Cluster analysis

Cluster Analysis

- One side-effect of discriminant analysis: could draw picture of data (if 1st 2s `LD`s 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

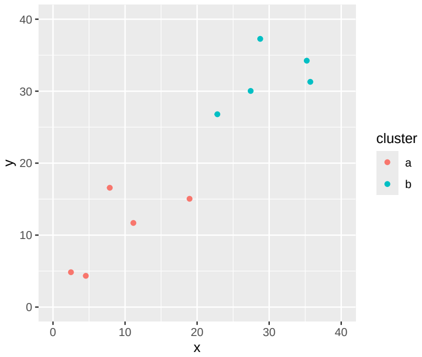
Dissimilarities and languages example

- 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`).

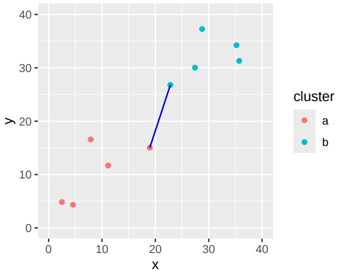
Two made-up clusters



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

Single-linkage distance

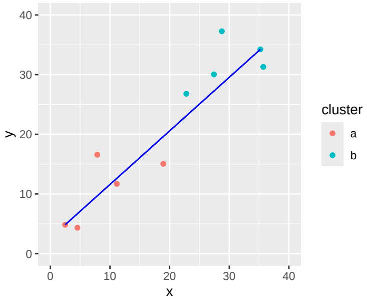
Find the red point and the blue point that are closest together:



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

Complete linkage

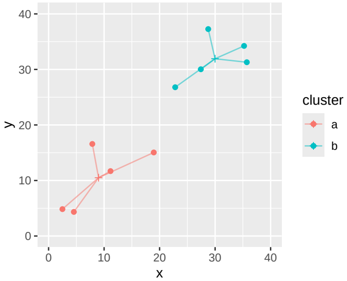
Find the red and blue points that are farthest apart:



Complete-linkage distance is distance between farthest points.

Ward's method

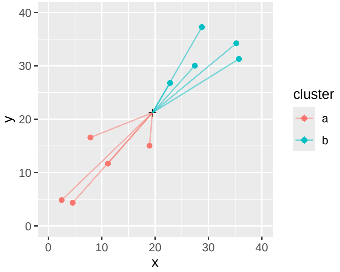
Work out mean of each cluster and join point to its mean:



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
```

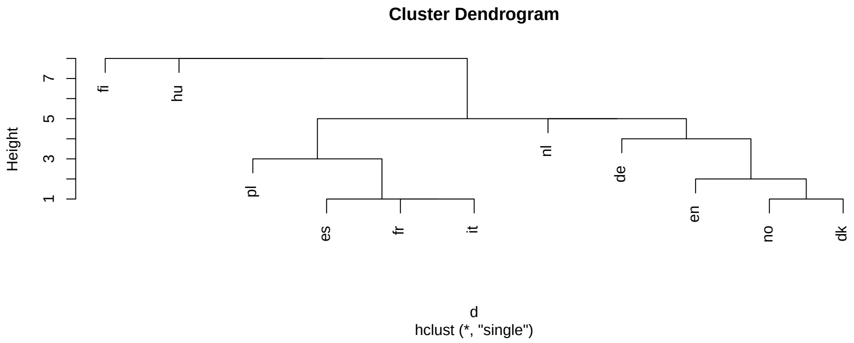
```
   en no dk nl de fr es it pl hu
no  2                           
dk  2  1                        
nl  7  5  6                     
de  6  4  5  5                  
fr  6  6  6  9  7               
es  6  6  5  9  7  2            
it  6  6  5  9  7  1  1         
pl  7  7  6 10  8  5  3  4      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

```
class(d)
```

```
[1] "dist"
```

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 1/2

```
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
```

