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

```r
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

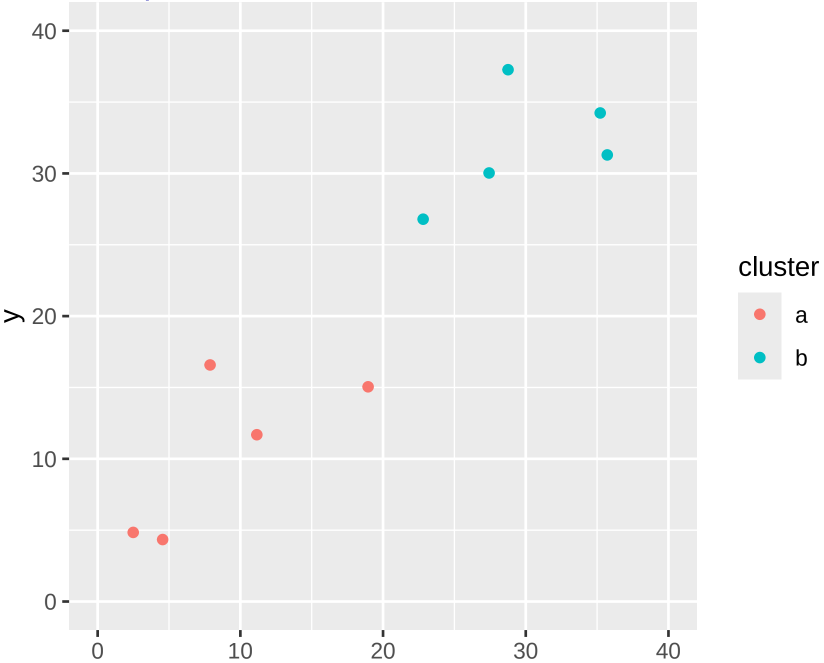
Dissimilarities and languages example

- 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

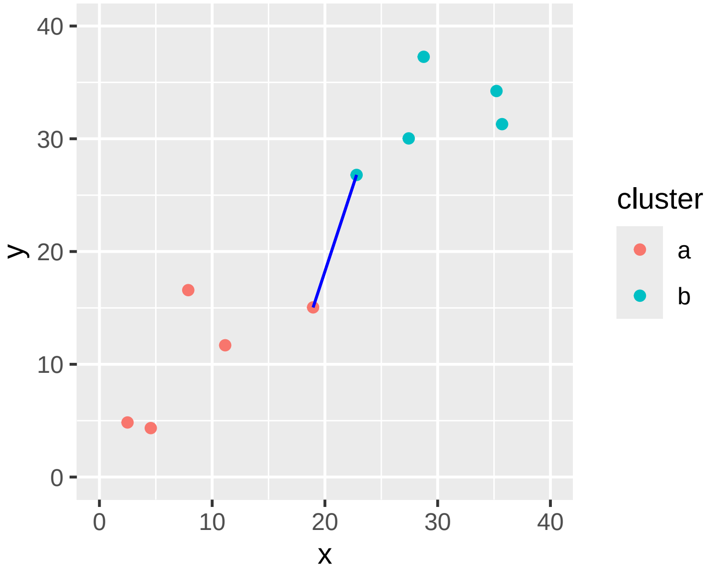
- Looking at process of forming clusters (of similar languages): **hierarchical cluster analysis** (`hclust`).
- Start with each individual in cluster by itself.
- Join "closest" clusters one by one until all individuals in one cluster.
- How to define closeness of two *clusters*? Not obvious, investigate 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



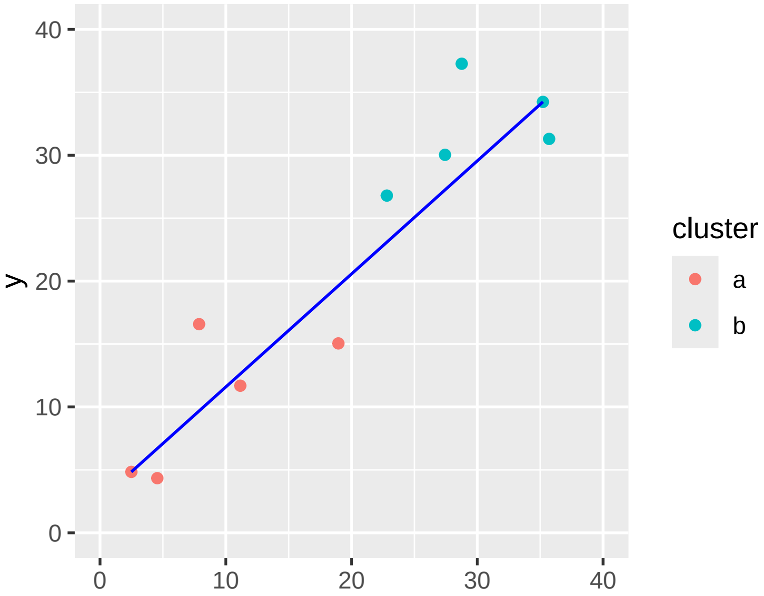
Single-linkage distance

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



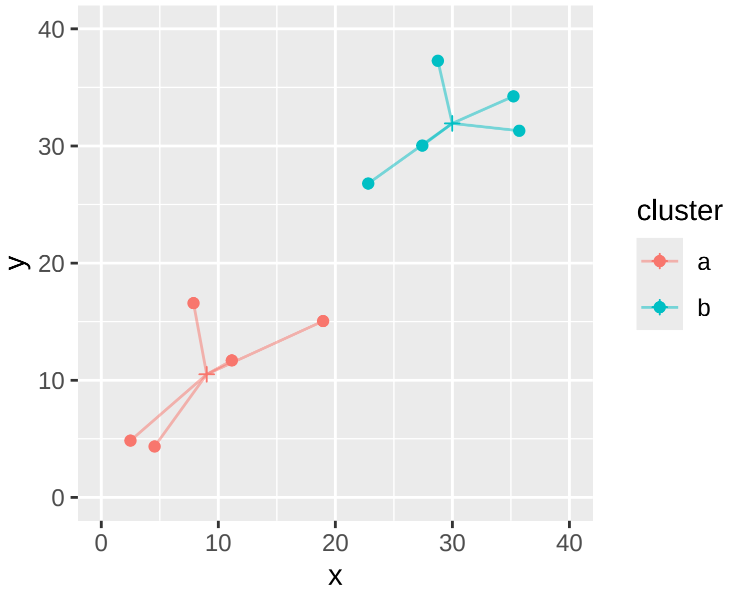
Complete linkage

Find the red and blue points that are farthest apart:



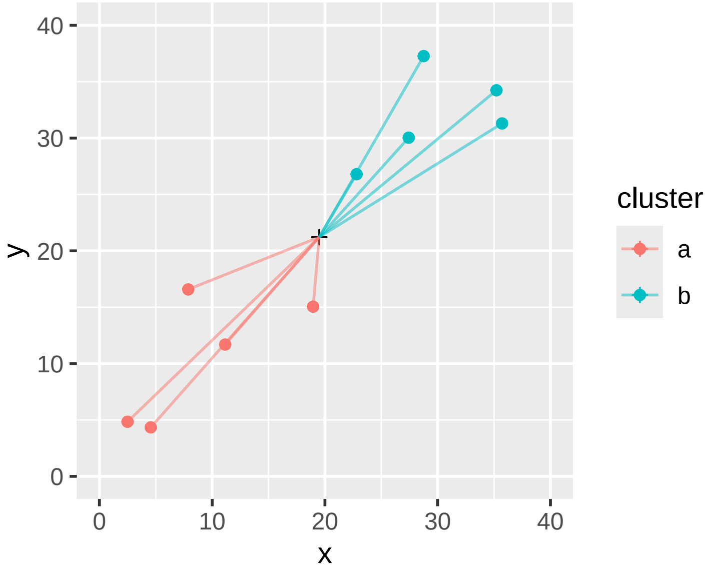
Ward's method

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



Ward's method part 2

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))
```

```
# 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
```

