

# R language basics, part 3: factor

## HUST Bioinformatics course series

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# section 1: TOC

# 前情提要

## data frame and tibble

- declaration & usage
- manipulation (更多相关内容会在介绍 dplyr 时讲到)
- differences between data.frame and tibble
- advantages of using tibble (更多内容以后会介绍)
- with, within, attach, detach 等的用法

## IO

- read from files of different formats
- write to files
- use GUI to read files (& get the corresponding code)

# 今次预报

- ① IO, project management, working enviroment management
- ② factors: R 中最重要的概念之一
- ③ exercises

## section 2: IO and working enviroment management

# R session 的概念

每个 R session 是一个单独的工作空间 (work space)，包含各自的数据、变量和操作历史。

```

wchen — R session 1 — R — 70x22
[wchen @mbp: 1] ~ > R
WARNING: ignoring environment value of R_HOME

R version 3.6.1 (2019-07-05) -- "Action of the Toes"
Copyright (C) 2019 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>

wchen — R session 2 — R — 74x22
[wchen @mbp: 1] ~ > R
WARNING: ignoring environment value of R_HOME

R version 3.6.1 (2019-07-05) -- "Action of the Toes"
Copyright (C) 2019 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
  
```

Figure 1: two R sessions

# R session in RStudio

Each RStudio session is automatically associated with a R session

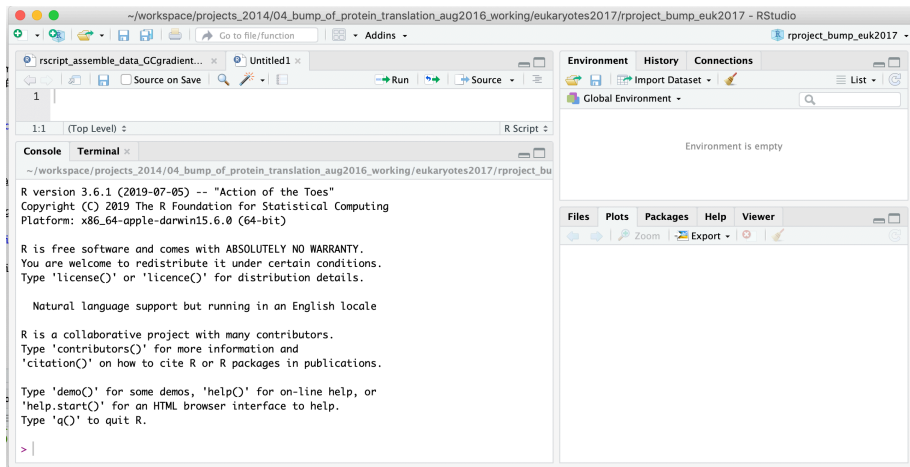


Figure 2: R session in RStudio

# start a new RStudio session by creating a new project

- 1 右上角的 Project 按钮，在弹出菜单里选 New Project ...

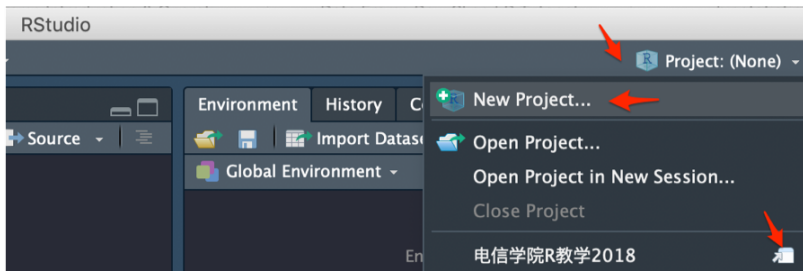


Figure 3: create new project, step 1



## create a new project, cont.

- 2 Select: New directory -> New Project in the popup window

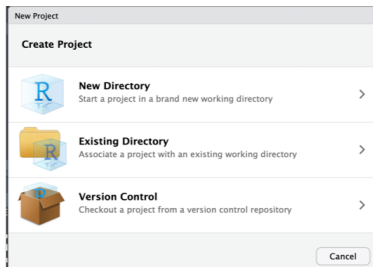
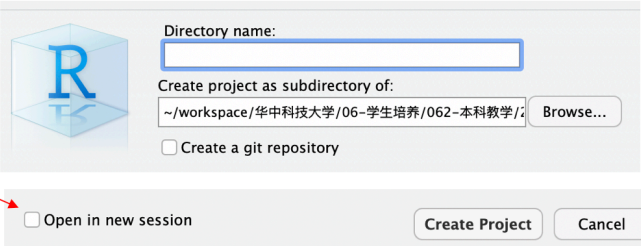


