Note for R Lec 4-5

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1 R 语言

首先，我们先介绍一个新的传递数据的方法：**Pipe operator**

1.1 Pipe operator

A key package: **tidyverse**

Suppose that we want to find the following summation:

$$\sqrt{\sum_{i=-10}^{10} |i|}.$$

Base-R, we can:

```
sqrt(sum(abs(-10:10)))
```

```
## [1] 10.48809
```

We can use pipe operator to deal with multiple functions like this:

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
## v ggplot2 3.3.6      v purrr   0.3.4
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.2      v forcats 0.5.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
-10:10 %>%
  abs() %>%
  sum() %>%
  sqrt()
```

```
## [1] 10.48809
```

More logical!

When you have multiple arguments in a function:

```
matrix(1:10, nrow = 2, byrow = TRUE)
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    2    3    4    5
## [2,]    6    7    8    9   10
```

```
1:10 %>%
matrix(nrow = 2, byrow = TRUE)
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    2    3    4    5
## [2,]    6    7    8    9   10
```

1.2 基本数据管理

```
library(tidyverse)
library(palmerpenguins)
```

1.2.1 mutate()

我们想再创建一个新的变量:

```
df <- penguins
attach(df)
df$bill_sum <- bill_length_mm + bill_depth_mm
detach(df)
```

在 tidyverse 包下，可以使用 mutate() 函数：

```
library(tidyverse)
mutate(.data = df, bill_sum = bill_length_mm + bill_depth_mm)
```

```
## # A tibble: 344 x 9
##   species island    bill_length_mm bill_d~1 flipp~2 body_~3 sex    year bill_~4
##   <fct>   <fct>              <dbl>    <dbl>   <int>   <int> <fct> <int>   <dbl>
## 1 Adelie  Torgersen           39.1     18.7     181    3750 male   2007    57.8
## 2 Adelie  Torgersen           39.5     17.4     186    3800 fema~  2007    56.9
## 3 Adelie  Torgersen           40.3     18       195    3250 fema~  2007    58.3
##  4 Adelie  Torgersen           NA       NA        NA      NA <NA>   2007    NA
##  5 Adelie  Torgersen           36.7     19.3     193    3450 fema~  2007    56
##  6 Adelie  Torgersen           39.3     20.6     190    3650 male   2007    59.9
##  7 Adelie  Torgersen           38.9     17.8     181    3625 fema~  2007    56.7
##  8 Adelie  Torgersen           39.2     19.6     195    4675 male   2007    58.8
##  9 Adelie  Torgersen           34.1     18.1     193    3475 <NA>   2007    52.2
## 10 Adelie  Torgersen           42       20.2     190    4250 <NA>   2007    62.2
## # ... with 334 more rows, and abbreviated variable names 1: bill_depth_mm,
## #   2: flipper_length_mm, 3: body_mass_g, 4: bill_sum
```

```
## or,
mutate(df, bill_sum = bill_length_mm + bill_depth_mm)
```

```
## # A tibble: 344 x 9
##    species island    bill_length_mm bill_d~1 flipp~2 body_~3 sex    year bill_~4
##    <fct>   <fct>              <dbl>    <dbl>   <int>   <int> <fct> <int>   <dbl>
##  1 Adelie  Torgersen           39.1     18.7     181    3750 male   2007    57.8
##  2 Adelie  Torgersen           39.5     17.4     186    3800 fema~  2007    56.9
##  3 Adelie  Torgersen           40.3     18       195    3250 fema~  2007    58.3
##  4 Adelie  Torgersen           NA       NA        NA      NA <NA>   2007    NA
##  5 Adelie  Torgersen           36.7     19.3     193    3450 fema~  2007    56
##  6 Adelie  Torgersen           39.3     20.6     190    3650 male   2007    59.9
##  7 Adelie  Torgersen           38.9     17.8     181    3625 fema~  2007    56.7
##  8 Adelie  Torgersen           39.2     19.6     195    4675 male   2007    58.8
##  9 Adelie  Torgersen           34.1     18.1     193    3475 <NA>   2007    52.2
## 10 Adelie  Torgersen           42       20.2     190    4250 <NA>   2007    62.2
## # ... with 334 more rows, and abbreviated variable names 1: bill_depth_mm,
## #   2: flipper_length_mm, 3: body_mass_g, 4: bill_sum
```

```
## or, using pipe operator:
df %>%
mutate(bill_sum = bill_length_mm + bill_depth_mm)
```

```
## # A tibble: 344 x 9
##    species island    bill_length_mm bill_d~1 flipp~2 body_~3 sex    year bill_~4
##    <fct>   <fct>              <dbl>    <dbl>   <int>   <int> <fct> <int>   <dbl>
##  1 Adelie  Torgersen           39.1     18.7     181    3750 male   2007    57.8
##  2 Adelie  Torgersen           39.5     17.4     186    3800 fema~  2007    56.9
##  3 Adelie  Torgersen           40.3     18       195    3250 fema~  2007    58.3
##  4 Adelie  Torgersen           NA       NA        NA      NA <NA>   2007    NA
##  5 Adelie  Torgersen           36.7     19.3     193    3450 fema~  2007    56
##  6 Adelie  Torgersen           39.3     20.6     190    3650 male   2007    59.9
##  7 Adelie  Torgersen           38.9     17.8     181    3625 fema~  2007    56.7
##  8 Adelie  Torgersen           39.2     19.6     195    4675 male   2007    58.8
##  9 Adelie  Torgersen           34.1     18.1     193    3475 <NA>   2007    52.2
## 10 Adelie  Torgersen           42       20.2     190    4250 <NA>   2007    62.2
## # ... with 334 more rows, and abbreviated variable names 1: bill_depth_mm,
## #   2: flipper_length_mm, 3: body_mass_g, 4: bill_sum
```

1.2.2 选取列 select()

```
df <- penguins # 初始化 df 变量
df %>% select(bill_length_mm, bill_depth_mm)
```

1.2.2.1 按名称选取

