talk05 练习与作业

目录

0.1 练习和作业说明

将相关代码填写入以 “‘{r} “‘ 标志的代码框中，运行并看到正确的结果；

完成后，用工具栏里的”Knit” 按键生成 PDF 文档；

将 PDF 文档改为：姓名-学号-`talk05` 作业`.pdf`，并提交到老师指定的平台/钉群。

0.2 Talk05 内容回顾

- dplyr 、tidyr (超级强大的数据处理) part 1
  - 长宽数据转换
  - dplyr 几个重要函数

0.3 练习与作业：用户验证

请运行以下命令，验证你的用户名。

如你当前用户名不能体现你的真实姓名，请改为拼音后再运行本作业！

```
Sys.info()[["user"]]
```

```
## [1] "mingyuwang"
```

```
Sys.getenv("HOME")
```

```
## [1] "C:/Users/rhong/Documents"
```

0.4 练习与作业 1：dplyr 练习

0.4.1 使用 mouse.tibble 变量做统计

- 每个染色体（或 scaffold）上每种基因类型的数量、平均长度、最大和最小长度，挑出最长和最短的基因
- 去掉含有 500 以下基因的染色体（或 scaffold），按染色体（或 scaffold）、数量高 -> 低进行排序

挑战题（可选做）：

实现上述目标（即：去掉少于 500 基因的染色体、排序、并统计）时不使用中间变量；

```
## 代码写这里，并运行；
options(warn = -1)
library("tidyverse")
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
## v ggplot2 3.3.6     v purrr   0.3.4
## v tibble  3.1.7     v dplyr   1.0.9
## v tidyr   1.2.0     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()
```

```
library("reshape2")
```

```
##
## 载入程辑包: 'reshape2'
##
## The following object is masked from 'package:tidyr':
##
##     smiths
```

```
options(warn = 0)
mouse_tibble <- read_delim("data/talk04/mouse_genes_biomart_sep2018.txt",
    delim = "\t", quote = "")
```

```
## Rows: 138532 Columns: 6
## -- Column specification --------------------------------------------------------
## Delimiter: "\t"
## chr (5): Gene stable ID, Transcript stable ID, Protein stable ID, Transcript...
## dbl (1): Transcript length (including UTRs and CDS)
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# 挑出最长和最短的基因
longest_gene <- mouse_tibble %>%
    group_by(`Chromosome/scaffold name`, `Transcript type`) %>%
    summarise(count = n(),
        mean_length = mean(`Transcript length (including UTRs and CDS)`),
        min_length = min(`Transcript length (including UTRs and CDS)`),
        max_length = max(`Transcript length (including UTRs and CDS)`))
```

```
## `summarise()` has grouped output by 'Chromosome/scaffold name'. You can
## override using the `.groups` argument.
```

```
# 挑出最长和最短的基因
longest_gene <- mouse_tibble %>%
    group_by(`Chromosome/scaffold name`) %>%
    top_n(1, `Transcript length (including UTRs and CDS)`) %>%
    ungroup() %>%
    select(longest_gene = `Gene stable ID`,
      `Chromosome/scaffold name`, `Transcript type`)
shortest_gene <- mouse_tibble %>%
    group_by(`Chromosome/scaffold name`, `Transcript type`) %>%
    top_n(-1, `Transcript length (including UTRs and CDS)`) %>%
    ungroup() %>%
    select(shortest_gene = `Gene stable ID`,
      `Chromosome/scaffold name`, `Transcript type`)

# 每个染色体（或 scaffold）上每种基因类型的数量、平均长度、最大和最小长度
summary_mouse <- mouse_tibble %>%
    group_by(`Chromosome/scaffold name`, `Transcript type`) %>%
    summarise(gene_count = n(),
        mean_length = mean(`Transcript length (including UTRs and CDS)`),
        min_length = min(`Transcript length (including UTRs and CDS)`),
        max_length = max(`Transcript length (including UTRs and CDS)`)) %>%
    left_join(longest_gene,
      by = c("Chromosome/scaffold name", "Transcript type")) %>%
    left_join(shortest_gene,
      by = c("Chromosome/scaffold name", "Transcript type")) %>%
    group_by(`Chromosome/scaffold name`) %>%
    # 去掉含有 500 以下基因的染色体（或 scaffold），按染色体（或 scaffold）、数量 高 -\> 低
    mutate(nr_genes_chrom = sum(gene_count)) %>%
    filter(nr_genes_chrom > 500) %>%
    arrange(`Chromosome/scaffold name`, desc(gene_count))
```

```
## `summarise()` has grouped output by 'Chromosome/scaffold name'. You can
## override using the `.groups` argument.
```

```
    # 平均长度这一列四舍五入到整数
summary_mouse$mean_length <- round(summary_mouse$mean_length)
summary_mouse
```

```
## # A tibble: 585 x 9
## # Groups:   Chromosome/scaffold name [21]
##    Chromosome/~1 Trans~2 gene_~3 mean_~4 min_l~5 max_l~6 longe~7 short~8 nr_ge~9
##    <chr>         <chr>     <int>   <dbl>   <dbl>   <dbl> <chr>   <chr>     <int>
##  1 1             protei~    3369    2700      75   40378 ENSMUS~ ENSMUS~    8553
##  2 1             retain~    1509    1748     230    8483 <NA>    ENSMUS~    8553
##  3 1             proces~     738     951      65    7640 <NA>    ENSMUS~    8553
##  4 1             proces~     627     728      30    4530 <NA>    ENSMUS~    8553
##  5 1             TEC         486    2241     133    8163 <NA>    ENSMUS~    8553
##  6 1             nonsen~     480    1844     284   10770 <NA>    ENSMUS~    8553
##  7 1             lincRNA     457    1207     154    9720 <NA>    ENSMUS~    8553
##  8 1             antise~     315    1236      78    7928 <NA>    ENSMUS~    8553
##  9 1             miRNA       128      98      53     442 <NA>    ENSMUS~    8553
## 10 1             snRNA       105     113      55     191 <NA>    ENSMUS~    8553
## # ... with 575 more rows, and abbreviated variable names
## #   1: `Chromosome/scaffold name`, 2: `Transcript type`, 3: gene_count,
## #   4: mean_length, 5: min_length, 6: max_length, 7: longest_gene,
## #   8: shortest_gene, 9: nr_genes_chrom
```