Figure 4: create new project, step 2

## create a new project, cont.

- 3 Enter a new directory name, choose its mother directory ...



The image shows the 'Create New Project' dialog box in RStudio. On the left is the R logo. The main area contains a 'Directory name:' text box, a 'Create project as subdirectory of:' text box with a file path, a 'Browse...' button, and a checkbox for 'Create a git repository'. At the bottom, there is a checkbox for 'Open in new session' which is highlighted by a red arrow, and two buttons: 'Create Project' and 'Cancel'.

Directory name:

Create project as subdirectory of:

~/workspace/华中科技大学/06-学生培养/062-本科教学/...

Browse...

☐ Create a git repository

☐ Open in new session

Create Project Cancel

Figure 5: create new project, step 3

# 现场演示

演示 ~~

# working space

当前工作空间，包括所有已装入的数据、包和自制函数  
可通过以下代码管理变量

```
ls(); ## 显示当前环境下所有变量
```

```
## [1] "color_block"
```

```
rm( x ); ## 删除一个变量
```

```
## Warning in rm(x): 找不到对象 'x'
```

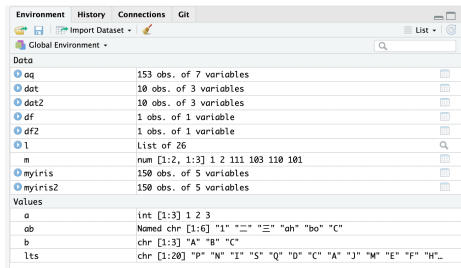
```
ls();
```

```
## [1] "color_block"
```

```
##rm(list=ls()); ## 删除当前环境下所有变量!!!
```

# variables in working space in RStudio

在 RStudio 右上角的 “Environment” 窗口显示了所有当前工作间的变量



**Figure 6:** RStudio environment window

# save and restore work space

```
## -- save all loaded variables into an external .RData file  
save.image( file = "prj_r_for_bioinformatics_aug3_2019.RData" );  
  
## -- restore ( load ) saved work space  
load( file = "prj_r_for_bioinformatics_aug3_2019.RData" );
```

## Notes

- existing variables will be kept, however, those with the same names will be replaced by loaded variables
- please consider using `rm( list=ls() )` to remove all existing variables to have a clean start
- you may need to reload all the packages

## save selected variables

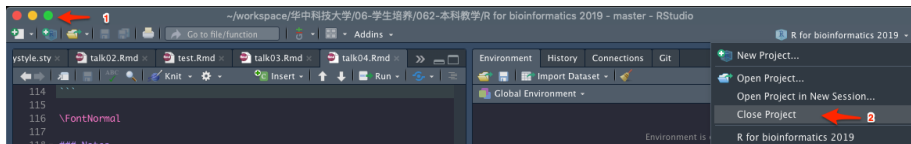
Sometimes you need to transfer processed data to a collaborator ...

```
## save selected variables to external
save(city, country, file="1.RData"); ## you can specify directory name

## --
load( "1.RData" );
```

# close and (re)open a project

close a project is easy:



**Figure 7:** Two ways of closing a project

however ...



