R for bioinformatics, data wrangler, part 2 HUST Bioinformatics course series

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section 1: TOC

前情提要

pipe

pipe

dplyr

- select()
- filter()
- mutate()
- summarise()
- arrange()
- group_by() ...

今次提要

tidyr

- pivot_longer(); ## 代替 gather
- pivot_wider(); ## 代替 spread

section 2: data wrangler - tidyr

tidyr

what is tidyr?

The goal of tidyr is to help you create **tidy** data.



Figure 1: dplyr logo

more to read

- tidyr offical page at tidyverse
- R for data science

tidyr 安装

只需安装一次即可!

```
# The easiest way to get tidyr is to install the whole tidyverse:
install.packages("tidyverse")

# Alternatively, install just tidyr:
install.packages("tidyr")

# Or the development version from GitHub:
# install.packages("devtools")
devtools::install_github("tidyverse/tidyr")
```

Get the cheatsheet at here

宽数据向长数据转变

get data ready

```
library(tidyverse); ## 先装入包;
grades2 <- read_tsv(file = "data/talk06/grades2.txt");
grades2;
## # A tibble: 3 x 6
```

```
Microbiology English Chinese Bioinformatics Chemistry
     name
                                 <dbl>
     <chr>>
                         <dbl>
                                          <dbl>
                                                          <dbl>
                                                                    <dbl>
## 1 7hi Liu
                           100
                                    50
                                             69
                                                             NA
                                                                       NΑ
## 2 Weihua Chen
                            89
                                    99
                                             NA
                                                             99
                                                                       NA
## 3 Kang Ning
                            NΑ
                                    NΑ
                                             20
                                                            100
                                                                       76
```

宽数据的特点

优点:

• 自然, 易理解;

缺点:

- 不易处理;
- 稀疏时问题较大;

宽数据向 长数据转变

```
library(kableExtra);
grades3 <- grades2 %>% pivot_longer( - name, names_to = "course", values_to = "grade" );
kbl( grades3 );
```

name	course	grade
Zhi Liu	Microbiology	100
Zhi Liu	English	50
Zhi Liu	Chinese	69
Zhi Liu	Bioinformatics	NA
Zhi Liu	Chemistry	NA
Weihua Chen	Microbiology	89
Weihua Chen	English	99
Weihua Chen	Chinese	NA
Weihua Chen	Bioinformatics	99
Weihua Chen	Chemistry	NA
Kang Ning	Microbiology	NA
Kang Ning	English	NA
Kang Ning	Chinese	20
Kang Ning	Bioinformatics	100
Kang Ning	Chemistry	76

pivot_longer explained!

```
grades3 <- grades2 %>% pivot_longer( - name, names_to = "course", values_to = "grade" );
```

-name: 此列保留

列名变为第一列,取名为 course

name	Bioinformatics	Chemistry	Chinese	English	Microbiology
Kang Ning	100	76	20	NA	NA
Weihua Chen	99	NA	NA	99	89
_ Zhi Liu	NA	NA	69	50	100

值变为第二列,取名为 grade

Figure 2: pivot_longer explained!

有 NA 值怎么办?

values_drop_na 即可消除;

有 NA 值怎么办?cont.

```
kbl( grades3_long );
```

name	course	grade
Zhi Liu	Microbiology	100
Zhi Liu	English	50
Zhi Liu	Chinese	69
Weihua Chen	Microbiology	89
Weihua Chen	English	99
Weihua Chen	Bioinformatics	99
Kang Ning	Chinese	20
Kang Ning	Bioinformatics	100
Kang Ning	Chemistry	76

长变宽

```
grades3_wide <- grades3_long %>%
  pivot_wider( names_from = "course", values_from = "grade" );
grades3_wide;
```

```
## # A tibble: 3 x 6
##
                 Microbiology English Chinese Bioinformatics Chemistry
     name
     <chr>>
                        <dbl>
                                 <dh1>
                                         <dh1>
                                                         <db1>
                                                                   <db1>
## 1 Zhi Liu
                           100
                                    50
                                            69
                                                            NA
                                                                      NA
## 2 Weihua Chen
                           89
                                    99
                                            NA
                                                            99
                                                                      NA
## 3 Kang Ning
                           NΑ
                                    NΑ
                                            20
                                                           100
                                                                      76
```

pivot_wider 怎么用?



