R language basics, part 3: factor

HUST Bioinformatics course series for '16 class

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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)

IO

- read from files of different formats
- write to files

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。

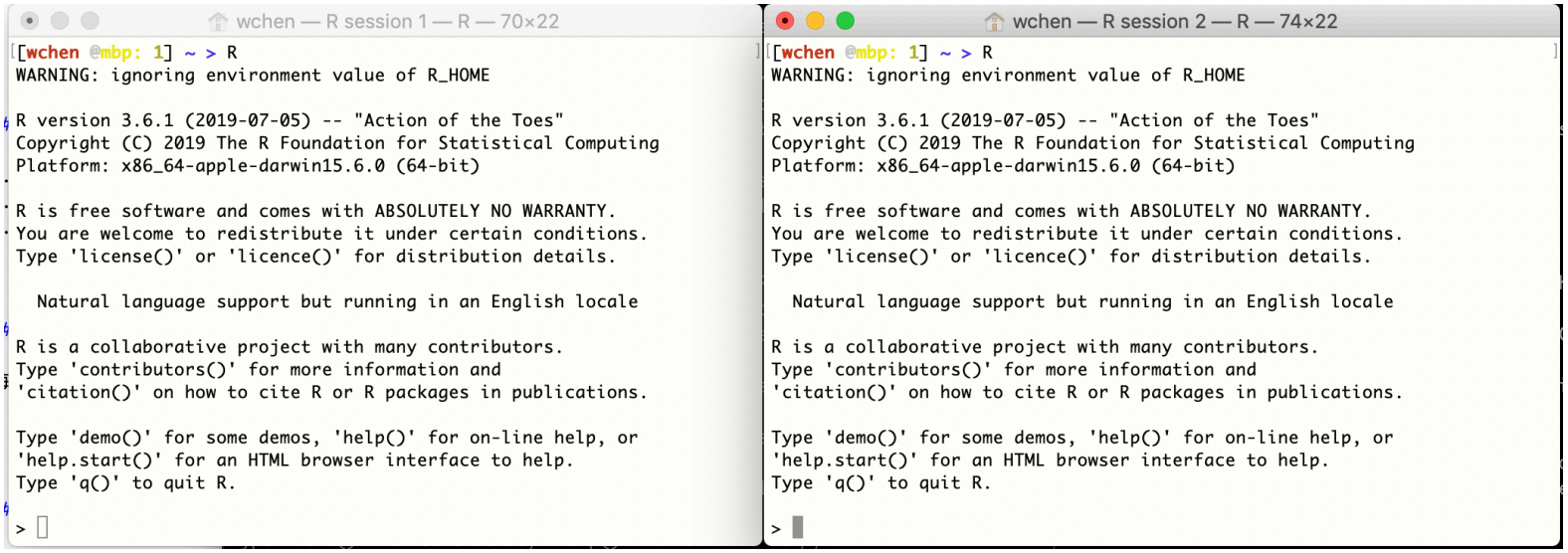