# 退出 projects 时的一些选项 (RStudio)

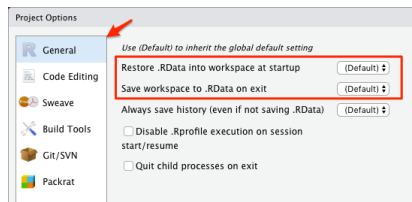
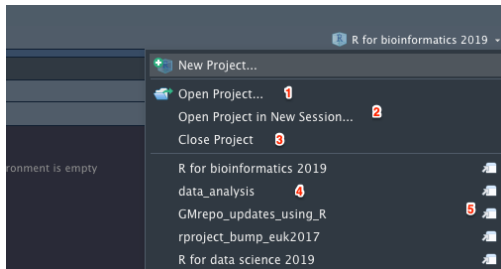


Figure 8: Project options

## notes

- 退出时保存
- 打开时装入
- 但数据较大时，装入时间可能过长 ...

# open a project



**Figure 9:** Open a project

演示项目的不同打开姿势（1-5）。

# 练习

- 创建一个项目
- 定义一些变量
- 从外部文件装入一些数据
- 保存 workspace 到.RData
- 退出 project
- 重新打开 project 并恢复 workspace

## section 3: factors

# 什么是 factors ?

Factor is a data structure used for fields that takes only predefined, finite number of values (categorical data).

Factor 用于限制某个字段 (列), 只允许其接受某些值

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

```
## chr [1:4] "single" "married" "married" "single"
```

```
## create factor as it is ...
```

```
x <- as.factor(x);
```

```
## please note the change in the displayed values ...
```

```
str(x);
```

```
## Factor w/ 2 levels "married","single": 2 1 1 2
```

```
## create factor from scratch ...
```

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

```
str(x);
```

```
## Factor w/ 2 levels "married","single": 2 1 1 2
```

# factors, cont.

## Factors 会限制输入数据的选择范围

```
str(x);
```

```
## Factor w/ 2 levels "married","single": 2 1 1 2
```

```
x[ length(x) + 1 ] <- "widowed";
```

```
## Warning in `[<-.factor`(`*tmp*`, length(x) + 1, value = "widowed"): invalid
## factor level, NA generated
```

```
x;
```

```
## [1] single married married single <NA>
## Levels: married single
```

Use levels() function to add new factors

```
levels(x) <- c(levels(x), "widowed");
x[ length(x) + 1 ] <- "widowed";
str(x);
```

```
## Factor w/ 3 levels "married","single",...: 2 1 1 2 NA 3
```

# factors, cont.

Play around with `levels()`:

```
## other ways of assigning factors ...
y <- as.factor( c( "single", "married", "married", "single" ) );
levels( y );
```

```
## [1] "married" "single"
```

```
levels(y) <- c("single", "married", "widowed");
str(y);
```

```
## Factor w/ 3 levels "single","married",...: 2 1 1 2
```

**\*\* 问题 \*\*** 如果运行以下代码，会报错吗？

```
y[ length(y) + 1 ] <- "widowed";
```

more to read

# factor 在做图中的应用（真正精髓）

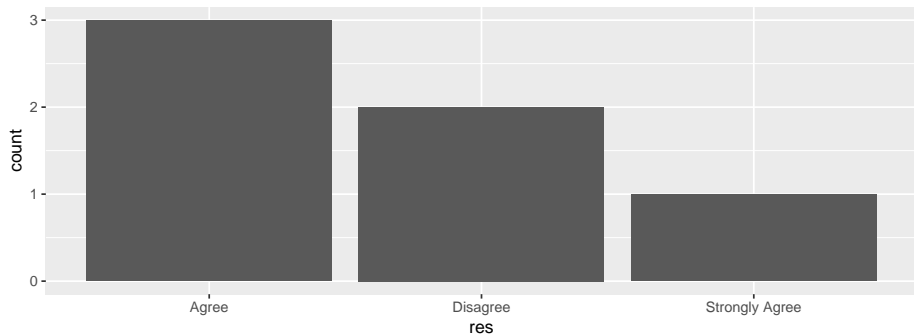
```
## 一项 mock 调查结果数据
( responses <- factor( c("Agree", "Agree", "Strongly Agree", "Disagree",
                        "Disagree", "Agree") ) );
```

```
## [1] Agree          Agree          Strongly Agree Disagree
## [5] Disagree        Agree
## Levels: Agree Disagree Strongly Agree
```

```
## -- plot the results --
library(ggplot2);
barplot <-
  ggplot( data = data.frame( res = responses ), aes( x = res ) ) +
  geom_bar();
```