```
## # A tibble: 344 x 2
##    bill_length_mm bill_depth_mm
##             <dbl>         <dbl>
##  1           39.1          18.7
##  2           39.5          17.4
##  3           40.3          18
##  4           NA            NA
##  5           36.7          19.3
##  6           39.3          20.6
##  7           38.9          17.8
##  8           39.2          19.6
##  9           34.1          18.1
## 10           42            20.2
## # ... with 334 more rows
```

```
df %>% select(-bill_length_mm, -bill_depth_mm) # 按名称删除不需要的列
```

```
## # A tibble: 344 x 6
##    species island    flipper_length_mm body_mass_g sex     year
##    <fct>   <fct>                 <int>       <int> <fct>  <int>
##  1 Adelie  Torgersen               181        3750 male    2007
##  2 Adelie  Torgersen               186        3800 female  2007
##  3 Adelie  Torgersen               195        3250 female  2007
##  4 Adelie  Torgersen                NA          NA <NA>    2007
##  5 Adelie  Torgersen               193        3450 female  2007
##  6 Adelie  Torgersen               190        3650 male    2007
##  7 Adelie  Torgersen               181        3625 female  2007
##  8 Adelie  Torgersen               195        4675 male    2007
##  9 Adelie  Torgersen               193        3475 <NA>    2007
## 10 Adelie  Torgersen               190        4250 <NA>    2007
## # ... with 334 more rows
```

名称选取

如果选取的列很多，我们也可以先观察其命名特征，用特定的函数进行选取。比如，在企

数据集中，类型为 double 的变量名都是以bill开始的，所以我们就可以

```
df %>% select(starts_with("bill"))
```

其他选择函数：

函数	作用
starts_with()	以某前缀开头
ends_with()	以某后缀结尾
contains()	包含某字符或字符串
matches()	匹配正则表达式
num_range()	匹配某数值范围

1.2.2.2 按名称所含字符选取

#### 按数值类型选取

```
df %>% select(where(is.numeric))
```

```
## # A tibble: 344 x 5
##    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g  year
##             <dbl>         <dbl>             <int>       <int> <int>
##  1           39.1          18.7               181        3750  2007
##  2           39.5          17.4               186        3800  2007
##  3           40.3          18                 195        3250  2007
##  4           NA            NA                  NA          NA  2007
##  5           36.7          19.3               193        3450  2007
##  6           39.3          20.6               190        3650  2007
##  7           38.9          17.8               181        3625  2007
##  8           39.2          19.6               195        4675  2007
##  9           34.1          18.1               193        3475  2007
## 10           42            20.2               190        4250  2007
## # ... with 334 more rows
```

```
df %>% select(where(is.double))
```

```
## # A tibble: 344 x 2
##    bill_length_mm bill_depth_mm
##             <dbl>         <dbl>
##  1           39.1          18.7
##  2           39.5          17.4
##  3           40.3          18
##  4           NA            NA
##  5           36.7          19.3
##  6           39.3          20.6
##  7           38.9          17.8
##  8           39.2          19.6
##  9           34.1          18.1
## 10           42            20.2
## # ... with 334 more rows
```

```
## 逻辑并
select(df, 条件一 & 条件二)
## 逻辑或
select(df, 条件一 | 条件二)
## 逻辑非
select(df, !条件一)
```

1.2.2.3 混合选取

1.2.3 修改列名

```
df %>%
rename(Bill.Length = bill_length_mm,
Bill.Depth = bill_depth_mm,
Flipper.Length = flipper_length_mm,
Body.Mass = body_mass_g) # 等号前是新名字，等号后面是老名字
```

```
## # A tibble: 344 x 8
##    species island    Bill.Length Bill.Depth Flipper.Length Body.Mass sex    year
##    <fct>   <fct>           <dbl>      <dbl>          <int>     <int> <fct> <int>
##  1 Adelie  Torgersen        39.1       18.7            181      3750 male   2007
##  2 Adelie  Torgersen        39.5       17.4            186      3800 fema~  2007
##  3 Adelie  Torgersen        40.3       18              195      3250 fema~  2007
##  4 Adelie  Torgersen        NA         NA               NA        NA <NA>   2007
##  5 Adelie  Torgersen        36.7       19.3            193      3450 fema~  2007
##  6 Adelie  Torgersen        39.3       20.6            190      3650 male   2007
##  7 Adelie  Torgersen        38.9       17.8            181      3625 fema~  2007
##  8 Adelie  Torgersen        39.2       19.6            195      4675 male   2007
##  9 Adelie  Torgersen        34.1       18.1            193      3475 <NA>   2007
## 10 Adelie  Torgersen        42         20.2            190      4250 <NA>   2007
## # ... with 334 more rows
```

1.2.4 按行选取 filter()

比如，我们想要选择 species 为"Adelie" 的这些样本点：

```
df %>% filter(species == "Adelie")
```

```
## # A tibble: 152 x 8
##    species island    bill_length_mm bill_depth_mm flipper_~1 body_~2 sex    year
##    <fct>   <fct>              <dbl>         <dbl>      <int>   <int> <fct> <int>
##  1 Adelie  Torgersen           39.1          18.7        181    3750 male   2007
##  2 Adelie  Torgersen           39.5          17.4        186    3800 fema~  2007
##  3 Adelie  Torgersen           40.3          18          195    3250 fema~  2007
##  4 Adelie  Torgersen           NA            NA           NA      NA <NA>   2007
##  5 Adelie  Torgersen           36.7          19.3        193    3450 fema~  2007
##  6 Adelie  Torgersen           39.3          20.6        190    3650 male   2007
##  7 Adelie  Torgersen           38.9          17.8        181    3625 fema~  2007
##  8 Adelie  Torgersen           39.2          19.6        195    4675 male   2007
##  9 Adelie  Torgersen           34.1          18.1        193    3475 <NA>   2007
## 10 Adelie  Torgersen           42            20.2        190    4250 <NA>   2007
## # ... with 142 more rows, and abbreviated variable names 1: flipper_length_mm,
## #   2: body_mass_g
```

进一步再选取 bill_length_mm 大于 40 的：

