

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)
library(conflicted)
conflict_prefer("select", "dplyr")
conflict_prefer("filter", "dplyr")
```

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

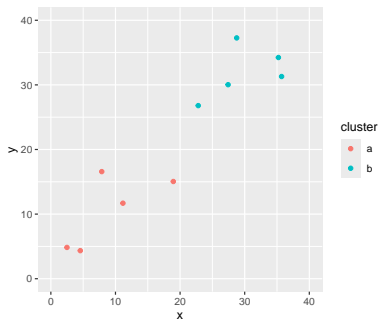
Dissimilarities and languages example

- ▶ 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`).

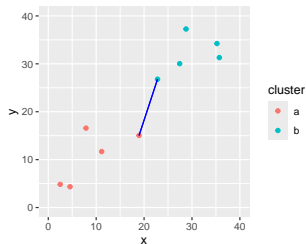
Two made-up clusters



How to measure distance between set of red points and set of blue ones?

Single-linkage distance

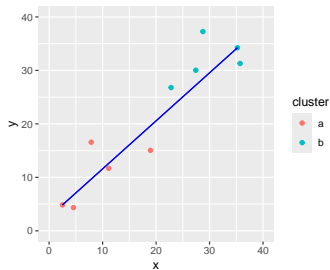
Find the red point and the blue point that are closest together:



Single-linkage distance between 2 clusters is distance between their closest points.

Complete linkage

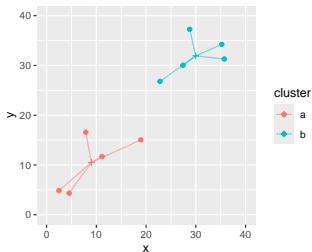
Find the red and blue points that are farthest apart:



Complete-linkage distance is distance between farthest points.

Ward's method

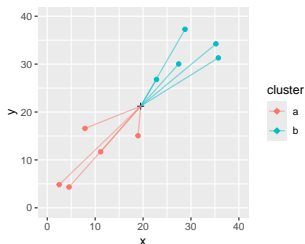
Work out mean of each cluster and join point to its mean:



Work out (i) sum of squared distances of points from means.

Ward's method part 2

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



Calc sum of squared distances (ii) of points to combined 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))
```

```
# A tibble: 11 x 12
```

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

```
# i 3 more variables: pl <dbl>, hu <dbl>, fi <dbl>
```

Making a distance object

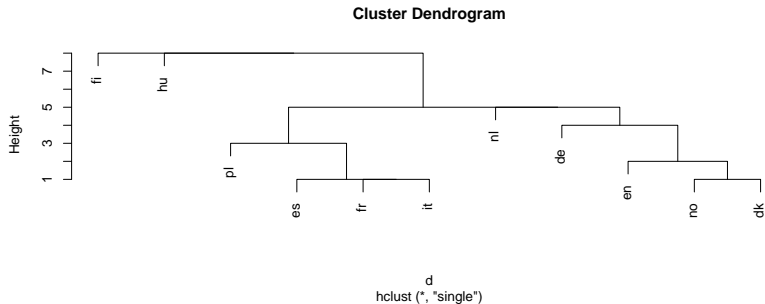
```
number.d %>%  
  select(-la) %>%  
  as.dist() -> d  
d
```

	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

```
class(d)
```


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

```
enframe(d.hc$labels)
```

```
# A tibble: 11 x 2
```

```
  name value
```

```
  <int> <chr>
```

1	1	en
2	2	no
3	3	dk
4	4	nl
5	5	de
6	6	fr
7	7	es
8	8	it
9	9	pl
10	10	hu
11	11	fi

```
d.hc$merge
```

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

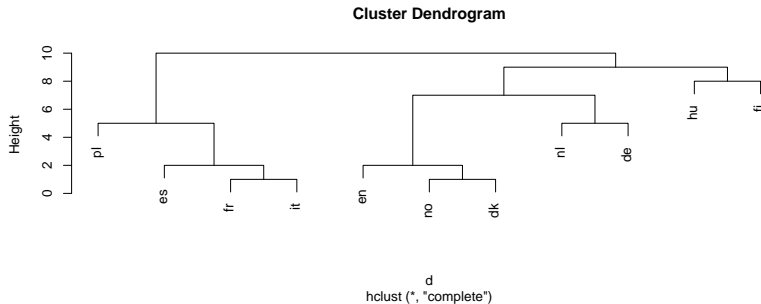
```
[1,] 1 2 2
```

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.

