R

Jeff Lin

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Contents

R , , , R . R (open-source, GNU General Public License), R {R} (R core-development team) , .

R , R Base , , ggplot2, tidyverse . . R , R Base . R , , ggplot2, tidyverse . , . R Base , R .

R , , , . , R . R **bookdown** package (Xie, 2020), .

, R , . R base R base , R , ggplot2, tidyverse , https://r4ds.had.co.nz/ https://rstudio-education.github.io/hopr/. , .

Chapter 1

R

R Ross Ihaka Robert Gentleman S , . R , R , , . S 1980 , AT&T , Rick Becker, John Chambers, Allan Wilks , 1990 , Insightful S , , Splus. R S (Splus) , R S , , S , SAS, SPSS . R (open-source, GNU General Public License), R {R} (R core-development team) , , , {R} , .

1.1 R

R , Microsoft Window, Unix/Linux, Apple Mac OS , windows . windows , , " ' ' (User), , . R , , .

R (Reproducible Research, Dynamic Documentation), Rtools, RStudio, Tex System, Pandoc, Git . (PATH) , PATH . R , .

R , R Rtools : 1. http://www.r-project.org 2. (Link) Download CRAN. 3. CRAN Mirrors (CRAN Mirrors), https://cloud.r-project.org/ 4. Download R for Windows. 5. R for Windows base. 6. , Download R X.Y.Z for Windows, X.Y.Z R , . 7. , R-X.Y.Z-win.exe, . 8. , 64 . 9. base , Rtools, Rtoolsxx.exe. , . 10. Windows, Mac Linux , google Youtube , .

1.2 RSudio

{R} {R} . , , , {R} . {R} / , RStudio {R} , RStudio {R} , . http://www.rstudio.com/, Product

, R premier IDE for R, Rstudio Desktop, RStudio. Rstudio , . , (User Name), , . RSudio , , . Tex/LaTeX, Rstudio PDF , Tex system, Pandoc, Git, TeX/LaTeX/XeLaTex , https://www.latex-project.org/get/, MikTeX: http://miktex.org/. Pandoc, http://pandoc.org/, http://pandoc.org/installing.html. Git, https://git-scm.com/. GitHub , . , (Xie, 2015), Xie (2020) https://bookdown.org/yihui/rmarkdown/, https://rmarkdown.rstudio.com/ .

1.3

{R} , {R}, {R}, , , {R} , . {R} RStudio console .

```
1+2            # calculator
log(3.14)      # log function
x = 1 + 2      # one plus two assign to x
x              # print x
x = c(1, 3, 5, 7) # get a vector
mean(x)        # mean function
log(x)         # log function
```

{R} {R}, google R Introduction, R Tutorial , YouTube . .

```
factorial(4)
sin(pi)
x.vec <- c(2:5)
exp(x.vec)
matrix(c(1:6), nrows=2, ncols=3)
weight = c(50, 45, 67, 53)
mean(weight)
sd(weight)
```

{R} , , , , , , . {R} .

```
## demo
demo(graphics)
demo(image)
example(contour)
demo(persp)
example(persp3d)
demo(plotmath)
demo(Hershey)
install.packages("lattice") # install package
library("lattice")          # load package
demo(lattice)
```

```
example(wireframe)
install.packages("rgl")
library("rgl")
demo(rgl)                        # Interact using your mouse.
```

{R} , , , . , ,

{R} , {R} , , 0.5$ $1.0 , , , . , google, . {R} :

- .
- .
- , Big5 utf-8 .
- : / , , $, },],).
- / , , : , , Tab .
- PDF Web copy .
- .

, , , , , .

1.4 Object

{R} **S** , (Object-Oriented Programming Language), {R} , , (**object**). {R} (vector), (matrix), (array), (Lists), (data frames) (function) .

{R} , . , {R} , `s` `S` . , (**object name**) **.** ( ) , **.** , , , (A-Z a-z), (0-9), /, ., _ (underscore) -, . .

{R} , , , `c`, `s`, `C`, `T`, `F` , (**reserved names**). :

```
FALSE Inf NA NaN NULL TRUE
break else for function if in next repeat while
F T
c q s t C D I
diff mean pi range rank var
```

, , , , , .

1.5

{R} , 2 , (**expression**), ,

```
1+2
log(x)
mean(x)
```

(**assignment**), ,

```
x <- 1+2
x = 4-5
```

{R} , (**prompt symbol**), > ( ). , , {R} . , {R} , ( ) , {R} . {R}

```
options(prompt = "R>")
```

> R>.

(**assignment symbol**) <- ``, , ,x <- 1 + 2, x`` '' $(1 + 2)$. {R} , =( ) ** **, ,x = 1 + 2, {R} ,=( ) , <- =, {R} <-‘.

, , print(), , .

```
## asign
x <- 1   # assign object x
x        # show x
## [1] 1
print(x) # print()
## [1] 1
msg <- "hello"
msg     # show x
## [1] "hello"
```

, {R} , <Enter> , {R} , + ( ), + , , {R} . , <Enter> , {R} . , ; ( ) , . ,

```
## input at the same line, use ;
x <- 1 + 2; y <- 3 + 4
## input 2 lines separately
x <- 1 + 2
y <- 3 + 4
```

, { \; }, , (**compound expression**), .

{R} , , , (**commands**), # ( ) , , {R} , . , , ##, #.

```
## This is my R code
log(pi)
## [1] 1.145
## simple calculation
3+4 # calculator: two plus one
## [1] 7
```

{R} Console , , , ↑ ( ) , , , <DEL> . , {R} .

```
# This is my R code
x = 1 + 2  # one plus two
x
## [1] 3
x + 4
## [1] 7
x - 1
## [1] 2
```

1.6

{R} (**object**), , , , . {R} object() ls() {R} .

```
## show objects
object()  # shiow all objects
ls()      # show all obkects
ls(x, y)  # show x and y object
```

rm(), , ,

```
## delete objects: x.vec and y.vec
rm(x.vec, y.vec)
```

x.vec y.vec.

1.7

, {R} . , <Esc> . ,

```
for (i in 1:1000000) print (i) # press <Esc>
```

<Esc> .

1.8

{R} , (**working directory**). {R} (PATH) // (, C://RData//) / (, C:/RData/). Windowns \\ (, C:\\RData). getwd(), . setwd(), . .

```
getwd() # show your current working directory
setwd("C:/RData/")
getwd()
## [1] "C:/RData"
```

.

```
setwd("C:/RData")
getwd()
setwd("C:/RData/")
getwd()
```

{R} , , , , , . , age, gender, m1.lm, m2.lm , , , , , , . RStudio (project), , , GitHub . (version control), (Xie, 2015), Xie (2020) https://bookdown.org/yihui/rmarkdown/, https://rmarkdown.rstudio.com/, https://happygitwithr.com/ .

1.9 RStudio

, . RStudio: Tools, Global Options.....

- General, Restore .RData, Save workspace to .RData on exit: Never.
- Default text encoding: UTF-8.
- Appearance, , , Zoom: 140%, Font size: 14, .
- Sweave, Waeve Rnw file using: knitr, Typest LaTeX into PDF using: XeLaTeX‘.
- Apply OK.

{RStudio} R .

- {RStudio}, {RStudio} .
- File → New File → R Script, R .
- , File, → Save as, C:\RData, Rlab00.r .
- .r .R , {R} .
- source , .
- , , File, Save.
- .

R , .

```
## Rlab00.r
x <- 1
print(x)
x
msg <- "hello"
msg
y <- 1:20
y
rm(x, msg, y)
```

R , , , (copy) {RSudio} Console , . , <control>+<Enter> , . {R} , {R} , . {RStudio}

Rlab00.r . , , {RSudio} Consol .

- {RStudio}, {RStudio} .
- File → New File, → R Notebook R Markdown, {RStudio} (template). (chunk) ```{r} ``` R . ,

~~~
```{r}
2.4*3.8
x.vec = rnorm(50)
y.vec = rnorm(50)
plot(x.vec, y.vec)
```
~~~

R Notebook R Markdown , , copy $\rightarrow$ paste word . , knit, , . R Notebook R Markdown , knit .

1.10 Function

{R} (**function**), , , , , , , {R} . (**argument**).

{R} (base) , , {R} (contribution) , {R} . , mean(), var(), sd(), log() . R .

```
## function
## function c() = concatenate elements, return a vector x.vec
x.vec = c(1:5)
x.vec # show x.vec
## [1] 1 2 3 4 5
mean(x = x.vec) # function mean() calculate mean, return a scalar
## [1] 3
var(x = x.vec)  # function mean() calculate variance
## [1] 2.5
log(x = x.vec)  # take log for all elements in vector x.vec
## [1] 0.0000 0.6931 1.0986 1.3863 1.6094
```

(**argument**) , , (**formals**). , , (**required argument**), , (**optional argument**), (**ellipsis argument**) , , , {R} . , log() :

```
log(x, base = exp(1))
```

log() {R} , x , . base = exp(1) , , log() *e* , , , 2 , log(x, base = 2).

```
## log function
x.vec <- c(1, 2, 3, 4, 5)
log(x = x.vec)
## [1] 0.0000 0.6931 1.0986 1.3863 1.6094
```

```
log(x = x.vec, base = 2)
## [1] 0.000 1.000 1.585 2.000 2.322
```

1.11 Packages

. } (**package**). , {R} , (**package**), , survival , , , tidyverse .

{R} , . {R} , ( ) base {R}, {R} , {R} , . , {R} , (**contributed package**).

{R} , . , , (1) {RStudio} . {RStudio} . Packages → Install. , , tidyverse, MASS .

(2) install.packages() .

```
install.packages("PackageName", dependencies = TRUE)
```

PackageName` . , `Console .

```
install.packages("survival")
library(survival)
```

{R} , , ,

- .
- library() require() .

library(), library() = loads a package, , require() = tries to load a package, , error , , foo() paa , require() pbb, pbb coo() foo(), paa paa , coo() , error , error , my.obj, , .

library(package.name) , package.name function.name(). , , , {::} package.name function.name() :

```
package.name::function.name()
```

package.name function.name().

```
ggplot2::ggplot()
```

ggplot2 ggplot().

1.12

{R} , Google {R} . {R} help.start(). Console

```
help.start()
```

funName , {R} , help(funName), ?funName, help.search("funName"), apropos("funName") . , mean() . {R} .

```
help(mean)
?mean
help.search("mean")
apropos("mean")
```

, args("funName").

1.13

{R} , {R} {R} , {R} , , {R} . sessionInfo() {R} .

```
sessionInfo()
```

version() {R} version[['version.string']], Sys.getlocale() {R} LC_COLLATE=Chinese (Traditional)_Taiwan.950;LC_CTYPE=Chinese (Traditional)_Taiwan.950;LC_MONETARY=Chinese (Traditional)_Taiwan.950;LC_NUMERIC=C;LC_TIME=C (Traditional)_Taiwan.950. cp950 (big5) . . Sys.timezone() {R} Asia/Taipei. {R} (local time) NA, , , , , Sys.setlocale("LC_TIME", "C"), UTC (Universal Time, Coordinated). ISO .

```
#   ->
Sys.setlocale("LC_CTYPE", "en_US.UTF-8")
# system("defaults write org.R-project.R force.LANG en_US.UTF-8") # linux/mac
#   ->
Sys.setlocale(category = "LC_ALL", locale = "cht")
# system("defaults write org.R-project.R force.LANG zh_TW.UTF-8") # linux/mac
```

, {R} .

Chapter 2

Vector

{R} , {R} , (**object**), , (vector), (matrix), (array), (Lists), (data frames) . {R} , , , . , . {R} , {R} .

2.1 Vector

{R} , (**mode**) . {R} (**basic mode**) **numeric**, **integer**, **logical**, **complex**, **character**. .

(scalar), , (double) ({numerical vector}). , {R} , (**scalar**) 1 , 1- , {R} (**no dimension**). , {R} `x.vec <- c(1, 2, 3)`, 1×3 , 3×1 , , `x.vec` / , `x.vec` , {R} , .

2.2

{R} , (**mode**) . {R} (**basic mode**) **numeric**, **integer**, **logical**, **complex**, **character**, `class()` .

- **numeric**, ( ), **single** **double** .

```
# numeric
x1 <- 10.1
x1
## [1] 10.1
class(x1)
## [1] "numeric"
x2 <- 10
x2
## [1] 10
```

```
class(x2)
## [1] "numeric"
is.numeric(x2)
## [1] TRUE
```

- **integer**, (1L, 2L, ...).

```
# integer
y1 <- 1L
y1
## [1] 1
class(y1)
## [1] "integer"
is.integer(y1)
## [1] TRUE
is.numeric(y1)
## [1] TRUE
```

- **logical**, (true or false), **TRUE** (**T**) **FALSE** (**F**) , 1 0 **T** **F**.

```
# logic
yes_id <- TRUE
yes_id
## [1] TRUE
no_id <- FALSE
no_id
## [1] FALSE
class(no_id)
## [1] "logical"
is.logical(no_id)
## [1] TRUE
2 == 3
## [1] FALSE
2 != 3
## [1] TRUE
2 > 3
## [1] FALSE
2 <= 3
## [1] TRUE
4 >= 1
## [1] TRUE
TRUE + 5
## [1] 6
TRUE * 5
## [1] 5
FALSE * 5
```

```
## [1] 0
TRUE + FALSE
## [1] 1
TRUE * FALSE
## [1] 0
```

- **complex**, .

```
x = 3+5i
x
## [1] 3+5i
class(x)
## [1] "complex"
```

- **character**, , (”).

```
# character
ca <- "yes"
ca
## [1] "yes"
cb <- "this is a book."
cb
## [1] "this is a book."
class(cb)
## [1] "character"
is.character(cb)
## [1] TRUE
"abc" > "abd"
## [1] FALSE
"date" < "dates"
## [1] TRUE
```

. ’Date,POSIXct POSIXt , , Sys.Date()‘ .

```
Sys.Date()
## [1] "2020-09-14"
date1 <- as.Date("2020-09-17")
date1
## [1] "2020-09-17"
class(date1)
## [1] "Date"
as.numeric(date1)
## [1] 18522
date2 <- as.POSIXct("2020-09-17 18:30")
class(date2)
## [1] "POSIXct" "POSIXt"
as.numeric(date2)
```

```
## [1] 1.6e+09
```

, .

2.2.1 c()

, c() . c() **concatenate** ( ), .

```
## c()
## numerical
x.vec <- c(1/1, 1/2, 1/3, 1/4, 1/5)
x.vec
## [1] 1.0000 0.5000 0.3333 0.2500 0.2000
## integer
x.vec <- c(1L, 2L, 3L)
x.vec
## [1] 1 2 3
## character
flavors.vec <- c("chocolate", "vanilla", "strawberry") # character
flavors.vec
## [1] "chocolate"  "vanilla"    "strawberry"
y.vec <- c("Hello", "What's your name?", "Your email?")
y.vec
## [1] "Hello"             "What's your name?" "Your email?"
## logical
z.vec <- c(F, T, T, F, F)
z.vec
## [1] FALSE  TRUE  TRUE FALSE FALSE
## complex
x.complex.vec <- c(8+3i, 9+0i, 2+4i)
x.complex.vec
## [1] 8+3i 9+0i 2+4i
## numerical
x.vec <- c(1/1, 1/2, 1/3, 1/4, 1/5)
y.vec <- c(1, 2, 3, 4, 5)
z.vec <- c(x.vec, 11, 12, y.vec)
z.vec
##  [1]  1.0000  0.5000  0.3333  0.2500  0.2000 11.0000 12.0000  1.0000  2.0000
## [10]  3.0000  4.0000  5.0000
```

2.3

{R} (**basic operators**), C , (arithmetic operator), (relation/comparison operator), (logical operator). {R} (programming language), (if-else), (switch), (loop) (function) , ,

. .

Table 2.1:

-	(Substraction, can be unary or binary)
+	(Addition, can be unary or binary)
!	(Unary not)
	(Multiplication, binary)
/	(Division, binary)
^	(Exponentiation, binary)
%%	(Modulus, binary)
%/%	(Integer divide, binary)
%*%	(Matrix product, binary)
%o%	(Outer product, binary)
%x%	Kronecker (Kronecker product, binary)
%in%	(Matching operator, binary, in model formulae: nesting)
<	Less than, binary
>	Greater than, binary
==	Equal to, binary
!=	Not equal to
>=	Greater than or equal to, binary
<=	Less than or equal to, binary
&	, (Logical AND, binary, vectorized)
&&	, (Logical AND, binary, not vectorized)
|	, (Logical OR, binary, vectorized)
||	, (Logical OR, binary, not vectorized)
xor	“ ’’, , 1 TRUE

2.4

{R} (**arithmetic operator**) , +, -, !, *, /, \^, %%, %/%, %*%, %o%, %x%, %in% : , , , , , .

```
## Arithmetic Operator
1 + 2
## [1] 3
1 + 2 + 3
## [1] 6
3 * 7 * 2
## [1] 42
4/2
## [1] 2
4/3
## [1] 1.333
```

```
2 * 3 + 4
## [1] 10
2 * (3 + 4)
## [1] 14
(3 + 11 * 2)/4
## [1] 6.25
#
x.complex <- (8+3i)+(1+2i)
x.complex
## [1] 9+5i
#
x.vec <- 1:5
y.vec <- c(-1, -2, 0, 2, 4)
z.vec <- c(2, 2, 3, 3, 4)
x.vec + y.vec
## [1] 0 0 3 6 9
x.vec - y.vec
## [1] 2 4 3 2 1
#
x.vec * 2
## [1]  2  4  6  8 10
x.vec * y.vec
## [1] -1 -4  0  8 20
x.vec/2
## [1] 0.5 1.0 1.5 2.0 2.5
x.vec/y.vec
## [1] -1.00 -1.00   Inf  2.00  1.25
#
x.vec^2
## [1]  1  4  9 16 25
x.vec^z.vec
## [1]   1   4  27  64 625
y.vec/2
## [1] -0.5 -1.0  0.0  1.0  2.0
y.vec/x.vec
## [1] -1.0 -1.0  0.0  0.5  0.8
#
y.vec %% 3  # modular arithmetic remainder
## [1] 2 1 0 2 1
y.vec %/% 3   # integer division
## [1] -1 -1  0  0  1
y.vec %/% x.vec
## [1] -1 -1  0  0  0
```

2.5

(**logic vector**) TRUE, FALSE. T F. {R} , (**relation/comparison operator**) . <, <=, >, >=, &, && (AND), | , || (OR), == != .

```
## Relation/Comparison Operator
x.vec <- 1:5
y.vec <- (x.vec > 2)
y.vec
## [1] FALSE FALSE  TRUE  TRUE  TRUE
any(x.vec > 2)
## [1] TRUE
all(x.vec > 2)
## [1] FALSE
#
x.vec <- 1:5
y.vec <- c(0, 2, 4, 6, 8)
#
x.vec < 2
## [1]  TRUE FALSE FALSE FALSE FALSE
x.vec<= 2
## [1]  TRUE  TRUE FALSE FALSE FALSE
x.vec == 2
## [1] FALSE  TRUE FALSE FALSE FALSE
x.vec != 2
## [1]  TRUE FALSE  TRUE  TRUE  TRUE
#
x.vec < y.vec
## [1] FALSE FALSE  TRUE  TRUE  TRUE
x.vec < (y.vec - 2)
## [1] FALSE FALSE FALSE FALSE  TRUE
x.vec <= y.vec
## [1] FALSE  TRUE  TRUE  TRUE  TRUE
x.vec <= (y.vec - 2)
## [1] FALSE FALSE FALSE  TRUE  TRUE
#
x.vec == y.vec
## [1] FALSE  TRUE FALSE FALSE FALSE
x.vec == (y.vec - 2)
## [1] FALSE FALSE FALSE  TRUE FALSE
x.vec != y.vec
## [1]  TRUE FALSE  TRUE  TRUE  TRUE
x.vec != (y.vec - 2)
## [1]  TRUE  TRUE  TRUE FALSE  TRUE
#
```

```
## Logical Operator: AND OR XOR
x.vec <- 1:5
y.vec <- c(0, 2, 4, 6, 8)
(x.vec > 0) &  (y.vec > 0)  # return vector AND
## [1] FALSE  TRUE  TRUE  TRUE  TRUE
(x.vec > 0) && (y.vec > 0)  # return scalar AND
## [1] FALSE
#
(x.vec > 0) &  ((y.vec - 3) > 0)      # return vector AND
## [1] FALSE FALSE  TRUE  TRUE  TRUE
((x.vec-2) > 0) && ((y.vec - 3) > 0) # return scalar AND
## [1] FALSE
#
(x.vec > 0) &  ((y.vec + 3) > 0)      # return vector AND
## [1] TRUE TRUE TRUE TRUE TRUE
((x.vec-2) > 0) && ((y.vec + 3) > 0) # return scalar AND
## [1] FALSE
#
(x.vec > 0) | (y.vec > 0) # return vector OR
## [1] TRUE TRUE TRUE TRUE TRUE
((x.vec- 2) > 0) | ((y.vec - 3) > 0)
## [1] FALSE FALSE  TRUE  TRUE  TRUE
#
(x.vec > 0) || (y.vec > 0) # return scalar OR
## [1] TRUE
((x.vec-2) > 0) || ((y.vec - 3) > 0)
## [1] FALSE
#
(x.vec > 0) || ((y.vec + 3) > 0) # return scalar OR
## [1] TRUE
((x.vec-2) > 0) || ((y.vec + 3) > 0)
## [1] TRUE
#
xor((x.vec > 0), (y.vec > 0)) # return vector exclusive OR
## [1]  TRUE FALSE FALSE FALSE FALSE
xor(((x.vec - 2) > 0), ((y.vec - 3) > 0))
## [1] FALSE FALSE FALSE FALSE FALSE
xor(((x.vec - 2) > 0), ((y.vec + 3) > 0))
## [1]  TRUE  TRUE FALSE FALSE FALSE
#
xx.vec <- (x.vec <= 3)
yy.vec <- (y.vec >= 4)
xx.vec
## [1]  TRUE  TRUE  TRUE FALSE FALSE
yy.vec
```

```
## [1] FALSE FALSE  TRUE  TRUE  TRUE
#
xx.vec && yy.vec
## [1] FALSE
xx.vec & yy.vec
## [1] FALSE FALSE  TRUE FALSE FALSE
xx.vec || yy.vec
## [1] TRUE
xx.vec | yy.vec
## [1] TRUE TRUE TRUE TRUE TRUE
xor(xx.vec, yy.vec)
## [1]  TRUE  TRUE FALSE  TRUE  TRUE
```

2.6

, , names() . , unname() , names(x.vec) <- NULL .

```
## vector names
x.vec <- c(
  age = 50,
  chol = 220,
  dbp = 84,
  sbp = 132
) # directly
x.vec
##  age chol  dbp  sbp
##   50  220   84  132
names(x.vec)
## [1] "age"  "chol" "dbp"  "sbp"
#
x.vec <- c(55, 236, 80, 140)
names(x.vec) <- c("age", "chol", "sbp", "dbp")
#
y.vec.name <- names(x.vec)
y.vec <- c(60, 214, 90, 144)
names(y.vec) <- y.vec.name
y.vec
##  age chol  sbp  dbp
##   60  214   90  144
```

2.7 Inxex

(length) , (index) , (**index**) `[i]`, ( ) . , , , .

```
## Vector Indexing
## positive integer
x.vec <- 1:50
x.vec[7]
## [1] 7
x.vec[11:15]
## [1] 11 12 13 14 15
y.vec <- x.vec[11:15]
y.vec
## [1] 11 12 13 14 15
## negative integer
z.vec <- 6:10
z.vec[-c(2, 4)]
## [1]  6  8 10
## character string
fruit.vec <- c(5, 10, 1, 20)
fruit.vec
## [1]  5 10  1 20
names(fruit.vec) <- c("orange", "banana", "apple", "peach")
fruit.vec
## orange banana  apple  peach
##      5     10      1     20
lunch.vec  <-  fruit.vec[c("apple", "orange")]
lunch.vec
##  apple orange
##      1      5
## logical index
x.vec <- c(NA, -2, -1, NA, 1, 2, NA) # NA = missing value
x.vec
## [1] NA -2 -1 NA  1  2 NA
y.vec <- x.vec[!is.na(x.vec)] # !is.na() = check missing value
y.vec
## [1] -2 -1  1  2
z.vec <- x.vec[x.vec > 0 & !is.na(x.vec)]
z.vec
## [1] 1 2
x.vec[x.vec < 0] # Note: NA
## [1] NA -2 -1 NA NA
y.vec[y.vec < 0]
## [1] -2 -1
z.vec[z.vec < 0]
```

```
## numeric(0)
```

2.8 ( ) Missing Values

, (**missing value**, incomplete data**), R , , NA , (NA = Not Available), R NaN = Not a Number , NULL 0. (NA) , (NA) . is.na(), is.nan() . . . , na.omit(), na.fail(), na.exclude(), na.action() . complete.cases() . , , R .

```
## missing value
z.vec <- c(1:2, NA)
is.na(z.vec)
## [1] FALSE FALSE  TRUE
log(z.vec)
## [1] 0.0000 0.6931     NA
z.vec / 0
## [1] Inf Inf  NA
0 / 0
## [1] NaN
Inf - Inf
## [1] NaN
#
is.na(z.vec)
## [1] FALSE FALSE  TRUE
is.nan(z.vec)
## [1] FALSE FALSE FALSE
is.nan(0 / 0)
## [1] TRUE
#
x.vec  <-  c(1, 2, NA, 4, NA, 5, 6)
bad  <-  is.na(x.vec)
x.vec[!bad]
## [1] 1 2 4 5 6
#
x.vec  <-  c(1, 2, NA, 4, NA, 5, 6)
y.vec  <-  c("a", "b", NA, "d", NA, "f", "g")
good  <-  complete.cases(x.vec, y.vec)
good
## [1]  TRUE  TRUE FALSE  TRUE FALSE  TRUE  TRUE
x.vec[good]
## [1] 1 2 4 5 6
y.vec[good]
## [1] "a" "b" "d" "f" "g"
#
```

```
data(airquality)
airquality[1:6,]
##   Ozone Solar.R Wind Temp Month Day
## 1    41     190  7.4   67     5   1
## 2    36     118  8.0   72     5   2
## 3    12     149 12.6   74     5   3
## 4    18     313 11.5   62     5   4
## 5    NA      NA 14.3   56     5   5
## 6    28      NA 14.9   66     5   6
good  <-  complete.cases(airquality)
airquality[good,][1:6,]
##   Ozone Solar.R Wind Temp Month Day
## 1    41     190  7.4   67     5   1
## 2    36     118  8.0   72     5   2
## 3    12     149 12.6   74     5   3
## 4    18     313 11.5   62     5   4
## 7    23     299  8.6   65     5   7
## 8    19      99 13.8   59     5   8
```

2.9 Factor

(**factor**) (**categorical data**), . , , (**nominal variable**) (**ordinal variable**), . , , . , , 1, 0; 1 = , 2 = , 3 = , 4 = , 5 = . , 2 , , 0 1, , (**dichotomous variable**, **binary variable**), . , , , . , 4 : , , , , I, II, III, IV 4 . $1, 2, 3, 4, \ldots$, , , .

, , , . {R} (**factor**) . , , , , ** *, ** *, ** * (**levels**), . , , , {R} , ", , {R} .

