

# Introduction to R

## Session 3 – Data manipulation

Statistical Consulting Centre

consulting@stat.auckland.ac.nz  
The Department of Statistics  
The University of Auckland

19 July, 2017



**SCIENCE**  
DEPARTMENT OF STATISTICS

# factor

## What is a factor?

*A variable which takes either qualitative values, ordinal values or a discrete set of quantitative values. The values of a factor are called its levels.*

Examples of factors:

- Gender with 2 *qualitative* levels: Male and Female.
- Education with 6 *ordinal* levels: None < "Primary compl < Incpl secondary < Secondary compl < Incpl university < University degree.
- Income has 9 *quantitative* levels when the mid-values of the income ranges are used: 5000, 12500, 17500, 22500, 27500, 35000, 45000, 60000 and 85000.

# factor

- R stores two *additional* pieces of information for each factor: (1) the unique set of levels and (2) an integer value, assigned by R, for each unique level.
- The integer values are assigned to factor levels so that they have an order associated with them.
- By default, the unique levels are assigned the values 1, 2, ..., according to ascending alphabetical order. This is not always appropriate!

```
typeof(Patient.df$Sex)
```

```
## [1] "character"
```

```
levels(Patient.df$Sex)
```

```
## NULL
```

```
Patient.df$BMI.group <- factor(Patient.df$BMI.group)
```

# Which other variables should also be factors?

```
str(Patient.df)
```

```
## 'data.frame':    17030 obs. of  9 variables:
## $ Patient.ID : int  3 4 9 10 11 19 34 44 45 48 ...
## $ Age        : int  21 32 48 35 48 44 42 24 67 56 ...
## $ Sex        : chr   "Male" "Female" "Female" "Male" ...
## $ Weight     : num   180 NA 150 204 155 ...
## $ Height     : num   70.4 63.9 61.8 69.8 NA 70.2 62.6 64.4
## $ Smoke.group: chr    NA NA "No" NA ...
## $ Race.group : chr   "Caucasian" "Caucasian" "Caucasian" "C
## $ BMI        : num   25.5 NA 27.6 29.4 NA ...
## $ BMI.group  : Factor w/ 3 levels "normal","overweight",..
```

# Which other variables should also be factors?

```
Patient.df$Sex <- factor(Patient.df$Sex)
Patient.df$Race.group <- factor(Patient.df$Race.group)
Patient.df$Smoke.group <- factor(Patient.df$Smoke.group)
```

# Converting numbers to factors

```
test <- factor(c(0, 1, 2))  
test
```

```
## [1] 0 1 2  
## Levels: 0 1 2
```

- then convert back to numbers?

## And convert back to numbers

- need to convert it to character, using `as.character()` first, then convert back to numbers, using `as.numeric()`.

```
test
```

```
## [1] 0 1 2  
## Levels: 0 1 2
```

```
as.numeric(test)
```

```
## [1] 1 2 3
```

```
as.numeric(as.character(test))
```

```
## [1] 0 1 2
```

## Your turn (Binning ages into age groups)

- Sometimes we are interested in examining responses by age group.
- Now, assign each of the 17030 patients to one of three age groups: “Under 35”, “36 to 60” and “Over 61”.
- Convert `Age.group` to a factor with levels in ascending order.



# Your turn

Assign each of the 17030 patients to one of three age groups: “Under 35”, “36 to 60” and “Over 61”.

```
Patient.df$Age.group <- ifelse(Patient.df$Age <= 35,  
  "Under 35", ifelse(Patient.df$Age <= 60, "36 to 60",  
    "Over 61"))  
table(Patient.df$Age.group)
```

```
##
```

```
## 36 to 60    Over 61 Under 35
```

```
##      5969      5476      5585
```

# Your turn

Convert Age.group to a factor with levels in ascending order.

```
Patient.df$Age.group <- factor(Patient.df$Age.group)  
table(Patient.df$Age.group)
```

```
##  
## 36 to 60    Over 61    Under 35  
##      5969      5476      5585
```

# Your turn

Convert Age.group to a factor with levels in ascending order.

```
Patient.df$Age.group <- factor(Patient.df$Age.group,  
  levels = c("Under 35", "36 to 60", "Over 61"))  
table(Patient.df$Age.group)
```

```
##
```

```
## Under 35 36 to 60 Over 61
```

```
##      5585      5969      5476
```

## Other way: if/else statement

```
if (test) {  
  # yes  
} else {  
  # no  
}
```

- test: a logical test.
- yes, what happens if the test is True.
- no, what happens if the test is False.

