

Cluster Analysis

Cluster Analysis

- One side-effect of discriminant analysis: could draw picture of data (if 1st 2s LDs told most of story) and see which individuals “close” to each other.
- Discriminant analysis requires knowledge of groups.
- Without knowledge of groups, use *cluster analysis*: see which individuals close together, which groups suggested by data.
- Idea: see how individuals group into “clusters” of nearby individuals.
- Base on “dissimilarities” between individuals.
- Or base on standard deviations and correlations between variables (assesses dissimilarity behind scenes).

Packages

```
library(MASS) # for lda later  
library(tidyverse)  
library(spatstat) # for crossdist later  
library(ggrepel)
```

One to ten in 11 languages

	English	Norwegian	Danish	Dutch	German
1	one	en	en	een	eins
2	two	to	to	twee	zwei
3	three	tre	tre	drie	drei
4	four	fire	fire	vier	vier
5	five	fem	fem	vijf	funf
6	six	seks	seks	zes	sechs
7	seven	sju	syv	zeven	sieben
8	eight	atte	otte	acht	acht
9	nine	ni	ni	negen	neun
10	ten	ti	ti	tien	zehn

One to ten

	French	Spanish	Italian	Polish	Hungarian	Finnish
1	un	uno	uno	jeden	egy	yksi
2	deux	dos	due	dwa	ketto	kaksi
3	trois	tres	tre	trzy	harom	kolme
4	quatre	cuatro	quattro	cztery	negy	nelja
5	cinq	cinco	cinque	piec	ot	viisi
6	six	seis	sei	szesc	hat	kuusi
7	sept	siete	sette	siedem	het	seitseman
8	huit	ocho	otto	osiem	nyolc	kahdeksan
9	neuf	nueve	nove	dziewiec	kilenc	yhdeksan
10	dix	diez	dieci	dziesiec	tiz	kymmenen

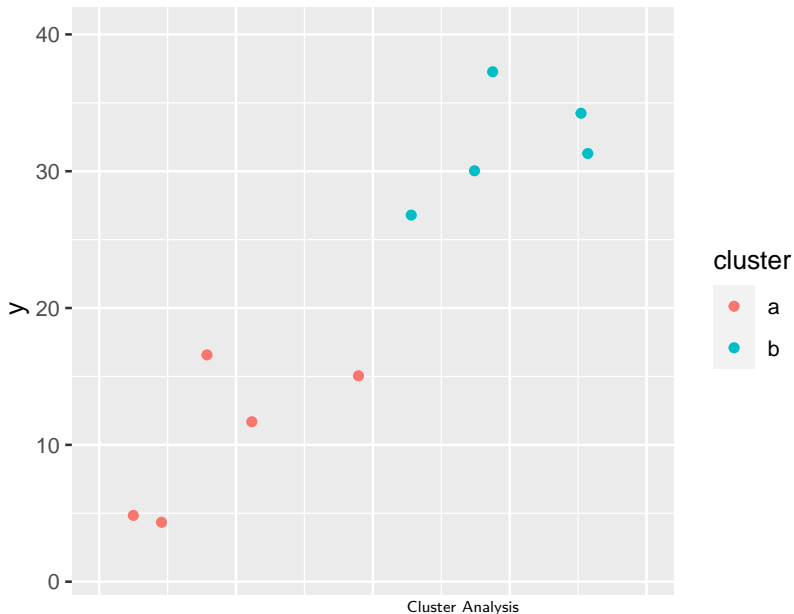
Dissimilarities and languages example

- Can define dissimilarities how you like (whatever makes sense in application).
- Sometimes defining “similarity” makes more sense; can turn this into dissimilarity by subtracting from some maximum.
- Example: numbers 1–10 in various European languages. Define similarity between two languages by counting how often the same number has a name starting with the same letter (and dissimilarity by how often number has names starting with different letter).
- Crude (doesn't even look at most of the words), but see how effective.

Two kinds of cluster analysis

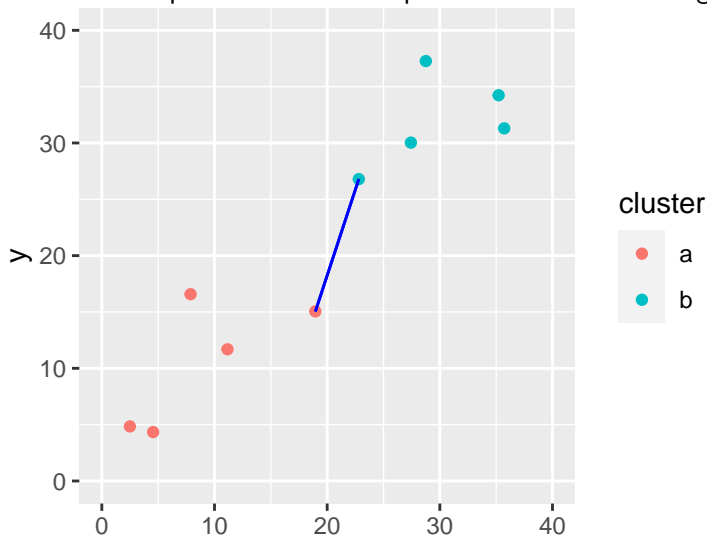
- Looking at process of forming clusters (of similar languages): **hierarchical cluster analysis** (`hclust`).
- Start with each individual in cluster by itself.
- Join “closest” clusters one by one until all individuals in one cluster.
- How to define closeness of two *clusters*? Not obvious, investigate in a moment.
- Know how many clusters: which division into that many clusters is “best” for individuals? **K-means clustering** (`kmeans`).