Figure 3: pivot_wider function explained

宽长数据转换练习

用 pivot_wider 和 pivot_longer 对下面的数据 mini_iris 进行宽长转换:

```
mini_iris <- iris[ c(1, 51, 101), ];
kbl( mini_iris);
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
51	7.0	3.2	4.7	1.4	versicolor
101	6.3	3.3	6.0	2.5	virginica

iris 是鸢尾属一些物种花瓣的量表

宽变长, cont.

```
## -- 注意: 第一、二个参数可以自行命名, 分别对应原始数据中的 column names 及 values ...
mini_iris.longer <- mini_iris %>%
    pivot_longer( - Species, names_to = "type", values_to = "dat" );
kbl( mini_iris.longer );
```

Species	type	dat
setosa	Sepal.Length	5.1
setosa	Sepal.Width	3.5
setosa	Petal.Length	1.4
setosa	Petal.Width	0.2
versicolor	Sepal.Length	7.0
versicolor	Sepal.Width	3.2
versicolor	Petal.Length	4.7
versicolor	Petal.Width	1.4
virginica	Sepal.Length	6.3
virginica	Sepal.Width	3.3
virginica	Petal.Length	6.0
virginica	Petal.Width	2.5

长变宽

```
## -- 注意: 第一、二个参数可以自行命名,分别对应原始数据中的 column names 及 values ...
mini_iris.wider <- mini_iris.longer %>%
pivot_wider( names_from = "type", values_from = "dat" );
kbl( mini_iris.wider );
```

Species	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
setosa	5.1	3.5	1.4	0.2
versicolor	7.0	3.2	4.7	1.4
virginica	6.3	3.3	6.0	2.5

比较复杂的例子

name	class	course	grade
CHEN	1	bioinformatics	90
CHEN	1	chemistry	92
CHEN	2	chinese	35
CHEN	3	german	62
LI	1	bioinformatics	44
LI	2	chinese	68
LI	3	microbiology	95
LI	3	japanese	90
WANG	1	bioinformatics	35
WANG	1	chemistry	76
WANG	1	mathmatics	82
WANG	3	german	100
WANG	3	spanish	78

这是哪种数据类型?长还是宽??

怎么变成宽数据?

```
grades2_wide <- grades2 %>%
  pivot wider( names from = course, values from = grade );
grades2 wide;
## # A tibble: 8 x 10
     name class bioinformatics chemistry chinese german microbiology japanese
                                               <dbl> <dbl>
     <chr> <dbl>
                           <dbl>
                                      <dbl>
                                                                    <dbl>
                                                                              <dbl>
## 1 CHEN
                                         92
                                                  NΑ
                                                         NΑ
                                                                       NA
                                                                                 NΑ
                               90
## 2 CHEN
                               NΑ
                                         NΑ
                                                  35
                                                         NΑ
                                                                       NΑ
                                                                                 NΑ
                                                         62
## 3 CHEN
                               NA
                                         NΑ
                                                  NA
                                                                       NA
                                                                                 NA
## 4 T.T
                               44
                                         NA
                                                  NA
                                                         NA
                                                                       NA
                                                                                 NA
## 5 T.T
                               NA
                                         NA
                                                  68
                                                         NA
                                                                       NA
                                                                                 NA
## 6 L.I
                3
                               NA
                                         NΑ
                                                  NA
                                                         NΑ
                                                                       95
                                                                                 90
## 7 WANG
                               35
                                         76
                                                  NΑ
                                                         NΑ
                                                                       NA
                                                                                 NA
                                                        100
## 8 WANG
                               NA
                                         NΑ
                                                  NA
                                                                       NA
                                                                                 NA
## # i 2 more variables: mathmatics <dbl>, spanish <dbl>
```

再变成长数据

又怎么把它变回来?