## Other way: if/else statement

```
if (test) {  
  # yes for (test)  
} else if (test1) {  
  # no for (test) but yes for (test1)  
} else {  
  # no for both (test) and (test1)  
}
```

- In general, it is rare in data analysis involves only a single table of data.
- Examples:
  - Patient information and blood test measurements
  - Experimental design and measurements from the high-throughput biological instrument

Serum Cholesterol level, mg/100ml, measured on:

- Day1
- Day5
- Day10

# Reading data into R

```
setwd("your working directory")
Patient.df <- read.csv("CholesterolNA.csv")
head(Cholesterol.df)
```

##	Patient.ID	Day1	Day5	Day10
## 1	3	268	276	281
## 2	4	160	170	170
## 3	9	236	245	252
## 4	10	225	231	235
## 5	11	260	256	257
## 6	19	187	194	195



## names(), dim() and str()

```
# Names of the variables
```

```
names(Cholesterol.df)
```

```
## [1] "Patient.ID" "Day1"          "Day5"
```

```
## [4] "Day10"
```

```
dim(Cholesterol.df)
```

```
## [1] 17030      4
```

```
str(Cholesterol.df)
```

```
## 'data.frame':    17030 obs. of  4 variables:
```

```
## $ Patient.ID: int  3 4 9 10 11 19 34 44 45 48 ...
```

```
## $ Day1      : int  268 160 236 225 260 187 216 137 NA 156
```

```
## $ Day5      : int  276 170 245 231 256 194 212 135 NA 157
```

```
## $ Day10     : int  281 170 252 235 257 195 222 136 NA 159
```

# Combining data-frame by columns (`cbind()`)

```
combined.df <- cbind(Patient.df, Cholesterol.df[, -1])
```

- Thus, the function for combining the data-frame by rows is `rbind()`.
- Make sure the dimensions are correct for two combining data-frames.
- Also, you need to make sure each row in `Patient.df` matches each row in `Cholesterol.df`.

# Reading data into R (Again)

```
setwd("your working directory")
Patient.df <- read.csv("Cholesterol.csv")
head(Cholesterol.df)
```

##	Patient.ID	Day1	Day5	Day10
## 1	3	268	276	281
## 2	4	160	170	170
## 3	9	236	245	252
## 4	10	225	231	235
## 5	11	260	256	257
## 6	19	187	194	195

## names(), dim() and str() (Again)

```
# Names of the variables
```

```
names(Cholesterol.df)
```

```
## [1] "Patient.ID" "Day1"          "Day5"
```

```
## [4] "Day10"
```

```
dim(Cholesterol.df)
```

```
## [1] 16062      4
```

```
str(Cholesterol.df)
```

```
## 'data.frame':    16062 obs. of  4 variables:
```

```
## $ Patient.ID: int  3 4 9 10 11 19 34 44 48 49 ...
```

```
## $ Day1      : int  268 160 236 225 260 187 216 137 156 179
```

```
## $ Day5      : int  276 170 245 231 256 194 212 135 157 183
```

```
## $ Day10     : int  281 170 252 235 257 195 222 136 159 183
```

## Combining data-frame by columns (cbind())

```
combined.df <- cbind(Patient.df, Cholesterol.df)
```

```
## Error in data.frame(..., check.names = FALSE): arguments in
```

# Better way

- Combining the based on the `Patient.ID` in both `Patient.df` and `Cholesterol.df`.
- First thing is to make sure the `Patient.ID` are unique in both data-frames.

## Better way

- Combining the based on the Patient.ID in both Patient.df and Cholesterol.df.
- First thing is to make sure the Patient.ID are unique in both data-frames.

```
sum(table(Patient.df$Patient.ID) > 1)
```

```
## [1] 0
```

```
sum(table(Cholesterol.df$Patient.ID) > 1)
```

```
## [1] 0
```

# dplyr R package

- dplyr R package provides some useful functions that correspond to the most data manipulation tasks.

```
library(dplyr)
```

- Mutating joins allow you to combine variables from multiple tables, there are four common types:
  - `left_join()`
  - `right_join()`
  - `full_join()`
  - `inner_join()`



# dplyr R package

```
x <- data.frame(key = c(1,2,3), val.x = c("x1","x2","x3"))  
y <- data.frame(key = c(1,2,4), val.y = c("y1","y2","y4"))
```

Data-frame x

key	val.x
1	x1
2	x2
3	x3

Data-frame y

key	val.y
1	y1
2	y2
4	y4

# left\_join()

```
left_join(x, y, by = "key")
```

Data-frame x

key	val.x
1	x1
2	x2
3	x3

Data-frame y

key	val.y
1	y1
2	y2
4	y4

left join

key	val.x	val.y
1	x1	y1
2	x2	y2
3	x3	NA

# right\_join()

```
right_join(x, y, by = "key")
```

Data-frame x

key	val.x
1	x1
2	x2
3	x3

Data-frame y

key	val.y
1	y1
2	y2
4	y4

right join

key	val.x	val.y
1	x1	y1
2	x2	y2
4	NA	y4

# full\_join()

```
full_join(x, y, by = "key")
```

Data-frame x

key	val.x
1	x1
2	x2
3	x3

Data-frame y

key	val.y
1	y1
2	y2
4	y4

full join

key	val.x	val.y
1	x1	y1
2	x2	y2
3	x3	NA
4	NA	y4

# inner\_join()

```
inner_join(x, y, by = "key")
```

Data-frame x

key	val.x
1	x1
2	x2
3	x3

Data-frame y

key	val.y
1	y1
2	y2
4	y4

inner join

key	val.x	val.y
1	x1	y1
2	x2	y2

These four types of mutating join are differ in their behaviour when a match is not found.