Two made-up clusters



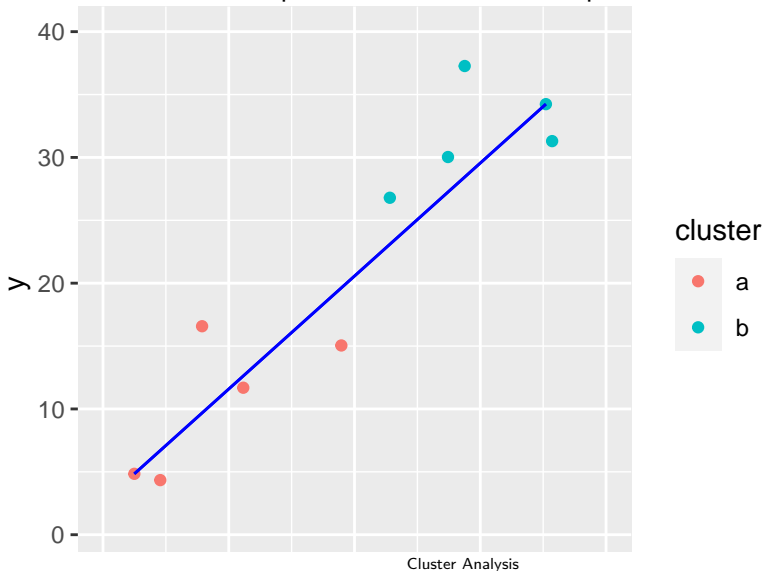
Single-linkage distance

Find the red point and the blue point that are closest together:



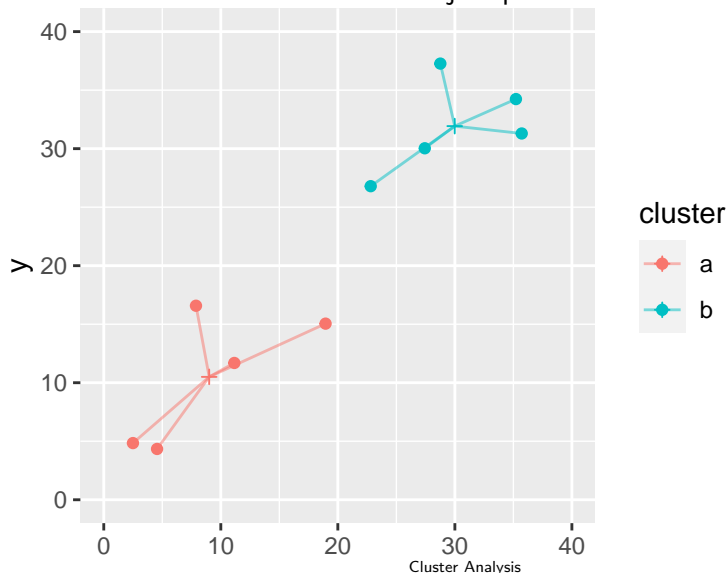
Complete linkage

Find the red and blue points that are farthest apart:



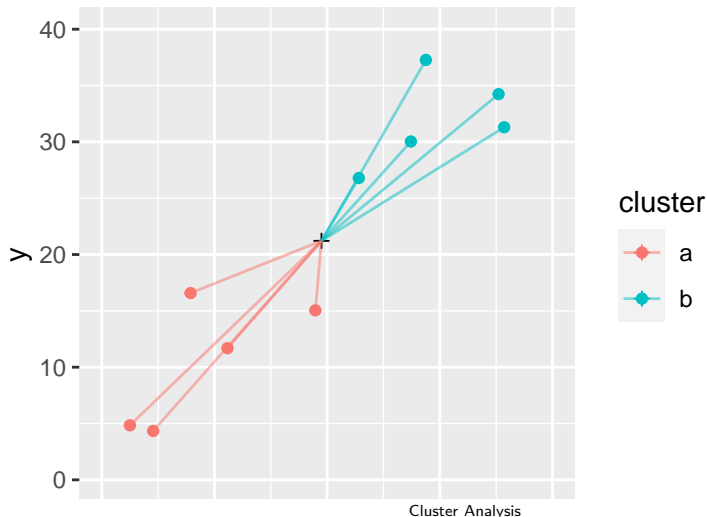
Ward's method

Work out mean of each cluster and join point to its mean:



Ward's method part 2 xxx

Now imagine combining the two clusters and working out overall mean.
Join each point to this mean:



Ward's method part 3

- Sum of squares (ii) will be bigger than (i) (points closer to own cluster mean than combined mean).
- Ward's distance is (ii) minus (i).
- Think of as “cost” of combining clusters:
- if clusters close together, (ii) only a little larger than (i)
- if clusters far apart, (ii) a lot larger than (i) (as in example).

Hierarchical clustering revisited

- Single linkage, complete linkage, Ward are ways of measuring closeness of clusters.
- Use them, starting with each observation in own cluster, to repeatedly combine two closest clusters until all points in one cluster.
- They will give different answers (clustering stories).
- Single linkage tends to make “stringy” clusters because clusters can be very different apart from two closest points.
- Complete linkage insists on whole clusters being similar.
- Ward tends to form many small clusters first.

Dissimilarity data in R

Dissimilarities for language data were how many number names had *different* first letter:

```
my_url <- "http://ritsokiguess.site/datafiles/languages.txt"  
(number.d <- read_table(my_url))
```

la	en	no	dk	nl	de	fr	es	it	pl	hu	fi
en	0	2	2	7	6	6	6	6	7	9	9
no	2	0	1	5	4	6	6	6	7	8	9
dk	2	1	0	6	5	6	5	5	6	8	9
nl	7	5	6	0	5	9	9	9	10	8	9
de	6	4	5	5	0	7	7	7	8	9	9
fr	6	6	6	9	7	0	2	1	5	10	9
es	6	6	5	9	7	2	0	1	3	10	9
it	6	6	5	9	7	1	1	0	4	10	9
pl	7	7	6	10	8	5	3	4	0	10	9
hu	9	8	8	8	9	10	10	10	10	0	8
fi	9	9	9	9	9	9	9	8	9	8	0