0.4.2 使用 grades 变量做练习

1. 装入 grades 变量;

```
library(dplyr); grades <- read_tsv( file = "data/talk05/grades.txt"
);
```

2. 尝试使用 spread 和 gather 函数将其变宽后再变长；

```
## 代码写这里，并运行；
grades <- read_tsv(file = "data/talk05/grades.txt")
```

```
## Rows: 9 Columns: 3
## -- Column specification --------------------------------------------------------
## Delimiter: "\t"
## chr (2): name, course
## dbl (1): grade
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
grades_spread <- spread(grades, key = `course`, value = `grade`)
grades_gather <- gather(grades_spread, key = `course`,
  value = `grade`, -name) %>%
  filter(!is.na(`grade`)) %>%
  arrange(desc(name))
grades_spread
```

```
## # A tibble: 3 x 6
##   name        Bioinformatics Chemistry Chinese English Microbiology
##   <chr>                <dbl>     <dbl>   <dbl>   <dbl>        <dbl>
## 1 Kang Ning              100        76      20      NA           NA
## 2 Weihua Chen             99        NA      NA      99           89
## 3 Zhi Liu                 NA        NA      69      50          100
```

```
grades_gather
```

```
## # A tibble: 9 x 3
##   name        course         grade
##   <chr>       <chr>          <dbl>
```

```
## 1 Zhi Liu     Chinese           69
## 2 Zhi Liu     English           50
## 3 Zhi Liu     Microbiology     100
## 4 Weihua Chen Bioinformatics    99
## 5 Weihua Chen English           99
## 6 Weihua Chen Microbiology      89
## 7 Kang Ning   Bioinformatics   100
## 8 Kang Ning   Chemistry         76
## 9 Kang Ning   Chinese           20
```