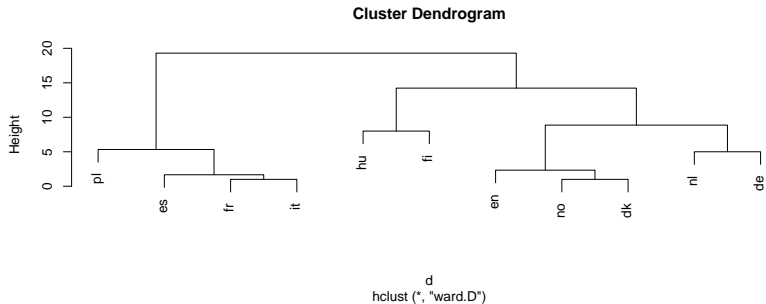
Complete linkage

```
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")
```

```
# A tibble: 11 x 2
```

```
  country cluster
```

```
  <chr>      <int>
```

```
1 en         1
```

```
2 no         1
```

```
3 dk         1
```

```
4 nl         1
```

```
5 de         1
```

```
6 fr         2
```

```
7 es         2
```

```
8 it         2
```

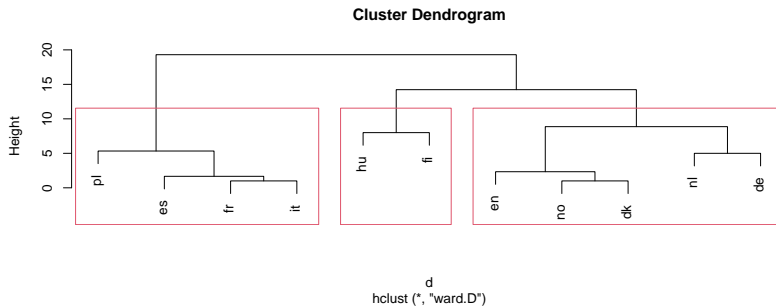
```
9 pl         2
```

```
10 hu        3
```

```
11 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
```

```
# A tibble: 10 x 11
  en    no    dk    nl    de    fr    es    it    pl
  <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
1 one   en    en    een   eins  un    uno   uno   jeden
2 two   to    to    twee zwei  deux  dos   due   dwa
3 three tre  tre  drie  drei  trois tres  tre   trzy
4 four  fire  fire  vier  vier  quatre quatre quatt~ czte~
5 five  fem   fem   vijf  funf  cinq  cinco cinque piec
6 six   seks  seks  zes   sechs six   seis  sei   szesc
7 seven sju   syv   zeven sieben sept  siete sette sied~
8 eight atte otte  acht  acht  huit  ocho  otto  osiem
9 nine  ni    ni    negen neun  neuf  nueve nove  dzie~
10 ten  ti    ti    tien  zehn  dix   diez  dieci dzie~
# i 2 more variables: hu <chr>, fi <chr>
```

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
```

```
# 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

```
# i 100 more rows
```

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
```

```
# A tibble: 10 x 4  
  number language name  first  
  <int> <chr>    <chr> <chr>  
1     1    en      one   o  
2     2    en      two   t  
3     3    en    three t  
4     4    en     four f  
5     5    en     five f  
6     6    en     six  s  
7     7    en   seven s  
8     8    en   eight e  
9     9    en    nine n  
10    10    en    ten  t
```

And then the lines for Norwegian

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

```
# A tibble: 10 x 4
  number language name first
  <int> <chr>      <chr> <chr>
1     1    no      en     e
2     2    no      to     t
3     3    no      tre    t
4     4    no      fire   f
5     5    no      fem    f
6     6    no      seks   s
7     7    no      sju    s
8     8    no      atte   a
9     9    no      ni     n
10    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, join_by(number))
```

