talk04 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-talk04 作业.pdf`，并提交到老师指定的平台/钉群。

0.2 Talk04 内容回顾

待写 …

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：R session 管理

0.4.1 完成以下操作

- 定义一些变量（比如 x, y , z 并赋值；内容随意）
- 从外部文件装入一些数据（可自行创建一个 4 行 5 列的数据，内容随意）
- 保存 workspace 到.RData
- 列出当前工作空间内的所有变量
- 删除当前工作空间内所有变量
- 从.RData 文件恢复保存的数据
- 再次列出当前工作空间内的所有变量，以确认变量已恢复
- 随机删除两个变量
- 再次列出当前工作空间内的所有变量

```
## 代码写这里，并运行；
x <- 1
y <- 2
z <- 3
data <- read.table("data/Table1.txt", header = TRUE)
# save.image(file = ".RData")
```

```
rm(list = ls())
ls()
```

```
## character(0)
```

```
load(file = ".RData")
ls()
```

```
## [1] "data" "x"    "y"    "z"
```

```
rm(list = c("x", "y"))
ls()
```

```
## [1] "data" "z"
```

0.5 练习与作业 2：Factor 基础

0.5.1 factors 增加

- 创建一个变量：

```
x <- c("single", "married", "married", "single");
```

- 为其增加两个 levels，`single`, `married`;
- 以下操作能成功吗？

```
x[3] <- "widowed";
```

- 如果不，请提供解决方案；

```
## 代码写这里，并运行;
x <- c("single", "married", "married", "single")
x <- factor(x, levels = c("single", "married"))
try(x[3] <- "widowed")
```

```
## Warning in `[<-.factor`(`*tmp*`, 3, value = "widowed"): 因子层次有错，产生了NA
```

```
# 解决方案
x <- factor(x, levels = c("single", "married", "widowed"))
try(x[3] <- "widowed")
x
```

```
## [1] single  married widowed single
## Levels: single married widowed
```

0.5.2 factors 改变

- 创建一个变量：

```
v = c("a", "b", "a", "c", "b")
```

- 将其转化为 `factor`，查看变量内容
- 将其第一个 levels 的值改为任意字符，再次查看变量内容

```
## 代码写这里，并运行;
v <- c("a", "b", "a", "c", "b")
v <- factor(v)
v
```

```
## [1] a b a c b
## Levels: a b c
```

```
levels(v)[1] <- "d"
v
```

```
## [1] d b d c b
## Levels: d b c
```

- 比较改变前后的 v 的内容，改变 levels 的操作使 v 发生了什么变化？

答：改变 levels 的操作使 v 的内容发生了变化，将原来的”a” 改为了”d”。

0.5.3 factors 合并

- 创建两个由随机大写字母组成的 factors
- 合并两个变量，使其 `factors` 得以在合并后保留

```
## 代码写这里，并运行；
x <- factor(sample(LETTERS, 10, replace = TRUE))
y <- factor(sample(LETTERS, 10, replace = TRUE))
x
```

```
##  [1] X G K O M P C R L Y
## Levels: C G K L M O P R X Y
```

```
y
```

```
##  [1] X L V E Y P V Y W U
## Levels: E L P U V W X Y
```

```
c(x, y)
```

```
##  [1] X G K O M P C R L Y X L V E Y P V Y W U
## Levels: C G K L M O P R X Y E U V W
```

0.5.4 利用 factor 排序

以下变量包含了几个月份，请使用 `factor`，使其能按月份，而不是英文字符串排序：

```
mon <- c("Mar","Nov","Mar","Aug","Sep","Jun","Nov","Nov","Oct","Jun","May","Sep","Dec",
```

```
## 代码写这里，并运行；
mon <- c("Mar","Nov","Mar","Aug","Sep","Jun","Nov",
  "Nov","Oct","Jun","May","Sep","Dec","Jul","Nov")
mon <- factor(mon, levels = c("Jan", "Feb", "Mar",
  "Apr", "May", "Jun", "Jul", "Aug", "Sep", "Oct", "Nov", "Dec"))
sort(mon)
```

```
##  [1] Mar Mar May Jun Jun Jul Aug Sep Sep Oct Nov Nov Nov Nov Dec
## Levels: Jan Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec
```

