### Cluster Analysis: Discovery Winter Institute in Data Science

Ryan T. Moore

2024 - 01 - 10

Supervised and Unsupervised Learning

Hierarchical Clustering

Partitional Clustering

Selecting k

Exercise

▶ matrix: rectangular array with a few more restrictions than data.frame

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- ▶ list: more general type of array that can be rectangular, but need not be. A data.frame is an example of a list

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In base R, can extract variable v1 from data frame df with

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- ► df\$v1
- df[["v1"]]

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- ▶ df[[6]]

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- ▶ df[[6]] (if v1 is 6th variable)
- ▶ df[, "v1"]
- ▶ df[, 6]
- ▶ df["v1"] (keeps col name)

1. Describe list 11 created below:

```
v1 <- 1:8
v2 <- letters[1:5]
m <- matrix(1:9, 3, 3)
l1 <- list(x = v1, y = v2, z = m)
```

- 2. What is 11\$y?
- 3. What is 11[[1]]?
- 4. What is 11[[3]][2, 2]?

# Distance Matrix for Clustering

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

	a	b	С	d
a	0	1	2	3
b	1	0	6	7
$\mathbf{c}$	2	6	0	8
d	3	7	8	0

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So, 
$$||(c,d)|| > ||(a,b)||$$
, e.g.,  $(8 > 1)$ 

Supervised and Unsupervised Learning

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Supervised: Modeling with **known** outcomes

## 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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- ▶ NLP (derive topics from documents)
- ► Clustering algorithms (most)

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  - ▶ no "home"/"work"/"leisure" labels

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- ► Partitional clustering
  - ► Find splits in full set
  - ▶ Units in only one cluster

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

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Divisive clustering

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Divisive clustering is "top-down"

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

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Agglomerative clustering

▶ Start at  $\{a\}$ ,  $\{b\}$ ,  $\{c\}$ ,  $\{d\}$ ,  $\{e\}$ 

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Agglomerative clustering is "bottom-up"

Each unit is in a clustering at every level.

# Agglomerative Hierarchical Clustering

Complete linkage clustering: greedily create clusters

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# Agglomerative Hierarchical Clustering

#### Complete linkage clustering: greedily create clusters

- 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	$\mathbf{c}$	d
a	0	1	2	3
b	1	0	6	7
$\mathbf{c}$	2	6	0	8
d	3	7	8	0

### Agglomerative Hierarchical Complete Linkage Clusters

a	0	1	2	3
1				0
b	1	0	6	7
$\mathbf{c}$	2	6	0	8
d	3	7	8	0

	(a,b)	c	d
(a,b)	0	6	7
$\mathbf{c}$	6	0	8
d	7	8	0

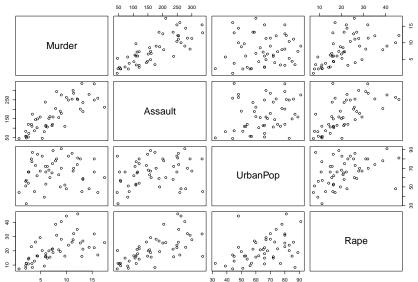
### Agglomerative Hierarchical Complete Linkage Clusters

a 0	1	_	
$a$ $\sigma$	1	2	3
b 1	0	6	7
c 2	6	0	8
d 3	7	8	0

	(a,b)	c	d
(a,b)	0	6	7
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("friends of friends")

pairs(USArrests)



## Delaware

## Florida

## Georgia ## Hawaii

## Illinois

## Indiana

## Idaho

## Iowa

##		Alabama	Alaska	Arizona	Arkansas	Californ
##	Alaska	37				
##	Arizona	63	47			
##	Arkansas	47	77	109		
##	California	56	45	23	98	