3. 研究并使用 tidyr 包里的 pivot_longer 和 pivot_wider 函数对 grades 变量进行宽长转换；

```
## 代码写这里，并运行；
grades.pivot_wider <- pivot_wider(grades, names_from = "course",
  values_from = "grade")
grades.pivot_longer <- pivot_longer(grades.pivot_wider, cols = 2:6,
  names_to = "course", values_to = "grade",
  # 去掉带 na 的行
  values_drop_na = TRUE)
grades.pivot_wider
```

```
## # A tibble: 3 x 6
##   name        Microbiology English Chinese Bioinformatics Chemistry
##   <chr>              <dbl>   <dbl>   <dbl>          <dbl>     <dbl>
## 1 Zhi Liu              100      50      69             NA        NA
## 2 Weihua Chen           89      99      NA             99        NA
## 3 Kang Ning             NA      NA      20            100        76
```

```
grades.pivot_longer
```

```
## # A tibble: 9 x 3
##   name        course         grade
##   <chr>       <chr>          <dbl>
```

```
## 1 Zhi Liu     Microbiology     100
## 2 Zhi Liu     English           50
## 3 Zhi Liu     Chinese           69
## 4 Weihua Chen Microbiology      89
## 5 Weihua Chen English           99
## 6 Weihua Chen Bioinformatics    99
## 7 Kang Ning   Chinese           20
## 8 Kang Ning   Bioinformatics   100
## 9 Kang Ning   Chemistry         76
```

4. 使用 pivot_longer 时，有时会产生 na 值，如何使用此函数的参数去除带 na 的行？

```
## 代码写这里，并运行；
message(" 使用 values_drop_na = TRUE 参数去除带 na 的行")
```

```
## 使用 values_drop_na = TRUE 参数去除带 na 的行
```

```
pivot_longer(grades.pivot_wider, cols = 2:6,
  names_to = "course", values_to = "grade", values_drop_na = TRUE)
```

```
## # A tibble: 9 x 3
##   name        course         grade
##   <chr>       <chr>          <dbl>
## 1 Zhi Liu     Microbiology     100
## 2 Zhi Liu     English           50
## 3 Zhi Liu     Chinese           69
## 4 Weihua Chen Microbiology      89
## 5 Weihua Chen English           99
## 6 Weihua Chen Bioinformatics    99
## 7 Kang Ning   Chinese           20
## 8 Kang Ning   Bioinformatics   100
## 9 Kang Ning   Chemistry         76
```

5. 以下代码有什么作用？

```
grades %>% complete( name, course )
```

答：complete 函数用于填充缺失值，这里是填充 name 和 course 的缺失值，使得每个 name 和 course 都有一个 grade 值。

0.4.3 使用 grades2 变量做练习

首先，用下面命令生成 grades2 变量：

```
grades2 <- tibble( "Name" = c("Weihua Chen", "Mm Hu", "John Doe", "Jane Doe",
                              "Warren Buffet", "Elon Musk", "Jack Ma"),
                   "Occupation" = c("Teacher", "Student", "Teacher", "Student",
                                    rep( "Entrepreneur", 3 ) ),
                   "English" = sample( 60:100, 7 ),
                   "ComputerScience" = sample(80:90, 7),
                   "Biology" = sample( 50:100, 7),
                   "Bioinformatics" = sample( 40:90, 7)
                   );
```