Figure 1: two R sessions

R session in RStudio

each RStudio session is automatically associated with a R session

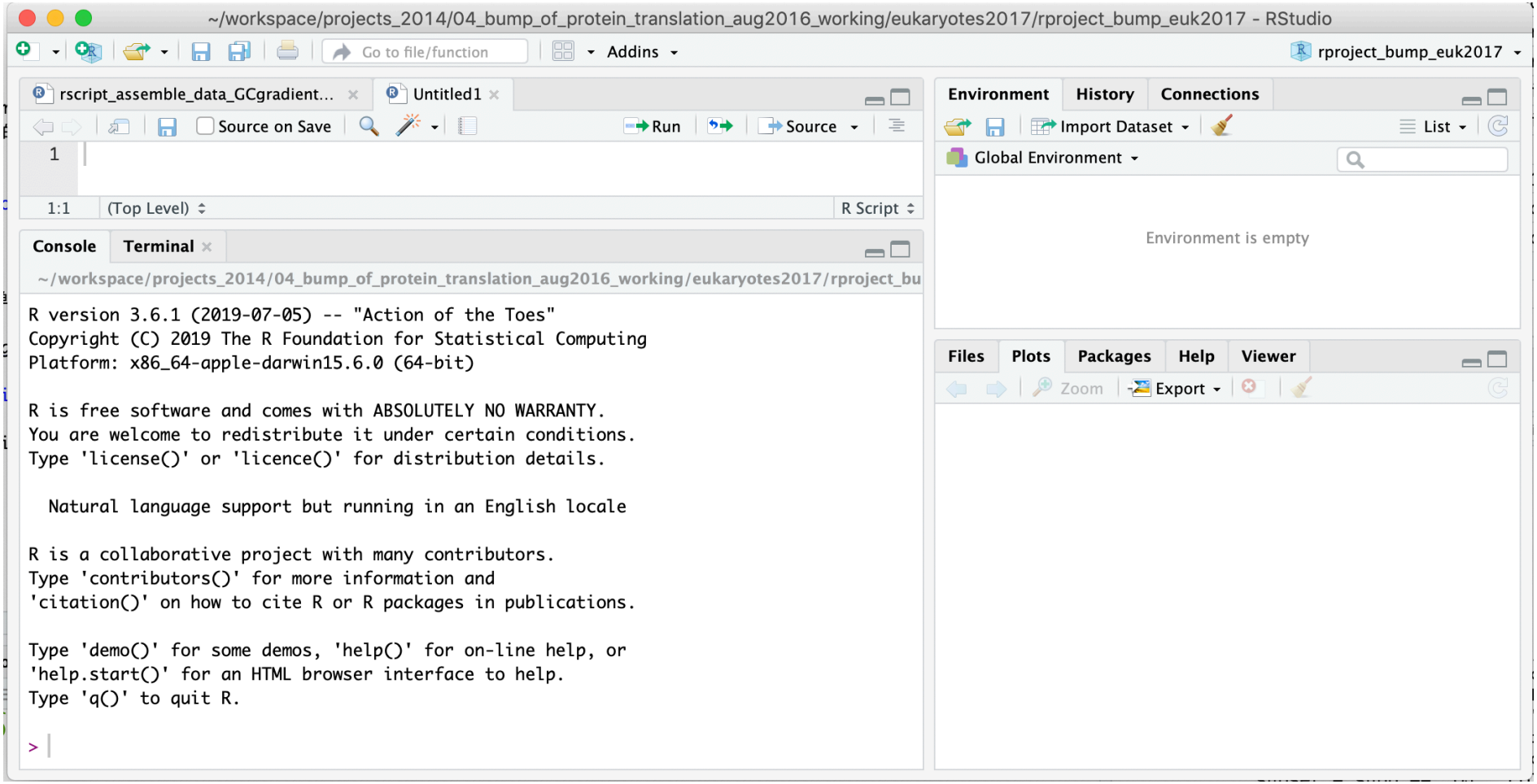


Figure 2: R session in RStudio

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 ...

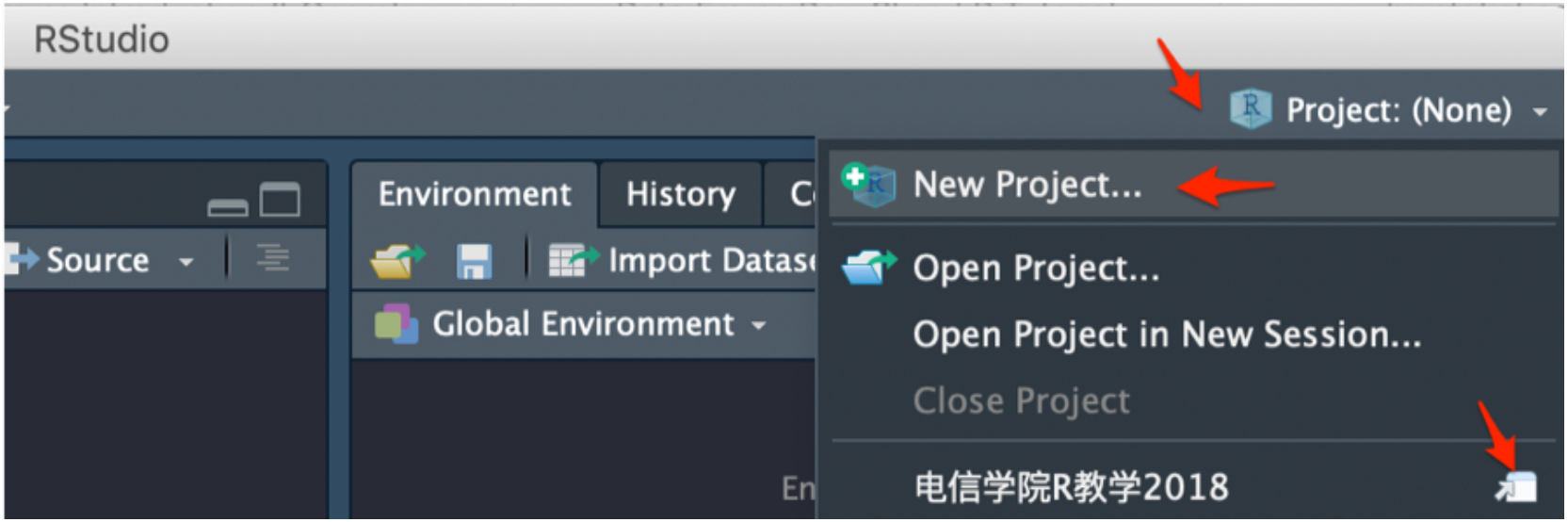


Figure 3: create new project, step 1

create a new project, cont.