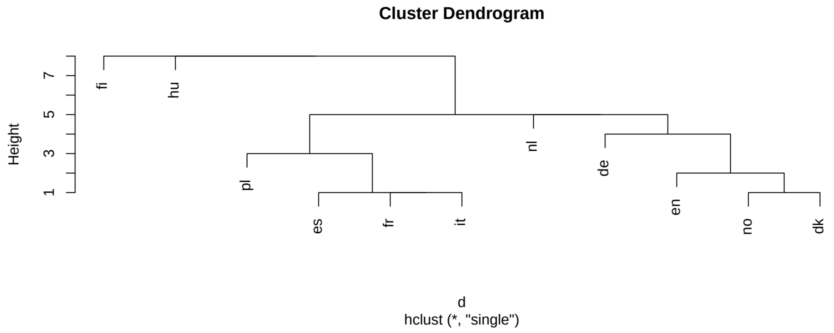
```
   en no dk nl de fr es it pl hu
no  2
dk  2  1
nl  7  5  6
de  6  4  5  5
fr  6  6  6  9  7
es  6  6  5  9  7  2
it  6  6  5  9  7  1  1
pl  7  7  6 10  8  5  3  4
hu  9  8  8  8  9 10 10 10 10
fi  9  9  9  9  9  9  9  8  9  8
```

```
class(d)
```

