MiCM Workshop Series

R - Beyond the Basics

Efficient Coding

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- March 7, 2020

Link to workshop material https://github.com/ly129/MiCM2020 (https://github.com/ly129/MiCM2020)

Outline

1. **An overview of efficiency**
    - General rules
    - R-specific rules
    - R object types (if necessary)
    - Record runtime of your code
2. **Efficient coding**
    - Powerful functions in R

    ```
    - aggregate(), by(), apply() family
    - ifelse(), cut() and split()
    ```

    - Write our own functions in R

    ```
    - function()
    ```

    - Examples
        - Categorization, conditional operations, etc..
3. **Exercises**

Important note! There are MANY advanced and powerful packages that do different things. There are too many and they are too diverse to be covered in this workshop.

Here is a list of some awesome packages. https://awesome-r.com/ (https://awesome-r.com/)

1.1 General rules

1.2 R-specific rules

1.3 R data types and structures

1.3.1 R data types

```
- numeric
    - integer
    - double precision (default)
- logical
- character
- factor
- ...
```

In [1]:
```
# double
class(5); is.double(5)
```

'numeric'

TRUE

In [2]:
```
class(5.0);
is.double(5.0)
```

'numeric'

TRUE

In [3]:
```
5L/2L
```

2.5

In [4]:
```
# integer
class(5L); is.double(5L)
```

'integer'

FALSE

In [5]:
```
# How precise is double precision?
options(digits = 22) # show more digits in output
print(1/3)
options(digits = 7) # back to the default
```

```
[1] 0.3333333333333333148296
```

In [6]:
```
object.size(rep(5, 5e6))
object.size(rep(5L, 5e6))
```

```
40000048 bytes
```

```
20000048 bytes
```

In [7]:
```
# logical
class(TRUE); class(F)
```

'logical'

'logical'

In [8]:
```
# character
class("TRUE")
```

'character'

In [9]:
```
# Not important for this workshop
fac <- as.factor(c(1, 5, 11, 3))
fac
```

1 5 11 3

▶ **Levels**:

In [10]:
```
class(fac)
```

'factor'

In [11]:
```
# R has an algorithm to decide the order of the levels
fac.ch <- as.factor(c("B", "a", "1", "ab", "b", "A"))
fac.ch
```

B a 1 ab b A

▶ **Levels**:

1.3.2 R data structures

```
- Scalar *
- Vector
- Matrix
- Array
- List
- Data frame
- ...
```

In [12]:
```
# Scalar - a vector of length 1
myscalar <- 5
myscalar
```

5

In [13]:
```
class(myscalar)
```

'numeric'

In [14]:
```
# Vector
myvector <- c(1, 1, 2, 3, 5, 8)
myvector
```

1 1 2 3 5 8

In [15]:
```
class(myvector)
```

'numeric'

In [16]:
```
# Matrix - a 2d array
mymatrix <- matrix(c(1, 1, 2, 3, 5, 8), nrow = 2, byrow = FALSE)
mymatrix
```

A matrix:
2 × 3 of
type dbl

1	2	5
1	3	8

In [17]:
```
class(mymatrix)
```

'matrix'

In [18]:
```
str(mymatrix)
```

```
 num [1:2, 1:3] 1 1 2 3 5 8
```

In [19]:
```
# Array - not important for this workshop
myarray <- array(c(1, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144), dim = c(2, 2, 3))
print(myarray) # print() is not needed if run in R or Rstudio.
```

```
, , 1

     [,1] [,2]
[1,]    1    2
[2,]    1    3

, , 2

     [,1] [,2]
[1,]    5   13
[2,]    8   21

, , 3

     [,1] [,2]
[1,]   34   89
[2,]   55  144
```

In [20]:
```
class(myarray)
```

'array'

In [21]:
```
# List - very important for the workshop
mylist <- list(Title = "R Beyond the Basics",
               Duration = c(2, 2),
               sections = as.factor(c(1, 2, 3, 4)),
               Date = as.Date("2020-03-06"),
               Lunch_provided = FALSE,
               Feedbacks = c("Amazing!", "Great workshop!", "Yi is the best!", "Wow!")
)
print(mylist) # No need for print if running in R or Rstudio
```

```
$Title
[1] "R Beyond the Basics"

$Duration
[1] 2 2

$sections
[1] 1 2 3 4
Levels: 1 2 3 4

$Date
[1] "2020-03-06"

$Lunch_provided
[1] FALSE

$Feedbacks
[1] "Amazing!"        "Great workshop!" "Yi is the best!" "Wow!"
```

In [22]:
```
class(mylist)
```

'list'

In [23]:
```
# Access data stored in lists
mylist$Title
```

'R Beyond the Basics'

In [24]:
```
# or
mylist[[6]]
```

'Amazing!' 'Great workshop!' 'Yi is the best!' 'Wow!'

In [25]:
```
# Further
mylist$Duration[1]
mylist[[6]][2]
```

2

'Great workshop!'

In [26]:
```
# Elements in lists can have different data types
lapply(mylist, class) # We will talk about lapply() later
```

$Title
'character'
$Duration
'numeric'
$sections
'factor'
$Date
'Date'
$Lunch_provided
'logical'
$Feedbacks
'character'

In [27]:
```
# Elements in list can have different lengths
lapply(mylist, length)
```

$Title
1
$Duration
2
$sections
4
$Date
1
$Lunch_provided
1
$Feedbacks
4

In [28]:
```
# Data frames - most commonly used for analyses
head(mtcars)
```

A data.frame: 6 × 11

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

In [29]:
```
# Access a column (variable) in data frames
mtcars$mpg
```

21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 17.8 16.4 17.3 15.2 10.4 10.4 14.7 32.4 30.4 33.9 21.5 15.5 15.2 13.3 19.2 27.3 26 30.4 15.8 19.7 15 21.4

1.4 Time your program in R

Illustrations of R rules for efficiency.

```
- proc.time(), system.time()
- microbenchmark
```

1.4.1 Vectorized operation vs. loop

Example Calculate the square root of 1 to 1,000,000 using vectorized operation vs. using a for loop.

In [30]:
```
# Vectorized operation
# system.time(operation)  returns the time needed to run the 'operation'
t <- system.time( x1 <- sqrt(1:1000000) )
head(x1)
```

1 1.4142135623731 1.73205080756888 2 2.23606797749979 2.44948974278318

In [31]:
```
# For loop with memory pre-allocation
x2 <- rep(NA, 1000000)
t0 <- proc.time()
for (i in 1:1000000) {
    x2[i] <- sqrt(i)
}
t1 <- proc.time()

identical(x1, x2) # Check whether results are the same
```

TRUE

In [32]:
```
# For loop without memory pre-allocation
x3 <- NULL
t2 <- proc.time()
for (i in 1:1000000) {
    x3[i] <- sqrt(i)
}
t3 <- proc.time()

identical(x1, x2) # Check whether results are the sa
```

TRUE

In [33]:
```
# As we can see, R is not very fast with loops.
t; t1 - t0; t3 - t2
# ?proc.time
```

```
   user  system elapsed 
  0.006   0.004   0.010 

   user  system elapsed 
  0.066   0.003   0.070 

   user  system elapsed 
  0.288   0.062   0.351 
```

How did R execute these three sets of codes?