然后统计：1. 每个人最差的学科和成绩分别是什么？2. 哪个职业的平均成绩最好？3. 每个职业的最佳学科分别是什么（按平均分排序）???

```
## 代码写这里，并运行;
grades2 <- tibble("Name" = c("Weihua Chen", "Mm Hu", "John Doe", "Jane Doe",
    "Warren Buffet", "Elon Musk", "Jack Ma"),
  "Occupation" = c("Teacher", "Student", "Teacher", "Student",
    rep("Entrepreneur", 3)),
  "English" = sample(60:100, 7),
  "ComputerScience" = sample(80:90, 7),
  "Biology" = sample(50:100, 7),
```

```
  "Bioinformatics" = sample(40:90, 7)
)
# 1. 每个人最差的学科和成绩分别是什么?
grades2 %>%
  gather(key = "course", value = "grade", -Name, -Occupation) %>%
  group_by(Name) %>%
  summarise(min_grade = min(grade)) %>%
  # 每个人成绩最差的学科
  left_join(grades2, by = c("Name")) %>%
  melt(id.vars = c("Name", "min_grade", "Occupation")) %>%
  tibble() %>%
  rename(course = variable, grade = value) %>%
  filter(grade == min_grade) %>%
  select(Name, poor_course = course, grade) %>%
  arrange(Name)
```

```
## # A tibble: 9 x 3
##   Name          poor_course    grade
##   <chr>         <fct>          <int>
## 1 Elon Musk     Biology           75
## 2 Jack Ma       Bioinformatics    45
## 3 Jane Doe      Biology           63
## 4 John Doe      Bioinformatics    55
## 5 Mm Hu         English           82
## 6 Mm Hu         Biology           82
## 7 Mm Hu         Bioinformatics    82
## 8 Warren Buffet Bioinformatics    58
## 9 Weihua Chen   English           70
```

```
# 2. 哪个职业的平均成绩最好?
grades2 %>%
  gather(key = "course", value = "grade", -Name, -Occupation) %>%
  group_by(Occupation) %>%
```

```
  summarise(avg_grade = mean(grade)) %>%
  arrange(desc(avg_grade))
```

```
## # A tibble: 3 x 2
##   Occupation   avg_grade
##   <chr>            <dbl>
## 1 Teacher           84.6
## 2 Student           80.2
## 3 Entrepreneur      78.6
```

```
# 3. 每个职业的最佳学科分别是什么（按平均分排序)???
grades2 %>%
  gather(key = "course", value = "grade", -Name, -Occupation) %>%
  group_by(Occupation, course) %>%
  summarise(avg_grade = mean(grade)) %>%
  arrange(Occupation, desc(avg_grade))
```

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

```
## # A tibble: 12 x 3
## # Groups:   Occupation [3]
##    Occupation   course          avg_grade
##    <chr>        <chr>               <dbl>
##  1 Entrepreneur Biology              86.7
##  2 Entrepreneur ComputerScience      83.7
##  3 Entrepreneur English              83.7
##  4 Entrepreneur Bioinformatics       60.3
##  5 Student      Bioinformatics       85
##  6 Student      ComputerScience      85
##  7 Student      English              78.5
##  8 Student      Biology              72.5
##  9 Teacher      Biology              94.5
```

```
## 10 Teacher      ComputerScience      88.5
## 11 Teacher      English              84.5
## 12 Teacher      Bioinformatics       71
```

0.4.4 使用 starwars 变量做计算

1. 计算每个人的 BMI；
2. 挑选出肥胖（BMI >= 30）的人类，并且只显示其 name, sex 和 homeworld；

```
## 代码写这里，并运行；
mutate(starwars, BMI = mass / (height / 100)^2)
```

```
## # A tibble: 87 x 15
##    name        height  mass hair_~1 skin_~2 eye_c~3 birth~4 sex   gender homew~5
##    <chr>        <int> <dbl> <chr>   <chr>   <chr>     <dbl> <chr> <chr>  <chr>
##  1 Luke Skywa~    172    77 blond   fair    blue       19   male  mascu~ Tatooi~
##  2 C-3PO          167    75 <NA>    gold    yellow    112   none  mascu~ Tatooi~
##  3 R2-D2           96    32 <NA>    white,~ red        33   none  mascu~ Naboo
##  4 Darth Vader    202   136 none    white   yellow     41.9 male  mascu~ Tatooi~
##  5 Leia Organa    150    49 brown   light   brown      19   fema~ femin~ Aldera~
##  6 Owen Lars      178   120 brown,~ light   blue       52   male  mascu~ Tatooi~
##  7 Beru White~    165    75 brown   light   blue       47   fema~ femin~ Tatooi~
##  8 R5-D4           97    32 <NA>    white,~ red        NA   none  mascu~ Tatooi~
##  9 Biggs Dark~    183    84 black   light   brown      24   male  mascu~ Tatooi~
## 10 Obi-Wan Ke~    182    77 auburn~ fair    blue-g~    57   male  mascu~ Stewjon
## # ... with 77 more rows, 5 more variables: species <chr>, films <list>,
## #   vehicles <list>, starships <list>, BMI <dbl>, and abbreviated variable
## #   names 1: hair_color, 2: skin_color, 3: eye_color, 4: birth_year,
## #   5: homeworld
```