## HINAHSAS	41	1.1	103		
## California	56	45	23	98	
## Colorado	42	66	90	37	

## California	56	45	23	98	
## Colorado	42	66	90	37	
## Connecticut	128	150	185	25	

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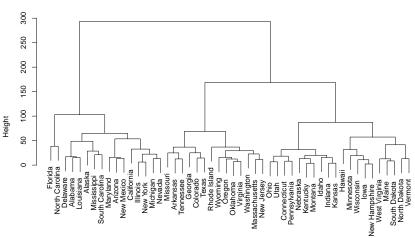
d > round(0)

d <- dist(USArrests, method = "euclidean")</pre>

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

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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))</pre> row.names(d\_mah) <- colnames(d\_mah) <- row.names(USArrests) d mah <- as.dist(d mah)</pre>

d mah |> round(1)

## Delaware

## Florida

## Georgia

## Illinois

## Hawaii ## Idaho

-	•		` '							
##				Alabam	a	Alaska	Arizona	Arkansas	Cali	forn
##	Alas	ka		4.	4					
				_	_					

ππ		ATaballa	нтарка	AI IZUIIa	ALValleas	Calliuli
## Alask	αa	4.4				
## Arizo	ona	3.2	3.9			
## Arkan	ısas	1.4	3.5	2.7		
## Calif	fornia	3.5	3.6	1.7	3.3	
## Color	rado	3.3	2.8	2.6	2 9	1

##	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	1
##	Connecticut	2.8	5.4	2.9	2.6	3

2.2 5.4

3.5 5.6

5.0

3.8

4.9

4.6 2.3

1.7

5.0

4.5

2.5

2.1

2.6

2.5

3.3

3.8

1.5

2.4

3

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##	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	

3.0 1.8

2.7

2.0

ππ	ATADAMA	итариа	ALIZUIIA	AI Nalibab	Callion
## Alaska	4.4				
## Arizona	3.2	3.9			
## Arkansas	1.4	3.5	2.7		
## California	a 3.5	3.6	1.7	3.3	

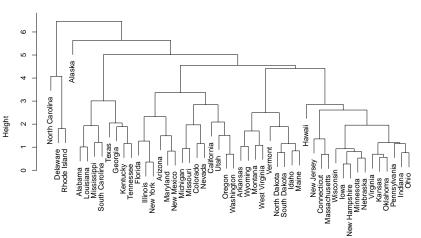
### Recluster w/ Alternative Distance Metric: Mahalanobis

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#### Cluster Dendrogram



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- ► E.g., euclidean clusters

##		Murder	Assault	UrbanPop	Rape
##	Ohio	7.3	120	75	21.4
##	Utah	3.2	120	80	22.9

- ➤ Small differences in Assault get over-weighted if euclidean dist
- ► (Assault has large variance, and cor w/ UrbanPop)
- ► Mahalanobis dist allows vars on different scales to all contribute.
- ► E.g., euclidean clusters

```
## Murder Assault UrbanPop Rape
## Ohio 7.3 120 75 21.4
## Utah 3.2 120 80 22.9
```

#### versus

##		Murder	${\tt Assault}$	UrbanPop	Rape
##	Indiana	7.2	113	65	21.0
##	Ohio	7.3	120	75	21.4

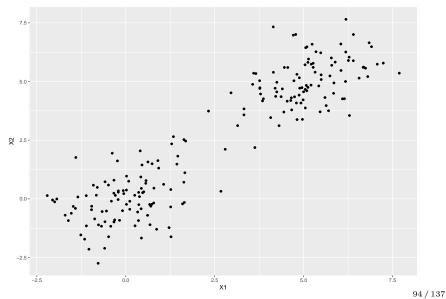
#### Partitional Clustering

#### k-means

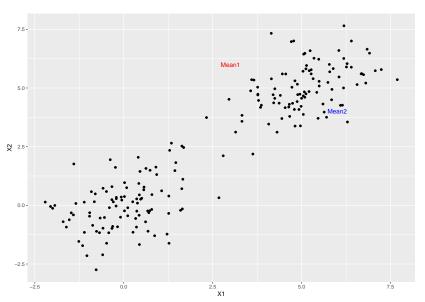
- 0. Standardize variables, or ensure comparable scales. A difference of 1 unit on x should be comparable to a difference of 1 unit on y.
- 1. Choose k, the number of clusters to identify.
- 2. Select the location of a center for each cluster.
- 3. Assign each observation to the cluster defined by the 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  $\mathtt{X1}$  and  $\mathtt{X2}$  on comparable scales.

