

# Array operations in the gRbase package

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# 1 Introduction

This note describes some operations on arrays in R. These operations have been implemented to facilitate implementation of graphical models and Bayesian networks in R.

## 2 Arrays/tables in R

The documentation of R states the following about arrays:

*An array in R can have one, two or more dimensions. It is simply a vector which is stored with additional attributes giving the dimensions (attribute "dim") and optionally names for those dimensions (attribute "dimnames"). A two-dimensional array is the same thing as a matrix. One-dimensional arrays often look like vectors, but may be handled differently by some functions.*

### 2.1 Cross classified data - contingency tables

Arrays appear for example in connection with cross classified data. The array `hec` below is an excerpt of the `HairEyeColor` array in R:

```
hec <- c(32, 53, 11, 50, 10, 25, 36, 66, 9, 34, 5, 29)
dim(hec) <- c(2, 3, 2)
dimnames(hec) <- list(Hair = c("Black", "Brown"),
                      Eye = c("Brown", "Blue", "Hazel"),
                      Sex = c("Male", "Female"))

hec
## , , Sex = Male
##
##      Eye
## Hair   Brown Blue Hazel
## Black   32   11   10
## Brown   53   50   25
##
## , , Sex = Female
##
##      Eye
## Hair   Brown Blue Hazel
## Black   36    9    5
## Brown   66   34   29
```

Above, `hec` is an array because it has a `dim` attribute. Moreover, `hec` also has a `dimnames` attribute naming the levels of each dimension. Notice that each dimension is given a name.

Printing arrays can take up a lot of space. Alternative views on an array can be obtained with `ftable()` or by converting the array to a dataframe with `as.data.frame.table()`. We shall do so in the following.

```
##flat <- function(x) {ftable(x, row.vars=1)}
flat <- function(x, n=4) {as.data.frame.table(x) %>% head(n)}
hec %>% flat
##   Hair Eye Sex Freq
## 1 Black Brown Male   32
## 2 Brown Brown Male   53
## 3 Black  Blue Male   11
## 4 Brown  Blue Male   50
```

An array with named dimensions is in this package called a *named array*. The functionality described below relies heavily on arrays having named dimensions. A check for an object being a named array is provided by `is.named.array()`<sub>[gRbase]</sub>

```
is.named.array(hec)
## [1] TRUE
```

## 2.2 Defining arrays

Another way is to use `tabNew()`<sub>[gRbase]</sub> from `gRbase`. This function is flexible wrt the input; for example:

```
dn <- list(Hair=c("Black", "Brown"), Eye=~Brown:Blue:Hazel, Sex=~Male:Female)
counts <- c(32, 53, 11, 50, 10, 25, 36, 66, 9, 34, 5, 29)
z3 <- tabNew(~Hair:Eye:Sex, levels=dn, value=counts)
z4 <- tabNew(c("Hair", "Eye", "Sex"), levels=dn, values=counts)
```

Notice that the levels list (`dn` above) when used in `tabNew()`<sub>[gRbase]</sub> is allowed to contain superfluous elements. Default `dimnames` are generated with

```
z5 <- tabNew(~Hair:Eye:Sex, levels=c(2, 3, 2), values = counts)
dimnames(z5) %>% str
## List of 3
## $ Hair: chr [1:2] "Hair1" "Hair2"
## $ Eye : chr [1:3] "Eye1" "Eye2" "Eye3"
## $ Sex : chr [1:2] "Sex1" "Sex2"
```

Using `tabNew`<sub>[gRbase]</sub>, arrays can be normalized to sum to one in two ways: 1) Normalization can be over the first variable for *each* configuration of all other variables and 2) over all configurations. For example:

```
z6 <- tabNew(~Hair:Eye:Sex, levels=c(2, 3, 2), values=counts, normalize="first")
z6 %>% flat
##   Hair Eye Sex   Freq
## 1 Hair1 Eye1 Sex1 0.3765
## 2 Hair2 Eye1 Sex1 0.6235
## 3 Hair1 Eye2 Sex1 0.1803
## 4 Hair2 Eye2 Sex1 0.8197
```

## 3 Operations on arrays

In the following we shall denote the `dimnames` (or variables) of the array `hec` by  $H$ ,  $E$  and  $S$  and we let  $(h, e, s)$  denote a configuration of these variables. The contingency table above shall be denoted by  $T_{HES}$  and we shall refer to the  $(h, e, s)$ -entry of  $T_{HES}$  as  $T_{HES}(h, e, s)$ .

