Rworkshop

Data processing in R

Bolin Wu
Aging Research Center
2022-03-24 (updated: 2022-10-24)

Reminder

- What we will talk about next usually can take 1-2 whole sessions for a master program in order to understand the technical details. Today the main purpose is to go through the tasks that R are capable of solving.
- R studio is very user-friendly. As explained before, whenever you have problem with a function, just type "?" + `function()`. For example:

```
?summary
?lm
?data.frame
```

--->R Studio

- If possible, please follow alone with your computer. It helps you to learn R faster! Welcome to ask question at any time.

Data

The example data we use are `paquid_cog.csv` and `paquid_cov.csv`.

Install and load package

We will mainly use the following two packages:

- `tidyverse`: A powerful package for data wrangling, which I will show later.
- `Hmisc`: We need this package for adding label to data.frame().
- However, please note that packages are not mandatory for solving the following tasks!

- To install package, you can use `install.package()` function.

```r
install.packages("tidyverse")
install.packages("Hmisc")
```

- we can load the package by using `library()` function.

```r
library(tidyverse)
library(Hmisc)
```

Import data

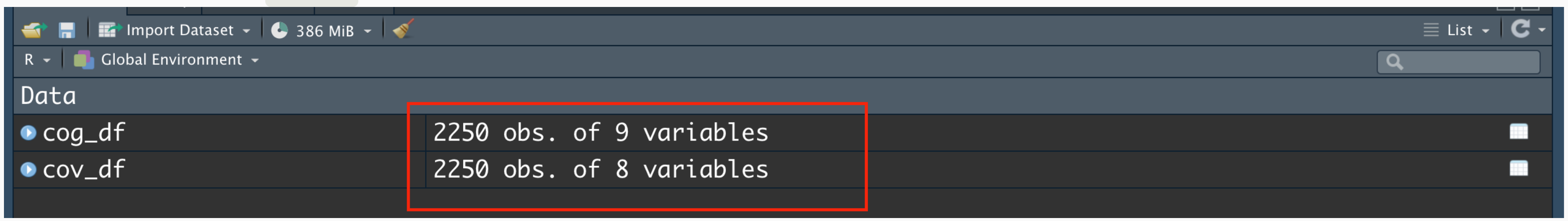
There are many different functions to read data, depending on the file's type. Since we have csv file, we can use `read.csv()` to read the data.

```r
cog_df ← read.csv(file = "data/paquid_cog.csv")
cov_df ← read.csv(file = "data/paquid_cov.csv")
# Use ?read.csv() to check what other arguments you can put in
```

Explore data

Usually the first thing we need to do is to check if the data are **correctly imported**.

- Looking at the `Data` panel



```
cog_df    2250 obs. of 9 variables
cov_df    2250 obs. of 8 variables
```

- Use `str()` function to check if the column types are as expected.

```
# check data's type
str(cog_df)
```

```
## 'data.frame':    2250 obs. of  9 variables:
##  $ X     : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ ID    : int  1 2 2 2 2 2 3 3 4 4 ...
##  $ MMSE  : int  26 26 28 25 24 22 28 25 NA 22 ...
##  $ BVRT  : int  10 13 13 12 13 9 13 6 NA 8 ...
##  $ IST   : int  37 25 28 23 16 15 28 16 NA 27 ...
##  $ dem   : int  0 1 1 1 1 1 0 0 0 0 ...
##  $ agedem: num  68.5 85.6 85.6 85.6 85.6 ...
##  $ age   : num  68.5 67 69.1 73.8 84.1 ...
##  $ wave  : int  1 1 2 3 4 5 1 2 1 2
```

Explore data

```
# check data's type
str(cov_df)
```

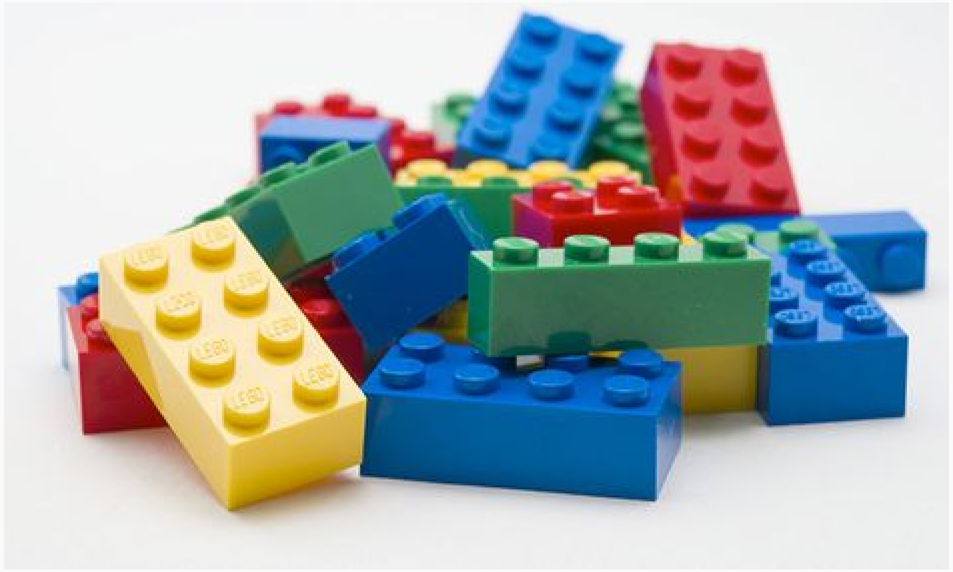
```
## 'data.frame':    2250 obs. of  8 variables:
##  $ X       : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ ID      : int  1 2 2 2 2 2 3 3 4 4 ...
##  $ age_init: num  67.4 65.9 65.9 65.9 65.9 ...
##  $ CEP     : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ male    : int  1 0 0 0 0 0 1 1 0 0 ...
##  $ HIER    : int  2 1 1 1 3 3 1 1 1 1 ...
##  $ age     : num  68.5 67 69.1 73.8 84.1 ...
##  $ wave    : int  1 1 2 3 4 5 1 2 1 2 ...
```