```
df %>% filter(species == "Adelie",
bill_length_mm > 40)
```

```
## # A tibble: 51 x 8
##    species island    bill_length_mm bill_depth_mm flipper_~1 body_~2 sex    year
##    <fct>   <fct>              <dbl>         <dbl>      <int>   <int> <fct> <int>
##  1 Adelie  Torgersen           40.3          18          195    3250 fema~  2007
##  2 Adelie  Torgersen           42            20.2        190    4250 <NA>   2007
##  3 Adelie  Torgersen           41.1          17.6        182    3200 fema~  2007
##  4 Adelie  Torgersen           42.5          20.7        197    4500 male   2007
##  5 Adelie  Torgersen           46            21.5        194    4200 male   2007
##  6 Adelie  Biscoe              40.6          18.6        183    3550 male   2007
##  7 Adelie  Biscoe              40.5          17.9        187    3200 fema~  2007
##  8 Adelie  Biscoe              40.5          18.9        180    3950 male   2007
##  9 Adelie  Dream               40.9          18.9        184    3900 male   2007
## 10 Adelie  Dream               42.2          18.5        180    3550 fema~  2007
## # ... with 41 more rows, and abbreviated variable names 1: flipper_length_mm,
## #   2: body_mass_g
```

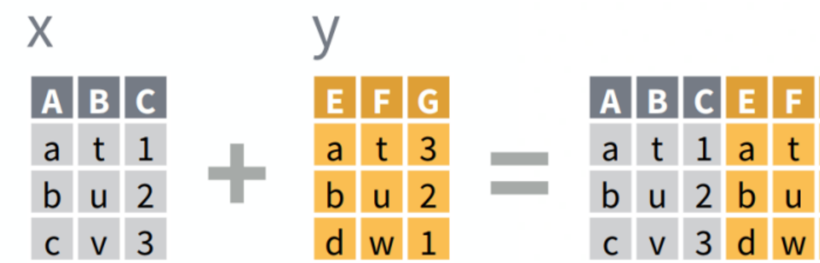
1.2.5 排序 arrange()

arrange(df, variable)（升序），或者 arrange(df, -variable)（降序）。

也可以对多个变量依次排序。比如先对变量一排序，再对变量二排序，其公式为：

```
arrange(df, var1, var2)
```

1.2.6 合并数据



x

A	B	C
a	t	1
b	u	2
c	v	3

y

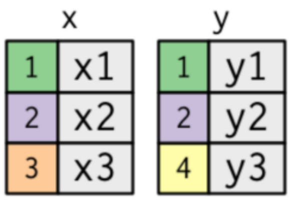
E	F	G
a	t	3
b	u	2
d	w	1

A	B	C	E	F
a	t	1	a	t
b	u	2	b	u
c	v	3	d	w

1.2.6.1 bind_cols(df1,df2,...)

1.2.6.2 连接数据 _join() 函数族

左联结 left_join():

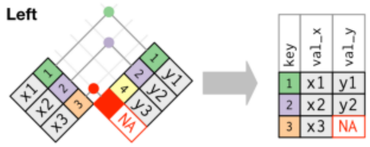


x

1	x1
2	x2
3	x3

y

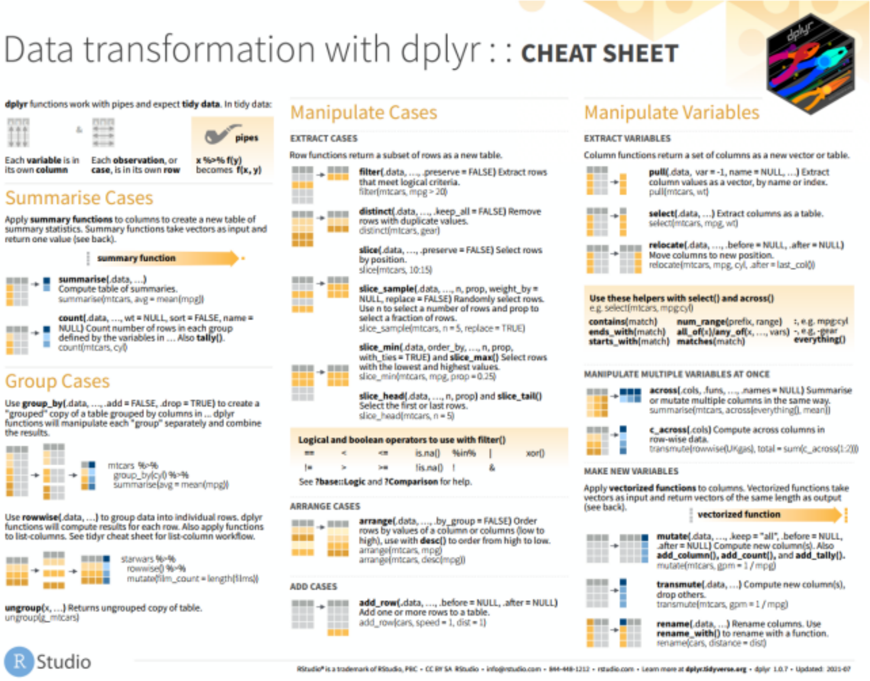
1	y1
2	y2
4	y3



key	val_x	val_y
1	x1	y1
2	x2	y2
3	x3	NA

还有右联结 right_join(), inner_join 和 full_join 等。

其他的数据处理函数



Data transformation with dplyr : : CHEAT SHEET

dplyr functions work with pipes and expect **tidy data**. In tidy data:

Each **variable** is in its own **column** & Each **observation**, or **case**, is in its own **row**

pipes **x %>% f(y)** becomes **f(x, y)**

Summarise Cases

Apply **summary functions** to columns to create a new table of summary statistics. Summary functions take vectors as input and return one value (see back).

summarise(.data, ...)
Compute table of summaries.
summarise(mtcars, avg = mean(mpg))

count(.data, ..., wt = NULL, sort = FALSE, name = NULL) Count number of rows in each group defined by the variables in ... Also **tally**().
count(mtcars, cyl)

Group Cases

Use **group_by**(.data, ..., .add = FALSE, .drop = TRUE) to create a "grouped" copy of a table grouped by columns in ... dplyr functions will manipulate each "group" separately and combine the results.