The better we know how programming languages work, how computers work in general, the better codes we can write.

1. Vectorized

```
x1 <- sqrt(1:1000000)

- sqrt 1, sqrt 2, ..., sqrt 1e6
- Save everything in x1 and put it in memory.
```

2. For loop with memory pre-allocation

```
x2 <- rep(NA, 1000000)
for (i in 1:1000000) { x2[i] <- sqrt(i) }

- Make a vector x2 of length 1e6 and set all elements to NA.
- Put it in memory.
- Setup for loop.
- 1st step
    - Find x2 in memory
    - Change the 1st element to sqrt 1
    - Put new x2 back in memory, delete old x2
- 2nd step
    - Find x2 in memory
    - Change the 2nd element to sqrt 2
    - Put new x2 back in memory, delete old x2
- ...
- - 1e6th step
    - Find x2 in memory
    - Change the 1e6th element to sqrt 1e6
    - Put new x2 back in memory, delete old x2
```

3. For loop without memory pre-allocation

```
x3 <- NULL
for (i in 1:1000000) { x3[i] <- sqrt(i) }

- Make an empty object x3 (NULL has length 0)
- Put it in memory
- Setup for loop.
- 1st step
    - Find x3 in memory
    - Change the 1st element to .., wait x3 has length 0
    - Make a new x3 that has length 1
    - Change the 1st element to sqrt 1
    - Put new x3 back in memory.., wait
      The memory allocated for old x3 is not enough for new x3
    - Find some new space in memory for new x3
    - Put new x3 back in memory, delete old x3
- 2nd step
    - Find x3 in memory
    - Change the 2nd element to .., wait x3 has length 1
    - Make a new x3 that has length 2
    - Copy the old x3 and paste as the first 1 element of new x3
    - Change the 2nd element to sqrt 2
    - Put new x3 back in memory.., wait
      The memory allocated for old x3 is not enough for new x3
    - Find some new space in memory for new x3
    - Put new x3 back in memory, delete old x3
- ...
- 1e6th step
    - Find x3 in memory
    - Change the 1e6th element to .., wait x3 has length 999999
    - Make a new x3 that has length 1e6
    - Copy the old x3 and paste as the first 999999 elements of new x3
    - Change the 1e6th element to sqrt 1e6
    - Put new x3 back in memory.., wait
      The memory allocated for old x3 is not enough for new x3
    - Find some new space in memory for new x3..
    - Put new x3 back in memory, delete old x3
```

Take-home message

- Use vectorized operations rather than loops for speed in R.
- Loops are more intuitive though.
- Balance between
  - speed
  - your need for speed
  - your level of comfortableness with linear algebra
  - your level of laziness
  - your typing speed
  - ...
- Based on what you are doing
  - dealing with big dataset and expensive calculations?
  - running the code only once or potentially many many times?

1.4.2 Use established functions

Example Calculate the square root using sqrt( ) vs. our own implementation.

In [34]:
```
# microbenchmark runs the code multiple times and take a summary
# Use well-developped R function
library(microbenchmark)
result <- microbenchmark(sqrt(500),
                         500^0.5,
                         unit = "ns", times = 1000
                        )
summary(result)
# Result in nanoseconds
```

A data.frame: 2 × 8

expr	min	lq	mean	median	uq	max	neval
<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
sqrt(500)	81	91	104.837	95	102	2968	1000
500^0.5	154	166	185.092	172	177	4313	1000

In summary, keep the rules in mind, know what you want to do, test your program, time your program.

2. Efficient coding

R has many powerful and useful functions that we can use to achieve efficient coding and computing.

2.1 Powerful functions in R

Let's play with some data.

In [35]:
```
data <- read.csv("https://raw.githubusercontent.com/ly129/MiCM2020/master/sample.csv", header =
TRUE)
head(data, 8)
```

A data.frame: 8 × 8

X	Sex	Wr.Hnd	NW.Hnd	Pulse	Smoke	Height	Age
<int>	<fct>	<dbl>	<dbl>	<int>	<fct>	<dbl>	<dbl>
1	Male	21.4	21.0	63	Never	180.00	19.000
2	Male	19.5	19.4	79	Never	165.00	18.083
3	Female	16.3	16.2	44	Regul	152.40	23.500
4	Female	15.9	16.5	99	Never	167.64	17.333
5	Male	19.3	19.4	55	Never	180.34	19.833
6	Male	18.5	18.5	48	Never	167.00	22.333
7	Female	17.5	17.0	85	Heavy	163.00	17.667
8	Male	19.8	20.0	NA	Never	180.00	17.417

In [36]:
```
summary(data)
```

```
       X              Sex         Wr.Hnd          NW.Hnd          Pulse       
 Min.   :  1.00   Female:47   Min.   :13.00   Min.   :12.50   Min.   : 40.00  
 1st Qu.: 25.75   Male  :53   1st Qu.:17.50   1st Qu.:17.45   1st Qu.: 50.25  
 Median : 50.50               Median :18.50   Median :18.50   Median : 71.50  
 Mean   : 50.50               Mean   :18.43   Mean   :18.39   Mean   : 69.90  
 3rd Qu.: 75.25               3rd Qu.:19.50   3rd Qu.:19.52   3rd Qu.: 84.75  
 Max.   :100.00               Max.   :23.20   Max.   :23.30   Max.   :104.00  
                                                              NA's   :6       
   Smoke        Height           Age       
 Heavy: 6   Min.   :152.0   Min.   :16.92  
 Never:79   1st Qu.:166.4   1st Qu.:17.58  
 Occas: 5   Median :170.2   Median :18.46  
 Regul:10   Mean   :171.8   Mean   :20.97  
            3rd Qu.:179.1   3rd Qu.:20.21  
            Max.   :200.0   Max.   :73.00  
            NA's   :13                     
```

a1. Calculate the mean writing hand span of all individuals

```
mean(x, trim = 0, na.rm = FALSE, ...)
```

In [37]:
```
mean(data$Wr.Hnd)
```

18.43

a2. Calculate the mean height of all individuals, exclude the missing values

In [38]:
```
mean(data$Height)
```

<NA>

In [39]:
```
mean(data$Height, na.rm = TRUE)
```

171.784597701149

a3. Calculate the mean of all continuous variables

```
apply(X, MARGIN, FUN, ...)
```

In [40]:
```
# Choose the continuous variables
var.cts <- sapply(data, FUN = is.numeric)
var.cts <- c("Wr.Hnd", "NW.Hnd", "Pulse", "Height", "Age")

cts.data <- data[, var.cts]
head(cts.data)
```

A data.frame: 6 × 5

Wr.Hnd	NW.Hnd	Pulse	Height	Age
<dbl>	<dbl>	<int>	<dbl>	<dbl>
21.4	21.0	63	180.00	19.000
19.5	19.4	79	165.00	18.083
16.3	16.2	44	152.40	23.500
15.9	16.5	99	167.64	17.333
19.3	19.4	55	180.34	19.833
18.5	18.5	48	167.00	22.333