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

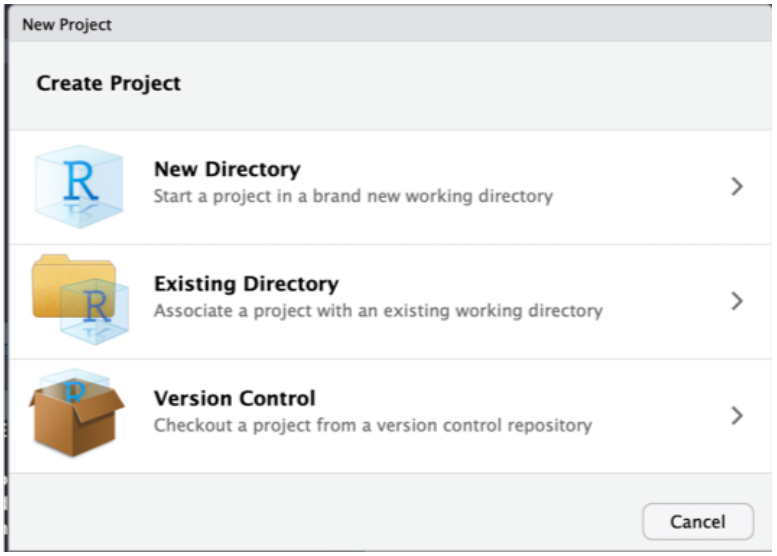


Figure 4: create new project, step 2

create a new project, cont.

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

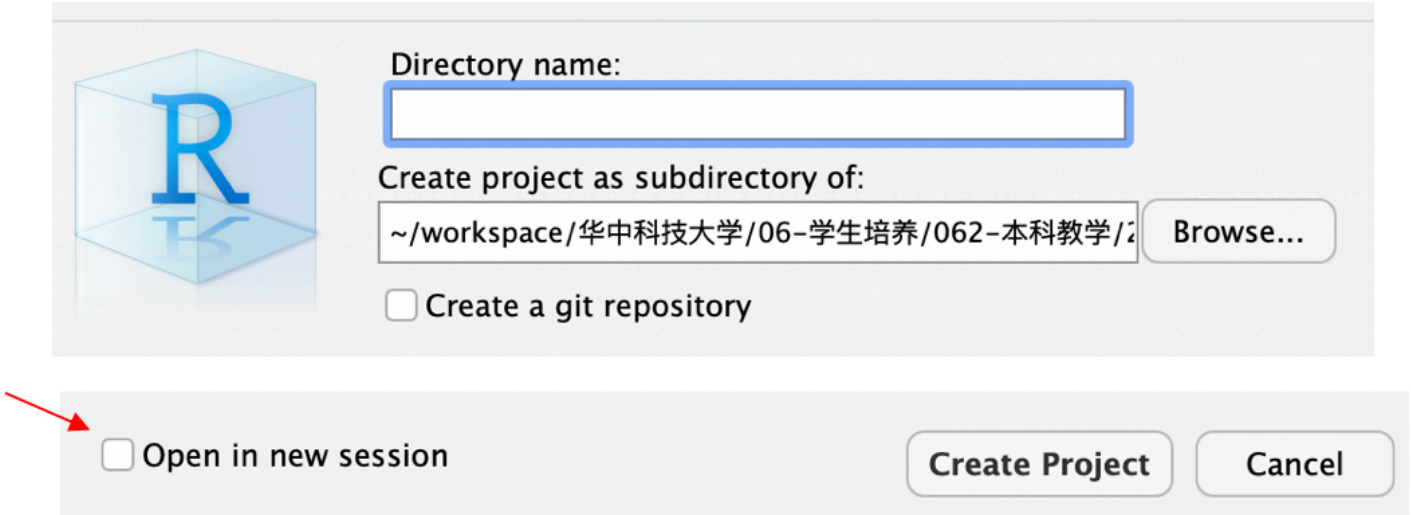


Figure 5: create new project, step 3

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): object 'x' not found
```

```
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 “Enviroment” 窗口显示了所有当前工作间的变量

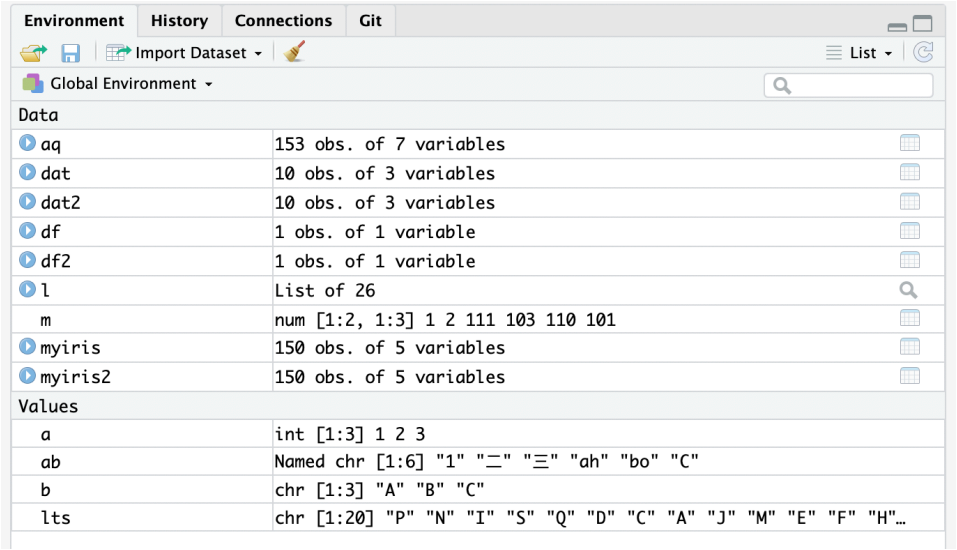


Figure 6: RStudio enviroment window

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 will 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:

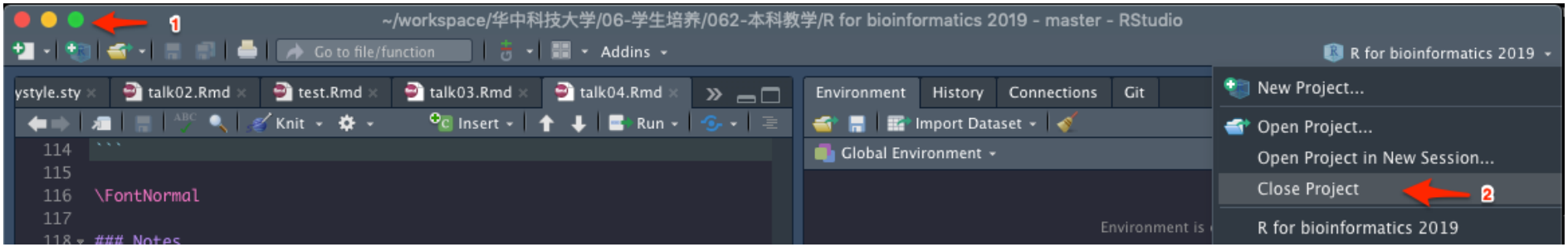


Figure 7: Two ways of closing a project

however ...

退出 projects 时的一些选项（RStudio）

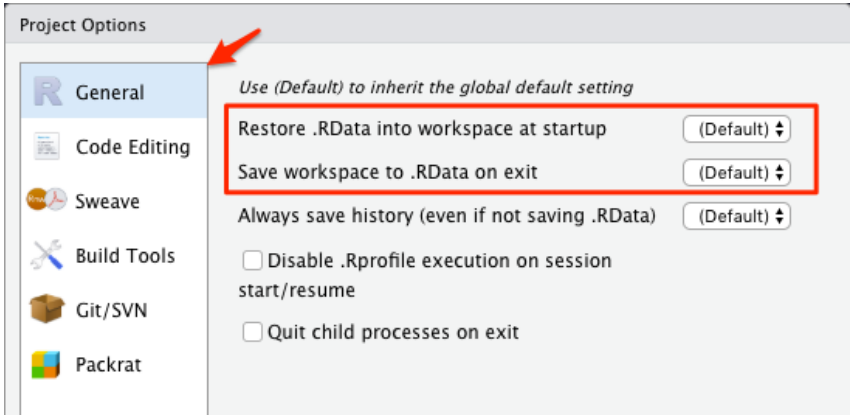


Figure 8: Project options

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

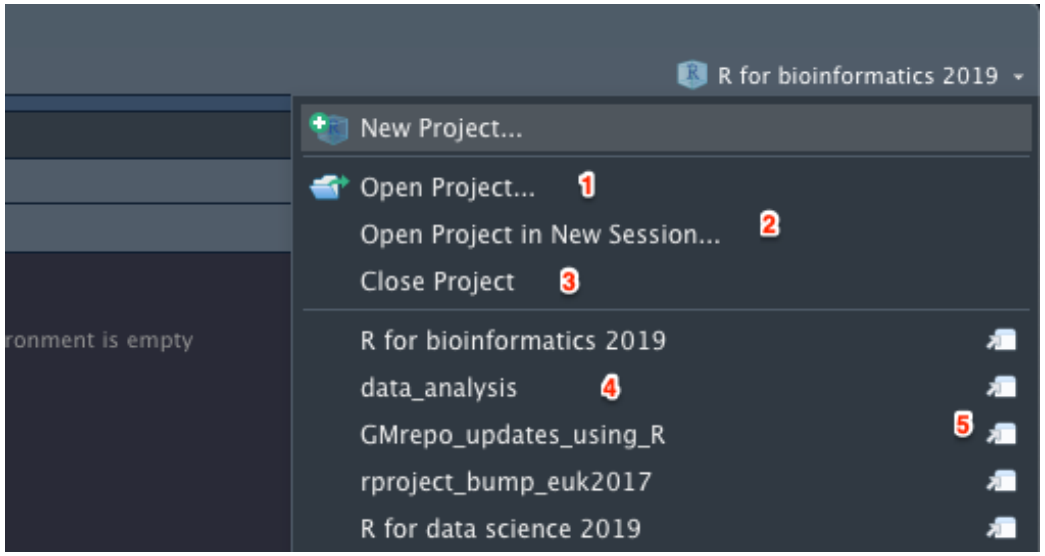


Figure 9: Open a project

演示项目的不同打开姿式（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).