Clustering process 2/2

```
d.hc$merge
```

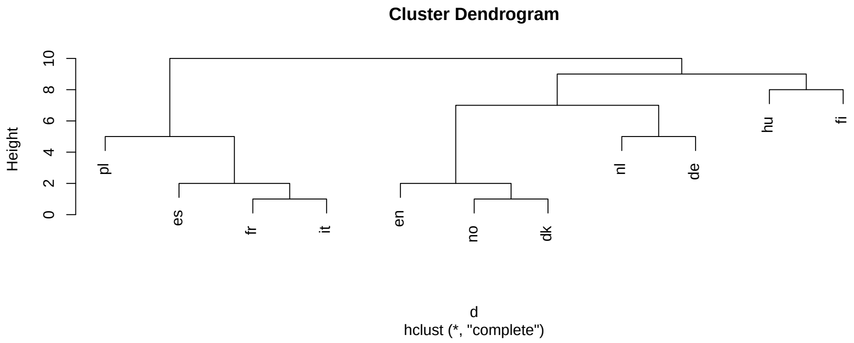
```
      [,1] [,2]
 [1,]   -2   -3
 [2,]   -6   -8
 [3,]   -7    2
 [4,]   -1    1
 [5,]   -9    3
 [6,]   -5    4
 [7,]   -4    6
 [8,]    5    7
 [9,]  -10    8
[10,]  -11    9
```

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.

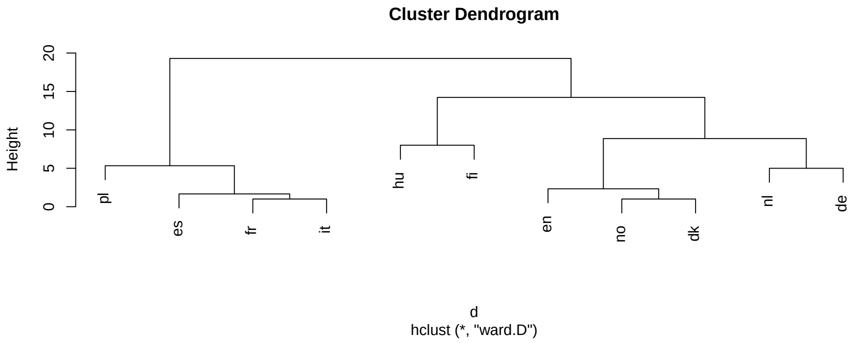
Complete linkage

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



Ward

```r
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
```

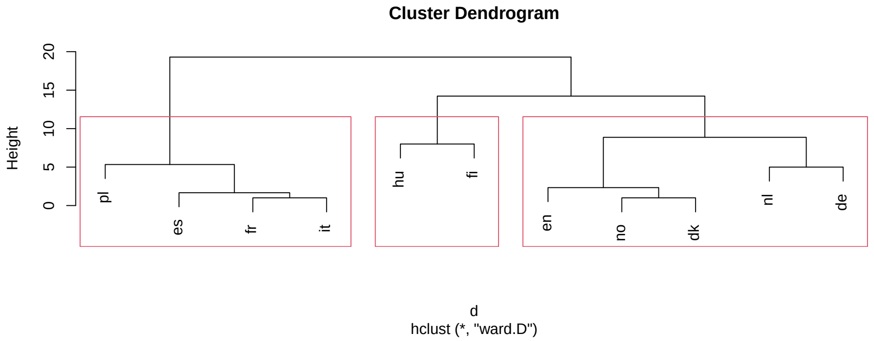
Turning the “named vector” into a data frame

```
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 cuatro 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

```r
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

```r
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

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

```
[1] 2
```

```r
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

```r
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._Gern
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_SS
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

```r
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
```

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.s
vital.s
```

```
# A tibble: 97 x 4
   birth[,1] death[,1] infant[,1] country
       <dbl>     <dbl>      <dbl> <chr>
 1    -0.334   -1.11       -0.524 Albania
 2    -1.17     0.186      -0.948 Czechoslovakia
 3    -1.30     0.552      -0.872 Hungary
 4    -1.15    -0.0293     -0.609 Romania
 5    -0.851   -0.180      -0.694 USSR
 6    -1.17     0.164      -0.911 Ukrainian_SSR
```

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
vital.km3
```

```
K-means clustering with 3 clusters of sizes 40, 25, 32

Cluster means:
       birth      death      infant
1 -1.0376994 -0.3289046 -0.90669032
2  1.1780071  1.3323130  1.32732200
3  0.3768062 -0.6297388  0.09639258