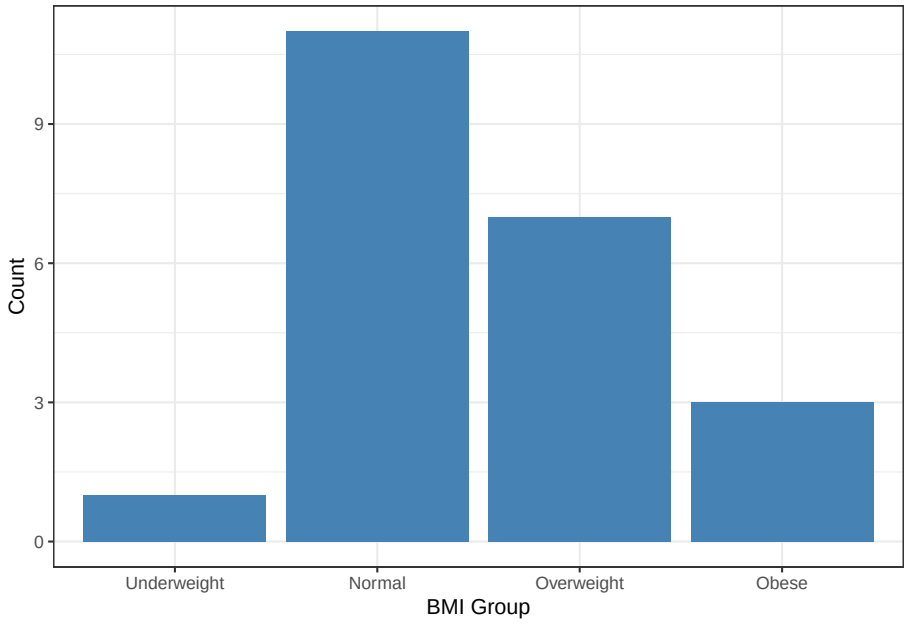
```
mutate(starwars, BMI = mass / (height / 100)^2) %>%
  filter(BMI >= 30) %>%
  select(name, sex, homeworld)
```

```
## # A tibble: 12 x 3
##    name                  sex           homeworld
##    <chr>                 <chr>         <chr>
##  1 R2-D2                 none          Naboo
##  2 Darth Vader           male          Tatooine
##  3 Owen Lars             male          Tatooine
##  4 R5-D4                 none          Tatooine
##  5 Jabba Desilijic Tiure hermaphroditic Nal Hutta
##  6 Jek Tono Porkins      male          Bestine IV
##  7 Yoda                  male          <NA>
##  8 IG-88                 none          <NA>
##  9 Bossk                 male          Trandosha
## 10 Sebulba               male          Malastare
## 11 Dud Bolt              male          Vulpter
## 12 Grievous              male          Kalee
```

3. 挑选出所有人类；
4. 按 BMI 将他们分为三组，<18, 18~25, >25，统计每组的人数，并用 barplot 进行展示；注意：展示时三组的按 BMI 从小到大排序；
5. 改变排序方式，按每组人数从小到大排序；

