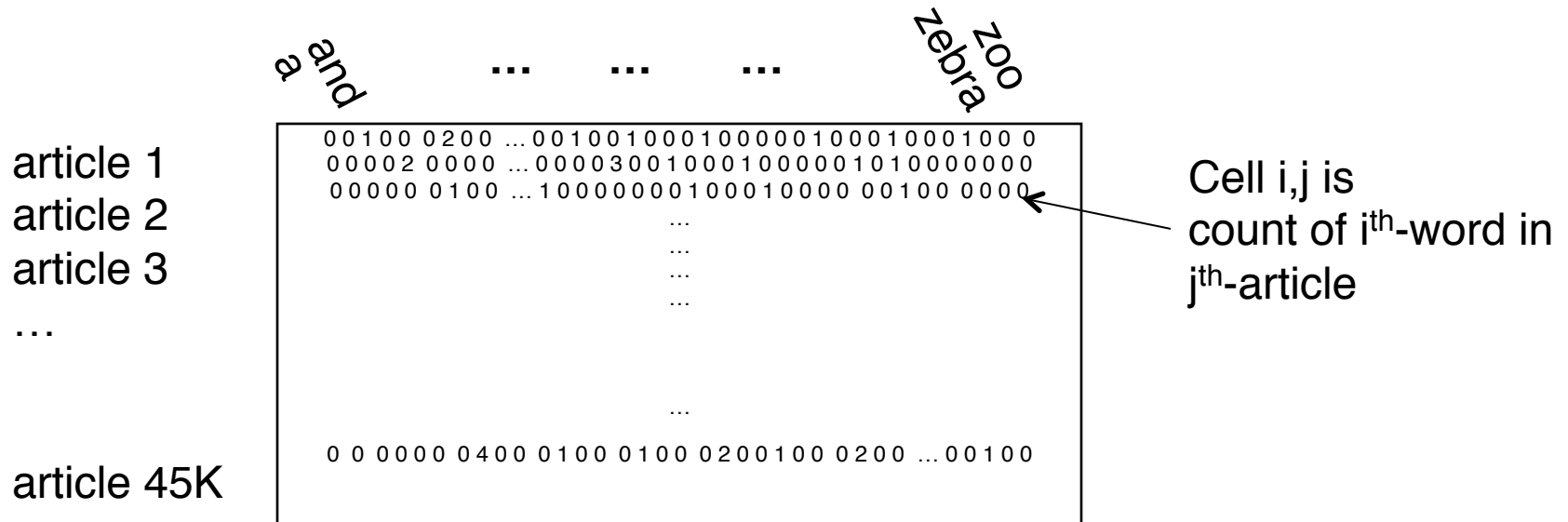
Total difference is 2

Kmeans big data example

- 45,000 NYTimes articles, 102,000 unique words

(UCI Machine Learning repository)

- Full Data Matrix: 45Kx102K ~ 40Gb



Kmeans results



*cluster means shown
with coordinates
determining fontsize*

7 viable clusters found

Kmeans for image segmentation

R snippet

get packages
read 1024X718X3 RGB image
convert to matrix 1024*718 X 3
Choose K by trial and error
run Kmeans and display

```
install.packages('ripa')  
library('ripa')
```

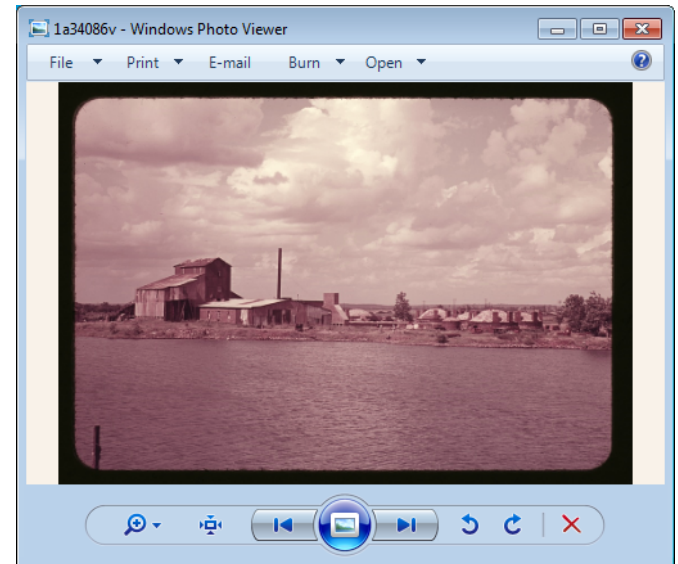
```
source("http://bioconductor.org/biocLite.R")  
biocLite()  
biocLite("EBImage")
```

```
library('EBImage')  
im=readImage('1a34086v.jpg')
```

```
library('ripa')  
img=rgb2grey(im, coefs=c(0.30, 0.59, 0.11))
```

```
imgx1 =as.vector(img)  
numk=8  
km_imgx1=kmeans(imgx1,numk,50,1);  
img_km_mat =matrix(km_imgx1$cluster,dim(im)[1],dim(im)[2])
```

```
display(img_km_mat/numk)
```

