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## 第 16 章: 列聯表函式

### 16: Cross Tabulation Function

在類別資料分析中, 常常會使用到 列聯表 (contingency table), 在 R 中, 一些函式用來製造或操作 列聯表 (contingency table), 例如, `table()`, `xtabs()`, `as.table()`, `is.table()`; `ftable()`, `read.ftable()`, `wirte.ftable()`; `as.data.frame()`; `margin.table()`, `prop.table()`, `addmargins()` 等. 除此之外, R 還有一些關於列聯表的套件, 例如, `xtable`, `vcd`, `reshape2`, `plyr`, `dplyr`, `tidyr`, `tidyverse` 等, 將資料產生或轉換成列聯表. R 本身有一些分析列聯表的函式, 也有許多許多流行病學的套件與函式, 對 列聯表 進行分析. 例如, `Epi`, `epibasix`, `epiDisplay` (之前為 `epicalc`), `epifit`, `epiR`, `epitools`, `RCOR`, `pROC` 等, 可以進行流行病學分析, 套件主要分析能力大至相同, 但各別套件仍有其特徵.

#### 16.1 類別資料型式

類別資料的輸入常見有 2 種型式, (a) 個別資料 (individual data, micro data, case data); (b) 聚集資料 (aggregated data, macro data, summarized data, ecological data). 個別資料內包含每一位 個體 (subject, individual), 研究者為目前的研究目的所蒐集的第一手資料, 記錄著每一為個體的測量值, 個別資料有時稱為 原始資料 (raw

data, primary data, original data). 資料只有摘要之後的結果, 是由其他來源所得到的資料, 沒有每一位個體的比變數觀測值, 例如沒有每一位個體的性別, 年紀等觀測值, 這種整理分析後的資料有時稱為 二手資料 或 次級資料 (secondary data).

個別資料可以經過整理成為聚集資料形態, 但是, 若遺失每一位個體的測量值, 只有聚集資料, 則無法回復原來的個別資料. 因此, 研究盡量使用每一位個體的測量值, 但有些時候, 無法得到每一位個體的測量值, 若資料內全是類別變數, 則 個別資料 與 聚集資料 分析結論部會有差別, 但資料內若有連續變數如年紀, BMI 等, 將連續變數轉換成類別變數, 只呈現或分析聚集資料, 則會造成所謂的 生態謬誤 (ecological fallacy), 是指由 聚集資料 (團體) 所得到的推論, 不能反應 個別資料 (個人的真實) 所得到的推論, 所產生研究推論的誤導.

#### 例 16.1. 小細胞肺癌臨床試驗

一個關於小細胞肺癌臨床試驗研究, 探討合併多種化學藥物治療的給藥方式對治療結果的影響. 病患依性別隨機分成 2 組: *sequence* 組 與 *alternating* 組, *sequence* 組 在每 1 治療療程中, 只給固定 1 種合併化學藥物, *alternating* 組 有 3 種不同合併化學藥物組合, 在每 1 治療療程中, 交替使用不同合併化學藥物組合, 反應變數有 4 個類別: *progressive disease*, *no change*, *partial remission*, *complete remission* (繼續惡化, 無變化, 部分緩解, 完全緩解), 其中定義 *progressive* 與 *no change* 是治療失敗 (fail), *partial remission* 與 *complete remission* 是治療成功 (success), 研究結果呈現在表 16.1, 變數定義在表 16.2, 資料在檔案 `CateLungcSsmallCellCombAgg.csv`, `CateLungcSsmallCellCombInd.csv`.

表 16.1: 小細胞肺癌臨床試驗

Treatment	Gender	Response				Outcome	
		Progress Disease	No Change	Partial Remission	Complete Remission	no	yes
sequence	male	28	45	29	26	73	55
	female	4	12	5	2	16	8
alternating	male	41	44	20	20	85	40
	female	12	7	3	1	19	44

表 16.2: 小細胞肺癌臨床試驗: 變數名稱與定義

變數	說明
treat	治療組別: 0 = sequence, 1 = alternating
gender	性別: 0 = 男性, 1 = 女性
response	治療反應: 1 = progressive disease, 2 = no change, 3 = partial remission, 4 = complete remission
outcome	治療結果: 0 = fail, 1 = success