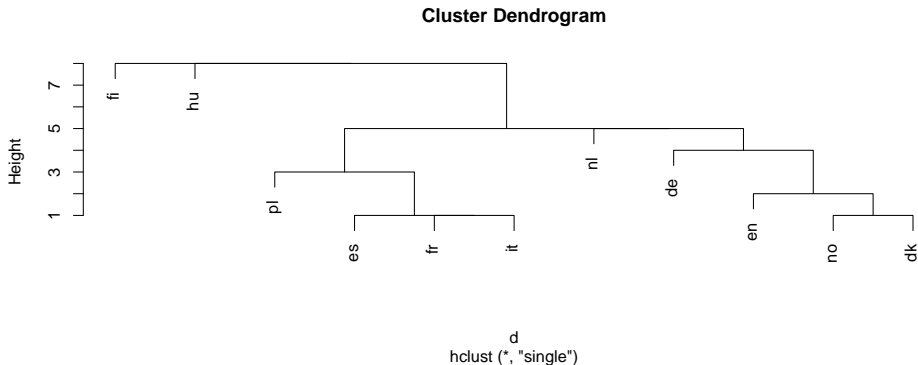
Making a distance object

```
d <- number.d %>%  
  select(-la) %>%  
  as.dist()  
d
```

```
##      en no dk nl de fr es it pl hu  
## no   2  
## dk   2  1  
## nl   7  5  6  
## de   6  4  5  5  
## fr   6  6  6  9  7  
## es   6  6  5  9  7  2  
## it   6  6  5  9  7  1  1  
## pl   7  7  6 10  8  5  3  4  
## hu   9  8  8  8  9 10 10 10 10  
## fi   9  9  9  9  9  9  9  8  9  8
```


Cluster analysis and dendrogram

```
d.hc <- hclust(d, method = "single")  
plot(d.hc)
```



Comments

- Tree shows how languages combined into clusters.
- First (bottom), Spanish, French, Italian joined into one cluster, Norwegian and Danish into another.
- Later, English joined to Norse languages, Polish to Romance group.
- Then German, Dutch make a Germanic group.
- Finally, Hungarian and Finnish joined to each other and everything else.

Clustering process

```
d.hc$labels
```

```
## [1] "en" "no" "dk" "nl" "de" "fr" "es" "it" "pl" "hu" "fi"
```

```
d.hc$merge
```

```
##      [,1] [,2]
```

```
## [1,]  -2  -3
```

```
## [2,]  -6  -8
```

```
## [3,]  -7   2
```

```
## [4,]  -1   1
```

```
## [5,]  -9   3
```

```
## [6,]  -5   4
```

```
## [7,]  -4   6
```

```
## [8,]   5   7
```

```
## [9,] -10   8
```

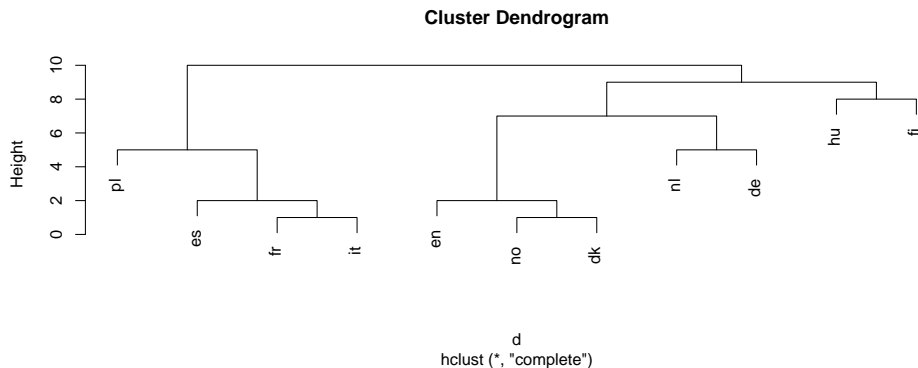
```
## [10,] -11  9
```

Comments

- Lines of merge show what was combined
 - First, languages 2 and 3 (no and dk)
 - Then languages 6 and 8 (fr and it)
 - Then #7 combined with cluster formed at step 2 (es joined to fr and it).
 - Then en joined to no and dk ...
 - Finally fi joined to all others.

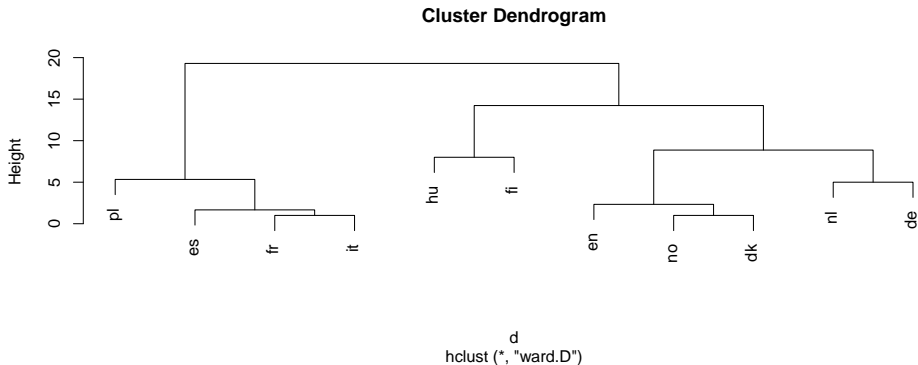
Complete linkage

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



Ward

```
d.hc <- hclust(d, method = "ward.D")  
plot(d.hc)
```



Chopping the tree

- Three clusters (from Ward) looks good:

```
cutree(d.hc, 3)
```

```
## en no dk nl de fr es it pl hu fi  
##  1  1  1  1  1  2  2  2  2  3  3
```

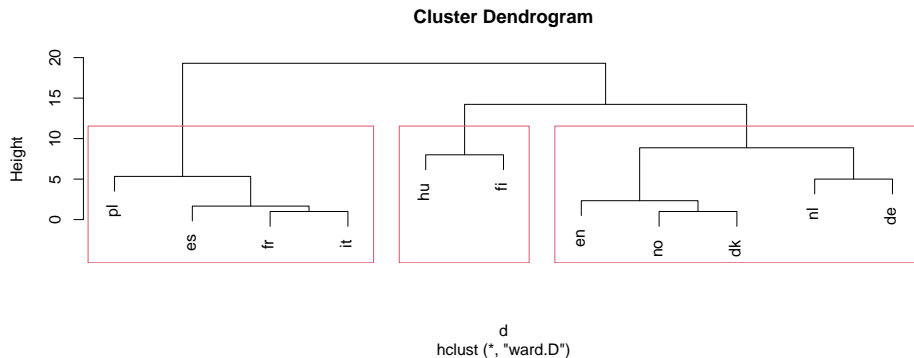
Turning the “named vector” into a data frame

```
cutree(d.hc, 3) %>% enframe(name="country", value="cluster")
```

country	cluster
en	1
no	1
dk	1
nl	1
de	1
fr	2
es	2
it	2
pl	2
hu	3
fi	3

Drawing those clusters on the tree

```
plot(d.hc)  
rect.hclust(d.hc, 3)
```



Comparing single-linkage and Ward

- In Ward, Dutch and German get joined earlier (before joining to Germanic cluster).
- Also Hungarian and Finnish get combined earlier.

