

# Primitive 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.

### 1.1 Arrays 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.*

Hence the defining characteristic of an array is that it is a vector with a dim attribute. For example

```
R> ## 1-dimensional array
R> ##
R> x1 <- 1:8
R> dim(x1) <- 8
R> x1

[1] 1 2 3 4 5 6 7 8

R> c(is.array(x1), is.matrix(x1))
```

```

[1] TRUE FALSE

R> ## 2-dimensional array (matrix)
R> ##
R> x2 <- 1:8
R> dim(x2) <- c(2,4)
R> x2

      [,1] [,2] [,3] [,4]
[1,]    1    3    5    7
[2,]    2    4    6    8

R> c(is.array(x2), is.matrix(x2))

[1] TRUE TRUE

R> ## 3-dimensional array
R> ##
R> x3 <- array(1:8, dim=c(2,2,2))
R> x3

, , 1

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

, , 2

      [,1] [,2]
[1,]    5    7
[2,]    6    8

R> c(is.array(x3), is.matrix(x3))

[1] TRUE FALSE

```

## 1.2 Terminology

Consider a set  $\Delta = \{\delta_1, \dots, \delta_K\}$  of  $|\Delta| = K$  factors where the factor  $\delta_k$  has levels  $I_k = \{1, \dots, L_k\}$ . The cross product  $I = I_1 \times \dots \times I_K$  defines an array where  $i = (i_1, \dots, i_K) \in I$  is a cell. It is the convention here that the first factor varies fastest. To each cell  $i \in I$  there is often a value  $f(i)$ .

As shown above, an array is implemented as a vector  $x$  of length  $L = |I|$ , that is  $x \equiv (f(i), i \in I)$ . In practice  $x$  is indexed by an entry  $e$  as  $x[e]$  for  $e = 1, \dots, L$ .

The factor levels  $(I_1, \dots, I_K)$  are denoted **adim** in the code below. As an example we take the following:

```

R> adim2222 <- c(2,2,2,2)
R> adim2323 <- c(2,3,2,3)

```

## 2 cell2entry() and entry2cell()

The map from a cell to the corresponding entry is provided by **cell2entry()**. The reverse operation, going from an entry to a cell (which is much less needed) is provided by **entry2cell()**.

```

R> cell2entry(c(1,1,1,1), adim2222)

```

```

[1] 1

```

```
R> entry2cell(1, adim2222)
```

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

```
R> cell2entry(c(2,1,2,1), adim2222)
```

```
[1] 6
```

```
R> entry2cell(6, adim2222)
```

```
[1] 2 1 2 1
```

### 3 nextCell() and nextCellSlice()

Given a cell, say  $i = (1, 1, 2, 1)$  we often want to find the next cell in the table following the convention that the first factor varies fastest, that is  $(2, 1, 2, 1)$ . This is provided by `nextCell()`.

```
R> nextCell(c(1,1,2,1), adim2222)
```

```
[1] 2 1 2 1
```

```
R> nextCell(c(2,2,2,1), adim2222)
```

```
[1] 1 1 1 2
```

Given  $A \subset \Delta$  and a cell  $i_A \in I_A$  consider the cells  $I(i_A) = \{j \in I | j_A = i_A\}$ . For example, the cells satisfying that factor 2 is at level 1. Given such a cell, say  $(2, 1, 1, 2)$  we often want to find the next cell also satisfying this constraint following the convention that the first factor varies fastest, that is  $(1, 1, 2, 2)$ . This is provided by `nextCellSlice()`.

```
R> nextCellSlice(c(2,1,1,2), sliceset=c(2), adim2323)
```

```
[1] 1 1 2 2
```

```
R> nextCellSlice(c(1,3,2,1), sliceset=c(2,3), adim2323)
```

```
[1] 2 3 2 1
```

### 4 slice2entry()

Given  $A \subset \Delta$  and a cell  $i_A \in I_A$ . This cell defines a slice of the original array, namely the cells  $I(i_A) = \{j \in I | j_A = i_A\}$ . We often want to find the entries in  $x$  for the cells  $I(i_A)$ . This is provided by `slice2entry()`. For example, we may want the entries for the cells  $(*, 1, 2, *)$  or  $(2, 2, *, *)$ :

```
R> (r1<-slice2entry(slicecell=c(1,2), sliceset=c(2,3), adim2222))
```

```
[1] 5 6 13 14
```

To verify that we indeed get the right cells:

```
R> do.call(rbind, lapply(r1, entry2cell, adim2222))
```

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

## 5 `permuteCellEntries()`

In a  $2 \times 3$  table, entries  $1, \dots, 6$  correspond to combinations  $(1, 1), (2, 1), (1, 2), (2, 2), (1, 3), (2, 3)$ . If we permute the table to a  $3 \times 2$  table the entries become as follows:

```
R> (p<-permuteCellEntries(perm=c(2,1), adim=c(2,3)))  
[1] 1 3 5 2 4 6
```

So for example,

```
R> (A <- array(11:16, dim=c(2,3)))
```

```
      [,1] [,2] [,3]  
[1,]    11    13    15  
[2,]    12    14    16
```

```
R> Ap <- A[p]  
R> dim(Ap) <- c(3,2)  
R> Ap
```

```
      [,1] [,2]  
[1,]    11    12  
[2,]    13    14  
[3,]    15    16
```

This corresponds to

```
R> aperm(A, c(2,1))
```

```
      [,1] [,2]  
[1,]    11    12  
[2,]    13    14  
[3,]    15    16
```

## 6 `factGrid()` – Factorial grid

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

```
R> ff <- factGrid(adim22222)  
R> head(ff)
```

```
      [,1] [,2] [,3] [,4]  
[1,]     1     1     1     1  
[2,]     2     1     1     1  
[3,]     1     2     1     1  
[4,]     2     2     1     1  
[5,]     1     1     2     1  
[6,]     2     1     2     1
```

```
R> tail(ff)
```

```
      [,1] [,2] [,3] [,4]  
[11,]     1     2     1     2  
[12,]     2     2     1     2  
[13,]     1     1     2     2  
[14,]     2     1     2     2  
[15,]     1     2     2     2  
[16,]     2     2     2     2
```

This is the same as (but faster)

```
R> aa <- expand.grid(list(1:2,1:2,1:2,1:2))
R> head(aa)
```

	Var1	Var2	Var3	Var4
1	1	1	1	1
2	2	1	1	1
3	1	2	1	1
4	2	2	1	1
5	1	1	2	1
6	2	1	2	1

There is a slice version as well:

```
R> factGrid(adim2222, slicecell=c(1,2), sliceset=c(2,3))
```

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