聚类模型案例: 癌细胞基因表达数据

吴翔

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概述

我们通过R语言 ISLR 包中64个细胞的6830个基因表达数据作为案例,来阐述如何使用如下聚类模型:

- 系统聚类
- K均值聚类

数据集 NCI60 包含基因表达数据矩阵 NCI60\$data 以及癌细胞系的类型 NCI60\$1abs。

```
# clean the work directory
rm(list = ls())

# set seeds
set.seed(123)

# read dataset
suppressMessages(library(ISLR))
suppressMessages(library(tidyverse))
data("NCI60")
# display the variables
str(NCI60)
```

```
## List of 2
## $ data: num [1:64, 1:6830] 0.3 0.68 0.94 0.28 0.485 ...
## ..- attr(*, "dimnames")=List of 2
## ....$ : chr [1:64] "V1" "V2" "V3" "V4" ...
## ....$ : chr [1:6830] "1" "2" "3" "4" ...
## $ labs: chr [1:64] "CNS" "CNS" "RENAL" ...
```

```
# summary of dataset
ncidat <- NCI60$data
ncilab <- NCI60$labs
# types of cancer cells
table(ncilab)</pre>
```

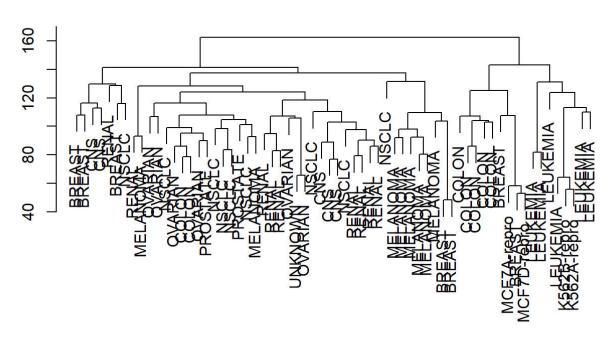
```
## ncilab
                    CNS
##
      BREAST
                             COLON K562A-repro K562B-repro
                                                          LEUKEMIA
                                7
                                     1
                         MELANOMA
                                       NSCLC
                                                OVARIAN
                                                          PROSTATE
## MCF7A-repro MCF7D-repro
##
                                           9
                                                     6
                                8
        1
                    1
##
       RENAL
             UNKNOWN
##
```

系统聚类

```
# scaling
ncidat <- scale(ncidat)

# clustering
nci.dist <- dist(ncidat, method = "euclidean", p = 2)
hc.out <- hclust(nci.dist)
plot(hc.out, labels = ncilab, main = "complete linkage", xlab = "", ylab = "")</pre>
```

complete linkage



hclust (*, "complete")

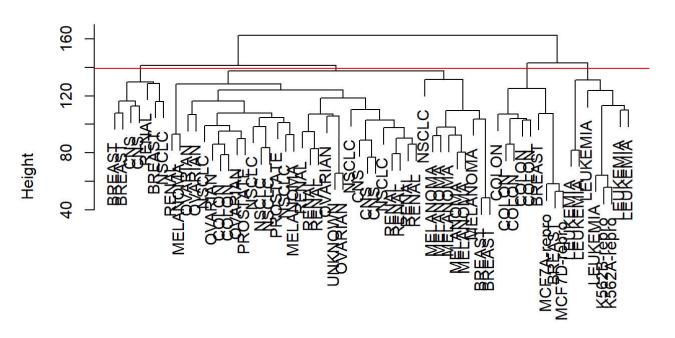
在以上谱系图上某个高度切割,可以得到指定类数的聚类,例如类别数量s = 4。

```
# four clusters
table(cutree(hc.out, 4))
```

```
## 1 2 3 4
## 40 7 8 9
```

```
# plot
plot(hc.out, labels = ncilab)
abline(h = 139, col = "red")
```

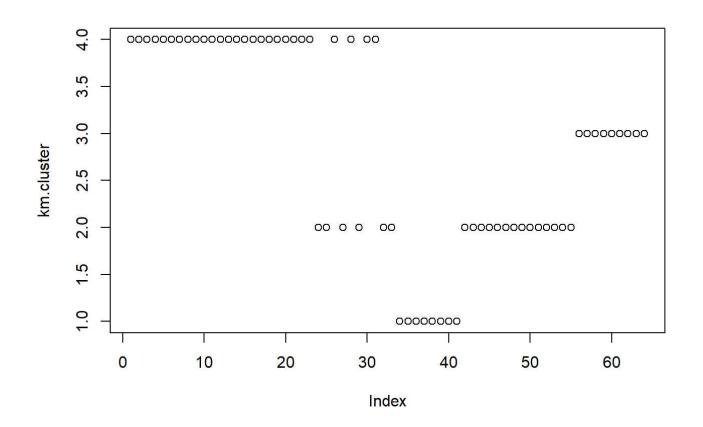
Cluster Dendrogram



nci.dist hclust (*, "complete")

K均值聚类

```
# kmeans
km.out <- kmeans(ncidat, 4, nstart = 20)
km.cluster <- km.out$cluster
names(km.cluster) <- ncilab
plot(km.cluster)</pre>
```



km. cluster

							_
##	CNS	CNS	CNS	RENAL	BREAST	CNS	3
##	4	4	4	4	4	4	Į.
##	CNS	BREAST	NSCLC	NSCLC	RENAL	RENAL	_
##	4	4	4	4	4	4	Į.
##	RENAL	RENAL	RENAL	RENAL	RENAL	BREAST	ì
##	4	4	4	4	4	4	ł
##	NSCLC	RENAL	UNKNOWN	OVARIAN	MELANOMA	PROSTATE	3
##	4	4	4	4	4	2	2
##	OVARIAN	OVARIAN	OVARIAN	OVARIAN	OVARIAN	PROSTATE	3
##	2	4	2	4	2	4	Į.
##			NSCLC	LEUKEMIA	K562B-repro	K562A-repro)
##	4	2	2	1	1	1	Ĺ
##	LEUKEMIA	LEUKEMIA	LEUKEMIA	LEUKEMIA	LEUKEMIA	COLON	1
##	1	1	1	1	1	2	2
##	COLON	COLON	COLON	COLON	COLON		
##	2	2	2	2	2	2	2
##	MCF7A-repro	BREAST	MCF7D-repro	BREAST	NSCLC	NSCLC)
##	2	2	2	2	2	2	2
##	NSCLC	MELANOMA	BREAST	BREAST	MELANOMA	MELANOMA	A
##	2	3	3	3	3	3	}
##	MELANOMA	MELANOMA	MELANOMA	MELANOMA			
##	3	3	3	3			