## factor 在做图中的应用, cont.



默认情况下, factor 按字母表排序: Agree -> Disagree -> Strong Agree 。  
ggplot2 也会按 factor 的排序作图

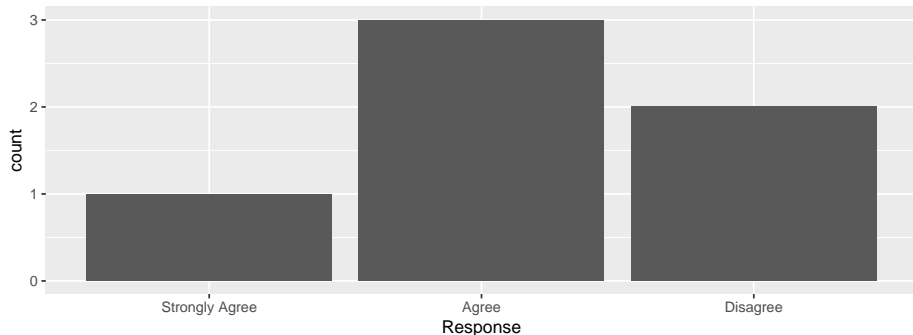
# 调整 factor 以调整画图顺序

```
res <- data.frame( res=responses );
## -- 按照同意程度从强-> 弱 排序
res$res <- factor( res$res, levels = c( "Strongly Agree", "Agree", "Disagree" ) );
str(res);
```

```
## 'data.frame':    6 obs. of  1 variable:
## $ res: Factor w/ 3 levels "Strongly Agree",...: 2 2 1 3 3 2
```

```
plot2 <-
  ggplot( data = res, aes( x = res ) ) +
  geom_bar() +
  xlab( "Response" );
```

# 调整 factor 以调整画图顺序, cont.



**\*\* 练习 \*\*** 按意程度从弱-> 强排序并作图!!

# ordered factor

通过 ordered 参数，让用户知道 factors 是经过精心排序的

```
( responses <- factor( c("Agree", "Agree", "Strongly Agree", "Disagree", "Disagree", "Agree"),
  ordered = T ) );
```

```
## [1] Agree          Agree          Strongly Agree Disagree
## [5] Disagree        Agree
## Levels: Agree < Disagree < Strongly Agree
```

```
is.ordered( responses );
```

```
## [1] TRUE
```

# 通过 factor 改变值

使用 dplyr 包的 recode() 函数改变 value

```
( x <- factor( c( "alpha", "beta", "gamma", "theta", "beta", "alpha" ) ) );
```

```
## [1] alpha beta  gamma theta beta  alpha
## Levels: alpha beta gamma theta
```

```
## --
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
```

```
x <- recode( x, "alpha" = "one", "beta" = "two" );
str(x);
```

```
## Factor w/ 4 levels "one","two","gamma",...: 1 2 3 4 2 1
```

# 去除不用的 levels

? 什么时候会用到:

```
mouse.genes <- read.delim( file = "data/talk04/mouse_genes_biomart_sep2018.txt",
                           sep = "\t", header = T, stringsAsFactors = T );
```