- Here we can see the data types are as expected.
- However, there is a non-sense column "X", we need to get rid of it. The easiest way to use `select()` function from `tidyverse` package.

```
# get rid of the first column 'X'
cog_df <- cog_df %>% select(-X)
cov_df <- cov_df %>% select(-X)
```

```
# get rid of the first column 'X'
cog_df <- cog_df %>% select(-X)
cov_df <- cov_df %>% select(-X)
```

Beautiful syntax with pipeline, just like playing LEGO. ---> R studio



Explore data

- Use `head()` function to check the first few rows of dataframe

```
head(cov_df)
```

```
##   ID age_init CEP male HIER      age wave
## 1  1  67.4167   1    1    2 68.50630    1
## 2  2  65.9167   1    0    1 66.99540    1
## 3  2  65.9167   1    0    1 69.09530    2
## 4  2  65.9167   1    0    1 73.80720    3
## 5  2  65.9167   1    0    3 84.14237    4
## 6  2  65.9167   1    0    3 87.09103    5
```

- Use `class()` function to check the type of cov_df: Is it a matrix, or data.frame, or list, or tibble?

```
class(cov_df)
```

```
## [1] "data.frame"
```

Personally I would love to convert `data.frame` to `tibble` for data wrangling. --> R studio...

Explore data

We may also interested in checking the descriptive statistics: `summary()`

```
# descriptive statistics
summary(cog_df)
```

```
##        ID             MMSE             BVRT
##  Min.   :  1.0   Min.   : 0.00   Min.   : 0.00
##  1st Qu.:132.2   1st Qu.:25.00   1st Qu.: 9.00
##  Median :263.0   Median :27.00   Median :11.00
##  Mean   :256.2   Mean   :25.99   Mean   :10.78
##  3rd Qu.:376.0   3rd Qu.:29.00   3rd Qu.:13.00
##  Max.   :500.0   Max.   :30.00   Max.   :15.00
##                  NA's   :36      NA's   :300
##       IST             dem              agedem
##  Min.   : 5.00   Min.   :0.0000   Min.   :66.87
##  1st Qu.:22.00   1st Qu.:0.0000   1st Qu.:82.03
##  Median :27.00   Median :0.0000   Median :86.61
##  Mean   :26.52   Mean   :0.3329   Mean   :85.89
##  3rd Qu.:31.00   3rd Qu.:1.0000   3rd Qu.:89.94
##  Max.   :40.00   Max.   :1.0000   Max.   :99.49
##  NA's   :198
##       age              wave
##  Min.   : 66.28   Min.   :1.000
```

Generate and label variables

1. Generate a variable “fu”, which means follow-up time and equals to age - age_init

- Let's first review cov_df:

```
head(cov_df)
```

```
##   ID age_init CEP male HIER      age wave
## 1  1  67.4167   1    1    2 68.50630    1
## 2  2  65.9167   1    0    1 66.99540    1
## 3  2  65.9167   1    0    1 69.09530    2
## 4  2  65.9167   1    0    1 73.80720    3
## 5  2  65.9167   1    0    3 84.14237    4
## 6  2  65.9167   1    0    3 87.09103    5
```

- How do we extract a specific column? By Google you can find many ways, one of them is to use `$` sign. "[1:10]" means take the elements one to ten.

```
cov_df$age_init[1:10]
```

```
##  [1] 67.4167 65.9167 65.9167 65.9167 65.9167 65.9167 71.5000
##  [8] 71.5000 66.0000 66.0000
```

Generate and label variables

1. Generate a variable “fu”, which means follow-up time and equals to age - age_init

- Now we are ready to generate the new variable:

```
fu ← cov_df$age - cov_df$age_init
# if you want to add the new variable to dataframe
cov_df$fu ← fu
head(cov_df)
```

```
##   ID age_init CEP male HIER      age wave       fu
## 1  1  67.4167   1    1    2 68.50630    1  1.08960
## 2  2  65.9167   1    0    1 66.99540    1  1.07870
## 3  2  65.9167   1    0    1 69.09530    2  3.17860
## 4  2  65.9167   1    0    1 73.80720    3  7.89050
## 5  2  65.9167   1    0    3 84.14237    4 18.22567
## 6  2  65.9167   1    0    3 87.09103    5 21.17433
```

Generate and label variables

2.Generate a variable “dem_young”, which means age of dementia onset (variable “agedem”) ≤70 years old (use the the if/else statement).

```
dem_young <- ifelse(cog_df$agedem <= 70, yes = 1, no = 0)
# put dem_young to cog_df
cog_df$dem_young <- dem_young
head(cog_df)
```

```
##   ID MMSE BVRT IST dem  agedem      age wave dem_young
## 1  1   26   10  37   0 68.5063 68.50630    1         1
## 2  2   26   13  25   1 85.6167 66.99540    1         0
## 3  2   28   13  28   1 85.6167 69.09530    2         0
## 4  2   25   12  23   1 85.6167 73.80720    3         0
## 5  2   24   13  16   1 85.6167 84.14237    4         0
## 6  2   22    9  15   1 85.6167 87.09103    5         0
```

Generate and label variables

3.**Rename** variable “CEP” as “education” and change the variable class to **factor**. **Label** the variable values as 0=“Below primary school”, 1=“Primary school and above”.

- We can rename a specific column "CEP" as follows:

```r
colnames(cov_df)[colnames(cov_df) == "CEP"] <- "education"
head(cov_df)
```

```
##   ID age_init education male HIER      age wave       fu
## 1  1  67.4167         1    1    2 68.50630    1  1.08960
## 2  2  65.9167         1    0    1 66.99540    1  1.07870
## 3  2  65.9167         1    0    1 69.09530    2  3.17860
## 4  2  65.9167         1    0    1 73.80720    3  7.89050
## 5  2  65.9167         1    0    3 84.14237    4 18.22567
## 6  2  65.9167         1    0    3 87.09103    5 21.17433
```

- Wait, what is going on here? ---> R studio

Generate and label variables

3.**Rename** variable “CEP” as “education” and change the variable class to **factor**. **Label** the variable values as 0=“Below primary school”, 1=“Primary school and above”.

