## **THE BIG-R BOOK**

## FROM DATA SCIENCE TO LEARNING MACHINES AND BIG DATA

- PART 04-

*Dr. Philippe J.S. De Brouwer* last compiled: September 1, 2021 Version 0.1.1

(c) 2021 Philippe J.S. De Brouwer - distribution allowed by John Wiley & Sons, Inc.

# THE BIG R-BOOK: From Data Science to Big Data and Learning Machines

## $\heartsuit$ – PART 04: Data Wrangling – $\heartsuit$

(c) 2021 by Philippe J.S. De Brouwer - distribution allowed by John Wiley & Sons, Inc.

These slides are to be used in with the book – for best experience, teachers will read the book before using the slides and students have access to the book and the code.

part 04: Data Wrangling  $\downarrow$  chapter 16:

## **Anonymous Data**

© DR. PHILIPPE J.S. DE BROUWER

3/156

```
-- Using AES 256 for example:
MariaDB [(none)]> SELECT AES_ENCRYPT("Hello World", "secret_key_string");
+-----+
| AES_ENCRYPT("Hello World", "secret_key_string") |
+-----+
| ïfiEwïfi*0ïfiïfiWïfiïfiïfiïfiïfiïfiïfiïfiïfiïfiïfi
| t-----+
1 row in set (0.00 sec)
-- Example:
SELECT AES_ENCRYPT(name, "secret_key_string"), AES_ENCRYPT(phone number, "secret_key_string"),
number_purchases, satifaction_rating, sustomer_since, etc.
FROM tbl_customers;
```

#### -- To decrypt, use AES\_DECRYPT(crypt\_str, key\_string)

Listing 1: SQL code for MySQL (or MariaDB) to encrypt using AES256. Note that those relational database systems (RDBMSs) provide much more methods for encryption. It is worth to go through the documentation of your particular system for more support.

There is also the package sodium, created by Jeroen Ooms. It is a wrapper around libsodium, which is a standard library. So you will need to install this first on your operating system (OS).

- deb: libsodium-dev (Debian, Ubuntu, etc.)
- rpm: libsodium-devel (Fedora, EPEL)
- csw: libsodium\_dev (Solaris)
- brew: libsodium (OSX)

This means – most probably – your will first need to open a terminal and run the following commands in the CLI (command line interface of your OS):

sudo apt-get install libsodium-dev

Then we can open R and install the sodium library for R.

library(sodium)

```
# Create the SHA256 key based on a secret password:
```

```
key <- sha256(charToRaw("My sweet secret"))</pre>
```

```
# Serialize the data to be encrypted:
```

msg <- serialize("Philippe J.S. De Brouwer", NULL)</pre>

```
# Encrypt:
```

```
msg_encr <- data_encrypt(msg, key)</pre>
```

```
orig <- data_decrypt(msg_encr, key)
stopifnot(identical(msg, orig))</pre>
```

```
# Tag the message with your key (HMAC):
tag <- data_tag(msg, key)</pre>
```

## part 04: Data Wrangling ↓ chapter 17: Data Wrangling in the tidyverse



## Reminder of the functions to connect to the database i

```
# --
library(RMySQL)
# -- The functions as mentioned earlier:
# db_get_data
# Get data from a MvSOL database
# Arguments:
     con_info -- MySQLConnection object -- containing the connection
#
                                             info to the MvSOL database
#
     sS0L
               -- character string
                                          -- the SOL statement that selects
#
#
                                             the records
# Returns
     data.frame, containing the selected records
db_get_data <- function(con_info, sSQL){</pre>
  con <- dbConnect(MySOL(),</pre>
                  user
                           = con_infosuser.
                 password = con_info$password.
                 dbname
                         = con infosdbname.
                           = con_infoshost
                 host
  df <- dbGetOuerv(con, sSOL)</pre>
  dbDisconnect(con)
  df
```

```
# db_run_sal
# Run a query that returns no data in an MySQL database
# Arguments:
     con_info -- MvSOLConnection object -- containing the connection
#
#
                                             info to the MySQL database
#
     sS0L
               -- character string
                                          -- the SOL statement to be run
db_run_sql <-function(con_info, sSQL)</pre>
  con <- dbConnect(MySQL(),</pre>
                  user
                           = con_info$user,
                  password = con_info$password.
                  dbname
                           = con_info$dbname,
                  host
                           = con_info$host
  rs <- dbSendOuerv(con,sSOL)</pre>
  dbDisconnect(con)
```

## Connecting to the library database

```
# Load dplyr via tidyverse:
library(tidyverse)
# Define the wrapper functions:
# Step 1: define the connection info.
my_con_info <- list()
my_con_info $password <- "librarian"
my_con_info $password <- "librarianPWD"
my_con_info $chaname <- "library"
my_con_info $host <- "localhost"
# -- The data import was similar to what we had done previously.
# -- However, now we import all tables separately
```

```
# Loop over the four tables and download their data:
for (n in 1:length(my_tables)) {
    my_sql <- paste("SELECT * FROM `",my_tables[n],"`;", sep="")
    df <- db_get_data(my_con_info, my_sql)
    # the next line uses tibbles are from the tidyverse
    as_tibble(assign(my_db_names[n],df)))
```

## Importing CSV files via the tidyverse

```
library(tidyverse)
s_csv = "'a'.'b'.'c'\n001.2.34..\n2.3.14.55\n3...43"
read csv(s csv)
## # A tibble: 3 x 3
## `'a'` `'b'` `'c'`
## <chr> <chr> <chr>
## 1 001 2.34 .
## 2 2 3.14 55
## 3 3 . 43
read_csv(s_csv, na = '.') # Tell R how to understand the '.'
## # A tibble: 3 x 3
## `'a'` `'b'` `'c'`
## <chr> <dbl> <dbl>
## 1 001 2.34
               NA
## 2 2 3.14 55
## 3 3 NA 43
read_csv(s_csv, na = '.'. guote = "'") # Tell how a string is guoted
## # A tibble: 3 x 3
       b c
## a
## <chr> <dbl> <dbl>
## 1 001 2.34
               NA
## 2 2 3.14 55
## 3 3
                 43
         NA
```

# Make a string that looks like a fixed-width table (s	(shortened):
--	--------------

txt <- "b	ook_id	year title	genre
1	1896	Les plaisirs et les jour	LITmod
2	1927	Albertine disparue	LITmod
3	1954	Contre Sainte-Beuve	LITmod
8	1687	PhilosophiÃę Naturalis Principia Mathematica	SCIphy
9	- 300	Elements (translated )	SCImat
10	2014	Big Data World	SCIdat
11	2016	Key Business Analytics	SCIdat
12	2011	Maslowian Portfolio Theory	FINinv
13	2016	R for Data Science	SCIdat"

Starting from this string variable, we will create a text file that has data in the fixed-width format.

```
fileConn <- file("books.txt")
writeLines(txt, fileConn)
close(fileConn)
mv_headers <- c("book_id","year","title","genre")</pre>
```

The previous code chunk has created the text file book.txt in the working path of R. Now, we can read it back in to illustrate how the read\_fwf() function works.

#### # Inspect the input:

## print(t)

##	#	A tibble: 9	Эх	4	
##		book_id ye	ear	title	genre
##		<dbl> <db< td=""><td>ol&gt;</td><td><chr></chr></td><td><chr></chr></td></db<></dbl>	ol>	<chr></chr>	<chr></chr>
##	1	1 18	396	Les plaisirs et les jour	LITmod
##	2	2 19	927	Albertine disparue	LITmod
##	3	3 19	954	Contre Sainte-Beuve	LITmod
##	4	8 16	587	PhilosophiÃę Naturalis Principia Mathematica	a SCIp
##	5	9 - 3	300	Elements (translated )	SCImat
##	6	10 20	914	Big Data World	SCIdat
##	7	11 20	916	Key Business Analytics	SCIdat
##	8	12 20	911	Maslowian Portfolio Theory	FINinv
##	9	13 20	916	R for Data Science	SCIdat

```
# -- > by guessing the columns
# The function fwf_empty can help to guess where the columns start
# based on white space
t3 <- read_fwf(
file = "books.txt",
    skip = 1,
    fwf_empty("books.txt")
    )</pre>
```

Note that this last method fails: it identifies a separate column for the word "Mathematica", while this is actually part of the column "title":

pr:	i.n1	<b>t</b> (t3)				
##	#	A tib	ble: 9	x 5		
##		X1	X2	ХЗ	X4	X5
##		<dbl></dbl>	<dbl></dbl>	<chr></chr>	<chr></chr>	<chr></chr>
##	1	1	1896	Les plaisirs et les jour	<na></na>	LITmod
##	2	2	1927	Albertine disparue	<na></na>	LITmod
##	3	3	1954	Contre Sainte-Beuve	<na></na>	LITmod
##	4	8	1687	PhilosophiÃę Naturalis Principi	a Mathematica	a SCIphy
##	5	9	-300	Elements (translated )	<na></na>	SCImat
##	6	10	2014	Big Data World	<na></na>	SCIdat
##	7	11	2016	Key Business Analytics	<na></na>	SCIdat
##	8	12	2011	Maslowian Portfolio Theory	<na></na>	FINinv
##	9	13	2016	R for Data Science	<na></na>	SCIdat



- a tibble/data-frame for each dataset,
- a column for each variable,
- a row for each observation,
- a value (or NA) in each cell the intersection between row and column.



### Importing one table that contains the whole database

#### # use the wrapper functions to get data.

#### # step 1: define the connection info

```
my_con_info <- list()
my_con_info$user <- "librarian"
my_con_info$password <- "librarianPWD"
my_con_info$dbname <- "library"
my_con_info$host <- "localhost"</pre>
```

```
## -- Import 2 tables combined
# step 2: get the data
my_sql <- "SELECT * FROM tbl_authors
JOIN tbl_author_book ON author_id = author
JOIN tbl_books ON book = book_id
JOIN tbl_genres ON genre = genre_id;"
t_mix <- db_get_data(my_con_info, my_sql)
t_mix <- as.tibble(t_mix)
# Show the result:</pre>
```

head(t\_mix)

## # A tibble: 6 x 16

## ;	author_id	pen_nar	ne	full_name	birth_date	death_date	ab_id	author
##	<dbl></dbl>	<dbl> <chr></chr></dbl>		<chr></chr>	<chr> <chr></chr></chr>		<dbl></dbl>	<dbl></dbl>
## 1	1	Marcel	Pr~	Valentin Lo~	1871-07-10	1922-11-18	1	1
## 2	1	Marcel	Pr∼	Valentin Lo~	1871-07-10	1922-11-18	2	1
## 3	1	Marcel	Pr~	Valentin Lo~	1871-07-10	1922-11-18	3	1
## 4		Marcel	Pr~	Valentin Lo~	1871-07-10	1922-11-18	4	1
© DR. PHILIPPE LS. DE	BROUWER 2	Miguel	de	Miguel de C	1547 00 20	1616 04 22	E	2

Ounderstand the data structure, eventually talk to the data owners and understand what is the job at hand. In this case, it is a mix of four tables: authors, a link-table to books, books, and genres.

```
# Make a table of how much each author_id occurs:
nbr_auth <- t_mix %>% count(author_id)
# Do the same and include all fields that are assumed to
# be part of the table authors.
nbr_auth2 <- t_mix %>%
count(author_id, pen_name, full_name, birth_date, death_date, book)
```

```
nbr_auth$n - nbr_auth2$n
## [1] 3 1 0 0 0 0 0 0 0 0 3 1 0 0
```

Learn from experiments till we find the right structure. In our case "book" is not unique for an "author," so we try again.

```
# Try without book:
```

nbr\_auth2 <- t\_mix %>%
 count(author\_id, pen\_name, full\_name, birth\_date, death\_date)

#### # Now these occurrences are the same:

nbr\_auth\$n - nbr\_auth2\$n ## [1] 0 0 0 0 0 0 0 0 0 0

- This looks better. But note that this exact match is only possible because our data is clean (because we took care and/or because we asked MySQL to help us to guard referential integrity). We still have to determine now which table takes which fields.
- Now, the heavy lifting is done and we can simply extract all data.