## 16.2 列聯表函式: table(), xtabs()

使用函式 `table()`, `xtabs()`, 可以從任何向量, 矩陣, 陣列, 資料框架創造一個列聯表, 回傳一個 列聯表 物件. 函式 `table()` 回傳的物件稱為 `_contingency table_`. 這是一個 R 物件類別 (class) 為 `table` 之特殊物件. 使用函式 `as.table()` 可用來強制將 矩陣 或 資料框架 形成列聯表物件. `as.matrix()` 強制將 列聯表物件 形成 矩陣. `as.data.frame()` 強制將 列聯表物件 形成 資料框架. `as.data.frame()` 是 `xtabs()` 的反函式. 使用函式 `is.table()` 可查看物件是否為列聯表物件.

```
1 > table(...,
2     exclude = if (useNA == "no") c(NA, NaN),
3     useNA = c("no", "ifany", "always"),
4     dnn = list.names(...), deparse.level = 1)
5
6 > xtabs(formula = ~., data = parent.frame(), subset, sparse = FALSE,
7     na.action, exclude = c(NA, NaN), drop.unused.levels = FALSE)
8
9 > as.data.frame(x, row.names = NULL, ...,
10     responseName = "Freq", stringsAsFactors = TRUE,
11     sep = "", base = list(LETTERS))
12
13 > is.table(x)
```

其中引數

- **formula**: 使用統計模型公式輸入.
- **data**: 資料框架名.
- **drop.unused.levels = FALSE**: 不排除類別水準的計數 (count) 為 0, 會造成卡方檢定的錯誤訊息.
- **na.action = "na.omit"**: 缺失值處理方式.
- **exclude**: 排除類別水準的細項, 自動內設排除缺失值.
- **useNA**: 處理缺失值選項.
  - "no": 排除缺失值.
  - "ifany": 納入缺失值, 若類別水準的計數 (count) 為正整數.
  - "always": 永遠納入缺失值成爲 1 類別水準.  
即使類別水準的計數 (count) 爲 0 仍然自成 1 個類別水準.
- **dnn**: **dimnames names**, 對回傳 **table** 物件的個別維度命名.
- **deparse.level**: 若 **dnn = NULL**, R 會對回傳 **table** 物件的個別維度命名.
  - **deparse.level = 0**: 個別維度沒有命名, **dnn = c("", "")**.

- `deparse.level = 1`: 維度命名僅列位為原有列位變數名,  
`dnn = c("var1.name", "")`.
- `deparse.level = 2`: 個別維度命名為原有變數名,  
`dnn = c("var1.name", "var2.name")`.
- `row.names`: 對 `as.data.frame()` 回傳的 `data frame` 的列位命名 (`row name`).
- `responseName = "Freq"`: 對 `as.data.frame()` 回傳的計數變數命名為 "Freq" (`count`).
- `stringsAsFactors`: 對 `as.data.frame()` 回傳的 `data frame` 變數設成因子變數.

使用函式 `xtabs()` 可以從資料框架中, 利用統計模型公式 (`model formula`) 創造一個列聯表. 函式 `as.data.frame()` 則是函式 `xtabs()` 的反函式, 從列聯表物件創造一個資料框架.

```

1 > ## Small Cell Lung Cancer Clinical Trial
2 > dd = read.table(file = "CateLungcSsmallCellCombInd.csv",
3                 header = TRUE, sep = ",",
4                 dec = ".", row.names = NULL)
5 > head(dd)
6   treat gender outcome response count
7 1     0     0     0         1     1
8 2     0     0     0         1     1
9 3     0     0     0         1     1
10 4     0     0     0         1     1
11 5     0     0     0         1     1
12 6     0     0     0         1     1
13 > #
14 > dim(dd)
15 [1] 299  5
16 > #
17 > str(dd)
18 'data.frame':  299 obs. of  5 variables:
19 $ treat   : int  0 0 0 0 0 0 0 0 0 0 ...
20 $ gender  : int  0 0 0 0 0 0 0 0 0 0 ...
21 $ outcome : int  0 0 0 0 0 0 0 0 0 0 ...
22 $ response: int  1 1 1 1 1 1 1 1 1 1 ...
23 $ count   : int  1 1 1 1 1 1 1 1 1 1 ...