In [41]:
```
# Calculate the mean
apply(cts.data, MARGIN = 2, FUN = mean)
```

Wr.Hnd	18.43
NW.Hnd	18.391
Pulse	<NA>
Height	<NA>
Age	20.96503

In [42]:
```
apply(cts.data, MARGIN = 2, FUN = mean, na.rm = TRUE)
```

Wr.Hnd	18.43
NW.Hnd	18.391
Pulse	69.9042553191489
Height	171.784597701149
Age	20.96503

b1. Calculate the count/proportion of females and males

```
table(...,
  exclude = if (useNA == "no") c(NA, NaN),
  useNA = c("no", "ifany", "always"),
  dnn = list.names(...), deparse.level = 1)

prop.table()
```

In [43]:
```
sex.tab <- table(data$Sex)
sex.tab
```

```
Female   Male
    47     53
```

In [44]:
```
prop.table(sex.tab)
```

```
Female   Male
  0.47   0.53
```

b2. Calculate the count in each Smoke group

In [45]:
```
table(data$Smoke)
```

```
Heavy Never Occas Regul 
    6    79     5    10 
```

b3. Calculate the count and proportion of males and females in each Smoke group

In [46]:
```
table(data$Sex, data$Smoke)
```

```
        
         Heavy Never Occas Regul
  Female     3    40     3     1
  Male       3    39     2     9
```

In [47]:
```
ss.tab <- table(data[, c("Sex", "Smoke")])
ss.tab
```

```
        Smoke
Sex      Heavy Never Occas Regul
  Female     3    40     3     1
  Male       3    39     2     9
```

In [48]:
```
prop.table(ss.tab, margin = 2)
```

```
        Smoke
Sex          Heavy     Never     Occas     Regul
  Female 0.5000000 0.5063291 0.6000000 0.1000000
  Male   0.5000000 0.4936709 0.4000000 0.9000000
```

In [49]:
```
prop.table(ss.tab, margin = 1)
```

```
        Smoke
Sex           Heavy      Never      Occas      Regul
  Female 0.06382979 0.85106383 0.06382979 0.02127660
  Male   0.05660377 0.73584906 0.03773585 0.16981132
```

In [50]:
```
sample(letters[1:3], size = 100, replace = T)
```

'c' 'b' 'c' 'b' 'c' 'b' 'c' 'c' 'c' 'b' 'a' 'b' 'a' 'c' 'c' 'a' 'c' 'a' 'c' 'b' 'a' 'a' 'a' 'b' 'c' 'a' 'a' 'c' 'a' 'c' 'a' 'c' 'c' 'b' 'c' 'b' 'a' 'a' 'c' 'b' 'c' 'b' 'b' 'c' 'a' 'c' 'b' 'c' 'c' 'a' 'b' 'c' 'c' 'b' 'a' 'a' 'c' 'c' 'a' 'b' 'c' 'c' 'c' 'b' 'a' 'a' 'c' 'a' 'c' 'c' 'c' 'c' 'b' 'a' 'a' 'a' 'c' 'a' 'a' 'c' 'c' 'b' 'a' 'b' 'b' 'a' 'c' 'a' 'b' 'b' 'a' 'a' 'c' 'c' 'a' 'b' 'c' 'a' 'a' 'b'

In [51]:
```r
tab3d <- table(data$Sex, data$Smoke,
               sample(letters[1:3], size = 100, replace = T))
tab3d
```

```
, ,  = a

        
         Heavy Never Occas Regul
  Female     2    17     1     0
  Male       0     9     1     2

, ,  = b

        
         Heavy Never Occas Regul
  Female     1    15     0     0
  Male       2    17     0     3

, ,  = c

        
         Heavy Never Occas Regul
  Female     0     8     2     1
  Male       1    13     1     4
```

In [52]:
```r
prop.table(tab3d, margin = c(1,3))
```

```
, ,  = a

        
              Heavy      Never      Occas      Regul
  Female 0.10000000 0.85000000 0.05000000 0.00000000
  Male   0.00000000 0.75000000 0.08333333 0.16666667

, ,  = b

        
              Heavy      Never      Occas      Regul
  Female 0.06250000 0.93750000 0.00000000 0.00000000
  Male   0.09090909 0.77272727 0.00000000 0.13636364

, ,  = c

        
              Heavy      Never      Occas      Regul
  Female 0.00000000 0.72727273 0.18181818 0.09090909
  Male   0.05263158 0.68421053 0.05263158 0.21052632
```

c1. Calculate the standard deviation of writing hand span of females

```
aggregate()
tapply()
by()
```

In [53]:
```
# Subset if we don't know these functions yet..
data.f <- data[data$Sex == "Female", ]
head(data.f)
sd(data.f$Wr.Hnd)
```

A data.frame: 6 × 8

	X	Sex	Wr.Hnd	NW.Hnd	Pulse	Smoke	Height	Age
	<int>	<fct>	<dbl>	<dbl>	<int>	<fct>	<dbl>	<dbl>
3	3	Female	16.3	16.2	44	Regul	152.40	23.500
4	4	Female	15.9	16.5	99	Never	167.64	17.333
7	7	Female	17.5	17.0	85	Heavy	163.00	17.667
9	9	Female	13.0	12.5	77	Never	165.00	18.167
10	10	Female	18.5	18.0	75	Never	173.00	18.250
11	11	Female	17.5	17.1	73	Never	167.00	18.417

1.51990797715501

In [54]:
```
# aggregate() syntax 1
aggregate(data$Wr.Hnd, by = list(sex = data$Sex), FUN = sd)
```

A data.frame: 2 × 2

sex	x
<fct>	<dbl>
Female	1.519908
Male	1.712066

In [55]:
```
# aggregate() syntax 2
aggregate(Wr.Hnd~Sex, data = data, FUN = sd)
```

A data.frame: 2 × 2

Sex	Wr.Hnd
<fct>	<dbl>
Female	1.519908
Male	1.712066

In [56]:
```
# by()
by(data = data$Wr.Hnd, INDICES = list(sex = data$Sex), FUN = sd)
```

```
sex: Female
[1] 1.519908
------------------------------------------------------------
sex: Male
[1] 1.712066
```

In [57]:
```
# tapply()
tapply(X = data$Wr.Hnd, INDEX = list(data$Sex), FUN = sd)
```

Female	1.51990797715501
Male	1.71206552443005

In [58]:
```
# Return a list using tapply()
tapply(X = data$Wr.Hnd, INDEX = list(data$Sex),
       FUN = sd, simplify = FALSE)
```

$Female
1.51990797715501
$Male
1.71206552443005

aggregate( ), by( ) and tapply( ) are all connected. They give different types of output.

c2. Calculate the standard deviation of writing hand span of all different Sex-Smoke groups

In [59]:
```
aggregate(data$Wr.Hnd,
          by = list(sex = data$Sex, smoke = data$Smoke),
          FUN = sd)
```

A data.frame: 8 × 3

sex	smoke	x
<fct>	<fct>	<dbl>
Female	Heavy	0.2309401
Male	Heavy	4.8569538
Female	Never	1.5762663
Male	Never	1.3857770
Female	Occas	1.9000000
Male	Occas	2.2627417
Female	Regul	NA
Male	Regul	1.6537835

