

# Cluster Analysis: Discovery Winter Institute in Data Science

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Matrices and Lists

Supervised and Unsupervised Learning

Hierarchical Clustering

Partitional Clustering

Selecting  $k$

Exercise

## Matrices and Lists

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- ▶ `df[, "v1"]`
- ▶ `df[, 6]`
- ▶ `df["v1"]` (keeps col name)

1. Describe list `ll` created below:

```
v1 <- 1:8  
v2 <- letters[1:5]  
m <- matrix(1:9, 3, 3)  
ll <- list(x = v1, y = v2, z = m)
```

2. What is `ll$y`?
3. What is `ll[[1]]`?
4. What is `ll[[3]][2, 2]`?

## Distance Matrix for Clustering

Each cell is a *distance* between unit **row** and unit **column**:

	a	b	c	d
a	0	1	2	3
b	1	0	6	7
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So,  $||(c, d)|| > ||(a, b)||$ , e.g.,  $(8 > 1)$

# Supervised and Unsupervised Learning

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Unsupervised: Discovery w/ **unknown** outcomes

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If you have  $y = f(X)$ , it's “supervised”.

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- ▶ Principal components analysis (PCA)
- ▶ (Some neural networks)
- ▶ NLP (derive topics from documents)
- ▶ Clustering algorithms (most)

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- ▶ Geographic clustering: daily activities
  - ▶ no “home”/“work”/“leisure” labels

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  - ▶ Find splits in full set
  - ▶ Units in only one cluster

# Hierarchical Clustering

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Consider a set of units open to cluster discovery,  
 $\{a, b, c, d, e\}$

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Divisive clustering is “top-down”

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Agglomerative clustering is “bottom-up”

## Hierarchical Clustering

Each unit is in a clustering at every level.

# Agglomerative Hierarchical Clustering

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1. Merge closest pair (into, say,  $\{a, b\}$ )
2. Update **dist**: delete rows/cols for  $a, b$ ; add row for  $\{a, b\}$  (with max)
3. Merge closest “pair”
4. Update **dist**
5. ...

# Agglomerative Hierarchical Complete Linkage Clusters

	a	b	c	d
a	0	1	2	3
b	1	0	6	7
c	2	6	0	8
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	(a,b)	c	d
(a,b)	0	6	7
c	6	0	8
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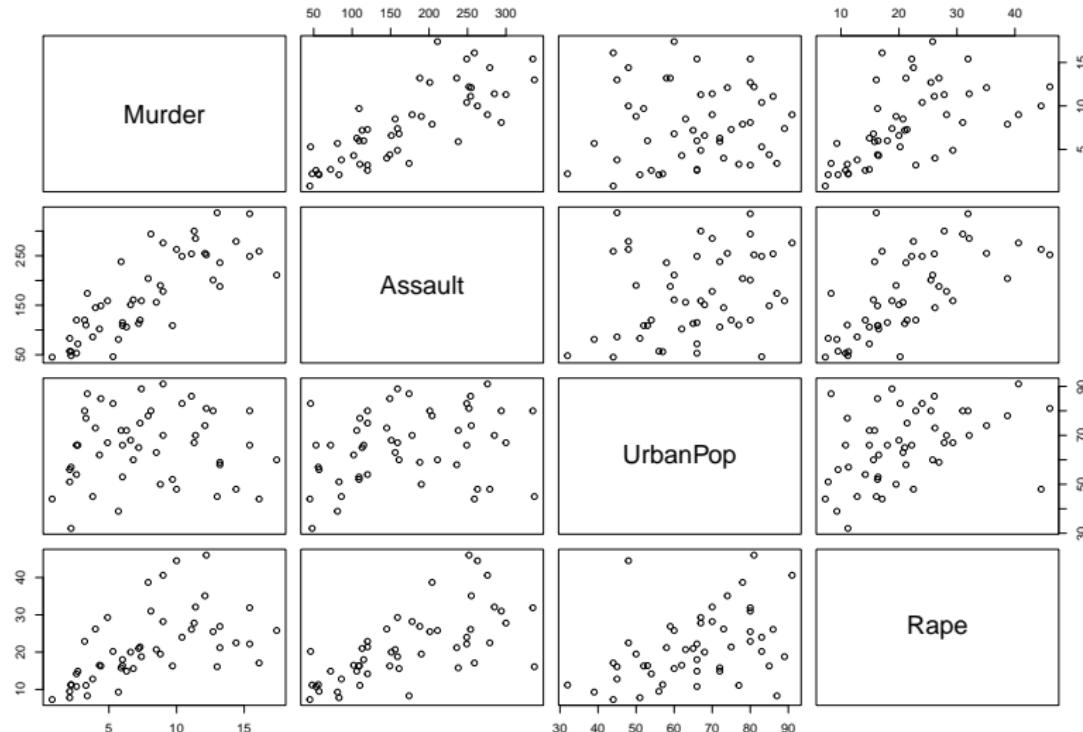
	(a,b)	c	d
(a,b)	0	6	7
c	6	0	8
d	7	8	0

("friends of friends")

# Agglomerative Hierarchical Clustering

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pairs(USArrests)



# Agglomerative Hierarchical Clustering

```
d <- dist(USArrests, method = "euclidean")
d |> round(0)
```

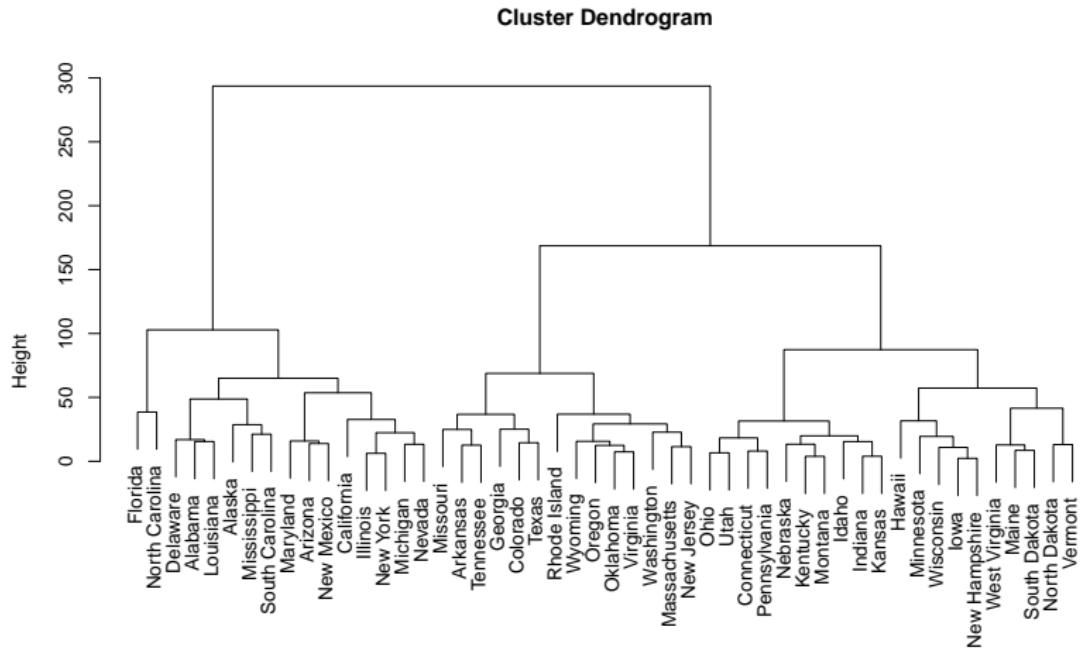
	Alabama	Alaska	Arizona	Arkansas	California	Colorado	Connecticut	Delaware	Florida	Georgia	Hawaii	Idaho	Illinois	Indiana	Iowa	Michigan	Minnesota	Mississippi	Missouri	Nebraska	Nebraska	North Carolina	North Dakota	Oklahoma	Oregon	Pennsylvania	Rhode Island	Tennessee	Texas	Utah	Vermont	Washington	West Virginia	Wisconsin	Wyoming
## Alaska		37																																	
## Arizona			63	47																															
## Arkansas				47	77	109																													
## California					56	45	23	98																											
## Colorado						42	66	90	37																										
## Connecticut						128	159	185	85																										
## Delaware						17	45	59	53																										
## Florida						102	80	42	149																										
## Georgia						26	57	86	26																										
## Hawaii						192	221	248	148																										
## Idaho						117	146	177	71																										
## Illinois						28	43	46	68																										
## Indiana						123	153	182	78																										
## Iowa						181	210	240	135																										

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```
hag <- hclust(d, method = "complete")
plot(hag)
```

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## Recluster w/ Alternative Distance Metric: Mahalanobis

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First, define function to make distance matrix:

```
mahal <- function(q, vc){  
  storage <- matrix(NA, nrow(q), nrow(q))  
  q <- as.matrix(q)  
  for(i in 1:nrow(q)){  
    storage[row(q), i] <- mahalanobis(x = q,  
                                      center=q[i, ],  
                                      cov = vc)  
  }  
  return(sqrt(storage))  
}
```

## Recluster w/ Alternative Distance Metric: Mahalanobis

