统计分析与建模

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数据预处理

- **数据过滤**
- 缺失值处理
- 异常值处理
- 数据去重
- 数据规范
- 数据采样
- 数据排序
- 数据向量化
- 列联表
- 分组汇总

数据过滤

- which()、subset()

```{r subset-1}
df=data.frame(year=c(2000,2001,2000,2003,2001),
   month=c(1,2,3,4,5))
df
```

year <dbl>	month <dbl>
2000	1
2001	2
2000	3
2003	4
2001	5

5 rows

```{r subset-2}
subset(df,year=='2000')
df[df$year==2000,]
df[which(df$year==2000),]
```

data.frame 2 x 2 | data.frame 2 x 2 | data.frame 2 x 2

	year <dbl>	month <dbl>
1	2000	1
3	2000	3

2 rows

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缺失值处理

一些特殊的数：

(1)FLASE（假）：以0计算

(2)NA（缺失值）：参与计算

(3)NULL：不参与计算

(4)NaN：无意义的数，比如sqrt(-2)

```
NA == NA
```

```
## [1] NA
```

```
NA+8
```

```
## [1] NA
```

```
NA^0
```

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

```
1/NA
```

```
## [1] NA
```

```
1/0
```

```
## [1] Inf
```

```
1/0-1/0
```

```
## [1] NaN
```

```
```{r NA}
x<-c(1,2,3,NA,4);
mean(x)
mean(x,na.rm=T)
```
```

```
[1] NA
[1] 2.5
```

缺失值检测

①判断x是否缺失值的函数是is.na(x)，是返回TRUE,否则返回FALSE。

②判断x是否完整的函数是complete.cases(x)。

③ summary可以显示每个变量的缺失值数量。

④返回数据缺失模式使用mice包中的md.pattern(x)函数。

缺失值处理

对于缺失数据通常有三种方法：

方法1：当缺失数据较少时直接删除相应样本

方法2：对缺失数据进行插补

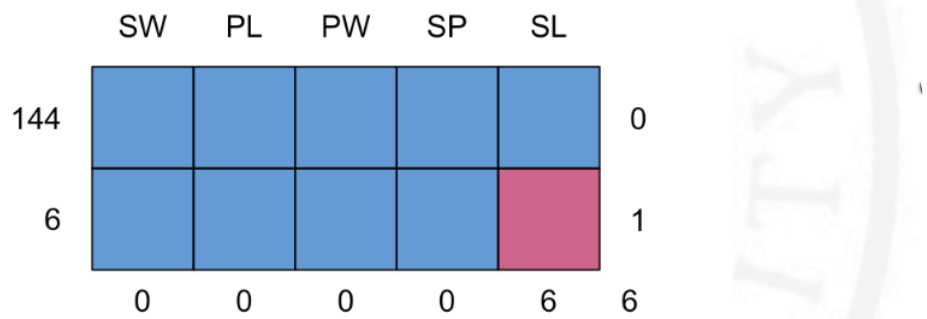
方法3：使用对缺失数据不敏感的分析方法，如决策树

```{r NA}
v=c(1,2,3,NA,4,NA,5)
print(v)
v[is.na(v)]=0
print(v)
```

```
[1]  1  2  3 NA  4 NA  5
[1] 1 2 3 0 4 0 5
```

缺失值检测

```{r kurtosis/skewness}
library(mice)
x=iris
x[sample(1:nrow(x), 6),1 ] <- NA
#随机在iris数据集第1列生成6行NA
colnames(x)<-c("SL","SW","PL","PW","SP")
md.pattern(x)
```