{R} , `factor()` .

```
factor(x = character(), levels, labels = levels,
       exclude = NA, ordered = is.ordered(x), nmax = NA)
```

- `x` , , , {R} .
- `levels` .
- `labels` .
- `exclude = NA` .
- `ordered = is.ordered(x)` , .
- `nmax = NA` .

```
## factor()
sex <- c("male", "female", "male", "male", "female")
sex
## [1] "male"   "female" "male"   "male"   "female"
class(sex)
## [1] "character"
sex <- factor(sex)
sex
## [1] male   female male   male   female
## Levels: female male
class(sex)
## [1] "factor"
## factor() + levels
sex <- c("male", "female", "male", "male", "female")
sex <- factor(sex, levels = c("female", "male"))
sex
## [1] male   female male   male   female
## Levels: female male
## factor() + levels + labels
x.chr = c("male", "male", "female", "female")
factor(x.chr, levels = c("male", "female", "bisex"))
## [1] male   male   female female
## Levels: male female bisex
factor(x.chr, levels = c("male", "female", "bisex"),
              labels = c("m", "f", "b"))
## [1] m m f f
## Levels: m f b
## factor() + exclude
## factor() + exclude
pain <- c("none", "mild", "moderate", "severe", NA)
factor(pain) # NA is NOT a level.
## [1] none     mild     moderate severe   <NA>
## Levels: mild moderate none severe
factor(pain, exclude = NA) # NA is NOT a level.
## [1] none     mild     moderate severe   <NA>
## Levels: mild moderate none severe
factor(pain, exclude = c(NA)) # NA is NOT a level.
## [1] none     mild     moderate severe   <NA>
## Levels: mild moderate none severe
factor(pain, exclude = NULL) # NA is a level.
## [1] none     mild     moderate severe   <NA>
## Levels: mild moderate none severe <NA>
factor(pain, exclude = "mild") # NA is a level.
## [1] none     <NA>     moderate severe   <NA>
## Levels: moderate none severe <NA>
```

```
pain <- factor(pain, exclude = c("mild", NA))
pain # mild and NA are NOT levels.
## [1] none     <NA>     moderate severe   <NA>
## Levels: moderate none severe
```

{R} factor() (**unordered factor**), (**nominal variable**), (level), , . {R} , , levels() ; levels() , {R} , levels() , .

, (**reference level**), (**contrast comparison**). relevel(), .

```
## unorder
## level()
gender <- c("M", "F", "M", "M", "F")
gender <- factor(gender)
gender
## [1] M F M M F
## Levels: F M
levels(gender)
## [1] "F" "M"
levels(gender) <- c("Female", "Male")
gender
## [1] Male   Female Male   Male   Female
## Levels: Female Male
hypertension <- c("Lo", "Mod", "Hi", "Mod", "Lo", "Hi", "Lo")
hypertension <- factor(hypertension)
hypertension
## [1] Lo  Mod Hi  Mod Lo  Hi  Lo
## Levels: Hi Lo Mod
# relevel()
relevel(hypertension, ref = "Lo") # reset a reference level
## [1] Lo  Mod Hi  Mod Lo  Hi  Lo
## Levels: Lo Hi Mod
```

as.integer() , 1 , , .

```
## convert to numerical values
hypertension <- c("Lo", "Mod", "Hi", "Mod", "Lo", "Hi", "Lo")
hypertension <- factor(hypertension)
levels(hypertension)
## [1] "Hi"  "Lo"  "Mod"
hypertension
## [1] Lo  Mod Hi  Mod Lo  Hi  Lo
## Levels: Hi Lo Mod
as.integer(hypertension)
## [1] 2 3 1 3 2 1 2
```

```
#
levels(hypertension) <- list("Low" = "Lo",
                             "Moderate" = "Mod",
                             "High" = "Hi")
hypertension
## [1] Low      Moderate High     Moderate Low      High     Low
## Levels: Low Moderate High
as.integer(hypertension)
## [1] 1 2 3 2 1 3 1
#
## convert to numerical values
pain <- c(7, 8, 6, 6, 8, 7)
pain <- factor(pain)
pain
## [1] 7 8 6 6 8 7
## Levels: 6 7 8
as.integer(pain)
## [1] 2 3 1 1 3 2
pain.chr = as.character(pain)
pain.chr
## [1] "7" "8" "6" "6" "8" "7"
pain.num = as.integer(pain.chr)
pain.num
## [1] 7 8 6 6 8 7
```

Chapter 3

Multidimensional Data

{R} , {R} , (**object**), , (vector), (matrix), (array), (Lists), (data frames) . {R} , , , . , . , {R} , (matrix), (array), (Lists), (data frames) .

3.1 Matrix

(**matrix**) (, mode) 2- (2-dimension) , (**dimension**) , dim() . , 2- (array).

3.1.1 matrix()

, × (×), , matrix().

```
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE, dimnames = NULL)
```

- `nrow = r` , (row numbers).
- `ncol = c` , (column number).
- `byrow = FALSE`: {R} , ( ) (column) . , `byrow = TRUE`.
- `dimnames = obj.list` .

dim() .

```
## numeric
x.mat <- matrix(c(1, 2, 3, 4, 5, 6), nrow = 2) # one row first
x.mat
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
```

```
dim(x.mat)
## [1] 2 3
y.mat <- matrix(c(1, 2, 3, 4, 5, 6), ncol = 2)
y.mat
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
z.mat <- matrix(c(1, 2, 3, 4, 5, 6), nrow = 2, byrow = T)
z.mat
##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]    4    5    6
p.mat <- matrix(c(1, 2, 3, 4, 5, 6), ncol = 2, byrow = T)
p.mat
##      [,1] [,2]
## [1,]    1    2
## [2,]    3    4
## [3,]    5    6
w.mat <- matrix(c(1:18), nrow = 3)
w.mat
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]    1    4    7   10   13   16
## [2,]    2    5    8   11   14   17
## [3,]    3    6    9   12   15   18
dim(y.mat)
## [1] 3 2
# character
x.vec <- c("a", "b", "c", "d", "e", "f")
x.vec
## [1] "a" "b" "c" "d" "e" "f"
y.mat <- matrix(x.vec, nrow = 2, ncol = 3) # byrow = F
y.mat
##      [,1] [,2] [,3]
## [1,] "a"  "c"  "e"
## [2,] "b"  "d"  "f"
y.mat <- matrix(x.vec,
                nrow = 2,
                ncol = 3,
                byrow = T)
y.mat
##      [,1] [,2] [,3]
## [1,] "a"  "b"  "c"
## [2,] "d"  "e"  "f"
dim(y.mat)
```

```
## [1] 2 3
# dim
m.vec.mat <- 1:10
dim(m.vec.mat) <- c(2, 5)
m.vec.mat
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    3    5    7    9
## [2,]    2    4    6    8   10
dim(m.vec.mat)
## [1] 2 5
```

3.1.2 dimnames()

, (column name) (row name), `dimnames()` . `dimnames()` matrix . (**row name**) (**column name**), `rownames()` `colnames()`.

```
# dimnames
x.mat  <-  matrix(1:6, nrow = 2, ncol = 3)
dimnames(x.mat) <- list(c("A1", "A2"),
                        c("B1", "B2", "B3"))
x.mat
##    B1 B2 B3
## A1  1  3  5
## A2  2  4  6
dim(x.mat)
## [1] 2 3
dimnames(x.mat)
## [[1]]
## [1] "A1" "A2"
##
## [[2]]
## [1] "B1" "B2" "B3"
rownames(x.mat)
## [1] "A1" "A2"
colnames(x.mat)
## [1] "B1" "B2" "B3"
#
m.mat <- matrix(
  c(1, 2, 3, 11, 12, 13),
  nrow = 2,
  ncol = 3,
  byrow = TRUE,
  dimnames = list(c("row1", "row2"),
                  c("C1", "C2", "C3"))
)
```

```
m.mat
##      C1 C2 C3
## row1  1  2  3
## row2 11 12 13
dim(m.mat)
## [1] 2 3
dimnames(m.mat)
## [[1]]
## [1] "row1" "row2"
##
## [[2]]
## [1] "C1" "C2" "C3"
rownames(m.mat)
## [1] "row1" "row2"
colnames(m.mat)
## [1] "C1" "C2" "C3"
```

3.2 Matrix Index

(**index**) , , 2- , , , , . , `matrix.name[i, j]` $[i, j]$; `matrix.name[i, ]` i (ith row), `matrix.name[ , j]` j (ith column). {R} , `[m, ]` , m (row) ; `[ , n]` , n (column) .

```
## matrix index
x.mat <- matrix(c(1:12), 3, 4)
x.mat
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    7   10
## [2,]    2    5    8   11
## [3,]    3    6    9   12
x.mat[2, 3] <- 30
x.mat
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    7   10
## [2,]    2    5   30   11
## [3,]    3    6    9   12
x.mat[2,]
## [1]  2  5 30 11
x.mat[, 3]
## [1]  7 30  9
x.mat[c(1, 3), c(2, 4)]
##      [,1] [,2]
## [1,]    4   10
## [2,]    6   12
```

```
#
m.mat <- matrix(
  c(1, 2, 3, 11, 12, 13),
  nrow = 2,
  ncol = 3,
  byrow = TRUE,
  dimnames = list(c("row1", "row2"),
                  c("C1", "C2", "C3"))
)
m.mat
##      C1 C2 C3
## row1  1  2  3
## row2 11 12 13
m.mat[, c("C1", "C2")]
##      C1 C2
## row1  1  2
## row2 11 12
m.mat[c("row2"),]
## C1 C2 C3
## 11 12 13
m.mat[c("row1"), c("C1", "C3")]
## C1 C3
##  1  3
```

1 1 , , , drop = FALSE.

```
## dimension reduction
x.mat <- matrix(1:8, 2, 4)
x.mat[1,] # reduces to a vector
## [1] 1 3 5 7
x.mat[1, , drop = FALSE] # remains as a matrix
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5    7
```

3.2.1 : rbind() cbind()

{R} (**no dimension**), , $1 \times k$ / , $k \times 1$ / , , / , , {R} / , $1 \times k$ {R} , , , , 1- k- , {R} $1 \times k$ $k \times 1$, . , (row number) (column number) , recycle .

```
## matrix cbind() and rbind()
x.vec <- c(1, 2, 3)
y.vec <- c(8, 9, 10)
rbind(x.vec, y.vec)  # vector as row vector
##       [,1] [,2] [,3]
## x.vec    1    2    3
## y.vec    8    9   10
cbind(x.vec, y.vec)  # vector as col vector
##      x.vec y.vec
## [1,]     1     8
## [2,]     2     9
## [3,]     3    10
#
x.mat <- matrix(c(11:16), 2, 3)
rbind(x.mat, x.vec) # vector as row vector
##       [,1] [,2] [,3]
##         11   13   15
##         12   14   16
## x.vec    1    2    3
cbind(x.mat, y.vec) # warning
## Warning in cbind(x.mat, y.vec): number of rows of result is not a multiple of
## vector length (arg 2)
##               y.vec
## [1,] 11 13 15     8
## [2,] 12 14 16     9
#
x.vec <- c(1, 2)
y.vec <- c(8, 9)
rbind(x.vec, y.vec) # vector as row vector
##       [,1] [,2]
## x.vec    1    2
## y.vec    8    9
cbind(x.vec, y.vec) # vector as col vector
##      x.vec y.vec
## [1,]     1     8
## [2,]     2     9
#
x.mat <- matrix(c(11:14), 2, 2)
z.mat <- rbind(x.mat, x.vec) # vector as row vector
z.mat
##       [,1] [,2]
##         11   13
##         12   14
## x.vec    1    2
cbind(x.mat, y.vec) # vector as col vector
##            y.vec
## [1,] 11 13     8
## [2,] 12 14     9
rbind(z.mat, y.vec) # vector as row vector
##       [,1] [,2]
##         11   13
##         12   14
## x.vec    1    2
## y.vec    8    9
cbind(z.mat, y.vec) # warning
## Warning in cbind(z.mat, y.vec): number of rows of result is not a multiple of
## vector length (arg 2)
##             y.vec
##       11 13      8
##       12 14      9
## x.vec  1  2      8
```

3.2.2 Array

(**array**) (mode) *p*- , *p*- . `array()` .

{R} 3- $m \times n \times k$, `[m, , ]` , m (row) ; `[ , n, ]` , n (column) , . `[ , , k]` 3- 1, 2- .

, , `dimnames()` . `dimnames()` array . (**index**) , , (`[i, j, k]`). 1 (, **row name**) { **2** (**,** column name**), `rownames()` `colnames()`.

```
## array()
a.vec <- 1:24
a.vec
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
b.array <- array(a.vec, dim = c(4, 3, 2),
                 dimnames = list(c("x1", "x2", "x3", "x4"),
                                 c("y1", "y2", "y3"),
                                 c("z1", "z2")))
b.array
## , , z1
##
##    y1 y2 y3
## x1  1  5  9
## x2  2  6 10
## x3  3  7 11
## x4  4  8 12
##
## , , z2
##
##    y1 y2 y3
## x1 13 17 21
## x2 14 18 22
## x3 15 19 23
## x4 16 20 24
```

```
mode(b.array)
## [1] "numeric"
dim(b.array)
## [1] 4 3 2
length(b.array)
## [1] 24
dimnames(b.array)
## [[1]]
## [1] "x1" "x2" "x3" "x4"
##
## [[2]]
## [1] "y1" "y2" "y3"
##
## [[3]]
## [1] "z1" "z2"
rownames(b.array)
## [1] "x1" "x2" "x3" "x4"
colnames(b.array)
## [1] "y1" "y2" "y3"
# array index
a.vec
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
b.array <- array(a.vec, dim = c(4, 3, 2),
                 dimnames = list(c("x1", "x2", "x3", "x4"),
                                 c("y1", "y2", "y3"),
                                 c("z1", "z2")))
b.array
## , , z1
##
##    y1 y2 y3
## x1  1  5  9
## x2  2  6 10
## x3  3  7 11
## x4  4  8 12
##
## , , z2
##
##    y1 y2 y3
## x1 13 17 21
## x2 14 18 22
## x3 15 19 23
## x4 16 20 24
b.array[3, 2, 1]
## [1] 7
b.array[4, 3, 2]
```

```
## [1] 24
b.array[2, c(1, 3), 1]
## y1 y3
##  2 10
b.array[3, c(2, 3), 1]
## y2 y3
##  7 11
b.array[2, ,]
##    z1 z2
## y1  2 14
## y2  6 18
## y3 10 22
b.array[, 2,]
##    z1 z2
## x1  5 17
## x2  6 18
## x3  7 19
## x4  8 20
b.array[, , 2]
##    y1 y2 y3
## x1 13 17 21
## x2 14 18 22
## x3 15 19 23
## x4 16 20 24
```

3.3 List

(**list**) , . (mode) (**complex mode**) , “ ’’, (**component**), , (order sequence), , , . , .

3.3.1 list()

list() . {R} , , , , , , .

```
## list()
## list w/o component names
x.vec <- 1:4
y.vec <- c("Male", "Female")
z.mat <- matrix(1:9, nrow = 3, ncol = 3)
xyz.list <- list(x.vec, y.vec, z.mat)
xyz.list
## [[1]]
## [1] 1 2 3 4
##
```

```
## [[2]]
## [1] "Male"   "Female"
##
## [[3]]
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
mode(xyz.list)
## [1] "list"
length(xyz.list)
## [1] 3
dim(xyz.list)
## NULL
names(xyz.list)
## NULL
class(xyz.list)
## [1] "list"
## list w/ component names
x.num <- c(1, 3, 6)
y.str <- c("chocolate", "vanilla", "strawberry")
xy.list <- list(x.num.var = x.num, y.str.var = y.str)
xy.list
## $x.num.var
## [1] 1 3 6
##
## $y.str.var
## [1] "chocolate"  "vanilla"    "strawberry"
# list = data matrix
id.vec <- c(1, 2, 3, 4)
age.vec <- c(35, 55, 45, 25)
sex.vec <- c("Male", "Male", "Female", "Female")
disease.vec <- c("Yes", "No", "No", "Yes")
x.list <- list(
  id  = id.vec,
  age = age.vec,
  sex = sex.vec,
  disease = disease.vec
)
x.list
## $id
## [1] 1 2 3 4
##
## $age
## [1] 35 55 45 25
```

```
##
## $sex
## [1] "Male"   "Male"   "Female" "Female"
##
## $disease
## [1] "Yes" "No"  "No"  "Yes"
```

3.3.2 List Index

, , List.Name , list i.number , List.Name[[3]]. , , [[i.number]] [i.number] .

```
## list index
## list w/o component names
x.vec <- 1:4
y.vec <- c("Male", "Female")
z.mat <- matrix(1:9, nrow = 3, ncol = 3)
xyz.list <- list(x.vec, y.vec, z.mat)
xyz.list
## [[1]]
## [1] 1 2 3 4
##
## [[2]]
## [1] "Male"   "Female"
##
## [[3]]
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
xyz.list[1]
## [[1]]
## [1] 1 2 3 4
xyz.list[[1]]
## [1] 1 2 3 4
xyz.list[2]
## [[1]]
## [1] "Male"   "Female"
xyz.list[[3]]
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
xyz.list[3]
## [[1]]
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
```

(component) comp.name, List.Name\$comp.name , List.Name[[comp.name]] . List.Name\$comp.name List.Name[[comp.name]] , List.Name\$comp.name . [[i.number]] , $.
.

```
# list w/ component names
x.vec <- 1:4
y.vec <- c("Male", "Female")
z.mat <- matrix(1:9, nrow = 3, ncol = 3)
xyz.list <- list(class = x.vec,
                 gender = y.vec,
                 score = z.mat)
xyz.list
## $class
## [1] 1 2 3 4
##
## $gender
## [1] "Male"   "Female"
##
## $score
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
xyz.list$class
## [1] 1 2 3 4
xyz.list[["class"]]
## [1] 1 2 3 4
xyz.list[["class"]][2]
## [1] 2
#
xyz.list$gender
## [1] "Male"   "Female"
xyz.list[["gender"]][1]
## [1] "Male"
#
xyz.list$score
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
xyz.list[["score"]][2, 3]
```

```
## [1] 8
```

3.4 Data Frame

, {R} , , , {R} (**list**) `list()`, .

(**data frame**) . ( ) , , , , (**data matrix**), . : {R} {R} , {R} {R} .

3.5 data.frame()

{R} `data.frame()` . ( ) , , .

```
## data frame
id.vec <- c(1, 2, 3, 4)
age.vec <- c(35, 55, 45, 25)
sex.vec <- c("Male", "Male", "Female", "Female")
disease.vec <- c("Yes", "No", "No", "Yes")
x.df  <-  data.frame(
  id  = id.vec,
  age = age.vec,
  sex = sex.vec,
  disease = disease.vec
)
mode(x.df)
## [1] "list"
class(x.df)
## [1] "data.frame"
x.df
##   id age    sex disease
## 1  1  35   Male     Yes
## 2  2  55   Male      No
## 3  3  45 Female      No
## 4  4  25 Female     Yes
x.df$age
## [1] 35 55 45 25
x.df$disease
## [1] "Yes" "No"  "No"  "Yes"
```

3.5.1 Data Frame Index

(**index**) , , , , , . 2- , , `dataframe.name[i, j]` $[i, j]$; `dataframe.name[i, ]` i (ith row), `dataframe.name[ , j]` j (ith column).

, (**index**) , . `data.Name` , ‘`i.number`'' ( ), data.Name[[3]]. , ,[[i.number]] [i.number] . variable.name, dataframe.Name$variable.name , dataframe.Name[[variable.name]] . `dataframe.Name\$variable.name` `dataframe.Name[[variable.name]]` `[i]` , `dataframe.Name\$variable.name` . `[[i.number]]` , $.

```
## data frame index
data(Puromycin)
Puromycin
##    conc rate     state
## 1  0.02   76   treated
## 2  0.02   47   treated
## 3  0.06   97   treated
## 4  0.06  107   treated
## 5  0.11  123   treated
## 6  0.11  139   treated
## 7  0.22  159   treated
## 8  0.22  152   treated
## 9  0.56  191   treated
## 10 0.56  201   treated
## 11 1.10  207   treated
## 12 1.10  200   treated
## 13 0.02   67 untreated
## 14 0.02   51 untreated
## 15 0.06   84 untreated
## 16 0.06   86 untreated
## 17 0.11   98 untreated
## 18 0.11  115 untreated
## 19 0.22  131 untreated
## 20 0.22  124 untreated
## 21 0.56  144 untreated
## 22 0.56  158 untreated
## 23 1.10  160 untreated
Puromycin$rate
##  [1]  76  47  97 107 123 139 159 152 191 201 207 200  67  51  84  86  98 115 131
## [20] 124 144 158 160
Puromycin$state
##  [1] treated   treated   treated   treated   treated   treated   treated  
##  [8] treated   treated   treated   treated   treated   untreated untreated
## [15] untreated untreated untreated untreated untreated untreated untreated
## [22] untreated untreated
## Levels: treated untreated
Puromycin[1]
##    conc
## 1  0.02
## 2  0.02
## 3  0.06
## 4  0.06
## 5  0.11
## 6  0.11
## 7  0.22
## 8  0.22
## 9  0.56
## 10 0.56
## 11 1.10
## 12 1.10
## 13 0.02
## 14 0.02
## 15 0.06
## 16 0.06
## 17 0.11
## 18 0.11
## 19 0.22
## 20 0.22
## 21 0.56
## 22 0.56
## 23 1.10
Puromycin[1][[1]]
##  [1] 0.02 0.02 0.06 0.06 0.11 0.11 0.22 0.22 0.56 0.56 1.10 1.10 0.02 0.02 0.06
## [16] 0.06 0.11 0.11 0.22 0.22 0.56 0.56 1.10
Puromycin$state[1:3]
## [1] treated treated treated
## Levels: treated untreated
Puromycin[1:3, 1:2]
##   conc rate
## 1 0.02   76
## 2 0.02   47
## 3 0.06   97
```

Chapter 4

{R} , , (vector), (matrix), (array), (Lists), (data frames) . , {R} , , , , {R} , {R} .

{R} ASCII , {R} , SAS, SPSS, STATA, EXCEL, , web open data (XML, HTML JSON), image, texts, stock market, social media . , , .

{R} , , , , , {R} , , {R} , {R} , , . , , , . ASCII , ASCII .

4.1

, , {R} (**data frame**). `SAS`, `STATA` dataset . , (**cross table**).

{R} , , , , , , , , , . (**mode**) .

Table 4.1: DMTKRtabsep.txt DMTKRblanksep.txt:

No	age	sex	DM	DMyr	preAC	prePC	postAC	postPC	Med	SIDE	PREKS	POSKS	ABS	I
1	67	0	0	10	120	160	140	180	0	0	56	92	1	0
2	67	0	0	11	100	150	150	220	0	1	62	62	0	1
3	72	1	0	4	150	200	120	150	2	0	60	94	1	0
4	82	1	0	8	150	200	160	250	0	1	47	90	1	0
5	73	1	0	3	85	110	140	200	0	0	44	88	0	0

, .

- 1 (, row), (**variable names**)
- 1 (row), (**column label**), 2 (row) .
- 1 (, row).
- 1 (, column) (label, identification), (**row label**).
- ( ) , , .
- (column) (**row label**).
- , , , `underscore _`.
- , , , , , .
- , , , , , , .
- , {R} , , .

4.2 ASCII R :

ASCII , ASCII . (**raw data**) , {R} ASCII , , {R} , ASCII .

{R} (data frame) , {R} `read.table()` `read.csv()` , . , , `scan()` , . {R} {R} , ASCII , :

- , , .
- (the first row) (**variable names**) , (**column name**) (**column label**).
- (the first column) (**row label**) (**row name**).
- (row), .
- () (blank space) , ’Tab‘ .
- , , , .
- ASCII , **.dat**, **.prn** **.txt**.
- **,** ( ) ASCII , **comma-separated-variable format CSV format**, **.csv** .
- (variable name) , , . (, dot), `_` (underscore). , . (observed value).
- `Tab` , 2 ASCII . , **CSV format**.

```
# DMTKRblanksep.txt = " " single space separate
Rblanksep.df = read.table("C:/RData/DMTKRblanksep.txt",
                          header = TRUE,
                          row.names = NULL,
                          dec = ".")
head(Rblanksep.df)
##   No age sex DM DMyr preAC prePC postAC postPC Med SIDE PREKS POSKS ABS INFECT
## 1  1  67   0  0   10   120   160    140    180   0    0    56    92   1      0
## 2  2  67   0  0   11   100   150    150    220   0    1    62    62   0      1
## 3  3  72   1  0    4   150   200    120    150   2    0    60    94   1      0
## 4  4  82   1  0    8   150   200    160    250   0    1    47    90   1      0
## 5  5  73   1  0    3    85   110    140    200   0    0    44    88   0      0
## 6  6  76   0  0    1   120   150    120    200   0    1    52    94   1      0
str(Rblanksep.df)
## 'data.frame':        78 obs. of  15 variables:
##  $ No    : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ age   : int  67 67 72 82 73 76 76 77 64 64 ...
##  $ sex   : int  0 0 1 1 1 0 0 0 0 0 ...
##  $ DM    : int  0 0 0 0 0 0 0 1 0 0 ...
##  $ DMyr  : int  10 11 4 8 3 1 1 35 5 5 ...
##  $ preAC : int  120 100 150 150 85 120 120 200 130 130 ...
##  $ prePC : int  160 150 200 200 110 150 150 250 180 180 ...
##  $ postAC: int  140 150 120 160 140 120 120 230 100 100 ...
##  $ postPC: int  180 220 150 250 200 200 200 300 150 150 ...
##  $ Med   : int  0 0 2 0 0 0 0 1 0 0 ...
##  $ SIDE  : int  0 1 0 1 0 1 0 1 0 1 ...
##  $ PREKS : int  56 62 60 47 44 52 48 42 40 45 ...
##  $ POSKS : int  92 62 94 90 88 94 96 90 94 96 ...
##  $ ABS   : int  1 0 1 1 0 1 0 1 1 0 ...
##  $ INFECT: int  0 1 0 0 0 0 0 0 0 0 ...
## complete read.table
## DMTKRblanksep.txt = " " single space separate
Rblanksep.df = read.table("C:/RData/DMTKRblanksep.txt",
                          header = TRUE,
                          sep = " ",
                          quote = "\"'",
                          dec = ".",
                          row.names = NULL,
                          # col.names,
                          as.is = TRUE,
                          # as.is = !stringsAsFactors,
                          na.strings = c(".", "NA"))
head(Rblanksep.df)
##   No age sex DM DMyr preAC prePC postAC postPC Med SIDE PREKS POSKS ABS INFECT
## 1  1  67   0  0   10   120   160    140    180   0    0    56    92   1      0
## 2  2  67   0  0   11   100   150    150    220   0    1    62    62   0      1
## 3  3  72   1  0    4   150   200    120    150   2    0    60    94   1      0
## 4  4  82   1  0    8   150   200    160    250   0    1    47    90   1      0
## 5  5  73   1  0    3    85   110    140    200   0    0    44    88   0      0
## 6  6  76   0  0    1   120   150    120    200   0    1    52    94   1      0
str(Rblanksep.df)
## 'data.frame':        78 obs. of  15 variables:
##  $ No    : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ age   : int  67 67 72 82 73 76 76 77 64 64 ...
##  $ sex   : int  0 0 1 1 1 0 0 0 0 0 ...
##  $ DM    : int  0 0 0 0 0 0 0 1 0 0 ...
##  $ DMyr  : int  10 11 4 8 3 1 1 35 5 5 ...
##  $ preAC : int  120 100 150 150 85 120 120 200 130 130 ...
##  $ prePC : int  160 150 200 200 110 150 150 250 180 180 ...
##  $ postAC: int  140 150 120 160 140 120 120 230 100 100 ...
##  $ postPC: int  180 220 150 250 200 200 200 300 150 150 ...
##  $ Med   : int  0 0 2 0 0 0 0 1 0 0 ...
##  $ SIDE  : int  0 1 0 1 0 1 0 1 0 1 ...
##  $ PREKS : int  56 62 60 47 44 52 48 42 40 45 ...
##  $ POSKS : int  92 62 94 90 88 94 96 90 94 96 ...
##  $ ABS   : int  1 0 1 1 0 1 0 1 1 0 ...
##  $ INFECT: int  0 1 0 0 0 0 0 0 0 0 ...
```

4.3 ASCII R :

ASCII , , (**comma**) ASCII , **csv format** (**comma-separated-variable format**), .csv. read.table() , ,. read.csv() , .

```
## read data file: DMTKRcsv.csv
read_table.df <- read.table("C:/RData/DMTKRcsv.csv",
                            header = TRUE,
                            row.names = NULL,
                            sep = ",",
                            dec = ".")
head(read_table.df, n = 3)
##   No age sex DM DMyr preAC prePC postAC postPC Med SIDE PREKS POSKS ABS INFECT
## 1  1  67   0  0   10   120   160    140    180   0    0    56    92   1      0
## 2  2  67   0  0   11   100   150    150    220   0    1    62    62   0      1
## 3  3  72   1  0    4   150   200    120    150   2    0    60    94   1      0
# simple one
read_csv.df <- read.csv("C:/RData/DMTKRcsv.csv")
head(read_csv.df, n = 3)
##   No age sex DM DMyr preAC prePC postAC postPC Med SIDE PREKS POSKS ABS INFECT
## 1  1  67   0  0   10   120   160    140    180   0    0    56    92   1      0
## 2  2  67   0  0   11   100   150    150    220   0    1    62    62   0      1
## 3  3  72   1  0    4   150   200    120    150   2    0    60    94   1      0
```

```
#
read_csv.df <- read.csv("C:/RData/DMTKRcsv.csv",
                        header = TRUE,
                        row.names = NULL,
                        sep = ",",
                        dec = ".")
head(read_csv.df, n = 3)
##   No age sex DM DMyr preAC prePC postAC postPC Med SIDE PREKS POSKS ABS INFECT
## 1  1  67   0  0   10   120   160    140    180   0    0    56    92   1      0
## 2  2  67   0  0   11   100   150    150    220   0    1    62    62   0      1
## 3  3  72   1  0    4   150   200    120    150   2    0    60    94   1      0
```

4.4 R

{R} , (contributed packages) , data() {R} , library(help = "datasets") {R} .

data(package = "package.name") package.name , , data(data.name) {R} data.name , data(package.data.name, package = "package.name") package.name , pack.data.name .

```
# data()     # check names of datasets
data(Orange) # use {R} build-in dataset = Orange
# help(Orange)
head(Orange)
## Grouped Data: circumference ~ age | Tree
##   Tree  age circumference
## 1    1  118            30
## 2    1  484            58
## 3    1  664            87
## 4    1 1004           115
## 5    1 1231           120
## 6    1 1372           142
#
library(MASS)
# help(package = MASS)
# data(package = "MASS")     # check MASS package data set
data(VA, package = "MASS")   # use MASS package dataset = VA
# help(VA)
head(VA)
##   stime status treat age Karn diag.time cell prior
## 1    72      1     1  69   60         7    1     0
## 2   411      1     1  64   70         5    1    10
## 3   228      1     1  38   60         3    1     0
## 4   126      1     1  63   60         9    1    10
## 5    118         1      1  65    70          11     1      10
## 6     10         1      1  49    20           5     1       0
```

4.5 {R}

{R} , . `write.table()` `write.csv()`. .