### 3.1 Normalizing an array

Normalize an array with `tabNormalize()`<sub>[gRbase]</sub> Entries of an array can be normalized to sum to one in two ways: 1) Normalization can be over the first variable for *each* configuration of all other variables and 2) over all configurations. For example:

```

tabNormalize(z5, "first") %>% flat
##   Hair Eye Sex  Freq
## 1 Hair1 Eye1 Sex1 0.3765
## 2 Hair2 Eye1 Sex1 0.6235
## 3 Hair1 Eye2 Sex1 0.1803
## 4 Hair2 Eye2 Sex1 0.8197

```

### 3.2 Subsetting an array – slicing

We can subset arrays (this will also be called “slicing”) in different ways. Notice that the result is not necessarily an array. Slicing can be done using standard R code or using `tabSlice[gRbase]`. The virtue of `tabSlice[gRbase]` comes from the flexibility when specifying the slice:

The following leads from the original  $2 \times 3 \times 2$  array to a  $2 \times 2$  array by cutting away the `Sex=Male` and `Eye=Brown` slice of the array:

```

tabSlice(hec, slice=list(Eye=c("Blue", "Hazel"), Sex="Female"))
## Notice: levels can be written as numerics
## tabSlice(hec, slice=list(Eye=2:3, Sex="Female"))

```

We may also regard the result above as a  $2 \times 2 \times 1$  array:

```

tabSlice(hec, slice=list(Eye=c("Blue", "Hazel"), Sex="Female"), drop=FALSE)
## , , Sex = Female
##
##      Eye
## Hair  Blue Hazel
## Black  9      5
## Brown 34     29

```

If slicing leads to a one dimensional array, the output will by default not be an array but a vector (without a `dim` attribute). However, the result can be forced to be a 1-dimensional array:

```

## A vector:
t1 <- tabSlice(hec, slice=list(Hair=1, Sex="Female")); t1
## A 1-dimensional array:
t2 <- tabSlice(hec, slice=list(Hair=1, Sex="Female"), as.array=TRUE); t2
## A higher dimensional array (in which some dimensions only have one level)
t3 <- tabSlice(hec, slice=list(Hair=1, Sex="Female"), drop=FALSE); t3

```

The difference between the last two forms can be clarified:

```

t2 %>% flat
##   Eye Freq
## 1 Brown 36
## 2 Blue  9
## 3 Hazel  5

t3 %>% flat
##   Hair Eye Sex Freq
## 1 Black Brown Female 36
## 2 Black Blue Female  9
## 3 Black Hazel Female  5

```

### 3.3 Collapsing and inflating arrays

Collapsing: The  $HE$ -marginal array  $T_{HE}$  of  $T_{HES}$  is the array with values

$$T_{HE}(h, e) = \sum_s T_{HES}(h, e, s)$$

Inflating: The “opposite” operation is to extend an array. For example, we can extend  $T_{HE}$  to have a third dimension, e.g. **Sex**. That is

$$\tilde{T}_{SHE}(s, h, e) = T_{HE}(h, e)$$

so  $\tilde{T}_{SHE}(s, h, e)$  is constant as a function of  $s$ .

With **gRbase** we can collapse arrays with<sup>1</sup>:

```
he <- tabMarg(hec, c("Hair", "Eye"))
he
##      Eye
## Hair   Brown Blue Hazel
## Black   68   20   15
## Brown  119   84   54
```

```
## Alternatives
tabMarg(hec, ~Hair:Eye)
tabMarg(hec, c(1, 2))
hec %a_% ~Hair:Eye
```

Notice that collapsing is a projection in the sense that applying the operation again does not change anything:

```
he1 <- tabMarg(hec, c("Hair", "Eye"))
he2 <- tabMarg(he1, c("Hair", "Eye"))
tabEqual(he1, he2)
## [1] TRUE
```