```
a <-
  grades2_wide %>%
  pivot longer( ! c( name, class ),
                names to = "course",
                 values_to = "grade",
                 values drop na = T
               );
kbl( a );
```

name class course grade CHEN bioinformatics 90 92 CHEN chemistry CHEN chinese 35 CHEN 62 german bioinformatics 44 68 chinese 95 microbiology an

iananese

另一种变法

又怎么把它变回来???

```
b <- grades2_wide %>%
pivot_longer( bioinformatics:spanish, ## 选择成绩所在的列!
names_to = "course", values_to = "grade",
values_drop_na = T
);
kbl( b );
```

name	class	course	grade
CHEN	1	bioinformatics	90
CHEN	1	chemistry	92
CHEN	2	chinese	35
CHEN	3	german	62
Ll	1	bioinformatics	44
LI	2	chinese	68
LI	3	microbiology	95
Ll	3	japanese	90
WANG	1	bioinformatics	35
WANG	1	chemistry	76

19987071

2000 2666 20595360

1999 37737 172006362

2000 80488 174504898

1999 212258 1272915272

tidyr::separate

将一列拆成多列

```
table3 <- read tsv(file = "data/talk06/table3.txt");</pre>
## Rows: 6 Columns: 3
## Delimiter: "\t"
## chr (2): country, rate
## dbl (1): year
##
## 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.
## 1. 将 rate 列拆分
table3 %>%
 separate(rate, into = c("cases", "population"). sep = "/"):
## # A tibble: 6 x 4
##
    country year cases population
##
    <chr>>
         <dbl> <chr> <chr>
```

1 Afghanistan 1999 745

2 Afghanistan ## 3 Brazil

4 Brazil

5 China

tidyr::separate 同时进行格式转换

如何把分拆后的列正确识别为数字??

```
table3 %>%
  separate(rate, into = c("cases", "population"), convert = TRUE)
```

```
## # A tibble: 6 x 4
    country
                 year cases population
    <chr>>
                <db1>
                     <int>
                                 <int>
## 1 Afghanistan 1999
                      745
                             19987071
  2 Afghanistan
                 2000 2666
                              20595360
## 3 Brazil
                 1999
                     37737 172006362
## 4 Brazil
                 2000
                      80488
                             174504898
## 5 China
                 1999 212258 1272915272
## 6 China
                 2000 213766 1280428583
```

tidyr::separate 按字符长度分割

把年拆分为世纪和年

A tibble: 6 x 4

```
table5 <- table3 %>%
  separate(year, into = c("century", "year"), sep = 2)
table5;
```

```
country
              century year
                              rate
    <chr>>
              <chr>
                       <chr> <chr>
## 1 Afghanistan 19
                       99
                              745/19987071
  2 Afghanistan 20
                   00
                              2666/20595360
## 3 Brazil
                19
                       99
                              37737/172006362
## 4 Brazil
                20
                       00
                             80488/174504898
## 5 China
                19
                        99
                              212258/1272915272
## 6 China
                20
                        00
                              213766/1280428583
```

tidyr::unite

A tibble: 6 x 3

```
## 将上页分拆的结果进行合并
table5 %>%
unite(new, century, year, sep = ""); ## sep 参数默认是 _
```

```
country
                new
                      rate
##
    <chr>
                <chr> <chr>
## 1 Afghanistan 1999 745/19987071
  2 Afghanistan 2000
                      2666/20595360
## 3 Brazil
                      37737/172006362
                1999
## 4 Brazil
                2000 80488/174504898
                      212258/1272915272
## 5 China
                1999
## 6 China
                2000
                      213766/1280428583
```

seperate 与 unit 小结

- 分割和合并后,原列会消失! 可使用 remove = FALSE 保留原列
- 更多示例见: https://r4ds.had.co.nz/tidy-data.html

section 3: 小结与作业

小结

今次提要

• tidyr (超级强大的数据处理) part 2

下次预告

• dplyr, tidyr 和 forcats 的更多功能与生信操作实例

important

 all codes are available at Github: https://github.com/evolgeniusteam/R-for-bioinformatics

练习 & 作业

- Exercises and homework 目录下 talk06-homework.Rmd 文件;
- 完成时间: 见钉群的要求