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

```
##  chr [1:4] "single" "married" "married" "single"
##  - attr(*, "levels")= chr [1:2] "single" "married"
```

** 问题 ** 如果运行以下代码，会报错吗？

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

more to read

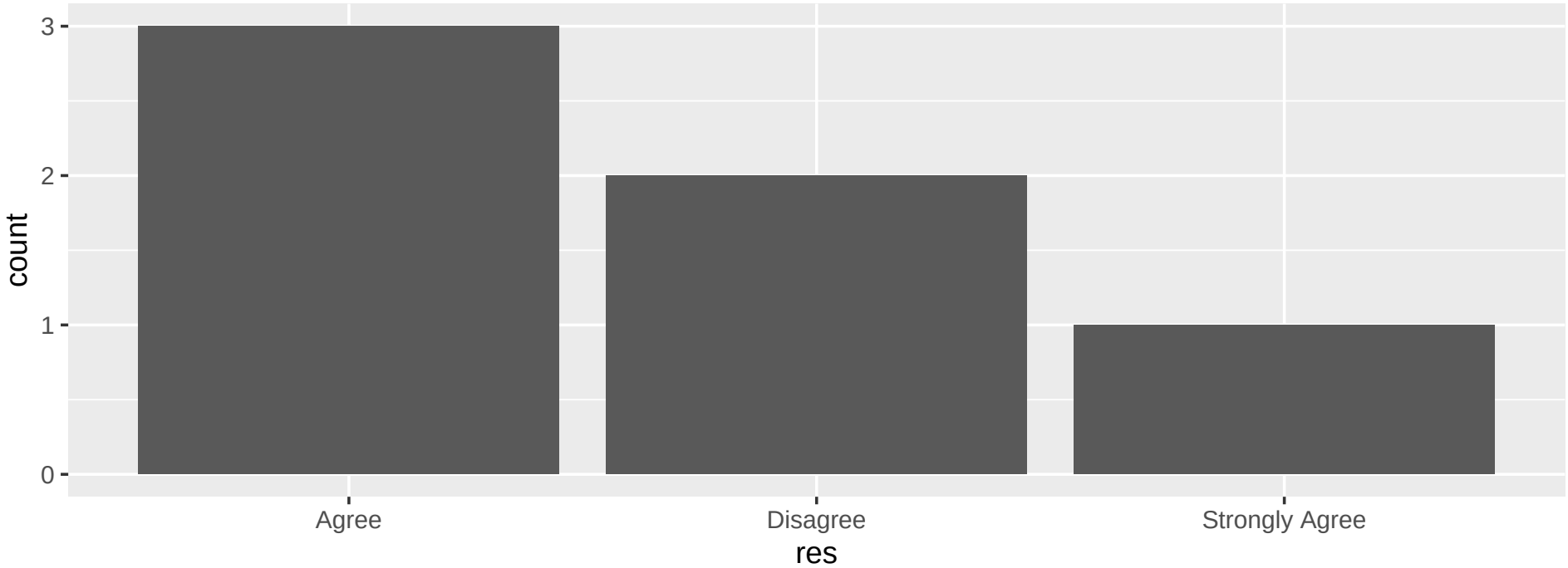
factor 在做图中的应用（真正精髓）

```
## 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

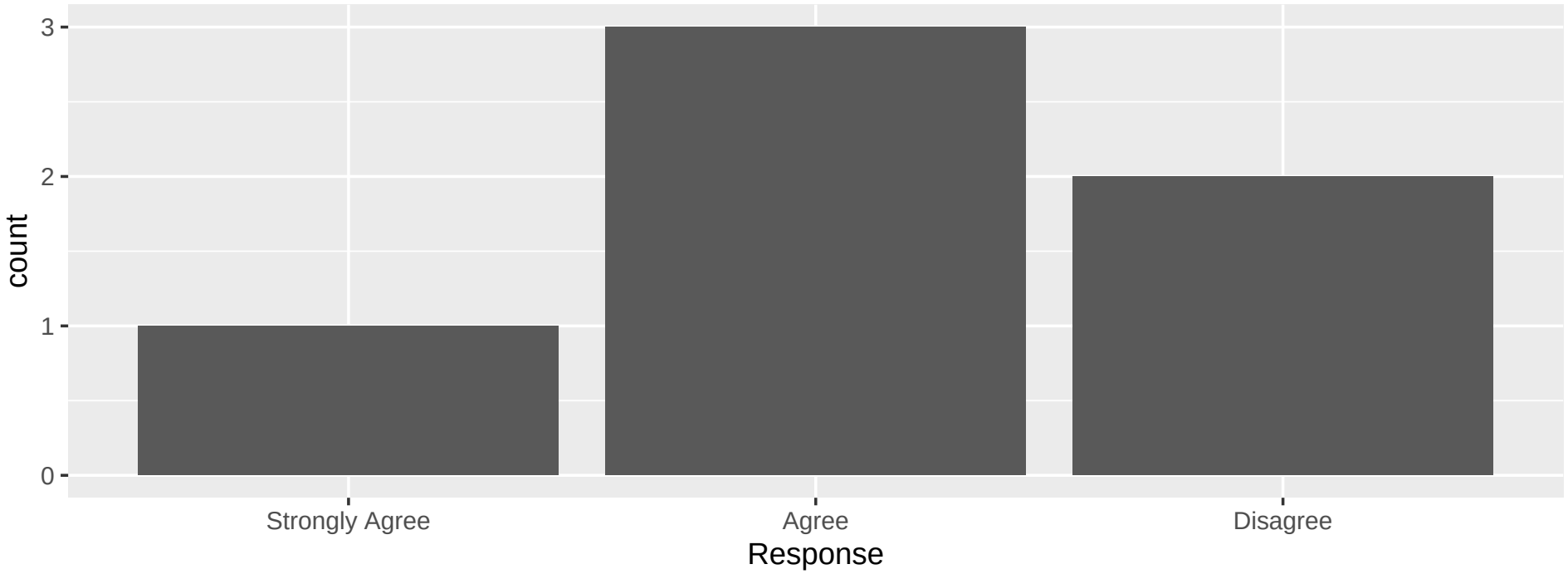
调整 factor 以调整画图顺序