- `left_join()`
- `right_join()`
- `full_join()`
- `inner_join()`

Which one should we use for this `Patient.df` and `Cholesterol.df` data-frames?

# Combining two tables

```
combined.df <- left_join(Patient.df, Cholesterol.df)
```

- Variable names:

```
names(combined.df)
```

```
## [1] "Patient.ID" "Age" "Sex"
## [4] "Weight" "Height" "Smoke.group"
## [7] "Race.group" "BMI" "BMI.group"
## [10] "Age.group" "Day1" "Day5"
## [13] "Day10"
```

# Combining two tables

```
str(combined.df)
```

```
## 'data.frame':    17030 obs. of  13 variables:
## $ Patient.ID : int  3 4 9 10 11 19 34 44 45 48 ...
## $ Age        : int  21 32 48 35 48 44 42 24 67 56 ...
## $ Sex        : Factor w/ 2 levels "Female","Male": 2 1 1 2 ...
## $ Weight     : num  180 NA 150 204 155 ...
## $ Height     : num  70.4 63.9 61.8 69.8 NA 70.2 62.6 64.4 ...
## $ Smoke.group: Factor w/ 2 levels "No","Yes": NA NA 1 NA 1 ...
## $ Race.group : Factor w/ 3 levels "African","Caucasian",...
## $ BMI        : num  25.5 NA 27.6 29.4 NA ...
## $ BMI.group  : Factor w/ 3 levels "normal","overweight",...
## $ Age.group  : Factor w/ 3 levels "Under 35","36 to 60",...
## $ Day1       : int  268 160 236 225 260 187 216 137 NA 156 ...
## $ Day5       : int  276 170 245 231 256 194 212 135 NA 157 ...
## $ Day10      : int  281 170 252 235 257 195 222 136 NA 159 ...
```



# Combining two tables

You can change the variable names.

```
names(combined.df)[c(1,11,12,13)] <-  
  c("ID", "Baseline", "PreTrt", "PostTrt")  
names(combined.df)
```

```
##   [1] "ID"           "Age"          "Sex"  
##   [4] "Weight"       "Height"       "Smoke.group"  
##   [7] "Race.group"   "BMI"          "BMI.group"  
##  [10] "Age.group"    "Baseline"     "PreTrt"  
##  [13] "PostTrt"
```

# Categorical Variables

```
table(combined.df$Age.group)
```

```
##  
## Under 35 36 to 60 Over 61  
##      5585      5969      5476
```

```
table(combined.df$Sex)
```

```
##  
## Female    Male  
##    9077    7953
```

```
. . .
```

## for loop to get column summary statistics

```
for (i in c("Age.group", "Sex", "Smoke.group", "Race.group",  
           "BMI.group")) {  
  print(i)  
  print(table(combined.df[, i]))  
}
```

# Continuous Variables

```
mean(combined.df$Age)
```

```
## [1] 48.7919
```

## for loop to get column summary statistics

```
for (i in c("Age", "Height", "Weight", "BMI", "Baseline",  
           "PreTrt", "PostTrt")) {  
  print(i)  
  print(mean(combined.df[, i]))  
}
```

```
## [1] "Age"  
## [1] 48.7919  
## [1] "Height"  
## [1] NA  
## [1] "Weight"  
## [1] NA  
## [1] "BMI"  
## [1] NA  
## [1] "Baseline"  
## [1] NA  
## [1] "PreTrt"
```

## for loop to get column summary statistics

```
for (i in c("Age", "Height", "Weight", "BMI", "Baseline",  
           "PreTrt", "PostTrt")) {  
  print(i)  
  print(mean(combined.df[, i], na.rm = TRUE))  
}
```

```
## [1] "Age"  
## [1] 48.7919  
## [1] "Height"  
## [1] 65.43787  
## [1] "Weight"  
## [1] 165.0315  
## [1] "BMI"  
## [1] 27.03084  
## [1] "Baseline"  
## [1] 206.0492  
## [1] "PreTrt"
```

# Easier way

```
summary(combined.df[, -1])
```

```
##           Age           Sex           Weight
## Min.      :20.00   Female:9077   Min.      : 48.0
## 1st Qu.:32.00   Male  :7953   1st Qu.:137.4
## Median :45.00
## Mean     :48.79
## 3rd Qu.:65.00
## Max.     :90.00
##
##           Height   Smoke.group   Race.group
## Min.      :46.70   No  :4255   African   : 4860
## 1st Qu.:62.60   Yes :4371   Caucasian:11612
## Median :65.30   NA's:8404   Other     :  553
## Mean     :65.44
## 3rd Qu.:68.20
## Max.     :81.20
```

# Summary

- factor
- Joining the data-sets
- for loop