Making those dissimilarities

Original data:

```
my_url <- "http://ritsokiguess.site/datafiles/one-ten.txt"
lang <- read_delim(my_url, " ")
lang
```

en	no	dk	nl	de	fr	es	it	pl	hu	fi
one	en	en	een	eins	un	uno	uno	jeden	egy	yksi
two	to	to	twee	zwei	deux	dos	due	dwa	ketto	kaksi
three	tre	tre	drie	drei	trois	tres	tre	trzy	harom	kolme
four	fire	fire	vier	vier	quatre	cuatro	quattro	cztery	negy	nelja
five	fem	fem	vijf	funf	cinq	cinco	cinque	piec	ot	viisi
six	seks	seks	zes	sechs	six	seis	sei	szesc	hat	kuusi
seven	sju	syv	zeven	sieben	sept	siete	sette	siedem	het	seitseman
eight	atte	otte	acht	acht	huit	ocho	otto	osiem	nyolc	kahdeksan
nine	ni	ni	negen	neun	neuf	nueve	nove	dziewiec	kilenc	yhdeksan
ten	ti	ti	tien	zehn	dix	diez	dieci	dziesiec	tiz	kymmenen

It would be a lot easier to extract the first letter if the number names were all in one column.

Tidy, and extract first letter

```
lang %>% mutate(number=row_number()) %>%  
  pivot_longer(-number, names_to="language", values_to="name") %>%  
  mutate(first=str_sub(name,1,1)) -> lang.long  
lang.long %>% print(n=12)
```

```
## # A tibble: 110 x 4  
##   number language name  first  
##   <int> <chr>    <chr> <chr>  
## 1     1 en      one   o  
## 2     1 no      en    e  
## 3     1 dk      en    e  
## 4     1 nl      een   e  
## 5     1 de      eins  e  
## 6     1 fr      un    u  
## 7     1 es      uno   u  
## 8     1 it      uno   u  
## 9     1 pl      jeden j  
## 10    1 hu      egy   e  
## 11    1 fi      yksi  y  
## 12    2 en      two   t
```

Calculating dissimilarity

- Suppose we wanted dissimilarity between English and Norwegian. It's the number of first letters that are different.
- First get the lines for English:

```
english <- lang.long %>% filter(language == "en")  
english
```

number	language	name	first
1	en	one	o
2	en	two	t
3	en	three	t
4	en	four	f
5	en	five	f
6	en	six	s
7	en	seven	s
8	en	eight	e
9	en	nine	n
10	en	ten	t

And then the lines for Norwegian

```
norwegian <- lang.long %>% filter(language == "no")  
norwegian
```

number	language	name	first
1	no	en	e
2	no	to	t
3	no	tre	t
4	no	fire	f
5	no	fem	f
6	no	seks	s
7	no	sju	s
8	no	atte	a
9	no	ni	n
10	no	ti	t

And now we want to put them side by side, matched by number. This is what `left_join` does. (A “join” is a lookup of values in one table using another.)

The join

```
english %>% left_join(norwegian, by = "number")
```

number	language.x	name.x	first.x	language.y	name.y	first.y
1	en	one	o	no	en	e
2	en	two	t	no	to	t
3	en	three	t	no	tre	t
4	en	four	f	no	fire	f
5	en	five	f	no	fem	f
6	en	six	s	no	seks	s
7	en	seven	s	no	sju	s
8	en	eight	e	no	atte	a
9	en	nine	n	no	ni	n
10	en	ten	t	no	ti	t

`first.x` is 1st letter of English word, `first.y` 1st letter of Norwegian word.

Counting the different ones

```
english %>%  
  left_join(norwegian, by = "number") %>%  
  count(different=(first.x != first.y))
```

different	n
FALSE	8
TRUE	2

or

```
english %>%  
  left_join(norwegian, by = "number") %>%  
  count(different=(first.x != first.y)) %>%  
  filter(different) %>% pull(n) -> ans  
ans
```

```
## [1] 2
```

Words for 1 and 8 start with different letter; rest are same.

A language with itself

The answer should be zero:

```
english %>%  
  left_join(english, by = "number") %>%  
  count(different=(first.x != first.y)) %>%  
  filter(different) %>% pull(n) -> ans  
ans
```

```
## integer(0)
```

- but this is “an integer vector of length zero”.
- so we have to allow for this possibility when we write a function to do it.

Function to do this for any two languages

```
countdiff <- function(lang.1, lang.2, d) {  
  d %>% filter(language == lang.1) -> lang1d  
  d %>% filter(language == lang.2) -> lang2d  
  lang1d %>%  
    left_join(lang2d, by = "number") %>%  
    count(different = (first.x != first.y)) %>%  
    filter(different) %>% pull(n) -> ans  
  # if ans has length zero, set answer to (integer) zero.  
  ifelse(length(ans)==0, 0L, ans)  
}
```

Testing

```
countdiff("en", "no", lang.long)
```

```
## [1] 2
```

```
countdiff("en", "en", lang.long)
```

```
## [1] 0
```

English and Norwegian have two different; English and English have none different.

Check.

For all pairs of languages?