Expand an array by adding additional dimensions with `tabExpand()`<sub>[gRbase]</sub>:

```
extra.dim <- list(Sex=c("Male", "Female"))
tabExpand(he, extra.dim)
## , , Sex = Male
##
##      Hair
## Eye   Black Brown
## Brown   68   119
## Blue    20    84
## Hazel   15    54
##
## , , Sex = Female
##
##      Hair
## Eye   Black Brown
## Brown   68   119
## Blue    20    84
## Hazel   15    54
```

<sup>1</sup>FIXME: Should allow for abbreviations in formula and character vector specifications.

```
## Alternatives
he %a~% extra.dim
```

Notice that expanding and collapsing brings us back to where we started:

```
(he %a~% extra.dim) %a_% c("Hair", "Eye")
##      Eye
## Hair   Brown Blue Hazel
## Black  136   40   30
## Brown  238  168  108
```

### 3.4 Permuting an array

A reorganization of the table can be made with `tabPerm[gRbase]` (similar to `aperm()`), but `tabPerm[gRbase]` allows for a formula and for variable abbreviation:

```
tabPerm(hec, ~Eye:Sex:Hair) %>% flat
##      Eye   Sex Hair Freq
## 1 Brown  Male Black   32
## 2 Blue   Male Black   11
## 3 Hazel  Male Black   10
## 4 Brown Female Black   36
```

Alternative forms (the first two also works for `aperm()`):

```
tabPerm(hec, c("Eye", "Sex", "Hair"))
tabPerm(hec, c(2, 3, 1))
tabPerm(hec, ~Ey:Se:Ha)
tabPerm(hec, c("Ey", "Se", "Ha"))
```

### 3.5 Equality

Two arrays are defined to be identical 1) if they have the same dimnames and 2) if, possibly after a permutation, all values are identical (up to a small numerical difference):

```
hec2 <- tabPerm(hec, 3:1)
tabEqual(hec, hec2)
## [1] TRUE
```

```
## Alternative
hec %a==% hec2
```

### 3.6 Aligning

We can align one array according to the ordering of another:

```
hec2 <- tabPerm(hec, 3:1)
tabAlign(hec2, hec)
```

```
## Alternative:
tabAlign(hec2, dimnames(hec))
## , , Sex = Male
##
##      Eye
## Hair   Brown Blue Hazel
## Black   32   11   10
## Brown   53   50   25
##
## , , Sex = Female
##
##      Eye
## Hair   Brown Blue Hazel
## Black   36    9    5
## Brown   66   34   29
```

### 3.7 Multiplication, addition etc: +, -, \*, /

The product of two arrays  $T_{HE}$  and  $T_{HS}$  is defined to be the array  $\tilde{T}_{HES}$  with entries

$$\tilde{T}_{HES}(h, e, s) = T_{HE}(h, e) + T_{HS}(h, s)$$

The sum, difference and quotient is defined similarly: This is done with `tabProd()[gRbase]`, `tabAdd()[gRbase]`, `tabDiff()[gRbase]` and `tabDiv()[gRbase]`:

```
hs <- tabMarg(hec, ~Hair:Eye)
tabMult(he, hs)
##      Eye
## Hair   Brown Blue Hazel
## Black 4624  400  225
## Brown 14161 7056 2916
```

Available operations:

```
tabAdd(he, hs)
tabSubt(he, hs)
tabMult(he, hs)
tabDiv(he, hs)
tabDiv0(he, hs) ## Convention 0/0 = 0
```

Shortcuts:

```
## Alternative
he %a+% hs
he %a-% hs
he %a*% hs
he %a/% hs
he %a/0% hs ## Convention 0/0 = 0
```

Multiplication and addition of (a list of) multiple arrays is accomplished with `tabProd()[gRbase]` and `tabSum()[gRbase]` (much like `prod()[gRbase]` and `sum()[gRbase]`):

```
es <- tabMarg(hec, ~Eye:Sex)
tabSum(he, hs, es)
```

```
## , , Sex = Male
##
##      Eye
## Hair   Brown Blue Hazel
## Black  221  101   65
## Brown  323  229  143
##
## , , Sex = Female
##
##      Eye
## Hair   Brown Blue Hazel
## Black  238   83   64
## Brown  340  211  142

## tabSum(list(he, hs, es))
```