- To label the variable we need to use the fore-mentioned `Hmisc` package.

Actually this is also new for me…

```
label(cov_df[["education"]]) <- "0='Below primary school', 1='Primary school and above
```

And then you can use View panel to check the label in the dataset.---> R Studio.

Or use the `factor` function:

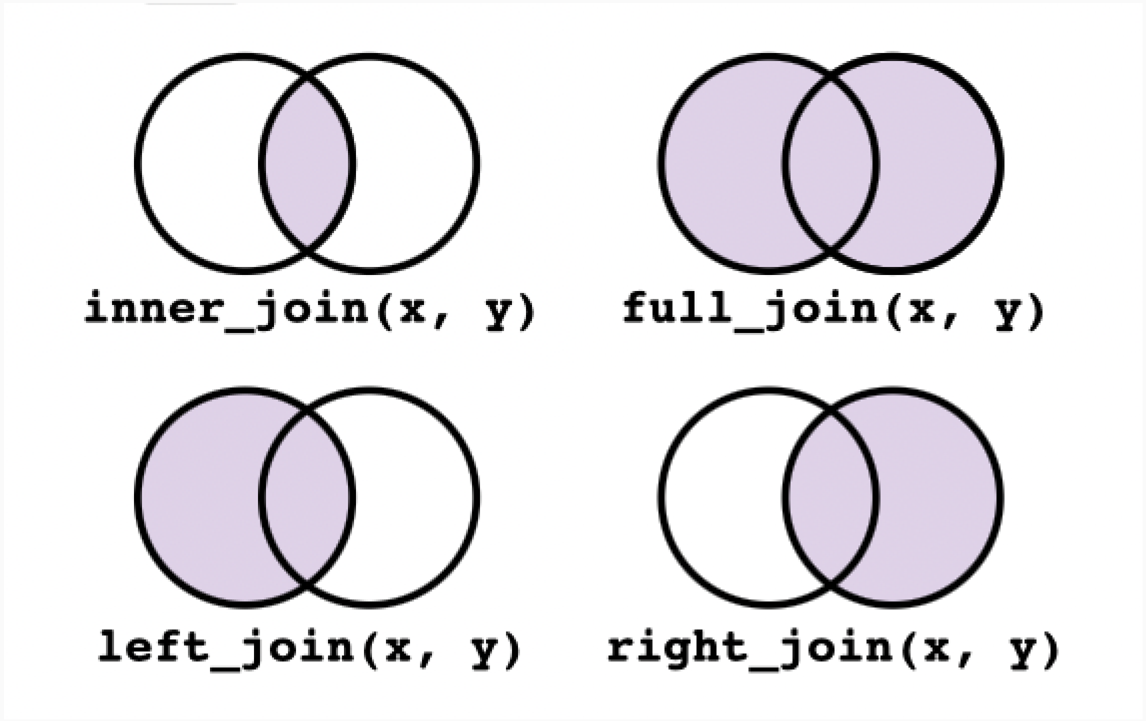
```
cov_label = factor(x = cov_df[["education"]],levels = c(0,1),labels = c('Below primary
head(cov_label)
```

```
## [1] Primary school and above Primary school and above
## [3] Primary school and above Primary school and above
## [5] Primary school and above Primary school and above
## Levels: Below primary school Primary school and above
```

Merge and reshape data sets

4.**Merge** datasets “paquid_cog” and “paquid_cov” to a data frame named “paquid”.

- With `join_` function: There are 4 common types of joins.



Merge and reshape data sets

4.**Merge** datasets “paquid_cog” and “paquid_cov” to a data frame named “paquid”.

```
paquid <- full_join(x = cog_df, y = cov_df, by = c("ID", "wave", "age"))
head(paquid)
```

```
##   ID MMSE BVRT IST dem  agedem      age wave dem_young age_init
## 1  1   26   10  37   0 68.5063 68.50630    1         1  67.4167
## 2  2   26   13  25   1 85.6167 66.99540    1         0  65.9167
## 3  2   28   13  28   1 85.6167 69.09530    2         0  65.9167
## 4  2   25   12  23   1 85.6167 73.80720    3         0  65.9167
## 5  2   24   13  16   1 85.6167 84.14237    4         0  65.9167
## 6  2   22    9  15   1 85.6167 87.09103    5         0  65.9167
##   education male HIER       fu
## 1         1    1    2  1.08960
## 2         1    0    1  1.07870
## 3         1    0    1  3.17860
## 4         1    0    1  7.89050
## 5         1    0    3 18.22567
## 6         1    0    3 21.17433
```

Merge and reshape data sets

- With `merge` function: In merge function, it finds columns with the same name by default. Therefore we only need to specify x and y data sets. You can recheck this by reading `?merge`.

```
paquid2 <- merge(x = cog_df, y = cov_df)
head(paquid2,n = 3)
```

```
##   ID     age wave MMSE BVRT IST dem   agedem dem_young age_init
## 1  1 68.5063    1   26   10  37   0 68.50630         1  67.4167
## 2 10 81.0601    1   30   12  35   0 88.01694         0  77.7500
## 3 10 83.0861    2   28    8  22   0 88.01694         0  77.7500
##   education male HIER     fu
## 1         1    1    2 1.0896
## 2         0    0    1 3.3101
## 3         0    0    1 5.3361
```

- This result is difficult to compare with paquid. We can reorder paquid2 so that it has the same column/row order as paquid.

```r
paquid2 <- paquid2[order(paquid2$ID), names(paquid)]
head(paquid2,n = 3)
```

```
##      ID MMSE BVRT IST dem  agedem     age wave dem_young
## 1     1   26   10  37   0 68.5063 68.5063    1         1
## 449   2   26   13  25   1 85.6167 66.9954    1         0
## 450   2   28   13  28   1 85.6167 69.0953    2         0
##      age_init education male HIER     fu
## 1     67.4167         1    1    2 1.0896
## 449   65.9167         1    0    1 1.0787
## 450   65.9167         1    0    1 3.1786
```