```

```
24 > #
25 > ## one-way table
26 > table(dd$response)
27
28 1 2 3 4
29 85 108 57 49
30 > dd$response = factor(dd$response)
31 > levels(dd$response) = c("progress", "nochange",
32 + "parital", "complete")
33 > #
34 > table(dd$response)
35
36 progress nochange parital complete
37 85 108 57 49
38 >
39 > ## one-way table
40 > table(dd$outcome)
41
42 0 1
43 193 106
44 > dd$outcome = factor(dd$outcome)
45 > levels(dd$outcome) = c("fail", "success")
46 > table(dd$outcome)
47
48 fail success
49 193 106
50 >
51 > ## one-way table
52 > table(dd$treat)
53
54 0 1
55 151 148
56 > dd$treat = factor(dd$treat)
57 > levels(dd$treat) = c("seq", "alt")
58 > table(dd$treat)
59
60 seq alt
61 151 148
62 >
63 > ## one-way table()
64 > table(dd$gender)
65
66 0 1
67 253 46
68 > dd$gender = factor(dd$gender)
69 > levels(dd$gender) = c("male", "female")
70 > table(dd$gender)
71
72 male female
73 253 46
```

```
74 >
75 > ## two-way table()
76 > table(dd$response, dd$outcome)
77
78           fail success
79 progress    85      0
80 nochange   108      0
81 parital     0     57
82 complete    0     49
83 > #
84 > t2.tab <- table(dd$treat, dd$response)
85 > t2.tab
86
87           progress nochange parital complete
88 seq           32      57      34      28
89 alt           53      51      23      21
90 > #
91 > class(t2.tab)
92 [1] "table"
93 > #
94 > typeof(t2.tab)
95 [1] "integer"
96 > #
97 > str(t2.tab)
98 'table' int [1:2, 1:4] 32 53 57 51 34 23 28 21
99 - attr(*, "dimnames") = List of 2
100 ..$ : chr [1:2] "seq" "alt"
101 ..$ : chr [1:4] "progress" "nochange" "parital" "complete"
102 > #
103 > attributes(t2.tab)
104 $dim
105 [1] 2 4
106
107 $dimnames
108 $dimnames[[1]]
109 [1] "seq" "alt"
110
111 $dimnames[[2]]
112 [1] "progress" "nochange" "parital" "complete"
113
114 $class
115 [1] "table"
116 >
117 > ## deparse.level
118 > table(dd$treat, dd$response, deparse.level = 0)
119
120           progress nochange parital complete
121 seq           32      57      34      28
122 alt           53      51      23      21
123 > #
```

```

124 > table(dd$treat, dd$response, deparse.level = 1)
125
126      progress nochange parital complete
127 seq         32      57      34      28
128 alt         53      51      23      21
129 > #
130 > table(dd$treat, dd$response, deparse.level = 2)
131      dd$response
132 dd$treat progress nochange parital complete
133 seq         32      57      34      28
134 alt         53      51      23      21
135 > #
136 > ## one-way table
137 > table(dd$response)
138
139 progress nochange parital complete
140      85      108      57      49
141 > dd$response = factor(dd$response)
142 > levels(dd$response) = c("progress", "nochange",
143                          "parital", "complete")
144 > table(dd$response)
145
146 progress nochange parital complete
147      85      108      57      49
148 >
149 > ## one-way table
150 > table(dd$outcome)
151
152 fail success
153  193    106
154 > dd$outcome = factor(dd$outcome)
155 > levels(dd$outcome) = c("fail", "success")
156 > table(dd$outcome)
157
158 fail success
159  193    106
160 >
161 > ## one-way table
162 > table(dd$treat)
163
164 seq alt
165 151 148
166 > dd$treat = factor(dd$treat)
167 > levels(dd$treat) = c("seq", "alt")
168 > table(dd$treat)
169
170 seq alt
171 151 148
172 >
173 > ## one-way table()