```
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

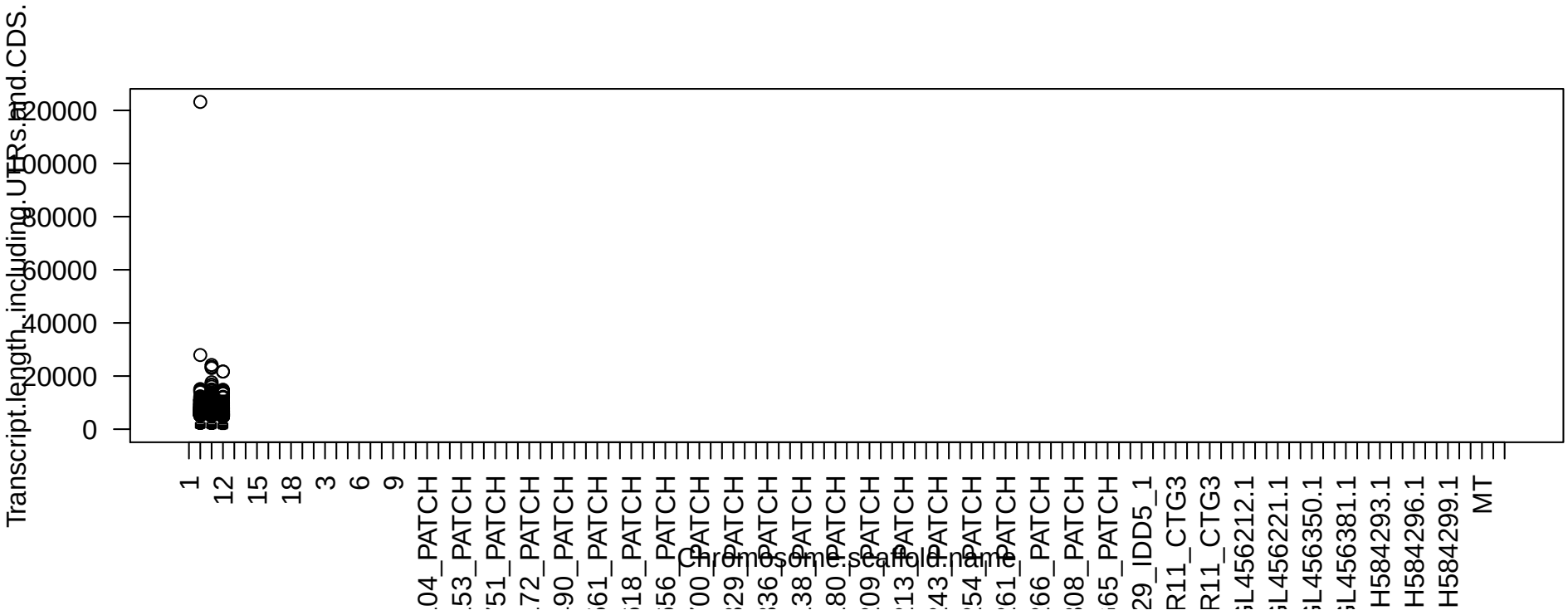
? 什么时候会用到:

```
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 "ENSMUSG00000000001",.
##  $ Transcript.stable.ID                    : Factor w/ 138532 levels "ENSMUST00000000001",
##  $ Protein.stable.ID                       : Factor w/ 65897 levels "","ENSMUSP00000000001
##  $ 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
```