In [60]:
```
aggregate(Wr.Hnd~Sex+Smoke, data = data, FUN = sd)
```

A data.frame: 8 × 3

Sex	Smoke	Wr.Hnd
<fct>	<fct>	<dbl>
Female	Heavy	0.2309401
Male	Heavy	4.8569538
Female	Never	1.5762663
Male	Never	1.3857770
Female	Occas	1.9000000
Male	Occas	2.2627417
Female	Regul	NA
Male	Regul	1.6537835

c3. Calculate the standard deviation of writing hand and non-writing hand span of all Sex-Smoke groups

In [61]:
```
cbind(1:5, 5:1); rbind(1:5, 5:1)
```

A matrix: 5 × 2 of type int

1	5
2	4
3	3
4	2
5	1

A matrix: 2 × 5 of type int

1	2	3	4	5
5	4	3	2	1

In [62]:
```
aggregate(cbind(data$Wr.Hnd, data$NW.Hnd),
          by = list(data$Sex, data$Smoke),
          FUN = sd)
```

A data.frame: 8 × 4

Group.1	Group.2	V1	V2
<fct>	<fct>	<dbl>	<dbl>
Female	Heavy	0.2309401	0.2886751
Male	Heavy	4.8569538	3.9828800
Female	Never	1.5762663	1.6625899
Male	Never	1.3857770	1.3760875
Female	Occas	1.9000000	1.3796135
Male	Occas	2.2627417	1.0606602
Female	Regul	NA	NA
Male	Regul	1.6537835	1.3991069

In [63]:
```
aggregate(cbind(Wr.Hnd, NW.Hnd)~Sex+Smoke, data = data, FUN = sd)
```

A data.frame: 8 × 4

Sex	Smoke	Wr.Hnd	NW.Hnd
<fct>	<fct>	<dbl>	<dbl>
Female	Heavy	0.2309401	0.2886751
Male	Heavy	4.8569538	3.9828800
Female	Never	1.5762663	1.6625899
Male	Never	1.3857770	1.3760875
Female	Occas	1.9000000	1.3796135
Male	Occas	2.2627417	1.0606602
Female	Regul	NA	NA
Male	Regul	1.6537835	1.3991069

Let's try to figure out what aggregate( ) is doing

```
print()
```

In [64]:
```
aggregate(Wr.Hnd~Smoke, data = data, FUN = print)
```

```
[1] 17.5 14.0 23.2 17.5 17.1 21.3
 [1] 21.4 19.5 15.9 19.3 18.5 19.8 13.0 18.5 17.5 22.0 20.0 18.6 16.0 13.0 18.0
[16] 19.6 21.0 17.5 19.5 18.9 18.1 16.0 18.8 19.5 16.4 18.5 17.2 19.4 17.0 17.8
[31] 18.0 16.9 21.0 16.5 17.0 18.5 17.6 16.5 19.1 18.8 17.7 15.5 21.0 18.0 19.0
[46] 17.6 19.5 21.5 20.8 19.0 18.9 17.5 19.0 18.5 18.5 19.2 15.0 17.7 17.5 16.0
[61] 18.5 17.5 18.0 18.0 19.0 18.5 19.2 21.5 17.5 17.5 19.5 17.6 18.7 17.0 18.2
[76] 18.0 19.5 19.5 20.5
[1] 19.1 22.2 15.4 16.5 19.0
 [1] 16.3 18.5 19.5 19.7 18.0 17.0 22.5 20.5 20.0 21.0
```

A data.frame: 4 × 2

Smoke	Wr.Hnd
<fct>	<list>
Heavy	17.5, 14.0, 23.2, 17.5, 17.1, 21.3
Never	21.4, 19.5, 15.9, 19.3, 18.5, 19.8, 13.0, 18.5, 17.5, 22.0, 20.0, 18.6, 16.0, 13.0, 18.0, 19.6, 21.0, 17.5, 19.5, 18.9, 18.1, 16.0, 18.8, 19.5, 16.4, 18.5, 17.2, 19.4, 17.0, 17.8, 18.0, 16.9, 21.0, 16.5, 17.0, 18.5, 17.6, 16.5, 19.1, 18.8, 17.7, 15.5, 21.0, 18.0, 19.0, 17.6, 19.5, 21.5, 20.8, 19.0, 18.9, 17.5, 19.0, 18.5, 18.5, 19.2, 15.0, 17.7, 17.5, 16.0, 18.5, 17.5, 18.0, 18.0, 19.0, 18.5, 19.2, 21.5, 17.5, 17.5, 19.5, 17.6, 18.7, 17.0, 18.2, 18.0, 19.5, 19.5, 20.5
Occas	19.1, 22.2, 15.4, 16.5, 19.0
Regul	16.3, 18.5, 19.5, 19.7, 18.0, 17.0, 22.5, 20.5, 20.0, 21.0

Exercise.

- Repeat b1-b3 using aggregate( )

In [65]:
```
aggregate(Wr.Hnd~Smoke, data = data, FUN = length)
```

A data.frame: 4 × 2

Smoke	Wr.Hnd
<fct>	<int>
Heavy	6
Never	79
Occas	5
Regul	10

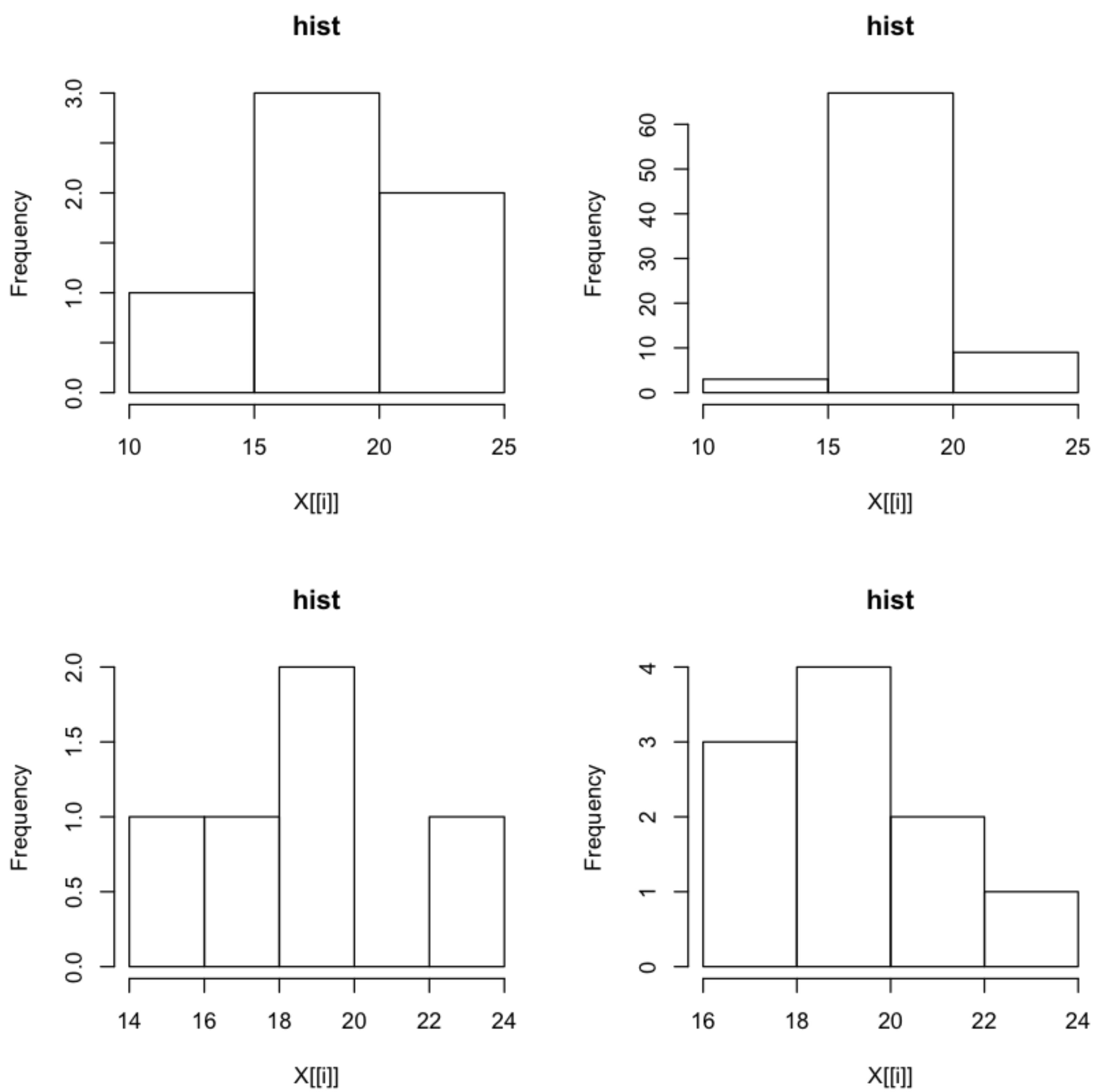
- Make histograms of writing hand span for all four Smoke groups using aggregate( )

```
hist()
```