```

```
174 > table(dd$gender)
175
176   male female
177   253     46
178 > dd$gender = factor(dd$gender)
179 > levels(dd$gender) = c("male", "female")
180 > table(dd$gender)
181
182   male female
183   253     46
184 >
185 > ## two-way table()
186 > table(dd$response, dd$outcome)
187
188           fail success
189 progress    85      0
190 nochange   108      0
191 parital     0     57
192 complete    0     49
193 > t2.tab <- table(dd$treat, dd$response)
194 > t2.tab
195
196   progress nochange parital complete
197   seq      32      57      34      28
198   alt      53      51      23      21
199 > #
200 > class(t2.tab)
201 [1] "table"
202 > #
203 > typeof(t2.tab)
204 [1] "integer"
205 > #
206 > str(t2.tab)
207 'table' int [1:2, 1:4] 32 53 57 51 34 23 28 21
208 - attr(*, "dimnames") = List of 2
209 ..$ : chr [1:2] "seq" "alt"
210 ..$ : chr [1:4] "progress" "nochange" "parital" "complete"
211 > #
212 > attributes(t2.tab)
213 $dim
214 [1] 2 4
215
216 $dimnames
217 $dimnames[[1]]
218 [1] "seq" "alt"
219
220 $dimnames[[2]]
221 [1] "progress" "nochange" "parital" "complete"
222
223 $class
```

```

224 [1] "table"
225 >
226 > ## deparse.level
227 > table(dd$treat, dd$response, deparse.level = 0)
228
229      progress nochange parital complete
230 seq         32      57      34      28
231 alt         53      51      23      21
232
233 > table(dd$treat, dd$response, deparse.level = 1)
234
235      progress nochange parital complete
236 seq         32      57      34      28
237 alt         53      51      23      21
238
239 > table(dd$treat, dd$response, deparse.level = 2)
240      dd$response
241 dd$treat progress nochange parital complete
242 seq         32      57      34      28
243 alt         53      51      23      21
244 > #
245 > ## one-way xtabs()
246 > table(dd$response)
247
248 progress nochange parital complete
249      85      108      57      49
250
251 > xtabs(~ response, data = dd)
252 response
253 progress nochange parital complete
254      85      108      57      49
255 >
256 > ## two-way xtabs()
257 > table(dd$response, dd$outcome)
258
259      fail success
260 progress  85      0
261 nochange 108      0
262 parital   0      57
263 complete  0      49
264 >
265 > xtabs(~ response + outcome, data = dd)
266      outcome
267 response fail success
268 progress  85      0
269 nochange 108      0
270 parital   0      57
271 complete  0      49
272 >
273 > xtabs(count ~ response + outcome, data = dd)

```

```

274           outcome
275 response  fail success
276 progress  85      0
277 nochange 108      0
278 parital   0       57
279 complete  0       49
280 >
281 > xtabs(count ~ treat + gender, data = dd)
282     gender
283 treat male female
284 seq  128    23
285 alt  125    23
286 > #
287 > ## three-way table()
288 > t3.tab = table(dd$treat, dd$response, dd$gender)
289 > t3.tab
290 , , = male
291     progress nochange parital complete
292 seq         28      45      29      26
293 alt         41      44      20      20
294
295 , , = female
296     progress nochange parital complete
297 seq          4      12       5       2
298 alt         12       7       3       1
299
300 > class(t3.tab)
301 [1] "table"
302 > typeof(t3.tab)
303 [1] "integer"
304 > str(t3.tab)
305 'table' int [1:2, 1:4, 1:2] 28 41 45 44 29 20 26 20 4 12 ...
306 - attr(*, "dimnames") = List of 3
307 ..$ : chr [1:2] "seq" "alt"
308 ..$ : chr [1:4] "progress" "nochange" "parital" "complete"
309 ..$ : chr [1:2] "male" "female"
310 > attributes(t3.tab)
311 $dim
312 [1] 2 4 2
313
314 $dimnames
315 $dimnames[[1]]
316 [1] "seq" "alt"
317
318 $dimnames[[2]]
319 [1] "progress" "nochange" "parital" "complete"
320
321 $dimnames[[3]]
322 [1] "male" "female"
323