```
mtcars %>%
  group_by(cyl) %>%
  summarise(avg = mean(mpg))
```

Use **rowwise**(.data, ...) to group data into individual rows. dplyr functions will compute results for each row. Also apply functions to list-columns. See tidyr cheat sheet for list-column workflow.

```
starwars %>%
  rowwise() %>%
  mutate(film_count = length(films))
```

ungroup(x, ...) Returns ungrouped copy of table.
ungroup(g_mtcars)

Manipulate Cases

EXTRACT CASES

Row functions return a subset of rows as a new table.

filter(.data, ..., .preserve = FALSE) Extract rows that meet logical criteria.
filter(mtcars, mpg > 20)

distinct(.data, ..., .keep_all = FALSE) Remove rows with duplicate values.
distinct(mtcars, gear)

slice(.data, ..., .preserve = FALSE) Select rows by position.
slice(mtcars, 10:15)

slice_sample(.data, ..., n, prop, weight_by = NULL, replace = FALSE) Randomly select rows. Use n to select a number of rows and prop to select a fraction of rows.
slice_sample(mtcars, n = 5, replace = TRUE)

slice_min(.data, order_by, ..., n, prop, with_ties = TRUE) and **slice_max**() Select rows with the lowest and highest values.
slice_min(mtcars, mpg, prop = 0.25)

slice_head(.data, ..., n, prop) and **slice_tail**() Select the first or last rows.
slice_head(mtcars, n = 5)

Logical and boolean operators to use with filter()

```
==   <   <=   is.na()    %in%   |   xor()
!=   >   >=   !is.na()   !      &
```

See **?base::Logic** and **?Comparison** for help.

ARRANGE CASES

arrange(.data, ..., .by_group = FALSE) Order rows by values of a column or columns (low to high), use with **desc**() to order from high to low.
arrange(mtcars, mpg)
arrange(mtcars, desc(mpg))

ADD CASES

add_row(.data, ..., .before = NULL, .after = NULL) Add one or more rows to a table.
add_row(cars, speed = 1, dist = 1)

Manipulate Variables

EXTRACT VARIABLES

Column functions return a set of columns as a new vector or table.

pull(.data, var = -1, name = NULL, ...) Extract column values as a vector, by name or index.
pull(mtcars, wt)

select(.data, ...) Extract columns as a table.
select(mtcars, mpg, wt)

relocate(.data, ..., .before = NULL, .after = NULL) Move columns to new position.
relocate(mtcars, mpg, cyl, .after = last_col())

Use these helpers with select() and across()
e.g. select(mtcars, mpg:cyl)

```
contains(match)      num_range(prefix, range)      :, e.g. mpg:cyl
ends_with(match)     all_of(x)/any_of(x, ..., vars) -, e.g. -gear
starts_with(match)   matches(match)                everything()
```

MANIPULATE MULTIPLE VARIABLES AT ONCE

across(.cols, .funs, ..., .names = NULL) Summarise or mutate multiple columns in the same way.
summarise(mtcars, across(everything(), mean))

c_across(.cols) Compute across columns in row-wise data.
transmute(rowwise(UKgas), total = sum(c_across(1:2)))

MAKE NEW VARIABLES

Apply **vectorized functions** to columns. Vectorized functions take vectors as input and return vectors of the same length as output (see back).

mutate(.data, ..., .keep = "all", .before = NULL, .after = NULL) Compute new column(s). Also **add_column(), add_count()**, and **add_tally()**.
mutate(mtcars, gpm = 1 / mpg)

transmute(.data, ...) Compute new column(s), drop others.
transmute(mtcars, gpm = 1 / mpg)

rename(.data, ...) Rename columns. Use **rename_with**() to rename with a function.
rename(cars, distance = dist)

RStudio

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1.2.7 缺失值

- 运算中的数据一旦出现了NA，结果就会出现问题：

```
c(1, 2, 3, NA) %>% sum()
```

```
## [1] NA
```

- 在运算的时候，可以强制忽略缺失值：

```
c(1, 2, 3, NA) %>% sum(na.rm = TRUE)
```

```
## [1] 6
```

- 很多函数都有na.rm这个选项，如mean()，var()等。

We can also do something to the origianl data to delete the NA value:

```
mean(penguins$body_mass_g)
```

```
## [1] NA
```

```
penguins1 <- penguins[complete.cases(penguins),]
mean(penguins1$body_mass_g)
```

```
## [1] 4207.057
```

1.2.8 数据规整

若我们有一组植物的高度数据

```
plant_height <- data.frame(
Day = 1:5,
A = c(0.7, 1.0, 1.5, 1.8, 2.2),
B = c(0.5, 0.7, 0.9, 1.3, 1.8),
C = c(0.3, 0.6, 1.0, 1.2, 2.2),
D = c(0.4, 0.7, 1.2, 1.5, 3.2)
)
```

此时的数据形如：

```
plant_height
```

```
##   Day   A   B   C   D
## 1   1 0.7 0.5 0.3 0.4
## 2   2 1.0 0.7 0.6 0.7
## 3   3 1.5 0.9 1.0 1.2
## 4   4 1.8 1.3 1.2 1.5
## 5   5 2.2 1.8 2.2 3.2
```

若我们想将其转化为：

```
## # A tibble: 20 x 3
##      Day plant height
##    <int> <chr>  <dbl>
##  1     1 A        0.7
##  2     1 B        0.5
##  3     1 C        0.3
##  4     1 D        0.4
##  5     2 A        1
##  6     2 B        0.7
##  7     2 C        0.6
##  8     2 D        0.7
##  9     3 A        1.5
## 10     3 B        0.9
## 11     3 C        1
## 12     3 D        1.2
## 13     4 A        1.8
## 14     4 B        1.3
## 15     4 C        1.2
## 16     4 D        1.5
## 17     5 A        2.2
## 18     5 B        1.8
## 19     5 C        2.2
## 20     5 D        3.2
```

则我们需要 pivot_longer() 来使表格变长：

1.2.8.1 pivot_longer() 上述步骤的代码为：