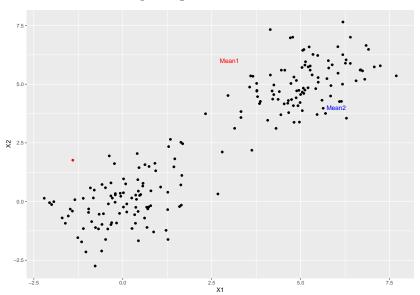
We will find k = 2 clusters. Ideas?



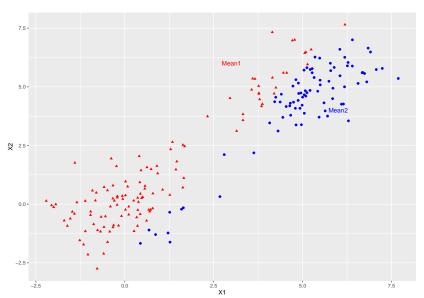
#### 2. Let's randomly select two centroids:



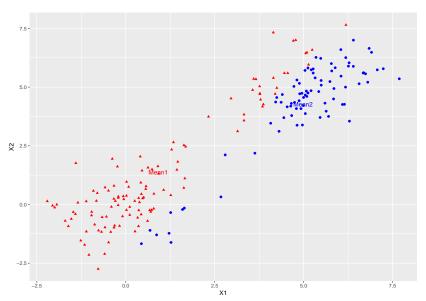
#### Where "should" this point go?



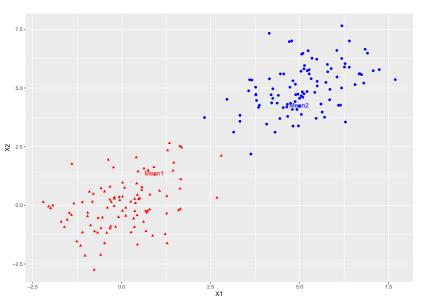
3. Find (Euclidean) distance between each point and the centroids; assign each point to closer centroid:



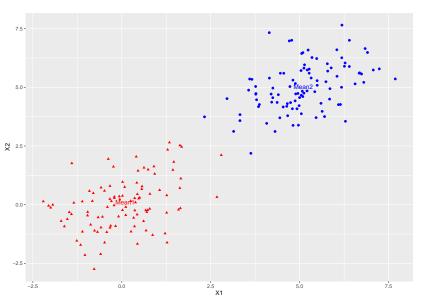
# 4. Relocate centroids to the mean $(\mathtt{X1},\,\mathtt{X2})$ value for each cluster:



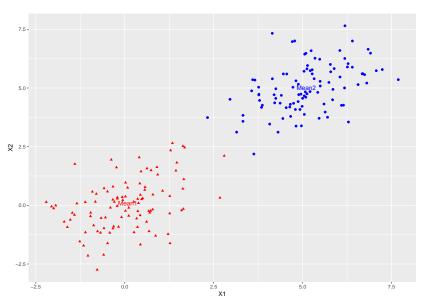
#### 3. Reassign each observation to the closer centroid:



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

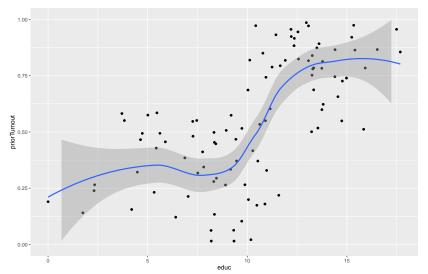


#### 3. Reassign points to clusters ...



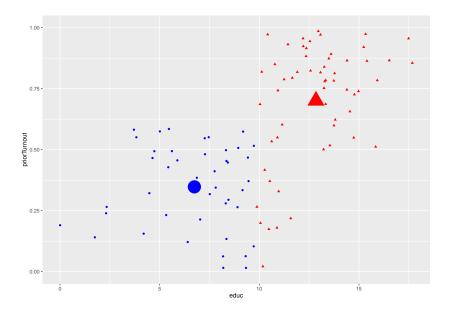
#### Standardization: Why, before clustering?