```

```

324 $class
325 [1] "table"
326 > #
327 > ## three-way xtabs()
328 > table(dd$treat, dd$outcome, dd$gender)
329 , , = male
330     fail success
331 seq   73     55
332 alt   85     40
333
334 , , = female
335     fail success
336 seq   16     7
337 alt   19     4
338
339 > dd.xtab = xtabs(~ treat + outcome + gender, data = dd)
340 > dd.xtab
341 , , gender = male
342     outcome
343 treat fail success
344 seq   73     55
345 alt   85     40
346
347 , , gender = female
348     outcome
349 treat fail success
350 seq   16     7
351 alt   19     4
352 > #
353 > class(dd.xtab)
354 [1] "xtabs" "table"
355 > #
356 > typeof(dd.xtab)
357 [1] "integer"
358 > #
359 > str(dd.xtab)
360 int [1:2, 1:2, 1:2] 73 85 55 40 16 19 7 4
361 - attr(*, "dimnames") = List of 3
362 ..$ treat : chr [1:2] "seq" "alt"
363 ..$ outcome: chr [1:2] "fail" "success"
364 ..$ gender : chr [1:2] "male" "female"
365 - attr(*, "class") = chr [1:2] "xtabs" "table"
366 - attr(*, "call") = language xtabs(formula = ~treat + outcome + gender, data = dd)
367 > #
368 > attributes(dd.xtab)
369 $dim
370 [1] 2 2 2
371
372 $dimnames
373 $dimnames$treat

```

```
374 [1] "seq" "alt"
375
376 $dimnames$outcome
377 [1] "fail" "success"
378
379 $dimnames$gender
380 [1] "male" "female"
381
382 $class
383 [1] "xtabs" "table"
384
385 $call
386 xtabs(formula = ~treat + outcome + gender, data = dd)
387 > #
388 > is.table(dd.xtab)
389 [1] TRUE
390 > #
391 > xtabs(count ~ treat + outcome + gender, data = dd)
392 , , gender = male
393
394   outcome
395 treat fail success
396 seq    73     55
397 alt    85     40
398
399 , , gender = female
400
401   outcome
402 treat fail success
403 seq    16      7
404 alt    19      4
405
406 > cd.xtab = xtabs(count ~ treat + response + gender, data = dd)
407 > cd.xtab
408 , , gender = male
409
410   response
411 treat progress nochange parital complete
412 seq         28     45     29     26
413 alt         41     44     20     20
414
415 , , gender = female
416
417   response
418 treat progress nochange parital complete
419 seq          4     12      5      2
420 alt         12      7      3      1
421 >
422 > class(cd.xtab)
423 [1] "xtabs" "table"
```

```
424 >
425 > typeof(cd.xtab)
426 [1] "integer"
427 >
428 > str(cd.xtab)
429 int [1:2, 1:4, 1:2] 28 41 45 44 29 20 26 20 4 12 ...
430 - attr(*, "dimnames") = List of 3
431 ..$ treat : chr [1:2] "seq" "alt"
432 ..$ response: chr [1:4] "progress" "nochange" "parital" "complete"
433 ..$ gender : chr [1:2] "male" "female"
434 - attr(*, "class") = chr [1:2] "xtabs" "table"
435 - attr(*, "call") = language xtabs(formula = count ~ treat + response + gender, data =
  dd)
436 >
437 > attributes(cd.xtab)
438 $dim
439 [1] 2 4 2
440
441 $dimnames
442 $dimnames$treat
443 [1] "seq" "alt"
444
445 $dimnames$response
446 [1] "progress" "nochange" "parital" "complete"
447
448 $dimnames$gender
449 [1] "male" "female"
450
451 $class
452 [1] "xtabs" "table"
453
454 $call
455 xtabs(formula = count ~ treat + response + gender, data = dd)
456 > #
457 > is.table(cd.xtab)
458 [1] TRUE
459 > #
460 > ## as.data.frame()
461 > dd.df = as.data.frame(dd.xtab, responseName = "Freq")
462 > dd.df
463   treat outcome gender Freq
464 1   seq   fail   male   73
465 2   alt   fail   male   85
466 3   seq success   male   55
467 4   alt success   male   40
468 5   seq   fail female   16
469 6   alt   fail female   19
470 7   seq success female    7
471 8   alt success female    4
472 > #
```

```
473 > cd.df = as.data.frame(cd.xtab, responseName = "count")
474 > cd.df
475   treat response gender count
476 1   seq progress  male   28
477 2   alt progress  male   41
478 .....
479 15  seq complete female    2
480 16  alt complete female    1
```