0.5.5 forcats 的问题

`forcats` 包中的 fct_inorder, fct_infreq 和 fct_inseq 函数的作用是什么？

请使用 `forcats` 包中的 `gss_cat` 数据举例说明

```
## 代码写这里，并运行；
library(forcats)
```

```
## Warning: 程辑包'forcats'是用R版本4.1.3 来建造的
```

```
head(gss_cat)
```

```
##   year       marital age  race       rincome            partyid
## 1 2000 Never married  26 White $8000 to 9999       Ind,near rep
## 2 2000      Divorced  48 White $8000 to 9999 Not str republican
## 3 2000       Widowed  67 White Not applicable        Independent
## 4 2000 Never married  39 White Not applicable       Ind,near rep
## 5 2000      Divorced  25 White Not applicable   Not str democrat
## 6 2000       Married  25 White $20000 - 24999    Strong democrat
##                relig            denom tvhours
## 1         Protestant Southern baptist      12
## 2         Protestant Baptist-dk which      NA
## 3         Protestant  No denomination       2
## 4 Orthodox-christian   Not applicable       4
## 5               None   Not applicable       1
## 6         Protestant Southern baptist      NA
```

```
# fct_inord er: 按出现顺序为 levels 排序
fct_inorder(gss_cat$marital) %>% levels()
```

```
## [1] "Never married" "Divorced"      "Widowed"       "Married"
## [5] "Separated"     "No answer"
```

```
# fct_infreq: 按出现频率为 levels 排序，出现频率高的拍在前面
fct_infreq(gss_cat$marital) %>% levels()
```

```
## [1] "Married"       "Never married" "Divorced"      "Widowed"
## [5] "Separated"     "No answer"
```

```
# fct_inseq: 根据 level 的数字大小为 levels 排序，要求 factor levels 为数字
factor(gss_cat$age, levels = 80:60) %>% levels()
```

```
##  [1] "80" "79" "78" "77" "76" "75" "74" "73" "72" "71" "70" "69" "68" "67" "66"
## [16] "65" "64" "63" "62" "61" "60"
```

```
factor(gss_cat$age, levels = 80:60) %>% fct_inseq() %>% levels()
```

```
##  [1] "60" "61" "62" "63" "64" "65" "66" "67" "68" "69" "70" "71" "72" "73" "74"
## [16] "75" "76" "77" "78" "79" "80"
```

0.6 练习与作业 3：用 mouse genes 数据做图

0.6.1 画图

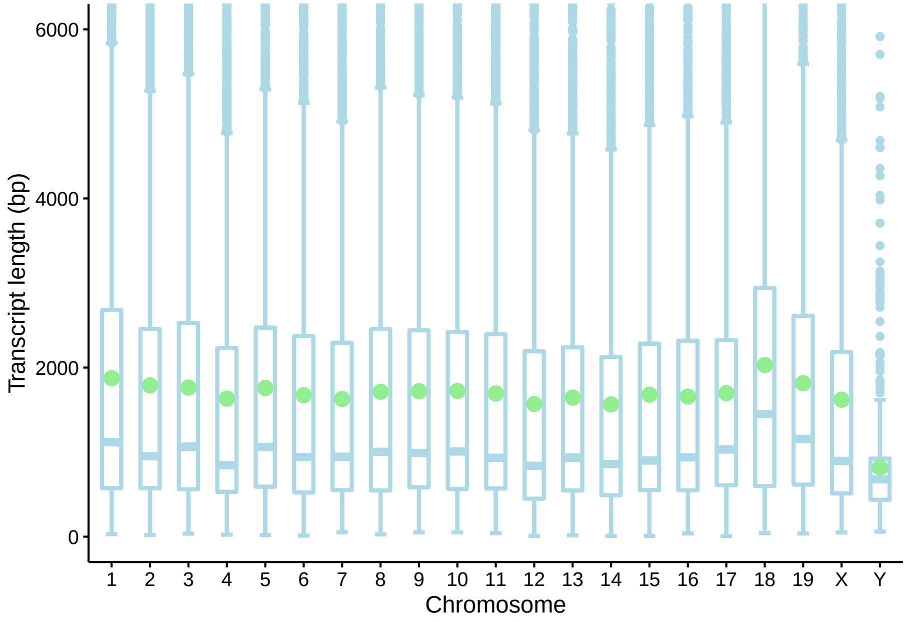
1. 用 readr 包中的函数读取 mouse genes 文件（从本课程的 Github 页面下载 data/talk04/ ）
2. 选取常染色体（1-19）和性染色体（X，Y）的基因
3. 画以下两个基因长度 boxplot :