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



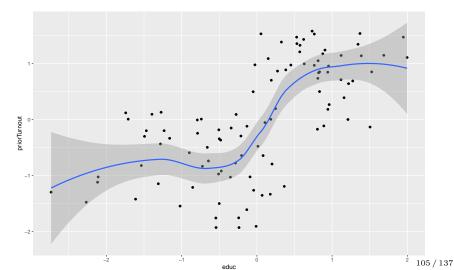
```
k2 <- kmeans(df2, centers = 2)
names(k2)
## [1] "cluster"
                    "centers"
                                  "totss"
                                                  "within
## [6] "betweenss" "size"
                                  "iter"
                                                  "ifault
table(k2$cluster)
##
## 1 2
## 57 43
k2$centers
```

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

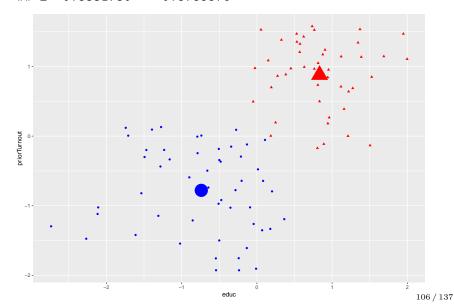


#### Standardized:

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



## 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

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

•

Total within-cluster sum of squares:

$$TSS_{\text{Within}} = \sum_{\text{(Clusters) (Obs in Cluster}_i)} \sum_{\text{(Distance (Obs - Cluster Mean))}}$$

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$$= \sum_{i=1}^k \sum_{x_j \in C_i} (\text{Distance}(x_j - \mu_i))^2$$

$$= \sum_{i=1}^k \sum_{x_j \in C_i} ||x_j - \mu_i||^2$$

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- $ightharpoonup TSS_{Within}$  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  $TSS_{Within}$

```
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</pre>
```

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max_k <- 10 # maximum number clusters to test
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   k_out <- kmeans(df2.standard, centers = idx_k)
   tot_within_ss[idx_k - 1] <- k_out$tot.withinss
}</pre>
```

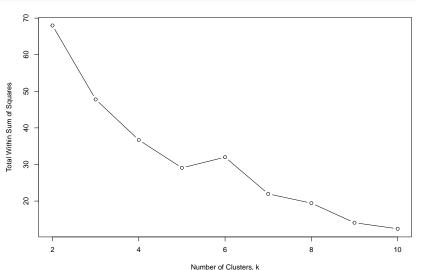
### Output:

```
tot_within_ss
```

```
## [1] 67.98793 47.78783 36.69742 29.07892 31.99645 21
## [9] 12.42197
```

### A Scree Plot

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



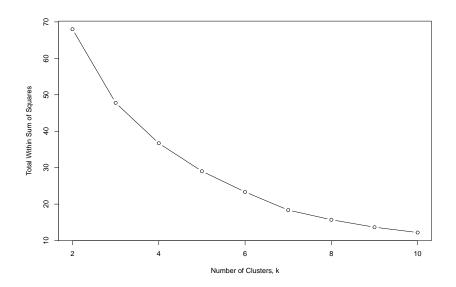
```
max k <- 10 # maximum clusters to test
tot within ss <- vector("numeric", length = max k - 1)
for(idx k in 2:max k){
 k out <- kmeans(df2.standard,
                  centers = idx k,
                  nstart = 10
 tot within ss[idx k - 1] <- k out$tot.withinss
```

tot within ss

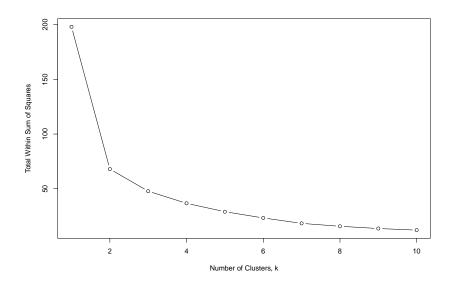
```
max k <- 10 # maximum clusters to test
tot within ss <- vector("numeric", length = max k - 1)
for(idx k in 2:max k){
 k out <- kmeans(df2.standard,
                  centers = idx k,
                  nstart = 10
 tot within ss[idx k - 1] <- k out$tot.withinss
```