## Workflow to split tables in R iii

my_	aut	hors <- t	<pre>ibble(author_id =</pre>	= t_mix <mark>\$</mark> author_id,		
			pen_name =	= t_mix <mark>\$</mark> pen_name,		
			full_name =	= t_mix <mark>\$</mark> full_name,		
			<pre>birth_date =</pre>	= t_mix <mark>\$</mark> birth_date,		
			death_date =	= t_mix <mark>\$</mark> death_date		
			) %>%			
		ur	nique %>%			
		р	rint			
##	# A	tibble: 3	10 × 5			
##		author_id	pen_name	full_name	birth_date	death_date
##		<dbl></dbl>	<chr></chr>	<chr></chr>	<chr></chr>	<chr></chr>
##	1	1	Marcel Proust	Valentin Louis G. $\sim$	1871-07-10	1922-11-18
##	2	2	Miguel de Cerv~	Miguel de Cervante~	1547-09-29	1616-04-22
##	3	4	E. L. James	Erika Leonard	1963-03-07	<na></na>
##	4	5	Isaac Newton	Isaac Newton	1642-12-25	1726-03-20
##	5	7	Euclid	Euclid of Alexandr~	<na></na>	<na></na>
##	6	11	Bernard Marr	Bernard Marr	<na></na>	<na></na>
##	7	13	Bart Baesens	Bart Baesens	1975-02-27	<na></na>
##	8	14	Philippe J.S. ~	Philippe J.S. De B $\sim$	1969-02-21	<na></na>
##	9	15	Hadley Wickham	Hadley Wickham	<na></na>	<na></na>
##	10	16	Garrett Grolem~	Garrett Grolemund	<na></na>	<na></na>

## Repeat this process for all other tables.

O Check the data and see once more if it all makes sense. In our case we will want to correct some of the data that has been imported and coerce them to the right type.

auth <- tibble(											
	<pre>author_id = as.integer(my_authors\$author_id),</pre>										
	<pre>pen_name = my_authors\$pen_name,</pre>										
	<pre>full_name = my_authors\$full_name,</pre>										
		birt	th_date	= as.Date	(my_authors\$birth_da	ate),					
		deat	th_date	= as.Date	(my_authors\$death_da	ate)					
			)	%>%							
		unique		%>%							
		print									
##	# A	tibble: :	10 x 5								
##		author_id	pen_na	me	full_name	birth_date	death_date				
##		<int></int>	<chr></chr>		<chr></chr>	<date></date>	<date></date>				
##	1	1	Marcel	Proust	Valentin Louis G. $\sim$	1871-07-10	1922-11-18				
##	2	2	Miguel	de Cerv~	Miguel de Cervante~	1547-09-29	1616-04-22				
##	3	4	E. L.	James	Erika Leonard	1963-03-07	NA				
##	4	5	Isaac	Newton	Isaac Newton	1642-12-25	1726-03-20				
##	5	7	Euclid		Euclid of Alexandr~	NA	NA				
##	6	11	Bernar	d Marr	Bernard Marr	NA	NA				
##	7	13	Bart B	aesens	Bart Baesens	1975-02-27	NA				
##	8	14	Philip	pe J.S. ~	Philippe J.S. De B~	1969-02-21	NA				
##	9	15	Hadley	Wickham	Hadley Wickham	NA	NA				
##	10	16	Garret	t Grolem~	Garrett Grolemund	NA	NA				

# First read in some data (using a flat file to remind

108

# how this works): x <- " January 100 102 February 106 105 105 March 104 104 106 April 120 122 118 Mav 130 100 133 141 139 135 lune July 175 176 180 August 170 188 187 September 142 148 155 October 133 137 145

```
November 122
                    128
                             131
December 102
                   108
                             110"
```

```
# Read in the flat file via read_fwf from readr:
t <- read_fwf(x, fwf_empty(x, col_names = my_headers))</pre>
```

```
# Set the column names:
```

colnames(t) <- c("month". "Sales2017". "Sales2018". "Sales2019")</pre>

```
# Finally, we can show the data as it appeared in the spreadsheet
        # from the sales department:
        print(t)
        ## # A tibble, 12 x 4
        ##
              month
                        Sales2017 Sales2018 Sales2019
              <chr>
                             <dbl>
                                       <dbl>
                                                  <dbl>
        ##
        ## 1 Januarv
                               100
                                         102
                                                   108
© DR. PHILIPPE LS. DE BROUWER
                             ....
                                        ....
                                                  . . .
```

t2 <- gather(t, "year", "sales", 2:4)
t2\$year <- str\_sub(t2\$year,6,9) # delete the sales word
t2\$year <- as.integer(t2\$year) # convert to integer</pre>

#### # Show the result:

t2

##	# A t	ibble	36	ъх	3	
##	mc	onth		yea	ar	sales
##	<0	:hr>	<	<int< td=""><td>t&gt;</td><td><dbl></dbl></td></int<>	t>	<dbl></dbl>
##	1 Ja	anuary		203	17	100
##	2 Fe	bruary	/	203	17	106
##	3 Ma	arch		203	17	104
##	4 Ap	oril		203	17	120
##	5 Ma	ау		203	17	130
##	6 Jι	ine		203	17	141
##	7 Ju	ıly		203	17	175
##	8 Au	igust		203	17	170
##	9 Se	eptembe	er	203	17	142
##	10 00	tober		203	17	133
##	#	with	26	mo	re	rows

### Spreading one column over many

```
library(dplyr)
sales_info <- data.frame(
    time = as.Date('2016-01-01') + 0:9 + rep(c(0,-1), times=5),
    type = rep(c("bought","sold"),5),
    value = round(runif(10, min = 0, max = 10001))
    )
</pre>
```

#### # Show the data frame:

sales\_info

## time type value 2016-01-01 bought 9949 ## 1 2016-01-01 sold 3717 ## 2 ## 3 2016-01-03 bought 1936 ## 4 2016-01-03 sold 1319 2016-01-05 bought 2131 ## 5 ## 6 2016-01-05 sold 9032 ## 7 2016-01-07 bought 5954 2016-01-07 sold 9344 ## 8 ## 9 2016-01-09 bought 3999 ## 10 2016-01-09 sold 6871

#### # Use the function spread():

spread(sales\_info, type, value) ## time bought sold ## 1 2016-01-01 9949 3717 ## 2 2016-01-03 1936 1319 ## 3 2016-01-05 2131 9032 ## 3 2016-01-05 5954 9344

## Split one column into many

```
library(tidvr)
# The original data frame:
turnover <- data.frame(</pre>
       what = paste(as.Date('2016-01-01') + 0:9 + rep(c(0,-1), times=5)),
                    rep(c("HSBC","JPM"),5), sep="/"),
       value = round(runif(10, min = 0, max = 50))
turnover
##
                 what value
## 1
      2016-01-01/HSBC
                         29
## 2
       2016-01-01/JPM
                         5
      2016-01-03/HSBC
## 3
                         32
## 4
       2016-01-03/JPM
                         13
## 5
      2016-01-05/HSBC
                         26
## 6
       2016-01-05/JPM
                         5
## 7
      2016-01-07/HSBC
                         11
## 8
       2016-01-07/JPM
                         36
      2016-01-09/HSBC
## 9
                         41
## 10 2016-01-09/JPM
                         14
# Use the function separate():
separate(turnover, what, into=c("date", "counterpart"), sep="/")
            date counterpart value
##
## 1
      2016-01-01
                        HSBC
                                29
## 2
      2016-01-01
                         JPM
                                 5
## 3
      2016-01-03
                        HSBC
                                32
## 4
     2016-01-03
                         1PM
                                13
                        HSBC
                                 26
```

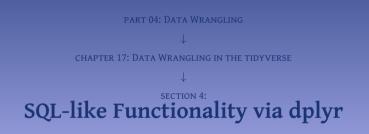
© DR. PHILIPPE J.S. DE BROUWER

### Merging multiple columns into one

#### library(tidyr)

# Define a data frame:

			une u	uutu	i i une i											
	df	<-	data.	frame	(year	=	2018,	mon	th	= (	) +	1:12	2,	day	=	5)
	pri	int (	(df)													
	##		year	month	day											
	##	1	2018	1	5											
	##	2	2018	2	5											
	##	3	2018	3	5											
	##	4	2018	4	5											
	##	5	2018	5	5											
	##	6	2018	6	5											
	##	7	2018	7	5											
	##	8	2018	8	5											
	##	9	2018	9	5											
	##	10	2018	10	5											
	##	11	2018	11	5											
	##	12	2018	12	5											
	# N	lero	e the	e colur	nns to		one va	riab	le:							
				date'							<i>r</i> .	sep	=	(1,1)	)	
	##			date	, ,		,		<i>'</i>	,					<i>'</i>	
	##	1	2018	3-1-5												
		2		3-2-5												
		3		3-3-5												
		4		3-4-5												
		5		3-5-5												
© Dr. Philipi	PË J.S	DE 1	BROUWE	R												



This functionality is provided by the library dplyr of the tidyverse. So, we will load it here and not repeat this in every sub-section.

library(dplyr)

# U	si	ing the ex	cample of the	ti	İbraı	ry:					
dpl	уı	::select	(genres,	#	the	fi	rst a	rgu	ment is	the	tibble
		genre_i	id, location)	#	ther	ı a	list	of	column	name	s
##		genre_id	location								
##	1	FINinv	405.08								
##	2	LITero	001.67								
##	3	LITmod	001.45								
##	4	SCIbio	300.10								
##	5	SCIdat	205.13								
##	6	SCImat	100.53								
##	7	SCIphy	200.43								

al <- filter(authors, birth\_date > as.Date("1900-01-01"))
paste(al\$pen\_name,"--", al\$birth\_date)
## [1] "E. L. James -- 1963-03-07"
## [2] "Bart Baesens -- 1975-02-27"
## [3] "Philippe J.S. De Brouwer -- 1969-02-21"

## Hint – Equivalence between dplyr and SQL

Note that

```
filter(count(author_book, author), n > 1}
```

```
is equivalent with the following in SQL
```

```
SELECT COUNT(author) FROM tbl_author_book
HAVING COUNT(author) > 1;
```

In the tidyverse, dplyr provides a series of join-functions, that all share a similar synthax:

```
*_join(x, y, by = NULL, copy = FALSE, ...)
```

We distinguish the following join functions.