Clustering vector:
 [1] 3 1 1 1 1 1 2 1 3 3 1 2 1 1 1 1 1 1 1 1 1 2 2 1 3 3 3 2
[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 3
```

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 1 has lower than average rates on everything; cluster 2 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 1 2 2 1 3 3 3 2
[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 3
[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 3
[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
)
vital.3
```

```
# A tibble: 97 x 2
   country       cluster
   <chr>           <int>
 1 Albania             3
 2 Czechoslovakia      1
 3 Hungary             1
 4 Romania             1
 5 USSR                1
 6 Ukrainian_SSR       1
 7 Bolivia             2
 8 Chile               1
```

Which countries in which cluster?

Write function to extract cluster number `i` from dataframe `d` with a column called `country`:

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

Cluster membership: cluster 2

```r
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

```r
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

```r
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"
```

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:

```r
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

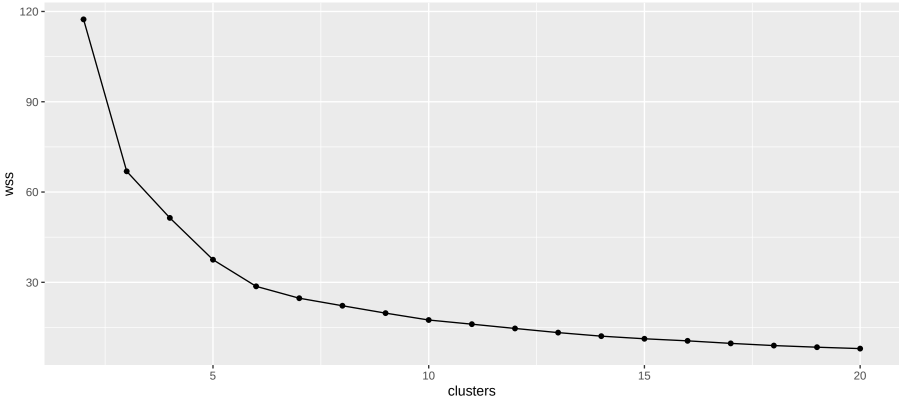
Make a data frame with desired numbers of clusters, and fill it with the total within-group sums of squares. `ss` expects a single number of clusters, not a vector of several, so run `rowwise`:

```
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
```

Scree plot

```r
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

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

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

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

```r
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        cluster
   <chr>            <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
```

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:

```r
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."
```

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
- Old cluster 2 split into new clusters 2 and 5 (two types of "developing" countries)
- Old cluster 3 split into new 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
```

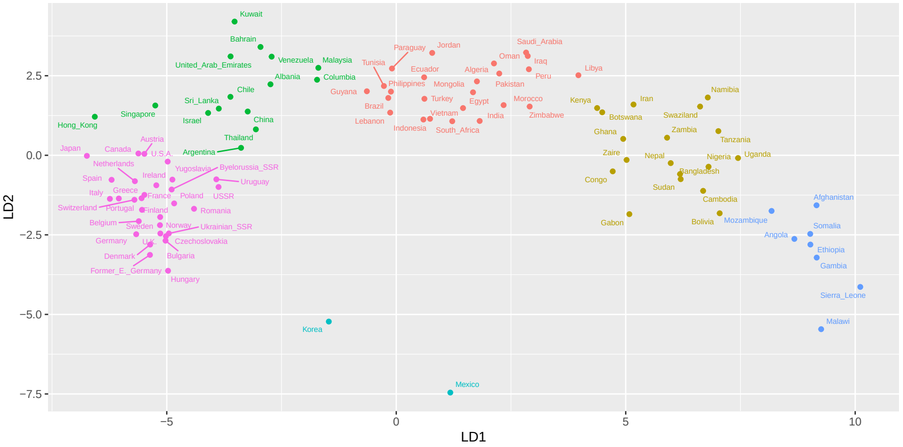
What's in there; making a plot

- `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
```