- x = {R}
- `file` =
- `append = FALSE`
- `quote = "\""`
- `sep = " "`
- `eol  = "\n"`
- `na = NA` NA
- `dec = '.'`
- `row.names = TRUE` row names
- `col.names = TRUE` (column names)
- `qmethod = c("escape", "double")`
- `fileEncoding` = ””

`write.csv()` `write.table()` , `sep = ","`.

4.6 {R}

`saveRDS()` {R} . `readRDS()` {R} . , , `data frame` {R} . `readRDS()` , . {R} `save()` `load()` , .

```
## saveRDS() and save()
x <- c(1:5)
saveRDS(x, file = "C:/RData/x.Rds")
save(x, file = "C:/RData/x.Rda")   # working directory
## readRDS()
new_x <- readRDS(file = "C:/RData/x.Rds")
new_x
## [1] 1 2 3 4 5
## load() -- note the result
new_x <- load(file = "C:/RData/x.Rda")
new_x
## [1] "x"
x
## [1] 1 2 3 4 5
```

Chapter 5

Data Visualization

, . \ Leland Wilkinson (1999), **The Grammar of Graphics**. {R} , . {R} , , . , . , (interactive) {R} , .

{R} , :

- (**high-levlel plotting functions**): , , , .
- (**low-level plotting functions**): , , .

, , **graphic device**), , {R} , `pdf`, `ps`, `jpg`, `png` .

{R} , `grid` , Splus `Trellis` . `grid` , `lattice`, `ggplot2` . . tidyverse , , `ggplot2` . `ggplot2` , .

5.1

Edward Tufte (2006) Beautiful Evidence .

- .
- .
- .
- .
- .
- .

5.2 ggplot2

`ggplot2` , `ggplot2` , , `ggplot2` R base . , , https://www.r-graph-gallery.com/index.html.

ggplot2 , , , , . . ggplot2 , + (layers), .

- data: .
- mapping (aes):
  - x- , y- , treat, fill, shape, size, etc.
- geoms: geometric object
  - point, line, bar, shapes, ribbon, polygon, smooth, text etc.
- stat: / , statistics
- position: position adjustments.

Table: ggplot2

ggplot() .

```
ggplot(data = data_name,
       aes(x = variable_name,
           y = variable_name,
           ... <other variable_name mappings>)) +
  geom_<type}() +
  ...
```

Prentice (1973) , , , % Veteran's Administration , , , . **survVATrial.csv**.

treat (therapy)	: 0 = ; 1 =
cellcode	; 1 = ; 2 = ; 3 = ; 4 =
time	, ,
censor	: 0 = ; 1 =
diagtime	Karnofsky performance score,
diagtime	,
age	( )
prior	; 0 = ; 1 =

```
dd <- read.table("./Data/survVATrial.csv",
                 header = TRUE,
                 sep = ",",
                 quote = "\"'",
                 dec = ".",
                 row.names = NULL,
                 # col.names,
                 as.is = TRUE,
                 # as.is = !stringsAsFactors,
                 na.strings = c(".", "NA"))
head(dd)
##   treat cellcode time censor diagtime kps age prior
## 1     0        1   72      1       60   7  69     0
## 2     0        1  411      1       70   5  64    10
## 3     0        1  228      1       60   3  38     0
## 4     0        1  126      1       60   9  63    10
## 5     0        1  118      1       70  11  65    10
## 6     0        1   10      1       20   5  49     0
str(dd)
## 'data.frame':        137 obs. of  8 variables:
##  $ treat   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ cellcode: int  1 1 1 1 1 1 1 1 1 1 ...
##  $ time    : int  72 411 228 126 118 10 82 110 314 100 ...
##  $ censor  : int  1 1 1 1 1 1 1 1 1 0 ...
##  $ diagtime: int  60 70 60 60 70 20 40 80 50 70 ...
##  $ kps     : int  7 5 3 9 11 5 10 29 18 6 ...
##  $ age     : int  69 64 38 63 65 49 69 68 43 70 ...
##  $ prior   : int  0 10 0 10 10 0 10 0 0 0 ...
dd$treat <- factor(dd$treat, labels = c("placebo", "test"))
dd$cellcode <- factor(dd$cellcode,
                      labels = c("squamous", "small", "adeno", "large"))
dd$censor <- factor(dd$censor, labels = c("survival", "dead"))
dd$prior <- factor(dd$prior, labels = c("no", "yes"))
head(dd)
##     treat cellcode time censor diagtime kps age prior
## 1 placebo squamous   72   dead       60   7  69    no
## 2 placebo squamous  411   dead       70   5  64   yes
## 3 placebo squamous  228   dead       60   3  38    no
## 4 placebo squamous  126   dead       60   9  63   yes
## 5 placebo squamous  118   dead       70  11  65   yes
## 6 placebo squamous   10   dead       20   5  49    no
str(dd)
## 'data.frame':        137 obs. of  8 variables:
##  $ treat   : Factor w/ 2 levels "placebo","test": 1 1 1 1 1 1 1 1 1 1 ...
##  $ cellcode: Factor w/ 4 levels "squamous","small",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ time    : int  72 411 228 126 118 10 82 110 314 100 ...
##  $ censor  : Factor w/ 2 levels "survival","dead": 2 2 2 2 2 2 2 2 2 1 ...
##  $ diagtime: int  60 70 60 60 70 20 40 80 50 70 ...
##  $ kps     : int  7 5 3 9 11 5 10 29 18 6 ...
##  $ age     : int  69 64 38 63 65 49 69 68 43 70 ...
##  $ prior   : Factor w/ 2 levels "no","yes": 1 2 1 2 2 1 2 1 1 1 ...
```

5.3

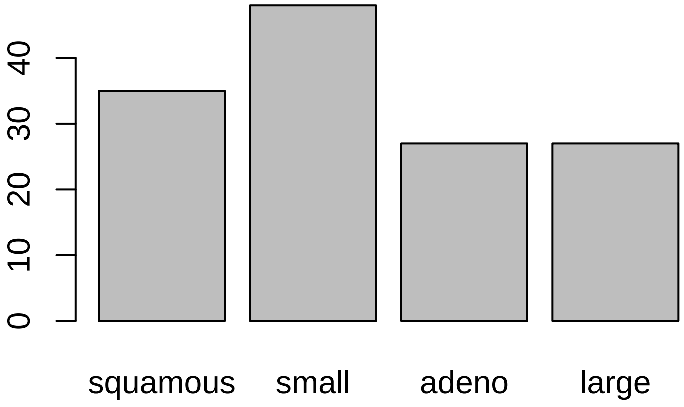
(**distribution**), . (frequency table), (bar plot) (pie chart).

, . , (Table) .

5.3.1

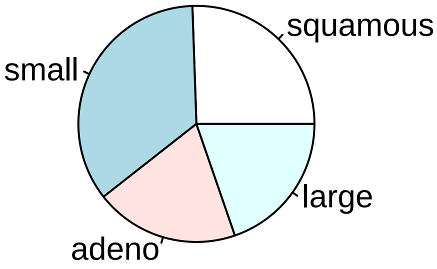
- : .

```
## pie chart: ggplot2 do not have a simple geom_pie()
## use R base pie()
cellcode.tab <- table(dd$cellcode)
cellcode.tab
##
## squamous    small    adeno    large
##       35       48       27       27
prop.table(cellcode.tab)
##
## squamous    small    adeno    large
##   0.2555   0.3504   0.1971   0.1971
barplot(cellcode.tab)
round(barplot(cellcode.tab), 4)
```

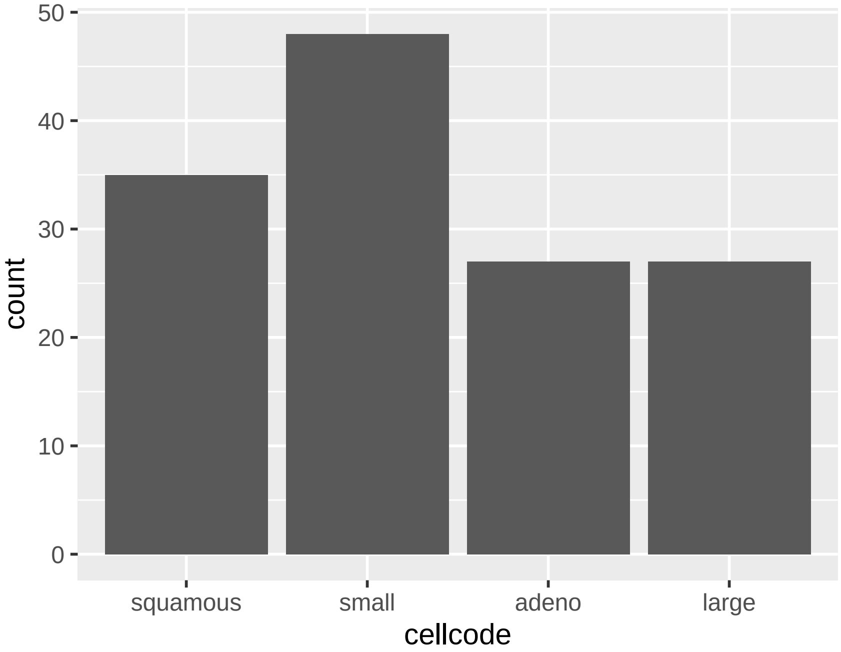


```
##      [,1]
## [1,]  0.7
## [2,]  1.9
## [3,]  3.1
## [4,]  4.3
```

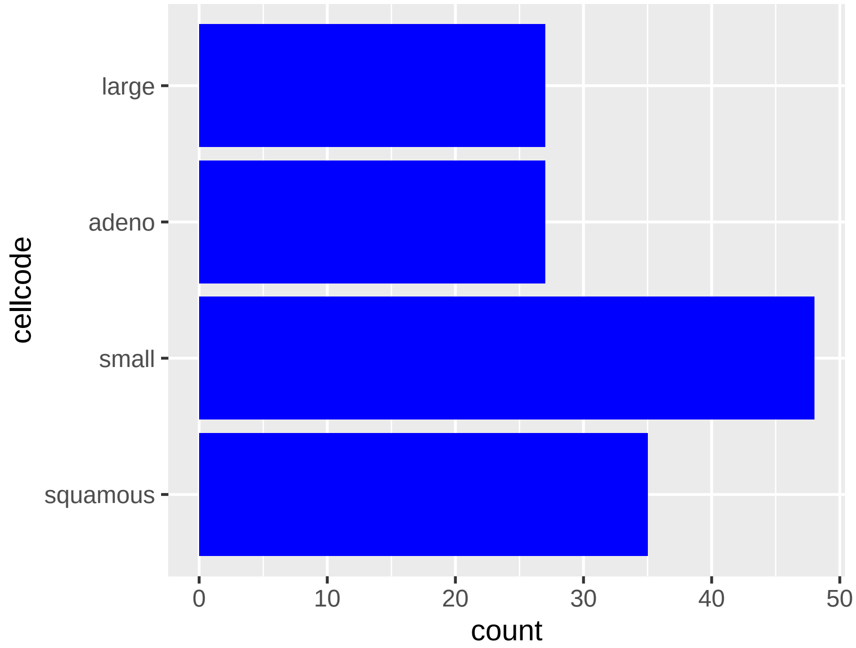
```
pie(cellcode.tab)
```



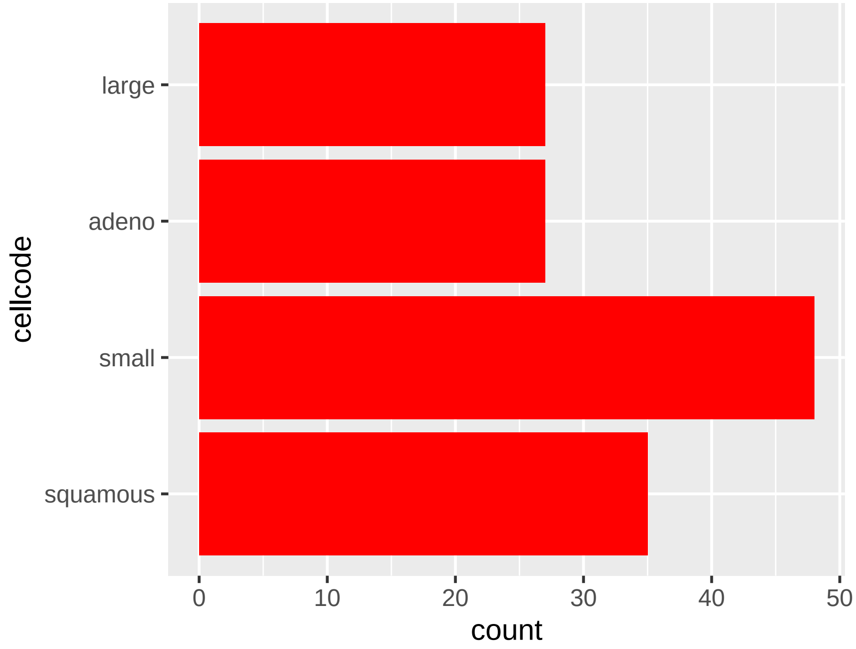
```
library(ggplot2)
## bar chart
ggplot(data = dd, aes(x = cellcode)) +
  geom_bar()
```



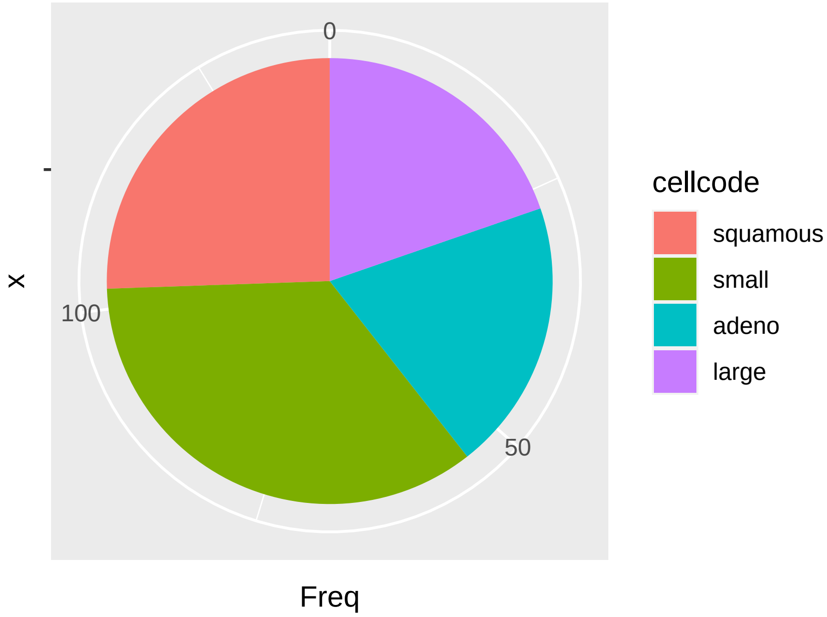
```
ggplot(data = dd, aes(x = cellcode)) +
  geom_bar(fill = "blue") +
  coord_flip()
```



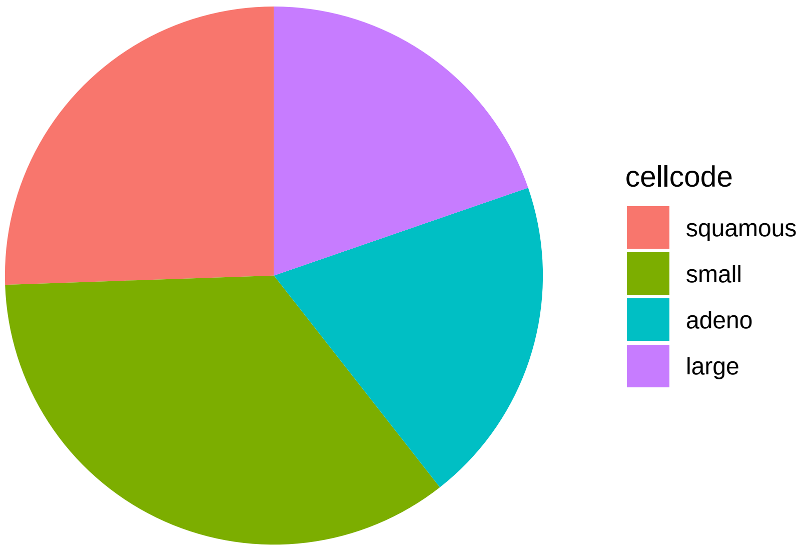
```
ggplot(data = dd, aes(y = cellcode)) +
  geom_bar(fill = "red")
```



```
# pie chart: no simple solution
clar.freq <- data.frame(cellcode.tab)
names(clar.freq)[1] <- "cellcode"
clar.freq
##   cellcode Freq
## 1 squamous   35
## 2    small   48
## 3    adeno   27
## 4    large   27
ggplot(data = clar.freq, aes(x = "", y = Freq, fill = cellcode)) +
  geom_bar(width = 1, stat = "identity") +
  coord_polar("y", start = 0)
```



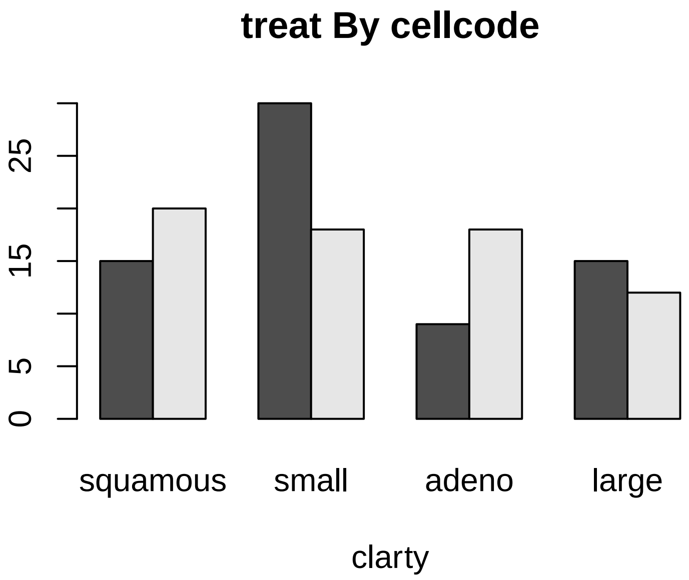
```
ggplot(data = clar.freq, aes(x = "", y = Freq, fill = cellcode)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y", start = 0) +
  theme_void() # remove background
```



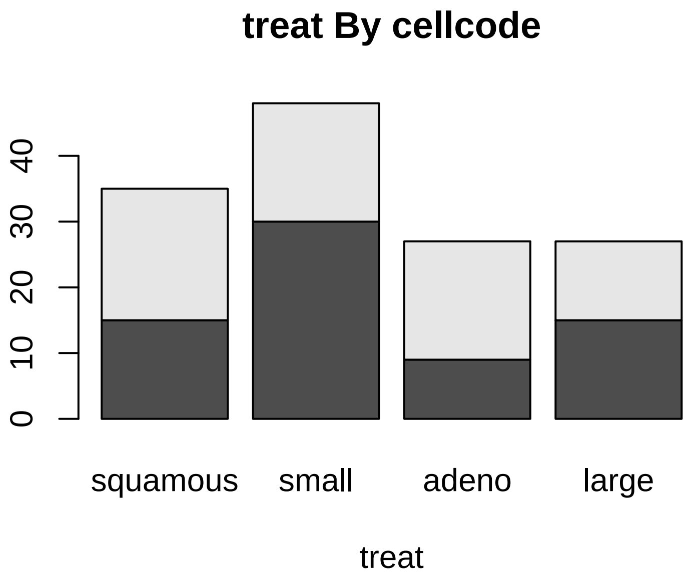
5.3.2

- : , .

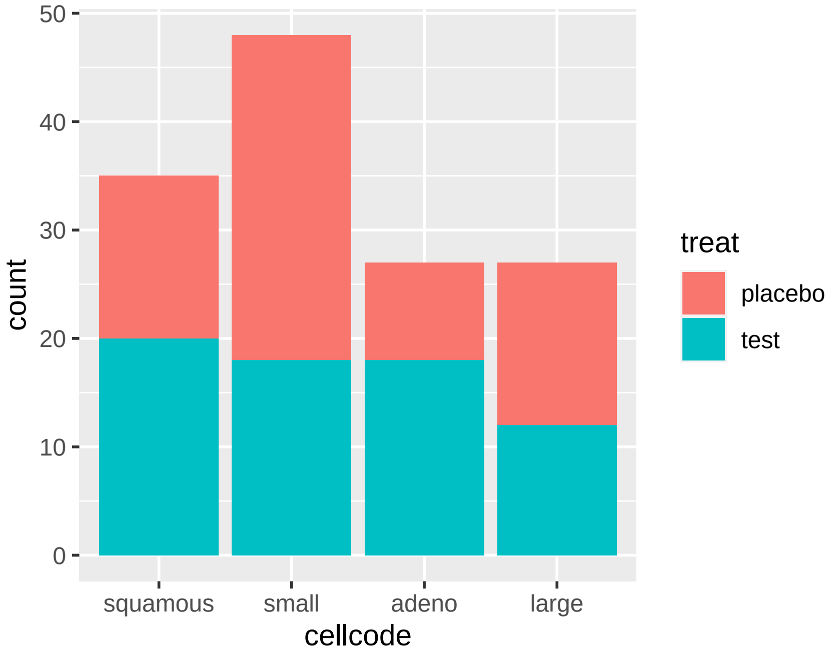
```
## two categorical vtriables
table(dd$treat)
##
## placebo    test
##      69      68
table(dd$cellcode)
##
## squamous    small    adeno    large
##       35       48       27       27
twoway.tab <- table(dd$treat, dd$cellcode)
twoway.tab
##
##             squamous small adeno large
##   placebo         15    30     9    15
##   test            20    18    18    12
## # cell proportion
cell.prop <- prop.table(twoway.tab, margin=NULL)
round(cell.prop, 3)
##
##             squamous small adeno large
##   placebo    0.109 0.219 0.066 0.109
##   test       0.146 0.131 0.131 0.088
## conditional on row sum to 1
cond_row_prop <- prop.table(twoway.tab, margin = 1)
round(cond_row_prop, 3)
##
##            squamous small adeno large
##   placebo    0.217 0.435 0.130 0.217
##   test       0.294 0.265 0.265 0.176
apply(cond_row_prop, 1, sum) # rows sum to 1
## placebo    test
##       1       1
## conditional on column sum to 1
cond_col_prop <- prop.table(twoway.tab, margin = 2)
round(cond_col_prop, 3)
##
##            squamous small adeno large
##   placebo    0.429 0.625 0.333 0.556
##   test       0.571 0.375 0.667 0.444
apply(cond_col_prop, 2, sum) # cols sum to 1
## squamous    small    adeno    large
##        1        1        1        1
## side-by-side bar plot
barplot(twoway.tab,
        beside = TRUE,
        main = "treat By cellcode",
        xlab = "clarty")
```



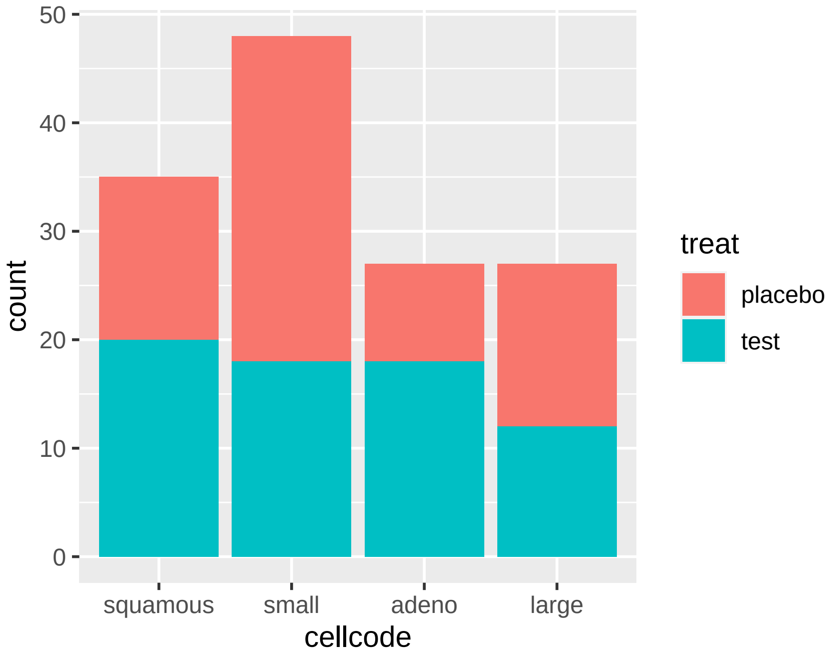
```
# Stacked Bar Plot
barplot(twoway.tab,
        beside = FALSE,
        main = "treat By cellcode",
        xlab = "treat")
```



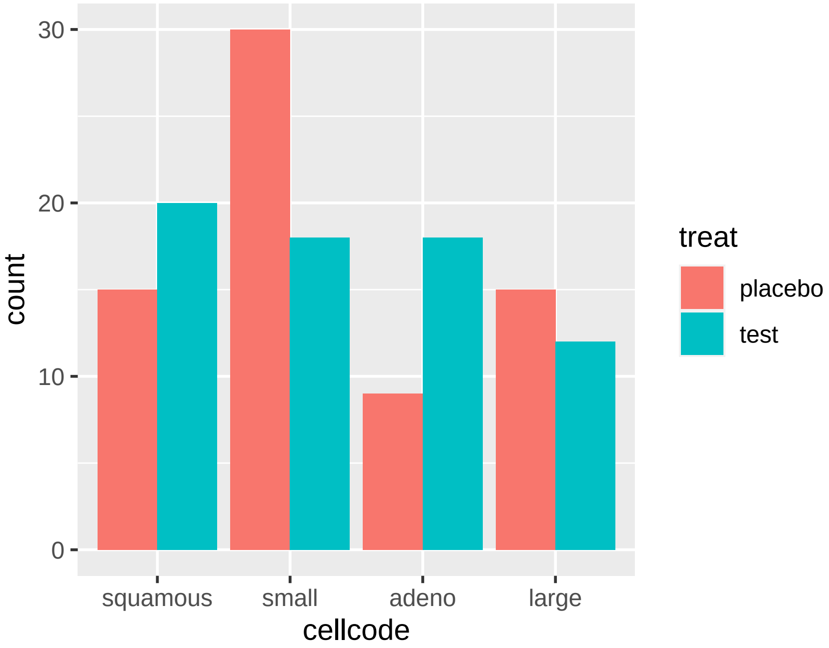
```
## ggplot2
## Automatically stack
library(ggplot2)
ggplot(data = dd, aes(x = cellcode, fill = treat)) +
  geom_bar()
```