```
# A tibble: 10 x 7
```

	number	language.x	name.x	first.x	language.y	name.y	first.y
	<int>	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>
1	1	en	one	o	no	en	e
2	2	en	two	t	no	to	t
3	3	en	three	t	no	tre	t
4	4	en	four	f	no	fire	f
5	5	en	five	f	no	fem	f
6	6	en	six	s	no	seks	s
7	7	en	seven	s	no	sju	s
8	8	en	eight	e	no	atte	a
9	9	en	nine	n	no	ni	n
10	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, join_by(number)) %>%  
  count(different=(first.x != first.y))
```

```
# A tibble: 2 x 2  
  different      n  
  <lgl>      <int>  
1 FALSE         8  
2 TRUE          2
```

or

```
english %>% left_join(norwegian, join_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, join_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, join_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)
```

The pairs

```
pairs
```

```
# A tibble: 121 x 2
  lang lang2
  <chr> <chr>
1 de    de
2 de    dk
3 de    en
4 de    es
5 de    fi
6 de    fr
7 de    hu
8 de    it
9 de    nl
10 de   no
# i 111 more rows
```

Run countdiff for all those language pairs

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

```
# A tibble: 121 x 3
```

```
# Rowwise:
```

	lang	lang2	diff
	<chr>	<chr>	<int>
1	de	de	0
2	de	dk	5
3	de	en	6
4	de	es	7
5	de	fi	9
6	de	fr	7
7	de	hu	9
8	de	it	7
9	de	nl	5
10	de	no	4

```
# i 111 more rows
```

Make square table of these

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

```
# A tibble: 11 x 12
  lang    de    dk    en    es    fi    fr    hu    it
<chr> <int> <int> <int> <int> <int> <int> <int> <int>
1 de      0     5     6     7     9     7     9     7
2 dk      5     0     2     5     9     6     8     5
3 en      6     2     0     6     9     6     9     6
4 es      7     5     6     0     9     2    10     1
5 fi      9     9     9     9     0     9     8     9
6 fr      7     6     6     2     9     0    10     1
7 hu      9     8     9    10     8    10     0    10
8 it      7     5     6     1     9     1    10     0
9 nl      5     6     7     9     9     9     8     9
10 no      4     1     2     6     9     6     8     6
11 pl      8     6     7     3     9     5    10     4
# i 3 more variables: nl <int>, no <int>, pl <int>
```

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._C
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
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)
vital
```

```
# A tibble: 97 x 4
  birth death infant country
  <dbl> <dbl>   <dbl> <chr>
1  24.7   5.7   30.8 Albania
2  13.4  11.7   11.3 Czechoslovakia
3  11.6  13.4   14.8 Hungary
4  13.6  10.7   26.9 Romania
5  17.7  10     23    USSR
6  13.4  11.6   13    Ukrainian_SSR
7  46.6  18    111    Bolivia
8  23.4   5.8   17.1 Chile
9  32.9   7.4   63    Ecuador
10 34.8   6.6   42    Paraguay
# i 87 more rows
```

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), \(x) scale(x))) -> vital
```

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  
[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"
[4]	"Iran"	"Bangladesh"	"Gabon"
[7]	"Ghana"	"Namibia"	"Sierra_Leone"
[10]	"Swaziland"	"Uganda"	"Zaire"
[13]	"Cambodia"	"Nepal"	"Angola"
[16]	"Congo"	"Ethiopia"	"Gambia"
[19]	"Malawi"	"Mozambique"	"Nigeria"
[22]	"Somalia"	"Sudan"	"Tanzania"
[25]	"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"
[29] "Denmark"	"Germany"
[31] "Ireland"	"Netherlands"

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
```

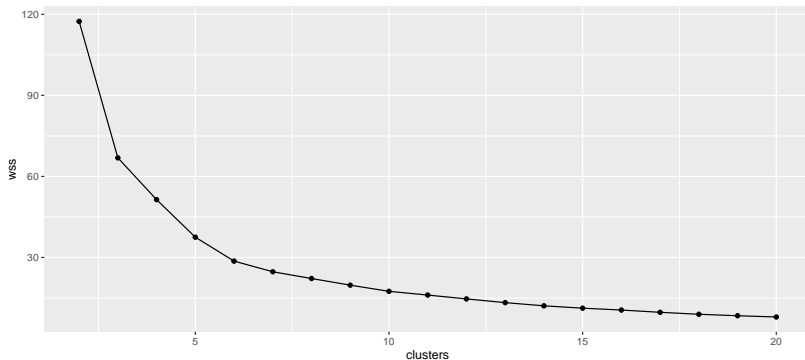
```
# A tibble: 19 x 2
```