- mutating joins: Contrary to what the name suggests, they do not mutate the tibbles on which they opearate. These joins output fields of both data frames. dplyr provides the following "mutating joins".
  - *inner\_join()* returns all the columns for x and y, but only those rows that have matching values in their respective field/columns mentioned in the by-clause, and all columns from "x" and "y." Note that it is possible that some of the join-fields are not unique and hence there can be multiple matches for the same record, then all combinations are all returned.
  - left\_join() returns all the columns for x and y, so that all rows of x will be returned at least once (with a match of y if it exists, otherwise with a match to NA (or NULL in SQL vocabulary) (matches are defined by the by-clause). Note that it is possible that some of the join-fields are not unique and hence there can be multiple matches for the same record or x, then all combinations are all returned.
  - *right\_join()* is similar to the previous but roles of x and y are inverted. Hence, it returns all rows from y, and all columns from x and y. Rows in y with no match in x will still be returned but have NA values in those rows of the y data frame.
  - full\_join() returns all rows and all columns from both data frames x and y. Where there are not matching values, returns "NA" for the one missing.
- filtering joins that only output the fields (columns) of the left data frame.

- semi\_join() returns all rows from x but only if there is a matching values in the field of y, while only keeping the columns of x. Note that unlike an inner join, the semi join will never duplicate rows of x
- anti\_join() returns all rows from x that do not have a matching value in y, while keeping only the columns of x.

```
library(sqldf)
# Because we have RMySQL loaded (and we don't want to unload it) sqldf will
# default to using that engine to run the queries. If we want it to use the
# R environment and data frames, then use the following line:
options(sqldf.driver = "SQLite")
```

```
ab <- authors %>%
inner_join(author_book, by = c("author_id" = "author")) %>%
inner_join(books, by = c("book" = "book_id")) %>%
add_count(author_id)
ab$n
## [1] 4 4 4 4 2 2 1 1 1 1 1 1 1
```

## Mutating data

```
t <- authors
                                                                        %>%
             mutate(short_name = str_sub(pen_name, 1, 7))
                                                                        %>%
             mutate(x_name = if_else(str_length(pen_name) > 15,
                                     paste(str_sub(pen_name.1.8).
                                           0....0
                                           str_sub(pen_name,
                                                  start = -3).
                                           sep=''),
                                     pen_name,
                                     "pen_name is NA"
                                                                        %>%
             mutate(is_alive =
               if_else(!is.na(birth_date) & is.na(death_date).
                    "YES",
                    if_else(death_date < Sys.Date(),</pre>
                        "no".
                        "maybe").
                      "NA")
                                                                         %>%
            dplvr::select(c(x_name, birth_date, death_date, is_alive)) %>%
            print()
        ##
                      x_name birth_date death_date is_alive
        ## 1
               Marcel Proust 1871-07-10 1922-11-18
                                                          no
        ## 2
              Miguel d...tes 1547-09-29 1616-04-22
                                                          no
        ## 3
                 James Jovce 1882-02-02 1941-01-13
                                                          no
        ## A
                 E. L. James 1963-03-07
                                               <NA>
                                                         YES
        ## 5
                Isaac Newton 1642-12-25 1726-03-20
                                                          no
© DR. PHILIPPELS. DE BROUWER Fuelid ANA
                                                        ....
```

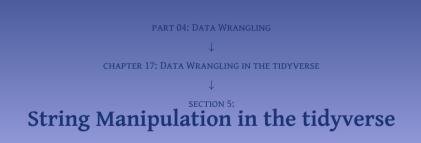
These functions are:

- intersect(x, y):  $A \cap B$  but with duplicates removed,
- union(x, y):  $A \cup B$  but with duplicates removed,
- union\_all(x, y):  $A \cup B$ ,
- setdiff(x, y): A B but with duplicates removed,
- setequal(x, y):  $A \cap B$ .

```
# Define two sets (with one column):
A <- tibble(coll = c(1L:4L))
B <- tibble(coll = c(4L,4L,5L))</pre>
```

```
# Study some of the set-operations:
dplyr::intersect(A,B)
## # A tibble: 1 x 1
     col1
##
## <int>
## 1
      4
union(A.B)
## # A tibble: 5 x 1
     col1
##
## <int>
## 1
        1
## 2
        2
## 3
        3
## 4
         4
## 5
         5
union_all(A.B)
## # A tibble: 7 x 1
     col1
##
## <int>
## 1
      1
## 2
        2
```

© DR. PHILIPP##S. DE BROUVER



library(tidyverse)
library(stringr)

#### # define strings

s1 <- "Hello" # double quotes are fine
s2 <- 'world.' # single quotes are also fine</pre>

```
# Return the length of a string:
str_length(s1)
## [1] 5
```

#### # Concatenate strings:

str\_c(s1, ", ", s2) # str\_c accepts many strings
## [1] "Hello, world."

```
str_c(s1, s2, sep = ", ") # str_c also has a
## [1] "Hello, world."
```

```
library(stringr)  # or library(tidyverse)
sVector <- c("Hello", ", ", "world", "Philippe")</pre>
```

# the first 3 characters

# convert to uppercase

```
str_sub (sVector,1,3)
## [1] "Hel" ", " "wor" "Phi"
```

```
str_sub (sVector,-3,-1)  # the last 3 characters
## [1] "llo" ", " "rld" "ppe"
```

```
str_to_lower(sVector[4])  # convert to lowercase
## [1] "philippe"
```

```
str_to_upper(sVector[4])
## [1] "PHILIPPE"
```

```
str_c(sVector, collapse=" ") # collapse into one string
## [1] "Hello , world Philippe"
```

```
str_flatten(sVector, collapse=" ") # flatten string
## [1] "Hello , world Philippe"
```

str\_sub(1,4) %>%
str\_to\_upper()
## [1] "PHIL"

One of the most simple string manipulations is duplicating them to form a longer string. Here we ask stringr to produce a dark shade of grey.

```
str <- "F0"
str_dup(str, c(2,3)) # duplicate a string
## [1] "F0F0" "F0F0F0"</pre>
```

## Manage White Space

str <- c(" 1 ", " abc", "Philippe De Brouwer ")
str\_pad(str, 5) # fills with white-space to x characters
## [1] " 1 " abc"
## [3] "Philippe De Brouwer "</pre>

# str\_pad never makes a string shorter!
# So to make all strings the same length we first truncate:
str\_trunc(10) %>%
str\_pad(10, "right") %>%
print
## [1] " 1 " " abc " "Philipp..."

#### # Remove trailing and leading white space:

**str\_trim**(str) ## [1] "1" "abc" "Philippe De Brouwer"

#### str\_trim(str,"left")

## [1] "1 " "abc" ## [3] "Philippe De Brouwer "

#### # Modify an existing string to fit a line length:

"The quick brown fox jumps over the lazy dog. " %>% str\_\_dup(5) %>% str\_\_c %>% # str\_\_flatten also removes existing \n str\_wrap(50) %>% # Make lines of 50 characters long. cat # or writeLines (print shows "\n") ## The quick brown fox jumps over the lazy dog. The

## Ine quick brown Tox jumps over the tazy dog. Ine ## quick brown fox jumps over the lazy dog. The quick ## brown fox jumps over the lazy dog. The quick brown ## fox jumps over the lazy dog. The quick brown fox ## jumps over the lazy dog.

### str <- c("a", "z", "b", "c")</pre>

#### # str\_order informs about the order of strings (rank number):

str\_order(str)
## [1] 1 3 4 2

# # Sorting is done with str\_sort: str\_sort(str) ## [1] "a" "b" "c" "z"

```
library(stringr) # or library(tidyverse)
sV <- c("philosophy", "physiography", "phis",
                "Hello world", "Philippe", "Philosophy",
                "physics", "philology")</pre>
```

# Extracting substrings that match a regex pattern:

str\_extract(sV, regex("Phi"))
## [1] NA NA NA NA "Phi" "Phi" NA NA

str\_extract(sV, "Phi") # the same, regex assumed
## [1] NA NA NA NA "Phi" "Phi" NA NA

str\_extract(sV, "(p|P)hi")
## [1] "phi" NA "phi" NA "Phi" "Phi" NA "phi"

# Or do it this way: str\_extract(sV, "(phi|Phi)") ## [1] "phi" NA "phi" NA "Phi" "Phi" NA "phi"

This logic is easy to extend:

# Match also i and y: str\_extract(sV, "(p|P)h(i|y)") ## [1] "phi" "phy" "phi" NA "Phi" "Phi" "phy" "phi"

# This is equivalent to: str\_extract(sV, "(phi|Phi|phy|Phy)") ## [1] "phi" "phy" "phi" NA "Phi" "Phi" "phy" "phi"

	Special characters
Anchors <ul> <li>begin of string or line</li> <li>endof string (or line)</li> <li>beginning of a word</li> <li>end of a word</li> </ul>	<pre>\n newline \r carriage return) \t tab \v vertical tab \f form feed</pre>

Character groups	
	any character, but \n
[abc]	accepted characters
[a-z]	character range
()	characters group

Quantifiers		
?	0 or 1 times	
*	0 or more	
+	1 or more	
{n}	n times	
[n,m}	between n and m times	
{n,}	n or more times	
{,m}	m or less times	

## Regex Syntax ii

Logic	
1	"OR," e.g. (a b) matches a or b
\1	content of group one, e.g. $r(w)g(1) \times matches "regex"$
\2	group two, e.g. r(\w)g(\1)x(\2)xpr matches "regexexpr"
(?:)	non capturing group = ignore that match in the string to return
[^a-d]	"not": no character in range a to d

	Other
Lookaround – requires PERL = TRUE a(?!b) a not followed by b a(?=b) a if followed by b (?<=b) a a if preceded by b	\Qa\E treat a verbatim, e.g. \QC++?\E matches "C++?" \K drop match so far, e.g.
(? b)a a if not preceded by b</td <td>x\K\dreturns from x1 only 1</td>	x\K\dreturns from x1 only 1

Line modifiers		
(?i)	makes all matches case insensitive	
(?s)	single line mode: . also matches \n	
(?m)	multi line mode: ^ and \$ become begin and end of line	

## Regex Syntax iii

(	POSIX Character classes
[[:digit:]] or \d	digit: [0-9]
\\D	not a digit: [^0-9]
[[:xdigit:]] or \x	hexadec. digits: [0-9A-Fa-f]
[[:lower:]]	lower-case: [a-z]
[[:upper:]]	upper-case: [A-Z]
[[:alnum:]]	alphanumeric: [A-z0-9]
\\w	word characters: [A-z0-9_]
\\W	not word characters: [^A-z0-9_]
[[:blank:]]	blank: [\\s\\t]
[[:space:]] or \s	space:\\s
\\S	not space: [^\\s]
[[:punct:]]	punctuation character :
	!"#\$%&'()*+,/:;<=>?@[]^_`{}~
[[:graph:]]	graphical character :
	[[:alnum:]] [[:punct:]]
[[:print:]]	printable character :
	[[:graph:]] [[:space:]]
[[:cntrl:]] or \c	control characters: e.g. [\\n\\rt]

The basic rule is that a quantifier applies to whatever is immediately left of it. For example:

- abcd+ matches "abcdddd" but not "abcdabcd" (the + applies only to the last letter);
- this behaviour can be modified with grouping characters: x(F1)+ will match "xF1F1F1," but also note that
- \QC++\E+ matches "C+++++' but not "C+C+C+"

However, there are more nuances that need to be understood.