In [66]:
```
par(mfrow = c(2,2))
aggregate(Wr.Hnd~Smoke, data = data, FUN = hist,
          main = "hist", breaks = 3)
```

A data.frame: 4 × 2

Smoke	Wr.Hnd
<fct>	<list[,6]>
Heavy	10, 15, 20, 25, 1, 3, 2, 0.03333333, 0.10000000, 0.06666667, 12.5, 17.5, 22.5, X[[i]], TRUE
Never	10, 15, 20, 25, 3, 67, 9, 0.007594937, 0.169620253, 0.022784810, 12.5, 17.5, 22.5, X[[i]], TRUE
Occas	14, 16, 18, 20, 22, 24, 1, 1, 2, 0, 1, 0.1, 0.1, 0.2, 0.0, 0.1, 15, 17, 19, 21, 23, X[[i]], TRUE
Regul	16, 18, 20, 22, 24, 3, 4, 2, 1, 0.15, 0.20, 0.10, 0.05, 17, 19, 21, 23, X[[i]], TRUE



d1. Categorize 'Age' - make a new binary variable 'Adult'

```
ifelse(test, yes, no)
```

In [67]:
```
vec <- 1:5
vec

ifelse(vec>3, yes = "big", no = "small")
```

1 2 3 4 5

'small' 'small' 'small' 'big' 'big'

In [68]:
```
data$Adult <- ifelse(data$Age >= 18, yes = "Yes", no = "No")
```

R has if (test) {opt1} else {opt2}, what is the advantage of ifelse( )?

In [69]:
```
if (data$Age >= 18) {
    data$Adult2 = "Yes"
} else {
    data$Adult2 = "No"
}
head(data)
```

```
Warning message in if (data$Age >= 18) {:
“the condition has length > 1 and only the first element will be used”
```

A data.frame: 6 × 10

X	Sex	Wr.Hnd	NW.Hnd	Pulse	Smoke	Height	Age	Adult	Adult2
<int>	<fct>	<dbl>	<dbl>	<int>	<fct>	<dbl>	<dbl>	<chr>	<chr>
1	Male	21.4	21.0	63	Never	180.00	19.000	Yes	Yes
2	Male	19.5	19.4	79	Never	165.00	18.083	Yes	Yes
3	Female	16.3	16.2	44	Regul	152.40	23.500	Yes	Yes
4	Female	15.9	16.5	99	Never	167.64	17.333	No	Yes
5	Male	19.3	19.4	55	Never	180.34	19.833	Yes	Yes
6	Male	18.5	18.5	48	Never	167.00	22.333	Yes	Yes

In [70]:
```
# Delete Adult2
data <- subset(data, select=-c(Adult2))
```

ifelse( ) is vectorized!!!

d2. Categorize 'Wr.Hnd' into 5 groups - make a new categorical variable with 5 levels

```
1. =< 16: TP/XS
2. 16~18 (16,18]: P/S
3. 18~20 (18,20]: M/M
4. 20~22: G/L
5. >  22: TG/XL
```

Can we still use ifelse( )?

```
cut(x, breaks, labels = NULL, right = TRUE, ...)
```

In [71]:
```r
cut.points <- c(-Inf, 16, 18, 20, 22, Inf)

data$Hn.Grp <- cut(data$Wr.Hnd, breaks = cut.points, right = T)

head(data, 12)
# labels as default
```

A data.frame: 12 × 10

X	Sex	Wr.Hnd	NW.Hnd	Pulse	Smoke	Height	Age	Adult	Hn.Grp
<int>	<fct>	<dbl>	<dbl>	<int>	<fct>	<dbl>	<dbl>	<chr>	<fct>
1	Male	21.4	21.0	63	Never	180.00	19.000	Yes	(20,22]
2	Male	19.5	19.4	79	Never	165.00	18.083	Yes	(18,20]
3	Female	16.3	16.2	44	Regul	152.40	23.500	Yes	(16,18]
4	Female	15.9	16.5	99	Never	167.64	17.333	No	(-Inf,16]
5	Male	19.3	19.4	55	Never	180.34	19.833	Yes	(18,20]
6	Male	18.5	18.5	48	Never	167.00	22.333	Yes	(18,20]
7	Female	17.5	17.0	85	Heavy	163.00	17.667	No	(16,18]
8	Male	19.8	20.0	NA	Never	180.00	17.417	No	(18,20]
9	Female	13.0	12.5	77	Never	165.00	18.167	Yes	(-Inf,16]
10	Female	18.5	18.0	75	Never	173.00	18.250	Yes	(18,20]
11	Female	17.5	17.1	73	Never	167.00	18.417	Yes	(16,18]
12	Male	22.0	21.5	73	Never	200.00	18.500	Yes	(20,22]

In [72]:
```
# Set labels to false
data$Hn.Grp <- cut(data$Wr.Hnd, breaks = cut.points, labels = F)
head(data)
```

A data.frame: 6 × 10

X	Sex	Wr.Hnd	NW.Hnd	Pulse	Smoke	Height	Age	Adult	Hn.Grp
<int>	<fct>	<dbl>	<dbl>	<int>	<fct>	<dbl>	<dbl>	<chr>	<int>
1	Male	21.4	21.0	63	Never	180.00	19.000	Yes	4
2	Male	19.5	19.4	79	Never	165.00	18.083	Yes	3
3	Female	16.3	16.2	44	Regul	152.40	23.500	Yes	2
4	Female	15.9	16.5	99	Never	167.64	17.333	No	1
5	Male	19.3	19.4	55	Never	180.34	19.833	Yes	3
6	Male	18.5	18.5	48	Never	167.00	22.333	Yes	3

