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
  - pipe
  - 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] "lucas"
```

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

```
## [1] "/Users/lucas"
```

```
getwd(); ## 显示当前工作目录
```

```
## [1] "/Users/lucas/Library/Mobile Documents/com~apple~CloudDocs/~~aa学习/大二上/学习/
```

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；

```
# Load the package
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v forcats   1.0.0     v readr     2.1.4
## v ggplot2   3.4.3     v stringr   1.5.0
## v lubridate 1.9.2     v tibble    3.2.1
## v purrr     1.0.2     v tidyr     1.3.0

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts
```

```
# read mouse.tibble
mouse_tibble =
  read_delim(file = "../data/talk04/mouse_genes_biomart_sep2018.txt",
             delim = "\t",
             quote = "",
             show_col_types = FALSE)

# Convert the mouse.tibble to tibble
if(!is.tibble(mouse_tibble))
  mouse_tibble = as_tibble(mouse_tibble)
```

```
## Warning: `is.tibble()` was deprecated in tibble 2.0.0.
## i Please use `is_tibble()` instead.
```

```
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
# Arrange the data
gene_summary = mouse_tibble %>%
  group_by(
    `Chromosome/scaffold name`,
    `Transcript type`) %>%
  summarize(
    Gene_Count = n(),
    Avg_Length =
      mean(`Transcript length (including UTRs and CDS)`),
    Max_Length =
      max(`Transcript length (including UTRs and CDS)`),
    Min_Length =
      min(`Transcript length (including UTRs and CDS)`),
    Longest_Gene =
      `Chromosome/scaffold name`[
        which.max(
          `Transcript length (including UTRs and CDS)`)],
    Shortest_Gene =
      `Chromosome/scaffold name`[
        which.min(
          `Transcript length (including UTRs and CDS)`)]
  )
```

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

```
# Remove the chromosome containing the following 500 genes
filtered_gene_summary =
  gene_summary %>%
  group_by(
```

```
    `Chromosome/scaffold name`) %>%
  filter(
    sum(Gene_Count) > 500)

# Descending order by number of chromosomes and genes
sorted_gene_summary =
  filtered_gene_summary %>%
  arrange(
    `Chromosome/scaffold name`, desc(Gene_Count))

# Print the data
sorted_gene_summary
```

```
## # A tibble: 521 x 8
## # Groups:   Chromosome/scaffold name [21]
##    `Chromosome/scaffold name` `Transcript type` Gene_Count Avg_Length Max_Length
##    <chr>                      <chr>                  <int>      <dbl>      <dbl>
##  1 1                          protein_coding          3369     2700.       40378
##  2 1                          retained_intron         1509     1748.        8483
##  3 1                          processed_transc~        738      951.        7640
##  4 1                          processed_pseudo~        627      728.        4530
##  5 1                          TEC                      486     2241.        8163
##  6 1                          nonsense_mediate~        480     1844.       10770
##  7 1                          lincRNA                  457     1207.        9720
##  8 1                          antisense                315     1236.        7928
##  9 1                          miRNA                    128       98.0        442
## 10 1                          snRNA                    105      113.         191
## # i 511 more rows
## # i 3 more variables: Min_Length <dbl>, Longest_Gene <chr>, Shortest_Gene <chr>
```

挑战题:

```r
# Load the packages
library(dplyr)
library(tidyverse)

# read mouse.tibble
mouse_tibble2 =
  read_delim(file = "../data/talk04/mouse_genes_biomart_sep2018.txt",
             delim = "\t",
             quote = "",
             show_col_types = FALSE)

# Convert the mouse.tibble to tibble
if(!is.tibble(mouse_tibble2))
  mouse_tibble2 = as_tibble(mouse_tibble2)

# Processing data
sorted_gene_summary2 =
  mouse_tibble2 %>%
  group_by(
    `Chromosome/scaffold name`,
    `Transcript type`) %>%
  summarize(
    Gene_Count = n(),
    Avg_Length =
      mean(`Transcript length (including UTRs and CDS)`),
    Max_Length =
      max(`Transcript length (including UTRs and CDS)`),
    Min_Length =
      min(`Transcript length (including UTRs and CDS)`),
    Longest_Gene =
      `Chromosome/scaffold name`[
        which.max(
          `Transcript length (including UTRs and CDS)`)],
```