```
d_mah <- mahal(USArrests, cov(USArrests))  
row.names(d_mah) <- colnames(d_mah) <- row.names(USArrests)  
d_mah <- as.dist(d_mah)  
d_mah |> round(1)
```

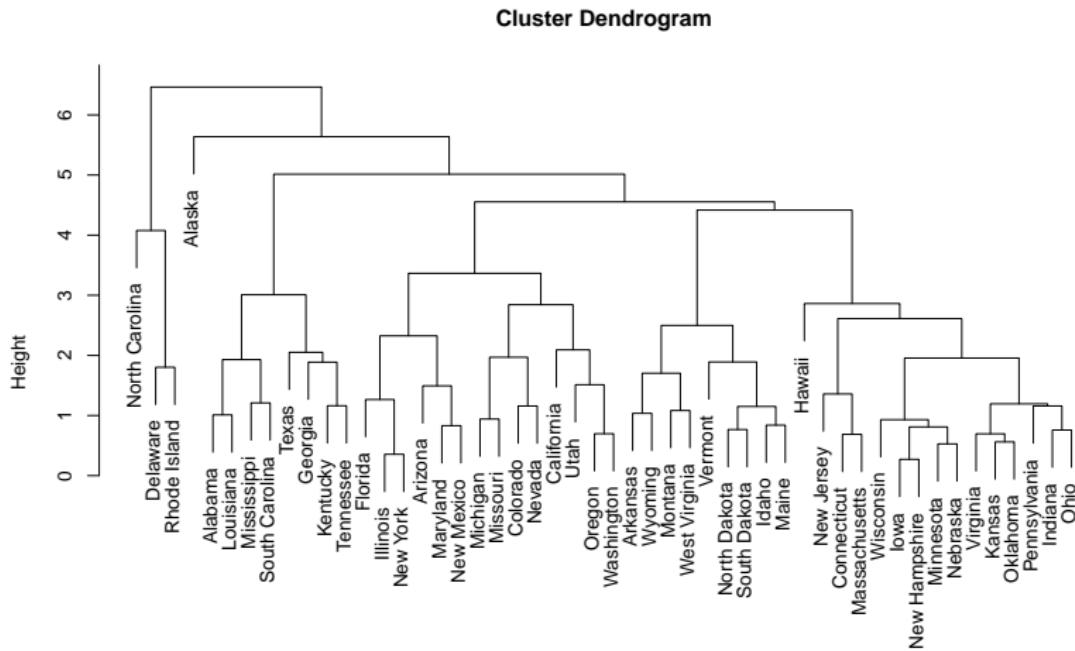
##	Alabama	Alaska	Arizona	Arkansas	California	Colorado	Connecticut	Delaware	Florida	Georgia	Hawaii	Idaho	Illinois	Michigan	Minnesota	Mississippi	Missouri	Nebraska	Nevada	New Hampshire	New Jersey	New Mexico	New York	Pennsylvania	Rhode Island	Tennessee	Utah	Vermont	Washington	West Virginia	Wisconsin	Wyoming
## Alaska		4.4																														
## Arizona			3.2		3.9																											
## Arkansas				1.4		3.5		2.7																								
## California					3.5		3.6		1.7		3.3																					
## Colorado						3.3		2.8		2.6		2.9																				
## Connecticut							2.8		5.4		2.9		2.6																			
## Delaware								3.0		5.0		1.7		2.6																		
## Florida									1.8		4.6		2.3		2.5																	
## Georgia										2.2		5.4		5.0		3.3																
## Hawaii											3.5		5.6		4.5		3.8															
## Idaho												2.7		3.8		2.5		1.5														
## Illinois													2.0		4.9		2.1		2.4													

## Recluster w/ Alternative Distance Metric: Mahalanobis

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hag <- hclust(d_mah, method = "complete")
plot(hag)
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```
##      Murder Assault UrbanPop Rape
## Ohio    7.3     120       75 21.4
## Utah    3.2     120       80 22.9
```

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```

versus

```
##      Murder Assault UrbanPop Rape
## Indiana 7.2      113       65 21.0
## Ohio    7.3      120       75 21.4
```

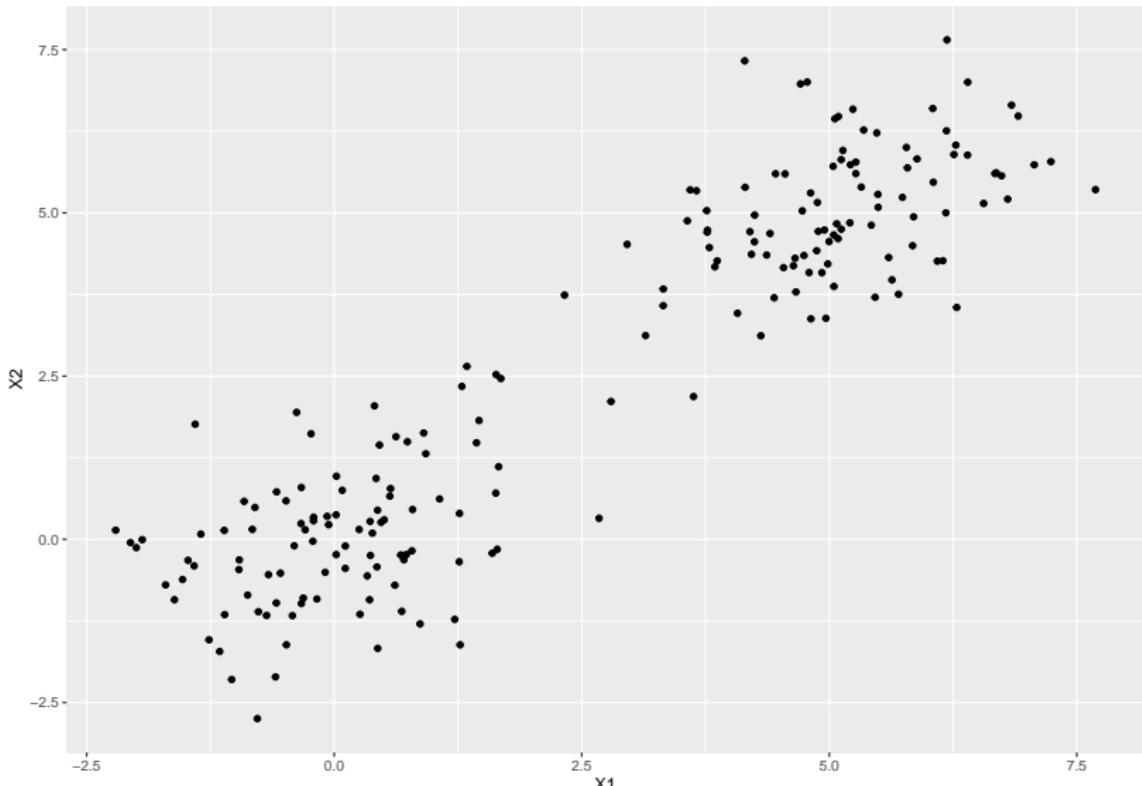
## Partitional Clustering

## *k*-means

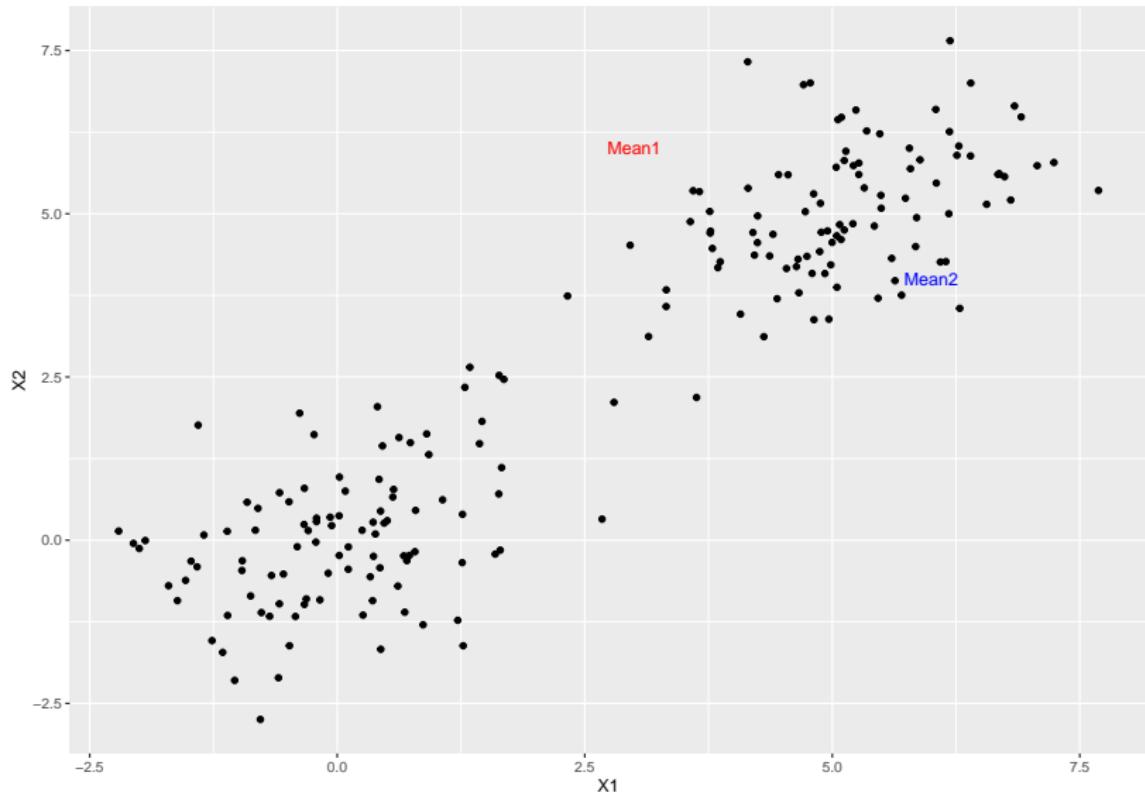
0. Standardize variables, or ensure comparable scales.  
(A diff of 1 unit on  $x_1$  should  $\approx$  a diff of 1 unit on  $x_2$ .)
1. Choose  $k$ , the number of clusters to identify.
2. Select the location of a center for each cluster.
3. Assign each observation to the cluster defined by the center closest to it.
4. Relocate each cluster's center to the mean of the observations currently in that cluster.
5. Repeat 3. and 4. until no observations gets assigned to a new cluster.