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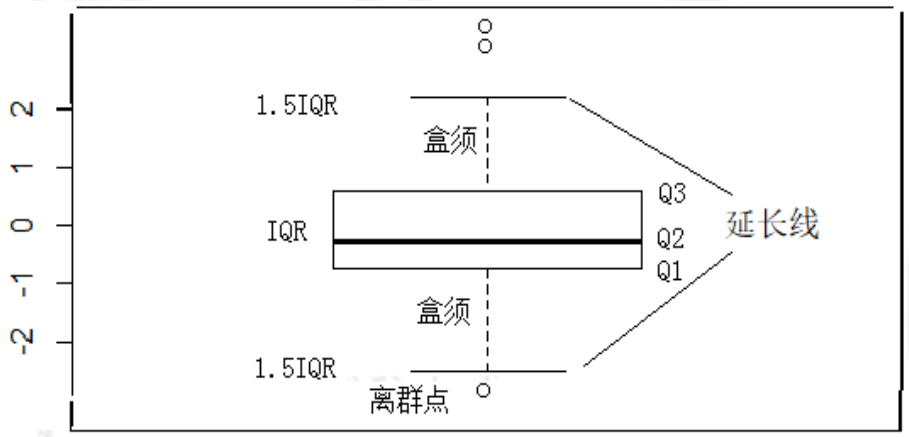
异常值检测

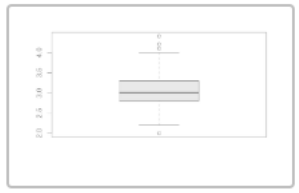
- 异常值（离群点）是指测量数据中的随机错误或偏差，包括错误值或偏离均值的孤立点值。在数据处理中，异常值会极大的影响回归或分类的效果。
- 为了避免异常值造成的损失，需要在数据预处理阶段进行异常值检测。另外，某些情况下，异常值检测也可能是研究的目的，如数据造假的发现、电脑入侵检测等。

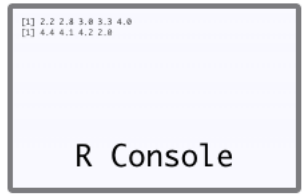
箱线图检测离群点(boxplot.stats)

在一条数轴上，以数据的上下四分位数（Q1-Q3）为界画一个矩形盒子（中间50%的数据落在盒内）；在数据的中位数位置画一条线段为中位线；默认延长线不超过盒长的1.5倍，延长线之外的点认为是异常值（用〇标记）




```{r noise}
y<-boxplot.stats(x[,2], coef=1.5, do.conf=TRUE, do.out=TRUE)
boxplot(x[,2])                    #绘制箱线图
y$stats
y$out
```

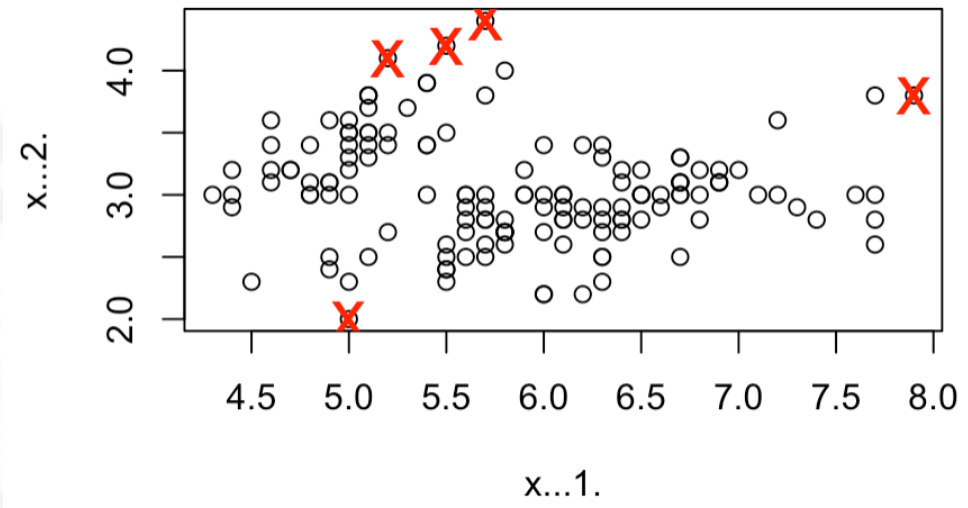





```
[1] 2.2 2.8 3.0 3.3 4.0
[1] 4.4 4.1 4.2 2.0
```