```
    Shortest_Gene =
      `Chromosome/scaffold name`[
        which.min(
          `Transcript length (including UTRs and CDS)`)]
  )%>%
  ungroup() %>%
  group_by(
    `Chromosome/scaffold name`) %>%
  filter(
    sum(Gene_Count) > 500) %>%
  # ungroup() %>%
  arrange(
    `Chromosome/scaffold name`, desc(Gene_Count))
```

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

```
# Print the data
sorted_gene_summary2
```

```
## # A tibble: 521 x 8
## # Groups:   Chromosome/scaffold name [21]
##    `Chromosome/scaffold name` `Transcript type` Gene_Count Avg_Length Max_Length
##    <chr>                      <chr>                  <int>      <dbl>      <dbl>
##  1 1                          protein_coding          3369     2700.       40378
##  2 1                          retained_intron         1509     1748.        8483
##  3 1                          processed_transc~        738      951.        7640
##  4 1                          processed_pseudo~        627      728.        4530
##  5 1                          TEC                      486     2241.        8163
##  6 1                          nonsense_mediate~        480     1844.       10770
##  7 1                          lincRNA                  457     1207.        9720
##  8 1                          antisense                315     1236.        7928
##  9 1                          miRNA                    128       98.0        442
```

```
## 10 1                          snRNA                  105      113.         191
## # i 511 more rows
## # i 3 more variables: Min_Length <dbl>, Longest_Gene <chr>, Shortest_Gene <chr>
```

0.4.2 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;

# Load the tibble
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))

# Question 1
# Use dplyr to find everyone's worst subjects and grades
worst_subject_per_person =
  grades2 %>%
  mutate(
    Min_Score = pmin(English,
                     ComputerScience,
                     Biology,
                     Bioinformatics)) %>%
  select(Name, Min_Score)

print(worst_subject_per_person)
```

```
## # A tibble: 7 x 2
##   Name          Min_Score
##   <chr>             <int>
## 1 Weihua Chen          81
## 2 Mm Hu                59
## 3 John Doe             40
## 4 Jane Doe             47
## 5 Warren Buffet        61
## 6 Elon Musk            42
## 7 Jack Ma              66
```

```
# Question 2
# Use dplyr to calculate the average score for each occupation
# Find the occupation with the highest average score
```

```
best_occupation =
  grades2 %>%
  group_by(Occupation) %>%
  summarise(
    Avg_Score =
      mean(English +
             ComputerScience +
             Biology +
             Bioinformatics)/4) %>%
  arrange(desc(Avg_Score)) %>%
  slice(1)

print(best_occupation)
```

```
## # A tibble: 1 x 2
##   Occupation Avg_Score
##   <chr>          <dbl>
## 1 Student         81.2
```

```
# Question 3
# Use dplyr to calculate the average score
# for each subject for each occupation
# Find the subject with the highest average score
best_subject_per_occupation =
  grades2 %>%
  group_by(Occupation) %>%
  summarise(
    Best_Subject =
      which.max(c(mean(English),
                  mean(ComputerScience),
                  mean(Biology),
                  mean(Bioinformatics)))) %>%
  ungroup() %>%
```

```
  mutate(
    Best_Subject =
      c("English",
        "ComputerScience",
        "Biology",
        "Bioinformatics")[Best_Subject])

print(best_subject_per_occupation)
```

```
## # A tibble: 3 x 2
##   Occupation   Best_Subject
##   <chr>        <chr>
## 1 Entrepreneur ComputerScience
## 2 Student      Biology
## 3 Teacher      ComputerScience
```

0.4.3 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;
# Loading the dplyr library
library(dplyr)