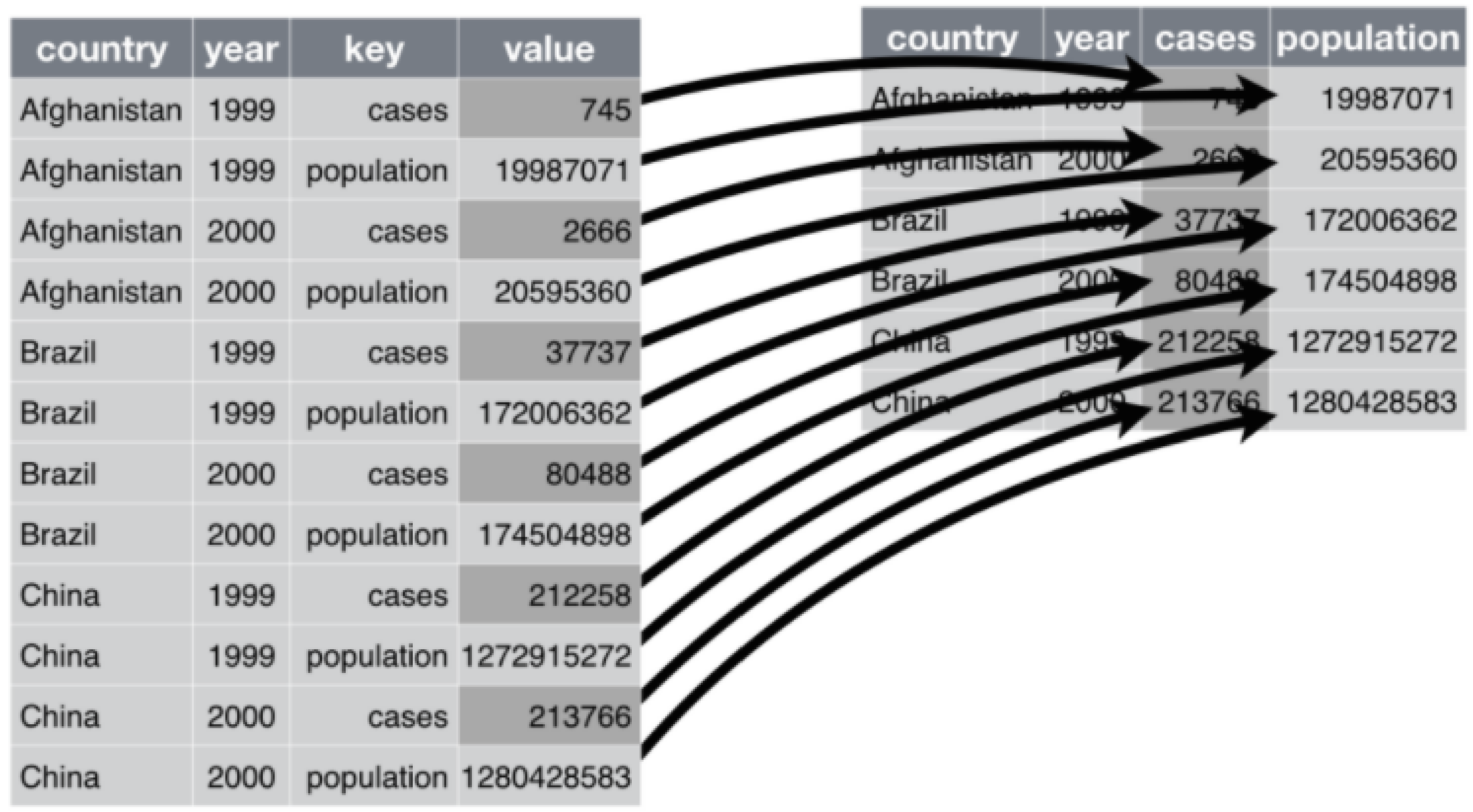
```r
head(paquid,n = 3)
```

```
##    ID MMSE BVRT IST dem  agedem     age wave dem_young age_init
## 1   1   26   10  37   0 68.5063 68.5063    1         1  67.4167
## 2   2   26   13  25   1 85.6167 66.9954    1         0  65.9167
## 3   2   28   13  28   1 85.6167 69.0953    2         0  65.9167
##    education male HIER     fu
## 1          1    1    2 1.0896
## 2          1    0    1 1.0787
## 3          1    0    1 3.1786
```

Merge and reshape data sets

5.Reshape the “paquid” data to **wide** format.

- Reshaping a data set is pretty tricky, usually I need to test out several times before I can arrive the final interested format.



country	year	key	value
Afghanistan	1999	cases	745
Afghanistan	1999	population	19987071
Afghanistan	2000	cases	2666
Afghanistan	2000	population	20595360
Brazil	1999	cases	37737
Brazil	1999	population	172006362
Brazil	2000	cases	80488
Brazil	2000	population	174504898
China	1999	cases	212258
China	1999	population	1272915272
China	2000	cases	213766
China	2000	population	1280428583

table2

country	year	cases	population
Afghanistan	1999	745	19987071
Afghanistan	2000	2666	20595360
Brazil	1999	37737	172006362
Brazil	2000	80488	174504898
China	1999	212258	1272915272
China	2000	213766	1280428583

Merge and reshape data sets

- Points to consider:

1. What is the variable that measures the time span?
2. What variables we would like to spread? Is it only one column to spread, or multiple?
3. What variables are unchanged?