```
long <- plant_height %>% pivot_longer(cols = A:D,names_to = "plant",values_to = "height
long
```

```
## # A tibble: 20 x 3
##      Day plant height
##    <int> <chr>  <dbl>
##  1     1 A         0.7
##  2     1 B         0.5
##  3     1 C         0.3
##  4     1 D         0.4
##  5     2 A         1
##  6     2 B         0.7
##  7     2 C         0.6
##  8     2 D         0.7
##  9     3 A         1.5
## 10     3 B         0.9
## 11     3 C         1
## 12     3 D         1.2
## 13     4 A         1.8
## 14     4 B         1.3
## 15     4 C         1.2
## 16     4 D         1.5
## 17     5 A         2.2
## 18     5 B         1.8
## 19     5 C         2.2
## 20     5 D         3.2
```

1.2.8.2 pivot_wider()

同样，我们也有使表格变宽的方法：

```
wide <- long %>% pivot_wider(names_from = "plant",
values_from = "height") # names_from= 表示转换后的表格的列的名字来源；values_from= 表示转
wide
```

```
## # A tibble: 5 x 5
##      Day     A     B     C     D
##   <int> <dbl> <dbl> <dbl> <dbl>
## 1     1   0.7   0.5   0.3   0.4
## 2     2   1     0.7   0.6   0.7
## 3     3   1.5   0.9   1     1.2
## 4     4   1.8   1.3   1.2   1.5
## 5     5   2.2   1.8   2.2   3.2
```

复杂一点的例子：

```
plant_record <- data.frame(
day = c(1L, 2L, 3L, 4L, 5L),
A_height = c(1.1, 1.2, 1.3, 1.4, 1.5),
A_width = c(2.1, 2.2, 2.3, 2.4, 2.5),
A_depth = c(3.1, 3.2, 3.3, 3.4, 3.5),
B_height = c(4.1, 4.2, 4.3, 4.4, 4.5),
B_width = c(5.1, 5.2, 5.3, 5.4, 5.5),
B_depth = c(6.1, 6.2, 6.3, 6.4, 6.5),
C_height = c(7.1, 7.2, 7.3, 7.4, 7.5),
C_width = c(8.1, 8.2, 8.3, 8.4, 8.5),
C_depth = c(9.1, 9.2, 9.3, 9.4, 9.5)
)
as_tibble(plant_record)
```

```
## # A tibble: 5 x 10
##     day A_height A_width A_depth B_hei~1 B_width B_depth C_hei~2 C_width C_depth
##   <int>    <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1     1      1.1     2.1     3.1     4.1     5.1     6.1     7.1     8.1     9.1
## 2     2      1.2     2.2     3.2     4.2     5.2     6.2     7.2     8.2     9.2
## 3     3      1.3     2.3     3.3     4.3     5.3     6.3     7.3     8.3     9.3
## 4     4      1.4     2.4     3.4     4.4     5.4     6.4     7.4     8.4     9.4
## 5     5      1.5     2.5     3.5     4.5     5.5     6.5     7.5     8.5     9.5
## # ... with abbreviated variable names 1: B_height, 2: C_height
```

```
plant_record_longer <- plant_record %>%
tidyr::pivot_longer(
cols = !day,
names_to = c("species", ".value"),
names_pattern = "(.*)_(.*)"
)
plant_record_longer %>% slice(1:10)
```

```
## # A tibble: 10 x 5
##      day species height width depth
##    <int> <chr>    <dbl> <dbl> <dbl>
##  1     1 A          1.1   2.1   3.1
##  2     1 B          4.1   5.1   6.1
##  3     1 C          7.1   8.1   9.1
##  4     2 A          1.2   2.2   3.2
##  5     2 B          4.2   5.2   6.2
##  6     2 C          7.2   8.2   9.2
##  7     3 A          1.3   2.3   3.3
##  8     3 B          4.3   5.3   6.3
##  9     3 C          7.3   8.3   9.3
## 10     4 A          1.4   2.4   3.4
```

变回去：

```
plant_record_wider <- plant_record_longer %>%
tidyr::pivot_wider(
names_from = species,
values_from = c(height, width, depth),
names_glue = "{species}_{.value}"
)
plant_record_wider
```

```
## # A tibble: 5 x 10
##     day A_height B_hei~1 C_hei~2 A_width B_width C_width A_depth B_depth C_depth
##   <int>    <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1     1      1.1     4.1     7.1     2.1     5.1     8.1     3.1     6.1     9.1
## 2     2      1.2     4.2     7.2     2.2     5.2     8.2     3.2     6.2     9.2
## 3     3      1.3     4.3     7.3     2.3     5.3     8.3     3.3     6.3     9.3
## 4     4      1.4     4.4     7.4     2.4     5.4     8.4     3.4     6.4     9.4
## 5     5      1.5     4.5     7.5     2.5     5.5     8.5     3.5     6.5     9.5
## # ... with abbreviated variable names 1: B_height, 2: C_height
```

1.3 From data set to a random variables

1.3.1 summary()

- Working with numbers:
  - center: sample mean, sample median, and so on
  - spread: standard deviation, range, quantiles, IQR(Interquartile range), and so on
  - skewness

```
body_mass_g <- penguins$body_mass_g
summary(body_mass_g)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    2700    3550    4050    4202    4750    6300       2
```

Or we can customize our summary output:

```
penguins %>%
  summarize(mean = mean(body_mass_g),
            median = median(body_mass_g),
            sd = sd(body_mass_g),
            IQR = IQR(body_mass_g,na.rm=TRUE))
```

```
## # A tibble: 1 x 4
##    mean median    sd   IQR
##   <dbl>  <int> <dbl> <dbl>
## 1    NA     NA    NA  1200
```

If we want to calculate the mean of one particular *species*, we can use **group_by()** and **summarize**