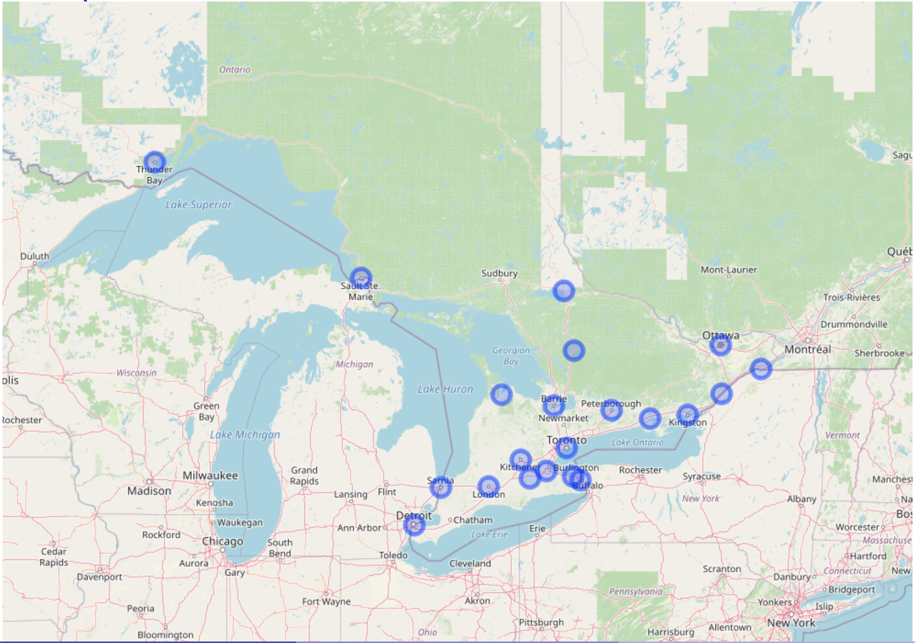


It would be better to zoom in on parts of this plot.

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



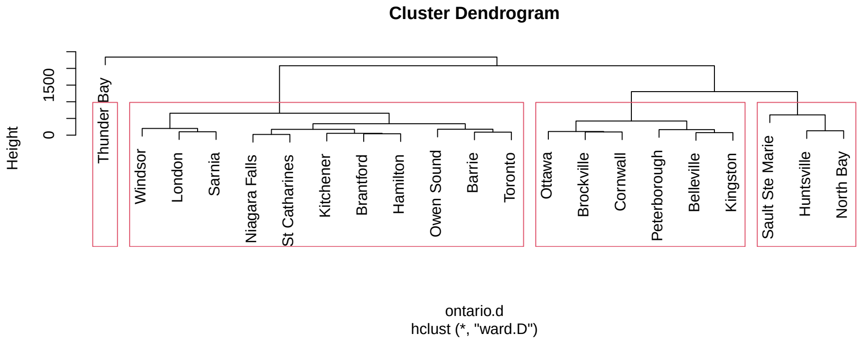
Ontario
Thunder Bay
Lake Superior
Duluth
Sault Ste. Marie
Sudbury
Mont-Laurier
Trois-Rivières
Drummondville
Ottawa
Montréal
Sherbrooke
Québ
Sagu
Georgian Bay
Michigan
Wisconsin
Lake Huron
Barrie
Newmarket
Peterborough
Kingston
Toronto
Lake Ontario
Vermont
Green Bay
Lake Michigan
Milwaukee
Madison
Grand Rapids
Lansing
Flint
Sarnia
London
Kitchener
Burlington
Buffalo
Rochester
Syracuse
New York
Albany
Manchest
Bos
Kenosha
Waukegan
Rockford
Chicago
South Bend
Ann Arbor
Detroit
Chatham
Lake Erie
Erie
Toledo
Cleveland
Worcester
Massachuse
Hartford
Cedar Rapids
Davenport
Aurora
Gary
Scranton
Danbury
Connecticut
New
Bridgeport
Pennsylvania
Yonkers
Islip
New York
Fort Wayne
Akron
Pittsburgh
Harrisburg
Allentown
Peoria
Bloomington
Ohio
Rochester
olis

Attempt 1

```
my_url <-
  "http://ritsokiguess.site/datafiles/ontario-road-distances.c
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)
```