```
## [1] 67.98793 47.78783 36.69742 29.02215 23.33501 18
## [9] 12.19779
```

## A Better Scree Plot



### An Even Better Scree Plot



# Other applications: Geolocations

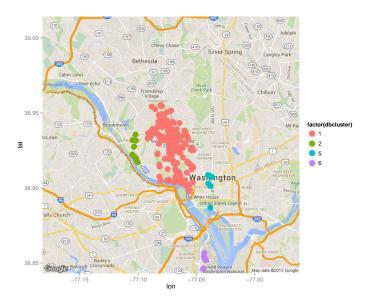


Figure 1: Clusters of Geolocations

## Other applications: Regimes

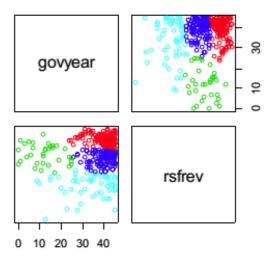


Figure 2: Comparative Regime Types

# Other applications: Senate Speeches

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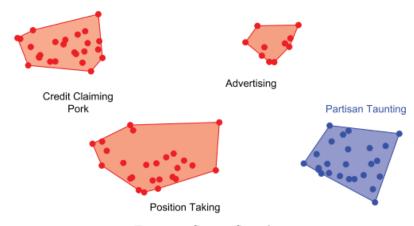


Figure 3: Senate Speeches

Density-based clustering

1. Find each point's neighbors

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- 2. ID *core* points with enough neighbors

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- 2. ID *core* points with enough neighbors
- 3. Connect nearby core points
- 4. Assign non-core points to near clusters (or noise)

#### Other applications:

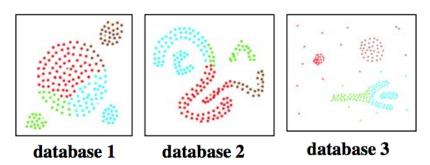


Figure 4: CLARANS: Not Great!

#### Other applications:

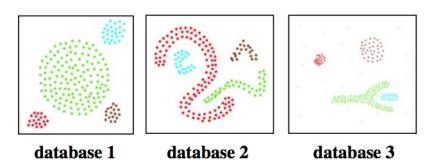
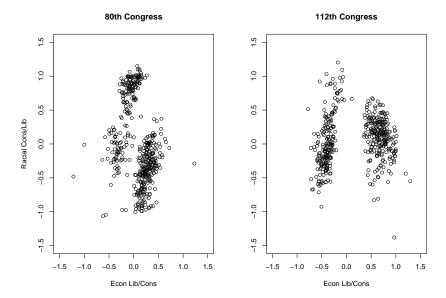
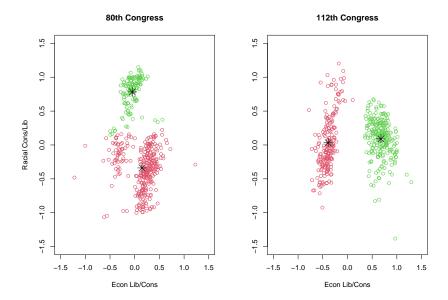


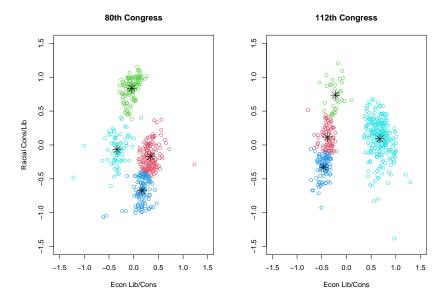
Figure 5: DBSCAN: Great!

### Congress Clusters

```
congress.url <- "http://j.mp/302nedz"
congress <- read_csv(congress.url)</pre>
dwnom80 <- cbind(congress$dwnom1[congress$congress == 80],</pre>
                  congress$dwnom2[congress$congress == 80])
dwnom112 <- cbind(congress$dwnom1[congress$congress == 112]</pre>
                   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"</pre>
ylab <- "Racial Cons/Lib"</pre>
```







## 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.)