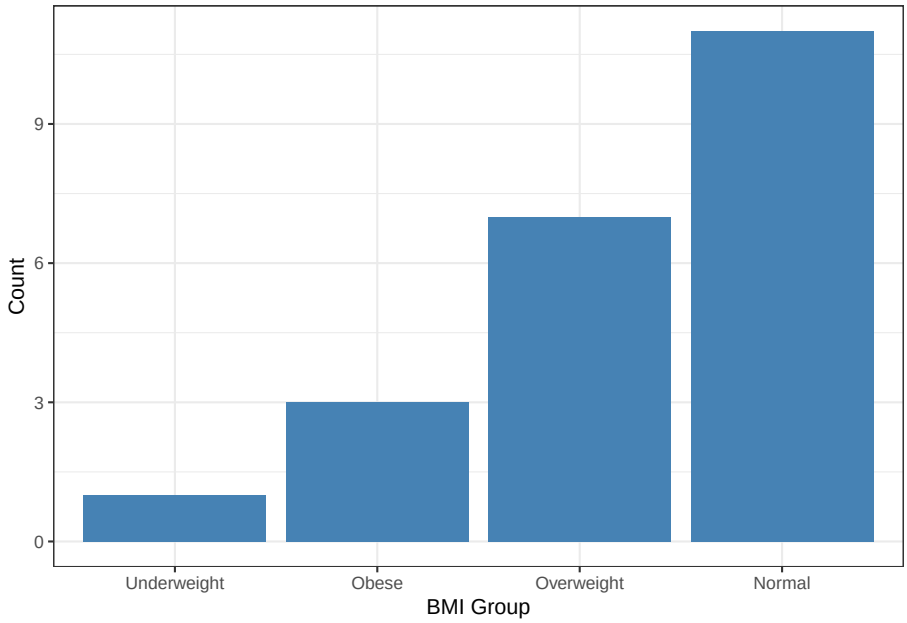
```
## 代码写这里，并运行；
human_bmi <- filter(starwars, species == "Human") %>%
    mutate(BMI = mass/(height/100)^2) %>%
    mutate(BMI_group = ifelse(BMI < 18, "Underweight",
                          ifelse(BMI < 25, "Normal",
                          ifelse(BMI < 30, "Overweight", "Obese")))) %>%
    group_by(BMI_group) %>%
    summarise(count = n())
```

```
human_bmi %>%
    filter(!is.na(BMI_group)) %>%
    ggplot(aes(x = factor(BMI_group,
        levels = c("Underweight", "Normal", "Overweight", "Obese")),
        y = count)) +
    # 调整颜色
    geom_bar(stat = "identity", fill = "steelblue") +
    labs(x = "BMI Group", y = "Count") +
    theme_bw()
```




```
# human_bmi 中的 BMI_group 按照相应的 count 重新设定 levels
human_bmi %>%
    filter(!is.na(BMI_group)) %>%
    ggplot(aes(x = factor(BMI_group,
        levels = human_bmi$BMI_group[order(human_bmi$count)]),
        y = count)) +
    geom_bar(stat = "identity", fill = "steelblue") +
```

```
    labs(x = "BMI Group", y = "Count") +
    theme_bw()
```



6. 查看 starwars 的 films 列，它有什么特点？data.frame 可以实现类似的功能吗？

答：films 列的每个元素是一个包含多个元素的列表，data.frame 不能实现类似的功能。

7. 为 starwars 增加一列，用于统计每个角色在多少部电影中出现。

```
## 代码写这里，并运行；
starwars %>%
    # 保持所有列不变，增加一列 nr_films
    mutate(nr_films = map_int(films, length)) %>%
    select(name, nr_films, 2:length(starwars))
```

```
## # A tibble: 87 x 15
```

```
##    name        nr_fi~1 height  mass hair_~2 skin_~3 eye_c~4 birth~5 sex   gender
##    <chr>         <int>  <int> <dbl> <chr>   <chr>   <chr>     <dbl> <chr> <chr>
##  1 Luke Skywa~       5    172    77 blond   fair    blue       19   male  mascu~
##  2 C-3PO             6    167    75 <NA>    gold    yellow    112   none  mascu~
##  3 R2-D2             7     96    32 <NA>    white,~ red        33   none  mascu~
##  4 Darth Vader       4    202   136 none    white   yellow     41.9 male  mascu~
##  5 Leia Organa       5    150    49 brown   light   brown      19   fema~ femin~
##  6 Owen Lars         3    178   120 brown,~ light   blue       52   male  mascu~
##  7 Beru White~       3    165    75 brown   light   blue       47   fema~ femin~
##  8 R5-D4             1     97    32 <NA>    white,~ red        NA   none  mascu~
##  9 Biggs Dark~       1    183    84 black   light   brown      24   male  mascu~
## 10 Obi-Wan Ke~       6    182    77 auburn~ fair    blue-g~    57   male  mascu~
## # ... with 77 more rows, 5 more variables: homeworld <chr>, species <chr>,
## #   films <list>, vehicles <list>, starships <list>, and abbreviated variable
## #   names 1: nr_films, 2: hair_color, 3: skin_color, 4: eye_color,
## #   5: birth_year
```