### 3.8 An array as a probability density

If an array consists of non-negative numbers then it may be regarded as an (unnormalized) discrete multivariate density. With this view, the following examples should be self explanatory:

```
tabDist(hec, marg=~Hair:Eye)
##      Eye
## Hair   Brown   Blue  Hazel
## Black 0.1889 0.05556 0.04167
## Brown 0.3306 0.23333 0.15000

tabDist(hec, cond=~Sex)
## , , Sex = Male
##
##      Eye
## Hair   Brown   Blue  Hazel
## Black 0.1768 0.06077 0.05525
## Brown 0.2928 0.27624 0.13812
##
## , , Sex = Female
##
##      Eye
## Hair   Brown   Blue  Hazel
## Black 0.2011 0.05028 0.02793
## Brown 0.3687 0.18994 0.16201

tabDist(hec, marg=~Hair, cond=~Sex)
##      Sex
## Hair   Male Female
## Black 0.2928 0.2793
## Brown 0.7072 0.7207
```

### 3.9 Miscellaneous

Multiply values in a slice by some number and all other values by another number:

```

tabSliceMult(es, list(Sex="Female"), val=10, comp=0)
##           Sex
## Eye      Male Female
## Brown    0    1020
## Blue     0     430
## Hazel    0     340

```

## 4 Examples

### 4.1 A Bayesian network

A classical example of a Bayesian network is the “sprinkler example”, see e.g. [http://en.wikipedia.org/wiki/Bayesian\\_network](http://en.wikipedia.org/wiki/Bayesian_network):

*Suppose that there are two events which could cause grass to be wet: either the sprinkler is on or it is raining. Also, suppose that the rain has a direct effect on the use of the sprinkler (namely that when it rains, the sprinkler is usually not turned on). Then the situation can be modeled with a Bayesian network.*

We specify conditional probabilities  $p(r)$ ,  $p(s|r)$  and  $p(w|s,r)$  as follows (notice that the vertical conditioning bar ( $|$ ) is replaced by the horizontal underscore:

```

yn <- c("y", "n")
lev <- list(rain=yn, sprinkler=yn, wet=yn)
r <- tabNew(~rain, levels=lev, values=c(.2, .8))
s_r <- tabNew(~sprinkler:rain, levels = lev, values = c(.01, .99, .4, .6))
w_sr <- tabNew( ~wet:sprinkler:rain, levels=lev,
               values=c(.99, .01, .8, .2, .9, .1, 0, 1))

r
## rain
## y n
## 0.2 0.8

s_r %>% flat
##   sprinkler rain Freq
## 1         y    y 0.01
## 2         n    y 0.99
## 3         y    n 0.40
## 4         n    n 0.60

w_sr %>% flat
##   wet sprinkler rain Freq
## 1   y         y    y 0.99
## 2   n         y    y 0.01
## 3   y         n    y 0.80
## 4   n         n    y 0.20

```

The joint distribution  $p(r, s, w) = p(r)p(s|r)p(w|s,r)$  can be obtained with `tabProd()`<sup>[gRbase]</sup> ways:

```

joint <- tabProd(r, s_r, w_sr); joint %>% flat
##   wet sprinkler rain   Freq
## 1   y         y    y 0.00198

```

```
## 2  n      y    y 0.00002
## 3  y      n    y 0.15840
## 4  n      n    y 0.03960
```

What is the probability that it rains given that the grass is wet? We find  $p(r, w) = \sum_s p(r, s, w)$  and then  $p(r|w) = p(r, w)/p(w)$ . Can be done in various ways: with `tabDist()` [gRbase]

```
tabDist(joint, marg=~rain, cond=~wet)
##      wet
## rain   y     n
##   y 0.3577 0.07182
##   n 0.6423 0.92818
```

```
## Alternative:
rw <- tabMarg(joint, ~rain + wet)
tabDiv(rw, tabMarg(rw, ~wet))
## or
rw %a/% (rw %a_% ~wet)
```

```
## Alternative:
x <- tabSliceMult(rw, slice=list(wet="y")); x
##      wet
## rain   y n
##   y 0.1604 0
##   n 0.2880 0

tabDist(x, marg=~rain)
## rain
##   y     n
## 0.3577 0.6423
```

## 4.2 Iterative Proportional Scaling (IPS)

We consider the 3-way lizard data from gRbase:

```
data(lizard, package="gRbase")
lizard %>% flat
##   diam height species Freq
## 1  <=4  >4.75   anoli   32
## 2  >4   >4.75   anoli   11
## 3  <=4  <=4.75  anoli   86
## 4  >4   <=4.75  anoli   35
```