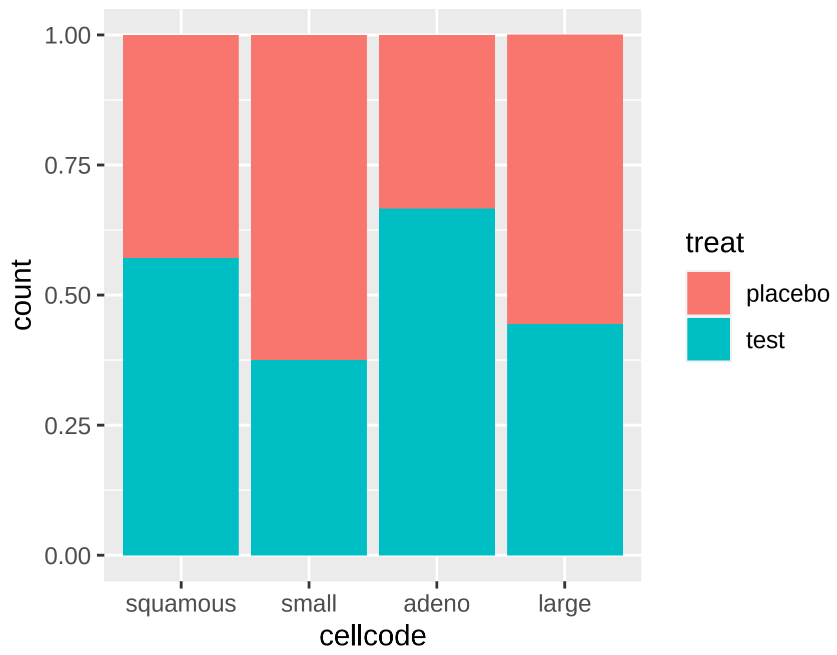
```r
ggplot(data = dd, aes(x = cellcode, fill = treat)) +
  geom_bar(position = "stack")
```



```
## side-by-side
ggplot(data = dd, aes(x = cellcode, fill = treat)) +
  geom_bar(position = "dodge")
```



```
ggplot(data = dd, aes(x = cellcode, fill = treat)) +
  geom_bar(position = "fill")
```



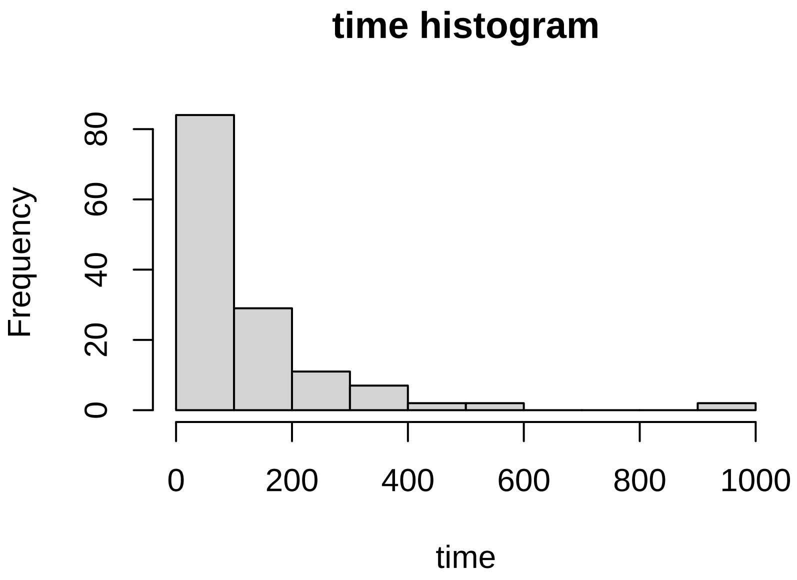
5.4

(**distribution**), . (dot plot),
(stem-and-leaf), , (histogram), (box plot), (density plot), , .
, , . , , .

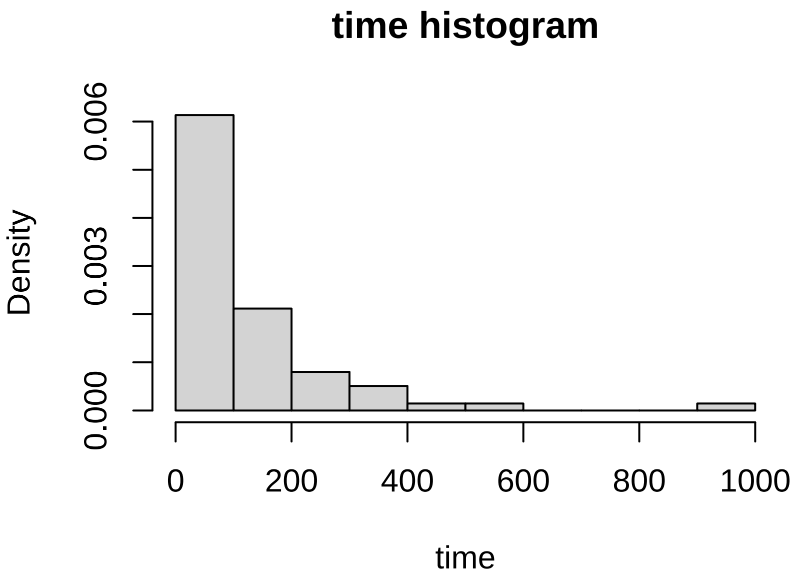
5.4.1

- : , , .

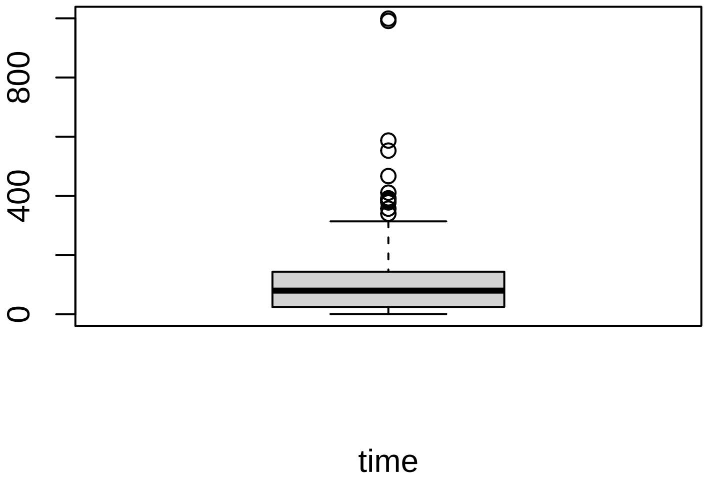
```r
## use R base pie()
## histogram
hist(dd$time,
     freq = TRUE,
     main = "time histogram",
     xlab = "time")
```



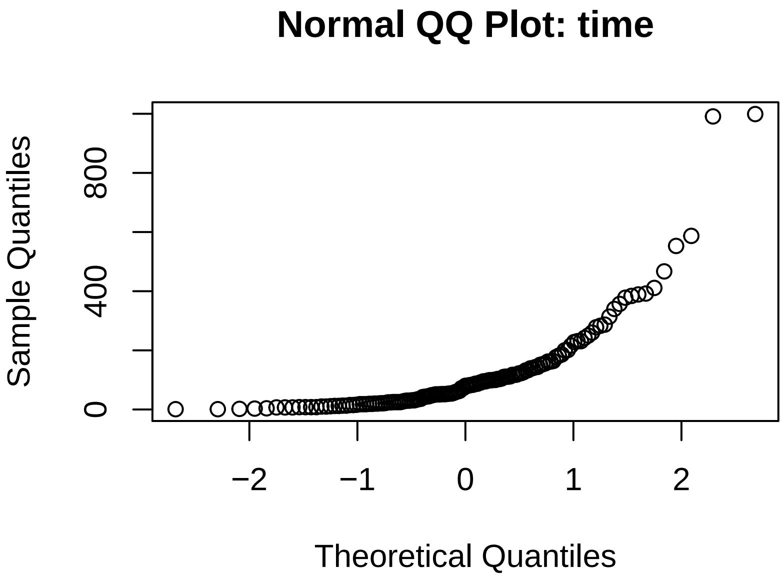
```r
hist(dd$time,
     freq = FALSE,
     main = "time histogram",
     xlab = "time")
```



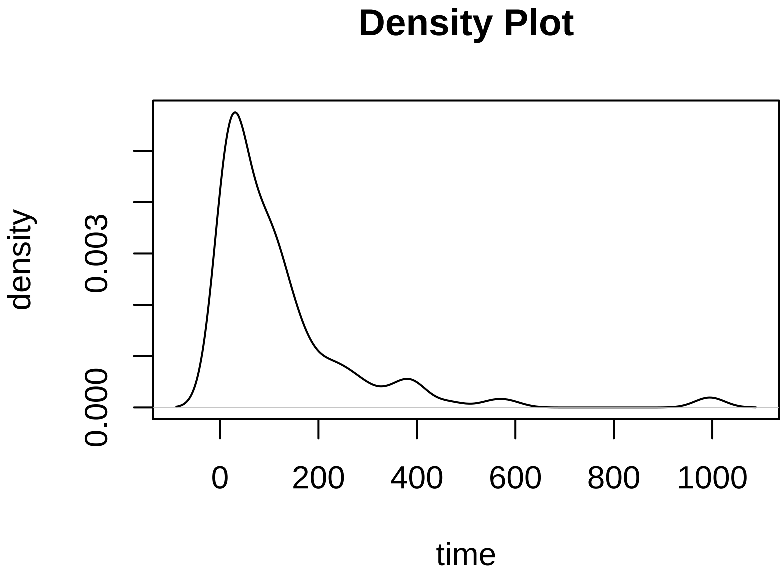
```
# box plot
boxplot(dd$time,
        xlab = "time")
```



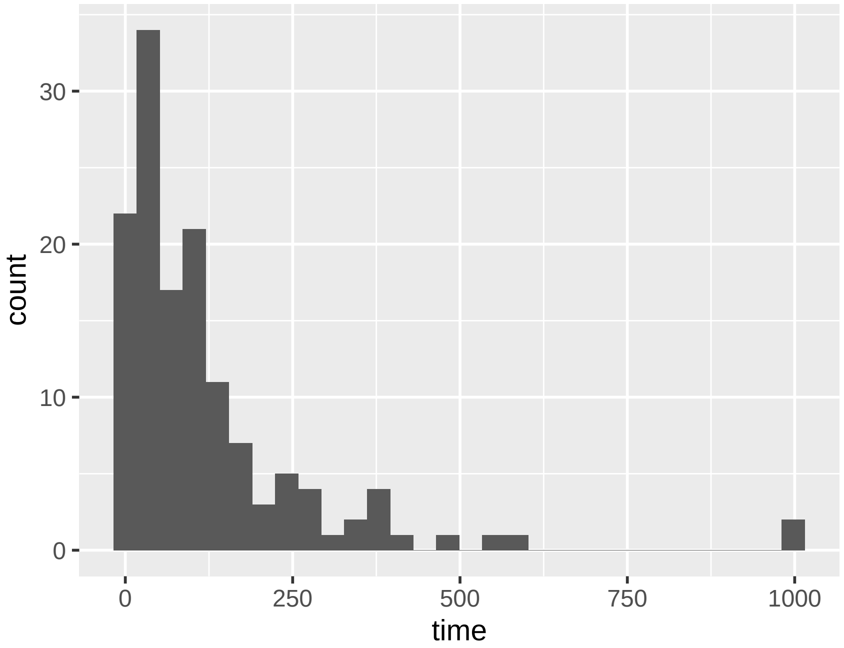
```
# QQ plot
qqnorm(dd$time,
       main = "Normal QQ Plot: time")
```



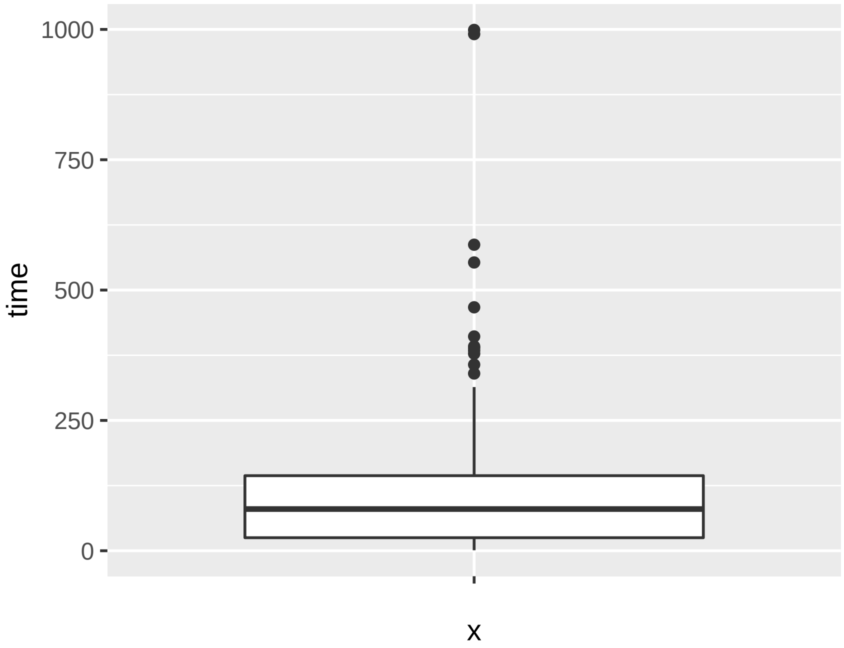
```r
# density plot
plot(density(dd$time),
     pch = 16,
     main = "Density Plot",
     xlab = "time",
     ylab = "density")
```



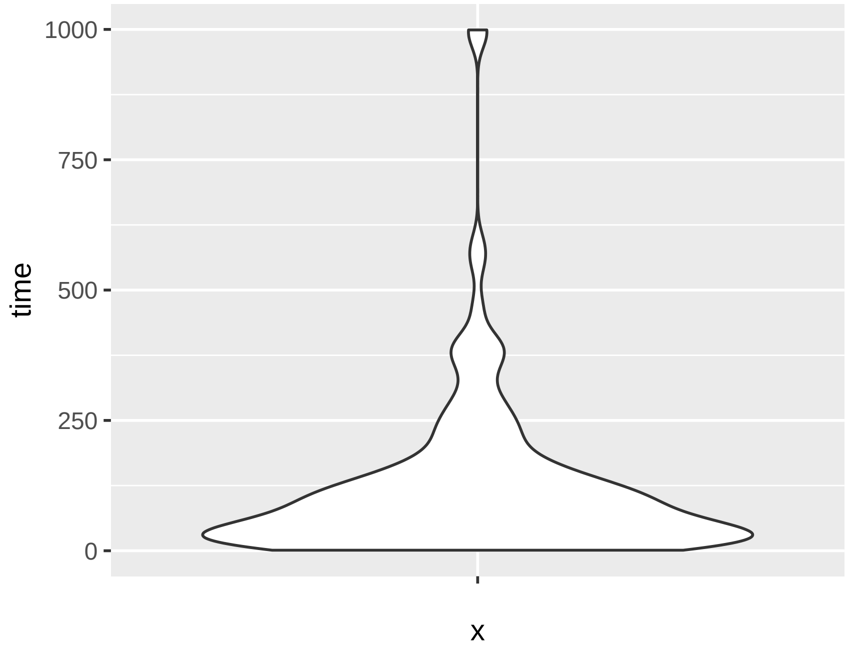
```
## ggplot2
## histogram
ggplot(data = dd, aes(x = time)) +
  geom_histogram()
```



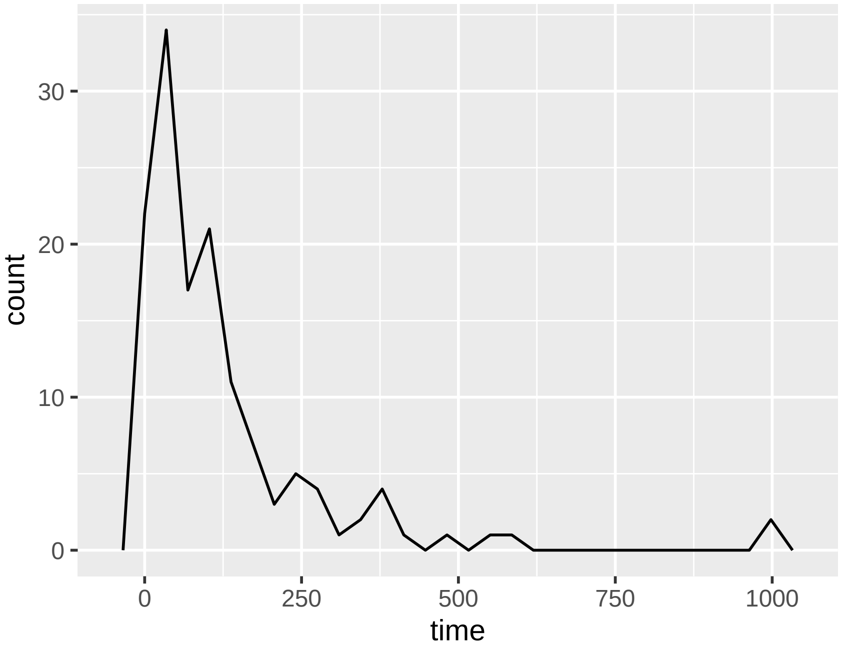
```
## box plot
ggplot(dd, aes(x = "", y = time)) +
  geom_boxplot()
```



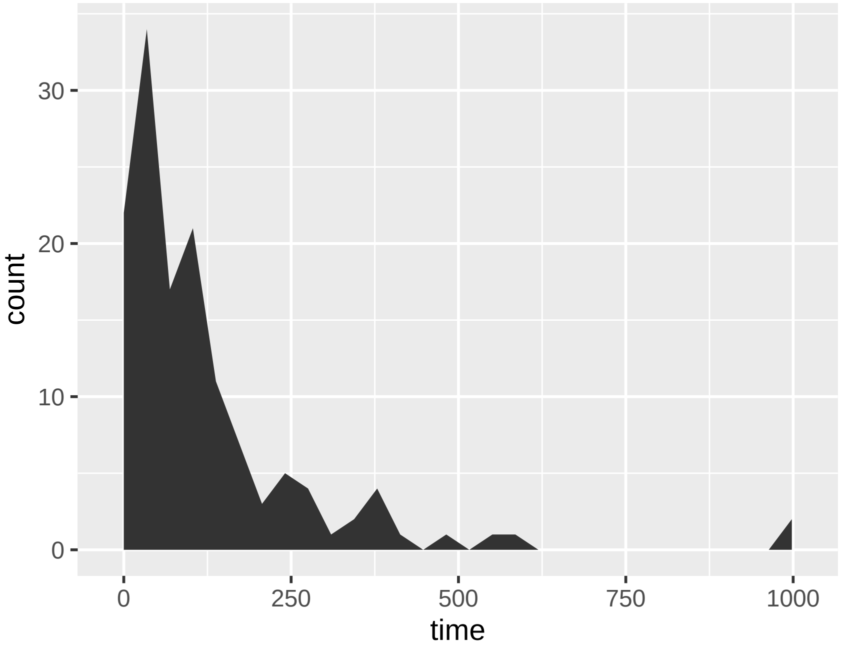
```
## violin plot
ggplot(dd, aes(x = "", y = time)) +
  geom_violin()
```



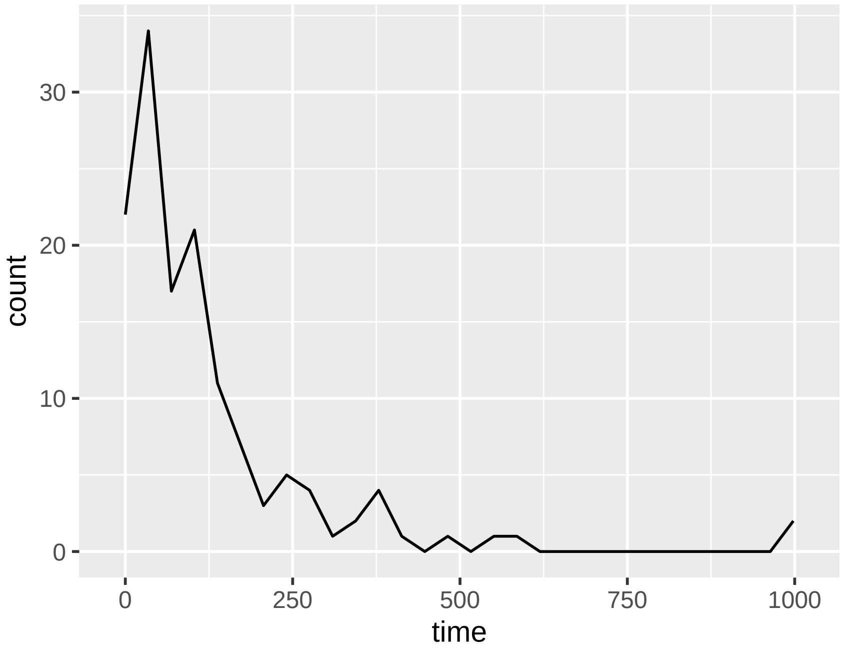
```
## density plot
ggplot(data = dd, aes(x = time)) +
  geom_freqpoly()
```



```
ggplot(data = dd, aes(x = time)) +
  stat_bin(geom = "area")
```



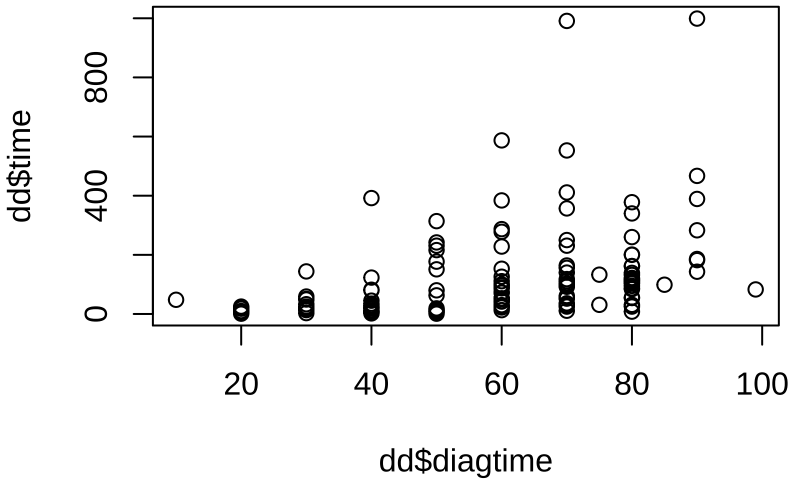
```
ggplot(data = dd, aes(x = time)) +
  stat_bin(geom = "line")
```



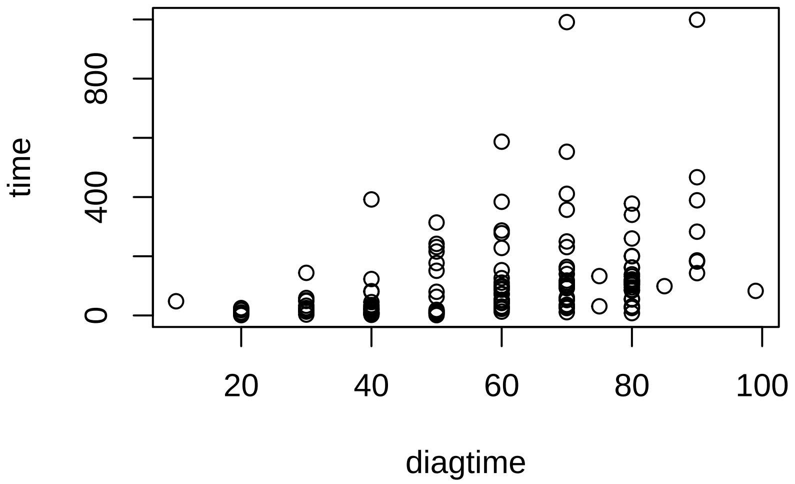
5.4.2

- **scatter plot** = X & Y =
- : , , , .