```
# Rowwise:
```

	clusters	wss
	<int>	<dbl>
1	2	117.
2	3	66.9
3	4	51.4
4	5	37.5
5	6	28.7
6	7	24.7

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

```
set.seed(457299)
```

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

```
[1] 24 18 15  2  8 30
```

```
vital.km6$centers
```

	birth	death	infant
1	0.4160993	-0.5169988	0.2648754
2	1.2092406	0.7441347	1.0278003
3	-0.4357690	-1.1438599	-0.7281108
4	-0.2199722	2.1116577	-0.4544435
5	1.3043848	2.1896567	1.9470306
6	-1.1737104	-0.1856375	-0.9534370

Make a data frame of countries and clusters

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

A tibble: 10 x 2

	country <chr>	cluster <int>
1	Ghana	2
2	Ukrainian_SSR	6
3	Ethiopia	5
4	Somalia	5
5	Oman	1
6	Botswana	2
7	Paraguay	1
8	Czechoslovakia	6
9	Peru	1

Cluster 1

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

```
get_countries(1, 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 2

High on everything:

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

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

Cluster 3

Low on everything:

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

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

Cluster 4

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

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

```
[1] "Mexico" "Korea"
```

Cluster 5

Very high on everything:

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

```
[1] "Afghanistan"  "Sierra_Leone" "Angola"  
[4] "Ethiopia"     "Gambia"       "Malawi"  
[7] "Mozambique"   "Somalia"
```

Cluster 6

A bit below average on everything:

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

[1]	"Czechoslovakia"	"Hungary"
[3]	"Romania"	"USSR"
[5]	"Ukrainian_SSR"	"Uruguay"
[7]	"Finland"	"France"
[9]	"Greece"	"Italy"
[11]	"Norway"	"Spain"
[13]	"Switzerland"	"Austria"
[15]	"Canada"	"Bulgaria"
[17]	"Former_E._Germany"	"Poland"
[19]	"Yugoslavia"	"Byelorussia_SSR"
[21]	"Belgium"	"Denmark"
[23]	"Germany"	"Ireland"
[25]	"Netherlands"	"Portugal"
[27]	"Sweden"	"U.K."
[29]	"Japan"	"U.S.A."

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	9	1	0	30
2	0	16	0	1	8	0
3	24	2	6	0	0	0

Compared to 3-cluster solution:

- ▶ most of (old) cluster 1 gone to (new) cluster 6
- ▶ cluster 2 split into clusters 2 and 5 (two types of “poor” countries)
- ▶ cluster 3 split into clusters 1 and 3 (two types of “intermediate” 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] 21.687195  8.851811  1.773006
```

```
vital.lda$scaling
```

	LD1	LD2	LD3
birth	2.6879695	1.1224202	-1.9483853
death	0.6652712	-2.7213044	-0.6049358
infant	2.1111801	0.7650912	2.3542296

- ▶ 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
)
d
```

	country	cluster	LD1
1	Albania	3	-2.74034473
2	Czechoslovakia	6	-5.01874312
3	Hungary	6	-4.97189595
4	Romania	6	-4.40612396
5	USSR	6	-3.87181416
6	Ukrainian_SSR	6	-4.95502329
7	Bolivia	2	7.04719692
8	Chile	3	-3.61284528
9	Ecuador	1	0.60813286
10	Paraguay	1	-0.09333631