0.4.5 使用 Theoph 变量做练习

注：以下练习请只显示结果的前 6 行；

1. 选取从 Subject 到 Dose 的列；总共有几列？

```
## 代码写这里，并运行；
theoph <- tibble(Theoph)
# 选取从 Subject 到 Dose 的列
select(theoph, Subject:Dose)
```

```
## # A tibble: 132 x 3
##    Subject    Wt  Dose
##    <ord>   <dbl> <dbl>
##  1 1        79.6  4.02
##  2 1        79.6  4.02
##  3 1        79.6  4.02
```

```
##  4 1        79.6  4.02
##  5 1        79.6  4.02
##  6 1        79.6  4.02
##  7 1        79.6  4.02
##  8 1        79.6  4.02
##  9 1        79.6  4.02
## 10 1        79.6  4.02
## # ... with 122 more rows
```

```
message(" 总共有", ncol(select(theoph, Subject:Dose)), " 列")
```

```
## 总共有3列
```

2. 用 filter 选取 Dose 大于 5，且 Time 高于 Time 列平均值的行；

```
## 代码写这里，并运行；
theoph %>%
    filter(Time > mean(Time)) %>%
    filter(Dose > 5)
```

```
## # A tibble: 12 x 5
##    Subject    Wt  Dose  Time  conc
##    <ord>   <dbl> <dbl> <dbl> <dbl>
##  1 5        54.6  5.86  7.02  7.09
##  2 5        54.6  5.86  9.1   5.9
##  3 5        54.6  5.86 12     4.37
##  4 5        54.6  5.86 24.4   1.57
##  5 10       58.2  5.5   7.08  8.02
##  6 10       58.2  5.5   9.38  7.14
##  7 10       58.2  5.5  12.1   5.68
##  8 10       58.2  5.5  23.7   2.42
##  9 12       60.5  5.3   7.07  6.59
## 10 12       60.5  5.3   9.03  6.11
## 11 12       60.5  5.3  12.0   4.57
```

```
## 12 12       60.5  5.3  24.2   1.17
```

3. 用 mutate 函数产生新列 trend，其值为 Time 与 Time 列平均值的差
   注意：请去除可能产生的 na 值；

```
## 代码写这里，并运行；
theoph %>%
    mutate(trend = Time - mean(Time, na.rm = TRUE)) %>%
    filter(!is.na(trend))
```

```
## # A tibble: 132 x 6
##    Subject    Wt  Dose  Time  conc  trend
##    <ord>   <dbl> <dbl> <dbl> <dbl>  <dbl>
##  1 1        79.6  4.02  0     0.74 -5.89
##  2 1        79.6  4.02  0.25  2.84 -5.64
##  3 1        79.6  4.02  0.57  6.57 -5.32
##  4 1        79.6  4.02  1.12 10.5  -4.77
##  5 1        79.6  4.02  2.02  9.66 -3.87
##  6 1        79.6  4.02  3.82  8.58 -2.07
##  7 1        79.6  4.02  5.1   8.36 -0.795
##  8 1        79.6  4.02  7.03  7.47  1.14
##  9 1        79.6  4.02  9.05  6.89  3.16
## 10 1        79.6  4.02 12.1   5.94  6.23
## # ... with 122 more rows
```