- The default quantifiers are **greedy:** \d+ will match 123 (as many digits as possible, not necessarily all the same). In other words, a greedy quantifier gives you the longest possible match (eg, ^\.\* will match always the whole line). However, quantifiers are actually **greedy, but with good manners**. We mean with that the engine will swallow as many matches as possible, but if that would hinder the rest of the pattern to be matched, it will back-track to allow for a match. That is why ^\.\*ippe will still match Philippe.
- A quantifier can be made **reluctant or lazy** by adding ? to it. For example, ^P\.\*? will match as little as possible within the possibilities of \* (which is "zero or more" and hence defaults to "zero").
- Actually, quantifiers might be reluctant or lazy but still benevolent. Meaning if the match was so small that
  this would hinder the rest of the match to be made, then they will start matching more in order for the further
  match to be made possible.

## Below we illustrate these concepts with greedy and lazy pattern matching:

```
str_extract("Philippe", "Ph\\w*") # is greedy
## [1] "Philippe"
str_extract("Philippe", "Ph\\w*?") # is lazy
## [1] "Ph"
```

Regex expressions easily get hard to read. To solve that, there is a library rex that provides a function rex() to make the process of creating a regular expression a lot easier and a lot more readable.

# Load the library rex: library(rex) # In this example we construct the regex to match a valid URL, and will # define the valid characters first:

valid\_chars <- rex(one\_of(regex('a-z0-9\u00a1-\uffff')))</pre>

## **Regex for Humans with** rex **i**i

```
# Then build the regex:
expr <- rex(
   start. # start of the string: ^</pre>
```

```
# Protocol identifier (optional) + //
group(list('http', maybe('s')) %or% 'ftp', '://'),
```

```
# User: pass authentication (optional)
maybe(non_spaces,
maybe(':', zero_or_more(non_space)),
    '@'),
```

```
# Top Level Domain (TLD) identifier
group('.', valid_chars %>% at_least(2)),
```

```
# Server port number (optional)
maybe(':', digit %>% between(2, 5)),
© Dr. Philippe J.S. De BROUWER
```

Now we have the regex stored in the variable expr and can use it:

We can check if an URL is valid as follows:

```
# for example:
str_extract("www.de-brouwer.com", expr)
## [1] NA
str_extract("http://www.de-brouwer.com", expr)
## [1] "http://www.de-brouwer.com"
str_extract("error=www.de-brouwer.com", expr)
```

## [1] NA

These functions will only report if a match is found, no information about starting positions of he match is given.

```
# grep() returns the whole string if a match is found:
grep(pattern, string, value = TRUE)
## [1] "one:1" "c5c5c5" "d123d" "123" "6"
```

# The default for value is FALSE -> only returns indexes: grep(pattern, string) ## [1] 1 3 4 5 6

#### # L for returning a logical variable:

grepl(pattern, string)
## [1] TRUE FALSE TRUE TRUE TRUE TRUE TRUE

```
# --- stringr ---
# similar to grepl (note order of arguments!)
str_detect(string, pattern)
## [1] TRUE FALSE TRUE TRUE TRUE TRUE
```

## Locate a Match

In many cases, it is not enough to know if there is a match, but also where the match occurs in the string; that is what we call "locating" a match in a string.

# Locate the first match (the numbers are the position in the string):
regexpr (pattern, string)
## [1] 5 -1 2 2 1 1
## attr(,"match.length")
## [1] 1 -1 1 1 1 1
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TUE

# grepexpr() finds all matches and returns a list:

```
gregexpr(pattern, string)
## [1]]
## [1] 5
## attr(,"match.length")
## [1] 1
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
##
## [[2]]
## [1] -1
## attr(,"match.length")
## [1] -1
```

Often we want to do more than just finding where a match occurs, but we want to change it with something else. This process is called "replacing" matches with strings.

```
# First, we need additionally a replacement (repl)
repl <- "___"</pre>
```

#### # sub() replaces the first match:

sub(pattern, repl, string)
## [1] "one:\_\_\_\_" "NO digit" "c\_\_\_\_c5c5" "d\_\_\_23d" "\_\_\_23" "\_\_\_"

#### # gsub() replaces all matches:

gsub(pattern, repl, string)
## [1] "one:\_\_\_" "NO digit" "c\_\_\_c\_\_\_" "d\_\_\_\_\_d"
## [5] "\_\_\_\_\_" "\_\_\_"

# --- stringr --# str\_replace() replaces the first match:
str\_replace(string, pattern, repl)
## [1] "one:\_\_\_" "NO diait" "c\_\_\_c5c5" "d\_\_23d" "\_\_23" "\_\_\_"

#### # str\_replace\_all() replaces all mathches:

str\_replace\_all(string, pattern, repl)
## [1] "one:\_\_\_" "NO digit" "c\_\_\_c\_\_\_c\_\_\_" "d\_\_\_\_\_d"
## [5] "\_\_\_\_\_" "\_\_\_"

## Extract

If it is not our aim to replace the match, then it might be the case that we want to extract it for further use and manipulation in other sections or functions. The following functions allow to extract matches to regular expressions. from strings. The output of these functions can be quite verbose such as the functions to locate matches.

```
# regmatches() with regexpr() will extract only the first match:
```

```
regmatches(string, regexpr(pattern, string))
## [1] "1" "5" "1" "1" "6"
```

```
# regmatches() with gregexpr() will extract all matches:
```

```
regmatches(string, gregexpr(pattern, string)) # all matches
## [[1]]
## [1] "1"
##
## [[2]]
## character(0)
##
## [[3]]
## [1] "5" "5" "5"
##
## [[4]]
## [1] "1" "2" "3"
##
## [[5]]
## [1] "1" "2" "3"
##
## [[6]]
## [1] "6"
```

Finally, it might be useful to split strings based on a separator (for example file-names and file-extensions, dates, etc.). This can be done with the function strsplit()

```
# --- base-R ---
strsplit(string, pattern)
## [[1]]
## [1] "one:"
##
## [[2]]
## [1] "NO digit"
##
## [[3]]
## [1] "c" "c" "c"
##
## [[4]]
## [1] "d" "" "d"
##
## [[5]]
## [1] "" "" ""
##
## [[6]]
## [1] ""
# --- stringr ---
str_split(string, pattern)
## [[1]]
## [1] "one:" ""
```



We will load the package here and show this part of the code only once. All sub-sections that follow will use this package.

# Load the tidyverse for its functionality such as pipes: library(tidyverse)

# Lubridate is not part of the core-tidyverse, so we need # to load it separately: library(lubridate) The first key concept is that of a date and a date-time. For most practical purposes, a date is something that can be stored as yyyy-mmm-dd.

It can be noted that R follows the ISO 8601 Notation and so will we do. Any person who believes in inclusion and not in imposing historical nation bound standards to the rest of the world will embrace the ISO standards, a fortiori any programmer or modeller with an inclusive world-view will also use the ISO 8601 standards. But there are many people who will not do this, and it is not uncommon to get dates in other formats or have to report dates in those formats. So, the format that we will use is the ISO format: yyyy-mm-dd, but we will also show how to convert to other systems.

```
Digression - R's internal date-format
Internally, R will store date-times as a Unix timestamp or POSIXct format:
as.numeric(Sys.time())  # the number of seconds passed since 1 January 1970
## [1] 1630480658
as.numeric(Sys.time()) / (60 * 60 * 24 * 365.2422)
## [1] 51.66792
```

```
# There is a list of functions that convert to a date
mdy("04052018")
## [1] "2018-04-05"
mdv("4/5/2018")
## [1] "2018-04-05"
mdy("04052018")
## [1] "2018-04-05"
mdv("4052018") # ambiguous formats are refused!
## [1] NA
dmy("04052018") # same string, different date
## [1] "2018-05-04"
```



## Warning - Dates as numbers can be confusing

The functions of the family ymd() do not only take strings as input, they can also can take a numerical input. This might lead to confusion as it is not what one would expect: the internal representation of a date.

```
dt <- ymd(20180505) %>% print
## [1] "2018-05-05"
as.numeric(dt)
## [1] 17656
ymd(17656)
## [1] NA
```

## Timezones

```
# Note it converts the system time-zone to UTC:
as_datetime("2006-07-22T14:00")
## [1] "2020-06-07 22:14:00 UTC"
```

# Force time-zone: as\_datetime("2006-07-22T14:00 UTC") ## [1] "2020-06-07 22:14:00 UTC"

as\_datetime("2006-07-22 14:00 Europe/Warsaw") #Fails silently!
## [1] "2020-06-07 22:14:00 UTC"

```
# Get the same date-time numerals in a different time-zone:
force_tz(dt, "Pacific/Tahiti")
## [1] "2020-06-07 22:14:00 -10"
```

```
# Get the same cosmic moment in a new time-zone
with_tz(dt, "Pacific/Tahiti")
## [1] "2020-06-07 10:14:00 -10"
```

## # We will use the date from previous hint: dt1 ## [1] "1890-12-29 08:00:00 MST" year(dt) # extract the year ## [1] 2020 month(dt) # extract the month ## [1] 6 week(dt) # extract the week ## [1] 23 dav(dt) # extract the day ## [1] 7 wday(dt) # extract the day of the week as number ## [1] 1 qday(dt) # extract the day of the guarter as number ## [1] 68 yday(dt) # extract the day of the year as number ## [1] 159

hour(dt)

```
moment1 <- as_datetime("2018-10-28 01:59:00", tz = "Europe/Warsaw")
moment2 <- as_datetime("2018-10-28 02:01:00", tz = "Europe/Warsaw")
moment2 - moment1 # Is it 2 minutes or 1 hour and 3 minutes?
## Time difference of 1.033333 hours
moment3 <- as_datetime("2018-10-28 03:01:00", tz = "Europe/Warsaw")
# The clocks were put back in this tz from 3 to 2am.
# So, there is 2 hours difference between 2am and 3am!
moment3 - moment1
# Time difference of 2.033333 hours</pre>
```