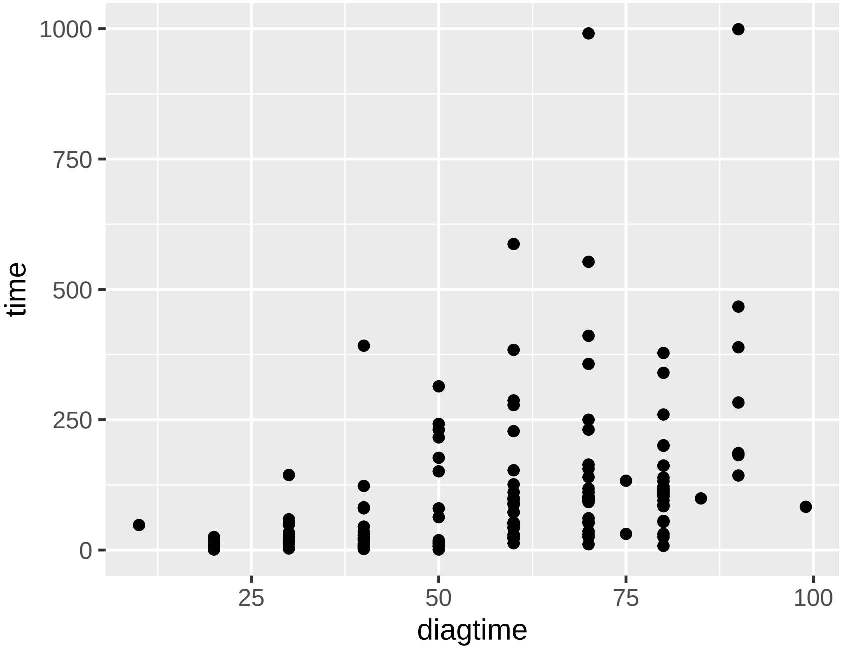
```
## R base
## scatter plot
## basic
plot(x = dd$diagtime, y = dd$time)
```



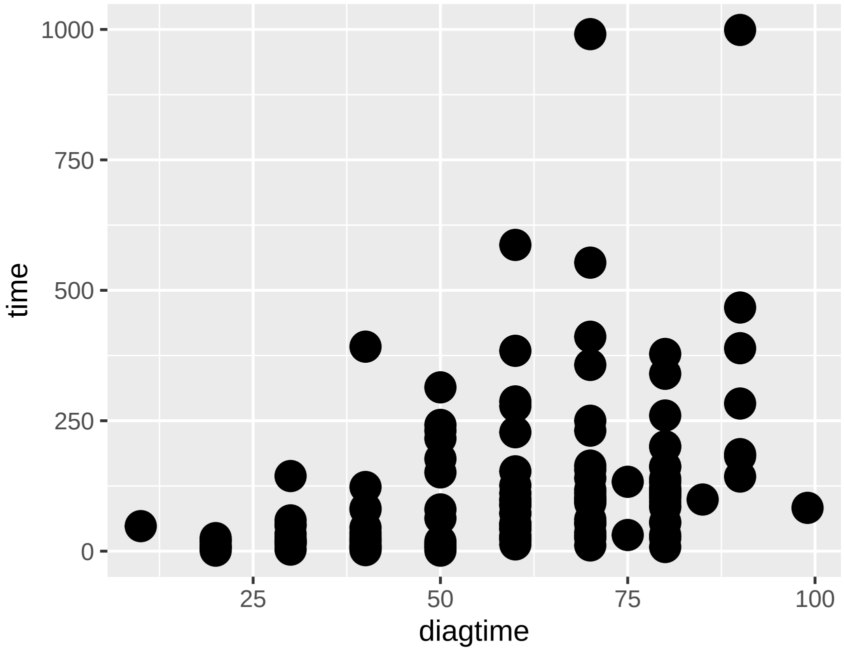
```
## formulat y ~ x, data = data_name)
plot(time ~ diagtime, data = dd)
```



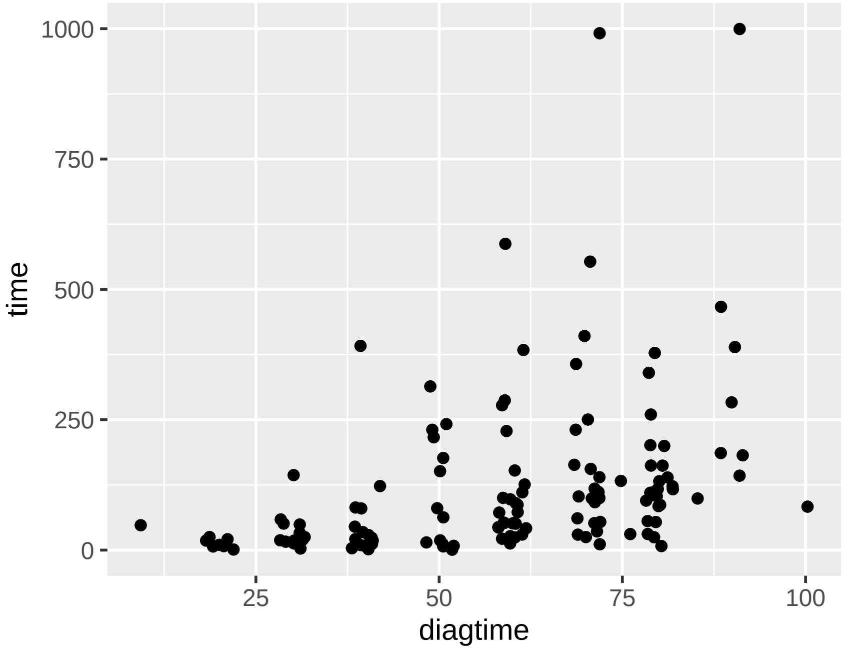
```
## ggplot
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_point()
```



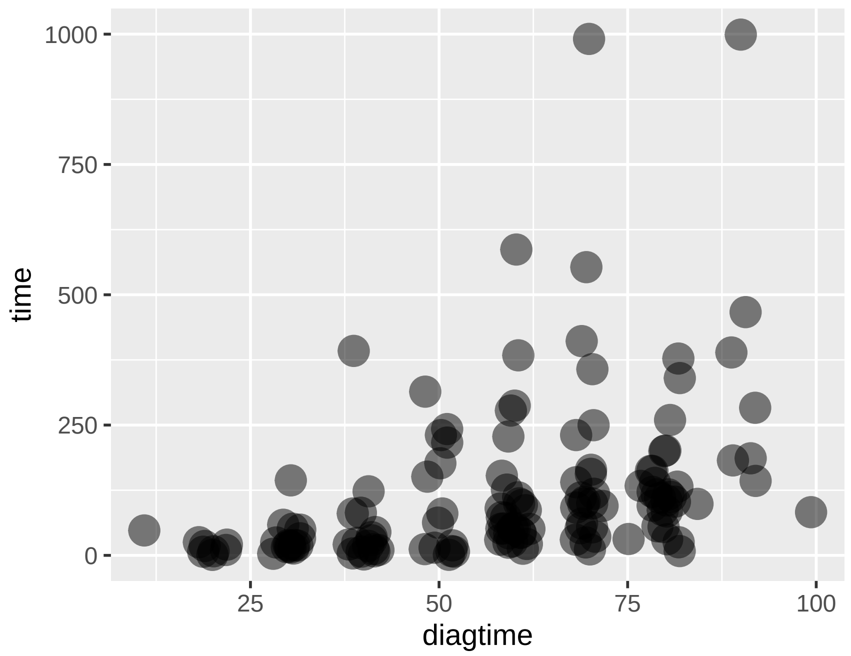
```
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_point(size = 5)
```



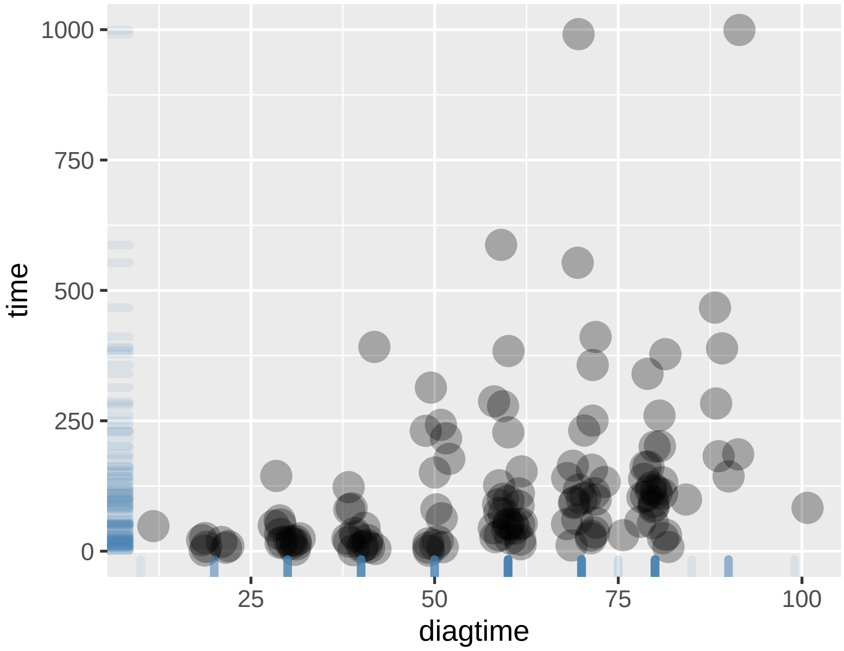
```r
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_jitter()
```



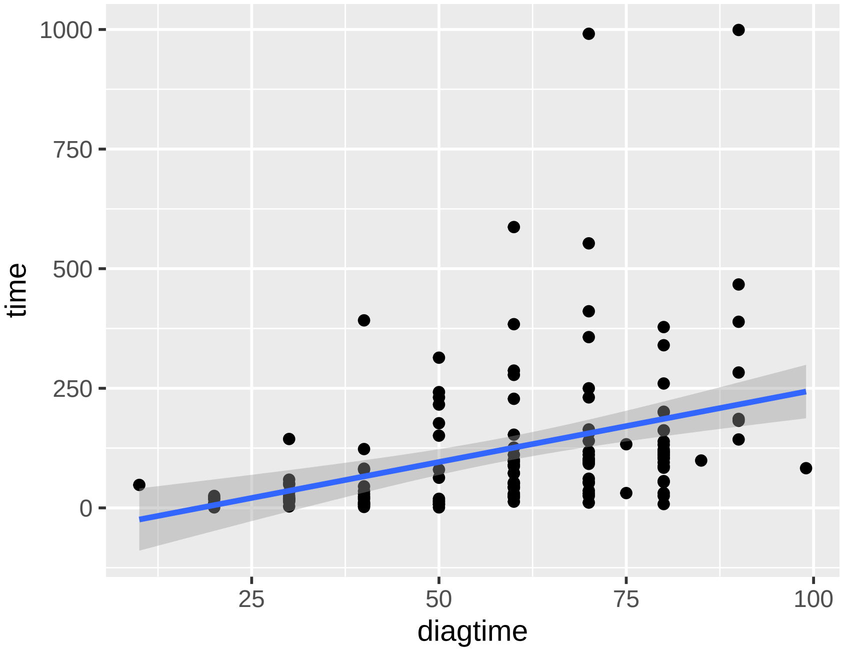
```
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_jitter(size = 5, alpha = 1/2)
```



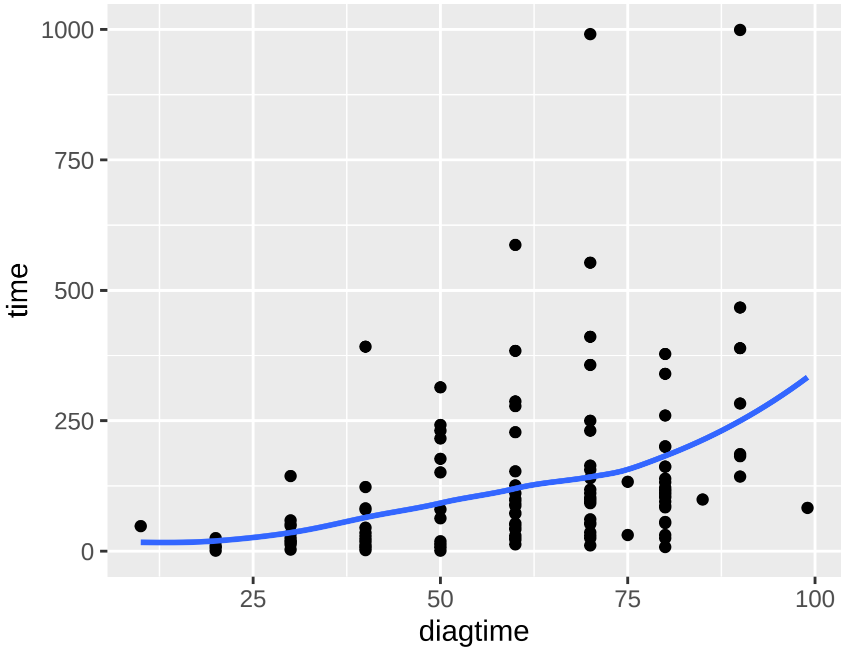
```
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_jitter(size = 5, alpha = 0.3) +
  geom_rug(col = "steelblue", alpha = 0.1, size = 1.5)
```



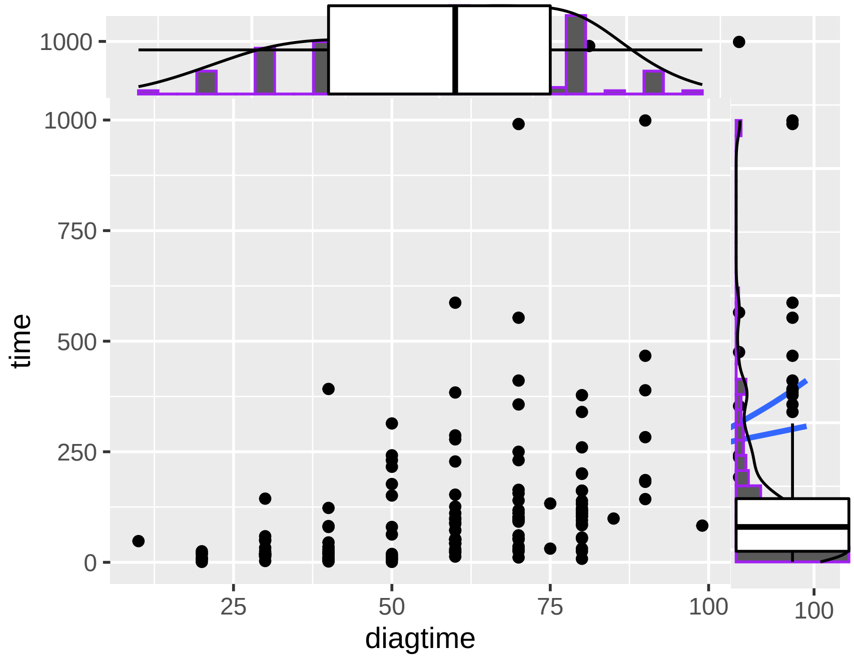
```
# add linear line or smoothing line
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_point() +
  geom_smooth(method = "lm")
```



```
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_point() +
  geom_smooth(se = FALSE)
```



```
ggplot(data = dd, aes(x = diagtime, y = time)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(se = FALSE)
## scatter plot + marginal distribution
library(ggExtra)
# classical
p <- ggplot(dd, aes(x = diagtime, y = time)) +
      geom_point() +
      theme(legend.position = "none")
# scatter plot + marginal histogram
ggMarginal(p, type = "histogram", color = "purple")
# scatter plot + marginal density
ggMarginal(p, type = "density")
# scatter plot + marginal boxplot
ggMarginal(p, type = "boxplot")
```

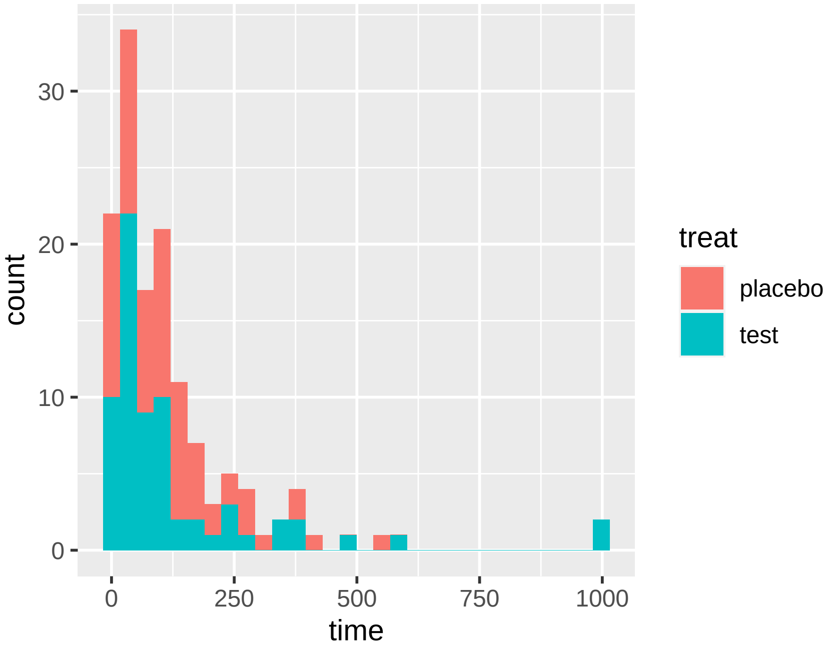


5.5

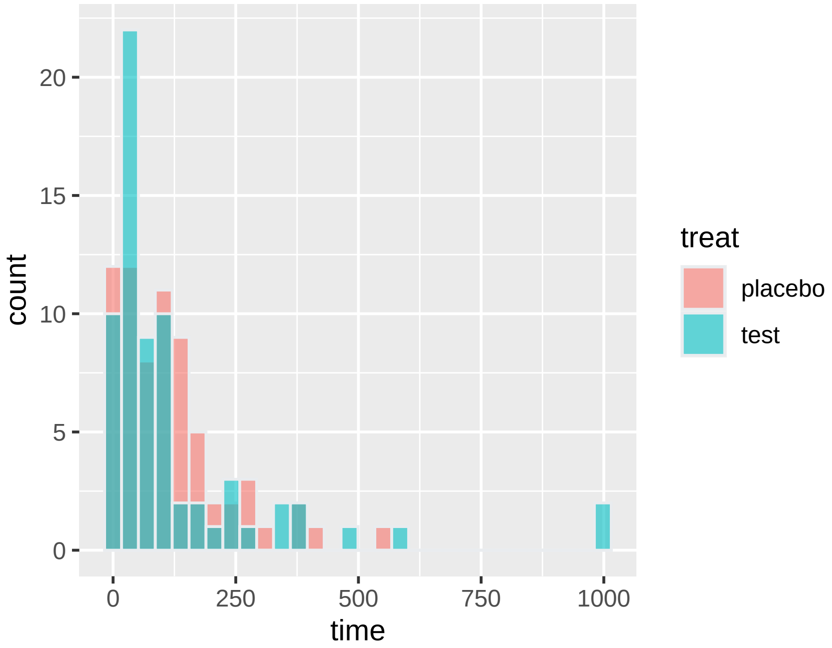
- +
- +
- + = +
-

5.5.1

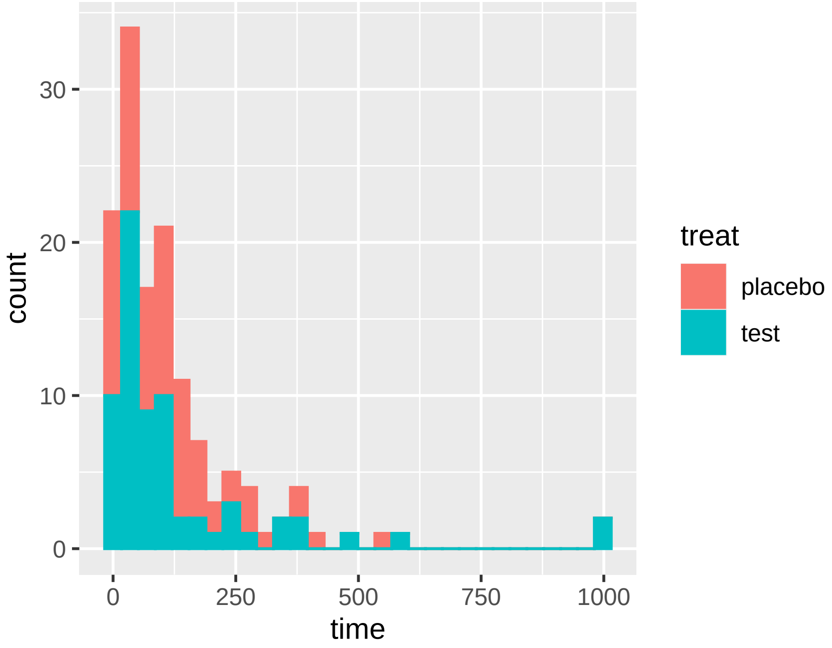
```
# one continuous + one categorical
ggplot(data = dd, aes(x = time)) +
  geom_histogram(aes(fill = treat))
```



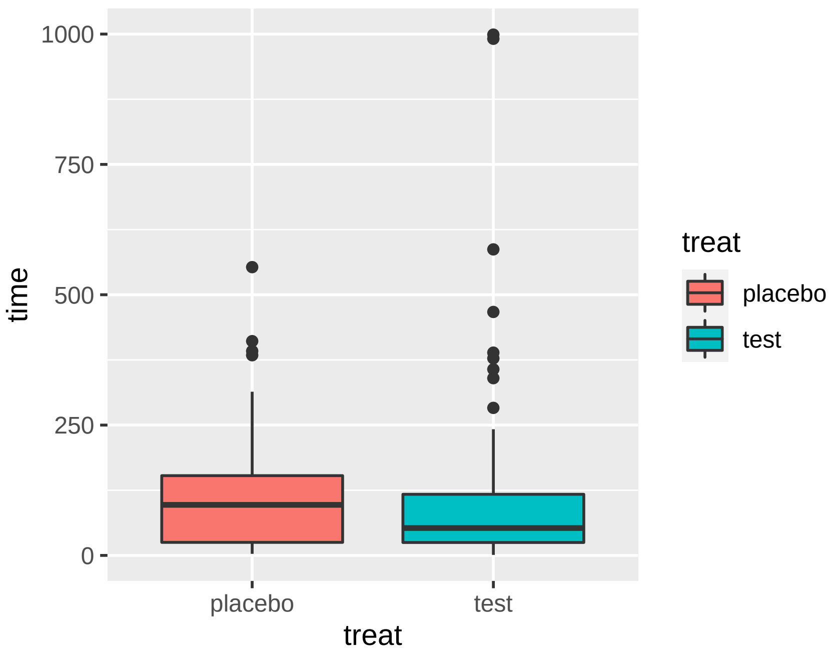
```r
ggplot(data = dd, aes(x = time, fill = treat)) +
    geom_histogram( color = "#e9ecef",
                    alpha = 0.6,
                    position = 'identity')
```



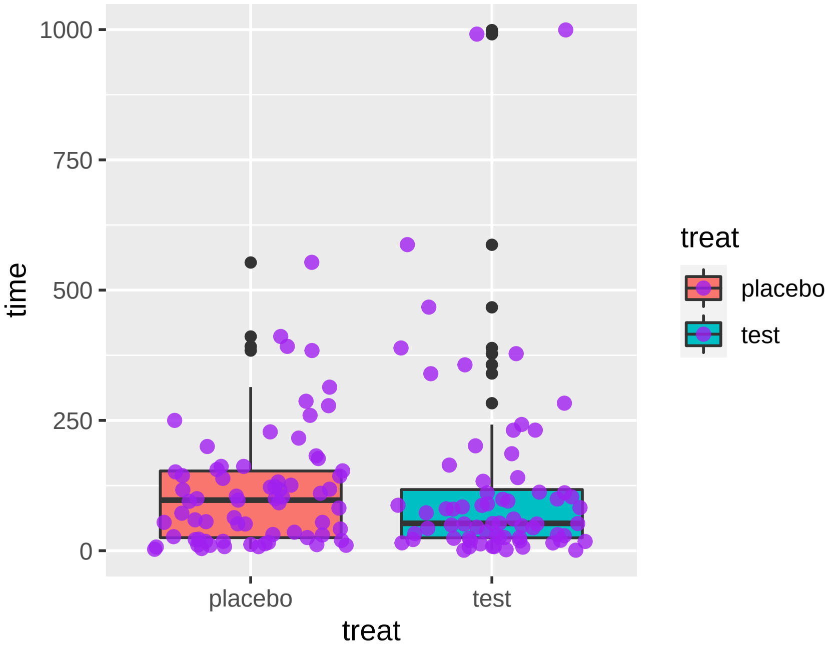
```r
ggplot(data = dd, aes(x = time, color = treat, fill = treat)) +
    geom_histogram()
```



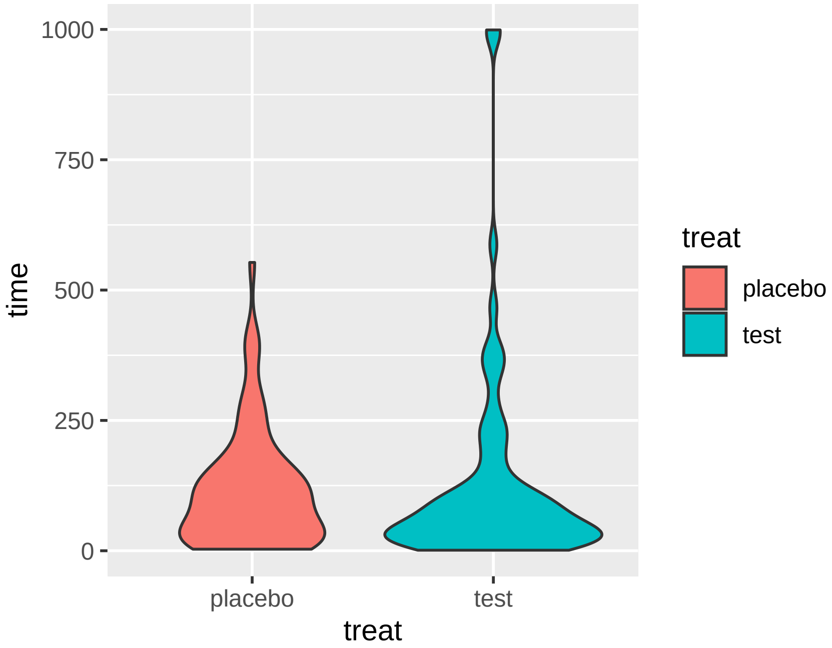
```
#
ggplot(data = dd, aes(x = treat, y = time, fill = treat)) +
    geom_boxplot()
```



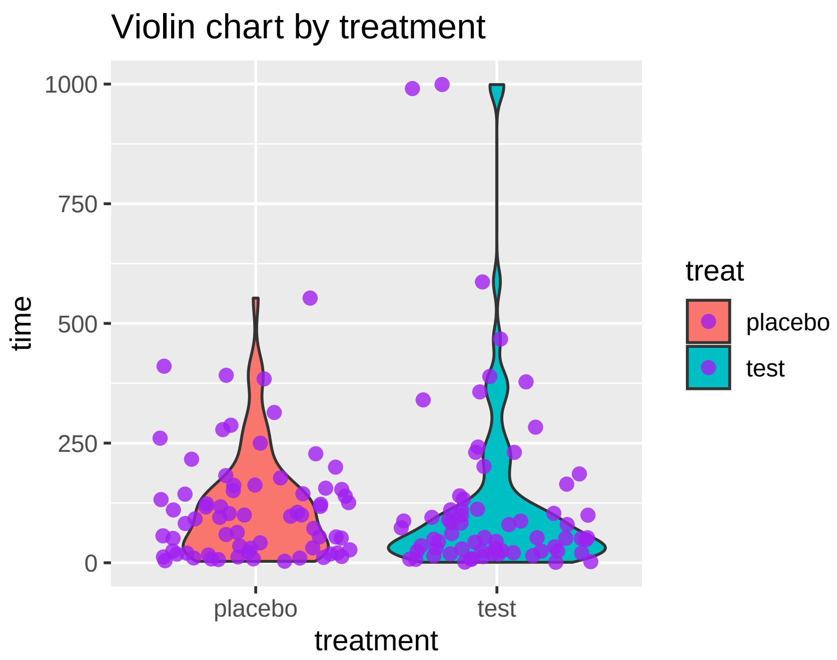
```
ggplot(data = dd, aes(x = treat, y = time, fill = treat)) +
    geom_boxplot() +
    geom_jitter(color = "purple", size = 2, alpha = 0.8)
```



```
#
ggplot(data = dd, aes(x = treat, y = time, fill = treat)) +
    geom_violin()
```

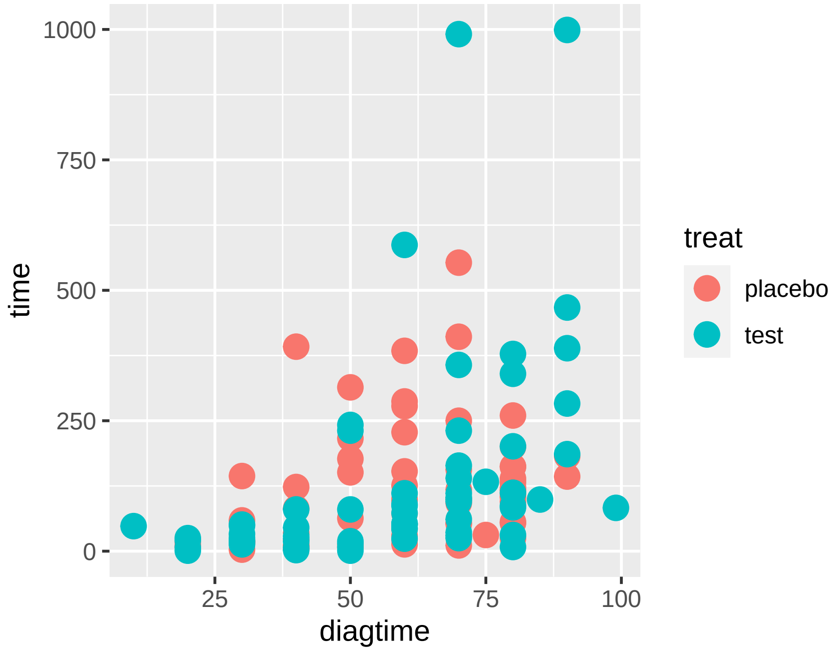


```
ggplot(data = dd, aes(x = treat, y = time, fill = treat)) +
    geom_violin() +
    geom_jitter(color = "purple", size = 2, alpha = 0.8) +
  ggtitle("Violin chart by treatment") +
    xlab("treatment")
```