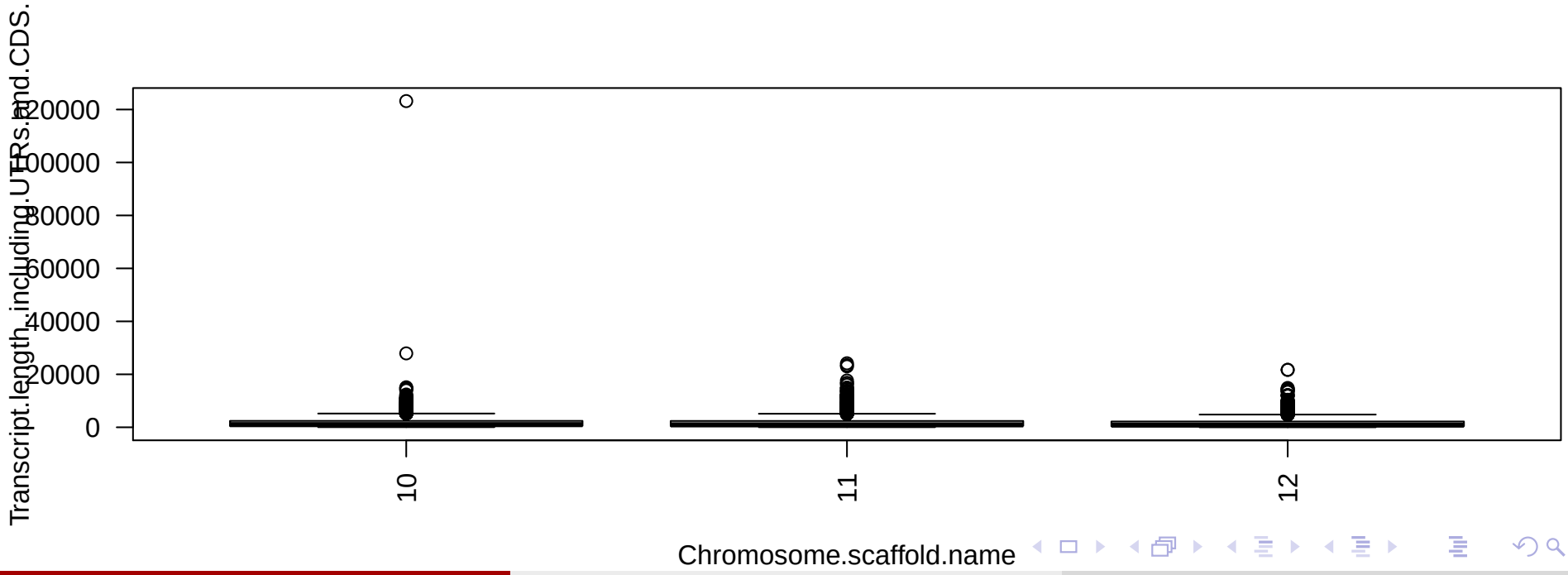
`subset()` 无法去除不用的 factors ...

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 ...

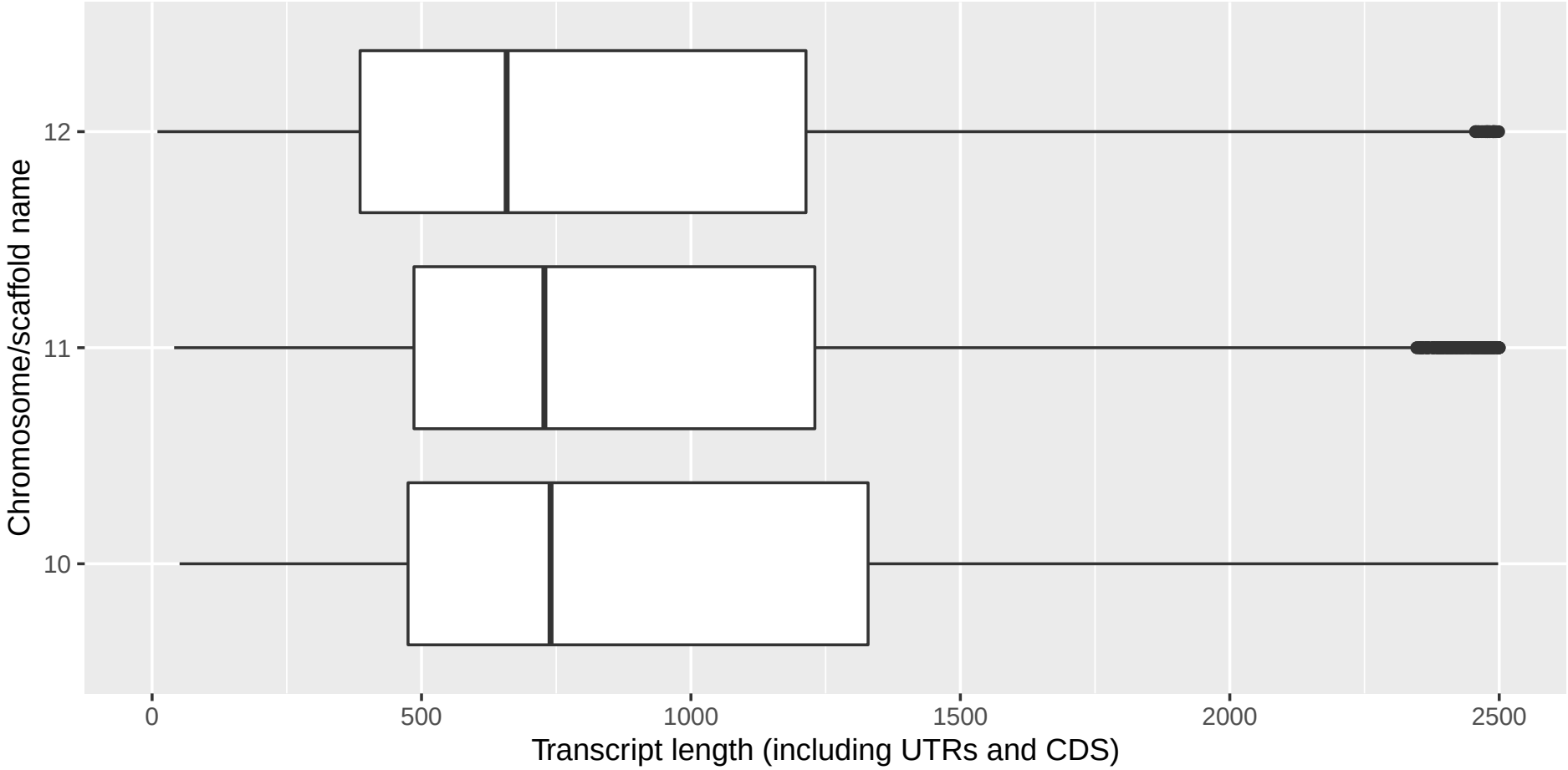
```
library( readr );
mouse.tibble <- read_delim( file = "data/talk04/mouse_genes_biomart_sep2018.txt",
                            delim = "\t", quote = "" )
```

```
## 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
```