Merge and reshape data sets

- Time span: column `wave` represents the time span.

```r
summary.factor(paquid$wave)
```

```
##   1   2   3   4   5   6   7   8   9
## 500 424 346 288 232 173 134 100  53
```

- Columns to change
  - If only spread `MMSE` column

```r
paquid_wide = spread(data = paquid, value = "MMSE", key = "wave", sep = "MMSE")
```

Merge and reshape data sets

```r
paquid_wide
```

```
##    ID BVRT IST dem   agedem      age dem_young age_init
## 1    1   10  37   0 68.50630 68.50630         1  67.4167
## 2    2   13  25   1 85.61670 66.99540         0  65.9167
## 3    2   13  28   1 85.61670 69.09530         0  65.9167
## 4    2   12  23   1 85.61670 73.80720         0  65.9167
## 5    2   13  16   1 85.61670 84.14237         0  65.9167
## 6    2    9  15   1 85.61670 87.09103         0  65.9167
## 7    3   13  28   0 74.73340 72.59240         0  71.5000
## 8    3    6  16   0 74.73340 74.73340         0  71.5000
## 9    4   NA  NA   0 87.63313 73.95350         0  66.0000
## 10   4    8  27   0 87.63313 87.63313         0  66.0000
## 11   5   10  34   0 88.12868 68.39840         0  67.3333
## 12   5   13  36   0 88.12868 72.52700         0  67.3333
## 13   5   12  36   0 88.12868 75.15260         0  67.3333
## 14   5   11  28   0 88.12868 77.52632         0  67.3333
## 15   5   11  35   0 88.12868 80.36547         0  67.3333
## 16   5    9  25   0 88.12868 85.01300         0  67.3333
## 17   5   12  27   0 88.12868 88.12868         0  67.3333
## 18   6   12  37   1 86.54336 71.15380         0  70.0833
## 19   6   14  38   1 86.54336 73.19080         0  70.0833
## 20   6   11  28   1 86.54336 75.28250         0  70.0833
## 21   6   10  30   1 86.54336 83.17296         0  70.0833
```

- Columns to change
  - If only spread `MMSE` column.
  - If we want to change all the columns varying at waves. (`reshape()` function)

```
# timevar: the variable in long format that differentiates multiple records from the s
# idvar: Columns that will not be affected, stay the same
unchange_column ← c("ID", "age_init", "education", "male", "agedem", "dem","dem_young
wide_paquid ← reshape(data = paquid, timevar = "wave", idvar = unchange_column, direc
wide_paquid
```

```
##     ID dem   agedem dem_young age_init education male MMSE_1
## 1    1   0 68.50630         1  67.4167         1    1     26
## 2    2   1 85.61670         0  65.9167         1    0     26
## 7    3   0 74.73340         0  71.5000         1    1     28
## 9    4   0 87.63313         0  66.0000         1    0     NA
## 11   5   0 88.12868         0  67.3333         1    0     29
## 18   6   1 86.54336         0  70.0833         1    1     29
## 24   7   0 89.82510         0  84.5000         1    0     23
## 27   8   0 88.18344         0  70.5000         1    0     25
## 34   9   0 84.93430         0  79.6667         1    1     26
## 37  10   0 88.01694         0  77.7500         0    0     30
## 41  11   0 83.67730         0  82.5000         1    0     25
```

Merge and reshape data sets

- The changing mentioned above is reversable, check:

```
?gather
?reshape
```

Row-wise calculation

6.Generate a variable named “MMSE_M”, which is the number of missing values across variables “MMSE_1”, “MMSE_2”, ..., “MMSE_9” per individual. Label the variable as “the number of missing values in MMSE”.

```r
# convert dataframe to tibble for faster data cleaning
wide_paquid ← as_tibble(wide_paquid)
paquid_MMSE ← wide_paquid %>% select(c("ID", contains("MMSE")))
paquid_MMSE
```

```
## # A tibble: 500 x 10
##       ID MMSE_1 MMSE_2 MMSE_3 MMSE_4 MMSE_5 MMSE_6 MMSE_7 MMSE_8
##    <int>  <int>  <int>  <int>  <int>  <int>  <int>  <int>  <int>
##  1     1     26     NA     NA     NA     NA     NA     NA     NA
##  2     2     26     28     25     24     22     NA     NA     NA
##  3     3     28     25     NA     NA     NA     NA     NA     NA
##  4     4     NA     22     NA     NA     NA     NA     NA     NA
##  5     5     29     27     30     28     28     27     26     NA
##  6     6     29     26     26     27     23     24     NA     NA
##  7     7     23     19     24     NA     NA     NA     NA     NA
##  8     8     25     27     23     29     24     27     25     NA
##  9     9     26     29     28     NA     NA     NA     NA     NA
## 10    10     30     28     24     25     NA     NA     NA     NA
## # ... with 490 more rows, and 1 more variable: MMSE_9 <int>
```

Row-wise calculation

- Use `rowSums` combined with `is.na`.

```r
MMSE_M <- rowSums(is.na(paquid_MMSE))
length(MMSE_M)
```

```
## [1] 500
```

```r
MMSE_M[1:10]
```

```
##  [1] 8 4 7 8 2 3 6 2 6 5
```

```r
# merge the vector to the tibble
paquid_MMSE$MMSE = MMSE_M
```

Row-wise calculation

7.View variables that contain “MMSE”.

- Use the `selection` from `tidyverse` package.

```
wide_paquid %>%
  select(contains("MMSE"))
```

Row-wise calculation

8.Generate variables “MEM_1”, “MEM_2”, ..., “MEM_9” which equals the mean of “BVRT” and “IST” at each time point.

- The original wide format data set has too many columns... Let's start with one babystep first:

```
# this tibble is the "ingredient"
wide_paquid %>% select(contains(c("ID","BVRT","IST")))
```

```
## # A tibble: 500 x 19
##        ID BVRT_1 BVRT_2 BVRT_3 BVRT_4 BVRT_5 BVRT_6 BVRT_7 BVRT_8
##     <int>  <int>  <int>  <int>  <int>  <int>  <int>  <int>  <int>
##   1     1     10     NA     NA     NA     NA     NA     NA     NA
##   2     2     13     13     12     13      9     NA     NA     NA
##   3     3     13      6     NA     NA     NA     NA     NA     NA
##   4     4     NA      8     NA     NA     NA     NA     NA     NA
##   5     5     10     13     12     11     11      9     12     NA
##   6     6     12     14     11     10      9      8     NA     NA
##   7     7      5      2     NA     NA     NA     NA     NA     NA
##   8     8     11     11     12      8     10      9      8     NA
##   9     9     11     12     12     NA     NA     NA     NA     NA
##  10    10     12      8      8     NA     NA     NA     NA     NA
## # ... with 490 more rows, and 10 more variables: BVRT_9 <int>,
```