```
penguins %>%
  group_by(species) %>%
  summarize(n = length(body_mass_g),
            mean = mean(body_mass_g,na.rm = TRUE),
            sd = sd(body_mass_g,na.rm = TRUE))
```

```
## # A tibble: 3 x 4
##   species       n  mean    sd
##   <fct>     <int> <dbl> <dbl>
## 1 Adelie      152 3701.  459.
## 2 Chinstrap    68 3733.  384.
## 3 Gentoo      124 5076.  504.
```

We can add more information like *sex*:

```
penguins[complete.cases(penguins),]%>%  # 去掉所有的 NA
  group_by(species,sex) %>%
  summarize(n = length(body_mass_g),
            mean = mean(body_mass_g,na.rm = TRUE),
            sd = sd(body_mass_g,na.rm = TRUE))
```

```
## `summarise()` has grouped output by 'species'. You can override using the
## `.groups` argument.
```

```
## # A tibble: 6 x 5
## # Groups:   species [3]
##   species   sex        n  mean    sd
##   <fct>     <fct>  <int> <dbl> <dbl>
## 1 Adelie    female    73 3369.  269.
## 2 Adelie    male      73 4043.  347.
## 3 Chinstrap female    34 3527.  285.
## 4 Chinstrap male      34 3939.  362.
## 5 Gentoo    female    58 4680.  282.
## 6 Gentoo    male      61 5485.  313.
```

1.3.2 Probability models

```
(joint_table <- penguins %>%
   xtabs(~species + sex, data = .)) %>% # 管道操作时，传过来的数据做为非第一参数时，必须用
  addmargins()   # 计算 sum
```

1.3.2.1 Joint count:

```
##            sex
## species     female male Sum
##   Adelie        73   73 146
##   Chinstrap     34   34  68
##   Gentoo        58   61 119
##   Sum          165  168 333
```

```
joint_table %>%
  prop.table() %>%
  round(digit = 3) %>% # 保留三位有效数字
  addmargins()
```

1.3.2.2 Joint probability

```
##            sex
## species     female  male   Sum
##   Adelie     0.219 0.219 0.438
##   Chinstrap  0.102 0.102 0.204
##   Gentoo     0.174 0.183 0.357
##   Sum        0.495 0.504 0.999
```

```
library(magrittr)
```

1.3.2.3 Marginal distribution

```
##
## 载入程辑包：'magrittr'

## The following object is masked from 'package:purrr':
##
##     set_names

## The following object is masked from 'package:tidyr':
##
##     extract
```

```
joint_table %>%
margin.table(1) %T>% # 向左传递值到 print()，但下一个%>% 仍然由 margin.table(1) 传递而不是
print() %>%
prop.table()
```

```
## species
##    Adelie Chinstrap    Gentoo
##       146        68       119

## species
##    Adelie Chinstrap    Gentoo
## 0.4384384 0.2042042 0.3573574
```

```
joint_table %>%
margin.table(2) %T>%
print() %>%
prop.table()
```

```
## sex
## female   male
##    165    168
```

```
## sex
##    female      male
## 0.4954955 0.5045045
```

```
joint_table %>% prop.table(margin = 1) # 已知第一个变量 species 求条件分布
```

1.3.2.4 Conditional distribution

```
##            sex
## species       female     male
##   Adelie    0.500000 0.500000
##   Chinstrap 0.500000 0.500000
##   Gentoo    0.487395 0.512605
```

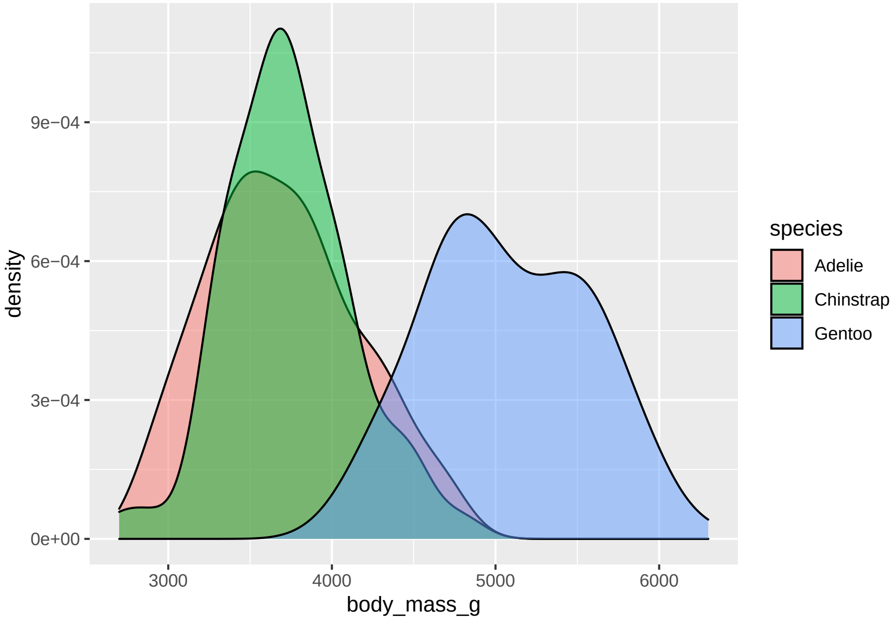
```
joint_table %>% prop.table(margin = 2)
```

```
##            sex
## species        female      male
##   Adelie    0.4424242 0.4345238
##   Chinstrap 0.2060606 0.2023810
##   Gentoo    0.3515152 0.3630952
```