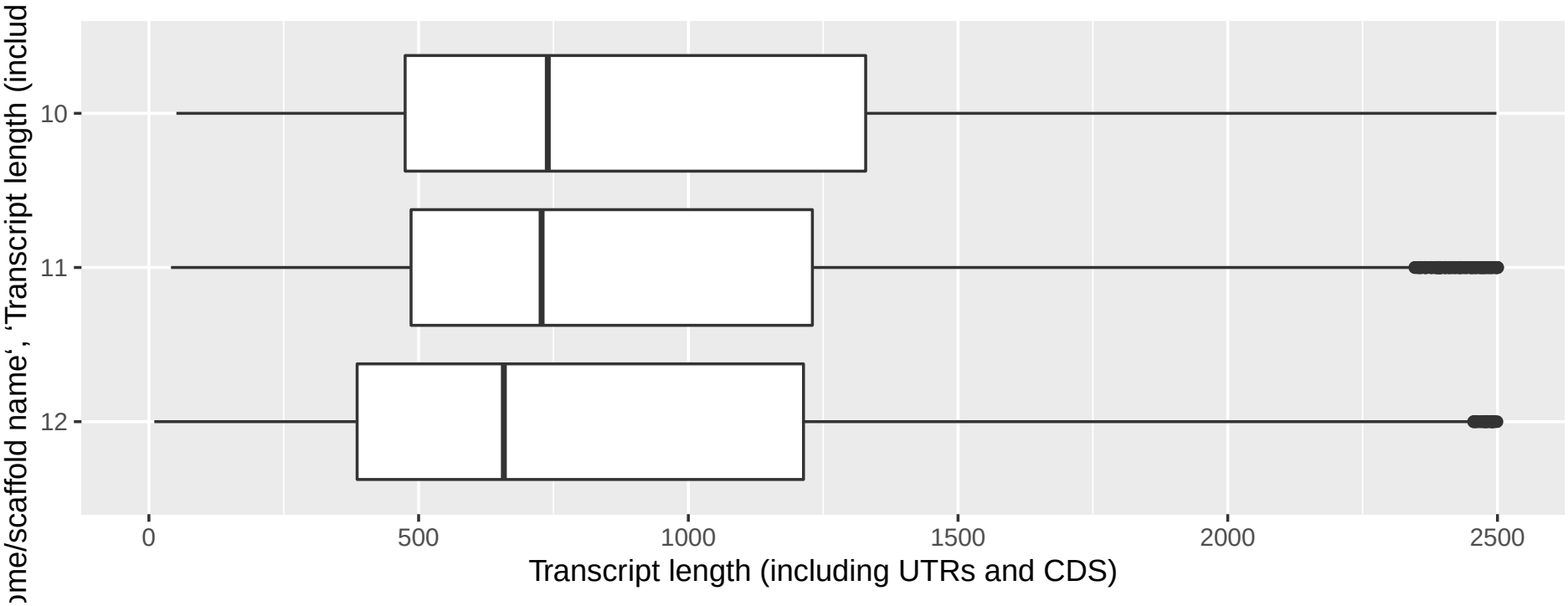
按基因长度中值从大 -> 小排序

```
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 ...