Row-wise calculation

- What should MEM_1 look like?

$$MEM_1 = (BVRT_1 + IST_1)/2$$

```r
wide_paquid %>%
  select(contains(c("ID", "BVRT_1", "IST_1"))) %>%
  rowwise("ID") %>% # indicate the row index
  mutate(MEM_1 = mean(c(BVRT_1, IST_1))) %>% # mutate: create new column
  ungroup() # need to ungroup for rowwise calculation
```

```
## # A tibble: 500 x 4
##        ID BVRT_1 IST_1 MEM_1
##     <int>  <int> <int> <dbl>
##   1     1     10    37  23.5
##   2     2     13    25  19
##   3     3     13    28  20.5
##   4     4     NA    NA  NA
##   5     5     10    34  22
##   6     6     12    37  24.5
##   7     7      5    16  10.5
##   8     8     11    29  20
##   9     9     11    25  18
##  10    10     12    35  23.5
## # … with 490 more rows
```

Row-wise calculation

- Can we do the above process directly on the whole wide dataframe? --- Yes!

```
wide_paquid  %>%
  rowwise("ID") %>%
  mutate(MEM_1 = mean(c(BVRT_1,IST_1))) %>%
  ungroup()
```

```
## # A tibble: 500 x 62
##        ID   dem agedem dem_young age_init education   male MMSE_1
##     <int> <int>  <dbl>     <dbl>    <dbl> <labelled> <int>  <int>
##   1     1     0   68.5         1     67.4 1              1     26
##   2     2     1   85.6         0     65.9 1              0     26
##   3     3     0   74.7         0     71.5 1              1     28
##   4     4     0   87.6         0     66   1              0     NA
##   5     5     0   88.1         0     67.3 1              0     29
##   6     6     1   86.5         0     70.1 1              1     29
##   7     7     0   89.8         0     84.5 1              0     23
##   8     8     0   88.2         0     70.5 1              0     25
##   9     9     0   84.9         0     79.7 1              1     26
## 10    10     0   88.0         0     77.8 0              0     30
## # … with 490 more rows, and 54 more variables: BVRT_1 <int>,
## #   IST_1 <int>, age_1 <dbl>, HIER_1 <int>, fu_1 <dbl>,
## #   MMSE_2 <int>, BVRT_2 <int>, IST_2 <int>, age_2 <dbl>,
## #   HIER_2 <int>, fu_2 <dbl>, MMSE_3 <int>, BVRT_3 <int>,
```

Row-wise calculation

- We can do the same procedure for the rest eight variables by loop and assign() function. This flexibility renders R an advantage concerning repetitive work.

```r
for (i in 1:9) {
  BVRT_i = paste0("BVRT_", i)
  IST_i = paste0("IST_", i)
  # create new variable name
  MEM_i = paste0("MEM_", i)
  # assign value to each new variable
  wide_paquid = wide_paquid  %>%
    rowwise("ID") %>%
    mutate( !! sym(MEM_i) := mean(c(get(BVRT_i),get(IST_i)))) %>%
    ungroup()
}
# sym(new_col_name) := is a dynamic way of writing MEM_1 = , MEM_2 = ,etc
# when using functions like mutate()
# in the tidyr package
```

Row-wise calculation

9.View variables that contain “MEM”, “BVRT”, or “IST”.:

```
wide_paquid %>%
  select(contains(c("ID", "MEM", "BVRT","IST")))
```

```
## # A tibble: 500 x 28
##       ID MEM_1 MEM_2 MEM_3 MEM_4 MEM_5 MEM_6 MEM_7 MEM_8 MEM_9
##    <int> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1     1  23.5  NA    NA    NA    NA       NA  NA       NA    NA
##  2     2  19    20.5  17.5  14.5  12       NA  NA       NA    NA
##  3     3  20.5  11    NA    NA    NA       NA  NA       NA    NA
##  4     4  NA    17.5  NA    NA    NA       NA  NA       NA    NA
##  5     5  22    24.5  24    19.5  23       17  19.5     NA    NA
##  6     6  24.5  26    19.5  20    17.5     17  NA       NA    NA
##  7     7  10.5   9    NA    NA    NA       NA  NA       NA    NA
##  8     8  20    18.5  20    18    18.5     16  11.5     NA    NA
##  9     9  18    18    18    NA    NA       NA  NA       NA    NA
## 10    10  23.5  15    16.5  NA    NA       NA  NA       NA    NA
## # ... with 490 more rows, and 18 more variables: BVRT_1 <int>,
## #   BVRT_2 <int>, BVRT_3 <int>, BVRT_4 <int>, BVRT_5 <int>,
## #   BVRT_6 <int>, BVRT_7 <int>, BVRT_8 <int>, BVRT_9 <int>,
## #   IST_1 <int>, IST_2 <int>, IST_3 <int>, IST_4 <int>,
## #   IST_5 <int>, IST_6 <int>, IST_7 <int>, IST_8 <int>,
## #   IST_9 <int>
```

Summarizing data

10.Summarize variable "age_init" (mean, sd, quantiles, etc), summarize "age_init" by variable "male".

- As is shown before, we can use `summary` function.

```
summary(wide_paquid$age_init)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   65.25   68.42   73.83   74.23   78.42   92.33
```

```
# sd is missing, we can calculate it with sd() function
sd(wide_paquid$age_init)
```

```
## [1] 6.392525
```

Summarizing data

- If we would like to summary by a specific group: Use `group_by` function and `summarise` function, connected by pipeline:

```
wide_paquid %>%
  group_by(male) %>%
  summarise(max = max(age_init),
            q3 = quantile(age_init, 0.75),
            mean = mean(age_init),
            q1 = quantile(age_init, 0.25),
            min = min(age_init),
            sd = sd(age_init)
            )
```

```
## # A tibble: 2 x 7
##    male   max    q3  mean    q1   min    sd
##   <int> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1     0  91.9  79.6  74.8  68.2  65.5  6.83
## 2     1  92.3  77.5  73.5  68.5  65.2  5.68
```

Summarizing data

11.Summarize variable “MMSE_1” (mean, sd, quantiles, etc), summarize “age_init” by variable “male”. Note how R deals with missing values.