- First need all the languages:

```
languages <- names(lang)
languages
```

```
## [1] "en" "no" "dk" "nl" "de" "fr" "es" "it" "pl"
## [10] "hu" "fi"
```

- and then all *pairs* of languages:

```
pairs <- crossing(lang = languages, lang2 = languages)
```

Some of these

```
pairs %>% slice(1:12)
```

lang	lang2
de	de
de	dk
de	en
de	es
de	fi
de	fr
de	hu
de	it
de	nl
de	no
de	pl
dk	de

Run countdiff for all those language pairs

```
pairs %>% rowwise() %>%  
  mutate(diff = countdiff(lang, lang2, lang.long)) -> thediff  
thediff
```

lang	lang2	diff
de	de	0
de	dk	5
de	en	6
de	es	7
de	fi	9
de	fr	7
de	hu	9
de	it	7
de	nl	5
de	no	4
de	pl	8
dk	de	5
dk	dk	0
dk	en	2
dk	es	5

Make square table of these

```
thediff %>% pivot_wider(names_from=lang2, values_from=diff)
```

lang	de	dk	en	es	fi	fr	hu	it	nl	no	pl
de	0	5	6	7	9	7	9	7	5	4	8
dk	5	0	2	5	9	6	8	5	6	1	6
en	6	2	0	6	9	6	9	6	7	2	7
es	7	5	6	0	9	2	10	1	9	6	3
fi	9	9	9	9	0	9	8	9	9	9	9
fr	7	6	6	2	9	0	10	1	9	6	5
hu	9	8	9	10	8	10	0	10	8	8	10
it	7	5	6	1	9	1	10	0	9	6	4
nl	5	6	7	9	9	9	8	9	0	5	10
no	4	1	2	6	9	6	8	6	5	0	7
pl	8	6	7	3	9	5	10	4	10	7	0

and that was where we began.

Another example

Birth, death and infant mortality rates for 97 countries (variables not dissimilarities):

24.7	5.7	30.8	Albania	12.5	11.9	14.4	Bulgaria
13.4	11.7	11.3	Czechoslovakia	12	12.4	7.6	Former_E._Germany
11.6	13.4	14.8	Hungary	14.3	10.2	16	Poland
13.6	10.7	26.9	Romania	14	9	20.2	Yugoslavia
17.7	10	23	USSR	15.2	9.5	13.1	Byelorussia_SSR
13.4	11.6	13	Ukrainian_SSR	20.7	8.4	25.7	Argentina
46.6	18	111	Bolivia	28.6	7.9	63	Brazil
23.4	5.8	17.1	Chile	27.4	6.1	40	Columbia
32.9	7.4	63	Ecuador	28.3	7.3	56	Guyana
...							

- Want to find groups of similar countries (and how many groups, which countries in each group).
- Tree would be unwieldy with 97 countries.
- More automatic way of finding given number of clusters?

Reading in

```
url <- "http://ritsokiguess.site/datafiles/birthrate.txt"
vital <- read_table(url)
```

```
##
```

```
## -- Column specification -----
```

```
## cols(
```

```
##   birth = col_double(),
```

```
##   death = col_double(),
```

```
##   infant = col_double(),
```

```
##   country = col_character()
```

```
## )
```

The data

vital

birth	death	infant	country
24.7	5.7	30.8	Albania
13.4	11.7	11.3	Czechoslovakia
11.6	13.4	14.8	Hungary
13.6	10.7	26.9	Romania
17.7	10.0	23.0	USSR
13.4	11.6	13.0	Ukrainian_SSR
46.6	18.0	111.0	Bolivia
23.4	5.8	17.1	Chile
32.9	7.4	63.0	Ecuador
34.8	6.6	42.0	Paraguay
18.0	9.6	21.9	Uruguay
29.0	23.2	43.0	Mexico
13.2	10.1	5.8	Finland

Standardizing

- Infant mortality rate numbers bigger than others, consequence of measurement scale (arbitrary).
- Standardize (numerical) columns of data frame to have mean 0, SD 1, done by scale.

```
vital %>%  
  mutate(across(where(is.numeric), ~scale(.))) -> vital.s
```

Three clusters

Pretend we know 3 clusters is good. Take off the column of countries, and run `kmeans` on the resulting data frame, asking for 3 clusters:

```
vital.s %>% select(-country) %>%  
  kmeans(3) -> vital.km3  
names(vital.km3)
```

```
## [1] "cluster"      "centers"      "totss"  
## [4] "withinss"     "tot.withinss" "betweenss"  
## [7] "size"         "iter"         "ifault"
```

A lot of output, so look at these individually.

What's in the output?

- Cluster sizes:

```
vital.km3$size
```

```
## [1] 40 25 32
```

- Cluster centres:

```
vital.km3$centers
```

```
##          birth      death    infant
## 1 -1.0376994 -0.3289046 -0.90669032
## 2  1.1780071  1.3323130  1.32732200
## 3  0.3768062 -0.6297388  0.09639258
```

- Cluster 2 has lower than average rates on everything; cluster 3 has much higher than average.

Cluster sums of squares and membership

```
vital.km3$withinss
```

```
## [1] 17.21617 28.32560 21.53020
```

Cluster 1 compact relative to others (countries in cluster 1 more similar).

```
vital.km3$cluster
```

```
## [1] 3 1 1 1 1 1 2 1 3 3 1 2 1 1 1 1 1 1 1 1 2 2 1 3 3 3
## [29] 1 3 1 3 3 1 1 3 3 3 2 2 3 3 2 2 3 2 2 2 3 1 1 1 1 1 1
## [57] 3 3 3 3 1 1 1 1 1 1 1 1 1 1 3 3 3 3 3 1 2 1 3 3 2 3 1
## [85] 2 2 2 2 3 2 2 2 2 2 3 2 2
```

The cluster membership for each of the 97 countries.

Store countries and clusters to which they belong

```
vital.3 <- tibble(  
  country = vital.s$country,  
  cluster = vital.km3$cluster  
)
```

Next, which countries in which cluster?