4. 用 mutate 函数产生新列 weight_cat ，其值根据 Wt 的取值范围而不
   同：

- 如果 Wt > 76.2，为 'Super-middleweight'，否则
- 如果 Wt > 72.57，为 'Middleweight'，否则
- 如果 Wt > 66.68，为 'Light-middleweight'
- 其它值，为 'Welterweight'

```
## 代码写这里，并运行；
theoph %>%
    mutate(weight_cat =
      ifelse(Wt > 76.2, "Super-middleweight",
      ifelse(Wt > 72.57, "Middleweight",
      ifelse(Wt > 66.68, "Light-middleweight", "Welterweight")))) %>%
      print(n = 50)
```

```
## # A tibble: 132 x 6
##    Subject    Wt  Dose  Time  conc weight_cat
##    <ord>   <dbl> <dbl> <dbl> <dbl> <chr>
##  1 1        79.6  4.02  0     0.74 Super-middleweight
##  2 1        79.6  4.02  0.25  2.84 Super-middleweight
##  3 1        79.6  4.02  0.57  6.57 Super-middleweight
##  4 1        79.6  4.02  1.12 10.5  Super-middleweight
##  5 1        79.6  4.02  2.02  9.66 Super-middleweight
##  6 1        79.6  4.02  3.82  8.58 Super-middleweight
##  7 1        79.6  4.02  5.1   8.36 Super-middleweight
##  8 1        79.6  4.02  7.03  7.47 Super-middleweight
##  9 1        79.6  4.02  9.05  6.89 Super-middleweight
## 10 1        79.6  4.02 12.1   5.94 Super-middleweight
## 11 1        79.6  4.02 24.4   3.28 Super-middleweight
## 12 2        72.4  4.4   0     0    Light-middleweight
## 13 2        72.4  4.4   0.27  1.72 Light-middleweight
## 14 2        72.4  4.4   0.52  7.91 Light-middleweight
## 15 2        72.4  4.4   1     8.31 Light-middleweight
## 16 2        72.4  4.4   1.92  8.33 Light-middleweight
## 17 2        72.4  4.4   3.5   6.85 Light-middleweight
## 18 2        72.4  4.4   5.02  6.08 Light-middleweight
## 19 2        72.4  4.4   7.03  5.4  Light-middleweight
## 20 2        72.4  4.4   9     4.55 Light-middleweight
## 21 2        72.4  4.4  12     3.01 Light-middleweight
## 22 2        72.4  4.4  24.3   0.9  Light-middleweight
```

```
## 23 3        70.5  4.53  0     0    Light-middleweight
## 24 3        70.5  4.53  0.27  4.4  Light-middleweight
## 25 3        70.5  4.53  0.58  6.9  Light-middleweight
## 26 3        70.5  4.53  1.02  8.2  Light-middleweight
## 27 3        70.5  4.53  2.02  7.8  Light-middleweight
## 28 3        70.5  4.53  3.62  7.5  Light-middleweight
## 29 3        70.5  4.53  5.08  6.2  Light-middleweight
## 30 3        70.5  4.53  7.07  5.3  Light-middleweight
## 31 3        70.5  4.53  9     4.9  Light-middleweight
## 32 3        70.5  4.53 12.2   3.7  Light-middleweight
## 33 3        70.5  4.53 24.2   1.05 Light-middleweight
## 34 4        72.7  4.4   0     0    Middleweight
## 35 4        72.7  4.4   0.35  1.89 Middleweight
## 36 4        72.7  4.4   0.6   4.6  Middleweight
## 37 4        72.7  4.4   1.07  8.6  Middleweight
## 38 4        72.7  4.4   2.13  8.38 Middleweight
## 39 4        72.7  4.4   3.5   7.54 Middleweight
## 40 4        72.7  4.4   5.02  6.88 Middleweight
## 41 4        72.7  4.4   7.02  5.78 Middleweight
## 42 4        72.7  4.4   9.02  5.33 Middleweight
## 43 4        72.7  4.4  12.0   4.19 Middleweight
## 44 4        72.7  4.4  24.6   1.15 Middleweight
## 45 5        54.6  5.86  0     0    Welterweight
## 46 5        54.6  5.86  0.3   2.02 Welterweight
## 47 5        54.6  5.86  0.52  5.63 Welterweight
## 48 5        54.6  5.86  1    11.4  Welterweight
## 49 5        54.6  5.86  2.02  9.33 Welterweight
## 50 5        54.6  5.86  3.5   8.74 Welterweight
## # ... with 82 more rows
```