Suppose we have a set of points measured in a two-dimensional space, with  $X_1$  and  $X_2$  on comparable scales.

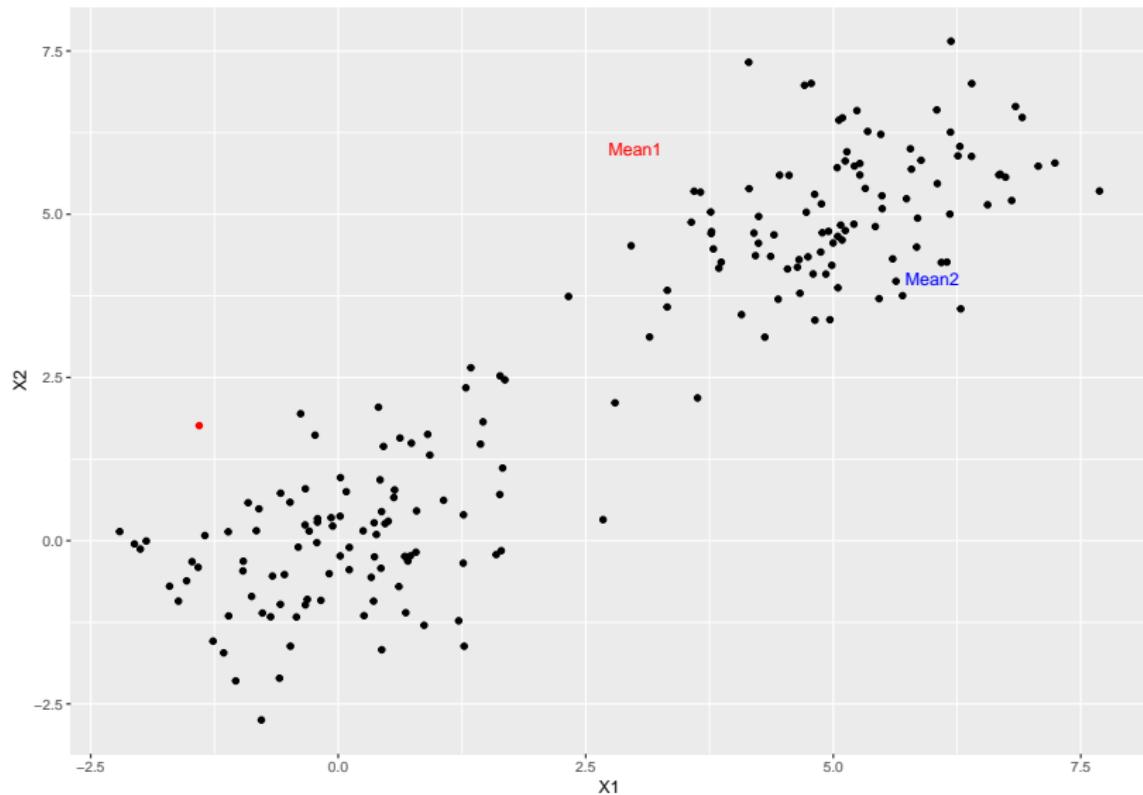
We will find  $k = 2$  clusters. Ideas?



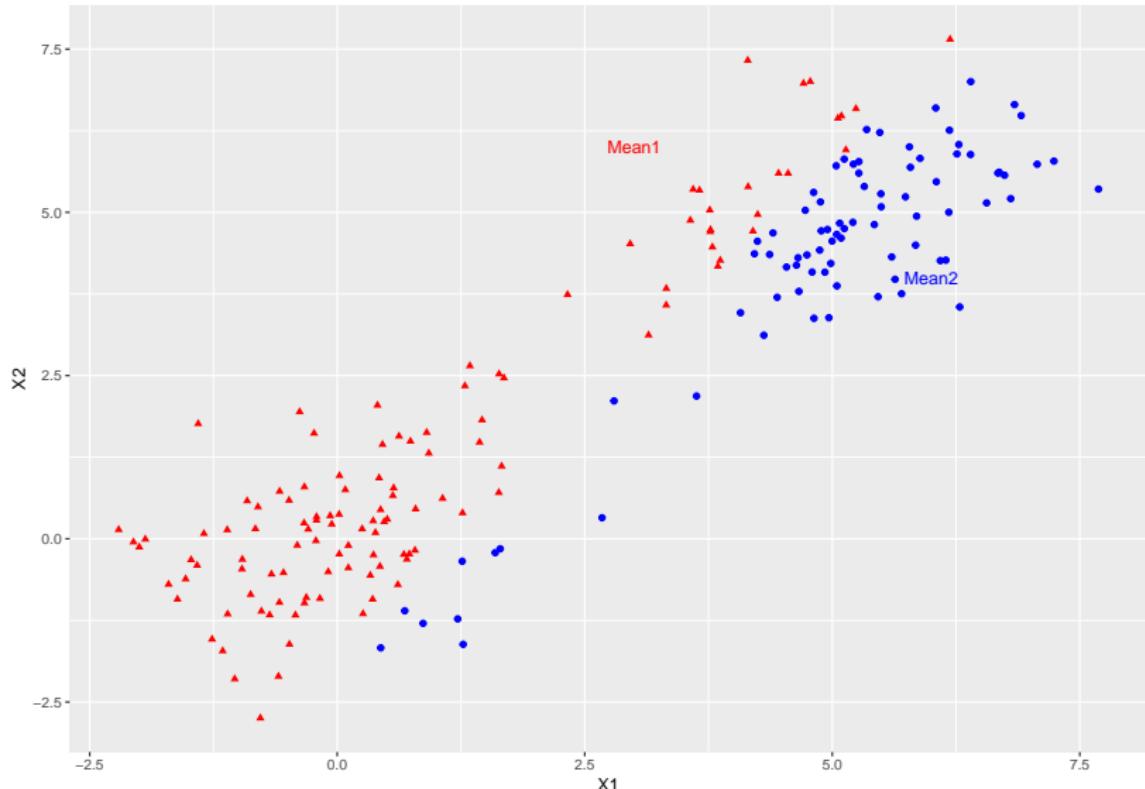
2. Let's randomly select two centroids:



Where “should” this point go?



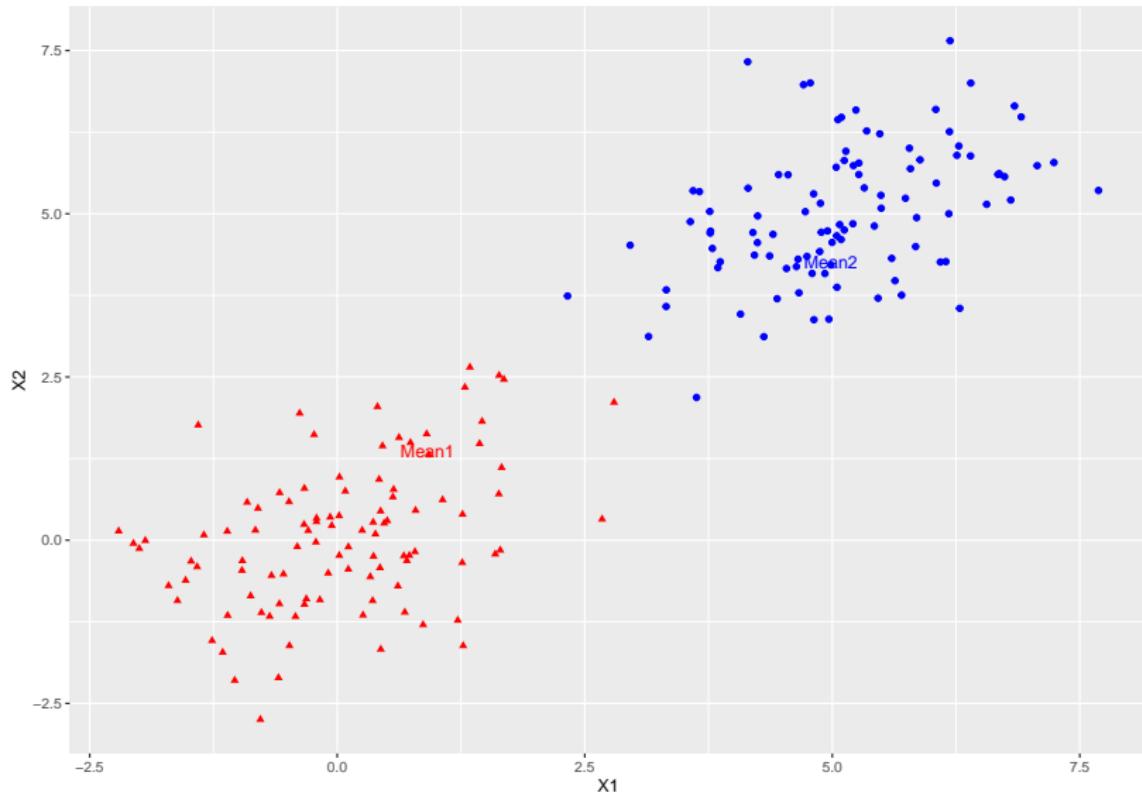
3. Find (Euclidean) distance between each point and the centroids; assign each point to closer centroid:



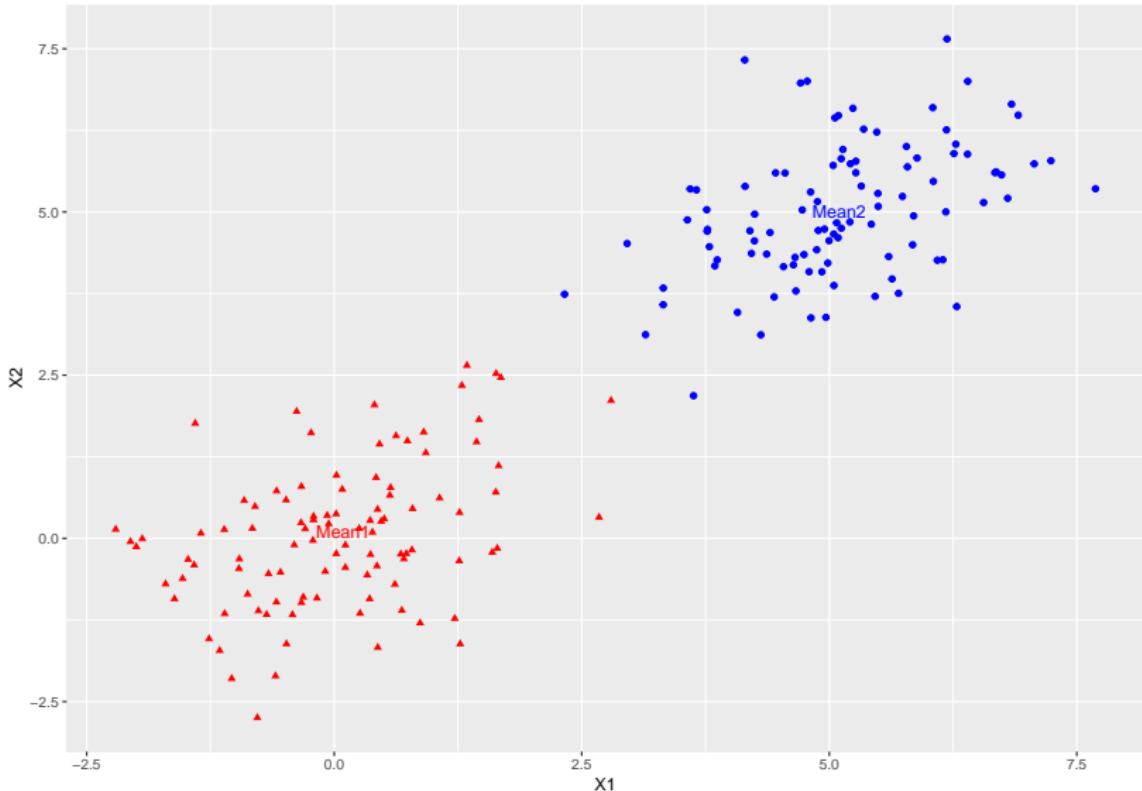
4. Relocate centroids to the mean ( $X_1$ ,  $X_2$ ) value for each cluster:



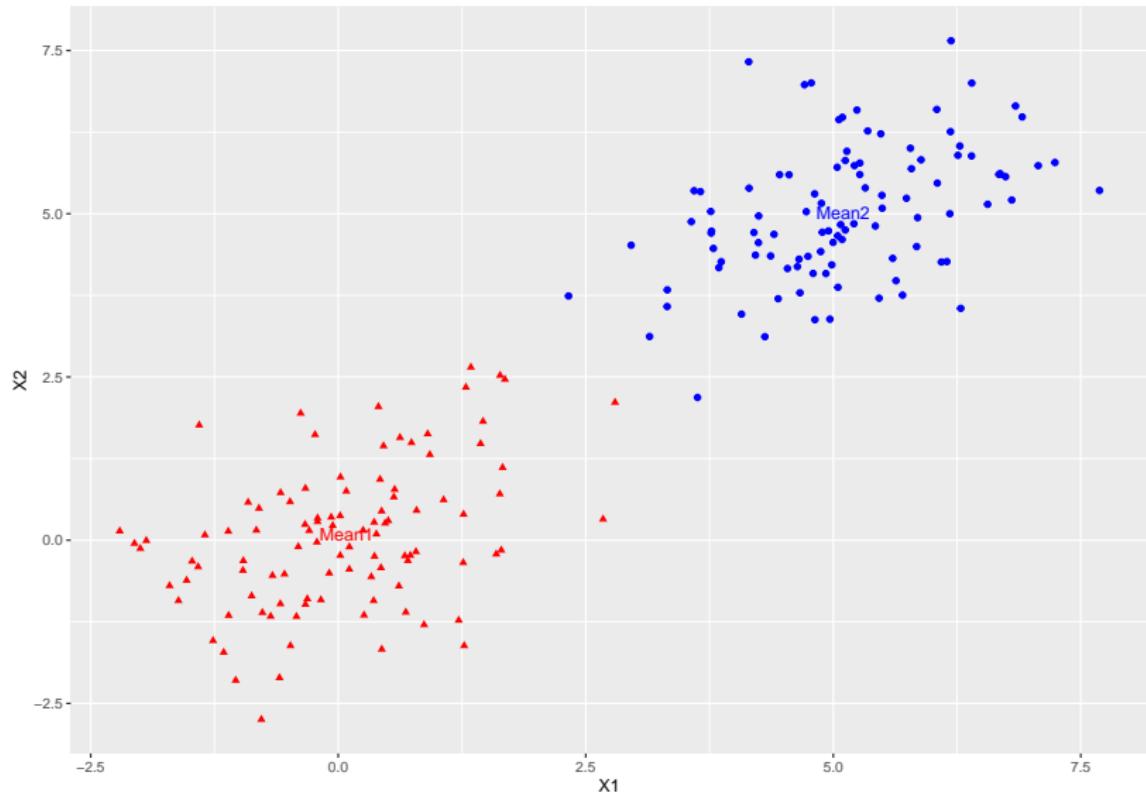
### 3. Reassign each observation to the closer centroid:



#### 4. Recalculate the centroid locations ...

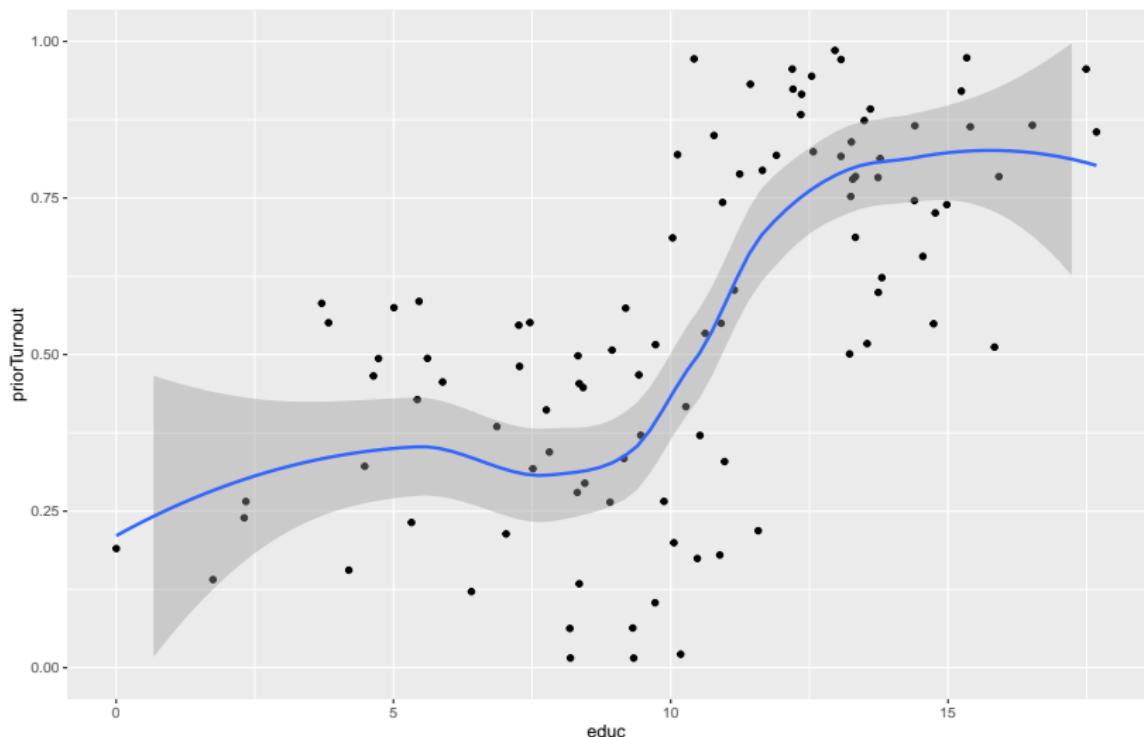


### 3. Reassign points to clusters ...



# Standardization: Why, before clustering?

Suppose we have prior turnout [0, 1] and education (yrs):



```
k2 <- kmeans(df2, centers = 2)
names(k2)

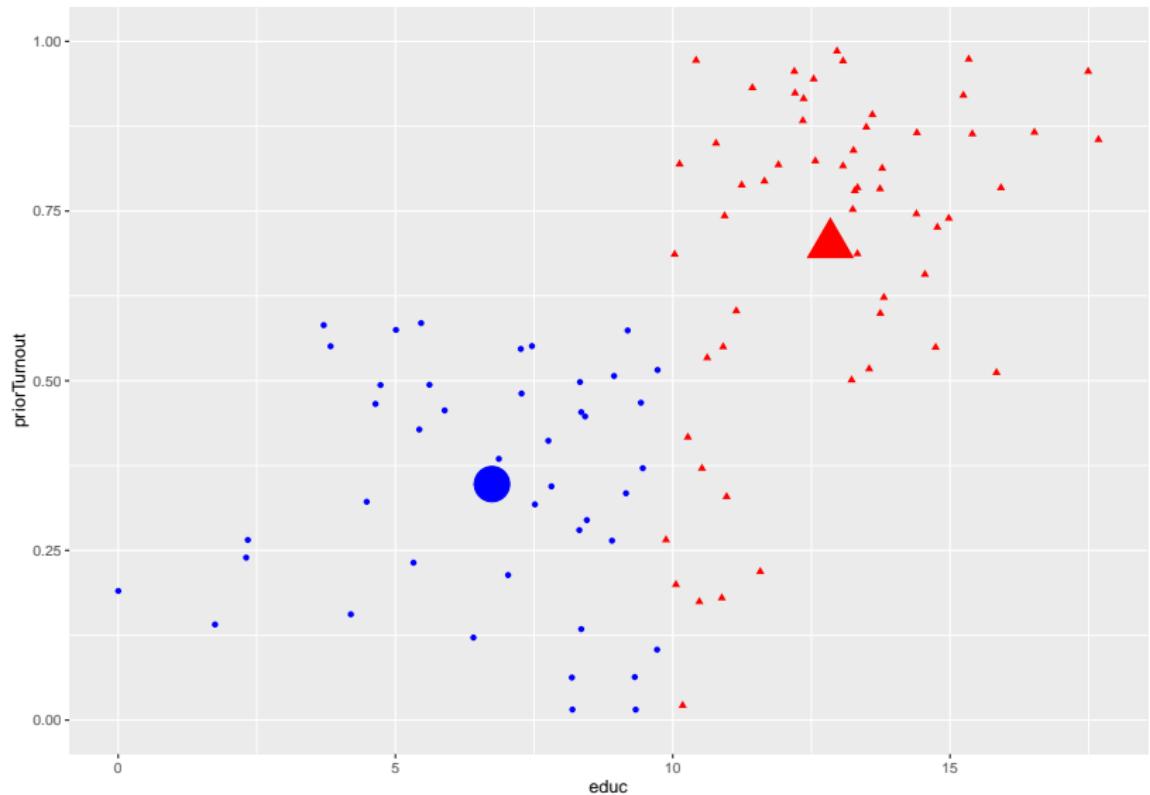
## [1] "cluster"         "centers"        "totss"          "withinss"
## [6] "betweenss"       "size"           "iter"           "ifault"

table(k2$cluster)

## 
## 1 2
## 57 43

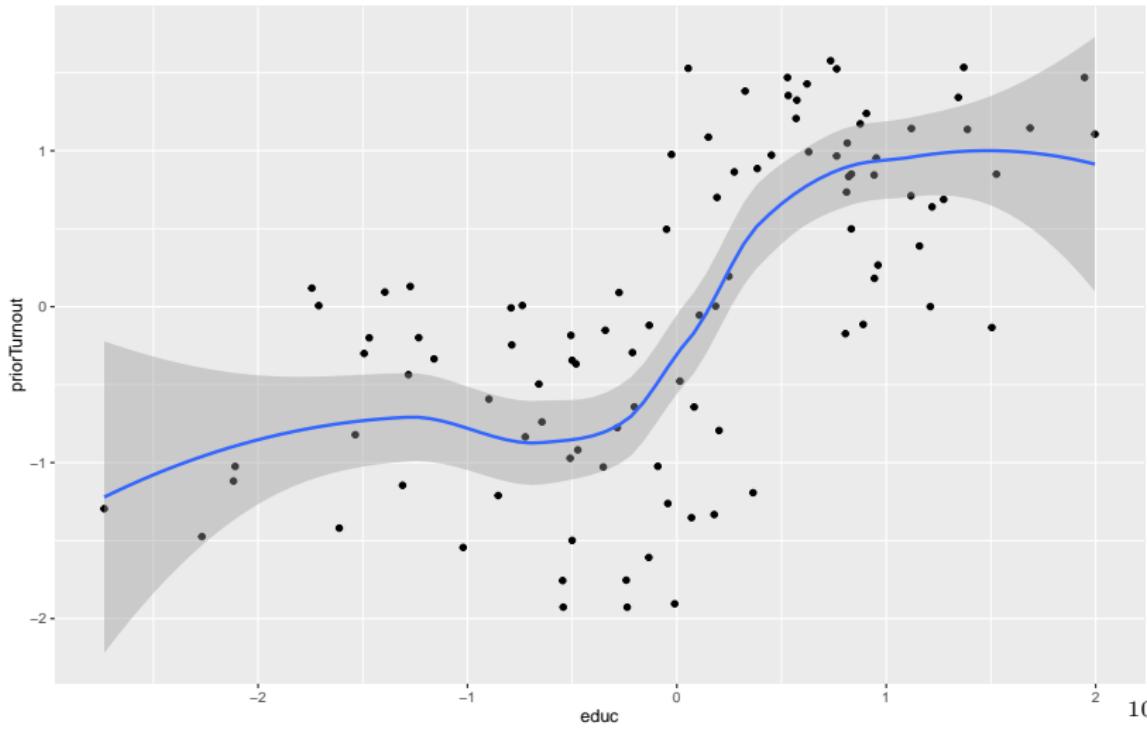
k2$centers

##             educ priorTurnout
## 1 12.841805    0.7007953
## 2 6.740813     0.3477128
```

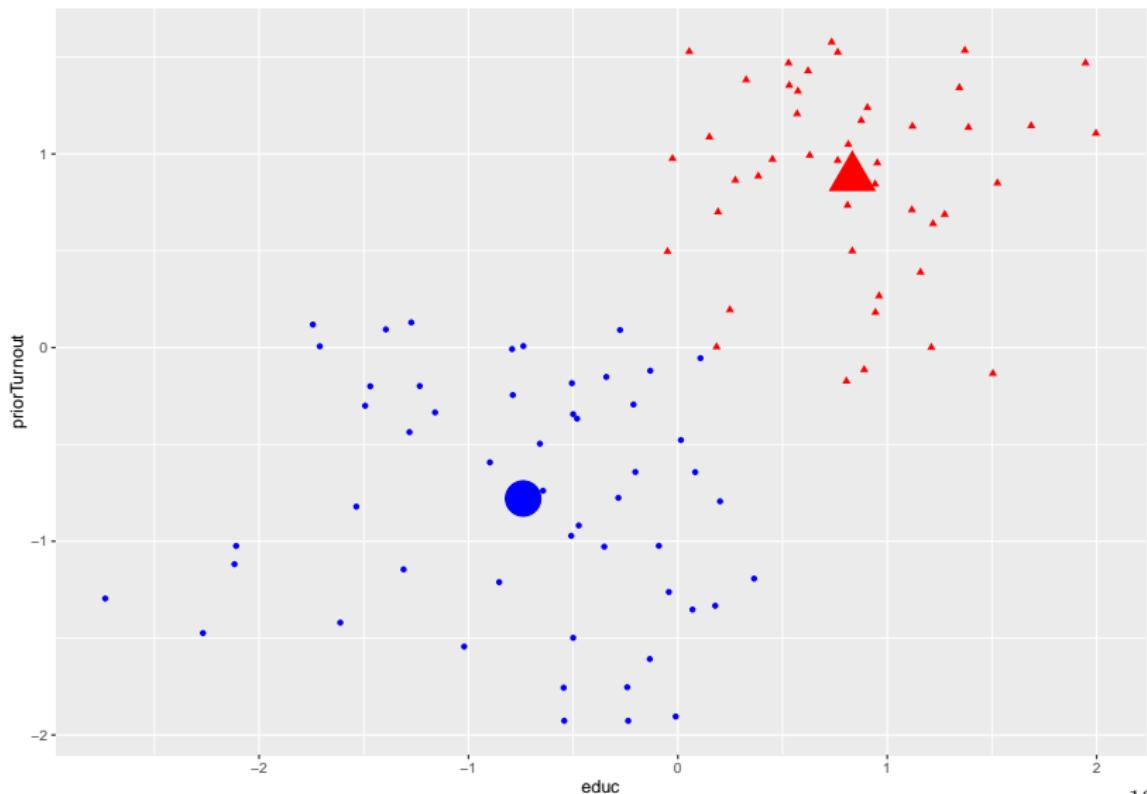


Standardized:

```
df2.standard <- data.frame(scale(df2))  
ggplot(df2.standard, aes(educ, priorTurnout)) +  
  geom_point() + geom_smooth()
```



```
##          educ priorTurnout
## 1 -0.7388515 -0.7791249
## 2  0.8331730  0.8785876
```



Selecting  $k$

## How do we select $k$ ?

Quick quiz:

Given  $y = (4, 2, 5, 9, 10)$ , calculate

$$\sum_{i=3}^4 y_i$$

.