Write function to extract them:

```
get_countries <- function(i, d) {  
  d %>% filter(cluster == i) %>% pull(country)  
}
```

Cluster membership: cluster 2

```
get_countries(2, vital.3)
```

##	[1]	"Bolivia"	"Mexico"	"Afghanistan"	"Iran"	"Bangladesh"
##	[6]	"Gabon"	"Ghana"	"Namibia"	"Sierra_Leone"	"Swaziland"
##	[11]	"Uganda"	"Zaire"	"Cambodia"	"Nepal"	"Angola"
##	[16]	"Congo"	"Ethiopia"	"Gambia"	"Malawi"	"Mozambique"
##	[21]	"Nigeria"	"Somalia"	"Sudan"	"Tanzania"	"Zambia"

Cluster 3

```
get_countries(3, vital.3)
```

##	[1]	"Albania"	"Ecuador"	"Paraguay"
##	[4]	"Kuwait"	"Oman"	"Turkey"
##	[7]	"India"	"Mongolia"	"Pakistan"
##	[10]	"Algeria"	"Botswana"	"Egypt"
##	[13]	"Libya"	"Morocco"	"South_Africa"
##	[16]	"Zimbabwe"	"Brazil"	"Columbia"
##	[19]	"Guyana"	"Peru"	"Venezuela"
##	[22]	"Bahrain"	"Iraq"	"Jordan"
##	[25]	"Lebanon"	"Saudi_Arabia"	"Indonesia"
##	[28]	"Malaysia"	"Philippines"	"Vietnam"
##	[31]	"Kenya"	"Tunisia"	

Cluster 1

```
get_countries(1, vital.3)
```

```
## [1] "Czechoslovakia" "Hungary"  
## [3] "Romania" "USSR"  
## [5] "Ukrainian_SSR" "Chile"  
## [7] "Uruguay" "Finland"  
## [9] "France" "Greece"  
## [11] "Italy" "Norway"  
## [13] "Spain" "Switzerland"  
## [15] "Austria" "Canada"  
## [17] "Israel" "China"  
## [19] "Korea" "Singapore"  
## [21] "Thailand" "Bulgaria"  
## [23] "Former_E._Germany" "Poland"  
## [25] "Yugoslavia" "Byelorussia_SSR"  
## [27] "Argentina" "Belgium"
```

Problem!

- `kmeans` uses randomization. So result of one run might be different from another run.
- Example: just run again on 3 clusters, table of results:

```
vital.s %>%  
  select(-country) %>% kmeans(3) -> vital.km3a  
table(  
  first = vital.km3$cluster,  
  second = vital.km3a$cluster  
)
```

```
##          second  
## first  1  2  3  
##      1 40  0  0  
##      2  0 24  1  
##      3  4  0 28
```

- Clusters are similar but *not same*.

Solution to this

- `nstart` option on `kmeans` runs that many times, takes best. Should be same every time:

```
vital.s %>%  
  select(-country) %>%  
  kmeans(3, nstart = 20) -> vital.km3b
```

How many clusters?

- Three was just a guess.
- Idea: try a whole bunch of `#clusters` (say 2–20), obtain measure of goodness of fit for each, make plot.
- Appropriate measure is `tot.withinss`.
- Run `kmeans` for each `#clusters`, get `tot.withinss` each time.

Function to get tot.withinss

...for an input number of clusters, taking only numeric columns of input data frame:

```
ss <- function(i, d) {  
  d %>%  
    select(where(is.numeric)) %>%  
    kmeans(i, nstart = 20) -> km  
  km$tot.withinss  
}
```

Note: writing function to be as general as possible, so that we can re-use it later.

Constructing within-cluster SS

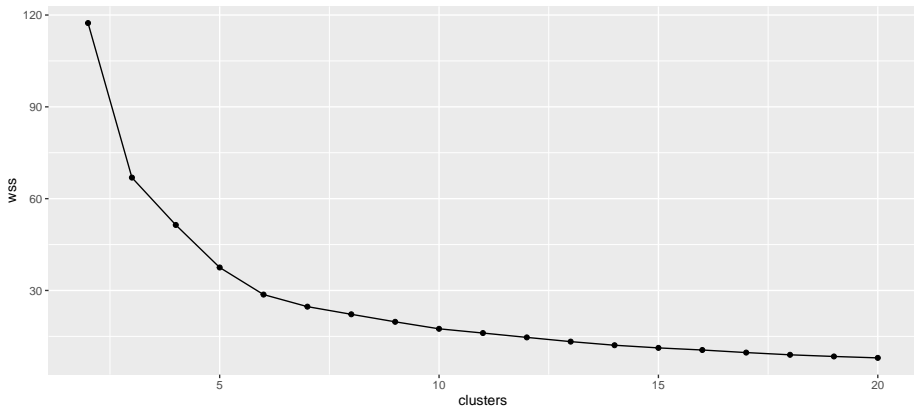
Make a data frame with desired numbers of clusters, and fill it with the total within-group sums of squares. `ss` expects a single number of clusters, not a vector of several, so run `rowwise`:

```
tibble(clusters = 2:20) %>%  
  rowwise() %>%  
  mutate(wss = ss(clusters, vital.s)) -> ssd  
ssd
```

clusters	wss
2	117.375682
3	66.883275
4	51.403362
5	37.513143
6	28.659864
7	24.714303
8	22.211262

Scree plot

```
ggplot(ssd, aes(x = clusters, y = wss)) + geom_point() +  
  geom_line()
```



Interpreting scree plot

- Lower wss better.
- But lower for larger #clusters, harder to explain.
- Compromise: low-ish wss and low-ish #clusters.
- Look for “elbow” in plot.
- Idea: this is where wss decreases fast then slow.
- On our plot, small elbow at 6 clusters. Try this many clusters.