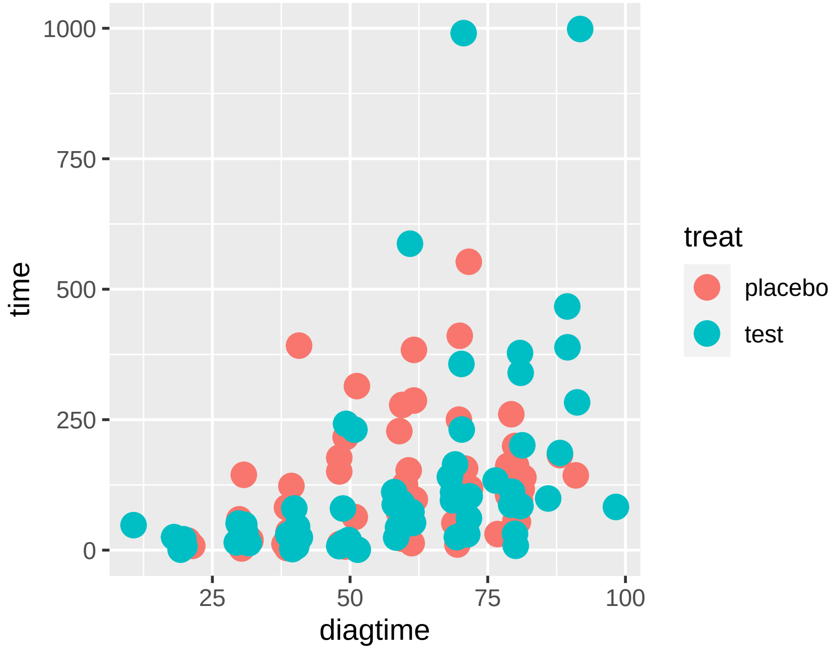


```r
## ggplot2
## two continuous + one categorical
ggplot(data = dd, aes(x = diagtime, y = time, color = treat)) +
  geom_point(size = 4)
```

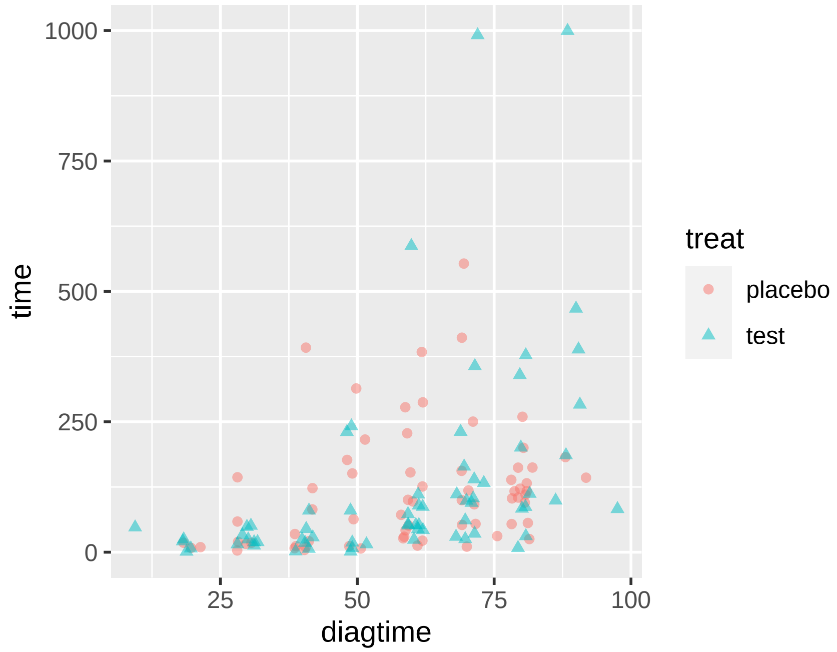
5.5.2 +



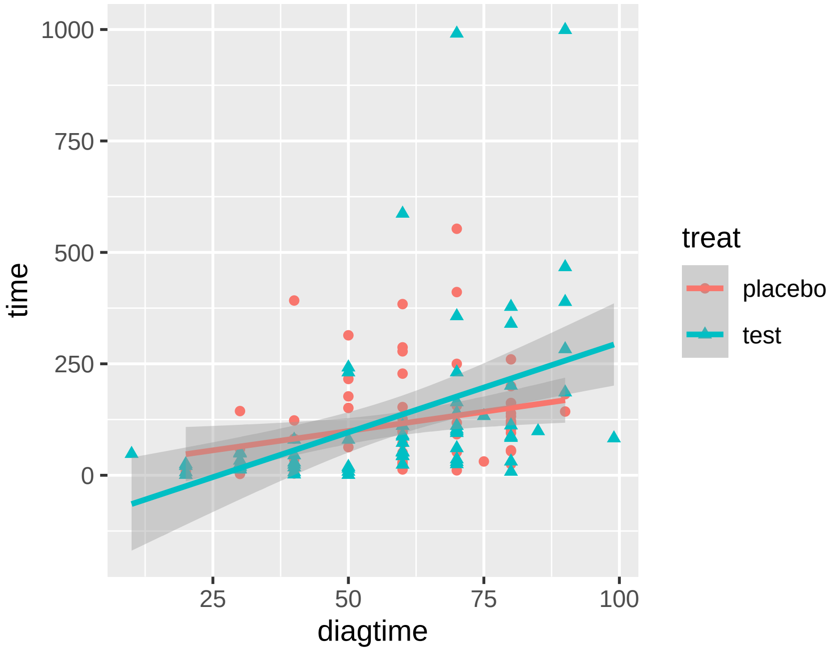
```
ggplot(data = dd, aes(x = diagtime, y = time, color = treat)) +
  geom_jitter(size = 4)
```



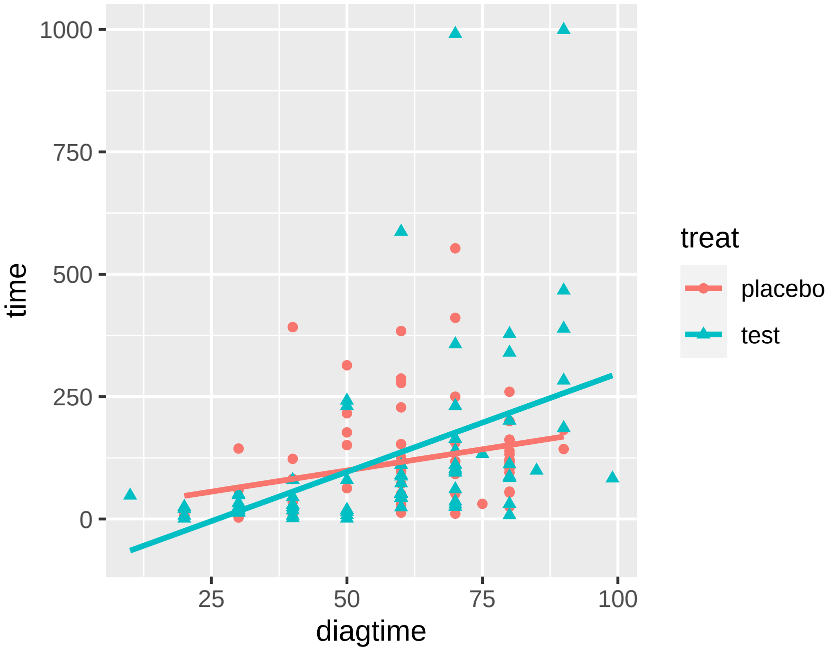
```
ggplot(data = dd, aes(x = diagtime, y = time,
                      color = treat, shape = treat)) +
  geom_jitter(alpha = 1/2)
```



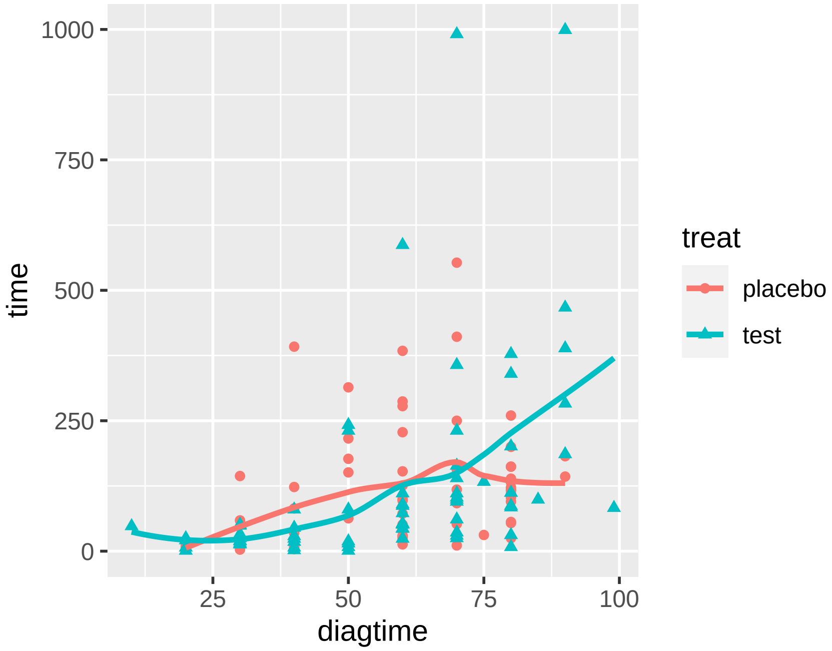
```
# add linear line or smoothing line
ggplot(data = dd, aes(x = diagtime, y = time,
                      color = treat, shape = treat)) +
  geom_point() +
  geom_smooth(method = "lm")
```



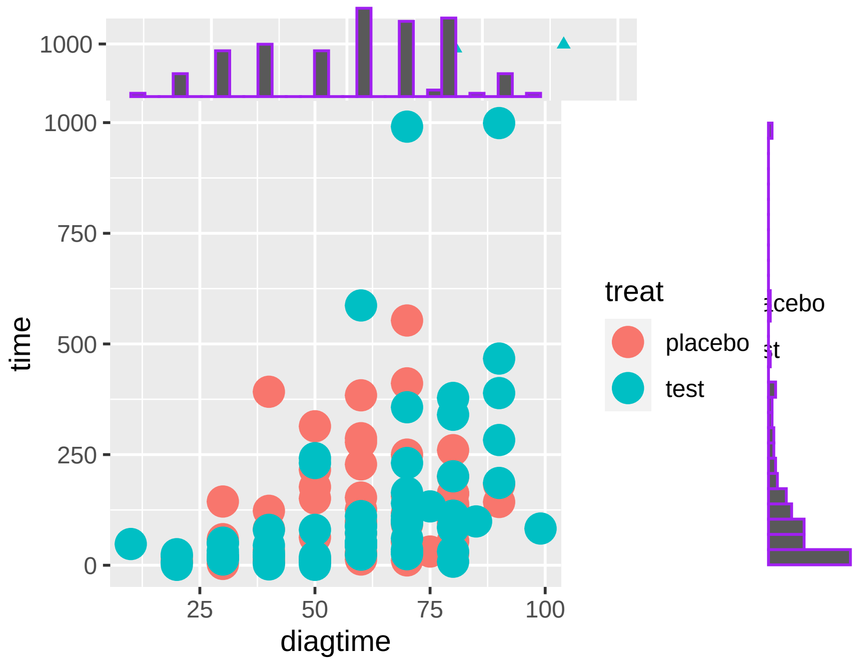
```r
ggplot(data = dd, aes(x = diagtime, y = time,
                      color = treat, shape = treat)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



```
#
ggplot(data = dd, aes(x = diagtime, y = time,
                      color = treat, shape = treat)) +
  geom_point() +
  geom_smooth(se = FALSE)
```



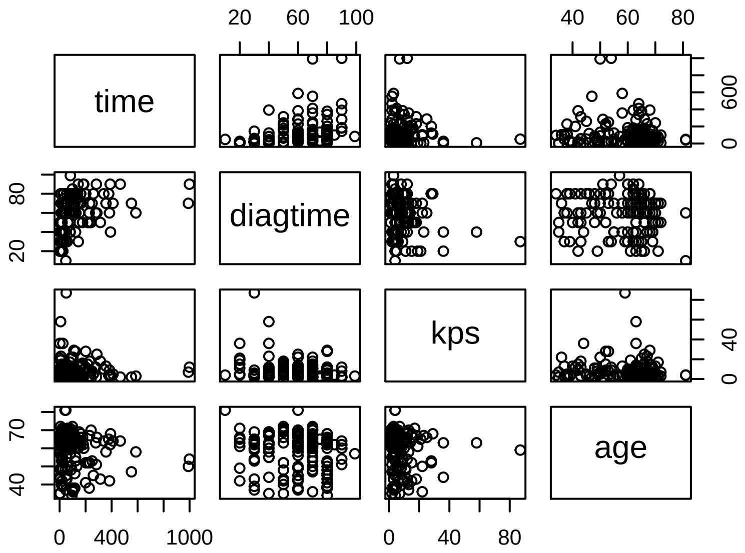
```
# BAD! too many lines
ggplot(data = dd, aes(x = diagtime, y = time,
                      color = treat, shape = treat)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(se = FALSE)
# classical
p <- ggplot(dd, aes(x = diagtime, y = time, color = treat)) +
      geom_point(size = 5)
# scatter plot + marginal histogram
ggExtra::ggMarginal(p, type = "histogram", color = "purple")
```



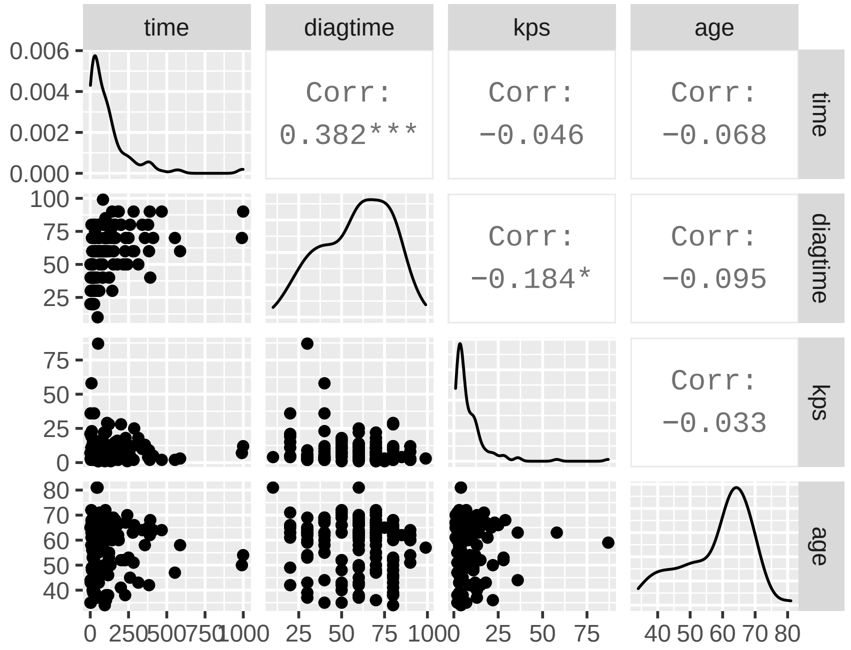
5.5.3

- : , , , .

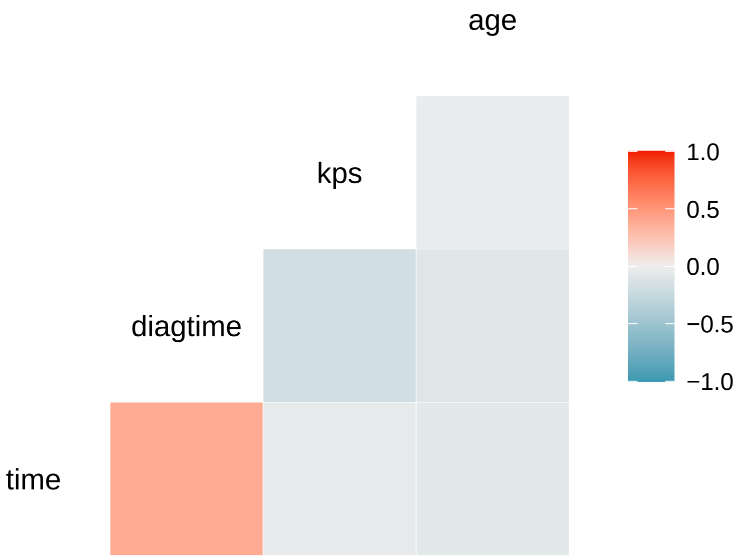
```
## pairwise scatter plot
## R base
con.df = dd[, c("time", "diagtime", "kps", "age")]
cor.mat = cor(con.df, use = "complete", method = "pearson")
round(cor.mat, 3)
##            time diagtime    kps    age
## time      1.000    0.382 -0.046 -0.068
## diagtime  0.382    1.000 -0.184 -0.095
## kps      -0.046   -0.184  1.000 -0.033
## age      -0.068   -0.095 -0.033  1.000
pairs(con.df)
```



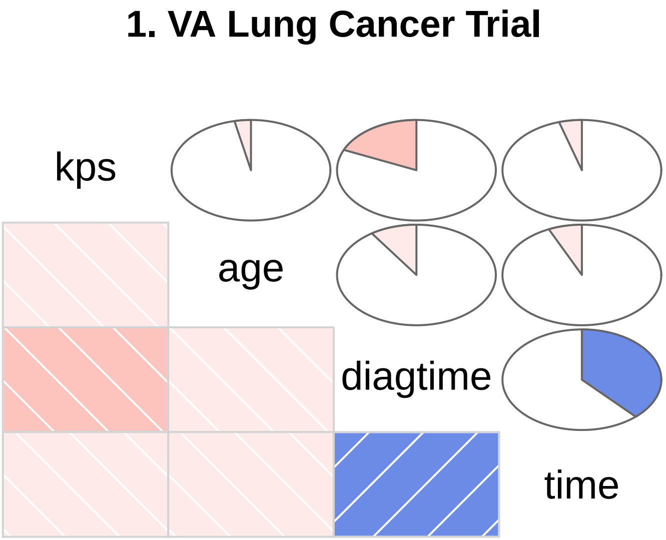
```r
## ggplot2
library(GGally)
GGally::ggpairs(data = con.df)
```



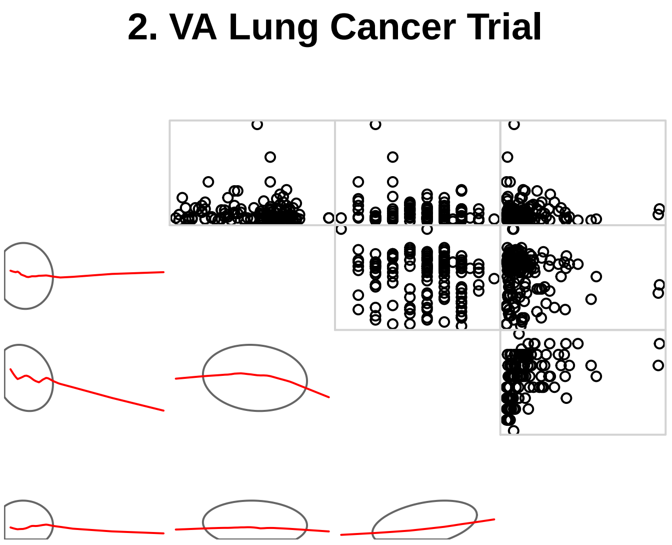
```
GGally::ggcorr(data = con.df,
               method = c("complete", "pearson"))
```



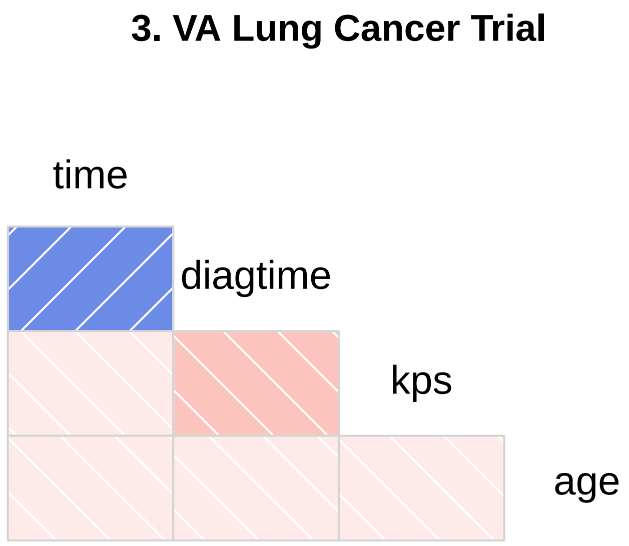
```r
## Correlogram
library(corrgram)
corrgram(x = dd,
         order = TRUE,
         lower.panel = panel.shade,
         upper.panel = panel.pie,
         text.panel = panel.txt,
         main = "1. VA Lung Cancer Trial")
```



```r
corrgram(x = dd,
         order = TRUE,
         lower.panel = panel.ellipse,
         upper.panel = panel.pts,
         text.panel = panel.minmax,
         main = "2. VA Lung Cancer Trial")
```

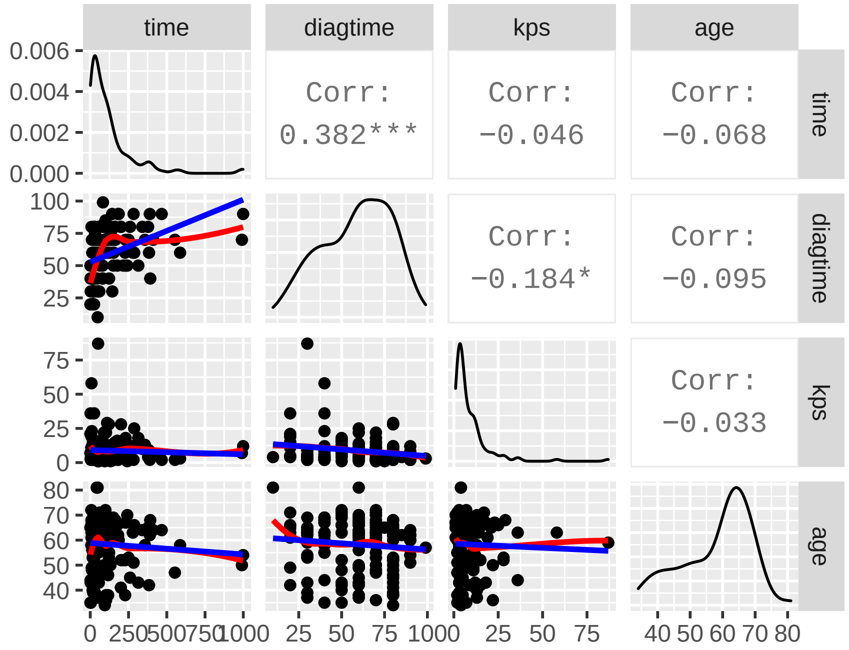


```r
corrgram(x = dd,
         order = NULL,
         lower.panel = panel.shade,
         upper.panel = NULL,
         text.panel = panel.txt,
         main = "3. VA Lung Cancer Trial")
```

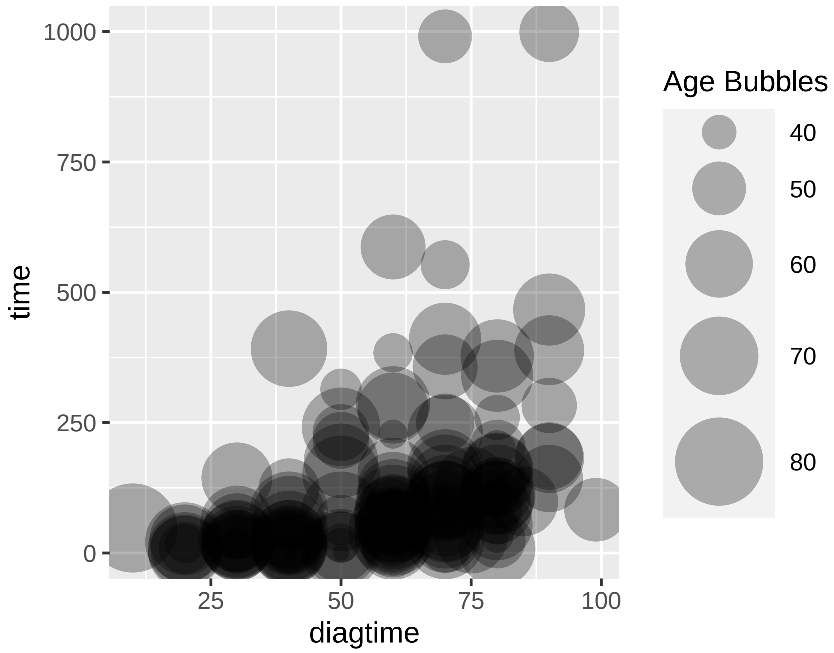


- Try by yourself!

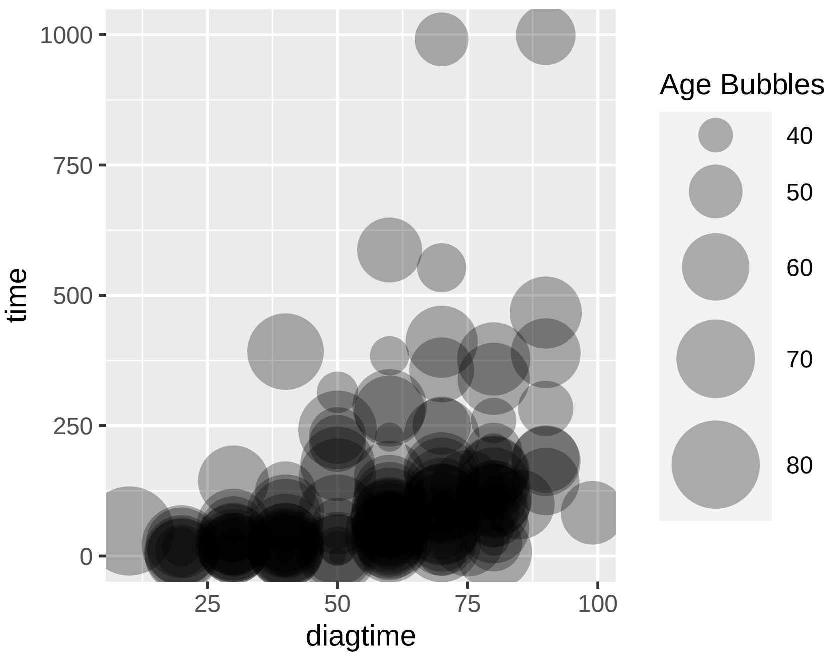
```
# more advanced
my_fn <- function(data, mapping, ...){
  p <- ggplot(data = data, mapping = mapping) +
    geom_point() +
    geom_smooth(method = loess, se = FALSE, fill = "red", color = "red", ...) +
    geom_smooth(method = lm, se = FALSE, fill = "blue", color = "blue", ...)
  p
}
GGally::ggpairs(data = con.df,
        lower = list(continuous = my_fn))
```



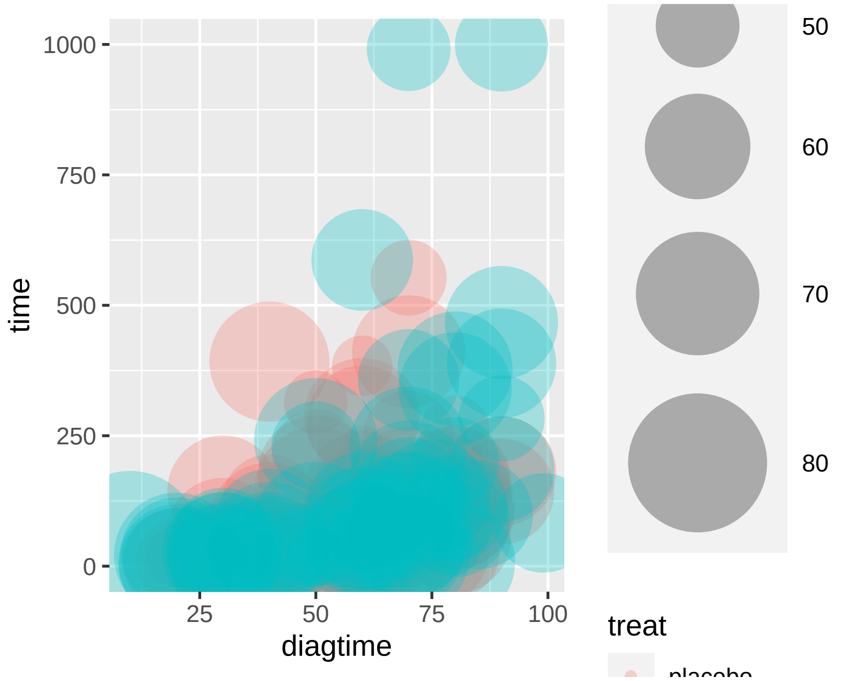
```
## Bubble plot
ggplot(data = dd, aes(x = diagtime, y = time, size = age)) +
  geom_point(alpha = 0.3) +
  scale_size(range = c(.1, 15), name = "Age Bubbles")
```



