Introduction to R Programming The Apply Family

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Built in datasets

R provides many built in datasets. For a complete list see:

```
library(help = "datasets")
```

In this lecture we will the following datasets:

- USArrests
- airquality

For information about a specific dataset see, for example:

?USArrests

The USArrests dataset

This data set contains:

- ➤ Arrests per 100.000 residents for assault, murder and rape in each of the 50 USA states in 1973.
- ► There is also a column with the percentage of population living in urban areas.

The USArrests dataset

head(USArrests)

##		Murder	Assault	${\tt UrbanPop}$	Rape
##	Alabama	13.2	236	58	21.2
##	Alaska	10.0	263	48	44.5
##	Arizona	8.1	294	80	31.0
##	Arkansas	8.8	190	50	19.5
##	${\tt California}$	9.0	276	91	40.6
##	Colorado	7.9	204	78	38.7

The USArrests dataset

Let's do some calculations with the arrests of four states:

```
USArrests_short <- USArrests[1:4, -3]
USArrests_short
```

##		Murder	Assault	Rape
##	Alabama	13.2	236	21.2
##	Alaska	10.0	263	44.5
##	Arizona	8.1	294	31.0
##	Arkansas	8.8	190	19.5

Row and column sums

270.4

##

```
colSums(USArrests_short)

## Murder Assault Rape
## 40.1 983.0 116.2

rowSums(USArrests_short)

## Alabama Alaska Arizona Arkansas
```

333.1

218.3

317.5

Row and column means

Alabama

##

##

```
colMeans(USArrests_short)

## Murder Assault Rape
## 10.025 245.750 29.050

rowMeans(USArrests_short)
```

Arkansas

Alaska Arizona

90.13333 105.83333 111.03333 72.76667

To collapse data frames across rows or columns using functions other than the sum and the mean we can use apply():

```
apply(X, MARGIN, FUN, ...)
```

- X is a data frame
- ► MARGIN = 1 for rows, MARGIN = 2 for columns
- FUN is a function
- ... are optional arguments to pass to FUN

```
Apply functions over the columns of USArrests short:
apply(USArrests_short, 2, mean)
## Murder Assault
                    Rape
## 10.025 245.750 29.050
apply(USArrests short, 2, median)
## Murder Assault
                     Rape
##
      9.4 249.5 26.1
apply(USArrests_short, 2, sd)
##
     Murder Assault
                           Rape
   2.257395 44.078528 11.479402
##
```

##

```
Apply functions the rows of USArrests short:
apply(USArrests_short, 1, max)
##
   Alabama Alaska Arizona Arkansas
##
       236
               263
                        294
                                 190
apply(USArrests short, 1, min)
##
   Alabama Alaska Arizona Arkansas
##
      13.2 10.0 8.1 8.8
apply(USArrests_short, 1, var)
```

Alabama Alaska Arizona Arkansas

15973.81 18823.58 25238.70 10336.36

apply() vs for loop

Loop over the columns of USArrests_short:

```
res <- vector()

for(i in 1:ncol(USArrests_short)){
   res[i] <- mean(USArrests_short[[i]], na.rm = TRUE)
   names(res)[i] <- names(USArrests_short)[i]
}
res</pre>
```

```
## Murder Assault Rape
## 10.025 245.750 29.050
```

apply() vs for loop

Loop over the rows of USArrests_short:

```
res <- vector()

for(j in 1:nrow(USArrests_short)){
   res[j] <- max(USArrests_short[j, ],na.rm = TRUE)
   names(res)[j] <- rownames(USArrests_short)[j]
}
res</pre>
```

```
## Alabama Alaska Arizona Arkansas
## 236 263 294 190
```

apply() with ...

Now let's see an example that requires using dot-dot-dot (\ldots) . Suppose you're working with the airquality the data frame:

head(airquality)

##		Ozone	Solar.R	Wind	Temp	Month	Day
##	1	41	190	7.4	67	5	1
##	2	36	118	8.0	72	5	2
##	3	12	149	12.6	74	5	3
##	4	18	313	11.5	62	5	4
##	5	NA	NA	14.3	56	5	5
##	6	28	NA	14.9	66	5	6

apply() with ...