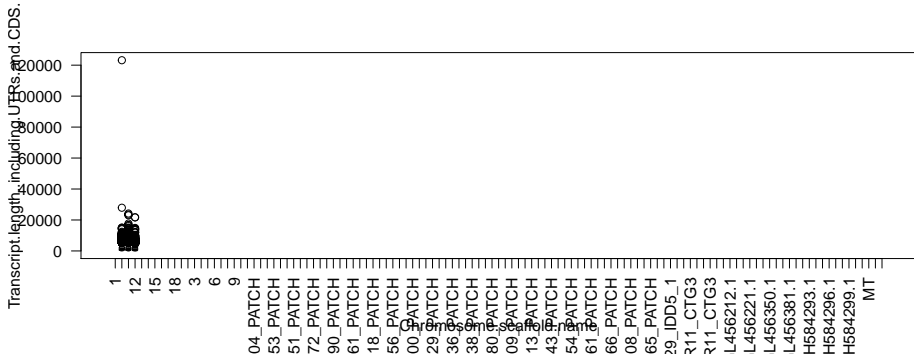
```
str(mouse.genes);
```

```
## 'data.frame':    138532 obs. of  6 variables:
## $ Gene.stable.ID          : Factor w/ 55029 levels "ENSMUSG000000000001",.
## $ Transcript.stable.ID    : Factor w/ 138532 levels "ENSMUST000000000001",
## $ Protein.stable.ID      : Factor w/ 65897 levels "", "ENSMUSP000000000001
## $ Transcript.length..including.UTRs.and.CDS.: int  67 67 1144 69 519 1824 71 59 67 1378 ..
## $ Transcript.type         : Factor w/ 48 levels "3prime_overlapping_ncRNA
## $ Chromosome.scaffold.name : Factor w/ 117 levels "1","10","11",...: 115 11
```

# 去除不用的 levels, cont.

```
mouse.chr_10_12 <- subset( mouse.genes, Chromosome.scaffold.name %in% c( "10", "11", "12" ) );
## plot length distribution --

boxplot( Transcript.length..including.UTRs.and.CDS. ~ Chromosome.scaffold.name, data = mouse.chr_10_12 )
```



subset() 无法去除不用的 factors ...

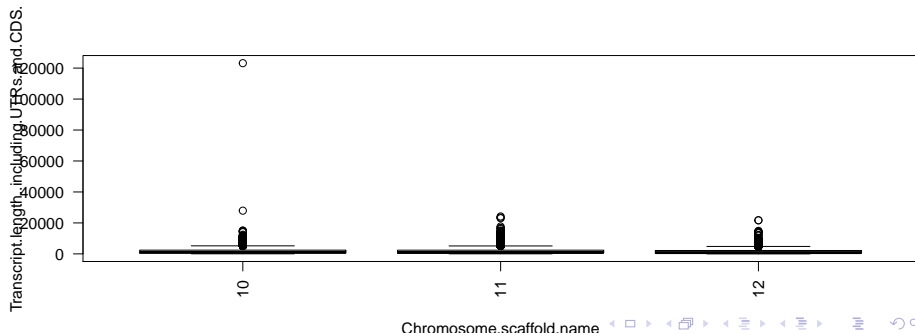
# 去除不用的 levels, cont.

```
mouse.chr_10_12$Chromosome.scaffold.name <-
  droplevels( mouse.chr_10_12$Chromosome.scaffold.name );

levels( mouse.chr_10_12$Chromosome.scaffold.name );
```

```
## [1] "10" "11" "12"
```

```
## 再次 plot ...
boxplot( Transcript.length..including.UTRs.and.CDS. ~ Chromosome.scaffold.name,
  data = mouse.chr_10_12, las = 2 );
```





## 也可以使用 tibble，完全不用担心 factor 的问题 ...

```
library( readr );
mouse.tibble <- read_delim( file = "data/talk04/mouse_genes_biomart_sep2018.txt",
                             delim = "\t", quote = "" )
```