## How do we select $k$ ?

Total within-cluster sum of squares:

$$TSS_{\text{Within}} = \sum_{(\text{Clusters})} \sum_{(\text{Obs in Cluster}_i)} (\text{Dist(Obs to Cluster Mean)})^2$$

## How do we select $k$ ?

Total within-cluster sum of squares:

$$\begin{aligned} TSS_{\text{Within}} &= \sum_{(\text{Clusters})} \sum_{(\text{Obs in Cluster}_i)} (\text{Dist(Obs to Cluster Mean)})^2 \\ &= \sum_{i=1}^k \sum_{x_j \in C_i} (\text{Distance}(x_j \text{ to } \mu_i))^2 \\ &= \sum_{i=1}^k \sum_{x_j \in C_i} \|x_j - \mu_i\|^2 \end{aligned}$$

## How do we select $k$ ?

Total within-cluster sum of squares:

$$\begin{aligned} TSS_{\text{Within}} &= \sum_{(\text{Clusters})} \sum_{(\text{Obs in Cluster}_i)} (\text{Dist(Obs to Cluster Mean)})^2 \\ &= \sum_{i=1}^k \sum_{x_j \in C_i} (\text{Distance}(x_j \text{ to } \mu_i))^2 \\ &= \sum_{i=1}^k \sum_{x_j \in C_i} \|x_j - \mu_i\|^2 \end{aligned}$$

- ▶  $TSS_{\text{Within}}$  should *always* decrease with more clusters

## How do we select $k$ ?

Total within-cluster sum of squares:

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- ▶  $TSS_{\text{Within}}$  should *always* decrease with more clusters
  - ▶ (But what's the point of 200 obs, 200 clusters?)

## How do we select $k$ ?

Total within-cluster sum of squares:

$$\begin{aligned} TSS_{\text{Within}} &= \sum_{(\text{Clusters})} \sum_{(\text{Obs in Cluster}_i)} (\text{Dist(Obs to Cluster Mean)})^2 \\ &= \sum_{i=1}^k \sum_{x_j \in C_i} (\text{Distance}(x_j \text{ to } \mu_i))^2 \\ &= \sum_{i=1}^k \sum_{x_j \in C_i} \|x_j - \mu_i\|^2 \end{aligned}$$

- ▶  $TSS_{\text{Within}}$  should *always* decrease with more clusters
  - ▶ (But what's the point of 200 obs, 200 clusters?)
- ▶ Select  $k$  s.t. additional cluster yields  $\downarrow\downarrow\downarrow$  in  $TSS_{\text{Within}}$

## How do we select $k$ ?

```
max_k <- 10 # maximum number clusters to test
tot_within_ss <- vector("numeric", length = max_k - 1)

for(idx_k in 2:max_k){

  k_out <- kmeans(df2.standard, centers = idx_k)
  tot_within_ss[idx_k - 1] <- k_out$tot.withinss

}
```

## How do we select $k$ ?

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max_k <- 10 # maximum number clusters to test
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  tot_within_ss[idx_k - 1] <- k_out$tot.withinss

}
```

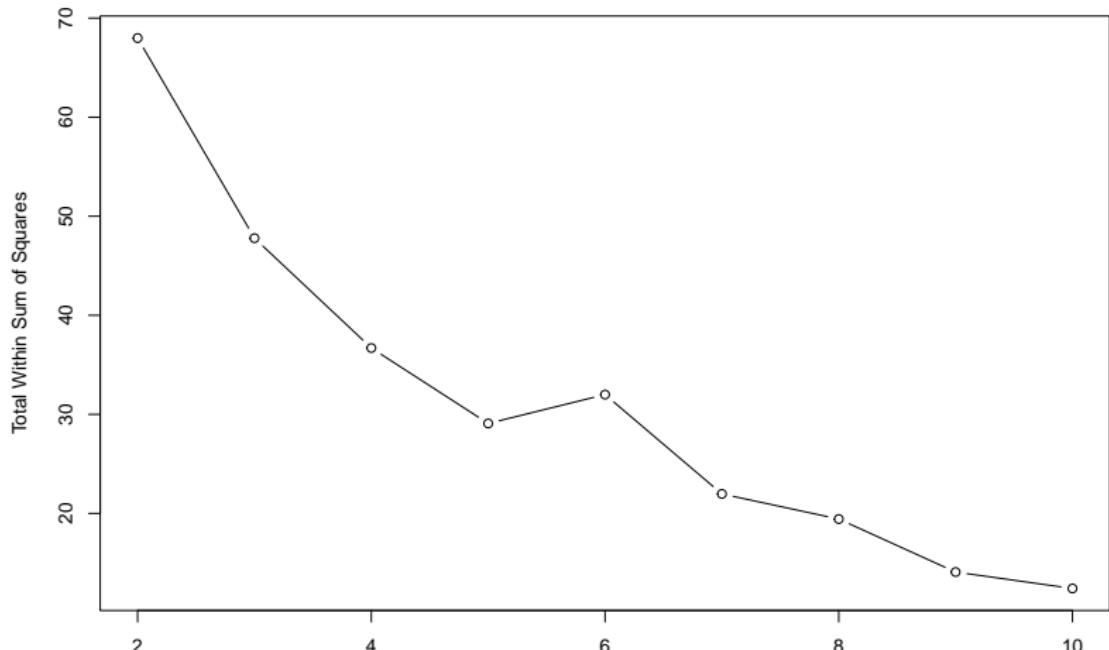
Output:

```
tot_within_ss |> round(1)
```

```
## [1] 68.0 47.8 36.7 29.1 32.0 22.0 19.4 14.1 12.4
```

# A Scree Plot

```
plot(2:max_k, tot_within_ss, xlab = "Number of Clusters, k",  
      ylab = "Total Within Sum of Squares", type = "b")
```



## How do we select $k$ ?

```
max_k <- 10 # maximum clusters to test
tot_within_ss <- vector("numeric", length = max_k - 1)

for(idx_k in 2:max_k){

  k_out <- kmeans(df2.standard,
                  centers = idx_k,
                  nstart = 10)

  tot_within_ss[idx_k - 1] <- k_out$tot.withinss
}
```

## How do we select $k$ ?

```
max_k <- 10 # maximum clusters to test
tot_within_ss <- vector("numeric", length = max_k - 1)

for(idx_k in 2:max_k){

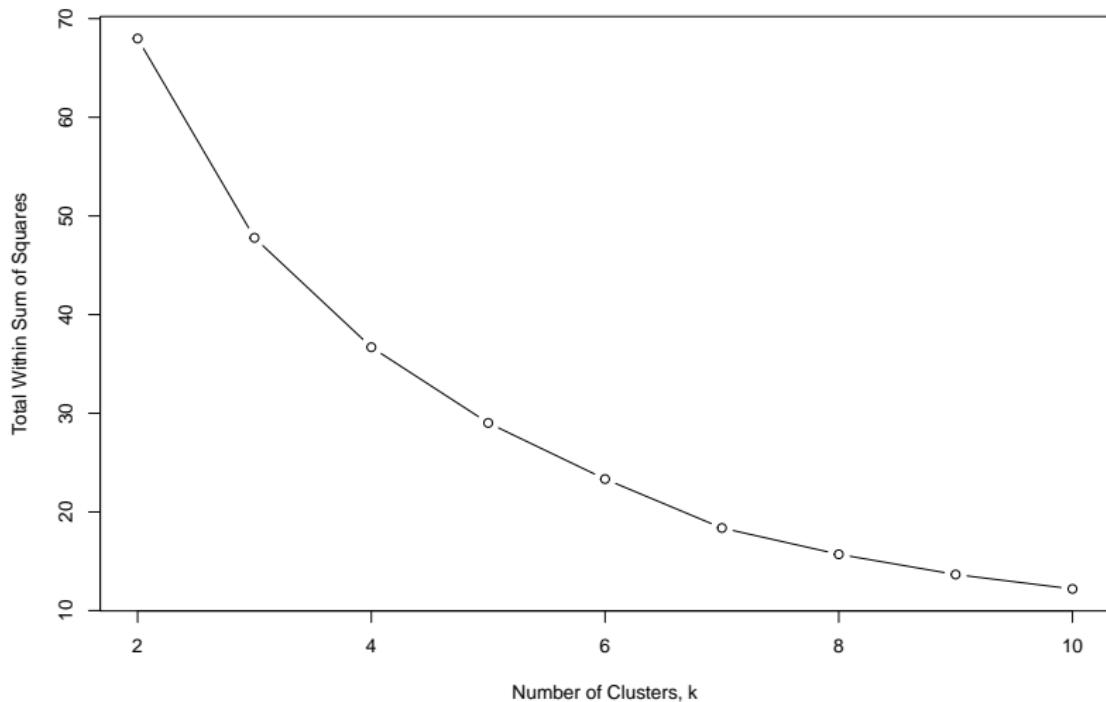
  k_out <- kmeans(df2.standard,
                  centers = idx_k,
                  nstart = 10)