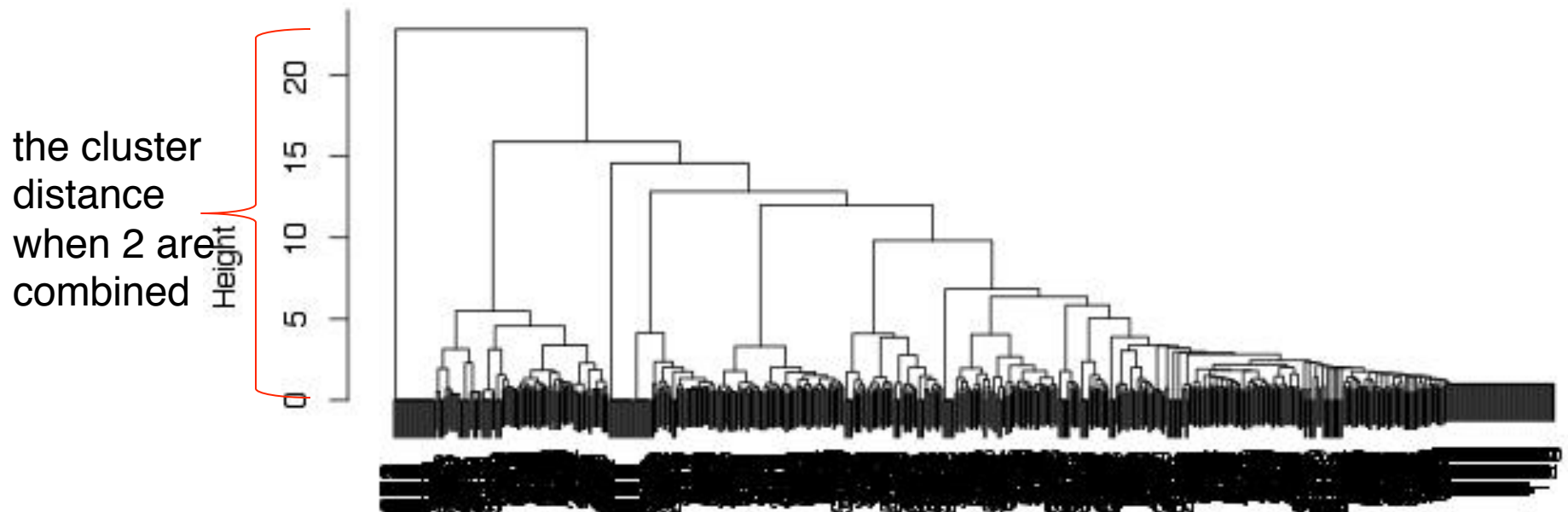


Other Clustering Methods

Hierarchical Clustering

- `hclust` with “Ward” distance gives spherical clusters

Cluster Dendrogram



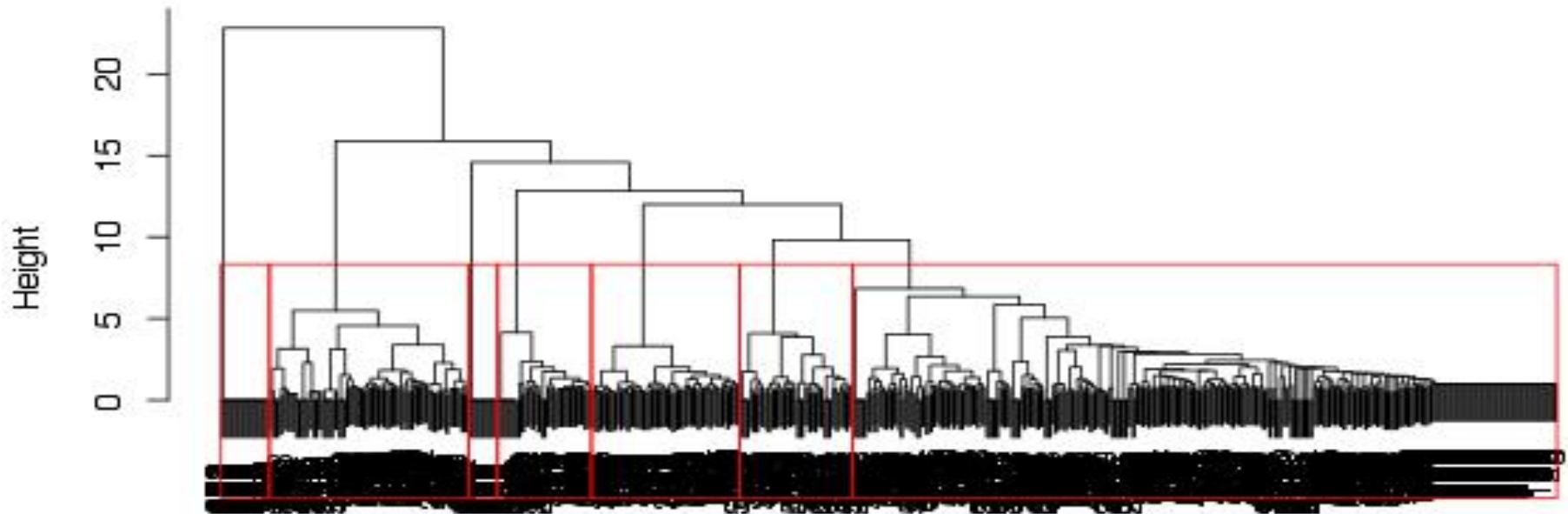
`d2use`
`hclust ("", "ward")`

Hierarchical Clustering

- Where height change looks big, cut off tree

```
groups <- cutree(fit, k=7)  
rect.hclust(fit, k=7, border="red")
```

Cluster Dendrogram



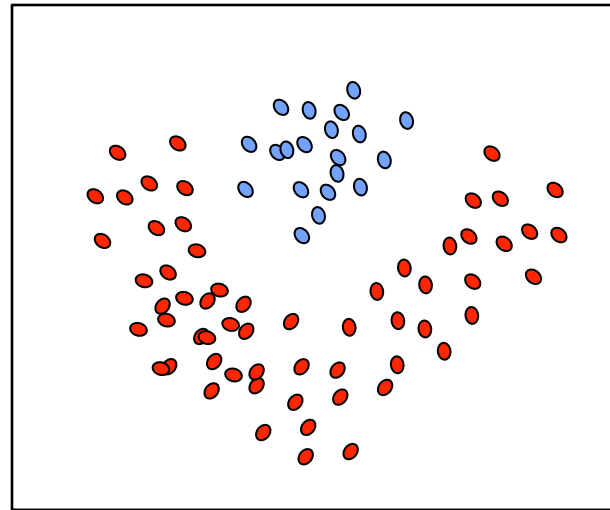
Other Clustering

- **Density based clustering**

build neighborhoods around seed points

link neighborhoods

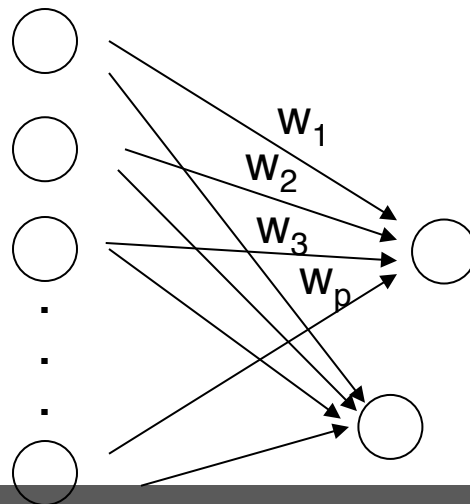
Results in arbitrary cluster shapes, good for image and spatial clustering



Other Clustering

- **Neural Network Based (e.g.)**

initialize weights to coordinate values for a seed point
set input nodes to coordinate values for data points
get best match to seed for each data point and adjust
weights toward the data point



Target node(s), starts as a seed point and ends up as a cluster mean