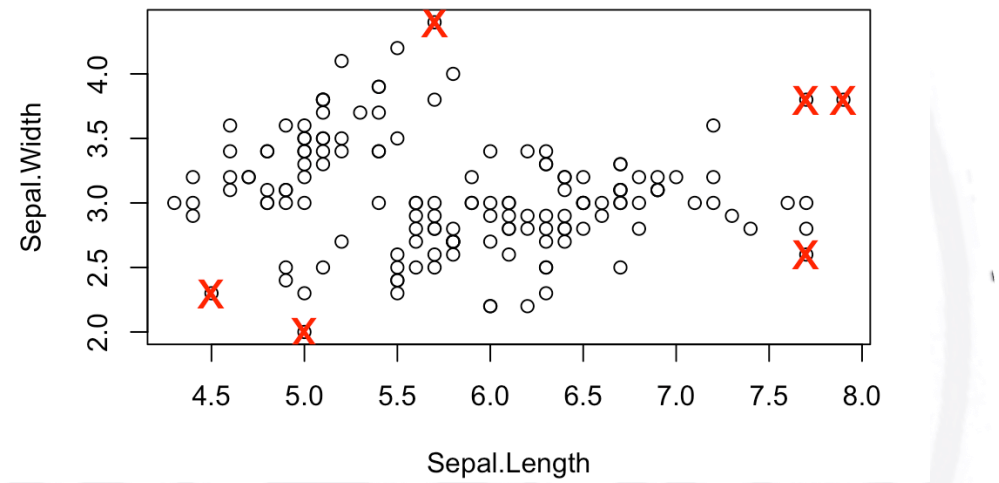
散点图检测离群点(boxplot.stats)

```r
```{r outliers-2}
#寻找a为异常值的坐标位置
a<-which(x[,2] %in% boxplot.stats(x[,2])$out)
#寻找b为异常值的坐标位置
b<-which(x[,1] %in% boxplot.stats(x[,1],coef=1.0)$out)
df<-data.frame(x[,1], x[,2])
plot(df) #绘制x, y的散点图
p2<-union(a,b) #寻找变量x或y为异常值的坐标位置
points(df[p2,],col="red",pch="x",cex=2) #标记异常值
```
```



聚类方法检测异常值

```{r outliers-3}
k<-kmeans(iris[,c(1,2)],centers=3) #kmeans聚类为3类
#k$cluster #输出聚类结果
#centers返回每个样本对应的聚类中心样本
centers <- k$centers[k$cluster, ]
#计算每个样本到其聚类中心的距离
distances<-sqrt(rowSums((iris[,1:2]-centers)^2))
#找到距离最大的6个样本，认为是异常值
out<-order(distances,decreasing=TRUE)[1:6]
plot(iris[,c(1,2)])
points(iris[out,c(1,2)],col="red",pch="x",cex=2) #标记异常值
```



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数据去重

- unique()
- duplicated()

(1)建立是否重复索引

```
index<-duplicated(data.set$Ensembl)
index
[1] FALSE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE
```

(2)去掉重复行

```
data.set2<-data.set[!index,]
```

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数据规范

(1)数据的中心化

scale(data, center=T,scale=F)

$x = x - \mu$

(2)数据的标准化

scale(data, center=T,scale=T)

$x = (x - \mu)/\sigma$

scale(data, center=F,scale=T)