  tot_within_ss[idx_k - 1] <- k_out$tot.withinss
}

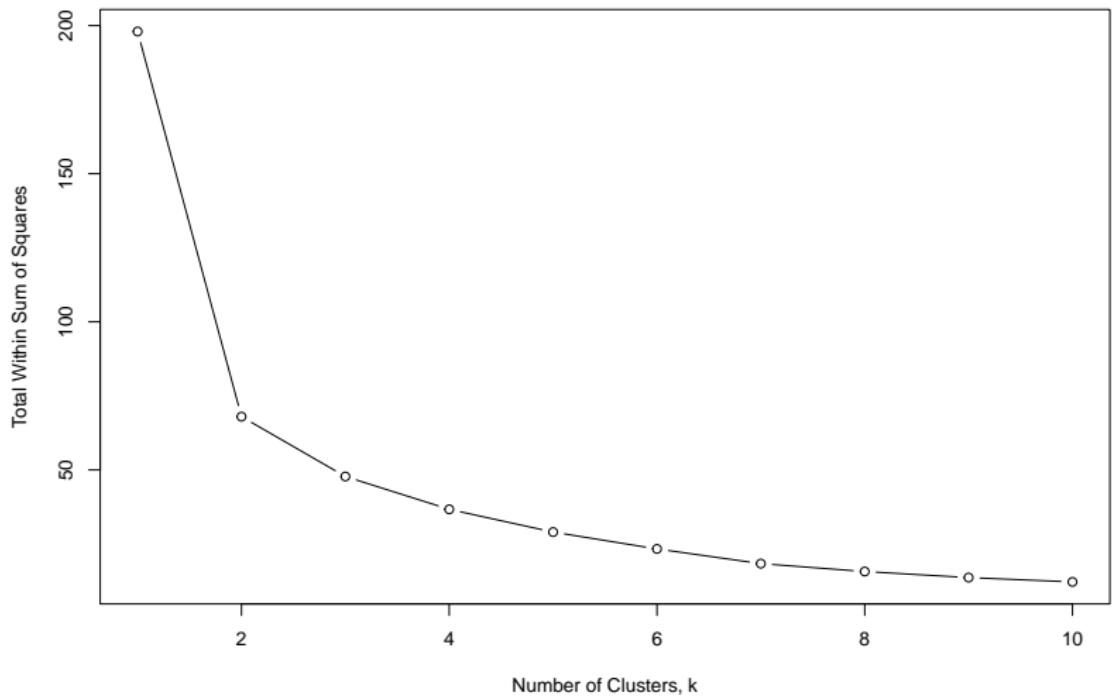
tot_within_ss |> round(1)

## [1] 68.0 47.8 36.7 29.0 23.3 18.4 15.7 13.7 12.2
```

# A Better Scree Plot



# An Even Better Scree Plot



# Other applications: Geolocations

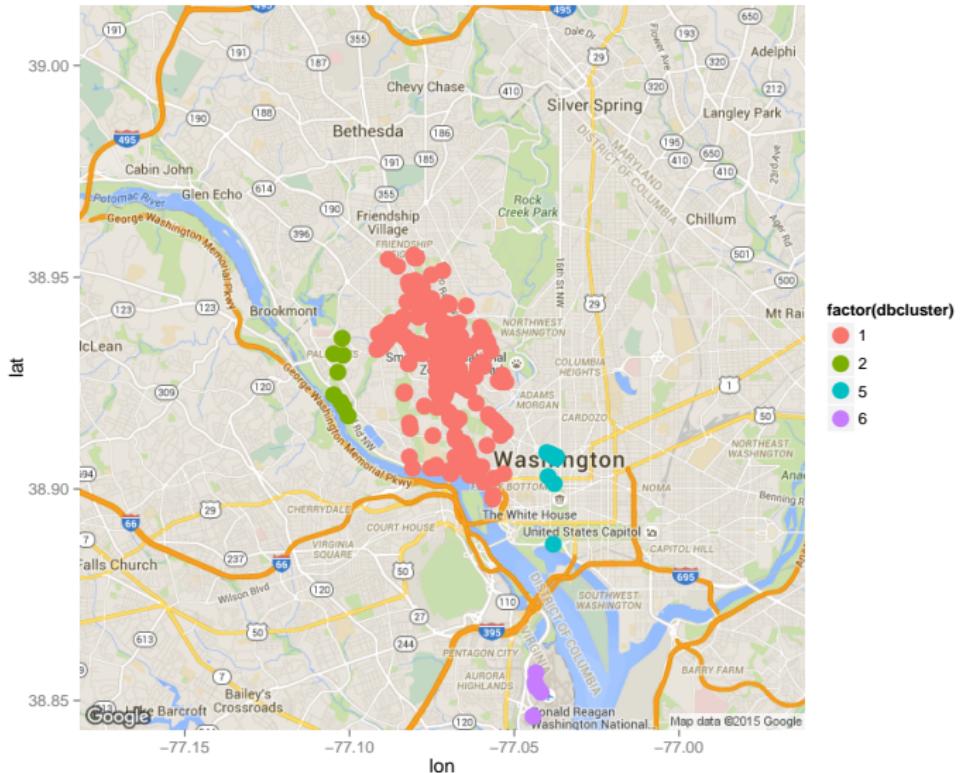


Figure 1: Clusters of Geolocations

## Other applications: Regimes

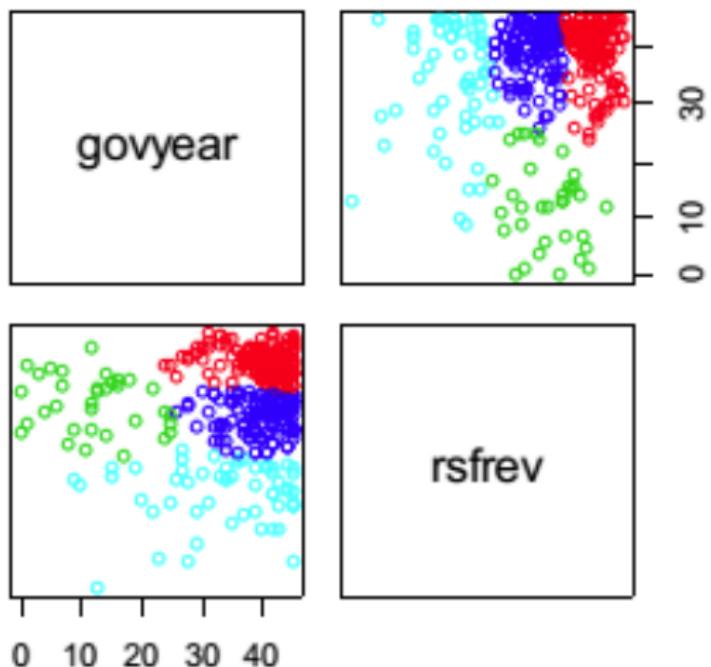


Figure 2: Comparative Regime Types

## Other applications: Senate Speeches

## Other applications: Senate Speeches

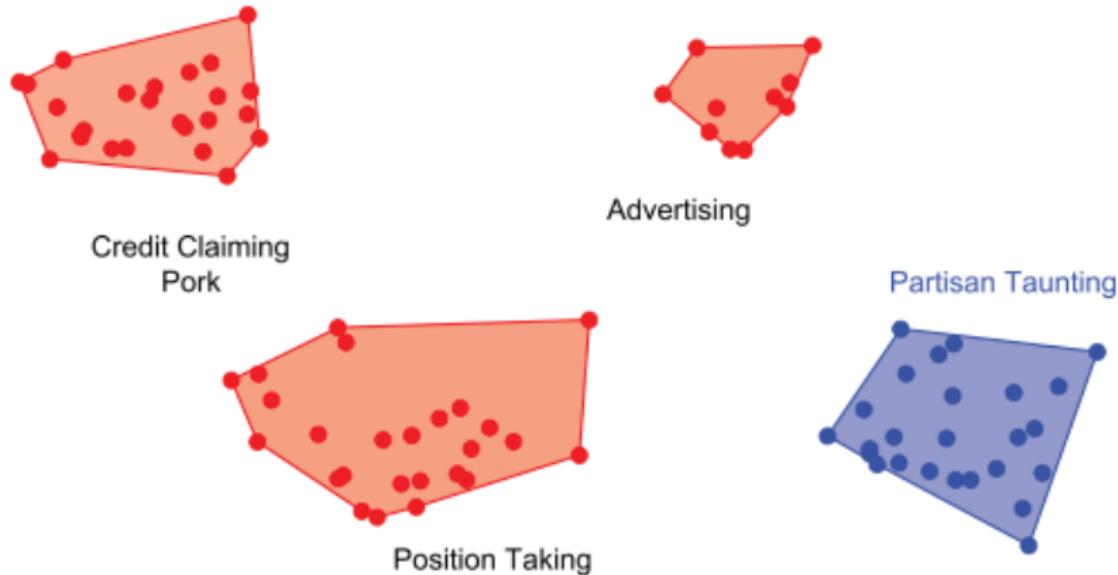


Figure 3: Senate Speeches

# DBSCAN (1996)

Density-based clustering

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1. Find each point's neighbors

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Density-based clustering

1. Find each point's neighbors
2. ID *core* points with enough neighbors

# DBSCAN (1996)

Density-based clustering

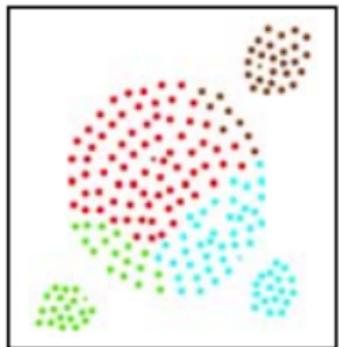
1. Find each point's neighbors
2. ID *core* points with enough neighbors
3. Connect nearby core points

## DBSCAN (1996)

Density-based clustering

1. Find each point's neighbors
2. ID *core* points with enough neighbors
3. Connect nearby core points
4. Assign non-core points to near clusters (or noise)

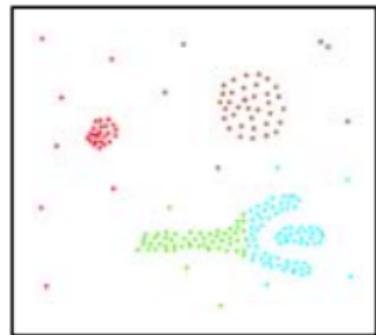
Other applications:



**database 1**



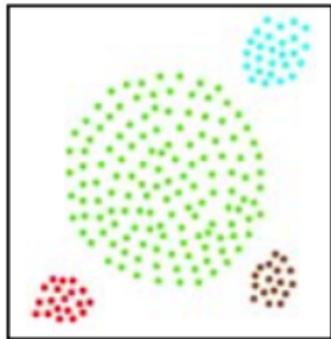
**database 2**



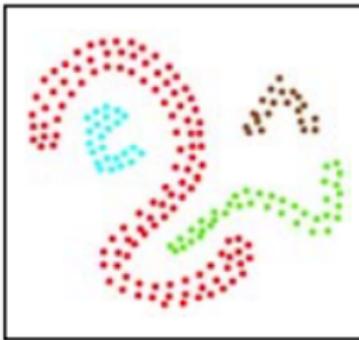
**database 3**

Figure 4: CLARANS: Not Great!

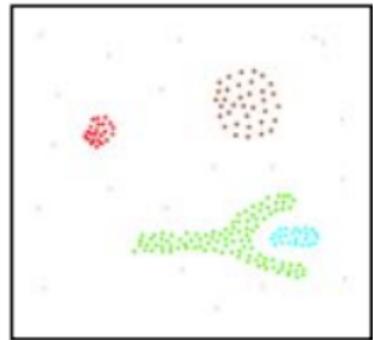
Other applications:



**database 1**



**database 2**



**database 3**

Figure 5: DBSCAN: Great!

## Congress Clusters

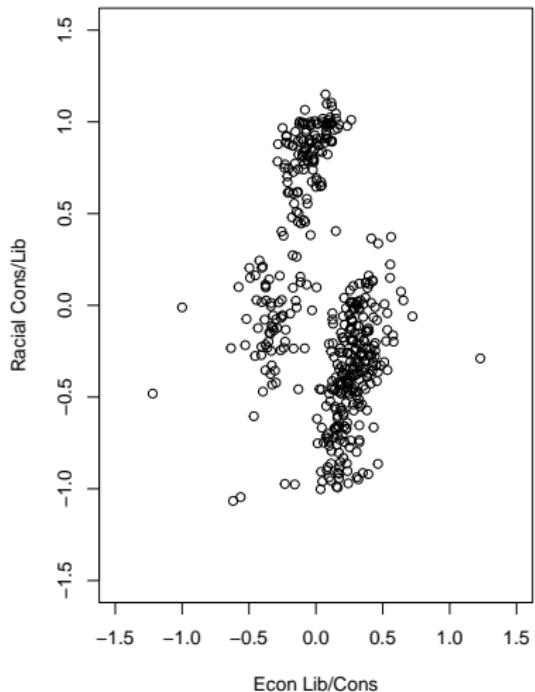
```
congress.url <- "https://tinyurl.com/2kcf3p9r"
congress <- read_csv(congress.url)
dwnom80 <- cbind(congress$dwnom1[congress$congress == 80],
                   congress$dwnom2[congress$congress == 80])
dwnom112 <- cbind(congress$dwnom1[congress$congress == 112],
                   congress$dwnom2[congress$congress == 112])