# Calculate BMI for each individual
starwars_bmi =
  starwars %>%
  mutate(
    BMI = mass / (height/100)^2)
```

```r
# Print the results of Q1
print(starwars_bmi)
```

```
## # A tibble: 87 x 15
##    name     height  mass hair_color skin_color eye_color birth_year sex   gender
##    <chr>     <int> <dbl> <chr>      <chr>      <chr>          <dbl> <chr> <chr>
##  1 Luke Sk~    172    77 blond      fair       blue            19   male  mascu~
##  2 C-3PO       167    75 <NA>       gold       yellow         112   none  mascu~
##  3 R2-D2        96    32 <NA>       white, bl~ red             33   none  mascu~
##  4 Darth V~    202   136 none       white      yellow          41.9 male  mascu~
##  5 Leia Or~    150    49 brown      light      brown           19   fema~ femin~
##  6 Owen La~    178   120 brown, gr~ light      blue            52   male  mascu~
##  7 Beru Wh~    165    75 brown      light      blue            47   fema~ femin~
##  8 R5-D4        97    32 <NA>       white, red red             NA   none  mascu~
##  9 Biggs D~    183    84 black      light      brown           24   male  mascu~
## 10 Obi-Wan~    182    77 auburn, w~ fair       blue-gray       57   male  mascu~
## # i 77 more rows
## # i 6 more variables: homeworld <chr>, species <chr>, films <list>,
## #   vehicles <list>, starships <list>, BMI <dbl>
```

```r
# Pick out obese humans and screen for columns that need to be
obese_humanoids =
  starwars_bmi %>%
  filter(
    species == "Human"
    & BMI >= 30) %>%
  select(name, sex, homeworld)

# Print the result of Q2
print(obese_humanoids)
```

```
## # A tibble: 3 x 3
##   name             sex   homeworld
```

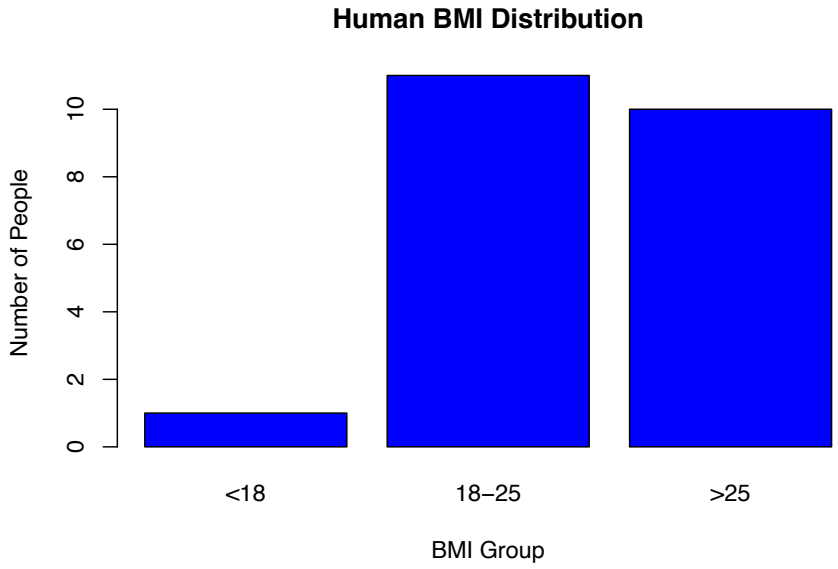
```
##   <chr>            <chr> <chr>
## 1 Darth Vader      male  Tatooine
## 2 Owen Lars        male  Tatooine
## 3 Jek Tono Porkins male  Bestine IV
```

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；
# Select all human beings
humans =
  starwars_bmi %>%
  filter(species == "Human")

# Create three BMI groupings
humans$BMI_Group =
  cut(humans$BMI,
      breaks =
        c(-Inf, 18, 25, Inf),
      labels =
        c("<18", "18-25", ">25"))

# Counting the number of people in each group
group_counts =
  table(humans$BMI_Group)

# Sort by BMI from smallest to largest
group_counts =
  group_counts[
    order(
      as.numeric(names(group_counts)))]
```