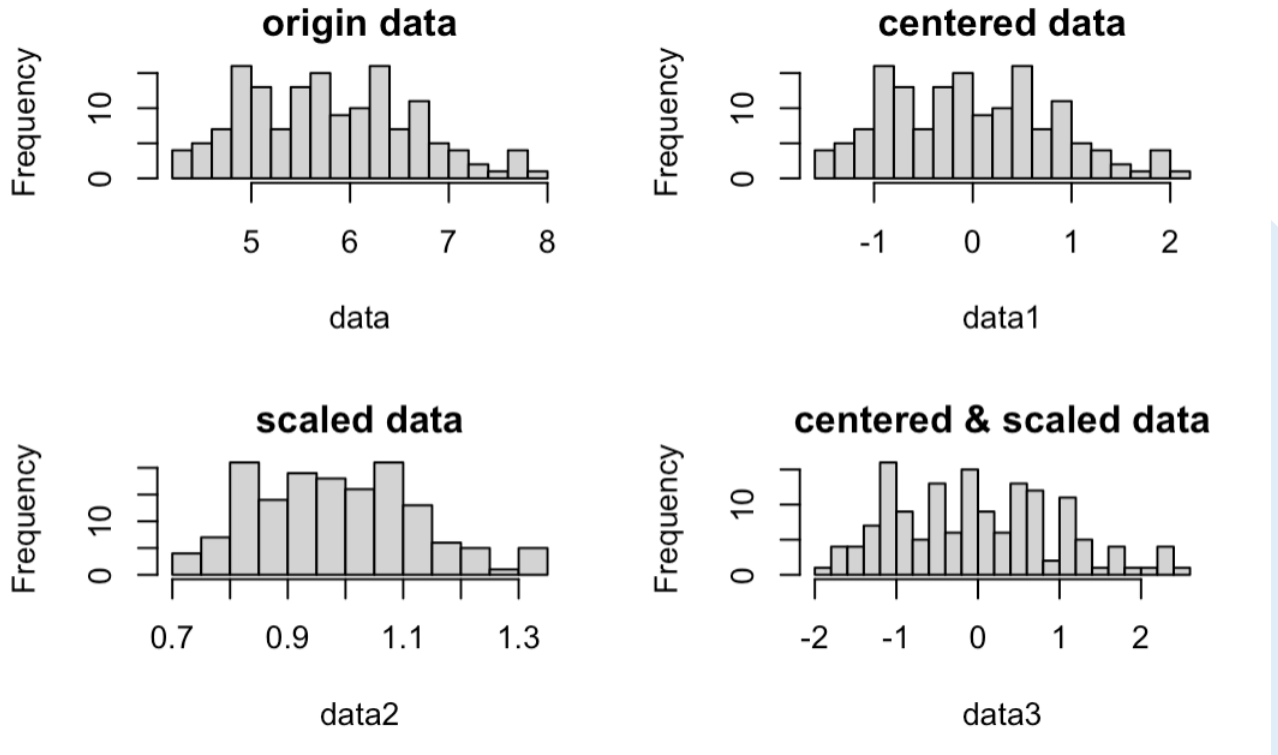
$$x = \frac{x}{\sqrt{\Sigma x^2/(n-1)}}$$

(3)小数定标规范化

移动变量的小数点位置来将变量映射到[-1,1]

options(digits = 4) #控制输出结果的有效位数

```{r scale}
data=iris[,1]
#summary(data)
data1=scale(data,center=T,scale=F)
#summary(data1)
data2=scale(data,center=F,scale=T)
#summary(data2)
data3=scale(data,center=T,scale=T)
#summary(data3)
par(mfrow=c(2,2))
hist(data,main="origin data",breaks = 20)
hist(data1,main="centered data",breaks = 20)
hist(data2,main="scaled data",breaks = 20)
hist(data3,main="centered & scaled data",breaks = 20)
```