- Duration: A duration is the physical amount of time that has been elapsed between two events.
- Periods: Track changes in clock times (so pretend that DST, leap seconds, and leap years do not exist).
- Intervals: Periods of time defined by start and end date-time (duration or period can be extracted)

## Calculating with Date-Times: Durations i

```
# Calculate the duration in seconds:
dvears(\mathbf{x} = 1/365)
## [1] "86459.1780821918s (~1 days)"
dweeks (x = 1)
## [1] "604800s (~1 weeks)"
ddays(x = 1)
## [1] "86400s (~1 days)"
dhours(x = 1)
## [1] "3600s (~1 hours)"
dminutes(x = 1)
## [1] "60s (~1 minutes)"
dseconds(x = 1)
## [1] "1s"
dmilliseconds(x = 1)
## [1] "0.001s"
dmicroseconds(x = 1)
## [1] "1e-06s"
```

```
# Note that a duration object times a number is again a Duration object
# and it allows arithmetic:
dpicoseconds(x = 1) * 10^12
## [1] "1s"
```

### # Investigate the object type:

dur <- dnanoseconds(x = 1)
class(dur)
## [1] "Duration"
## attr(,"package")
## [1] "lubridate"</pre>

str(dur)
## Formal class 'Duration' [package "lubridate"] with 1 slot
## ..@ .Data: num 1e-09

print(dur)
## [1] "1e-09s"

# Calculating with Date-Times: Durations iii

If the duration is not given in one number, but for example in with units expressed as a string, we can use the function duration(). There is also a series of functions that can coerce to a duration, check if something is a duration:

```
# Useful for automation:
duration(5, unit = "years")
## [1] "157788000s (~5 years)"
# Coerce and logical:
dur <- dyears (x = 10)
as.duration(60 * 60 * 24)
## [1] "86400s (~1 davs)"
as.duration(dur)
## [1] "315576000s (~10 years)"
is.duration(dur)
## [1] TRUE
is.difftime(dur)
## [1] FALSE
as.duration(dur)
## [1] "315576000s (~10 vears)"
make_difftime(60. units="minutes")
```

## Time difference of 1 mins © Dr. Philippe J.S. De Brouwer

## Calculating with Date-Times: Periods

```
vears(x = 1)
## [1] "1y Om Od OH OM OS"
months(x = 1)
## [1] "1m 0d 0H 0M 0S"
weeks (x = 1)
## [1] "7d OH OM OS"
days(x = 1)
## [1] "1d OH OM OS"
hours(x = 1)
## [1] "1H OM OS"
minutes(x = 1)
## [1] "1M 0S"
seconds(x = 1)
## [1] "1S"
milliseconds(x = 1)
## [1] "0.001S"
microseconds(x = 1)
```

## [1] "1e-06S" © DR. PHILIPPE J.S. DE BROUWER

```
d1 <- ymd_hm("1939-09-01 09:00", tz = "Europe/Warsaw")
d2 <- ymd_hm("1945-08-15 12:00", tz = "Asia/Tokyo")</pre>
```

interval(d1, d2) # defines the interval ## [1] 1939-09-01 09:00:00 CET--1945-08-15 05:00:00 CEST

```
# Or use the operator %--%:
ww2 <-- d1 %--% d2 # defines the same interval</pre>
```

```
ww2 / days(1) # the period expressed in days
## [1] 2174.833
```

```
ww2 / ddays(1) # duration in terms of days
## [1] 2174.792
```

```
# The small difference is due to DST and equals one hour:
(ww2 / ddays(1) - ww2 / days(1)) * 24
## [1] -1
```

```
# Allow the interval to report on its length:
int_length(ww2) / 60 / 60 / 24
## [1] 2174.792
```

The package lubridate provides a set of functions that allow to check if a date is in an interval, move the interval forward, etc.

## Calculating with Date-Times: the Intervals iii

```
d_date <- vmd("19450430")</pre>
# Ts a date or interval in another:
d date %within% ww2
## [1] TRUE
ph <- interval(ymd_hm("1941-12-07 07:48", tz = "US/Hawaii"),</pre>
                      ymd_hm("1941-12-07 09:50", tz = "US/Hawaii")
ph %within% ww2
                   # is ph in ww2?
## [1] TRUE
int_aligns(ph, ww2) # do ww2 and ph share start or end?
## [1] FALSE
# Shift forward or backward:
int_shift(ww2. years(1))
## [1] 1940-09-01 09:00:00 CEST--1946-08-15 05:00:00 CEST
int_shift(ww2, years(-1))
## [1] 1938-09-01 09:00:00 CET--1944-08-15 05:00:00 CEST
# Swap start and end moment
flww2 <- int_flip(ww2)</pre>
# Coerce all to "positive" (start-date before end-date)
```

© DR. PHILIPPE LS. DE BROUWER



# Building Data for an Example: Survey Data

```
set.seed(1911)
s <- tibble(reply = runif(n = 1000, min = 0, max = 13))</pre>
hml <- function (\mathbf{x} = 0) {
 if (x < 0) return(NA)</pre>
 if (x <= 4) return("L")
 if (x <= 8) return("M")
 if (x <= 12) return("H")</pre>
  return(NA)
surv <- apply(s, 1, FUN = hml) # output is a vector</pre>
surv <- tibble(reply = surv) # coerce back to tibble</pre>
surv
## # A tibble: 1.000 x 1
## reply
## <chr>
## 1 H
## 2 M
## 3 L
## 4 M
## 5 L
## 6 H
## 7 L
## 8 H
## 9 <NA>
## 10 L
## # ... with 990 more rows
```

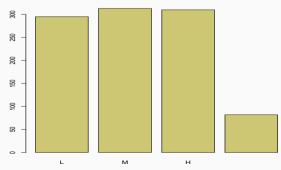
To put the labels in the right orders, we have to make clear to R that they are factors and that we have a specific order for our factors. This can be done with the argument levels in the function parse\_factor().

```
# 1. Define the factor-levels in the right order:
f_levels <- c("L", "M", "H")</pre>
```

# 2. Define our data as factors: survey <- parse\_factor(surv\$reply, levels = f\_levels)</pre>

# Building Data for an Example: Visualizing the Data

```
summary(survey)
## L M H <NA>
## 295 313 310 82
plot(survey, col="khaki3",
    main = "Customer Satisfaction",
    xlab = "Response to the last survey"
)
```



#### Customer Satisfaction

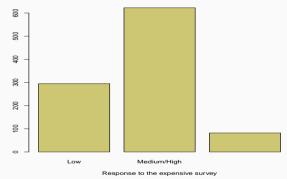
Response to the last survey

# Count the labels:
fct\_count(survey)

## Error: Tibble columns must have compatible sizes.
## \* Size 4: Existing data.
## \* Size 3: Column 'n'.
## i Only values of size one are recycled.

```
# Relabel factors with fct relabel:
HML <- function (x = NULL) {
  x[x == "L"] <- "Low"
  x[x == "M"] <- "Medium/High"</pre>
  x[x == "H"] <- "Medium/High"</pre>
  x[!(x %in% c("High", "Medium/High", "Low"))] <- NA</pre>
  return(x)
f <- fct_relabel(survey, HML)</pre>
summary(f)
           Low Medium/High
                                    <NA>
##
##
           295
                        623
                                      82
plot(f, col="khaki3",
     main = "Only one third of customers is not happy",
     xlab = "Response to the expensive survey"
```

# The Functions of forcats: Changing Labels ii



Only one third of customers is not happy

Figure 2: Maybe you would prefer to show this plot to the board meeting? This plot takes the two best categories together and creates the impression that more people are happy. Compare this to previous plot.

# The Functions of forcats: More Examples

```
num obs < - 1000 # the number of observations in the survey
# Start from a new survey: srv
srv <- tibble(reply = 1:num_obs)</pre>
srv$age <- rnorm(num_obs, mean=50, sd=20)</pre>
srv$age[srv$age < 15] <- NA</pre>
srv$age[srv$age > 85] <- NA</pre>
hml <- function (\mathbf{x} = \mathbf{0}) {
  if (x < 0) return(NA)
  if (x <= 4) return("L")
  if (x <= 8) return("M")
  if (x \le 12) return("H")
  return(NA)
for (n in 1:num_obs) {
  if (!is.na(srv$age[n])) {
     srv$replv[n] <- hml(rnorm(n = 1, mean = srv$age[n] / 7, sd = 2))</pre>
   else {
     srv$reply[n] <- hml(runif(n = 1, min = 1, max = 12))</pre>
f_levels <- c("L". "M". "H")</pre>
srv$fct <- parse_factor(srv$reply, levels = f_levels)</pre>
```

Now that we have the data of the survey, we can showcase forcats and use it to visualize and manipulate the data.

# From most frequent to least frequent: srv\$fct %>% fct\_infreq(ordered = TRUE) %>% levels() ## [1] "M" "H" "L" NA

```
# From least frequent to more frequent:
srv$fct %>%
fct_infreq %>%
fct_rev %>%
levels
## [1] NA "L" "H" "M"
```

```
# Reorder the reply variable in function of median age:
fct_reorder(srv$reply, srv$age) %>%
    levels
## [1] "H" "L" "M"
```

# Add the function min() to order based on the minimum
# age in each group (instead of default median):
fct\_reorder(srv\$reply, srv\$age, min) %>%
 levels
## [1] "H" "L" "M"

# The Functions of forcats: More Examples iv

### # Show the means per class of satisfaction in base-R style:

by(srv\$age, srv\$fct, mean, na.rm = TRUE)
## srv\$fct: L
## [1] 30.65112
##
## srv\$fct: M
## [1] 44.41898
##
## srv\$fct: H
## [1] 60.01358
##
## srv\$fct: NA
## [1] 62.67211

### # Much more accessible result with the dplyr:

```
satisf <- srv %>%
                 group_by(fct) %>%
                 summarize(
                    age = median(age, na.rm = TRUE),
                    \mathbf{n} = \mathbf{n}()
                                %>%
                 print
        ## # A tibble: 4 x 3
           fct age
        ##
                         n
           <fct> <dbl> <int>
        ##
        ## 1 L
               29.9 173
        ## 2 M 43.6 432
© DR. PHILIPPE J.S. DE BROUWER 61.0 328
```

# part 04: Data Wrangling ↓ chapter 18: Dealing with Missing Data



Typically data is missing for one of the following reasons:

- input and pre-processing (e.g. conversion of units: some dates were in American format, others in UK format, some dates got misunderstood and others rejected; a decimal comma is not understood, data is copied to a system that does not recognize large number, etc.);
- unclear or incomplete formulated questions (e.g. asking "are you male or female?", while the possible answers in the questionnaire are "yes" and "no");
- fraud or other intend (if we know that young males will pay higher for a car insurance we might omit the box where the gender is put);
- random reason (e.g. randomly skipped a question, interruption of financial markets due to external reason, mistake, typing a number too much, etc.)