Consider the two factor log-linear model for the lizard data. Under the model the expected counts have the form

$$\log m(d, h, s) = a_1(d, h) + a_2(d, s) + a_3(h, s)$$

If we let  $n(d, h, s)$  denote the observed counts, the likelihood equations are: Find  $m(d, h, s)$  such that

$$m(d, h) = n(d, h), \quad m(d, s) = n(d, s), \quad m(h, s) = n(h, s)$$

where  $m(d, h) = \sum_s m(d, h, s)$  etc. The updates are as follows: For the first term we have

$$m(d, h, s) \leftarrow m(d, h, s) \frac{n(d, h)}{m(d, h)}$$

After iterating the updates will not change and we will have equality:  $m(d, h, s) = m(d, h, s) \frac{n(d, h)}{m(d, h)}$  and summing over  $s$  shows that the equation  $m(d, h) = n(d, h)$  is satisfied.

A rudimentary implementation of iterative proportional scaling for log-linear models is straight forward:

```
myips <- function(indata, glist){
  fit <- indata
  fit[] <- 1
  ## List of sufficient marginal tables
  md <- lapply(glist, function(g) tabMarg(indata, g))

  for (i in 1:4){
    for (j in seq_along(glist)){
      mf <- tabMarg(fit, glist[[j]])
      # adj <- tabDiv( md[[ j ]], mf)
      # fit <- tabMult( fit, adj )
      ## or
      adj <- md[[ j ]] %a/% mf
      fit <- fit %a*% adj
    }
  }
  pearson <- sum((fit - indata)^2 / fit)
  list(pearson=pearson, fit=fit)
}

glist <- list(c("species", "diam"),c("species", "height"),c("diam", "height"))

fm1 <- myips(lizard, glist)
fm1$pearson
## [1] 664.6

fm1$fit %>% flat
##   species diam height Freq
## 1  anoli  <=4  >4.75 32.8
## 2  dist  <=4  >4.75 60.2
## 3  anoli  >4   >4.75 10.2
## 4  dist  >4   >4.75 41.8

fm2 <- loglin(lizard, glist, fit=T)
## 4 iterations: deviation 0.009619

fm2$pearson
## [1] 0.1506

fm2$fit %>% flat
##   diam height species Freq
## 1  <=4  >4.75  anoli 32.8
## 2  >4   >4.75  anoli 10.2
## 3  <=4  <=4.75  anoli 85.2
## 4  >4   <=4.75  anoli 35.8
```

## 5 Some low level functions

For e.g. a  $2 \times 3 \times 2$  array, the entries are such that the first variable varies fastest so the ordering of the cells are (1, 1, 1), (2, 1, 1), (1, 2, 1), (2, 2, 1), (1, 3, 1) and so on. To find the value of such a cell, say,  $(j, k, l)$  in the array (which is really just a vector), the cell is mapped into an entry of a vector.

For example, cell (2, 3, 1) (Hair=Brown, Eye=Hazel, Sex=Male) must be mapped to entry 4 in

```
hec
## , , Sex = Male
##
##      Eye
## Hair   Brown Blue Hazel
## Black   32   11   10
## Brown   53   50   25
##
## , , Sex = Female
##
##      Eye
## Hair   Brown Blue Hazel
## Black   36    9    5
## Brown   66   34   29

c(hec)
## [1] 32 53 11 50 10 25 36 66  9 34  5 29
```

For illustration we do:

```
cell2name <- function(cell, dimnames){
  unlist(lapply(1:length(cell), function(m) dimnames[[m]][cell[m]]))
}
cell2name(c(2,3,1), dimnames(hec))
## [1] "Brown" "Hazel" "Male"
```

### 5.1 cell2entry(), entry2cell() and next\_cell()

The map from a cell to the corresponding entry is provided by `cell2entry()`<sub>[gRbase]</sub>. The reverse operation, going from an entry to a cell (which is much less needed) is provided by `entry2cell()`<sub>[gRbase]</sub>.

```
cell2entry(c(2,3,1), dim=c(2, 3, 2))
## [1] 6

entry2cell(6, dim=c(2, 3, 2))
## [1] 2 3 1
```

