___ Demo1 Intro to RStudio___

刘玉婷

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1. R/RStudio download and install

R www.r-project.org.

Rstudio https://www.rstudio.com/products/rstudio/download/

2. RStudio 界面介绍

3. R object

- 数据类型

```r
x <- 1
class(x)
```

```
## [1] "numeric"
```

```r
x <- 'genomic'
class(x)
```

```
## [1] "character"
```

```r
x <- '1.5e23'
class(x)
```

```
## [1] "character"
```

```r
x <- 'TRUE'
class(x)
```

```
## [1] "character"
```

- 对象

```r
a <- seq(1,9,1)
a
```

```
## [1] 1 2 3 4 5 6 7 8 9
```

```r
a <- matrix(data = seq(1,9,1), nrow = 3)
a
```

```
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
```

```r
class(a)
```

```
## [1] "matrix"
```

```r
dim(a)
```

```
## [1] 3 3
```

```r
b <- data.frame(a)
class(b)
```

```
## [1] "data.frame"
```

4. 文件读写

```r
library(data.table)
library(openxlsx)

df <- fread(file = '/lustre/user/liclab/liuyt/Genomic-Class/data/HAR.hg19.name.bed', header =
df[1:3,]
```

```
##      V1      V2      V3              V4
## 1: chr1 3089753 3089889 HAR98;2xHAR.305
## 2: chr1 7310704 7310825       HACNS_512
## 3: chr1 7651263 7651536          ANC163
```

```r
dim(df)
```

```
## [1] 2701    4
```

```r
class(df)
```

```
## [1] "data.table" "data.frame"
```

```r
colnames(df) <- c('chr', 'start', 'end', 'id')
df[1:3,]
```

```
##      chr   start     end               id
## 1: chr1 3089753 3089889 HAR98;2xHAR.305
## 2: chr1 7310704 7310825        HACNS_512
## 3: chr1 7651263 7651536           ANC163
```

```
mat <- read.xlsx('/lustre/user/liclab/liuyt/Genomic-Class/data/D190724.genes.fpkm_table.xlsx',
dim(mat)
```

```
## [1] 26255     16
```

```
mat[1:3,1:3]
```

```
##           B20-1_0    B20-2_0  B20PD_0
## A1BG      8.813990 4.23518000 8.091700
## A1BG-AS1 0.918168 0.17718900 0.236635
## A1CF      0.000000 0.00917955 0.000000
```

```
write.table(df, file = "/lustre/user/liclab/liuyt/Genomic-Class/data/HAR.hg19.name.bed",
            row.names = F, col.names = F, quote = F,
            sep = "\t")
```

5. 统计

6. 绘图