```r
ggplot(data = penguins, aes(x = body_mass_g, y = ..density.., fill = species)) +
  geom_density(color = "black", alpha = 0.5)
```

1.3.2.5 Draw distribute plot

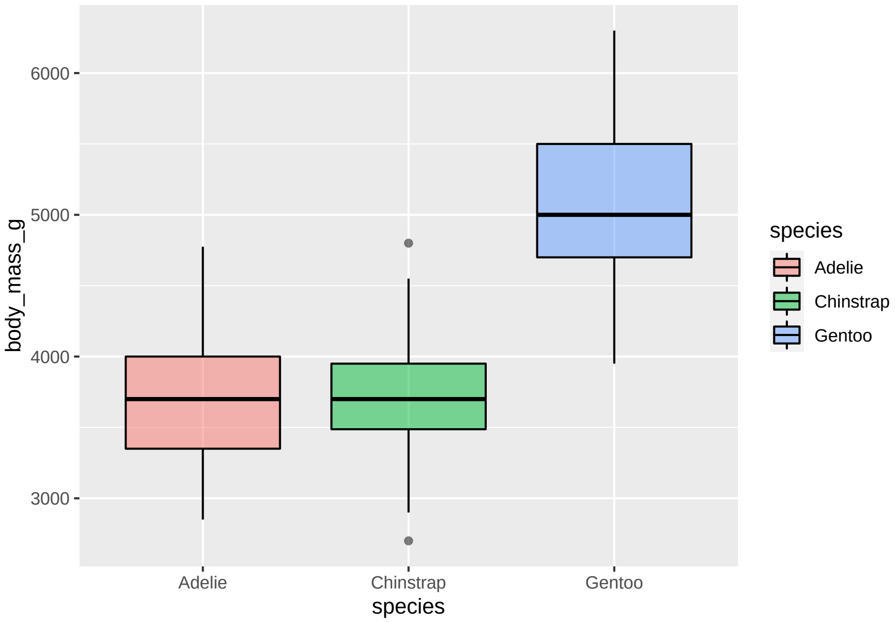
```
## Warning: Removed 2 rows containing non-finite values (stat_density).
```



Sometimes we can also use **boxplot()**

```r
ggplot(data = penguins, aes(x=species, y=body_mass_g, fill=species)) +
  geom_boxplot(color="black", alpha=0.5)
```

```
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```



1.3.2.6 Calculate Sample Mean and Covariance Mean

```
penguins1 %>%
  select(where(is.numeric)) %>%
  colMeans() %>%
  knitr::kable()  # 用表格表示
```

	x
bill_length_mm	43.99279
bill_depth_mm	17.16486
flipper_length_mm	200.96697
body_mass_g	4207.05706
year	2008.04204

Covariance Matrix

```
penguins1 %>%
  select(where(is.numeric)) %>%
  rename(X1 = bill_length_mm,
         X2 = bill_depth_mm,
         X3 = flipper_length_mm,
         X4 = body_mass_g,
         X5 = year) %>%  # 改名防止矩阵名字过长影响美观
  var() %>%
  round(digit = 2) %>%
  knitr:: kable()
```

	X1	X2	X3	X4	X5
X1	29.91	-2.46	50.06	2595.62	0.15
X2	-2.46	3.88	-15.95	-748.46	-0.08
X3	50.06	-15.95	196.44	9852.19	1.72
X4	2595.62	-748.46	9852.19	648372.49	14.31
X5	0.15	-0.08	1.72	14.31	0.66

Correlation Matrix

```
penguins1 %>%
  select(where(is.numeric)) %>%
  rename(X1 = bill_length_mm,
         X2 = bill_depth_mm,
         X3 = flipper_length_mm,
         X4 = body_mass_g,
         X5 = year) %>%  # 改名防止矩阵名字过长影响美观
  cor() %>%
  round(digit = 2) %>%
  knitr:: kable()
```

	X1	X2	X3	X4	X5
X1	1.00	-0.23	0.65	0.59	0.03
X2	-0.23	1.00	-0.58	-0.47	-0.05
X3	0.65	-0.58	1.00	0.87	0.15
X4	0.59	-0.47	0.87	1.00	0.02
X5	0.03	-0.05	0.15	0.02	1.00

1.4 Generate random variables by the build-in functions

1.4.1 Common probability distributions

Letter	Description
d	density
p	probability, distribution function
q	quantile function
r	random generation

For example:

```
dnorm(0)#Normal distribution 的 f(x) 在 x=0 处的值
```

```
## [1] 0.3989423
```

```
pnorm(0)#F(0)
```

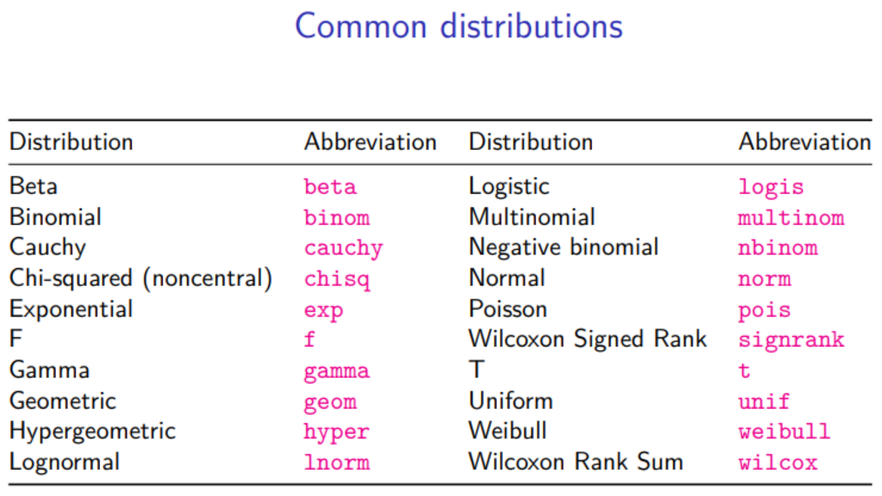
```
## [1] 0.5
```

```
qnorm(0.25)#Normal distribution 的 F(x) 小于等于 0.25 时 x 的值
```

```
## [1] -0.6744898
```

```
rnorm(100) # 生成 n 个服从 Normal distribution 的点
```

```
##   [1]  0.91042246  1.30051615 -0.15632530  1.03827771  0.60078149  0.08197316
##   [7]  0.75716874  0.01572915  0.53504882  0.08197983 -0.61039920 -0.21939325
##  [13]  0.32235670 -0.28615564  0.12074337  0.53893889  0.23477276 -2.79557243
##  [19]  1.70301087 -1.37533719 -2.12701424  1.11752100 -1.32748275  0.13085013
##  [25]  0.54190657 -0.96162230 -0.43122228 -0.45348243  0.58338815  0.32969995
##  [31] -0.13618782 -1.07651517 -0.41933581  0.89875303  1.89589993  2.10347674
##  [37] -1.74895543  1.28243933  1.11763420 -0.58785007  1.41029660  0.23911747
##  [43]  0.30763068 -0.73646567  2.50749014 -0.35787946  0.93203286  1.82171953
##  [49]  0.95598089  0.66374993  0.96202650 -1.19291145  0.12532804 -0.12068604
##  [55]  1.01066323 -1.38276165 -0.45066957 -1.14961735 -0.10016193 -0.10245828
##  [61] -0.16352543  0.71934533  0.88153839  1.68019513 -1.16779894  0.82686081
##  [67]  0.55091111 -0.35137248  0.72399147  0.19662018 -2.48402215  0.49543918
##  [73] -0.42581290  0.13104051 -0.44585107  0.40809023 -0.25318276  0.22665706
##  [79]  0.24347304 -0.39507716  0.03600709  0.08494616  0.53811249  0.02393861
##  [85] -0.91437330 -1.42142677 -0.20410372  0.28641367 -0.50467861  2.18677658
##  [91] -1.87696424  1.09340833  1.71875305  0.79254963 -0.77698722  1.19237565
##  [97] -0.98041794 -1.30406564  0.01093546  0.40756647
```