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数据采样(sample)

```r
```{r sample}
set.seed(1234)
data=data.frame(c1=c(1:10),c2=c(11:20))
k=nrow(data)
idx=sample(k,round(0.8*k))
train=data[idx,]
(test=data[-idx,])
```
```

	c1 <int>	c2 <int>
3	3	13
9	9	19

2 rows

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数据排序

- sort()

```{r srot}
data=data.frame(v1=c(1,3,2,5,4),v2=c('a','c','b','e','d'))
#data frame对象 含有v1,v2两列
data[sort(data$v1,index.return=TRUE)$ix,]
#对data的数据按v1排列,v1须为numeric
```

	v1 <dbl>	v2 <chr>
1	1	a
3	2	b
2	3	c
5	4	d
4	5	e

5 rows

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数据向量化

- as.vector()
  1. matrix
  2. array

```
```{r as.vector}
 (m=matrix(c(1,2,3,4),nrow=2))
 as.vector(m)
```
```

```
     [,1] [,2]
[1,]    1    3
[2,]    2    4
[1] 1 2 3 4
```

- unlist()
  1. list
  2. data frame

unlist simplifies it to produce a vector which contains all the atomic components which occur in x

```
```{r unlist}
 l=list(c1=c(1,2,3),c2=c('a','b'),c3=data.frame(c31=c(4,5),c32=c('c','d')))
 print(l)
 unlist(l)
```
```

```
$c1
[1] 1 2 3

$c2
[1] "a" "b"

$c3
  c31 c32
1   4   c
2   5   d

    c11     c12     c13     c21     c22 c3.c311 c3.c312 c3.c321 c3.c322
    "1"     "2"     "3"     "a"     "b"     "4"     "5"     "c"     "d"
```

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列联表

列联表

员工	产品X	产品Y	总计
甲	23	27	50
乙	22	33	55
总计	45	60	105

- table()

```{r contingency table}
(v=sample(letters[1:5],10,replace=TRUE))
(t=table(v))
length(t);names(t)
```

```
 [1] "a" "c" "c" "c" "e" "a" "d" "d" "c" "b"
v
a b c d e
2 1 4 2 1
[1] 5
[1] "a" "b" "c" "d" "e"
```

```{r contingency_table_2}
(a<-rep(letters[1:3],each=4))
(b<-sample(LETTERS[1:3],12,replace=T))
(t=table(a,b))
nrow(t);colnames(t);rownames(t)
```

```
 [1] "a" "a" "a" "a" "b" "b" "b" "b" "c" "c" "c" "c"
 [1] "A" "C" "A" "A" "A" "A" "C" "C" "B" "A" "B" "B"
   b
a   A B C
  a 3 0 1
  b 2 0 2
  c 1 3 0
[1] 3
[1] "A" "B" "C"
[1] "a" "b" "c"
```

列联表

```{r contingency_table_3}
library(vcd)
#风湿性关节炎新疗法的双盲临床实验
#Improved:
  #none: 无改善
  #some: 一定程度改善
  #marked: 显著改善
#Treatment
  #Treated: 用药治疗
  #Placebo: 安慰剂治疗
head(Arthritis)
```

	ID <int>	Treatment <fctr>	Sex <fctr>	Age <int>	Improved <ord>
1	57	Treated	Male	27	Some
2	46	Treated	Male	29	None
3	77	Treated	Male	30	None
4	17	Treated	Male	32	Marked
5	36	Treated	Male	46	Marked
6	23	Treated	Male	58	Marked

```{r contingency_table_4}
library(vcd)
(mytable=with(Arthritis,table(Improved)))
prop.table(mytable)
```

```
Improved
  None   Some Marked 
    42     14     28 
Improved
     None      Some    Marked 
0.5000000 0.1666667 0.3333333 
```