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

Cluster analysis and dendrogram

```r
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

```r
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
```

```r
d.hc$merge
```

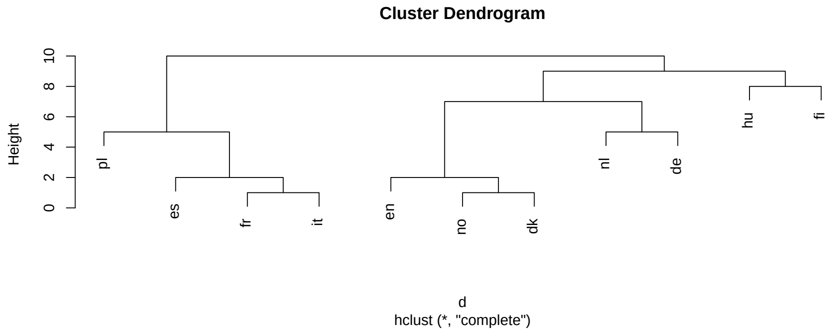
```
      [,1] [,2]
 [1,]   -2   -3
 [2,]   -6   -8
```

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.

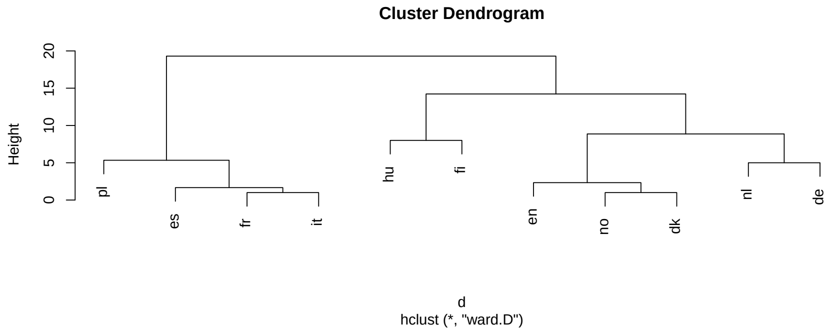
Complete linkage

```r
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:

```r
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
```

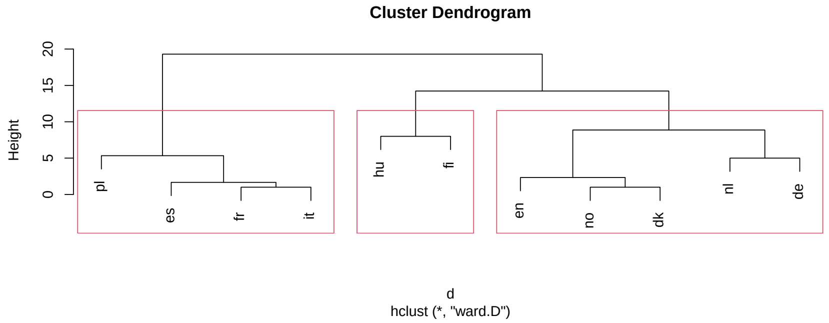
Turning the “named vector” into a data frame

```
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

```
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

```r
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

```r
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._
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 Byelorussi
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 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

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

Next, which countries in which cluster?