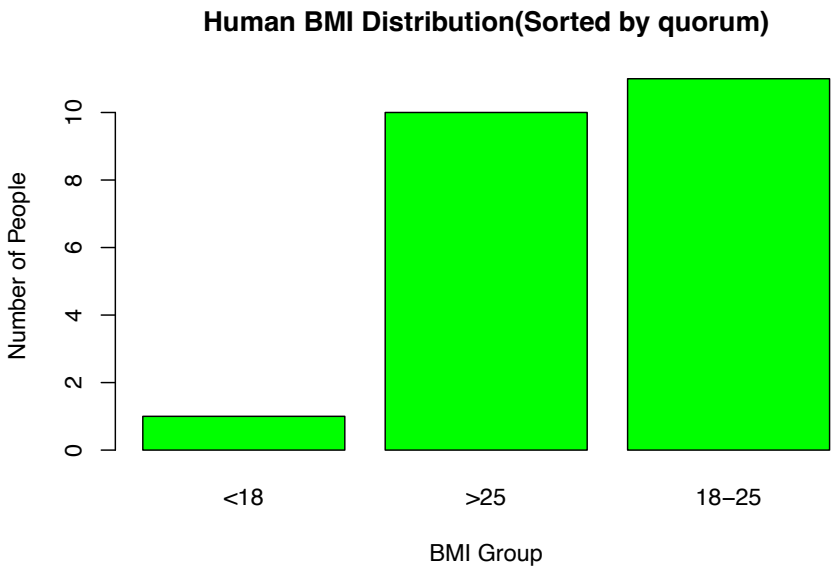
```
## Warning in order(as.numeric(names(group_counts))): NAs introduced by coercion
```

```r
# Displayed using barplot
barplot(
  group_counts,
  main = "Human BMI Distribution",
  xlab = "BMI Group",
  ylab = "Number of People",
  col = "blue")
```




```r
# Ordered from smallest to largest
group_counts =
  group_counts[order(group_counts)]

# Displayed using barplot,
# sorted by quorum
# from smallest to largest
barplot(
  group_counts,
```

```
  main = "Human BMI Distribution(Sorted by quorum)",
  xlab = "BMI Group",
  ylab = "Number of People",
  col = "green")
```



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：

这一列中的所有元素都是以列表的形式存储在 tibble 中。

data.frame 不能够直接存储一些列表在某特定单元格内，但是可以通过其他的方式来实现类似的效果。

- List Column: 使用 data.frame 的一列来存储列表（list）数据，每个元素表示一个包含电影信息的子列表。这样可以模拟 films 列的结构。

```
films_list_colmn =
  data.frame(
  Name =
    c("Luke Skywalker",
      "Darth Vader"),
  Films =
    list(
      list(
        "A New Hope",
        "The Empire Strikes Back"),
    list(
      "A New Hope",
      "The Empire Strikes Back",
      "Return of the Jedi")
    )
  )

print(films_list_colmn)
```

```
##             Name Films..A.New.Hope. Films..The.Empire.Strikes.Back.
## 1 Luke Skywalker         A New Hope         The Empire Strikes Back
## 2    Darth Vader         A New Hope         The Empire Strikes Back
##   Films..A.New.Hope..1 Films..The.Empire.Strikes.Back..1
## 1           A New Hope           The Empire Strikes Back
## 2           A New Hope           The Empire Strikes Back
##   Films..Return.of.the.Jedi.
## 1         Return of the Jedi
## 2         Return of the Jedi
```

- 使用 Tidy Data Structure

```
# 创建一个整洁数据结构示例
films_tidy_data_str =
```

```
  data.frame(
  Name = c(
    "Luke Skywalker",
    "Luke Skywalker",
    "Darth Vader",
    "Darth Vader"),
  Film = c(
    "A New Hope",
    "The Empire Strikes Back",
    "A New Hope",
    "The Empire Strikes Back")
)

print(films_tidy_data_str)
```

```
##             Name                     Film
## 1 Luke Skywalker             A New Hope
## 2 Luke Skywalker The Empire Strikes Back
## 3    Darth Vader             A New Hope
## 4    Darth Vader The Empire Strikes Back
```

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;
# Adding a new column using the mutate function
starwars_with_appearances =
  starwars %>%
  mutate(
    Appearances =
      rowSums(!is.na(.[5:12])))