In [73]:
```
# Customized labels
custom.label <- c("TP/XS", "P/S", "M/M", "G/L", "TG/XL")
data$Hn.Grp <- cut(data$Wr.Hnd, breaks = cut.points,
                   right = T, labels = custom.label)
head(data)
```

A data.frame: 6 × 10

X	Sex	Wr.Hnd	NW.Hnd	Pulse	Smoke	Height	Age	Adult	Hn.Grp
<int>	<fct>	<dbl>	<dbl>	<int>	<fct>	<dbl>	<dbl>	<chr>	<fct>
1	Male	21.4	21.0	63	Never	180.00	19.000	Yes	G/L
2	Male	19.5	19.4	79	Never	165.00	18.083	Yes	M/M
3	Female	16.3	16.2	44	Regul	152.40	23.500	Yes	P/S
4	Female	15.9	16.5	99	Never	167.64	17.333	No	TP/XS
5	Male	19.3	19.4	55	Never	180.34	19.833	Yes	M/M
6	Male	18.5	18.5	48	Never	167.00	22.333	Yes	M/M

e1. Calculate the mean Wr.Hnd span of each Hnd.group

In [74]:
```
aggregate(Wr.Hnd~Hn.Grp, data = data, FUN = mean)
```

A data.frame: 5 × 2

Hn.Grp	Wr.Hnd
<fct>	<dbl>
TP/XS	14.98000
P/S	17.37941
M/M	19.04634
G/L	21.12500
TG/XL	22.63333

e2. Calcuate the mean Wr.Hnd span of each Hnd.group without using aggregate, by, tapply

```
split(x, f, ...)
lapply(X, FUN, ...)
sapply(X, FUN, ..., simplify = TRUE)
```

In [75]:
```
numbers <- 1:10
groups <- sample(letters[1:3], size = 10, replace = T)
rbind(numbers, groups)
```

A matrix: 2 × 10 of type chr

numbers	1	2	3	4	5	6	7	8	9	10
groups	c	b	c	a	a	c	b	b	b	c

In [76]:
```
split(x = numbers, f = groups)
```

$a
4 5

$b
2 7 8 9

$c
1 3 6 10

In [77]:
```
wr.hnd.grp <- split(data$Wr.Hnd, f = data$Hn.Grp)
wr.hnd.grp
```

$`TP/XS`
15.9 13 16 13 14 16 15.5 15.4 15 16

$`P/S`
16.3 17.5 17.5 18 17.5 16.4 17.2 17 17.8 18 18 17 16.9 16.5 17 17.6 16.5 17.5 17.7 17.1 18 17.6 17.5 17.7 17.5 17.5 18 18 16.5 17.5 17.5 17.6 17 18

$`M/M`
19.5 19.3 18.5 19.8 18.5 20 18.6 18.5 19.1 19.6 19.5 19.5 18.9 18.1 19.7 18.8 19.5 18.5 19.4 18.5 19.1 18.8 20 19 19.5 19 18.9 19 18.5 18.5 19.2 18.5 19 18.5 19.2 19.5 18.7 18.2 19.5 19 19.5

$`G/L`
21.4 22 21 21 20.5 21 21.5 20.8 21.3 21.5 21 20.5

$`TG/XL`
22.2 23.2 22.5

In [78]:
```
# lapply
la <- lapply(X = wr.hnd.grp, FUN = mean);
la
```

$`TP/XS`
14.98
$`P/S`
17.3794117647059
$`M/M`
19.0463414634146
$`G/L`
21.125
$`TG/XL`
22.6333333333333

In [79]:
```
# sapply
sapply(X = wr.hnd.grp, FUN = mean, simplify = T)
```

TP/XS	14.98
P/S	17.3794117647059
M/M	19.0463414634146
G/L	21.125
TG/XL	22.6333333333333

In [80]:
```
sapply(X = wr.hnd.grp, FUN = mean, simplify = F)
```

$`TP/XS`
14.98
$`P/S`
17.3794117647059
$`M/M`
19.0463414634146
$`G/L`
21.125
$`TG/XL`
22.6333333333333

In [81]:
```
summary(1:10)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   1.00    3.25    5.50    5.50    7.75   10.00 
```

In [82]:
```
# vapply *
# Safer than sapply(), and a little bit faster
# because FUN.VALUE has to be specified that length and type should match

va <- vapply(wr.hnd.grp, summary, FUN.VALUE = c("Min." = numeric(1),
                                                "1st Qu." = numeric(1),
                                                "Median" = numeric(1),
                                                "Mean" = numeric(1),
                                                "3rd Qu." = numeric(1),
                                                "Max." = numeric(1)))
va
```

A matrix: 6 × 5 of type dbl

	TP/XS	P/S	M/M	G/L	TG/XL
Min.	13.000	16.30000	18.10000	20.500	22.20000
1st Qu.	14.250	17.00000	18.50000	20.950	22.35000
Median	15.450	17.50000	19.00000	21.000	22.50000
Mean	14.980	17.37941	19.04634	21.125	22.63333
3rd Qu.	15.975	17.70000	19.50000	21.425	22.85000
Max.	16.000	18.00000	20.00000	22.000	23.20000

f. Calculate the 95% sample confidence intervals of Wr.Hnd in each Smoke group.

One variable for lower bound and one variable for upper bound.

$$CI = \bar{x} \pm t_{n-1,0.025} \times \sqrt{\frac{s^2}{n}}$$

where $\bar{x}$ is the sample mean and s^2 is the sample variance.

In [83]:
```
# aggregate(Wr.Hnd~Smoke, data = data, FUN = ...)
# tapply(X = data$Wr.Hnd, INDEX = list(data$Smoke), FUN = ...)
```

Unfortunately, I do not know any function in R that does this calculation.

But we know how to do it step by step.

In [84]:
```
sample.mean <- aggregate(Wr.Hnd~Smoke, data = data, FUN = mean)[,2]
sample.var <- aggregate(Wr.Hnd~Smoke, data = data, FUN = var)[,2]
sample.size <- aggregate(Wr.Hnd~Smoke, data = data, FUN = length)[,2]

# sample.mean; sample.var; sample.size

t <- qt(p = 0.025, df = sample.size - 1, lower.tail = FALSE)

lb <- sample.mean - t * sqrt(sample.var/sample.size); lb
ub <- sample.mean + t * sqrt(sample.var/sample.size); ub


# How many times did we aggregate according to the group?
# Can we aggregate only once?
```

14.9809186861126 17.9392216758363 15.1612075858683 17.9536416263331

21.8857479805541 18.698753007708 21.7187924141317 20.6463583736669

Or, we can make our own function and integrate it into aggregate( ), by( ), or tapply( ) !!!