Write function to extract them:

```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"
[31] "Ireland"             "Netherlands"
[33] "Portugal"            "Sweden"
```

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

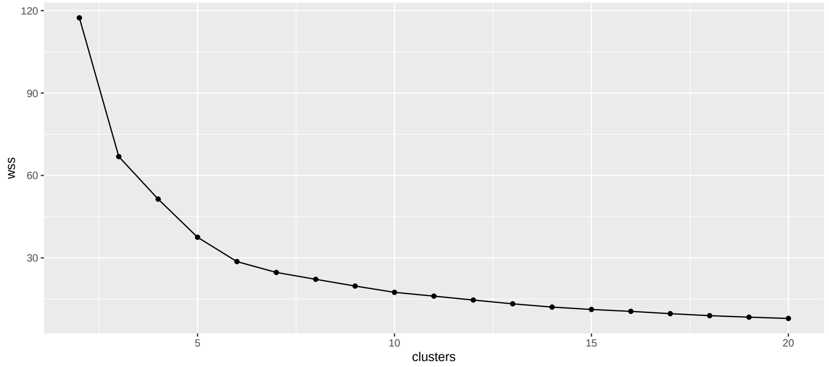
Make a data frame with desired numbers of clusters, and fill it with the total within-group sums of squares. `ss` expects a single number of clusters, not a vector of several, so run `rowwise`:

```
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
 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        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
 9 Peru                 1
10 Afghanistan          5
```

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:

```r
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

```r
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:

```r
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
```