## Example (Unclear questions)

Often, data is missing because questionnaires are written carelessly and formulated ambiguously. What to think about questions such as these:

- rate the quality of the printed materials (1 ... 5);
- parent name, student name, study level;
- it is never so that the teacher is too late: yes/no;
- is the DQP sufficient to monitor the IMRDP and in line with GADQP? yes/no
- I belong to a minority group (when applying for a job).

These example questions have - at least - the following issues.

- The reader will assume that this question is there because the teacher will be assessed on the quality of printed materials and it also assumes that the student cares. Which is an assumption, that should be asked first. What would you do with this question if you did not want printed materials in the first place? Another common mistake is asking "how important are printed materials?" also this question does not help to find whethere people assess the printed materials as positive or negative.
- Whose study level are we asking here? That of the student or that of the parent?
- Assume that the teacher is often late, then you can answer both "yes" or "no," assume the opposite and the same holds. So what to answer?

© DR. PHILIPPE JS ALE REQUERTURESTION has two common problems. First it uses acronyms that might not be clear to everyone:



- Leave out the rows with missing data. If there is no underlying reason why data is missing, then leaving out the missing data is most probably harmless. This will work fine if the dataset is sufficiently large and of sufficient quality (even a dataset with hundred thousand lines but with 500 columns can lead to problems when we leave out all rows that miss one data point).
- Carefully leave out rows with missing data. Same as above, but first make up our mind which variable will be in the model and then only leave out those rows that miss data on those rows.
- Somehow fill in the missing data based on some rules or models. For example, we can replace the missing value by:
  - the mean value for that column;
  - median value for that column;
  - conditional mean or median (e.g. fill in missing value for height with gender based mean) where some pre-existing logic or clear and well accepted rules hold;
  - an educated guess (e.g. someone who scored all requested dimensions as "4/5" probably intended the missing value for "quality of printed materials" to be a "4/5" as well);
  - the mid-value (if that makes sense for example the "3/5" could be a mid-value for "rate on a scale from 1 to 5"), this means choosing the middle of the possible values regardless which values occur more;
  - replace the missing value by a more complex model, eventually based on machine learning, such as:
    - regression substitution, which tries to guess the missing value based on a multiple linear regression on other variables,
    - multiple imputation, which uses statistical methods to guess plausible values based on the data that is not missing (linear
      regression or machine learning) and then reset averages of the variables back by adding random errors in the predictions.

## Example

For the purpose of this example, we will use this database and introduce some missing values.

## # Show a part of the resulting dataset:

head(d1, n=10L)

##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	NA	NA	1.3	0.2	setosa
##	4	4.6	3.1	1.5	0.2	setosa
##	5	5.0	3.6	1.4	0.2	setosa
##	6	5.4	3.9	1.7	0.4	setosa
##	7	4.6	NA	1.4	0.3	setosa
##	8	NA	NA	1.5	0.2	setosa
##	9	4.4	2.9	1.4	0.2	setosa
##	10	4.9	3.1	1.5	0.1	setosa

For each observation that has a variable with a missing value, the method finds an observation (that has no missing value on this variable) with the closest predictive mean to that variable. The observed value from this observation is used as imputed value. This means that it preserves automatically many important characteristics such as skew, boundness (e.g. only positive data), base type (e.g. integer values only), etc.

The PMM process is as follows:

- Take all observations that have no missing values and fit a linear regression of variable x that has the missing values – to one or more variables y, and produce a set of coefficients b.
- Draw random coefficients b\* from the posterior predictive distribution of b. Typically, this would be a random draw from a multivariate normal distribution with mean b and the estimated covariance matrix of b (with an additional random draw for the residual variance). This step will ensure that there is sufficient variability in the imputed values.
- Using  $b^*$ , generate predicted values for x for all cases (as well for those that have missing values in x as those that do not.
- For each observation with missing *x*, identify a set of cases with observed *x* whose predicted values are close to the predicted value for the observation with missing data.
- From those observations, randomly choose one and assign its observed value as value to be imputed to the missing *x*.
- Repeat steps 2 5 till all the missing variables for *x* have an impute candidate.
- Repeat steps 1 6 for all variables that have missing values.



#install.packages('mice') # uncomment if necessary
library(mice) # load the package

# mice provides the improved visualization function md.pattern(): md.pattern(dl) # function provided by mice mice ii

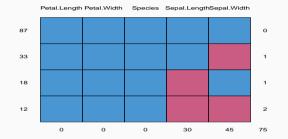


Figure 4: The visualization of missing data with the function md.pattern() of the package mice. This simple visualisation shows the contingents of data with missing values.

102/156

##		Petal.Length	Petal.Width	Species	Sepal.Length	Sepal.Width	
##	87	1	1	1	1	1	0
##	33	1	1	1	1	0	1
##	18	1	1	1	0	1	1
##	12	1	1	1	0	0	2
##		Θ	Θ	0	30	45	75

The table shows that the dataset *d*1 has 87 complete cases, 33 missing observations in Sepal.Width, 18 observations, where Sepal.Length is missing, and 12 cases where both are missing.

```
d2_imp <- mice(d1, m = 5, maxit = 25, method = 'pmm', seed = 1500)</pre>
```

This created five possible datasets and we can select one completed set as follows.

```
# Choose set number 3:
d3_complete <- complete(d2_imp, 3)</pre>
```

## # install.packages('missForest') # only first time

librory(miccForest)					<pre># load the library</pre>			
<pre>library(missForest)</pre>						# toad the tibrary		
	$d\_\text{mf}$	<- missFore	est(d1)			# using the same data as before		
	##	missForest	iteration	1	in	progressdone!		
	##	missForest	iteration	2	in	progressdone!		
	##	missForest	iteration	3	in	progressdone!		
	##	missForest	iteration	4	in	progressdone!		
	##	missForest	iteration	5	in	progressdone!		
	##	missForest	iteration	6	in	progressdone!		
	##	missForest	iteration	7	in	progressdone!		

### # access the imputed data in the ximp attribute:

### head(d\_mf\$ximp)

##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.100000	3.500000	1.4	0.2	setosa
##	2	4.900000	3.000000	1.4	0.2	setosa
##	3	4.516867	3.205947	1.3	0.2	setosa
##	4	4.600000	3.100000	1.5	0.2	setosa
##	5	5.000000	3.600000	1.4	0.2	setosa
##	6	5.400000	3.900000	1.7	0.4	setosa

## # normalized MSE of imputation:

d\_mf\$00Berror ## NRMSE PFC ## 0.1080024 0.0000000

# missForest ii

## Hmisc i

### # Install the package first via: # install.packages('Hmisc') library(Hmisc)

# impute using mean: SepLImp mean <- with(d1, impute(Sepal,Length, mean))</pre>

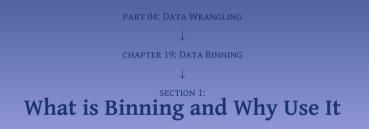
# impute a randomly chosen value: SepLImp\_rand <- with(d1, impute(Sepal.Length, 'random'))</pre>

# impute the maximum value: SepLImp\_max <- with(d1, impute(Sepal.Length, max))</pre>

# impute the minimum value: SepLImp\_min <- with(d1, impute(Sepal.Length, min))</pre>

# note the '\*' next to the imputed values"
head(SepLInp\_min, n = 10L)
## 1 2 3 4 5 6 7 8 9 10
## 5.1 4.9 4.3\* 4.6 5.0 5.4 4.6 4.3\* 4.4 4.9

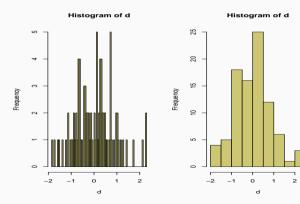
part 04: Data Wrangling ↓ chapter 19: Data Binning



## Histograms are a Binning Method

Consider the following simple example where we start with data drawn from a known distribution and plot the histogram (the output of this code is in Figure 5):

```
set.seed(1890)
d <- rnorm(90)
par(mfrow=c(1,2))
hist(d, breaks=70, col="khaki3")
hist(d, breaks=12, col="khaki3")</pre>
```

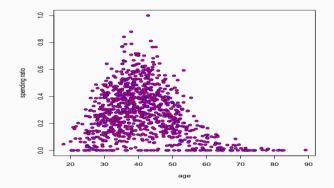


```
# Try a possible cut
c \le cut(d, breaks = c(-3, -1, 0, 1, 2, 3))
table(c)
## C
## (-3,-1] (-1,0] (0,1] (1,2] (2,3]
## 9 34 37
                         7 3
# This is not good, it will not make solid predictions for the last bin.
# So, we neet to use other bins:
c \leftarrow cut(d, breaks = c(-3, -0.5, 0.5, 3))
table(c)
## c
## (-3,-0.5] (-0.5,0.5] (0.5,3]
## 27 41 22
# We have now a similar number of observations in each bin.
```

# Is that the only thing to think about?



## Generating the Data for this Section ii



**Figure 6:** A plot of the fabricated dataset with the spending ratio in function of the age of the customers. The spending ratio is defined as  $\frac{S_n}{S_{n-1}+S_n}$ , where  $S_n$  is the spending in period *n*. If both spends are 0, then the spending ratio is defined as 0.

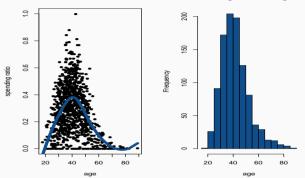
```
# Assume this data is:
# age = age of customer
# spending_ratio = R := S_n/ (S_{n-1} + S_n)
# (zero if both are zero)
# with S_n the spending in month n
dt <- tibble (age = age, spending_ratio = y)</pre>
```

```
# Leave out NAs (in this example redundant):
d1 <- dt[complete.cases(dt),]</pre>
```

```
# order() returns sorted indices, so this orders the vector:
dl <- dl[order(dl$age),]</pre>
```

```
# Fit a loess:
d1_loess <- loess(spending_ratio ~ age, d1)</pre>
```

```
# Add predictions:
d1_pred_loess <- predict(d1_loess)</pre>
```



Histogram of d1\$age

Figure 7: A simple aid to select binning borders is plotting a non-parametric fit (left) and the histogram (right). The information from both plots combined can be used to decide on binning.

par(mfrow=c(1,1))

From the histogram and loess estimate in Figure 7 on slide 117, we can see that:

- the spending ratio does not simply increase or decrease with age the relation is non-linear;
- the local volatility is not constant (the dataset is "heteroscedastic");
- we have little young customers and little older ones (it even looks as if some of those have a definite reason to be inactive on our Internet-shop).