列联表

```{r contingency_table_5}
(mytable=xtabs(~Treatment+Improved,data=Arthritis))
margin.table(mytable,1)
margin.table(mytable,2)
```

```
          Improved
Treatment None Some Marked
  Placebo   29    7      7
  Treated   13    7     21
Treatment
Placebo Treated
     43      41
Improved
  None   Some Marked
    42     14     28
```

```{r contingency_table_6}
(mytable=xtabs(~Treatment+Improved,data=Arthritis))
prop.table(mytable,1)
prop.table(mytable,2)
prop.table(mytable)
```

```
          Improved
Treatment None Some Marked
  Placebo   29    7      7
  Treated   13    7     21
          Improved
Treatment      None      Some    Marked
  Placebo 0.6744186 0.1627907 0.1627907
  Treated 0.3170732 0.1707317 0.5121951
          Improved
Treatment      None      Some    Marked
  Placebo 0.6904762 0.5000000 0.2500000
  Treated 0.3095238 0.5000000 0.7500000
          Improved
Treatment       None       Some     Marked
  Placebo 0.34523810 0.08333333 0.08333333
  Treated 0.15476190 0.08333333 0.25000000
```

列联表

```{r contingency_table_7}
(mytable=xtabs(~Treatment+Improved,data=Arthritis))
addmargins(mytable)
addmargins(prop.table(mytable))
```

```
          Improved
Treatment None Some Marked
  Placebo   29    7      7
  Treated   13    7     21
          Improved
Treatment None Some Marked Sum
  Placebo   29    7      7  43
  Treated   13    7     21  41
  Sum       42   14     28  84
          Improved
Treatment       None       Some     Marked        Sum
  Placebo 0.34523810 0.08333333 0.08333333 0.51190476
  Treated 0.15476190 0.08333333 0.25000000 0.48809524
  Sum     0.50000000 0.16666667 0.33333333 1.00000000
```

```{r contingency_table_8}
(mytable=xtabs(~Treatment+Improved,data=Arthritis))
addmargins(prop.table(mytable,1),2)
addmargins(prop.table(mytable,2),1)
```

```
          Improved
Treatment None Some Marked
  Placebo   29    7      7
  Treated   13    7     21
          Improved
Treatment      None      Some    Marked       Sum
  Placebo 0.6744186 0.1627907 0.1627907 1.0000000
  Treated 0.3170732 0.1707317 0.5121951 1.0000000
          Improved
Treatment      None      Some    Marked
  Placebo 0.6904762 0.5000000 0.2500000
  Treated 0.3095238 0.5000000 0.7500000
  Sum     1.0000000 1.0000000 1.0000000
```

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分组汇总

- aggregate(x, by, FUN, ...)

```{r aggregate-1}
table(state.region)
```

```
state.region
    Northeast         South North Central          West
            9            16            12            13
```

```{r aggregate-2}
aggregate(state.x77, list(Region = state.region), mean)
```

Region <fctr>	Population <dbl>	Income <dbl>	Illiteracy <dbl>	Life Exp <dbl>	Murder <dbl>	HS Grad <dbl>	Frost <dbl>	Area <dbl>
Northeast	5495.111	4570.222	1.000000	71.26444	4.722222	53.96667	132.7778	18141.00
South	4208.125	4011.938	1.737500	69.70625	10.581250	44.34375	64.6250	54605.12
North Central	4803.000	4611.083	0.700000	71.76667	5.275000	54.51667	138.8333	62652.00
West	2915.308	4702.615	1.023077	71.23462	7.215385	62.00000	102.1538	134463.00

4 rows

分组汇总

- aggregate(x, by, FUN, ...)

```
```{r aggregate-3}
aggregate(state.x77,
          list(Region = state.region,
               Cold = state.x77[,"Frost"] > 130),
          mean)
```
```