# Printing results
# Including the new Appearances column
```

```
print(starwars_with_appearances)
```

```
## # A tibble: 87 x 15
##    name     height  mass hair_color skin_color eye_color birth_year sex   gender
##    <chr>     <int> <dbl> <chr>      <chr>      <chr>          <dbl> <chr> <chr>
##  1 Luke Sk~    172    77 blond      fair       blue            19   male  mascu~
##  2 C-3PO       167    75 <NA>       gold       yellow         112   none  mascu~
##  3 R2-D2        96    32 <NA>       white, bl~ red             33   none  mascu~
##  4 Darth V~    202   136 none       white      yellow          41.9 male  mascu~
##  5 Leia Or~    150    49 brown      light      brown           19   fema~ femin~
##  6 Owen La~    178   120 brown, gr~ light      blue            52   male  mascu~
##  7 Beru Wh~    165    75 brown      light      blue            47   fema~ femin~
##  8 R5-D4        97    32 <NA>       white, red red             NA   none  mascu~
##  9 Biggs D~    183    84 black      light      brown           24   male  mascu~
## 10 Obi-Wan~    182    77 auburn, w~ fair       blue-gray       57   male  mascu~
## # i 77 more rows
## # i 6 more variables: homeworld <chr>, species <chr>, films <list>,
## #   vehicles <list>, starships <list>, Appearances <dbl>
```

0.4.4 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；
# Loading the Theoph dataset
data("Theoph")

# Select the columns from Subject to Dose.
selected_columns =
  Theoph[, c("Subject", "Wt", "Dose")]
```

```r
# Calculate the total number of columns
num_columns =
  ncol(selected_columns)

# Show first 6 rows
head(selected_columns)
```

```
##   Subject   Wt Dose
## 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
```

```r
# Total number of columns displayed
cat("There are ",
    num_columns,
    "columns in total.")
```

```
## There are  3 columns in total.
```

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

```r
## 代码写这里，并运行；

# Calculate the average of the Time columns
mean_time =
  mean(Theoph$Time)

# Use the filter function to
# select the rows that match the conditions
filtered_data =
```

```
  filter(Theoph, Dose > 5,
         Time > mean_time)

# Display the first 6 rows of results
head(filtered_data)
```

```
##   Subject   Wt Dose  Time conc
## 1       5 54.6 5.86  7.02 7.09
## 2       5 54.6 5.86  9.10 5.90
## 3       5 54.6 5.86 12.00 4.37
## 4       5 54.6 5.86 24.35 1.57
## 5      10 58.2 5.50  7.08 8.02
## 6      10 58.2 5.50  9.38 7.14
```

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；
# Calculate the average
# of the Time columns
mean_time =
  mean(Theoph$Time,
       na.rm = TRUE)

# Using the mutate function
# to create a new column trend
Theoph =
  mutate(Theoph,
         trend = Time - mean_time)

# Removal of possible NA values
Theoph =
  na.omit(Theoph)
```

```r
# Display the first 6 rows of results
head(Theoph)
```

```
##   Subject   Wt Dose Time  conc     trend
## 1       1 79.6 4.02 0.00  0.74 -5.894621
## 2       1 79.6 4.02 0.25  2.84 -5.644621
## 3       1 79.6 4.02 0.57  6.57 -5.324621
## 4       1 79.6 4.02 1.12 10.50 -4.774621
## 5       1 79.6 4.02 2.02  9.66 -3.874621
## 6       1 79.6 4.02 3.82  8.58 -2.074621
```

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'

```r
# Using the mutate function to create a new column weight_cat
Theoph =
  mutate(
    Theoph,
    weight_cat = case_when(
      Wt > 76.2 ~ 'Super-middleweight',
      Wt > 72.57 ~ 'Middleweight',
      Wt > 66.68 ~ 'Light-middleweight',
      TRUE ~ 'Welterweight'
    )
  )

# Display the first 6 rows of results
head(Theoph)
```

```
##   Subject   Wt Dose Time  conc     trend         weight_cat
## 1       1 79.6 4.02 0.00  0.74 -5.894621 Super-middleweight
## 2       1 79.6 4.02 0.25  2.84 -5.644621 Super-middleweight
## 3       1 79.6 4.02 0.57  6.57 -5.324621 Super-middleweight
## 4       1 79.6 4.02 1.12 10.50 -4.774621 Super-middleweight
## 5       1 79.6 4.02 2.02  9.66 -3.874621 Super-middleweight
## 6       1 79.6 4.02 3.82  8.58 -2.074621 Super-middleweight
```