```
ggplot(data = dd, aes(x = diagtime, y = time, size = age)) +
  geom_point(alpha = 0.3) +
  scale_size(range = c(.1, 15), name = "Age Bubbles")
```



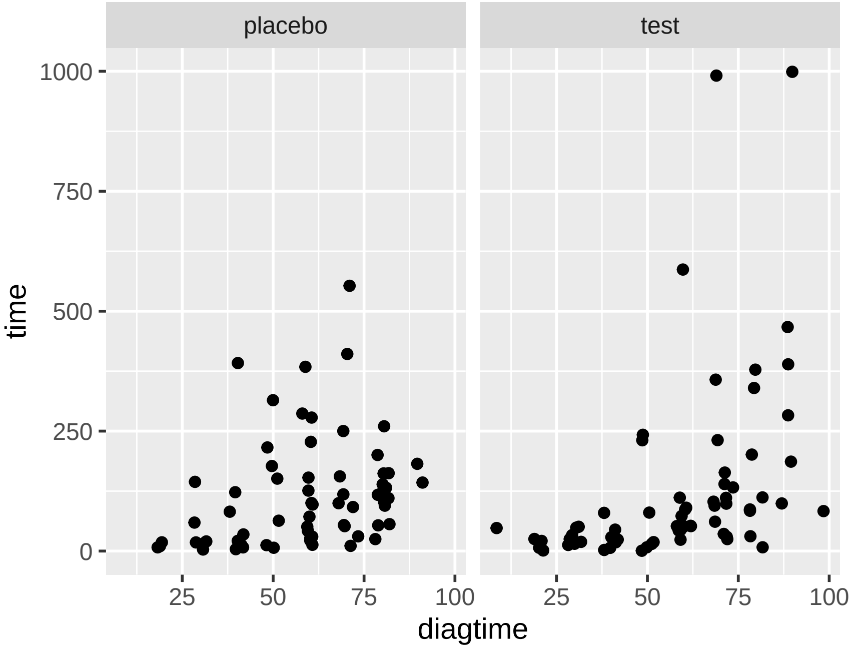
```
ggplot(data = dd, aes(x = diagtime, y = time, size = age, color = treat)) +
  geom_point(alpha = 0.3) +
scale_size(range = c(.1, 24), name = "")
```



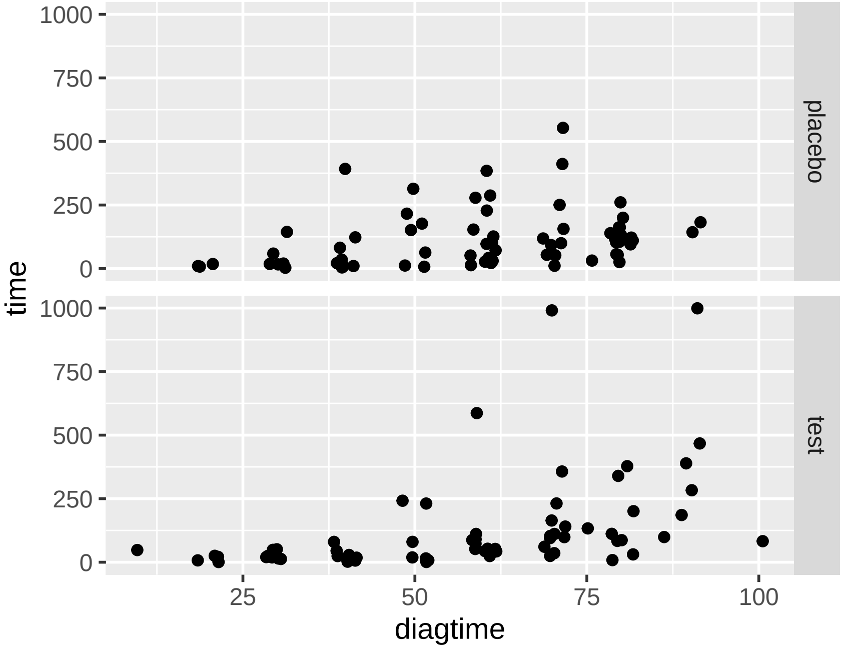
5.6

-
-
-

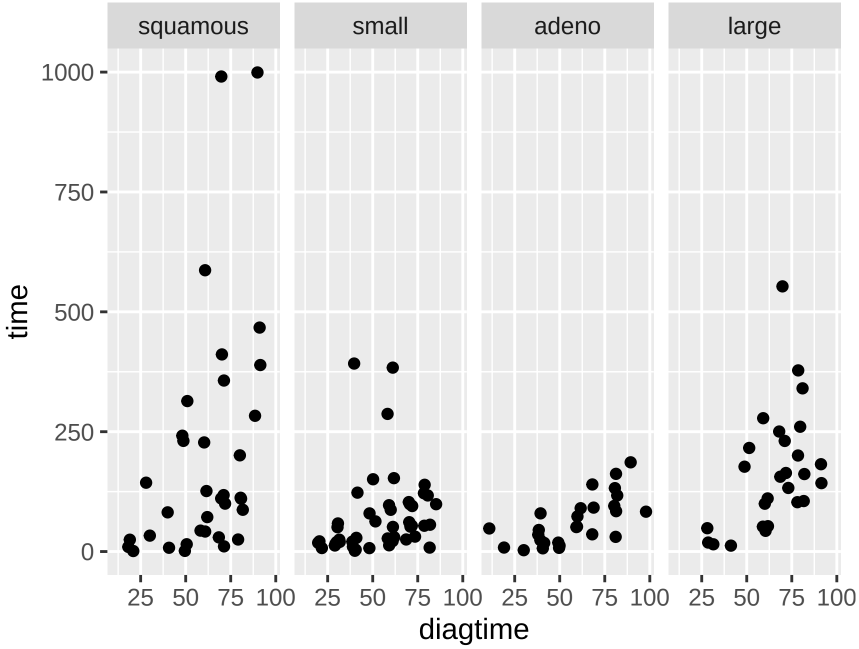
```
# plot by treat
ggplot(data = dd, aes(x = diagtime, y = time)) + geom_jitter() +
  facet_grid(. ~ treat)
```



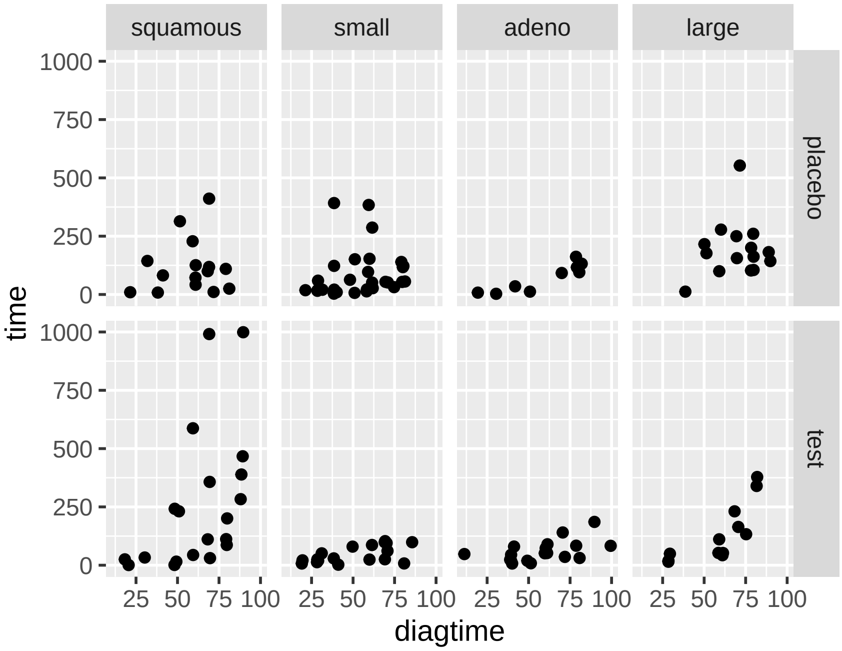
```r
ggplot(data = dd, aes(x = diagtime, y = time)) + geom_jitter() +
  facet_grid(treat ~ .)
```



```
# plot by cellcode
ggplot(data = dd, aes(x = diagtime, y = time)) + geom_jitter() +
  facet_grid(. ~ cellcode)
```



```
# two factors
ggplot(data = dd, aes(x = diagtime, y = time)) + geom_jitter() +
  facet_grid(treat ~ cellcode)
```


squamous
small
adeno
large
placebo
test
time
1000
750
500
250
0
diagtime
25
50
75
100

Chapter 6

Basic Function

{R} (**function**), , , , , , , {R} . (**argument**).

{R} (base) , , {R} (contribution) , {R} . , mean(), var(), sd(), log() .

6.1

(**argument**) , , (**formals**). , , (**required argument**), , (**optional argument**), (**ellipsis argument**) , , , {R} . , log() :

```
log(x, base = exp(1))
```

log() {R} , x , . base = exp(1) , , log() e , , , 2 , log(x, base = 2).

```
## basic function
x.vec = c(1:5)
x.vec            # show x.vec
## [1] 1 2 3 4 5
mean(x = x.vec) # function mean() calculate mean, return a scalar
## [1] 3
var(x = x.vec)   # function mean() calculate variance
## [1] 2.5
sd(x.vec)        # function mean() calculate standard deviation
## [1] 1.581
summary(x.vec)   # summarized statistics
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##       1       2       3       3       4       5 
log(x = x.vec)   # take log for all elements in vector x.vec
```

```
## [1] 0.0000 0.6931 1.0986 1.3863 1.6094
## log function
x.vec <- c(1, 2, 3, 4, 5)
log(x = x.vec)
## [1] 0.0000 0.6931 1.0986 1.3863 1.6094
log(x = x.vec, base = 2)
## [1] 0.000 1.000 1.585 2.000 2.322
```

6.2

{R} S3 classes S4 classes , , {R} , S3 classes . , `function.name()`, . `methods("function.name")`, `getAnywhere("function.name")`, `stats:::function.name` , `sd`, `sd` .

```
## methods()
sd
## function (x, na.rm = FALSE)
## sqrt(var(if (is.vector(x) || is.factor(x)) x else as.double(x),
##     na.rm = na.rm))
## <bytecode: 0x0000000014b1b560>
## <environment: namespace:stats>
t
## function (x)
## UseMethod("t")
## <bytecode: 0x0000000009aa46d0>
## <environment: namespace:base>
methods(t)
##  [1] t,ANY-method            t,CsparseMatrix-method  t,dgCMatrix-method
##  [4] t,dgeMatrix-method      t,diagonalMatrix-method t,dppMatrix-method
##  [7] t,dsCMatrix-method      t,dspMatrix-method      t,dsTMatrix-method
## [10] t,dsyMatrix-method      t,dtpMatrix-method      t,dtrMatrix-method
## [13] t,dtTMatrix-method      t,indMatrix-method      t,lgeMatrix-method
## [16] t,lspMatrix-method      t,lsTMatrix-method      t,lsyMatrix-method
## [19] t,ltpMatrix-method      t,ltrMatrix-method      t,ltTMatrix-method
## [22] t,Matrix-method         t,ngeMatrix-method      t,nspMatrix-method
## [25] t,nsTMatrix-method      t,nsyMatrix-method      t,ntpMatrix-method
## [28] t,ntrMatrix-method      t,ntTMatrix-method      t,pMatrix-method
## [31] t,RsparseMatrix-method  t,sparseVector-method   t,TsparseMatrix-method
## [34] t.data.frame            t.default               t.fractions*
## [37] t.gtable*               t.trellis*              t.ts*
## [40] t.vctrs_sclr*           t.vctrs_vctr*
## see '?methods' for accessing help and source code
methods(class = "ts")
##  [1] [             [<-           aggregate     as.data.frame as_tibble
##  [6] cbind         coerce        cycle         diff          diffinv
## [11] filter        initialize    kernapply     lines         Math
## [16] Math2         monthplot     na.omit       Ops           plot
## [21] print         show          slotsFromS3   t             time
## [26] window        window<-
## see '?methods' for accessing help and source code
```

S4 classes , showClass("function.namme"), showMethods("function.namme"), getMethod("function.namme"), selectMethod(), existsMethod(), hasMethod(), removeClass(), removeMethod(), getClass(), getSlots(), slotNames(), slot(). , .

```
download.packages(pkgs = "package.name",
                  destdir = "C:/RData",
                  type = "source")
```

6.3

{R} , :, sequence(), rep() .

6.3.1 : seq() sequence()

, , [1,2,3,4,5], [1,3,5,7,9] , : ( ), seq() sequence() .

```
## :
1:5
## [1] 1 2 3 4 5
5:1
## [1] 5 4 3 2 1
- 1:3
## [1] -1  0  1  2  3
```

seq() sequence() , , .

```
seq(from = 1, to = 1,
    by = ((to - from)/(length.out - 1)),
    length.out = NULL,
    along.with = NULL, ...)
```

- from = 1
- to = 1
- by
- length.out ( )

```
## seq()
seq(from = 1, to = 5, by = 0.5)
```

```
## [1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
seq(1, 5, 0.5)
## [1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
seq(1, 5, length = 3)
## [1] 1 3 5
seq(from = 0, to = 1, by = 0.1)
##  [1] 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
seq(from = 0, to = 2, by = 0.33)
## [1] 0.00 0.33 0.66 0.99 1.32 1.65 1.98
sequence(c(3, 4, 5))
##  [1] 1 2 3 1 2 3 4 1 2 3 4 5
```

6.4 : rep()

seq() rep(), . :

```
rep(x, times = 1, length.out = NA, each = 1)
```

- x .
- times x .
- each x .
- length.out = NA x .

```
## rep()
rep(0, times = 3)
## [1] 0 0 0
rep(1, 5)
## [1] 1 1 1 1 1
x.vec <- c(4, 5, 6)
rep(x.vec, times = 2)
## [1] 4 5 6 4 5 6
rep(x.vec, each = 2)
## [1] 4 4 5 5 6 6
rep(x.vec, each = 2, times = 3)
##  [1] 4 4 5 5 6 6 4 4 5 5 6 6 4 4 5 5 6 6
rep(x.vec, times = c(2, 2, 2))
## [1] 4 4 5 5 6 6
rep(x.vec, times = c(1, 2, 3))
## [1] 4 5 5 6 6 6
rep(x.vec, each = 2, len = 4)    # first 4 only.
## [1] 4 4 5 5
```

6.5 Arithmetic Computing Function

{R} (**arithmetic function**), , , Gamma , Beta , , , ,
.

Table 6.1: Arithmetic Computing Function

-	(Substraction, can be unary or binary)
+	(Addition, can be unary or binary)
!	(Unary not)
	(Multiplication, binary)
/	(Division, binary)
^	(Exponentiation, binary)
%%	(Modulus, binary)
%/%	(Integer divide, binary)
%*%	(Matrix product, binary)
%o%	(Outer product, binary)
%x%	Kronecker (Kronecker product, binary)
%in%	(Matching operator, binary, in model formulae: nesting)
`round(x,  digits = 0)`	( )
`signif(x, digits = 6)`	( )
`trunc(x)`	x , 0
`ceiling(x)`	x
`floor(x)`	x
`sign(x)`	x , 1, 0, -1.
`abs(x)`	x
`sqrt(x)`	$\sqrt{x}$
`exp(x)`	e^x
`expm1(x)`	$\vert x\vert << 1,\quad e^x - 1$
`log(x)`	$\log(x)$
`log10(x)`	$log_{10}(x)$
`log2(x)`	$\log_2(x)$
`logb(x, base = z)`	$\log_z(x)$
`log1p(x)`	$\vert x\vert << 1,\quad \log(1+x)$
`gamma(x)`	$\Gamma(x) = (x-1)! = \int_0^\infty t^{(x-1)} \exp(-t)dt$
`lgamma(x)`	$\log_e[\Gamma(x)]$
`beta(a, b)`	$B(a,b) = (\Gamma(a)\Gamma(b)) \,/\, (\Gamma(a+b))$ $ = _0^1 t^{(a-1)} (1-t)^{(b-1)} d t$
`lbeta(a, b)`	$\log_e[B(a,b)]$
`digamma(x)`	$\frac{d}{dx} \log_e[\Gamma(x)]$
`trigamma(x)`	$\frac{d^2}{dx^2} \log_e[\Gamma(x)]$
`psigamma(x, deriv = 0)`	$\frac{d^p}{dx^p} \log_e[\Gamma(x)]$
`sin(x) cos(x) tan(x)`	(trigonometric functions)
`asin(x) acos(x) atan(x)`	(inverse functions)

`sinh(x) cosh(x) tanh(x)`	(hyperbolic functionsx)
`asinh(x) acosh(x) atanh(x)`	(inverse hyperbolic functions)

```
## Arithmetic Computing
## rounding
(x.vec <- 0.5 + c(-2:2))
## [1] -1.5 -0.5  0.5  1.5  2.5
round(x.vec) # IEEE rounding
## [1] -2  0  0  2  2
(y.vec <- seq(-2, 2, by = 0.5))
## [1] -2.0 -1.5 -1.0 -0.5  0.0  0.5  1.0  1.5  2.0
(y.round <- round(y.vec)) # IEEE rounding
## [1] -2 -2 -1  0  0  0  1  2  2
(y.trunc <- trunc(y.vec))
## [1] -2 -1 -1  0  0  0  1  1  2
(y.signif <- signif(y.vec))
## [1] -2.0 -1.5 -1.0 -0.5  0.0  0.5  1.0  1.5  2.0
(y.ceil <- ceiling(y.vec))
## [1] -2 -1 -1  0  0  1  1  2  2
(y.floor <- floor(y.vec))
## [1] -2 -2 -1 -1  0  0  1  1  2
cbind(y.vec, y.round, y.trunc, y.signif, y.ceil, y.floor)
##       y.vec y.round y.trunc y.signif y.ceil y.floor
##  [1,]  -2.0      -2      -2     -2.0     -2      -2
##  [2,]  -1.5      -2      -1     -1.5     -1      -2
##  [3,]  -1.0      -1      -1     -1.0     -1      -1
##  [4,]  -0.5       0       0     -0.5      0      -1
##  [5,]   0.0       0       0      0.0      0       0
##  [6,]   0.5       0       0      0.5      1       0
##  [7,]   1.0       1       1      1.0      1       1
##  [8,]   1.5       2       1      1.5      2       1
##  [9,]   2.0       2       2      2.0      2       2
#
(x.vec <-  0.5 + c(-2:3))
## [1] -1.5 -0.5  0.5  1.5  2.5  3.5
round(x.vec) # IEEE rounding
## [1] -2  0  0  2  2  4
(y.vec <- seq(-2, 3, by = 0.5))
##  [1] -2.0 -1.5 -1.0 -0.5  0.0  0.5  1.0  1.5  2.0  2.5  3.0
(y.round <- round(y.vec)) # IEEE rounding
##  [1] -2 -2 -1  0  0  0  1  2  2  2  3
(y.trunc <- trunc(y.vec))
##  [1] -2 -1 -1  0  0  0  1  1  2  2  3
```

```
(y.signif <- signif(y.vec))
##  [1] -2.0 -1.5 -1.0 -0.5  0.0  0.5  1.0  1.5  2.0  2.5  3.0
(y.ceil <- ceiling(y.vec))
##  [1] -2 -1 -1  0  0  1  1  2  2  3  3
(y.floor <- floor(y.vec))
##  [1] -2 -2 -1 -1  0  0  1  1  2  2  3
cbind(y.vec, y.round, y.trunc, y.signif, y.ceil, y.floor)
##       y.vec y.round y.trunc y.signif y.ceil y.floor
##  [1,]  -2.0      -2      -2     -2.0     -2      -2
##  [2,]  -1.5      -2      -1     -1.5     -1      -2
##  [3,]  -1.0      -1      -1     -1.0     -1      -1
##  [4,]  -0.5       0       0     -0.5      0      -1
##  [5,]   0.0       0       0      0.0      0       0
##  [6,]   0.5       0       0      0.5      1       0
##  [7,]   1.0       1       1      1.0      1       1
##  [8,]   1.5       2       1      1.5      2       1
##  [9,]   2.0       2       2      2.0      2       2
## [10,]   2.5       2       2      2.5      3       2
## [11,]   3.0       3       3      3.0      3       3
#
(y.vec <- seq(-2, 3, by = 0.5))
##  [1] -2.0 -1.5 -1.0 -0.5  0.0  0.5  1.0  1.5  2.0  2.5  3.0
y.vec[trunc(y.vec) != floor(y.vec)]
## [1] -1.5 -0.5
y.vec[round(y.vec) != floor(y.vec + 0.5)]
## [1] -1.5  0.5  2.5
#
(z.vec <- pi * 100 ^ (-1:3))
## [1] 3.142e-02 3.142e+00 3.142e+02 3.142e+04 3.142e+06
round(z.vec, 3)
## [1] 3.100e-02 3.142e+00 3.142e+02 3.142e+04 3.142e+06
signif(z.vec, 3)
## [1] 3.14e-02 3.14e+00 3.14e+02 3.14e+04 3.14e+06
#
## sign() abs()
sign(pi) # == 1
## [1] 1
sign(-2:3)# -1 -1 0 1 1 1
## [1] -1 -1  0  1  1  1
abs(-2:3)
## [1] 2 1 0 1 2 3
#
## log(), exp() calculation
(x.vec <- 1:3)
## [1] 1 2 3
```

```
log(exp(x.vec))
## [1] 1 2 3
(y.vec <- 10 ^ (x.vec))
## [1]   10  100 1000
log10(y.vec)
## [1] 1 2 3
log10(1e7) # = 7
## [1] 7
#
## options(digits, scipen)
options(digits = 4, scipen = 0)
z.vec <- pi * 100^(-1:3)
print(z.vec / 1000, digits = 4)
## [1] 3.142e-05 3.142e-03 3.142e-01 3.142e+01 3.142e+03
options(digits = 4, scipen = 100)
print(z.vec / 1000, digits = 4)
## [1]    0.00003142    0.00314159    0.31415927   31.41592654 3141.59265359
#
options(digits = 4, scipen = 100)
x.vec <- 100 ^ -(1 + 2 * 1:3)
cbind(
  x = x.vec,
  log1px = log(1 + x.vec),
  log1p  = log1p(x.vec),
  exp    = exp(x.vec) - 1,
  expm1  = expm1(x.vec)
)
##                      x               log1px            log1p
## [1,] 0.00000100000000 0.000000999999499918 0.00000099999950
## [2,] 0.00000000010000 0.000000000100000008 0.00000000010000
## [3,] 0.00000000000001 0.000000000000009992 0.00000000000001
##                       exp            expm1
## [1,] 0.000001000000499962 0.00000100000050
## [2,] 0.000000000100000008 0.00000000010000
## [3,] 0.000000000000009992 0.00000000000001
#
options(digits = 4, scipen = 0)
x.vec <- 100^(-(1 + 2 * 1:3))
cbind(
  x = x.vec,
  log1px = log(1 + x.vec),
  log1p  = log1p(x.vec),
  exp    = exp(x.vec) - 1,
  expm1  = expm1(x.vec)
)
```

```
##          x    log1px log1p       exp expm1
## [1,] 1e-06 1.000e-06 1e-06 1.000e-06 1e-06
## [2,] 1e-10 1.000e-10 1e-10 1.000e-10 1e-10
## [3,] 1e-14 9.992e-15 1e-14 9.992e-15 1e-14
```

6.6 : choose() factorial()

{R} choose(), lchoose(), factorial(), lfactorial(), .

- choose(n, k) $= \binom{n}{k}$
- fractorial(x) $= x!$
- k .
- x n .
- factorial(), lfactorial() .

```
## combination
## choose()
choose(n = 5, k = 2)
## [1] 10
log(choose(n = 5, k = 2))
## [1] 2.303
lchoose(n = 5, k = 2)
## [1] 2.303
for (n in 0:5)
  print(choose(n, k = 0:n))
## [1] 1
## [1] 1 1
## [1] 1 2 1
## [1] 1 3 3 1
## [1] 1 4 6 4 1
## [1]  1  5 10 10  5  1
## factorial
factorial(x = 100)
## [1] 9.333e+157
log(factorial(x = 100))
## [1] 363.7
lfactorial(x = 100)
## [1] 363.7
lfactorial(x = 10000)
## [1] 82109
factorial(x = c(1, 3, 5))
## [1]   1   6 120
```

6.7 : all(), any(), which()

all(x) any(x) obj.vec , TRUE FALSE. which() obj.vec , , . which.max() which.min() which() .

```
all(..., na.rm = FALSE)
any(..., na.rm = FALSE)
which(x, arr.ind = FALSE, useNames = TRUE)
```

... . all(x) any(x) (scalar) TRUE FALSE. all(x) x TRUE? , any(x) x TRUE? which(x) , x TRUE (index). which(x) arr.ind = TRUE x array (matrix) , array (matrix) .

```
## all(), any(), which()
(x.vec <- c(-1:2))
## [1] -1  0  1  2
all(x.vec > 0)
## [1] FALSE
any(x.vec > 0)
## [1] TRUE
which(x.vec > 0)
## [1] 3 4
which.max(x.vec)
## [1] 4
which.min(x.vec)
## [1] 1
#
(x.mat <- matrix(c(2, -1, -3,
                   -1,  2,  4,
                   -3,  4,  9),
                 nrow = 3, byrow = T))
##      [,1] [,2] [,3]
## [1,]    2   -1   -3
## [2,]   -1    2    4
## [3,]   -3    4    9
all(x.mat > 0)
## [1] FALSE
any(x.mat > 0)
## [1] TRUE
which(x.mat > 0)
## [1] 1 5 6 8 9
#
which(x.mat %% 2 == 0)
## [1] 1 5 6 8
which(x.mat %% 2 == 0, arr.ind = TRUE)
```

```
##      row col
## [1,]   1   1
## [2,]   2   2
## [3,]   3   2
## [4,]   2   3
```

6.8 Ranking and Sorting

{R} , rev(), sort(), order() rank().

Table 6.2:

rev(x)	x	(reverse order)
rank(x)	x	(returns the sample ranks of the values) ties.method = "average"
sort(x)	x	(sort a vector or factor, partially) into ascending or descending order).
order(x)	x	

```
rev(x)
sort(x, decreasing = FALSE, na.last = NA, ...)
rank(x, na.last = TRUE,
     ties.method = c("average", "first", "last", "random", "max", "min"))
order(x, ..., na.last = TRUE, decreasing = FALSE,
        method = c("shell", "radix"))
```

:

- x x.
- decreasing:
  - decreasing = FALSE {R} .
  - decreasing = TRUE .
- na.last:
  - na.last = TRUE {R} NA .
  - na.last = FALSE {R} NA .
  - na.last = NA {R} NA .
- rev(x) z, x .
- sort(x) z, x .
- % rank(x) z, x , x (rank).

- "average": .
- "first": .
- "last": .
- "random": .
- "max": .
- "min": .

```
## reverse, rank, sort and order
## rev(): reverse elements
x.vec <- c(7, 7, 7, 6, 10, 9, 9, 9, NA, 8)
rev(x.vec)
##  [1]  8 NA  9  9  9 10  6  7  7  7
## sort(): from the smallest to the largest
sort(x.vec)
## [1]  6  7  7  7  8  9  9  9 10
## rank():
rank(x.vec, na.last = TRUE)
##  [1]  3  3  3  1  9  7  7  7 10  5
rank(x.vec, na.last = FALSE)
##  [1]  4  4  4  2 10  8  8  8  1  6
set.seed(1)
rank(x.vec, ties.method = "average")
##  [1]  3  3  3  1  9  7  7  7 10  5
rank(x.vec, ties.method = "first")
##  [1]  2  3  4  1  9  6  7  8 10  5
rank(x.vec, ties.method = "last")
##  [1]  4  3  2  1  9  8  7  6 10  5
rank(x.vec, ties.method = "random")
##  [1]  2  3  4  1  9  7  8  6 10  5
rank(x.vec, ties.method = "max")
##  [1]  4  4  4  1  9  8  8  8 10  5
rank(x.vec, ties.method = "min")
##  [1]  2  2  2  1  9  6  6  6 10  5
## order(): retrun index
## x.vec[] is the smallest one
order(x.vec)
##  [1]  4  1  2  3 10  6  7  8  5  9
x.vec[order(x.vec)]
##  [1]  6  7  7  7  8  9  9  9 10 NA
## rank(): ties.method = "average"
x <- c(7, 9, 6, 7, 8, NA)
sort(x, na.last = FALSE)
## [1] NA  6  7  7  8  9
```

```
rank(x, ties.method = "average", na.last = TRUE)
## [1] 2.5 5.0 1.0 2.5 4.0 6.0
(x.ord <- order(x, na.last = FALSE))
## [1] 6 3 1 4 5 2
x[x.ord] # = sort(x)
## [1] NA  6  7  7  8  9
```

{R} NA , na.last = TRUE {R} , , NA .

6.9

{R} is.object(), is.na(), is.vector() , .

{R} as.object(), as.vector(), as.matrix(() , .