To illustrate the effect of binning, we will use a logistic regression.<sup>1</sup> First, without binning and then with binning. Fitting the logistic regression worsk as follows:

```
# Investigate the model:
summary(lReg1)
##
## Call:
## glm(formula = spending_ratio ~ age, family = guasibinomial, data = dt)
##
## Deviance Residuals:
       Min
##
                  10
                        Median
                                     30
                                              Max
## -0.96344 -0.35725 -0.03202 0.25994
                                          1.62106
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) -0.09892
                       0.11733 -0.843 0.399
         -0.02107 0.00282 -7.473 1.71e-13 ***
## age
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.1652355)
##
##
      Null deviance: 195.63 on 999 degrees of freedom
## Residual deviance: 185.93 on 998 degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

#### # Calculate predictions and means square error:

120/156

Inspired by Figure 7 on slide 117, we can make an educated guess of what bins would make sense. We choose bins that capture the dynamics of our data and make sure to have a bin for values with high spending rations and bins that have low spending ratios.

Now, we will introduce a simple data binning, calculate the logistic mode and show the results:

```
# Bin the variable age:
        c \le cut(dtsage, breaks = c(15, 30, 55, 90))
        # Check the binning:
        table(c)
        ## c
        ## (15.30] (30.55] (55.90]
         ##
               118
                        781
                                101
        # We have one big bucket and two smaller (with the smallest
        # more than 10% of our dataset.
        lvls <- unique(c) # find levels</pre>
                                # check levels order
        lvls
        ## [1] (30.55] (15.30] (55.90]
        ## Levels: (15.30] (30.55] (55.90]
        # Create the tibble (a data-frame also works):
        dt <- as_tibble(dt)</pre>
                                                          2.5%
               mutate(is_L = if_else(age <= 30, 1, 0)) %>%
               mutate(is_H = if_else(age > 55 . 1. 0))
© DR. PHILIPPE I.S. DE BROUWER
```

# Investigate the logistic model:

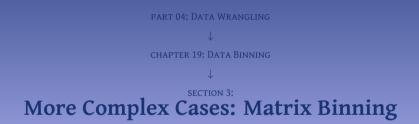
```
summary(lReg2)
##
## Call:
## glm(formula = spending_ratio ~ is_L + is_H. family = guasibinomial.
##
      data = dt)
##
## Deviance Residuals:
##
       Min
                 10
                       Median
                                     30
                                             Max
## -0.88247 -0.31393 -0.03812
                                0.22173
                                         1.50439
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) -0.74222 0.02791 -26.595 <2e-16 ***
## is_L -0.85871 0.09404 -9.132 <2e-16 ***
## is H
        -2.20235 0.16876 -13.050 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.132909)
##
      Null deviance: 195.63 on 999 degrees of freedom
##
## Residual deviance: 144.92 on 997 degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

Finally, we can compare the MSE of both models:

# Compare the MSE of the two models: MSE1 ## [1] 0.03294673

MSE2 ## [1] 0.02603179

We see that indeed the mean square error (MSE) is improved.<sup>2</sup> That is great: our model will make better predictions. However, what is even more important: the significance of our coefficients is up: we have now 3 stars for each *and* the significance of the intercept is up from 0 to 3 stars. That means that the model 2 is much more significant and hence robust to predict the future.



## Generating the Data for Matrix Binning i

## Generating the Data for Matrix Binning ii

```
# Load libraries and define parameters:
library(tidyverse) # provides tibble (only used in next block)
set.seed(1880) # to make results reproducible
N <- 500 # number of rows
# Ladies first:
# age will function as our x-value:
age_f <- rlnorm(N, meanlog = log(40), sdlog = log(1.3))
# x is a temporary variable that will become the propensity to buy:
x_f <- abs(age_f + rnorm(N, 0, 20)) # Add noise & keep positive
x_f <- 1 - (x_f - min(x_f)) / max(x_f) # Scale between 0 and 1
x_f <- 0.5 * x_f / mean(x_f) # Coerce mean to 0.5</pre>
```

```
# This last step will produce some outliers above 1
x_f[x_f > 1] <-1 # Coerce those few that are too big to 1
```

```
# Then the gentlemen:
age_m <- rlnorm(N, meanlog = log(40), sdlog = log(1.3))
x_m <- abs(age_m + rnorm(N, 0, 20))  # Add noise & keep positive
x_m <- 1 - (x_m - min(x_m)) / max(x_m) # Scale between 0 and 1
x_m <- 0.5 * x_m / mean(x_m)  # Coerce mean to 0.5
# This last step will produce some outliers above 1
x_m[x_m > 1] <- 1  # Coerce those few that are too big to 1
x_m <- 1 - x_m  # relation to be increasing</pre>
```

```
# Rename (p_x is not the gendered propensity to buy)
D_f <- x_f</pre>
```

```
p_m <- x_m
```

© Dr. Philippe J.S. De Brouwer

126/156

This first step was only to prepare the data and show what is exactly inside. In the next step, we will merge the data, and assume that this merged data set is what we got to work with. The following block of code will do this and then plot the histogram for the all observations (combined males and females) in Figure 9 on slide 128:

```
tf <- tibble("age" = age_f, "sex" = "F", "is_good" = p_f)
tm <- tibble("age" = age_m, "sex" = "M", "is_good" = p_m)
t <- full_join(tf, tm, by = c("age", "sex", "is_good"))</pre>
```

#### # Change plot parameters and capture old values:

```
oldparams <- par(mfrow=c(1,2))
plot(t$age, t$is_good,
    pch = 21, col = "black", bg = "khaki3",
    xlab = "Age",
    ylab = "Spending probability",
    main = "Dependence on age"
    )
    fct_sex <- factor(t$sex, levels=c("F", "M"), labels=c(0,1))
t$sexM <- as.numeric(fct_sex)  # store for later use
plot(fct_sex, t$is_good,
    col="khaki3",
    main="Dependence on sex",
    xlab="female Male")</pre>
```

## Step 2 to Create the Data: Merge the Sets i

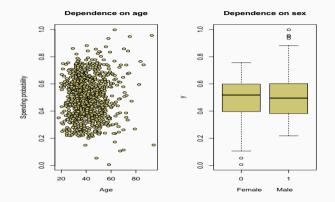


Figure 9: The dataset "as received from the customer service department" does not show any clear relationship between Age or Sex and the variable that we want to explain: the spending ratio.

par(oldparams) # Reset the plot parameters

```
d1 <- t[complete.cases(t),]</pre>
```

```
dl <- dl[order(d1$age),]
dl_age_loess <- loess(is_good ~ age, d1)
dl_age_pred_loess <- predict(d1_age_loess)</pre>
```

```
dl <- dl[order(dl$sexM),]
dl_sex_loess <- loess(is_good ~ sexM, dl)
dl_sex_pred_loess <- predict(dl_sex_loess)</pre>
```

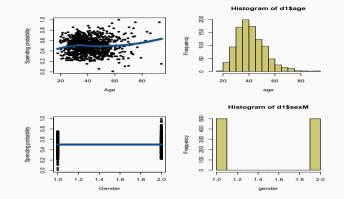


Figure 10: The data does not reveal much patterns for any of the variables (Gender and Age).

par(mfrow=c(1,1))

```
# assess the model:
        summary(regr1)
        ##
        ## Call:
        ## glm(formula = is good ~ age + sexM, family = guasibinomial, data = t)
        ##
        ## Deviance Residuals:
                Min
                           10
                                 Median
                                               30
                                                        Max
        ##
        ## -1.15510 -0.21981 0.00556 0.20597
                                                    1.14979
        ##
        ## Coefficients:
        ##
                         Estimate Std. Error t value Pr(>|t|)
        ## (Intercept) -6.990e-02 9.133e-02 -0.765
                                                       0.444
                  1.684e-03 1.680e-03 1.002
        ## age
                                                        0.316
        ## sexM
                 6.015e-05 3.730e-02 0.002
                                                        0.999
        ##
        ## (Dispersion parameter for quasibinomial family taken to be 0.08694359)
        ##
               Null deviance: 91.316 on 999 degrees of freedom
        ##
        ## Residual deviance: 91.229 on 997 degrees of freedom
        ## AIC: NA
        ##
        ## Number of Fisher Scoring iterations: 3
        pred1 <- 1 / (1+ exp(-(coef(regr1)[1] + t$age * coef(regr1)[2]
                             + t$sexM * coef(regr1)[3])))
        SE1 <- (pred1 - t$is good)^2
MSE1 <- sum(SE1) / length(SE1)
© DR. PHILIPPE J.S. DE BROUWER
```

```
# 1. Check the potential cut:
c <- cut(t$age, breaks = c(min(t$age), 35, 55, max(t$age)))
table(c)
## c
## (17.9,35] (35,55] (55,94.2]
## 300 591 108
```

#### # 2. Create the matrix variables:

```
t <- as_tibble(t)</pre>
                                                              %>%
    mutate(is_LF = if_else((age <= 35) & (sex == "F"), 1L, 0L)) %>%
    mutate(is_HF = if_else((age > 50) & (sex == "F"), 1L, 0L)) %>%
    mutate(is_LM = if_else((age <= 35) & (sex == "M"), 1L, 0L)) %>%
    mutate(is_HM = if_else((age > 50) & (sex == "M"), 1L, 0L)) %>%
    print
## # A tibble: 1.000 x 8
       age sex is good sexM is LF is HF is LM is HM
##
     <dbl> <chr> <dbl> <dbl> <int> <int> <int> <int> <int><</pre>
##
                            1
##
   1 44.3 F
                  0.564
                                   0
                                         0
                                               0
                                                    0
## 2 38.3 F
                  0.636
                          1
                                   0
                                        0
                                               0
                                                    0
## 3 38.9 F
                   0.552
                                   0
                                         0
                           1
                                               0
                                                    0
## 4 58.5 F
                  0.351
                           1
                                   0
                                        1
                                               0
                                                    0
## 5 31.5 E
                   0.623
                            1
                                   1
                                         0
                                               0
                                                    0
                                         0
## 6 48.4 F
                   0.487
                           1
                                   0
                                               0
                                                    0
## 7 28.9 F
                  0.552
                           1
                                   1
                                         0
                                               0
                                                    0
## 8 29.9 F
                   0.493
                             1
                                   1
                                         0
                                               0
                                                    0
## 9 30.1 F
                   0.549
                             1
                                   1
                                         0
                                               0
                                                    0
## 10 51.1 F
                   0.241
                                   0
                                         1
                                               0
                                                    0
                             1
## # ... with 990 more rows
```

#### # 3. Check if the final bins aren't too small:

t[,5:8] %>% map\_int(sum) ## is\_LF is\_HF is\_LM is\_HM ## 154 104 147 101

# Assess the model: summary(regr2) ## ## Call: ## glm(formula = is good ~ is LF + is HF + is LM + is HM, family = guasibinomial.## data = t) ## ## Deviance Residuals: ## Min 10 Median 30 Max ## -0.98606 -0.18858 -0.00424 0.18159 0.98651 ## ## Coefficients: Estimate Std. Error t value Pr(>|t|) ## ## (Intercept) -0.01768 0.02467 -0.716 0.474 ## is\_LF 0.27945 0.05094 5.485 5.23e-08 \*\*\* ## is\_HE -0.35564 0.06002 -5.925 4.29e-09 \*\*\* ## is\_LM -0.22844 0.05183 -4.408 1.16e-05 \*\*\* ## is\_HM 0.45028 0.06106 7.375 3.46e-13 \*\*\* ## ---## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 ## ## (Dispersion parameter for quasibinomial family taken to be 0.07518569) ## Null deviance: 91.316 on 999 degrees of freedom ## ## Residual deviance: 78.274 on 995 degrees of freedom ## AIC: NA ##

```
## Number of Fisher Scoring iterations: 3
© Dr. PHILIPPE J.S. DE BROUWER
```

## Finally, we also note that the MSE has improved too:

MSE1 ## [1] 0.02166756

MSE2 ## [1] 0.01844601

# Question #1 Binary dependent variables

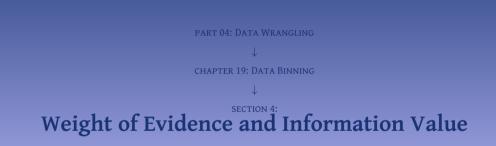
In many cases, the dependent variable will be binary (0 or 1, "yes" or "no"). That means that we are trying to model a yes/no decision. For example, 1 can be a customer that defaulted on a loan, a customer to receive a special offer, etc.

t <- mutate(t, "is\_good" = if\_else(is\_good >= 0.5, 1L, 0L))

Remake model 1 (logistic regression in function of age and sexM) and model 2 (logistic regression for the variables is\_LF, is\_HF, is\_LM, and is\_HM). What does this change? Are the conclusions different?