## 16.3 列聯表函式:

### `fTable()`, `read.fTable()`, `write.fTable()`

函式 `table()` 或 `xtabs()` 對高維度列聯表的呈現類似 `list` 形式, 較不方便操作, 改使用函式 `fTable()`, 可以從任何向量, 矩陣, 陣列, 資料框架創造一個 扁平列聯表 (flat contingency table), 扁平列聯表 是一個 "fTable" 類別 (class) 的矩陣物件, 其中變數 (欄位, column) 為分類因子變數, 另外再加上各組頻率數目, 每一列 (row) 代表每一種分類的類別水準 (level). 使用函式 `fTable()` 得到 `fTable` 物件, 在 R 的列印上, 會比 `table()` 或 `xtabs()` 得到 `_contingency table_` 物件好看. 使用函式 `read.fTable()` 與 `write.fTable()`, 可以用來讀寫 "fTable" 的扁平列聯表矩陣物件.

```
1 > fTable(..., exclude = c(NA, NaN), row.vars = NULL,
2   col.vars = NULL)
3
4 > read.fTable(file, sep = ",", quote = "\"",
5   row.var.names, col.vars, skip = 0)
6
7 > write.fTable(x, file = "", quote = TRUE, append = FALSE,
8   digits = getOption("digits"), ...)
```

其中引數

- `exclude`: 排除類別水準的細項, 自動內設排除缺失值.
- `row.vars`: 向量, 選定 flat contingency table 列位名.

- `col.vars`: 向量, 選定 flat contingency table 變數名 (欄位名).
- `dnn`: `dimnames names`, 對回傳 `table` 物件的個別維度命名.
- `row.var.names`: 設定讀入 `fable` 資料列位名.

```

1 > ## ftable()
2 > head(dd)
3   treat gender outcome response count
4 1   seq  male   fail progress     1
5 2   seq  male   fail progress     1
6 3   seq  male   fail progress     1
7 4   seq  male   fail progress     1
8 5   seq  male   fail progress     1
9 6   seq  male   fail progress     1
10 > #
11 > t1.ftab = ftable(dd$treat, dd$gender, dd$outcome)
12 > t1.ftab
13           fail success
14 seq male      73     55
15   female    16      7
16 alt male     85     40
17   female    19      4
18 >
19 > t2.ftab = ftable(data = dd, row.vars = c("treat", "gender"),
20                   col.vars = c("outcome"))
21 > t2.ftab
22           outcome fail success
23 treat gender
24 seq  male           73     55
25     female         16      7
26 alt  male           85     40
27     female         19      4
28 > #
29 > t3.ftab = ftable(data = dd, row.vars = c("treat", "gender"),
30                   col.vars = c("response"))
31 > t3.ftab
32           response progress nochange parital complete
33 treat gender
34 seq  male           28     45     29     26
35     female           4     12      5      2
36 alt  male           41     44     20     20
37     female           12      7      3      1
38 > #
39 > is.table(t3.ftab)
40 [1] FALSE
41 > #
42 > class(t3.ftab)
43 [1] "fable"

```

```

44 > #
45 > typeof(t3.ftab)
46 [1] "integer"
47 > #
48 > str(t3.ftab)
49 'ftable' int [1:4, 1:4] 28 4 41 12 45 12 44 7 29 5 ...
50 - attr(*, "row.vars") = List of 2
51 ..$ treat : chr [1:2] "seq" "alt"
52 ..$ gender: chr [1:2] "male" "female"
53 - attr(*, "col.vars") = List of 1
54 ..$ response: chr [1:4] "progress" "nochange" "parital" "complete"
55 > #
56 > attributes(t3.ftab)
57 $dim
58 [1] 4 4
59
60 $row.vars
61 $row.vars$treat
62 [1] "seq" "alt"
63
64 $row.vars$gender
65 [1] "male" "female"
66
67 $col.vars
68 $col.vars$response
69 [1] "progress" "nochange" "parital" "complete"
70
71 $class
72 [1] "ftable"
73 >
74 > ## write.ftable()
75 > write.ftable(t3.ftab, file = "LungCAftab.txt", quote = FALSE)
76 > # check file "C:/RData/LungCAftab.txt"
77 > #
78 > write.ftable(t3.ftab, quote = FALSE)
79           response progress nochange parital complete
80 treat gender
81 seq   male           28      45      29      26
82      female          4      12       5       2
83 alt   male           41      44      20      20
84      female          12       7       3       1
85 > #
86 > write.ftable(t3.ftab, quote = FALSE, method = "row.compact")
87 treat gender response progress nochange parital complete
88 seq   male           28      45      29      26
89      female          4      12       5       2
90 alt   male           41      44      20      20
91      female          12       7       3       1
92 > #
93 > write.ftable(t3.ftab, quote = FALSE, method = "col.compact")