This question is similar to the previous one. I would leave it to the audience.

Summarizing data

12.Tabulate variable “male”, tabulate variable “male” and “education”, add row-wise and column-wise proportions.

- Find frequency of elements in male

```
table(wide_paquid$male)
```

```
##
##   0   1
## 288 212
```

- Male and education

```
tab_male_edu = table(wide_paquid %>% select("male", "education"))
prop.table(tab_male_edu)
```

```
##      education
## male      0     1
##     0 0.202 0.374
##     1 0.088 0.336
```

Summarizing data

- It seems difficult to add column to table() directly, so we convert it to tibble first

```
tib_male_edu = as_tibble(table(wide_paquid %>% select("male", "education")))
tib_male_edu
```

```
## # A tibble: 4 x 3
##   male  education     n
##   <chr> <chr>     <int>
## 1 0     0           101
## 2 1     0            44
## 3 0     1           187
## 4 1     1           168
```

Summarizing data

- Add proportion column to the tibble:

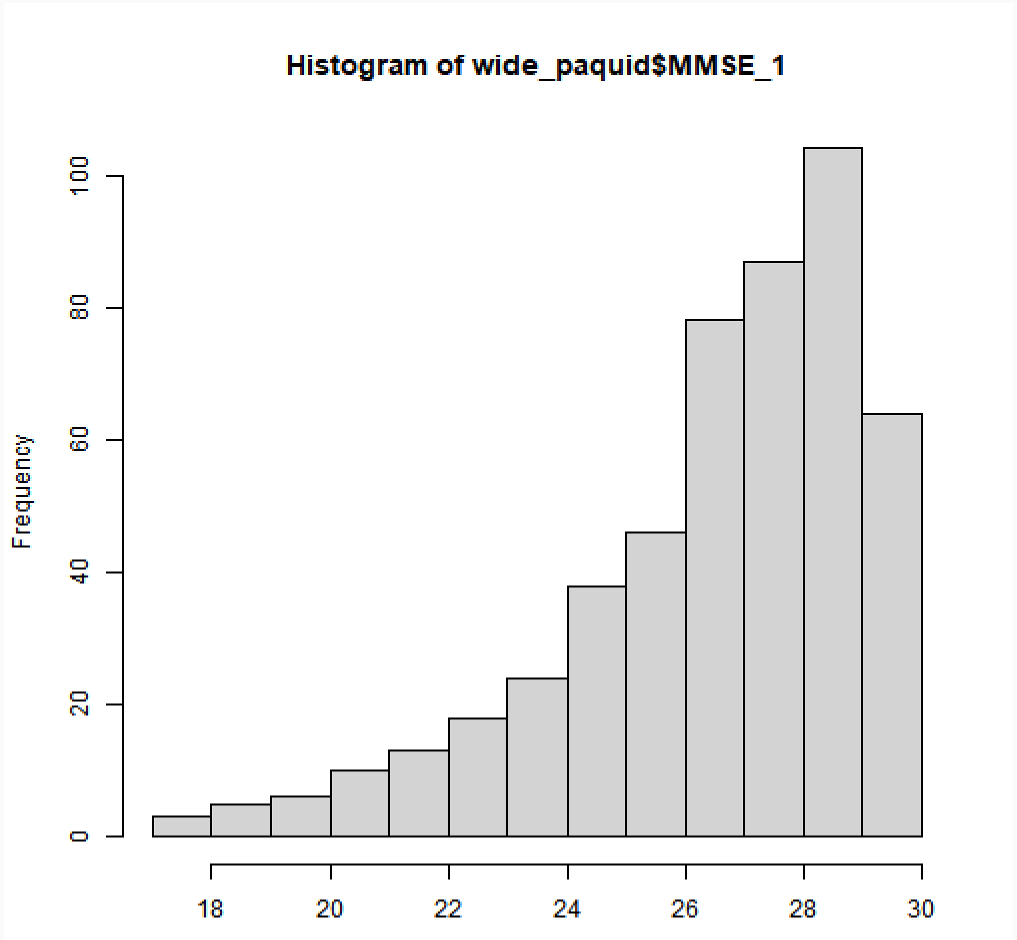
```
tib_male_edu$proportion = tib_male_edu$n / 500
tib_male_edu
```

```
## # A tibble: 4 x 4
##   male  education     n proportion
##   <chr> <chr>     <int>      <dbl>
## 1 0     0           101      0.202
## 2 1     0            44      0.088
## 3 0     1           187      0.374
## 4 1     1           168      0.336
```