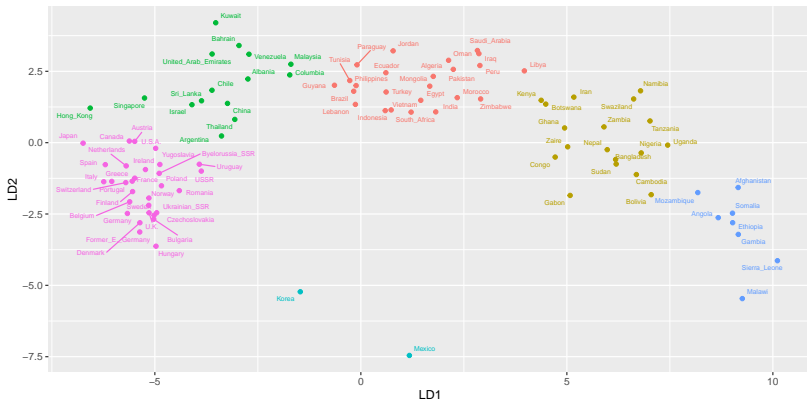
What's in there; making a plot

- ▶ 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

α

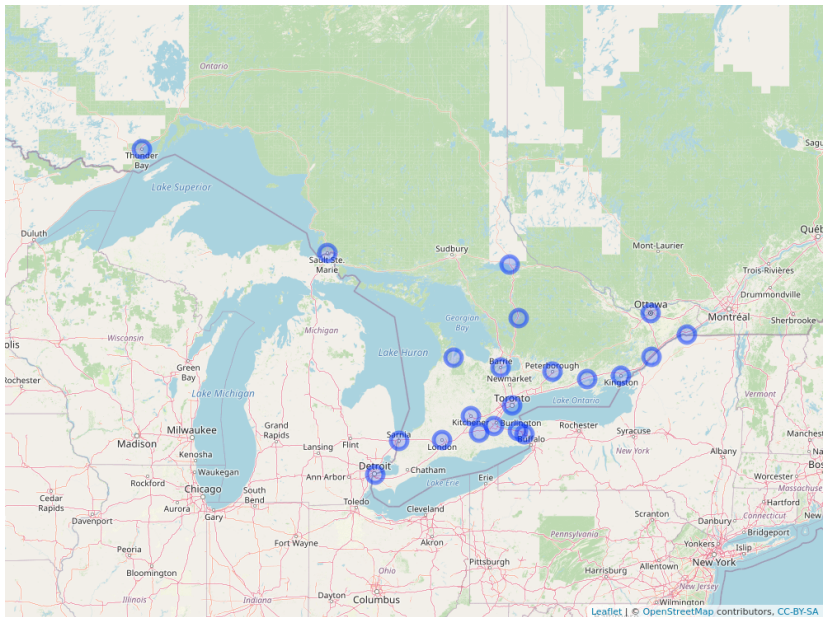


It would be better to zoom in on parts of this plot.

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

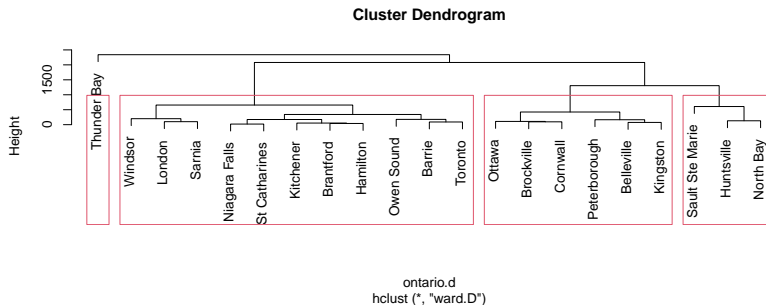


Attempt 1

```
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)
```

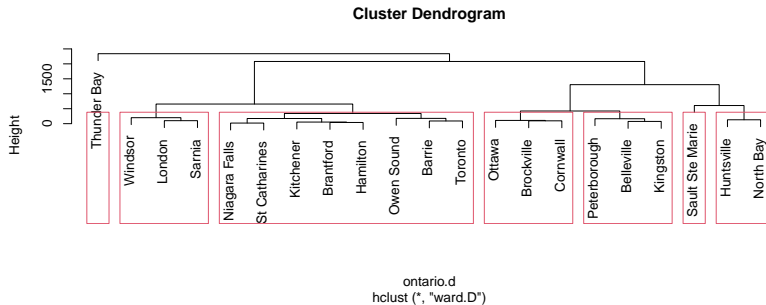


Comments

- ▶ 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