Given a cell, say  $i = (2, 3, 1)$  in a  $2 \times 3 \times 2$  array we often want to find the next cell in the table following the convention that the first factor varies fastest, that is (1, 1, 2). This is provided by `next_cell()`<sub>[gRbase]</sub>.

```
next_cell(c(2,3,1), dim=c(2, 3, 2))
## [1] 1 1 2
```

## 5.2 next\_cell\_slice() and slice2entry()

Given that we look at cells for which the index in dimension 2 is at level 3 (that is Eye=Hazel), i.e. cells of the form  $(j, 3, l)$ . Given such a cell, what is then the next cell that also satisfies this constraint. This is provided by `next_cell_slice()`<sup>2</sup>.

```
next_cell_slice(c(1,3,1), slice_marg=2, dim=c( 2, 3, 2 ))
## [1] 2 3 1

next_cell_slice(c(2,3,1), slice_marg=2, dim=c( 2, 3, 2 ))
## [1] 1 3 2
```

Given that in dimension 2 we look at level 3. We want to find entries for the cells of the form  $(j, 3, l)$ .<sup>3</sup>

```
slice2entry(slice_cell=3, slice_marg=2, dim=c( 2, 3, 2 ))
## [1] 5 6 11 12
```

To verify that we indeed get the right cells:

```
r <- slice2entry(slice_cell=3, slice_marg=2, dim=c( 2, 3, 2 ))
lapply(lapply(r, entry2cell, c( 2, 3, 2 )),
       cell2name, dimnames(hec))
## [[1]]
## [1] "Black" "Hazel" "Male"
##
## [[2]]
## [1] "Brown" "Hazel" "Male"
##
## [[3]]
## [1] "Black" "Hazel" "Female"
##
## [[4]]
## [1] "Brown" "Hazel" "Female"
```

## 5.3 fact\_grid() – Factorial grid

Using the operations above we can obtain the combinations of the factors as a matrix:

```
head( fact_grid( c(2, 3, 2) ), 6 )
##      [,1] [,2] [,3]
## [1,]  1   1   1
## [2,]  2   1   1
## [3,]  1   2   1
## [4,]  2   2   1
## [5,]  1   3   1
## [6,]  2   3   1
```

A similar dataframe can also be obtained with the standard R function `expand.grid` (but `factGrid` is faster)

---

<sup>2</sup>FIXME: sliceset should be called margin.

<sup>3</sup>FIXME:slicecell and sliceset should be renamed

```
head( expand.grid(list(1:2, 1:3, 1:2)), 6 )
##   Var1 Var2 Var3
## 1    1    1    1
## 2    2    1    1
## 3    1    2    1
## 4    2    2    1
## 5    1    3    1
## 6    2    3    1
```

## A More about slicing

Slicing using standard R code can be done as follows:

```
hec[, 2:3, ] %>% flat ## A 2 x 2 x 2 array
##   Hair   Eye Sex Freq
## 1 Black  Blue Male   11
## 2 Brown  Blue Male   50
## 3 Black  Hazel Male   10
## 4 Brown  Hazel Male   25

hec[1, , 1] ## A vector
## Brown  Blue Hazel
##    32    11    10

hec[1, , 1, drop=FALSE] ## A 1 x 3 x 1 array
## , , Sex = Male
##
##      Eye
## Hair   Brown Blue Hazel
## Black    32   11   10
```

Programmatically we can do the above as

```
do.call("[", c(list(hec), list(TRUE, 2:3, TRUE))) %>% flat
do.call("[", c(list(hec), list(1, TRUE, 1)))
do.call("[", c(list(hec), list(1, TRUE, 1), drop=FALSE))
```

`gRbase` provides two alternatives for each of these three cases above:

```
tabSlicePrim(hec, slice=list(TRUE, 2:3, TRUE)) %>% flat
tabSlice(hec, slice=list(c(2, 3)), margin=2) %>% flat

tabSlicePrim(hec, slice=list(1, TRUE, 1))
tabSlice(hec, slice=list(1, 1), margin=c(1, 3))

tabSlicePrim(hec, slice=list(1, TRUE, 1), drop=FALSE)
tabSlice(hec, slice=list(1, 1), margin=c(1, 3), drop=FALSE)
```