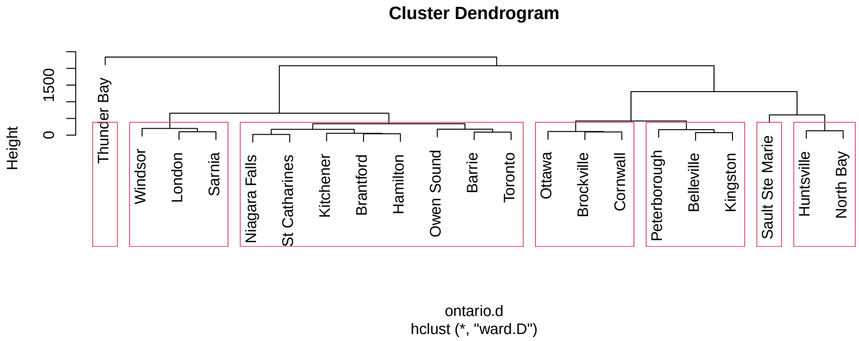


Comments

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

Seven clusters

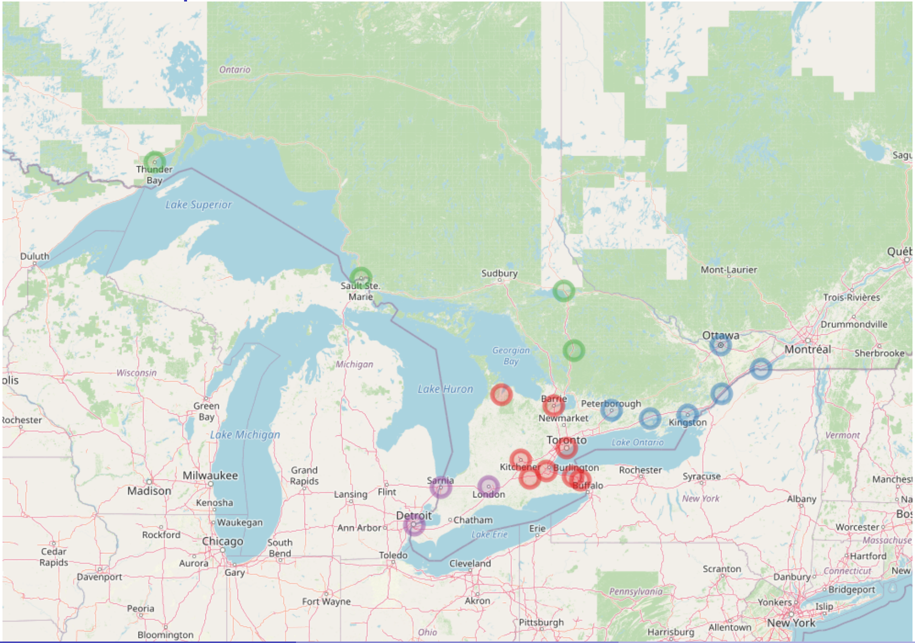
```
plot(ontario.hc)
rect.hclust(ontario.hc, 7)
```



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



Ontario
Thunder Bay
Lake Superior
Duluth
Sault Ste. Marie
Sudbury
Mont-Laurier
Trois-Rivières
Drummondville
Ottawa
Montréal
Sherbrooke
Georgian Bay
Michigan
Wisconsin
Lake Huron
Green Bay
Lake Michigan
Barrie
Peterborough
Newmarket
Kingston
Toronto
Lake Ontario
Vermont
Kitchener
Burlington
Rochester
Syracuse
Buffalo
Sarnia
London
Milwaukee
Madison
Grand Rapids
Lansing
Flint
Kenosha
Waukegan
Detroit
Chatham
Ann Arbor
Rockford
Chicago
South Bend
Toledo
Lake Erie
Erie
Cedar Rapids
Aurora
Gary
Davenport
Cleveland
New York
Albany
Worcester
Hartford
Scranton
Danbury
Bridgeport
Pennsylvania
Peoria
Fort Wayne
Akron
Pittsburgh
Yonkers
Islip
Bloomington
Ohio
Harrisburg
Allentown