# **Question #2 Think outside the box**

In this particular case, what other approach would you suggest?



For each bin *i* of variable *j* (or for each binary variable *j*) is defined as

$$\textit{NOE}_{ij} = \log \left\{ rac{rac{\#G_{ij}}{\#G}}{rac{\#B_{ij}}{\#B}} 
ight\}$$

Where  $\#G_{ij}$  is the number of "good observations" (binary variable is 1) in bin *i* for variable *j*. #Gis the number of good observations for the whole dataset, and "B" refers to the "bad observations" (i.e. where the dependent variable is 0).

This makes WOE a measure of predicting power of a binned variable.

The information value of bin *i* for variable *j* is defined as

$$\mathsf{IV}_{ij} = \left(rac{\# \mathsf{G}_{ij}}{\# \mathsf{G}} - rac{\# \mathsf{B}_{ij}}{\# \mathsf{B}}
ight)$$
 .WOE $_{ij}$ 

Rule of thumb:

IV	Predictability
< 0.02	Not predictive
0.02 - 0.3	Weak
0.1 - 0.3	Medium
0.3 - 0.5	Strong
> 0.5	Suspicious

Table 1: Different levels of information value and their commonly accepted interpretation – which works good in the environment of credit data for example.

# WOE and IV in R i

# We	start	from	this	da	ataset	used	in	previous	section:
prin	t(t)								
## #	A tib	ole: 3	1.000	х	8				

is\_good sexM is\_LF is\_HF is\_LM is\_HM ## age sex ## ## 1 44.3 F ## 2 38.3 F ## 3 38.9 F 4 58.5 F ## ## 5 31.5 E ## 6 48.4 F ## 7 28.9 F 1 1 ## 8 29.9 F ## 9 30.1 F ## 10 51.1 E ## # ... with 990 more rows

This dataset contains a specific property where males and females have a similar propensity to spend as an average population. However, this propensity is decreasing for females and increasing for males. This situation is particularly difficult, since at first glance the variables Age and Sex will not be predictive at all. We need to look at the interactions between the variables in order to find the underlying relations.

Now, that we have data, we can load the package InformationValue, create a weight of evidence table and calculate the information value for a given variable:

```
#install.packages("InformationValue")
```

library(InformationValue)

```
WOETable(X = factor(t$sexM), Y = t$is_good, value0fGood=1) %>%
knitr::kable(format.args = list(big.mark = " ", digits=2))
```

CAT	GOODS	BADS	TOTAL	PCT_G	PCT_B	WOE	IV
1	267	233	500	0.52	0.48	0.088	0.0039
2	245	255	500	0.48	0.52	-0.088	0.0039

## also functions WOE() and IV(), e.g. # IV of a categorical variable is the sum of IV of its categories IV(X = factor(t\$sexM), Y = t\$is\_good, valueOfGood=1) ## [1] 0.007757952 ## attr(,"howgood")

## [1] "Not Predictive"

Dividing the data based on gender is not sufficient, and it does not work. Using our variables, such as is\_LF (female from the lower age group), which combine the information of age and gender should work better.

```
WOETable(X = factor(t$is_LF), Y = t$is_good, value0fGood=1) %>%
knitr::kable(digits=2)
```

CAT	GOODS	BADS	TOTAL	PCT_G	PCT_B	WOE	IV
0	396	450	846	0.77	0.92	-0.18	0.03
1	116	38	154	0.23	0.08	1.07	0.16

```
# The package porvides also functions WOE() and IV().
# The IV of a categorical variable is the sum of IV of its categories.
IV(X = factor(t$is_LF), Y = t$is_good, value0fGood=1)
## [1] 0.1849507
## attr(,"howgood")
## [1] "Highly Predictive"
```



Consider the dataset mtcars and investigate if the gearbox type (the variable am is a good predictor for the layout of the motor (the variable vs, V-motor or not). Do this by using WOE and IV.

# part 04: Data Wrangling $\downarrow$ chapter 20:

## **Factoring Analysis and Principle Components**



#### fit <- princomp(mtcars, cor=TRUE)</pre>

<pre>summary(fit)  # print the variance explained by PC</pre>								
## Importance of components:								
##	Comp.1 Comp.2 Comp.3 Comp.4							
## Standard deviation	2.5706809 1.6280258 0.79195787 0.51922773							
## Proportion of Variance	0.6007637 0.2409516 0.05701793 0.02450886							
## Cumulative Proportion	0.6007637 0.8417153 0.89873322 0.92324208							
##	Comp.5 Comp.6 Comp.7 Comp.8							
## Standard deviation	0.47270615 0.45999578 0.36777981 0.35057301							
## Proportion of Variance	$0.02031374 \ 0.01923601 \ 0.01229654 \ 0.01117286$							
## Cumulative Proportion	0.94355581 0.96279183 0.97508837 0.98626123							
##	Comp.9 Comp.10 Comp.11							
## Standard deviation	0.277572792 0.228112781 0.148473587							
## Proportion of Variance	0.007004241 0.004730495 0.002004037							
## Cumulative Proportion	0.993265468 0.997995963 1.000000000							

#### PCA in R and Visualising Results ii

#### loadings(fit) # show PC loadings

##

## Loadings:

m m	Loudings.										
##		Comp.1	Comp.2	Comp.3	Comp.4	Comp.5	Comp.6	Comp.7	Comp.8	Comp.9	
##	mpg	0.363		0.226		0.103	0.109	0.368	0.754	0.236	
##	cyl	-0.374		0.175			-0.169		0.231		
##	disp	-0.368			-0.257	0.394	0.336	0.214		0.198	
##	hp	-0.330	0.249	-0.140		0.540			0.222	-0.576	
##	drat	0.294	0.275	-0.161	-0.855		-0.244				
##	wt	-0.346	-0.143	-0.342	-0.246		0.465			0.359	
##	qsec	0.200	-0.463	-0.403		-0.165	0.330		0.232	-0.528	
##	VS	0.307	-0.232	-0.429	0.215	0.600	-0.194	-0.266		0.359	
##	am	0.235	0.429	0.206			0.571	-0.587			
##	gear	0.207	0.462	-0.290	0.265		0.244	0.605	-0.336		
##	carb	-0.214	0.414	-0.529	0.127	-0.361	-0.184	-0.175	0.396	0.171	
##		Comp.10	O Comp.	11							
##	mpg	0.139	0.12	5							
##	cyl	-0.846	0.14	1							
##	disp		-0.663	1							
##	hp	0.248	0.250	5							
##	drat	-0.101									
##	wt		0.56	7							
##	qsec	-0.271	-0.18	1							
##	VS	-0.159									
##	am	-0.178									
##	gear	-0.214									
##	carb		-0.320	Э							

##

© DR. PHILIPPELS. DE BROUWER

Comp 1 Comp 2 Comp 2 Comp 4 Comp 5 Comp 6 Comp 7

150/156

### Hint – Executing PCA before fitting a model

Since a lot of variance is explained in the first PCs, it is a good idea to fit any model (such as a logistic regression or any other model) not directly on mtcars, but rather on its principal components. This will make the model more stable and one can expect the model to perform better out of sample, the only cost is the loss of transparency of the model.<sup>a</sup>

<sup>&</sup>lt;sup>a</sup> If the first principal components can be summarizes as a certain concept, then there is little to no loss of transparency. However, usually, the PCs are composed of too many variables and do not summarize as one concept.



# Maximum Likelihood Factor Analysis # Extracting 3 factors with varimax rotation: fit <- factanal(mtcars, 3, rotation = "varimax")</pre> print(fit, digits = 2, cutoff = .3, sort = TRUE) ## ## Call: ## factanal(x = mtcars, factors = 3, rotation = "varimax") ## ## Uniquenesses: ## mpg cvl disp hp drat wt gsec vs am gear carb ## 0.13 0.06 0.09 0.13 0.29 0.06 0.05 0.22 0.21 0.12 0.16 ## ## Loadings: Factor1 Factor2 Factor3 ## ## mpg 0.64 -0.48 -0.47 ## disp -0.72 0.54 0.32 ## drat 0.80 ## wt -0.78 0.52 ## am 0.88 ## gear 0.91 ## cvl -0.62 0.70 ## hp 0.72 0.51 ## asec -0.95 ## vs -0.80 ## carb 0.56 0.72 ## ## Factor1 Factor2 Factor3

DR. PHILIPPELS DE BROUWER 4 20 2 52 1 50

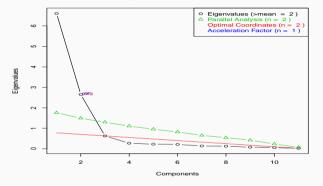
# load the library nFactors: library(nFactors)

Then we can perform the analysis, get the optimal number of factors, and plot a visualisation:

```
# Get the eigenvectors:
eigV <- eigen(cor(mtcars))</pre>
# Get mean and selected quantile of the distribution of eigen-
# values of correlation or a covariance matrices of standardized
# normally distributed variables:
aPar <- parallel(subject = nrow(mtcars), var = ncol(mtcars),
                 rep = 100, cent = 0.05)
# Get the optimal number of factors analysis:
nScr <- nScree(x = eigV$values, aparallel = aPar$eigen$gevpea)</pre>
# See the result
nScr
## noc naf nparallel nkaiser
## 1 2 1
                     2
                        2
```

```
# and plot it.
plotnScree(nScr)
```

#### Factor Analysis: Deciding How Many Factors to Use ii



Non Graphical Solutions to Scree Test

Figure 14: Visual aids to select the optimal number of factors.