```
## is() and as()
# vector
x.vec <- c(1 / 1, 1 / 2, 1 / 3, 1 / 4, 1 / 5)
x.vec
## [1] 1.0000 0.5000 0.3333 0.2500 0.2000
is.vector(x.vec)
## [1] TRUE
is.character(x.vec)
## [1] FALSE
x.vec <- as.character(x.vec)
x.vec
## [1] "1"                 "0.5"               "0.333333333333333"
## [4] "0.25"              "0.2"
##
b.df <- as.data.frame(matrix(c(1:24), nrow = 6, byrow = T))
is.matrix(b.df)
## [1] FALSE
b.mat <- as.matrix(b.df)
b.mat
##      V1 V2 V3 V4
## [1,]  1  2  3  4
## [2,]  5  6  7  8
## [3,]  9 10 11 12
## [4,] 13 14 15 16
## [5,] 17 18 19 20
## [6,] 21 22 23 24
b.mat <- as.vector(b.mat)
b.mat
##  [1]  1  5  9 13 17 21  2  6 10 14 18 22  3  7 11 15 19 23  4  8 12 16 20 24
```

Chapter 7

{R} , , {R} , , `sum()`, `cumsum()`, `diff()`, `prod()`, `cumprod()`; , , `mean()`, `median()`, `var()`, `sd()`, `range()`, `min()`, `max()`, `quantile()`, `sample()` .

{R} , , , {R} , , `na.omit()` , , , `mean(na.omit(x))`. , , `na.rm = T`, , `mean(x, na.rm = T)` , , , .

Table 7.1:

`sum(x)`	(scalar)	$y = \sum_i x_i$
`cumsum(x)`	(vector)	$z_j = \sum_{i \leq j} x_i$
`diff(x)`	`x[i+1]-x[i]`	$z_i = x_{i+1} - x_i$
`lag(x, k)`	`x[i-k]`	$z_i = x_{i-k}$, `x[i]` `x[i-k]`
`lead(x, k)`	`x[i+k]`	$z_i = x_{i+k}$, `x[i]` `x[i+k]`
`prod(x)`	(product)	$y = \prod_i x_i$
`cumprod(x)`		$z_j = _{i j} x_i
`mean(x)`	(mean)	$\bar{x} = \frac{1}{n} \sum_i x_i)$
`median(x)`	(median)	0.5 quantile, 50^{th} percentile
`var(x)`	,	$s^2 = \frac{1}{n-1} \sum_i (x_i - \bar{x})^2$
`sd(x)`	(SD)	$s = \sqrt{s^2}$
`range(x)`	(range)	$(\min(x), \max(x))$
`min(x)`		$\min(x)$
`max(x)`		$\max(x)$
`quantile(x)`		
`fivenum(x)`		(five-number summary) $(\min, Q_1, \text{median}, Q_3, \max)$
`sample(x)`		random sample

7.1

{R} , . `z <- range(x)` , $(\min(x), \max(x))$; `min(x)`, `max(x)`; `quantile()`, `quantile(x, probs = c(0.05, 0.25, 0.5, 0.75, 0.95)`. `fivenum(x)` `x` $(\min, Q_1, \text{median}, Q_3, \max)$.

```
## basic descriptive statistics
x <- seq(-2, 3, 0.3)
x
##  [1] -2.0 -1.7 -1.4 -1.1 -0.8 -0.5 -0.2  0.1  0.4  0.7  1.0  1.3  1.6  1.9  2.2
## [16]  2.5  2.8
sum(x)
## [1] 6.8
cumsum(x)
##  [1] -2.0 -3.7 -5.1 -6.2 -7.0 -7.5 -7.7 -7.6 -7.2 -6.5 -5.5 -4.2 -2.6 -0.7  1.5
## [16]  4.0  6.8
diff(x)
##  [1] 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3
prod(x)
## [1] -0.7138
cumprod(x)
##  [1] -2.00000  3.40000 -4.76000  5.23600 -4.18880  2.09440 -0.41888 -0.04189
##  [9] -0.01676 -0.01173 -0.01173 -0.01525 -0.02440 -0.04635 -0.10197 -0.25493
## [17] -0.71381
mean(x)
## [1] 0.4
median(x)
## [1] 0.4
var(x)
## [1] 2.295
sd(x)
## [1] 1.515
range(x)
## [1] -2.0  2.8
min(x)
## [1] -2
max(x)
## [1] 2.8
## quantile
y <- quantile(x, probs = c(0.05, 0.25, 0.5, 0.75, 0.95))
y
##    5%   25%   50%   75%   95%
## -1.76 -0.80  0.40  1.60  2.56
# IQR: inter-quantile range
iqr = y[4] - y[2]
iqr
```

```
## 75%
## 2.4
## five numnber summary
fivenum(x)
## [1] -2.0 -0.8  0.4  1.6  2.8
# missing values
x[3] <- NA
x[7] <- NA
x
##  [1] -2.0 -1.7   NA -1.1 -0.8 -0.5   NA  0.1  0.4  0.7  1.0  1.3  1.6  1.9  2.2
## [16]  2.5  2.8
mean(x)
## [1] NA
mean(na.omit(x))
## [1] 0.56
mean(x, na.rm = T)
## [1] 0.56
var(x, na.rm = T)
## [1] 2.338
```

7.2

, (**contingency table**), {R} , (**contingency table**), , `table()`, `xtabs()`, `as.table()`, `is.table()`; `ftable()`, `read.ftable()`, `wirte.ftable()`; `as.data.frame()`; `margin.table()`, `prop.table()`, `addmargins()` . , {R} , , `xtable`, `vcd**`, reshape2, plyr, dplyr, tidyr, tidyverse , . {R} , , ** ** . , Epi, epibasix, epiDisplay(epicalc), epifit, epiR, epitools, RC , , , .

2 , (a) (**individual data**, **micro data**, **case data**); (b) (**aggregated data**, **macro data**, **summarized data**, **ecological data**). (**subject**, **individual**), , , (**raw data**, **primary data**, **original data**). , , , , , (**secondary data**).

, , , , . , , , , , , BMI , , , (**ecological fallacy**), ( ) , ( ) , .

7.2.1 : table(), xtabs()

`table()`, `xtabs()`, , , , , . `table()` `_contingency table_`. {R} (class) `table` . `as.table()` . `as.matrix()` . `as.data.frame()` . `as.data.frame()` `xtabs()` . `is.table()` . `table()`

. `xtabs()` , (model formula) . `as.data.frame()` `xtabs()` , .

```
table(variable_name, ...)
xtabs(formula, data)
```

.

- `formula`: .
- `data`: .
- `na.action = "na.omit"`: .
- `exclude`: , .
- `useNA`: .
  - `"no"`: .
  - `"ifany"`: , (count) .
  - `"always"`: 1 . (count) 0 1 .

Prentice (1973) , , , % Veteran's Administration , , , . **survVATrial.csv**.

treat (therapy)	: 0 = ; 1 =
cellcode	; 1 = ; 2 = ; 3 = ; 4 =
time	, ,
censor	: 0 = ; 1 =
diagtime	Karnofsky performance score,
diagtime	,
age	( )
prior	; 0 = ; 1 =

```
dd <- read.table("./Data/survVATrial.csv",
                 header = TRUE,
                 sep = ",",
                 quote = "\"'",
                 dec = ".",
                 row.names = NULL,
                 # col.names,
                 as.is = TRUE,
                 # as.is = !stringsAsFactors,
                 na.strings = c(".", "NA"))
head(dd)
##   treat cellcode time censor diagtime kps age prior
## 1     0        1   72      1       60   7  69     0
## 2     0        1  411      1       70   5  64    10
## 3     0        1  228      1       60   3  38     0
## 4     0        1  126      1       60   9  63    10
## 5     0        1  118      1       70  11  65    10
## 6     0        1   10      1       20   5  49     0
str(dd)
## 'data.frame':        137 obs. of  8 variables:
##  $ treat   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ cellcode: int  1 1 1 1 1 1 1 1 1 1 ...
##  $ time    : int  72 411 228 126 118 10 82 110 314 100 ...
##  $ censor  : int  1 1 1 1 1 1 1 1 1 0 ...
##  $ diagtime: int  60 70 60 60 70 20 40 80 50 70 ...
##  $ kps     : int  7 5 3 9 11 5 10 29 18 6 ...
##  $ age     : int  69 64 38 63 65 49 69 68 43 70 ...
##  $ prior   : int  0 10 0 10 10 0 10 0 0 0 ...
dd$treat <- factor(dd$treat, labels = c("placebo", "test"))
dd$cellcode <- factor(dd$cellcode,
                      labels = c("squamous", "small", "adeno", "large"))
dd$censor <- factor(dd$censor, labels = c("survival", "dead"))
dd$prior <- factor(dd$prior, labels = c("no", "yes"))
head(dd)
##     treat cellcode time censor diagtime kps age prior
## 1 placebo squamous   72   dead       60   7  69    no
## 2 placebo squamous  411   dead       70   5  64   yes
## 3 placebo squamous  228   dead       60   3  38    no
## 4 placebo squamous  126   dead       60   9  63   yes
## 5 placebo squamous  118   dead       70  11  65   yes
## 6 placebo squamous   10   dead       20   5  49    no
str(dd)
## 'data.frame':        137 obs. of  8 variables:
##  $ treat   : Factor w/ 2 levels "placebo","test": 1 1 1 1 1 1 1 1 1 1 ...
##  $ cellcode: Factor w/ 4 levels "squamous","small",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ time    : int  72 411 228 126 118 10 82 110 314 100 ...
##  $ censor  : Factor w/ 2 levels "survival","dead": 2 2 2 2 2 2 2 2 2 1 ...
##  $ diagtime: int  60 70 60 60 70 20 40 80 50 70 ...
##  $ kps     : int  7 5 3 9 11 5 10 29 18 6 ...
##  $ age     : int  69 64 38 63 65 49 69 68 43 70 ...
##  $ prior   : Factor w/ 2 levels "no","yes": 1 2 1 2 2 1 2 1 1 1 ...
## one-way table
## table()
table(dd$censor)
##
## survival     dead
##        9      128
table(dd$cellcode)
##
## squamous    small    adeno    large
##       35       48       27       27
## xtabs()
xtabs(~ censor, data = dd)
## censor
## survival     dead
##        9      128
## two-way table()
## table()
dd.2tab = table(dd$cellcode, dd$censor)
dd.2tab
##
##             survival dead
##   squamous        4   31
##   small           3   45
##   adeno           1   26
##   large           1   26
class(dd.2tab)
## [1] "table"
## xtabs()
dd.2xtabs = xtabs(~ cellcode + censor, data = dd)
dd.2xtabs
##           censor
## cellcode   survival dead
##   squamous        4   31
##   small           3   45
##   adeno           1   26
##   large           1   26
class(dd.2xtabs)
## [1] "xtabs" "table"
## three-way table()
## table()
dd.3tab = table(dd$treat, dd$censor, dd$cellcode)
dd.3tab
## , ,  = squamous
##
##
##           survival dead
##   placebo        2   13
##   test           2   18
##
## , ,  = small
##
##
##           survival dead
##   placebo        2   28
##   test           1   17
```

```
##
## , ,  = adeno
##
##
##              survival dead
##   placebo        0    9
##   test           1   17
##
## , ,  = large
##
##
##              survival dead
##   placebo        1   14
##   test           0   12
## xtabs()
dd.3xtabs = xtabs(~ treat + censor + cellcode, data = dd)
dd.3xtabs
## , , cellcode = squamous
##
##             censor
## treat        survival dead
##   placebo           2   13
##   test              2   18
##
## , , cellcode = small
##
##             censor
## treat        survival dead
##   placebo           2   28
##   test              1   17
##
## , , cellcode = adeno
##
##             censor
## treat        survival dead
##   placebo           0    9
##   test              1   17
##
## , , cellcode = large
##
##             censor
## treat        survival dead
##   placebo           1   14
##   test              0   12
```

7.2.2 : ftable()

`table()` `xtabs()` list , , `ftable()`, , , , (**flat contingency table**), `ftalbe` (class) , (, column) , , (row) (level). `ftable()` `ftable` , {R} , `table()` `xtabs()` `_contingency table_` .

```
## three-way table()
## ftable()
dd.3ftab = ftable(dd$cellcode, dd$treat, dd$censor)
dd.3ftab
##                    survival dead
##
## squamous placebo          2   13
##          test             2   18
## small    placebo          2   28
##          test             1   17
## adeno    placebo          0    9
##          test             1   17
## large    placebo          1   14
##          test             0   12
```

7.2.3 : margin.table(), prop.table()

`margin.table()` (class) `table` , (array, matrix) (**marginal total**). `prop.table()` (array, matrix) , (**relative frequency**). `addmargins()` .

`margin.table()` `prop.table()` (class) `ftable` . `addmargins()` (class) `table` `ftable` .

```
margin.table(x, margin = NULL)
prop.table(x, margin = NULL)
addmargins(A, margin, ...)
```

- `x`: `table` .
- `A`: `table` `ftable` .
- `margin`: (index/vector), .
    - `margin = NULL`: (cell count/proportion).
    - `margin = 1`: (row) (row marginal total/proportion).
- `margin = 2`: (column) (column marginal total/proportion).
- `margin = k`: .

```
## one-way table
## table()
dd.1tab = table(dd$cellcode)
dd.1tab
```

```
##
## squamous    small    adeno    large
##       35       48       27       27
margin.table(dd.1tab)
## [1] 137
prop.table(dd.1tab)
##
## squamous    small    adeno    large
##   0.2555   0.3504   0.1971   0.1971
## xtabs()
dd.1xtabs = xtabs(~ censor, data = dd)
margin.table(dd.1xtabs)
## [1] 137
prop.table(dd.1xtabs)
## censor
## survival     dead
##  0.06569  0.93431
## two-way table()
## table()
dd.2tab = table(dd$cellcode, dd$censor)
dd.2tab
##
##            survival dead
##   squamous        4   31
##   small           3   45
##   adeno           1   26
##   large           1   26
## cell count total and proportion
margin.table(dd.2tab)
## [1] 137
prop.table(dd.2tab)
##
##            survival     dead
##   squamous 0.029197 0.226277
##   small    0.021898 0.328467
##   adeno    0.007299 0.189781
##   large    0.007299 0.189781
## condition on row
margin.table(dd.2tab, margin = 1)
##
## squamous    small    adeno    large
##       35       48       27       27
prop.table(dd.2tab, margin = 1)
##
##            survival    dead
##   squamous  0.11429 0.88571
##   small     0.06250 0.93750
##   adeno     0.03704 0.96296
##   large     0.03704 0.96296
## condition on column
margin.table(dd.2tab, margin = 2)
##
## survival     dead
##        9      128
prop.table(dd.2tab, margin = 2)
##
##             survival   dead
##   squamous   0.4444 0.2422
##   small      0.3333 0.3516
##   adeno      0.1111 0.2031
##   large      0.1111 0.2031
## xtabs()
dd.2xtabs = xtabs(~ cellcode + censor, data = dd)
dd.2xtabs
##            censor
## cellcode   survival dead
##   squamous        4   31
##   small           3   45
##   adeno           1   26
##   large           1   26
## cell count total and proportion
margin.table(dd.2xtabs)
## [1] 137
prop.table(dd.2xtabs)
##            censor
## cellcode   survival     dead
##   squamous 0.029197 0.226277
##   small    0.021898 0.328467
##   adeno    0.007299 0.189781
##   large    0.007299 0.189781
## condition on row
margin.table(dd.2xtabs, margin = 1)
## cellcode
## squamous    small    adeno    large
##       35       48       27       27
prop.table(dd.2xtabs, margin = 1)
##            censor
## cellcode   survival    dead
##   squamous  0.11429 0.88571
##   small     0.06250 0.93750
##   adeno     0.03704 0.96296
##   large     0.03704 0.96296
## condition on column
margin.table(dd.2xtabs, margin = 2)
## censor
## survival     dead
##        9      128
prop.table(dd.2xtabs, margin = 2)
##           censor
## cellcode   survival   dead
##   squamous   0.4444 0.2422
##   small      0.3333 0.3516
##   adeno      0.1111 0.2031
##   large      0.1111 0.2031
```

7.3

{R} \ref{tab:RDistFun**, X (random variable), .

$$f = f(X = x) = \qquad F(x) = \int f(x)dx =$$

$$\begin{aligned}
p &= F(q) = P(X \leq q) = \qquad \text{, cumulative distribution function}\\
q &= Q(u) = F^{-1}(p) = \quad \text{, quantile function,} \quad p \leq P(X \leq q)\\
d &= f(x) = F'(x) = P(X = x) = \qquad \text{, probability density function}\\
r &= R(r) = f^{-1}(x) = \quad \text{, random number,}
\end{aligned}$$

{R} , (probability function), , `ProbFun`, , `ProbFun`, , 4 , `p`, `q`, `d`, `r`, . , `fProbFun`, , . (non-centrality parameter), `ncp` , `ptukey()` `qtukey()` Studentized Range Distribution.

Table 7.3:

	{R} (ProbFun)	
beta	`beta`	shape1, shape2, ncp
binomial	`binom`	size, prob
Cauchy	`cauchy`	location, scale
chi-squared	`chisq`	df, ncp
exponential	`exp`	rate
F	`f`	df1, df1, ncp
gamma	`gamma`	shape, scale
geometric	`geom`	prob
hypergeometric	`hyper`	m, n, k
log-normal	`lnorm`	meanlog, sdlog

	{R} (ProbFun)	
logistic	logis	location, scale
negative binomial		nbinom
normal	norm	mean, sd
Poisson	pois	lambda
Student's	t	t df, ncp
uniform	unif	min, max
Weibull	weibull	shape, scale
Wilcoxon	wilcox	m, n

- `p` (**cumulative distribution function, CDF**).
- `q` (**quantile**), $u \le P(X <= x)$ x.
- `d` (**probability density function, pdf**).
- `r` , (**pseudo-random number generation function**, **random number**).
- `dProbFun` x.
- `pProbFun` q.
- `qProbFun` p.
- `rProbFun` n, .
- `pProbFun` `qProbFun` `lower.tail**` log.p‘.
  - `lower.tail = TRUE` (default), $P(X <= x)$.
  - `lower.tail = FALSE` $P(X > x)$.
  - `log.p = TRUE`, p `log(p)` .
- `dProbFun` `log`, .

```
# normal distribution
pnorm(1.96)
## [1] 0.975
qnorm(0.975)
## [1] 1.96
dnorm(1.96)
## [1] 0.05844
# Poisson distribution
rpois(10, 1)
##  [1] 0 0 0 1 1 2 1 1 4 1
rpois(10, 2)
##  [1] 3 4 1 2 0 1 1 0 1 4
rpois(10, 20)
##  [1] 18 21 16 23 22 24 23 20 11 22
## Cumulative distribution
## Pr(x <= 2)
ppois(2, 2)
## [1] 0.6767
ppois(4, 2)
## [1] 0.9473
```

```
ppois(6, 2)
## [1] 0.9955
# t distribution
qt(0.995, df = 2)
## [1] 9.925
2*pt(-1.96, df = 2)
## [1] 0.1891
2*pt(-1.96, df = 30)
## [1] 0.05934
# upper 1% point for an F(1, 2) distribution
sqrt(qf(0.99, 1, 2))
## [1] 9.925
```

, , {R} , , (current time), (**seed**) ,
(uniform random number), {R}, , , , ,
`set.seed()`, , .

```
## generate random number
## set.seed(): set initial value
## Caution use set.seed() everytime!
## uniform
runif(5)
## [1] 0.86121 0.43810 0.24480 0.07068 0.09947
runif(5)
## [1] 0.3163 0.5186 0.6620 0.4068 0.9129
set.seed(10)
runif(5)
## [1] 0.50748 0.30677 0.42691 0.69310 0.08514
set.seed(10)
runif(5)
## [1] 0.50748 0.30677 0.42691 0.69310 0.08514
# norm
rnorm(5)
## [1] -0.7540 -0.6059 -0.1772  0.1706  0.2428
rnorm(5)
## [1] -0.1794 -0.6305  0.9787  0.2933 -0.3703
set.seed(10)
rnorm(5)
## [1]  0.01875 -0.18425 -1.37133 -0.59917  0.29455
set.seed(10)
rnorm(5)
## [1]  0.01875 -0.18425 -1.37133 -0.59917  0.29455
##  normal + uniform
set.seed(10)
runif(5)
## [1] 0.50748 0.30677 0.42691 0.69310 0.08514
```

```
rnorm(5)
## [1] -0.7540 -0.6059 -0.1772  0.1706  0.2428
set.seed(10)
runif(5)
## [1] 0.50748 0.30677 0.42691 0.69310 0.08514
rnorm(5)
## [1] -0.7540 -0.6059 -0.1772  0.1706  0.2428
set.seed(10)
rnorm(5)
## [1]  0.01875 -0.18425 -1.37133 -0.59917  0.29455
runif(5)
## [1] 0.6517 0.5677 0.1135 0.5959 0.3580
```

7.4 sample()

{R} , `sample()`, . , (**seed**).

```
sample(x, size, replace = FALSE, prob = NULL)
```

- `x` 1 , .
- `size = k` .
- `prob` ,
  — , .
- `replace = FALSE` , .

```
## random sampling
letters
##  [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q" "r" "s"
## [20] "t" "u" "v" "w" "x" "y" "z"
sample(letters, 5)
## [1] "g" "j" "b" "m" "h"
sample(letters, 5)
## [1] "n" "g" "f" "y" "v"
set.seed(1)
sample(letters, 5)
## [1] "y" "d" "g" "a" "b"
sample(letters, 5)
## [1] "w" "k" "n" "r" "s"
set.seed(1)
sample(letters, 5)
## [1] "y" "d" "g" "a" "b"
sample(letters, 5)
## [1] "w" "k" "n" "r" "s"
## sampling 5 subjects from 10 subjects
## without or with replacement
set.seed(1)
```

```
x <- 1:10
sample(x, size = 5, replace = FALSE) # (a) no resampling
## [1] 9 4 7 1 2
sample(x, size = 5, replace = TRUE)  # (b) resampling
## [1] 7 2 3 1 5
# permutation
set.seed(1)
x <- 1:10
sample(x, size = 10, replace = FALSE) # no resampling
##  [1]  9  4  7  1  2  5  3 10  6  8
# equal probability
set.seed(1)
x <- 1:10
sample(x, size = 5, replace = FALSE, prob = c(1:10))
## [1]  9  8  6  2 10
sample(x, size = 5, replace = FALSE, prob = c(rep(1, 10) / 10.0))
## [1] 10  1  7  6  2
# unequal rpobability
set.seed(1)
x <- 1:10
(prob.rs = c(seq(1, 10) / sum(seq(1, 10))))
##  [1] 0.01818 0.03636 0.05455 0.07273 0.09091 0.10909 0.12727 0.14545 0.16364
## [10] 0.18182
sum(prob.rs)
## [1] 1
sample(x, size = 5, replace = TRUE,  prob = seq(1, 10))
## [1] 9 8 7 3 9
```

, , sample(), , . , (**seed**).

```
## clinical trials or experiments
## randomization
## random assign to two groups, total 20 subjects
## random assigning treatment groups
## 20 Bernoulli trials
set.seed(1)
sample(c(0, 1), size = 20, replace = TRUE)
##  [1] 0 1 0 0 1 0 0 0 1 1 0 0 0 0 0 1 1 1 1 0
sample(2, size = 20, replace = TRUE)
##  [1] 1 1 1 1 1 1 2 1 1 2 2 2 1 2 1 1 2 1 2 2
# random choose 10 subjects to group 1
set.seed(1)
sample(20, size = 10, replace = FALSE)
##  [1]  4  7  1  2 13 19 11 17 14  3
# block randomization
# total 5 blocks, block size 4, choose 2 subjects to group 1
```

```r
set.seed(1)
replicate(5, sample(c(1:4), size = 2, replace = FALSE))
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    1    1    3    2
## [2,]    3    2    3    2    3
```

Chapter 8

tidyverse , .

- tidyverse
  - `ggplot2` .
  - `purrr` .
  - `tibble` .
  - `dplyr` .
  - `tidyr` ,
  - `stringr` .
  - `readr` .
  - ‘forcats (factors).

- import
  - `readxl` excel .

  - `haven` SPSS, Stata SAS .
  - `jsonlite` JSON .
  - `xml2` XML .
  - `httr` web APIs .
  - `rvest` web scraping .
- DBI , `RSQLite`, `RPostgres` `odbc`.
- tidy/wrangle
  - `stringr` .
  - `lubridate` .
  - `forcats` (factors).
  - `hms` .
  - `blob` .
- program
  - `rlang` tidyverse.

  - magrittr %>%.
  - glue .
- model
  - broom .
  - modelr .

8.1 readr

tidyverse readr . read_csv() .csv , read_excel excel , read_delim() . (help(read_delim)).

- file =
- delim =
- quote = ( )
- escape_backslash = FALSE,
- escape_double = TRUE,
- col_names = (T F)
- col_types =
- na = NA
- comment = ,
- trim_ws =
- skip = (row)
- n_max =

```
# .csv
library(tidyverse)
library(readr)
dd <- readr::read_csv("C:/RData/DMTKAInfMo.csv")
print(dd, n = 5, width = Inf)
## # A tibble: 78 x 16
##      No   age   sex    DM  DMyr preAC prePC postAC postPC medication  SIDE PREKS
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>  <dbl>      <dbl> <dbl> <dbl>
## 1     1    67     0     0    10   120   160    140    180          0     0    56
## 2     2    67     0     0    11   100   150    150    220          0     1    62
## 3     3    72     1     0     4   150   200    120    150          2     0    60
## 4     4    82     1     0     8   150   200    160    250          0     1    47
## 5     5    73     1     0     3    85   110    140    200          0     0    44
##   POSKS   ABS INFECT INFMO
##   <dbl> <dbl>  <dbl> <dbl>
## 1    92     1      0     0
## 2    62     0      1     2
## 3    94     1      0     0
## 4    90     1      0     0
## 5    88     0      0     0
## # ... with 73 more rows
# .xls
```

```
library(readxl)
dd <- readxl::read_excel("C:/RData/DMTKAInfMo.xls")
print(dd, n = 5, width = Inf)
## # A tibble: 78 x 16
##      No   age   sex    DM  DMyr preAC prePC postAC postPC medication  SIDE PREKS
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>  <dbl>      <dbl> <dbl> <dbl>
## 1     1    67     0     0    10   120   160    140    180          0     0    56
## 2     2    67     0     0    11   100   150    150    220          0     1    62
## 3     3    72     1     0     4   150   200    120    150          2     0    60
## 4     4    82     1     0     8   150   200    160    250          0     1    47
## 5     5    73     1     0     3    85   110    140    200          0     0    44
##   POSKS   ABS INFECT IOFECTMO
##   <dbl> <dbl>  <dbl>    <dbl>
## 1    92     1      0        0
## 2    62     0      1        2
## 3    94     1      0        0
## 4    90     1      0        0
## 5    88     0      0        0
## # ... with 73 more rows
```

8.2 Tidy Data

, , {R} (**data frame**). SAS, STATA dataset . , (**cross table**), (** data table**). **tidverse** **tidy‘** ** (**tidy data**) . 1 (, row), (, row) . , , . , , . .

-
- (EXCEL sheet).
- (, Column) , .
- , (inxex) (id) .

. , EXCEL sheel , . , / . **DMTKAORI.xls**. , , .

8.3 Pipe

8.4

{R} , , . , , , , , , , . , .

Bibliography

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