```

```

94      response progress nochange parital complete
95 treat gender
96 seq  male           28      45      29      26
97      female          4      12       5       2
98 alt  male           41      44      20      20
99      female          12       7       3       1
100 > #
101 > write.ftable(t3.ftab, quote = FALSE, method = "compact")
102 treat gender response progress nochange parital complete
103 seq  male           28      45      29      26
104      female          4      12       5       2
105 alt  male           41      44      20      20
106      female          12       7       3       1
107 > #
108 > ## read.ftable()
109 > t4.ftab = read.ftable(file = "LungCAftab.txt")
110 > t4.ftab
111      response progress nochange parital complete
112 treat gender
113 seq  male           28      45      29      26
114      female          4      12       5       2
115 alt  male           41      44      20      20
116      female          12       7       3       1
117 > #
118 > ## read.ftable()
119 > t4.ftab = read.ftable(file = "LungCAftab.txt")
120 > t4.ftab
121      response progress nochange parital complete
122 treat gender
123 seq  male           28      45      29      26
124      female          4      12       5       2
125 alt  male           41      44      20      20
126      female          12       7       3       1
127 > tc.ftab = ftable(data = dd, row.vars = c("treat", "gender", "outcome"),
128                   col.vars = c("count"))
129 > #
130 > tc.ftab
131      count  1
132 treat gender outcome
133 seq  male  fail      73
134      success  55
135      female fail      16
136      success  7
137 alt  male  fail      85
138      success  40
139      female fail      19
140      success  4

```

## 16.4 列聯表函式: `margin.table()`, `prop.table()`, `addmargins()`

使用函式 `margin.table()` 可以使用類別 (class) 為 `table` 的列聯表物件, 或是使用陣列型式 (array) 的列聯表物件計算 邊際總合 (marginal total). 函式 `prop.table()` 從陣列型式之列聯表物件, 計算列聯表物件的 相對頻率 (relative frequency). 函式 `addmargins()` 對列聯表物件進行邊際維度計算總和.

函式 `margin.table()` 與函式 `prop.table()` 無法對類別 (class) 為 `"ftable"` 的列聯表物件進行操作. 函式 `addmargins()` 可以對類別 (class) 為 `"table"` 或 `"ftable"` 的列聯表物件進行操作.

```
1 > margin.table(x, margin = NULL)
2 > prop.table(x, margin = NULL)
3 > addmargins(A, margin = seq_along(dim(A)), FUN = sum, quiet = FALSE)
```

其中引數

- `x`: `table` 物件.
  - `A`: `table` 或 `ftable` 物件.
  - `margin`: 維度下標或向量 (index/vector), 設定計算的邊際維度.
    - `margin = NULL`: 計算列聯表內 總和 或 個別空格分率 (cell count/proportion).
    - `margin = 1`: 計算列聯表的列位 (row) 邊際總和 或 分率 (row marginal total/proportion).
    - `margin = 2`: 計算列聯表的欄位 (column) 邊際總和 或 分率 (column marginal total/proportion)..
    - `margin = k`: 其餘維度則依此列推.
-