k80two.out <- kmeans(dwnom80, centers = 2)
k112two.out <- kmeans(dwnom112, centers = 2)

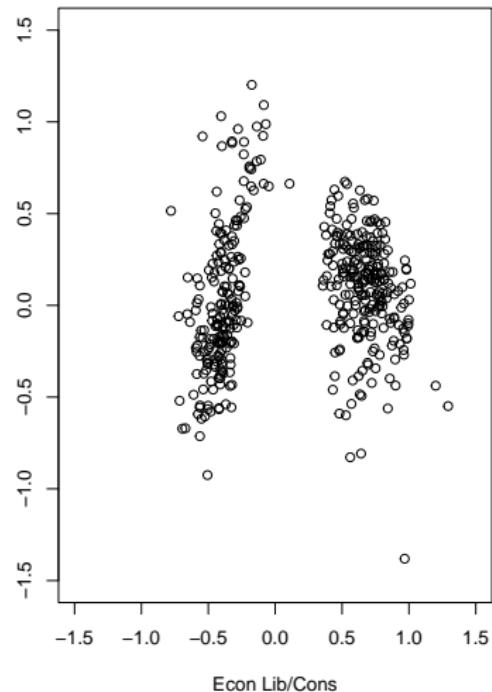
k80four.out <- kmeans(dwnom80, centers = 4)
k112four.out <- kmeans(dwnom112, centers = 4)

lim <- c(-1.5, 1.5)
xlab <- "Econ Lib/Cons"
ylab <- "Racial Cons/Lib"
```

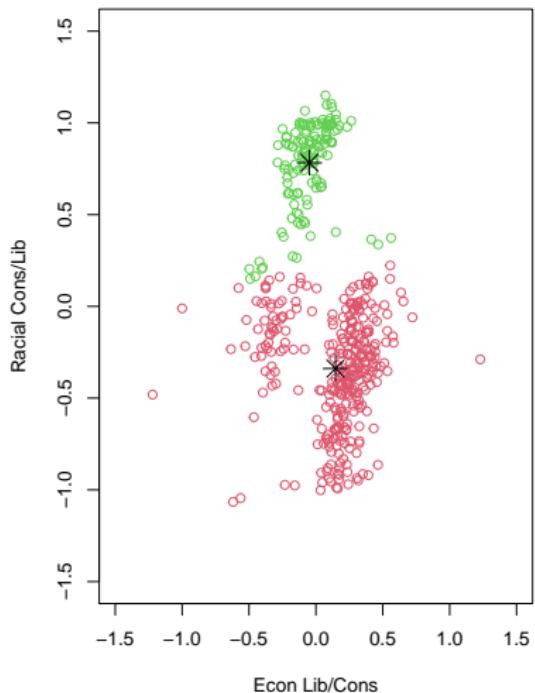
**80th Congress**



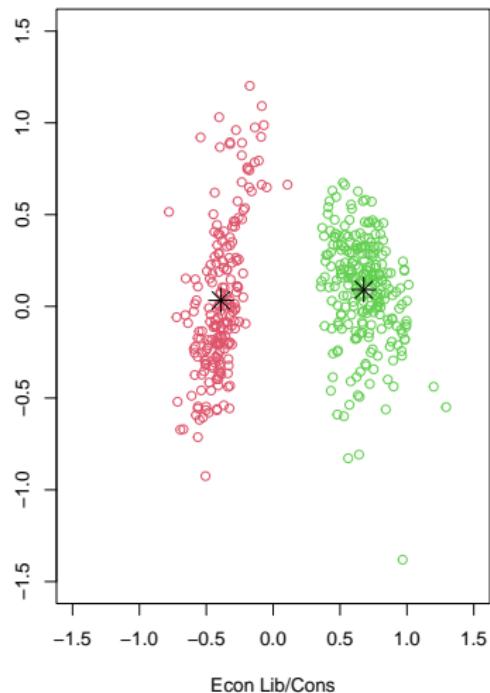
**112th Congress**



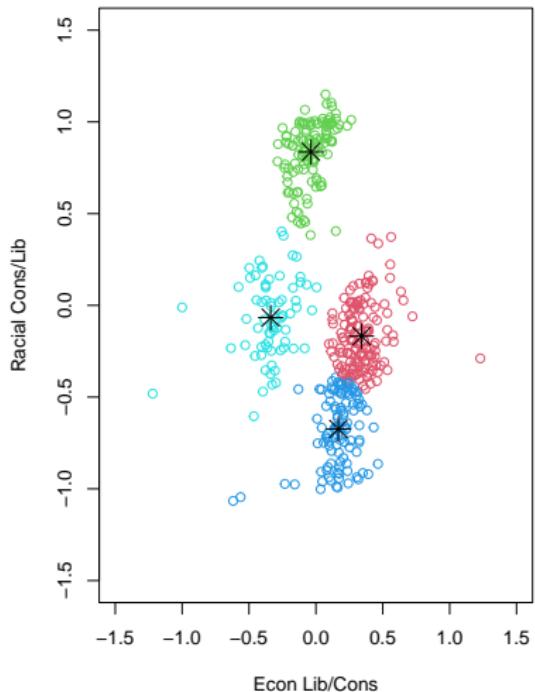
**80th Congress**



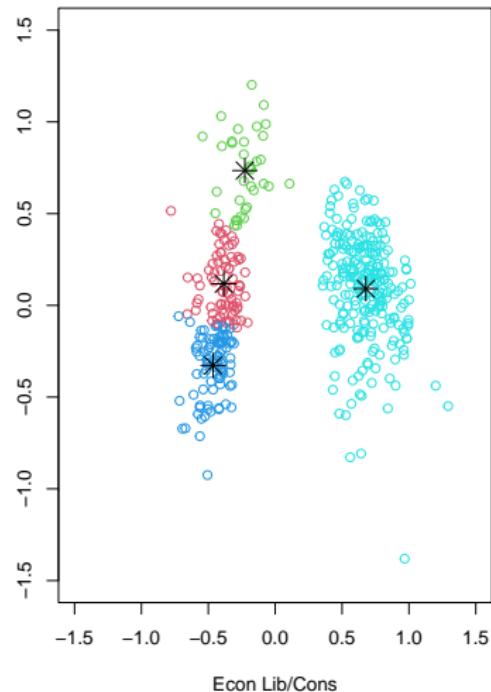
**112th Congress**



**80th Congress**



**112th Congress**



## Exercise

## Exercise

1. Checkout CRAN Task View for Clustering:

<https://cran.r-project.org/web/views/Cluster.html>

2. Discover clusters in your final project data!

(Use 2 predictors to visualise; more predictors to discover higher-dim clusters.)