Six clusters, using nstart

```
vital.s %>%  
  select(-country) %>%  
  kmeans(6, nstart = 20) -> vital.km6  
vital.km6$size
```

```
## [1] 17 24 13 20 13 10
```

```
vital.km6$centers
```

```
##          birth          death          infant  
## 1  1.2049466  0.6972333  1.0165097  
## 2  0.4160993 -0.5169988  0.2648754  
## 3 -1.1458296  0.2636810 -0.9301055  
## 4 -1.1331101 -0.4617719 -0.9428918  
## 5 -0.3548334 -1.1812663 -0.7096686  
## 6  1.1700347  2.1719052  1.6537224
```

Make a data frame of countries and clusters

```
vital.6 <- tibble(  
  country = vital.s$country,  
  cluster = vital.km6$cluster  
)  
vital.6 %>% sample_n(10)
```

country	cluster
Swaziland	1
Switzerland	4
Philippines	2
Guyana	2
Finland	4
Vietnam	2
Paraguay	2
Portugal	4
Mongolia	2

Cluster 1

Below-average death rate, though other rates a little higher than average:

```
get_countries(1, vital.6)
```

```
## [1] "Iran"          "Bangladesh" "Botswana"    "Gabon"
## [5] "Ghana"         "Namibia"     "Swaziland"   "Uganda"
## [9] "Zaire"         "Cambodia"    "Nepal"       "Congo"
## [13] "Kenya"         "Nigeria"     "Sudan"       "Tanzania"
## [17] "Zambia"
```

Cluster 2

High on everything:

```
get_countries(2, vital.6)
```

##	[1]	"Ecuador"	"Paraguay"	"Oman"
##	[4]	"Turkey"	"India"	"Mongolia"
##	[7]	"Pakistan"	"Algeria"	"Egypt"
##	[10]	"Libya"	"Morocco"	"South_Africa"
##	[13]	"Zimbabwe"	"Brazil"	"Guyana"
##	[16]	"Peru"	"Iraq"	"Jordan"
##	[19]	"Lebanon"	"Saudi_Arabia"	"Indonesia"
##	[22]	"Philippines"	"Vietnam"	"Tunisia"

Cluster 3

Low on everything, though death rate close to average:

```
get_countries(3, vital.6)
```

```
## [1] "Czechoslovakia" "Hungary"  
## [3] "Romania"        "Ukrainian_SSR"  
## [5] "Norway"         "Korea"  
## [7] "Bulgaria"       "Former_E._Germany"  
## [9] "Belgium"        "Denmark"  
## [11] "Germany"        "Sweden"  
## [13] "U.K."
```

Cluster 4

Low on everything, especially death rate:

```
get_countries(4, vital.6)
```

```
## [1] "USSR" "Uruguay"
## [3] "Finland" "France"
## [5] "Greece" "Italy"
## [7] "Spain" "Switzerland"
## [9] "Austria" "Canada"
## [11] "Poland" "Yugoslavia"
## [13] "Byelorussia_SSR" "Argentina"
## [15] "Ireland" "Netherlands"
## [17] "Portugal" "Japan"
## [19] "U.S.A." "Hong_Kong"
```

Cluster 5

Higher than average on everything, though not the highest:

```
get_countries(5, vital.6)
```

```
## [1] "Albania"           "Chile"
## [3] "Israel"            "Kuwait"
## [5] "China"             "Singapore"
## [7] "Thailand"           "Columbia"
## [9] "Venezuela"         "Bahrain"
## [11] "United_Arab_Emirates" "Malaysia"
## [13] "Sri_Lanka"
```


Cluster 6

Very high death rate, just below average on all else:

```
get_countries(6, vital.6)
```

```
## [1] "Bolivia"      "Mexico"      "Afghanistan"  
## [4] "Sierra_Leone" "Angola"      "Ethiopia"  
## [7] "Gambia"       "Malawi"      "Mozambique"  
## [10] "Somalia"
```

Comparing our 3 and 6-cluster solutions

```
table(three = vital.km3$cluster, six = vital.km6$cluster)
```

```
##          six
## three  1  2  3  4  5  6
##       1  0  0 13 20  7  0
##       2 15  0  0  0  0 10
##       3  2 24  0  0  6  0
```

Compared to 3-cluster solution:

- most of (old) cluster 3 gone to (new) cluster 2
- cluster 1 split into clusters 3 and 4 (two types of “richer” countries)
- cluster 3 split into clusters 2 and 5 (two types of “poor” countries, divided by death rate).

Getting a picture from kmeans

- Use discriminant analysis on clusters found, treating them as “known” groups.

Discriminant analysis

- So what makes the groups different?
- Uses package MASS (loaded):

```
vital.lda <- lda(vital.km6$cluster ~ birth + death + infant,  
                data = vital.s)  
vital.lda$svd
```

```
## [1] 17.407851  8.743023  1.000331
```

```
vital.lda$scaling
```

```
##           LD1           LD2           LD3  
## birth  -2.088306  1.6066337 -1.7791031  
## death  -1.359398 -2.5075513 -0.6581161  
## infant -1.184993  0.4780262  2.2687506
```

- LD1 is some of everything (high=poor, low=rich).
- LD2 mainly death rate, high or low.

A data frame to make plot from

- Get predictions first:

```
vital.pred <- predict(vital.lda)
d <- data.frame(
  country = vital.s$country,
  cluster = vital.km6$cluster,
  vital.pred$x
)
glimpse(d)
```

```
## Rows: 97
## Columns: 5
## $ country <chr> "Albania", "Czechoslovakia", "Hu~
## $ cluster <int> 5, 3, 3, 3, 4, 3, 6, 5, 2, 2, 4,~
## $ LD1      <dbl> 2.8215814, 3.3109528, 3.0010047,~
## $ LD2      <dbl> 1.983429, -2.796716, -3.891051, ~
## $ LD3      <dbl> 0.13334944, -0.19415639, -0.0258~
```

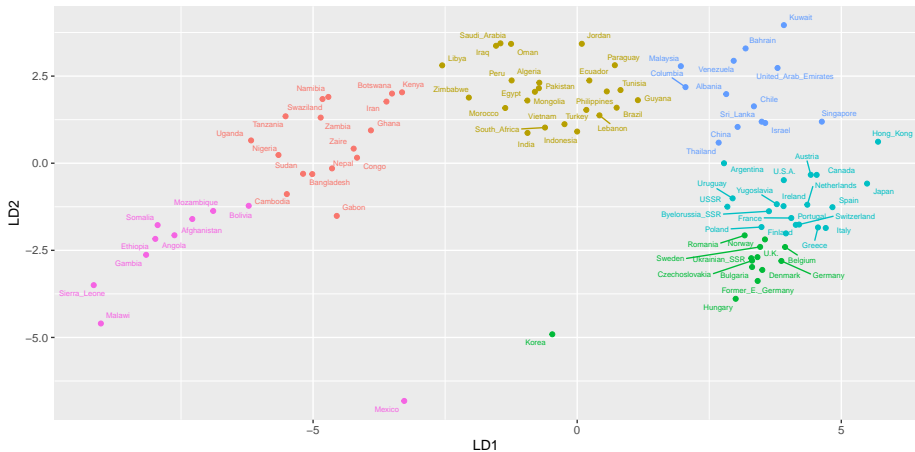
What's in there; making a plot

- d contains country names, cluster memberships and discriminant scores.
- Plot LD1 against LD2, colouring points by cluster and labelling by country:

```
g <- ggplot(d, aes(  
  x = LD1, y = LD2, colour = factor(cluster),  
  label = country  
)) + geom_point() +  
  geom_text_repel(size = 2, max.overlaps = Inf) + guides(colour = 'none')
```