2.2 Write our own functions in R

A function takes in some arguments and gives some outputs

Arguments include

```
- inputs
- options
```

In [85]:
```
# The structure
func_name <- function(argument){
    statement
}
```

Example 1. Make a function for $f(x) = 2x$

In [86]:
```
# Build the function
times2 <- function(x) {
    fx <- 2 * x
    return(fx)
}
# Use the function
times2(x = 5)
# or
times2(3)
```

10

6

Example 2. Make a function to calculate the integer division of a **by** b**, return the integer part and the modulus.**

In [87]:
```
# R has operators that do this
9 %/% 2
9 %% 2
```

4

1

```
 floor( ) takes a single numeric argument x and returns a numeric vector containing the largest int
egers not greater than the corresponding elements of x.
```

In [88]:
```
int.div <- function(a, b){
    int <- floor(a/b)
    mod <- a - int*b
    return(list(integer = int, modulus = mod))
}
```

In [89]:
```
# class(result)
# Recall: how do we access the modulus?
result <- int.div(21, 4)
result
```

$integer
5
$modulus
1

In [90]:
```
int.div <- function(a, b){
    int <- a%/%b
    mod <- a%%b
    return(cat(a, "%%", b, ": \n integer =", int,"\n ------------------", " \n modulus =", mod,
"\n"))
}
int.div(33,5)
```

```
33 %% 5 :
 integer = 6
 ------------------
 modulus = 3
```

In [91]:
```
int.div <- function(a, b){
    int <- a%/%b
    mod <- a%%b
    out <- rbind(a, b, int, mod)
    out
}
int.div(21:25, 1:5)
```

A matrix: 4 × 5 of type int

a	21	22	23	24	25
b	1	2	3	4	5
int	21	11	7	6	5
mod	0	0	2	0	0

Example 3. Make the simplest canadian AI chatbot

A function can return something other than an R object, say some voice.

In [92]:
```
# No need to worry about the details here.
# Just want to show that functions do not always have to return() something.
AIcanadian <- function(who, reply_to) {
    system(paste("say -v", who, "Sorry!"))
}
# AIcanadian("Alex", "Sorry I stepped on your foot.")
```

In [93]:
```
# Train my chatbot - AlphaGo style.
# I'll let Alex and Victoria talk to each other.
# MacOS has their voices recorded.
# chat_log <- rep(NA, 8)
# for (i in 1:8) {
#     if (i == 1) {
#         chat_log[1] <- "Sorry I stepped on your foot."
#         system("say -v Victoria Sorry, I stepped on your foot.")
#     } else {
#         if (i %% 2 == 0)
#             chat_log[i] <- AIcanadian("Alex", chat_log[i - 1])
#         else
#             chat_log[i] <- AIcanadian("Victoria", chat_log[i - 1])
#     }
# }
# chat_log
```

Example 4. Check one summary statistic by Smoke group of our 'data' data.

Function arguments can be basically anything, say another function.

In [94]:
```
data_summary <- function(func) {
    data <- read.csv("https://raw.githubusercontent.com/ly129/MiCM2020/master/sample.csv", head
er = TRUE)
    by(data = data$Wr.Hnd, INDICES = list(data$Smoke), FUN = func)
}
data_summary(mean)
```

```
: Heavy
[1] 18.43333
------------------------------------------------------------
: Never
[1] 18.31899
------------------------------------------------------------
: Occas
[1] 18.44
------------------------------------------------------------
: Regul
[1] 19.3
```

Example 5. Default argument value & stop execution & warning message

In [95]:
```
a_times_2_unless_you_want.something.else.but.I.refuse.3 <- function(a, b=2){
    if (b == 3) {
        stop("I refuse 3!")
    }

    if (b == 4) {
        warning("4 sucks too.")
    }

    a*b
}
```

In [96]:
```
a_times_2_unless_you_want.something.else.but.I.refuse.3(a = 5)
```

10

In [97]:
```
a_times_2_unless_you_want.something.else.but.I.refuse.3(a = 5, b = 4)
```

```
Warning message in a_times_2_unless_you_want.something.else.but.I.refuse.3(a = 5, :
“4 sucks too.”
```

20

In [118]:
```
a_times_2_unless_you_want.something.else.but.I.refuse.3(a = 5, b = 3)
```

```
Error in a_times_2_unless_you_want.something.else.but.I.refuse.3(a = 5, : I refuse 3!
Traceback:

1. a_times_2_unless_you_want.something.else.but.I.refuse.3(a = 5,
 .     b = 3)
2. stop("I refuse 3!")   # at line 3 of file <text>
```

In [99]:
```
# Multiple optional arguments fed to different functions called in our own function
# Still needs a lot of refinement

fancy.mean <- function(vec, ...) {
    args <- list(...)
    print(args)
#     print(as.list(match.call(expand.dots = FALSE)))
    mean.args <- c("trim", "na.rm")
    sample.args <- c("size", "replace", "prob")

# Could use a for loop to go over all args.

#     cat("arguments in mean()", mean.args, "\n")

    args.names <- names(args)

#     cat("argument names in ...", args.names, "\n")

    m.args <- args.names[args.names %in% mean.args]
    s.args <- args.names[args.names %in% sample.args]

#     cat("args names that will be used in mean", m.args, "\n")

    print(args[["m.args"]])
    m <- list(trim = 0, na.rm = args[[m.args]])
    s <- list(args[[s.args]], replace = FALSE, prob = NULL)

#     print(m)
#     print("args that will be used in mean", m, "\n")

    fancy.mean <- mean(vec, trim = 0, na.rm = args[[m.args]])
    fancy.sample <- sample(vec, size = args[[s.args]])
    return(list(fancy.mean,fancy.sample))
}
```

In [100]:
```
fancy.mean(c(1:5, NA, NA, 234,123,4,123,41,234),
           na.rm = T, size = 1)
```

```
$na.rm
[1] TRUE

$size
[1] 1

NULL
```

1. 70.3636363636364
2. 234

Exercise:

- Make a function to calculate sample confidence intervals (2.1 f)

In [101]:
```
sample.ci <- function(x, digits = 2) {
    mu <- mean(x)
    variance <- var(x)
    size <- length(x)
    t.stat <- qt(p = 0.025, df = size - 1, lower.tail = FALSE)

    lb <- mu - t.stat * sqrt(variance/size)
    ub <- mu + t.stat * sqrt(variance/size)

    return(round(c(lower = lb, upper = ub), digits))

    # Think carefully whether this output can be put
    # inside of a data.frame
}
```

- Use the function in 1 with aggregate( ), by( ) or apply( ) to calculate the sample confidence intervals (2.1 f)

In [102]:
```
aggregate(Wr.Hnd~Smoke, data = data, FUN = sample.ci)
```

A data.frame: 4 × 2

Smoke	Wr.Hnd
<fct>	<dbl[,2]>
Heavy	14.98, 21.89
Never	17.94, 18.70
Occas	15.16, 21.72
Regul	17.95, 20.65

3. Exercises

A fake dataset is generated. Results should make no biological sense.