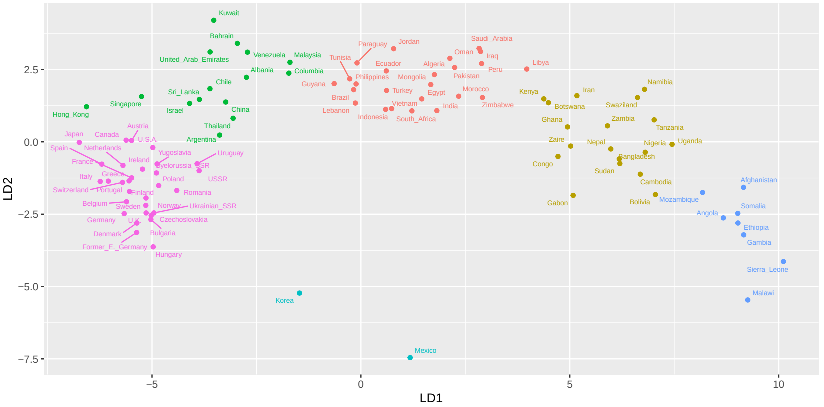
What's in there; making a plot

- `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(co
```

The plot

```
g
```

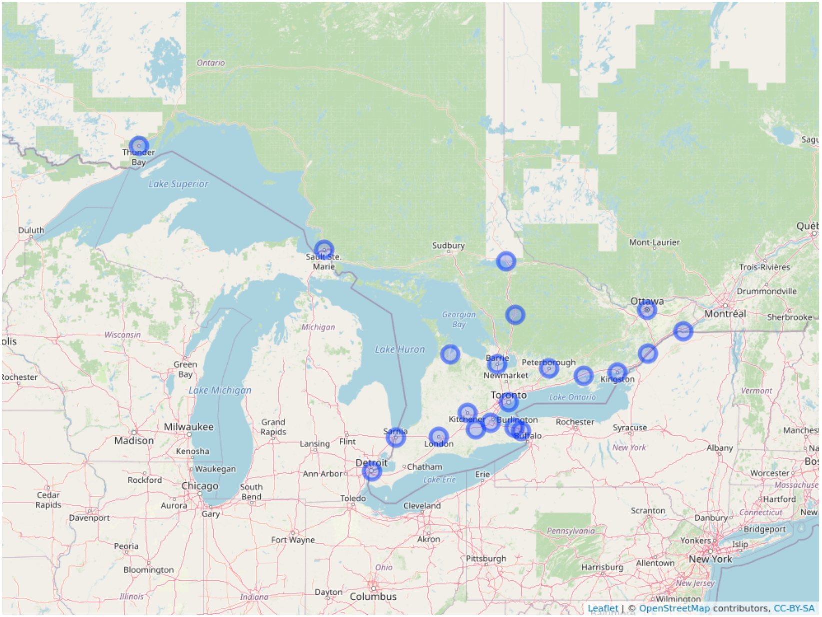


It would be better to zoom in on parts of this plot.

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

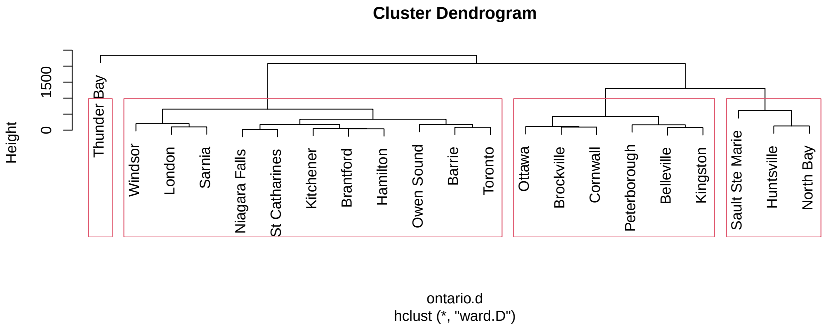


Attempt 1

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

Plot, with 4 clusters

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

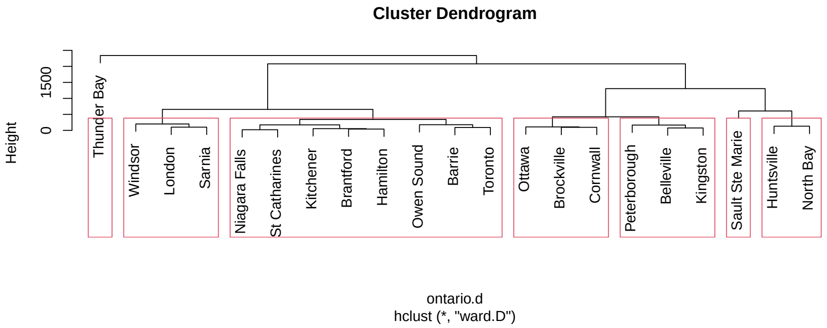


Comments

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

Seven clusters

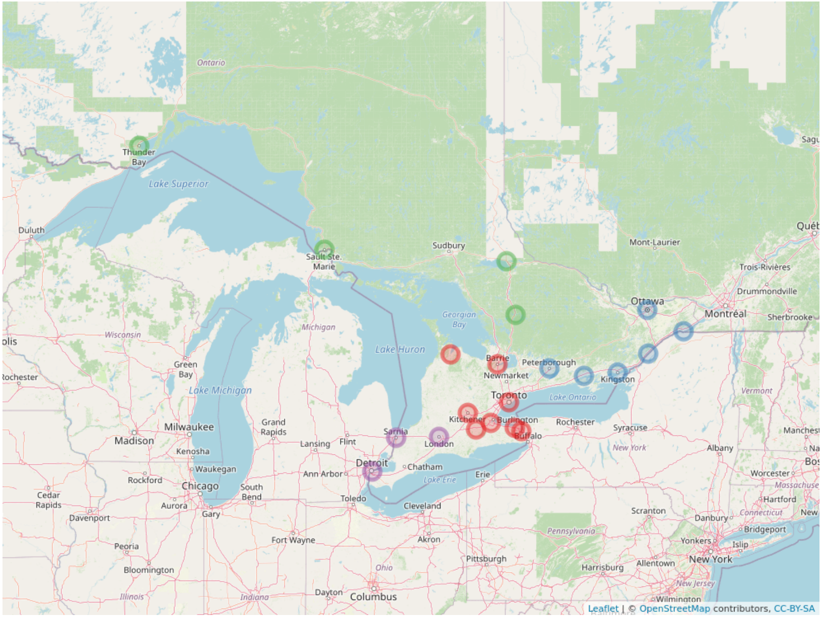
```r
plot(ontario.hc)
rect.hclust(ontario.hc, 7)
```



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


Leaflet | © OpenStreetMap contributors, CC-BY-SA