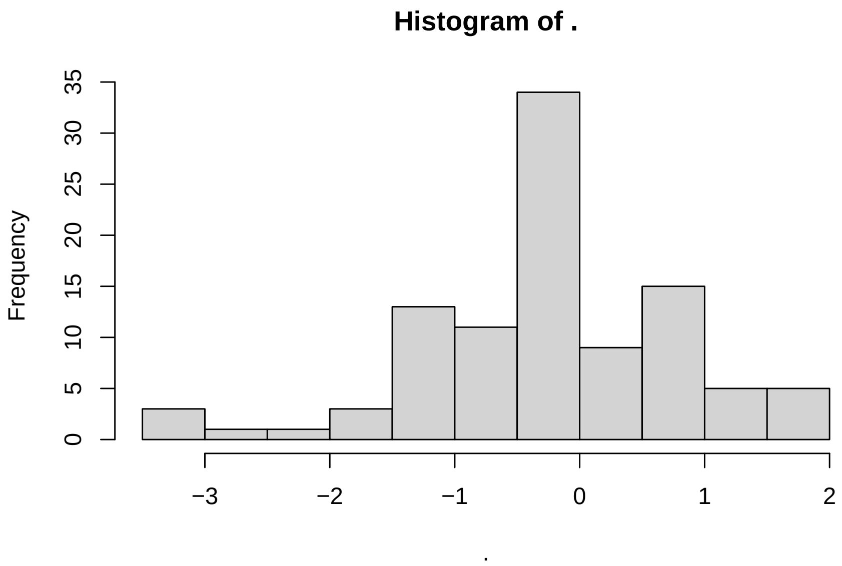


Common distributions

Distribution	Abbreviation	Distribution	Abbreviation
Beta	beta	Logistic	logis
Binomial	binom	Multinomial	multinom
Cauchy	cauchy	Negative binomial	nbinom
Chi-squared (noncentral)	chisq	Normal	norm
Exponential	exp	Poisson	pois
F	f	Wilcoxon Signed Rank	signrank
Gamma	gamma	T	t
Geometric	geom	Uniform	unif
Hypergeometric	hyper	Weibull	weibull
Lognormal	lnorm	Wilcoxon Rank Sum	wilcox

1.4.2 Generate normal random variables

```
rnorm(100,mean=0,sd=1) %>%
  hist()
```



```
rnorm(100) %>%
  summary()
```

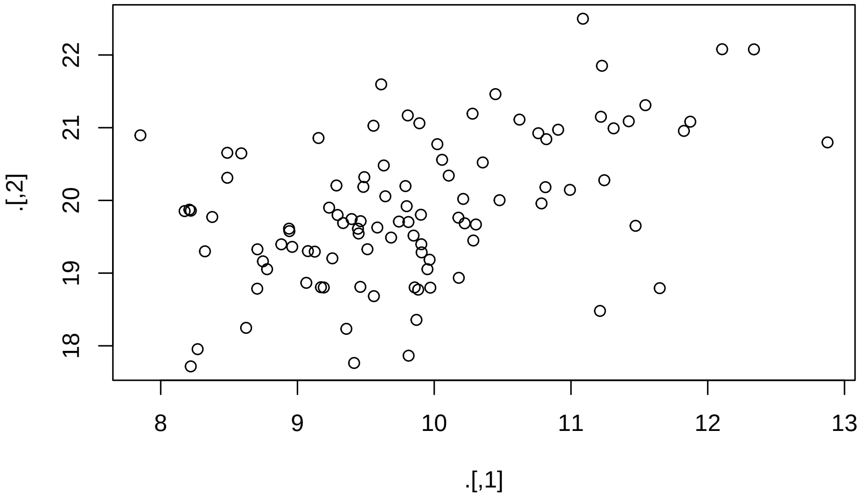
```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max. 
## -3.260109 -0.690097  0.054221 -0.006459  0.640251  2.782867
```

1.4.3 Generate multivariate normal random variables

```
library(MASS)
```

```
## 
## 载入程辑包：'MASS'
## The following object is masked from 'package:dplyr':
##
##     select
```

```
set.seed(1234)
mu <- c(10, 20)
sigma <- matrix(c(1, 0.5, 0.5, 1), nrow = 2)
mvrnorm(100, mu, sigma) %>%
plot()
```


22
21
20
19
18
.[,2]
8
9
10
11
12
13
.[,1]