函式 `margin.table()` 是函式 `apply(x, margin, sum)` 的簡化, 函式 `prop.table()` 是函式 `sweep(x, margin, margin.table(x, margin), "/")` 的簡化. 但是, 函式 `margin.table()` 與函式 `prop.table()` 無法對類別 (class) 為 "ftable" 的列聯表物件進行操作.

```
1 > head(dd)
2   treat gender outcome response count
3 1  seq  male   fail progress    1
4 2  seq  male   fail progress    1
5 3  seq  male   fail progress    1
6 4  seq  male   fail progress    1
7 5  seq  male   fail progress    1
8 6  seq  male   fail progress    1
9 >
10 > ## 2-way table
11 > tr.tab = table(dd$treat, dd$response)
12 > #
13 > margin.table(tr.tab) # total count
14 [1] 299
15 > prop.table(tr.tab) # cell proportion
16
17   progress nochange parital complete
18 seq 0.10702341 0.19063545 0.11371237 0.09364548
19 alt 0.17725753 0.17056856 0.07692308 0.07023411
20 > #
21 > margin.table(tr.tab, margin = 1) # row (treat) marginal total
22
23 seq alt
24 151 148
25 > #
26 > prop.table(tr.tab, margin = 1) # row (response) marginal proportion
27
28   progress nochange parital complete
29 seq 0.2119205 0.3774834 0.2251656 0.1854305
30 alt 0.3581081 0.3445946 0.1554054 0.1418919
31 > #
32 > margin.table(tr.tab, margin = 2) # column (treat) marginal total
33
34 progress nochange parital complete
35 85 108 57 49
36 > #
37 > prop.table(tr.tab, margin = 2) # column (response) marginal proportion
38
39   progress nochange parital complete
40 seq 0.3764706 0.5277778 0.5964912 0.5714286
41 alt 0.6235294 0.4722222 0.4035088 0.4285714
42 > #
43 > #
```

```
44 > ## 3-way table
45 > tgr.tab = table(dd$treat, dd$response, dd$gender)
46 > prop.table(tgr.tab) # cell proportion
47
48 , , = male
49     progress  nochange  parital  complete
50 seq 0.093645485 0.150501672 0.096989967 0.086956522
51 alt 0.137123746 0.147157191 0.066889632 0.066889632
52
53 , , = female
54     progress  nochange  parital  complete
55 seq 0.013377926 0.040133779 0.016722408 0.006688963
56 alt 0.040133779 0.023411371 0.010033445 0.003344482
57
58 > #
59 > margin.table(tgr.tab, margin = 1) # row (treat) marginal total
60
61 seq alt
62 151 148
63 > #
64 > prop.table(tgr.tab, margin = 1) # row (response) marginal proportion
65
66 , , = male
67     progress  nochange  parital  complete
68 seq 0.185430464 0.298013245 0.192052980 0.172185430
69 alt 0.277027027 0.297297297 0.135135135 0.135135135
70
71 , , = female
72     progress  nochange  parital  complete
73 seq 0.026490066 0.079470199 0.033112583 0.013245033
74 alt 0.081081081 0.047297297 0.020270270 0.006756757
75
76 > #
77 > margin.table(tgr.tab, margin = 2) # column (treat) marginal total
78
79 progress nochange  parital complete
80      85      108      57      49
81 > #
82 > prop.table(tgr.tab, margin = 2) # column (response) marginal proportion
83
84 , , = male
85     progress  nochange  parital  complete
86 seq 0.32941176 0.41666667 0.50877193 0.53061224
87 alt 0.48235294 0.40740741 0.35087719 0.40816327
88
89 , , = female
90     progress  nochange  parital  complete
91 seq 0.04705882 0.11111111 0.08771930 0.04081633
92 alt 0.14117647 0.06481481 0.05263158 0.02040816
93
```

```
94 > #
95 > margin.table(tgr.tab, margin = 3)
96
97   male female
98   253     46
99 > #
100 > prop.table(tgr.tab, margin = 3)
101
102 , , = male
103      progress  nochange  parital  complete
104 seq 0.11067194 0.17786561 0.11462451 0.10276680
105 alt 0.16205534 0.17391304 0.07905138 0.07905138
106
107 , , = female
108      progress  nochange  parital  complete
109 seq 0.08695652 0.26086957 0.10869565 0.04347826
110 alt 0.26086957 0.15217391 0.06521739 0.02173913
111
112 > #
113 > margin.table(tgr.tab, margin = c(1, 3))
114
115      male female
116 seq  128     23
117 alt  125     23
```