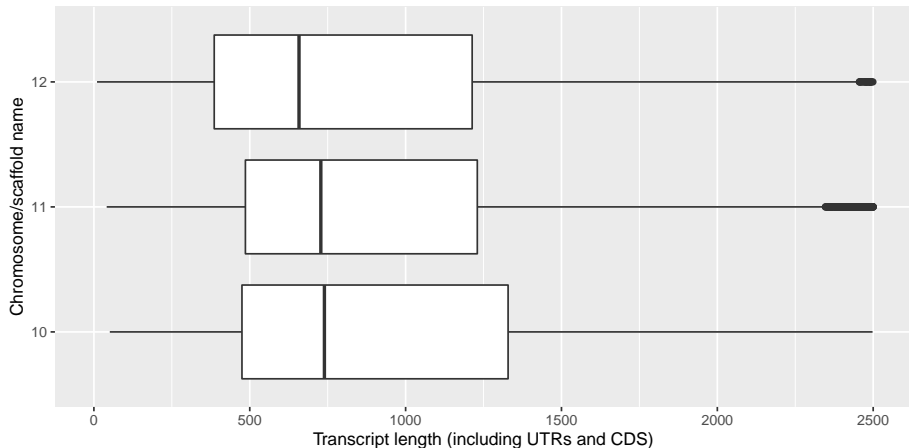
```
## Parsed with column specification:
## cols(
##   `Gene stable ID` = col_character(),
##   `Transcript stable ID` = col_character(),
##   `Protein stable ID` = col_character(),
##   `Transcript length (including UTRs and CDS)` = col_double(),
##   `Transcript type` = col_character(),
##   `Chromosome/scaffold name` = col_character()
## )
```

```
mouse.tibble.chr10_12 <-
  mouse.tibble %>% filter( `Chromosome/scaffold name` %in% c( "10", "11", "12" ) );
```

```
plot3 <-
  ggplot( data = mouse.tibble.chr10_12,
    aes( x = `Chromosome/scaffold name`,
      y = `Transcript length (including UTRs and CDS)` ) ) +
  geom_boxplot() +
  coord_flip() +
  ylim( 0, 2500 ) ;
```

## 用 tibble 解决 factor 的问题, cont.

```
## Warning: Removed 4770 rows containing non-finite values (st
```



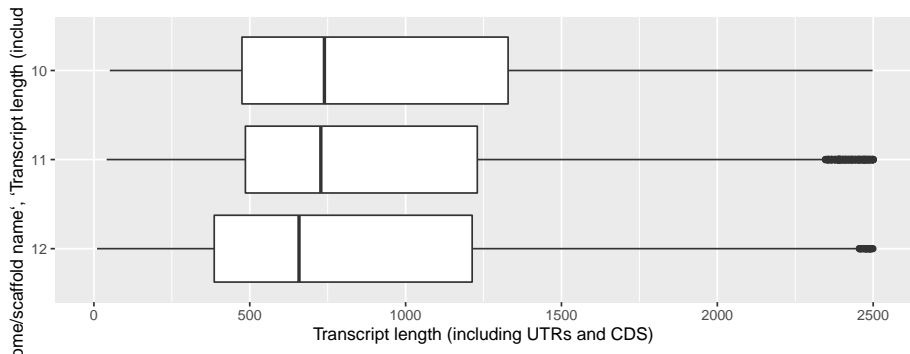
## 按基因长度中值从大 -> 小排序

```
plot4 <-
  ggplot( data = mouse.tibble.chr10_12,
    aes( x = reorder( `Chromosome/scaffold name`,
                      `Transcript length (including UTRs and CDS)`,
                      median ),
        y = `Transcript length (including UTRs and CDS)` ) ) +
  geom_boxplot() +
  coord_flip() +
  ylim( 0, 2500 ) ;
```

`reorder( vector_with_factor, numeric_value , FUN = mean )` 的用法

## 按基因长度中值从大 -> 小排序, cont.

```
## Warning: Removed 4770 rows containing non-finite values (st
```



**\*\* 注意 \*\*** `reorder( `Chromosome/scaffold name`, - `Transcript length (including UTRs and CDS)`, median )` 的作用

## 按基因长度中值从大 -> 小排序, cont.

**\*\* 问题 \*\***

- ① 如果要按小 -> 大的顺序排序呢 ? ( `reorder(Chromosome/scaffold name, -Transcript length (including UTRs and CDS)', median )` )
- ② `reorder` 的作用是什么 ?? 只在 `ggplot2` 里有用吗 ??

more to read!

## section 4: 练习与作业

## more to read & 练习:

- ① R factors 基础
- ② R 阅读和练习 2, 必读!!
- ③ R 练习 1
- ④ rename columns using dplyr
- ⑤ ggplot2 boxplot
- ⑥ ordering a plot in ggplot2

# 作业

- 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 选取常染色体的基因
- 3 画以下两个基因长度 boxplot :
  - 按染色体序号排列，从 1 开始
  - 按基因长度中值排列，从短 -> 长 ...

**\*\* 要求 \*\***

- 1 一周内提交
- 2 代码和两个 pdf 文件 ...