Region <fctr>	Cold <lgl>	Population <dbl>	Income <dbl>	Illiteracy <dbl>	Life Exp <dbl>	Murder <dbl>	HS Grad <dbl>	Frost <dbl>	Area <dbl>
Northeast	FALSE	8802.8000	4780.400	1.1800000	71.12800	5.580000	52.06000	110.6000	21838.60
South	FALSE	4208.1250	4011.938	1.7375000	69.70625	10.581250	44.34375	64.6250	54605.12
North Central	FALSE	7233.8333	4633.333	0.7833333	70.95667	8.283333	53.36667	120.0000	56736.50
West	FALSE	4582.5714	4550.143	1.2571429	71.70000	6.828571	60.11429	51.0000	91863.71
Northeast	TRUE	1360.5000	4307.500	0.7750000	71.43500	3.650000	56.35000	160.5000	13519.00
North Central	TRUE	2372.1667	4588.833	0.6166667	72.57667	2.266667	55.66667	157.6667	68567.50
West	TRUE	970.1667	4880.500	0.7500000	70.69167	7.666667	64.20000	161.8333	184162.17

7 rows

分组汇总

- aggregate(x, by, FUN, ...)

```r
testDF <- data.frame(v1 = c(1,3,5,7,8,3,5,NA,4,5,7,9),
                     v2 = c(11,33,55,77,88,33,55,NA,44,55,77,99) )
by1 <- c("red", "blue", 1, 2, NA, "big", 1, 2, "red", 1, NA, 12)
by2 <- c("wet", "dry", 99, 95, NA, "damp", 95, 99, "red", 99, NA, NA)
aggregate(x = testDF, by = list(by1, by2), FUN = "mean")
```

Group.1 <chr>	Group.2 <chr>	v1 <dbl>	v2 <dbl>
1	95	5	55
2	95	7	77
1	99	5	55
2	99	*NA*	*NA*
big	damp	3	33
blue	dry	3	33
red	red	4	44
red	wet	1	11

8 rows

```r
fby1 <- factor(by1, exclude = "")
fby2 <- factor(by2, exclude = "")
aggregate(x = testDF, by = list(fby1, fby2), FUN = "mean")
```

Group.1 <fctr>	Group.2 <fctr>	v1 <dbl>	v2 <dbl>
1	95	5.0	55.0
2	95	7.0	77.0
1	99	5.0	55.0
2	99	*NA*	*NA*
big	damp	3.0	33.0
blue	dry	3.0	33.0
red	red	4.0	44.0
red	wet	1.0	11.0
12	*NA*	9.0	99.0
NA	*NA*	7.5	82.5

1–10 of 10 rows

分组汇总

- aggregate(formula, data, FUN, ...)

```{r aggregate-one~one}
aggregate(weight ~ feed, data = chickwts, mean)
```

feed <fctr>	weight <dbl>
casein	323.5833
horsebean	160.2000
linseed	218.7500
meatmeal	276.9091
soybean	246.4286
sunflower	328.9167

6 rows

```{r aggregate-one~many}
aggregate(breaks ~ wool + tension, data = warpbreaks, mean)
```

wool <fctr>	tension <fctr>	breaks <dbl>
A	L	44.55556
B	L	28.22222
A	M	24.00000
B	M	28.77778
A	H	24.55556
B	H	18.77778

6 rows

```{r aggregate-many~one}
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, mean)
```

Month <int>	Ozone <dbl>	Temp <dbl>
5	23.61538	66.73077
6	29.44444	78.22222
7	59.11538	83.88462
8	59.96154	83.96154
9	31.44828	76.89655

5 rows

```{r aggregate-many~many}
aggregate(cbind(ncases, ncontrols) ~ alcgp + tobgp, data = esoph, sum)
```

alcgp <ord>	tobgp <ord>	ncases <dbl>	ncontrols <dbl>
0-39g/day	0-9g/day	9	261
40-79	0-9g/day	34	179
80-119	0-9g/day	19	61
120+	0-9g/day	16	24
0-39g/day	10-19	10	84
40-79	10-19	17	85
80-119	10-19	19	49

数据预处理

- 数据过滤
- 缺失值处理
- 异常值处理
- 数据去重
- 数据规范
- 数据采样
- 数据排序
- 数据向量化
- 列联表
- 分组汇总

Thanks

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