Summarizing data

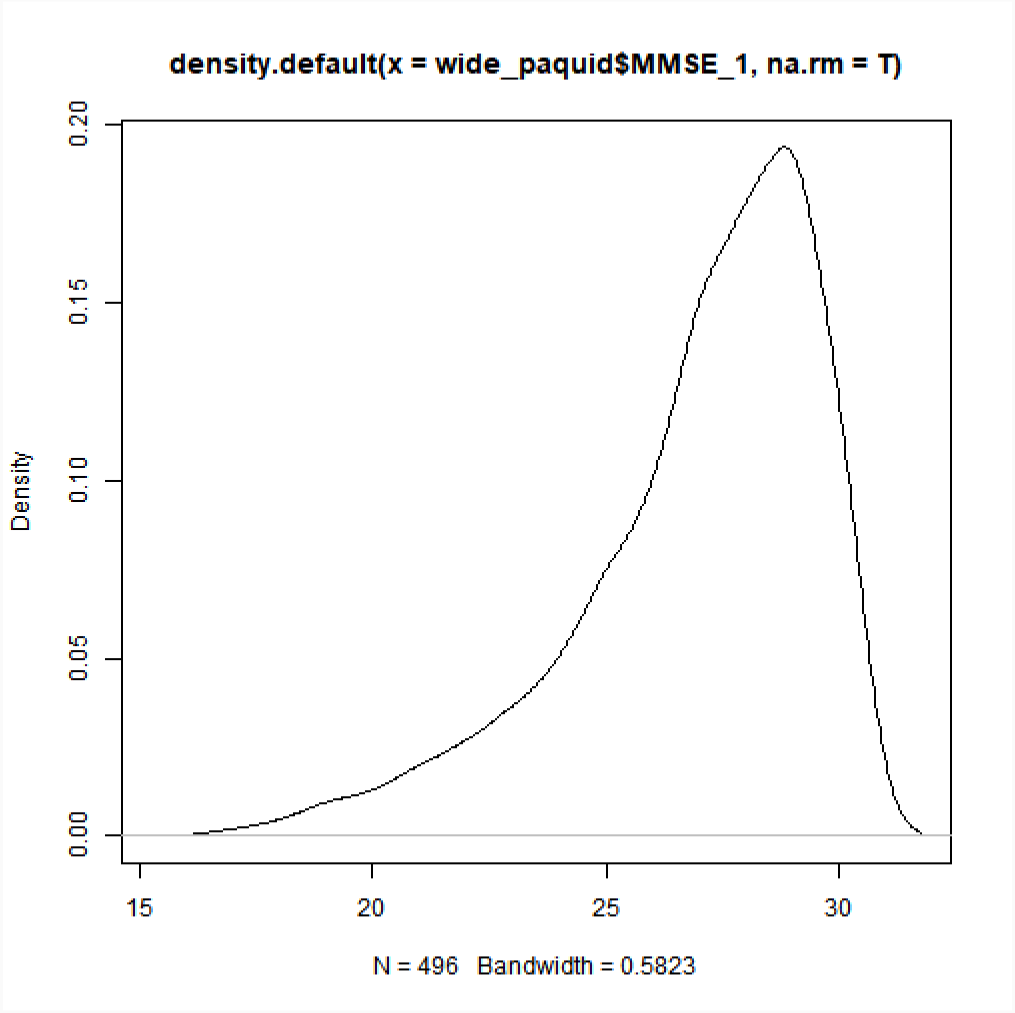
13.Draw a histogram and a density plot of "MMSE_1": Use `hist` and `plot` function:

```
hist(wide_paquid$MMSE_1)
```



Summarizing data

```
plot(density(wide_paquid$MMSE_1,na.rm = T))
```



Run simple models and check model

14.Run a linear regression, with **“MMSE_1”** as **dependent** variable and **“age_init”** and **“male”** as the **independent** variables, assuming “MMSE_1” has a normal distribution. Check model output.

- Use `lm` function. --->R studio

```
linear_m = lm(formula = MMSE_1 ~ age_init + male,data = wide_paquid)
```

Run simple models and check model

- Output from `summary` function:

```
summary(linear_m)
```

```
##
## Call:
## lm(formula = MMSE_1 ~ age_init + male, data = wide_paquid)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.9013 -1.0920  0.5365  1.7564  4.6739
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 36.69160    1.31023  28.004  < 2e-16 ***
## age_init    -0.13127    0.01740  -7.542 2.24e-13 ***
## male         0.06449    0.22498   0.287    0.775
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.463 on 493 degrees of freedom
```

Run simple models and check model

- Extract certain information from `summary` function:

```
summary(linear_m)$coefficients
```

```
##                Estimate Std. Error    t value      Pr(>|t|)
## (Intercept) 36.69160077 1.31022670 28.0040093 5.656499e-104
## age_init    -0.13126706 0.01740399 -7.5423524  2.238581e-13
## male         0.06448892 0.22498083  0.2866418  7.745070e-01
```

This output is super useful, when we have many combinations of dependent ~ independent. For example:

- Assuming we have 12 air pollution variables & 10 MRI variables. There are 120 pairs in total.
- We want to find which air pollutants could be significant in linear regression with MRI. Controlling for age, education, gender, etc...
- A loop can easily solve this problem! (Code script is available if anyone needs.)

Run simple models and check model

- Check the residual for model evaluation: ---> R studio

```
# residuals
linear_m$residuals
plot(linear_m)
```

Run simple models and check model

15.Run a logistic regression, with “dem_young” as dependent variable and “male” as the independent variables.

- Use `glm` function, set family = binomial. It is similar to `lm` function.

```
logi_m = glm(formula = dem_young ~ male,data = wide_paquid, family = "binomial")
logi_m
```

```
##
## Call:  glm(formula = dem_young ~ male, family = "binomial", data = wide_paquid)
##
## Coefficients:
## (Intercept)         male
##     -3.6924       0.4538
##
## Degrees of Freedom: 499 Total (i.e. Null);  498 Residual
## Null Deviance:        134.7
## Residual Deviance: 134     AIC: 138
```

Run simple models and check model

```
# output
summary(logi_m)
summary(logi_m)$coefficients
# similar to lm function's output

# residuals
logi_m$residuals

# fitted values
fitted.values(logi_m)
```

Run simple models and check model

- For binary estimation, we are usually interested in the predicted probability for each observation and the overall prediction accuracy.

$$\text{accuracy} = \frac{\text{Number of correct prediction}}{\text{Number of ovservation}}$$

```r
# probability
probabilities  = predict(logi_m,type = "response")
probabilities[1:5]
```

```
##          1          2          3          4          5 
## 0.03773585 0.02430556 0.03773585 0.02430556 0.02430556
```

```r
# overall accuracy, assume threshold = 0.5
predicted.classes <- ifelse(probabilities > 0.5, 1, 0)
mean(predicted.classes == wide_paquid$dem_young)
```

```
## [1] 0.97
```

Ending

- At first you may feel difficult. But don't worry, R has a strong user community, basically you can solve most of the problems by Google.
- After using R several years, I still rely heavily on Google and I keep learning new things.
- Because of its strong community, R now has many extensions. For example, this whole slide is written by R...
- R code for all the exercises is available on my github page: https://github.com/Bolin-Wu/Rworkshop_KI. If you have any question please feel free to ask and we can discuss together!