In [103]:
```
set.seed(20200306)
N <- 200
height <- round(rnorm(n = N, mean = 180, sd = 10)) # in centimeter
weight <- round(rnorm(n = N, mean = 80, sd = 10)) # in kilograms
age <- round(rnorm(n = N, mean = 50, sd = 10))
treatment <- sample(c(TRUE, FALSE), size = N,
                    replace = T, prob = c(0.3,0.7))
HF <- sample(c(TRUE, FALSE), size = N, replace = T,
             prob = c(0.1,0.9))

fake <- data.frame(height, weight, age, treatment, HF)
head(fake)
```

A data.frame: 6 × 5

height	weight	age	treatment	HF
<dbl>	<dbl>	<dbl>	<lgl>	<lgl>
186	92	60	FALSE	FALSE
155	74	58	FALSE	TRUE
182	79	62	FALSE	FALSE
178	101	54	FALSE	FALSE
182	72	54	FALSE	FALSE
159	66	41	FALSE	TRUE

1. (Vectorized operation) Calculate BMI for every individual

$$\text{BMI} = \text{weight}(kg)/\text{height}(m)^2$$

In [104]:
```
names(fake)
fake$BMI <- fake$weight/(fake$height/100)^2
head(fake)
```

'height' 'weight' 'age' 'treatment' 'HF'

A data.frame: 6 × 6

height	weight	age	treatment	HF	BMI
<dbl>	<dbl>	<dbl>	<lgl>	<lgl>	<dbl>
186	92	60	FALSE	FALSE	26.59267
155	74	58	FALSE	TRUE	30.80125
182	79	62	FALSE	FALSE	23.84978
178	101	54	FALSE	FALSE	31.87729
182	72	54	FALSE	FALSE	21.73651
159	66	41	FALSE	TRUE	26.10656

2. (Categorization) BMI Categories:

```
- Underweight = <18.5
- Normal weight = 18.5–24.9
- Overweight = 25–29.9
- Obesity = BMI of 30 or greater
```

In [105]:
```
cut.pts <- c(-Inf, 18.5, 25, 30, Inf)
labs <- c("Underweight", "Normal weight", "Overweight", "Obesity")
fake$BMI.cat <- cut(fake$BMI, breaks = cut.pts, labels = labs, right = F)
head(fake)
```

A data.frame: 6 × 7

height	weight	age	treatment	HF	BMI	BMI.cat
<dbl>	<dbl>	<dbl>	<lgl>	<lgl>	<dbl>	<fct>
186	92	60	FALSE	FALSE	26.59267	Overweight
155	74	58	FALSE	TRUE	30.80125	Obesity
182	79	62	FALSE	FALSE	23.84978	Normal weight
178	101	54	FALSE	FALSE	31.87729	Obesity
182	72	54	FALSE	FALSE	21.73651	Normal weight
159	66	41	FALSE	TRUE	26.10656	Overweight

3. (*apply) Mean BMI of each BMI group

In [106]:
```
# aggregate()
aggregate(BMI~BMI.cat, data = fake, FUN = mean)
```

A data.frame: 4 × 2

BMI.cat	BMI
<fct>	<dbl>
Underweight	16.17253
Normal weight	22.09822
Overweight	26.94884
Obesity	32.79935

In [107]:
```
# split() and lapply()
BMI.grp <- split(fake$BMI, f = fake$BMI.cat)
lapply(BMI.grp, FUN = mean)
```

$Underweight
16.1725259238271
$`Normal weight`
22.0982178055369
$Overweight
26.9488351034313
$Obesity
32.7993482108602

4. (Aggregation) Proportion with heart failure in each BMI-treatment group

In [108]:
```
# Trick:
FALSE+TRUE+TRUE
```

2

In [109]:
```
aggregate(HF~BMI.cat+treatment, data = fake, FUN = sum)
```

A data.frame: 8 × 3

BMI.cat	treatment	HF
<fct>	<lgl>	<int>
Underweight	FALSE	0
Normal weight	FALSE	9
Overweight	FALSE	3
Obesity	FALSE	4
Underweight	TRUE	1
Normal weight	TRUE	5
Overweight	TRUE	2
Obesity	TRUE	0

5. Write a function that allow user to specify

```
- a dataset
- the (binary) treatment variable
- the (binary) outcome variable
```

and return a cross-tabulation (a 2x2 table).

In [110]:
```
tab2by2 <- function(data, treatment, outcome){
    sub <- data[, c(treatment, outcome)]
    return(table(sub))
}
```

In [111]:
```
tab2by2(fake, treatment = "treatment", outcome = "HF")
```

```
          HF
treatment FALSE TRUE
    FALSE   130   16
    TRUE     46    8
```

5 Pro. The function should be able to check whether the treatment/outcome variables are binary or not. Continuous variables will be dichotomized based on a user-defined threshold.

In [112]:
```
tab2by2.pro <- function(data, treatment, outcome, treatment.threshold, outcome.threshold){
    tx <- data[, treatment]
    rx <- data[, outcome]

    if (length(table(tx))>2) {
        if (missing(treatment.threshold)) {
            stop("Non-binary treatment. Please provide a threshold.")
        } else {
            binary.treatment <- ifelse(tx<=treatment.threshold,
                                       yes = paste("<=", treatment.threshold),
                                       no = paste(">", treatment.threshold))
        }
    } else {
        binary.treatment <- tx
    }

    if (length(table(rx))>2) {
        if (missing(outcome.threshold)) {
            stop("Non-binary outcome. Please provide a threshold.")
        } else {
            binary.outcome <- ifelse(rx<=outcome.threshold,
                                     yes = paste("<=", outcome.threshold),
                                     no = paste(">", outcome.threshold))
        }
    } else {
        binary.outcome <- rx
    }


    return(table(treatment = binary.treatment, outcome = binary.outcome))
}
```

In [113]:
```
tab2by2.pro(fake, treatment = "age", outcome = "BMI")
```

```
Error in tab2by2.pro(fake, treatment = "age", outcome = "BMI"): Non-binary treatment. Please p
rovide a threshold.
Traceback:

1. tab2by2.pro(fake, treatment = "age", outcome = "BMI")
2. stop("Non-binary treatment. Please provide a threshold.")   # at line 7 of file <text>
```

In [114]:
```
tab2by2.pro(fake, treatment = "age", outcome = "BMI", treatment.threshold = 50)
```

```
Error in tab2by2.pro(fake, treatment = "age", outcome = "BMI", treatment.threshold = 50): Non-
binary outcome. Please provide a threshold.
Traceback:

1. tab2by2.pro(fake, treatment = "age", outcome = "BMI", treatment.threshold = 50)
2. stop("Non-binary outcome. Please provide a threshold.")   # at line 19 of file <text>
```

In [115]:
```
tab2by2.pro(fake, treatment = "age", outcome = "BMI", treatment.threshold = 50, outcome.thresho
ld = 20)
```

```
         outcome
treatment <= 20 > 20
    <= 50      6   93
    > 50      11   90
```

In [116]:
```
tab2by2.pro(fake, treatment = "age", outcome = "HF")
```

```
Error in tab2by2.pro(fake, treatment = "age", outcome = "HF"): Non-binary treatment. Please pr
ovide a threshold.
Traceback:

1. tab2by2.pro(fake, treatment = "age", outcome = "HF")
2. stop("Non-binary treatment. Please provide a threshold.")   # at line 7 of file <text>
```

In [117]:
```
# HF is binary, so it is OK if "outcome.threshold" is missing.
tab2by2.pro(fake, treatment = "age", outcome = "HF", treatment.threshold = 50)
```

```
         outcome
treatment FALSE TRUE
    <= 50    93    6
    > 50     83   18
```

6. Specific task in your own research

In [ ]:
```
```