The plot

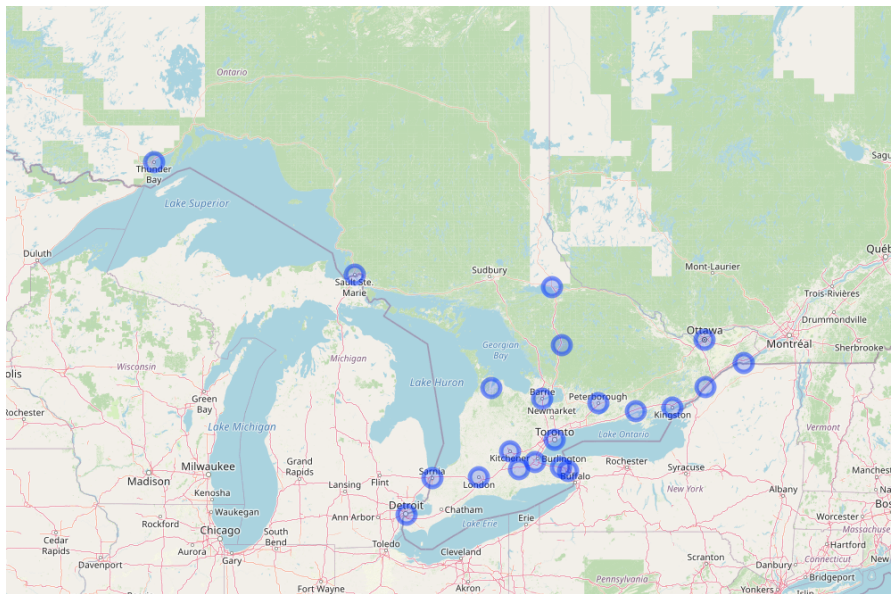
g



Final example: a hockey league

- An Ontario hockey league has teams in 21 cities. How can we arrange those teams into 4 geographical divisions?
- Distance data in spreadsheet.
- Take out spaces in team names.
- Save as “text/csv”.
- Distances, so back to `hclust`.

A map

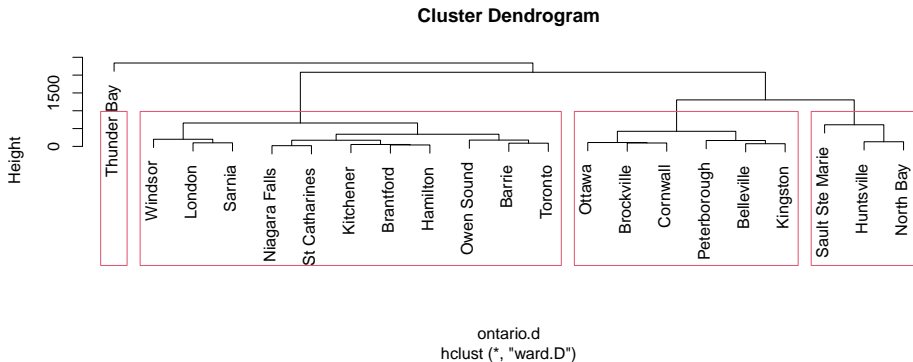


Attempt 1

```
my_url <-  
  "http://ritsokiguess.site/datafiles/ontario-road-distances.csv"  
ontario <- read_csv(my_url)  
ontario.d <- ontario %>% select(-1) %>% as.dist()  
ontario.hc <- hclust(ontario.d, method = "ward.D")
```

Plot, with 4 clusters

```
plot(ontario.hc)  
rect.hclust(ontario.hc, 4)
```

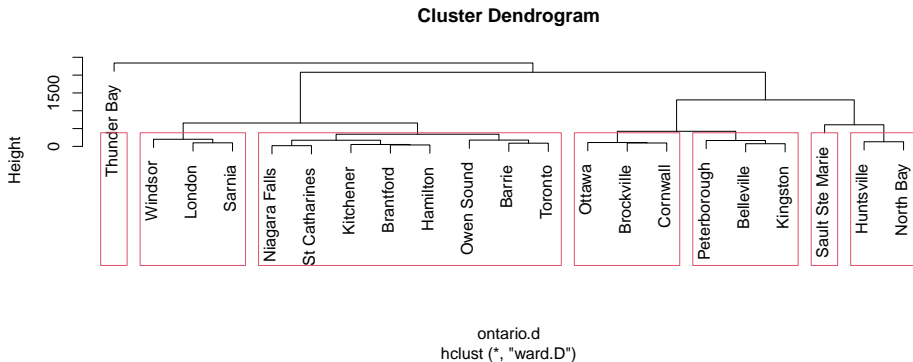


Comments

- Can't have divisions of 1 team!
- “Southern” divisions way too big!
- Try splitting into more. I found 7 to be good:

Seven clusters

```
plot(ontario.hc)  
rect.hclust(ontario.hc, 7)
```



Divisions now

- I want to put Huntsville and North Bay together with northern teams.
- I'll put the Eastern teams together. Gives:
- North: Sault Ste Marie, Sudbury, Huntsville, North Bay
- East: Brockville, Cornwall, Ottawa, Peterborough, Belleville, Kingston
- West: Windsor, London, Sarnia
- Central: Owen Sound, Barrie, Toronto, Niagara Falls, St Catharines, Brantford, Hamilton, Kitchener
- Getting them same size beyond us!

Another map