- 按染色体序号排列，比如 1, 2, 3 …. X, Y
- 按基因长度中值排列，从短 -> 长 …

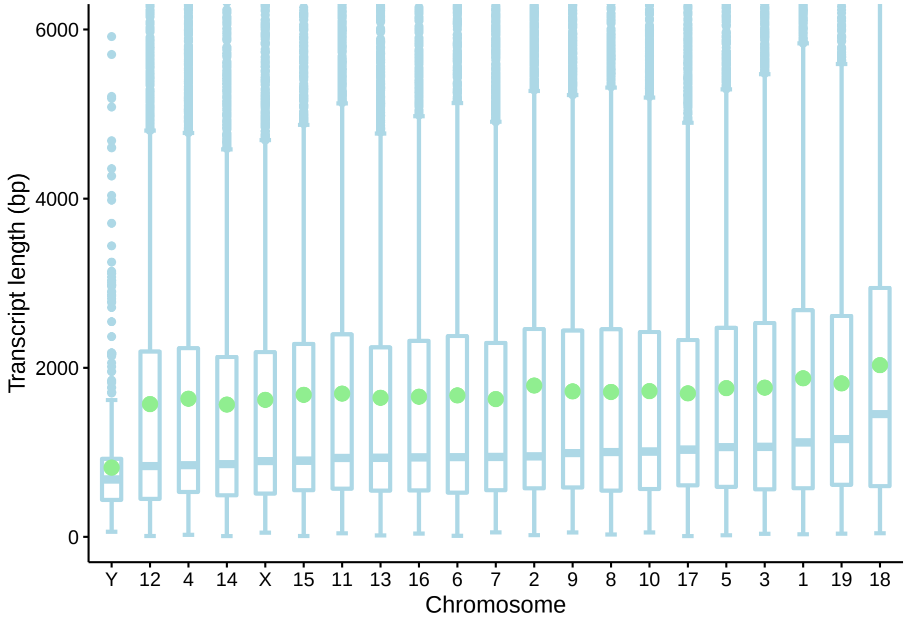
```
## 代码写这里，并运行；
# 不显示 warning 信息 和 message
options(warn = -1, message = -1)

library(readr)
library(ggplot2)
library(dplyr)
```

```
##
## 载入程辑包：'dplyr'

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

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

```r
options(warn = 0, message = 0)
mouse_genes <- read_tsv("../data/talk04/mouse_genes_biomart_sep2018.txt",
  col_names = TRUE, show_col_types = FALSE)

colnames(mouse_genes) <- gsub(" ", "_", colnames(mouse_genes))
colnames(mouse_genes) <- gsub("/", "_", colnames(mouse_genes))
colnames(mouse_genes) <- gsub("\\(", "", colnames(mouse_genes))
colnames(mouse_genes) <- gsub("\\)", "", colnames(mouse_genes))
autosome_genes <- filter(mouse_genes,
  Chromosome_scaffold_name %in% c(1:19, "X", "Y"))

# 按染色体序号排列
ggplot(autosome_genes,
  aes(x = factor(Chromosome_scaffold_name, levels = c(1:19, "X", "Y")),
  y = Transcript_length_including_UTRs_and_CDS)) +
  stat_boxplot(geom = "errorbar", width = 0.3, lwd = 1, color = "lightblue") +
  geom_boxplot(width = 0.5, lwd = 1, color = "lightblue") +
  theme_minimal() +
  theme(panel.grid.major.x = element_blank(),
    panel.grid.minor.x = element_blank(),
    panel.grid.major.y = element_blank(),
    panel.grid.minor.y = element_blank(),
    panel.background = element_blank(),
    panel.border = element_blank(),
    axis.line = element_line(color = "black", size = 0.5),
    axis.ticks = element_line(color = "black", size = 0.5),
    axis.text.x = element_text(size = 10, color = "black"),
    axis.text.y = element_text(size = 10, color = "black"),
    axis.title.x = element_text(size = 12, color = "black"),
    axis.title.y = element_text(size = 12, color = "black"),
    legend.position = "none") +
  coord_cartesian(ylim = c(0, 6000)) +
  stat_summary(fun = mean, geom = "point", shape = 20,
    size = 5, color = "lightgreen", fill = "lightgreen") +
  xlab("Chromosome") +
  ylab("Transcript length (bp)")
```



```
# 按基因长度 中值 排列，从 短 -> 长
ggplot(autosome_genes, aes(x = reorder(Chromosome_scaffold_name,
    Transcript_length_including_UTRs_and_CDS, median),
    y = Transcript_length_including_UTRs_and_CDS)) +
  stat_boxplot(geom = "errorbar", width = 0.3, lwd = 1, color = "lightblue") +
  geom_boxplot(width = 0.5, lwd = 1, color = "lightblue") +
  theme_minimal() +
  theme(panel.grid.major.x = element_blank(),
    panel.grid.minor.x = element_blank(),
    panel.grid.major.y = element_blank(),
    panel.grid.minor.y = element_blank(),
    panel.background = element_blank(),
    panel.border = element_blank(),
    axis.line = element_line(color = "black", size = 0.5),
    axis.ticks = element_line(color = "black", size = 0.5),
    axis.text.x = element_text(size = 10, color = "black"),
    axis.text.y = element_text(size = 10, color = "black"),
    axis.title.x = element_text(size = 12, color = "black"),
    axis.title.y = element_text(size = 12, color = "black"),
    legend.position = "none") +
  coord_cartesian(ylim = c(0, 6000)) +
  stat_summary(fun = mean, geom = "point", shape = 20,
    size = 5, color = "lightgreen", fill = "lightgreen") +
  xlab("Chromosome") +
  ylab("Transcript length (bp)")
```


Transcript length (bp)
Y
X
Chromosome