Try to use apply() to compute the means of the first four columns: apply(airquality[, 1:4], 2, mean)

Ozone Solar.R Wind Temp ## NA NA 9.957516 77.882353

We get NA for the first two columns. Why?

```
apply() with ...
```

```
Problem: Some columns have NAs.

sum(is.na(airquality$0zone))

## [1] 37

sum(is.na(airquality$Solar.R))

## [1] 7
```

apply() with ...

```
Solution: use ... to pass the na.rm argument to mean(): apply(airquality[, 1:4], 2, mean, na.rm = TRUE)
```

Ozone Solar.R Wind Temp ## 42.129310 185.931507 9.957516 77.882353

apply() user-defined functions

Checking for NAs one column at a time is not be feasible when we have many columns. How can we check how many NAs there there in each column?

```
count_nas <- function(x){sum(is.na(x))}
apply(airquality, 2, count_nas)</pre>
```

##	Ozone	Solar.R	Wind	Temp	Month	Day
##	37	7	0	0	0	0

```
Syntax: lapply(X, FUN, ...)
```

lapply() is similar to apply() but:

- X is a vector (atomic or list)
- ► There is no MARGINS argument
- Always returns a list

lapply() returns a list of the same length as X, each element of which is the result of applying FUN to the corresponding element of X.

```
lapply(c(1:3), log, base = 10)

## [[1]]
## [1] 0
##
## [[2]]
## [1] 0.30103
##
## [[3]]
## [1] 0.4771213
```

```
A <- matrix(1:10, ncol = 5)
B <- matrix(c(1, 5, 7, -1), ncol = 4)
C <- matrix(letters[1:4], ncol = 2)

my_list <- list(A, B, C)</pre>
```

```
my_list
## [[1]]
## [,1] [,2] [,3] [,4] [,5]
## [1,] 1 3 5 7 9
## [2,] 2 4 6
                    8 10
##
## [[2]]
## [,1] [,2] [,3] [,4]
## [1,] 1 5 7 -1
##
## [[3]]
## [,1] [,2]
## [1,] "a" "c"
## [2,] "b" "d"
```

Every element of my_list, except the last, contain a numerical matrix. Sum the elements of each of those matrices:

```
lapply(my_list[-3], sum)
## [[1]]
## [1] 55
```

```
##
## [[2]]
## [1] 12
```

Extract the element in position (1, 2) from each matrix:

```
lapply(my_list,"[", 1, 2)

## [[1]]
## [1] 3
##
## [[2]]
## [1] 5
##
## [[3]]
## [1] "c"
```

Extract the first row from each matrix:

```
lapply(my_list,"[", 1 , )

## [[1]]
## [1] 1 3 5 7 9

##
## [[2]]
## [1] 1 5 7 -1

##
## [[3]]
## [1] "a" "c"
```

Extract the 2nd column from each matrix:

```
lapply(my_list,"[", , 2)

## [[1]]
## [1] 3 4
##
## [[2]]
## [1] 5
##
## [[3]]
## [1] "c" "d"
```

lapply() vs for loop

Extract the 2nd column from each matrix:

```
res <- vector(mode = "list")
for(i in seq_along(my_list)){
 res[[i]] <- my_list[[i]][, 2]
res
## [[1]]
## [1] 3 4
##
## [[2]]
## [1] 5
##
## [[3]]
## [1] "c" "d"
```

- ► Works like lapply(), but simplifies the output to the most elementary data structure that is possible.
- Returns vectors or matrices.

```
sapply(my_list[-3], sum)
## [1] 55 12
sapply(my_list,"[", 1, 2)
## [1] "3" "5" "c"
```

```
sapply(airquality, function(x) sum(is.na(x)))
```

##	Uzone	Solar.R	Wind	Temp	Month	рау
##	37	7	0	0	0	0

```
set.seed(123)
our_list <- list(</pre>
 w = 1:6
 x = sample(1:5, 4, replace = TRUE),
  y = matrix(sample(1:100, 9), nrow = 3),
 z = sample(1:10, 3, replace = TRUE)
str(our list)
## List of 4
## $ w: int [1:6] 1 2 3 4 5 6
## $ x: int [1:4] 3 3 2 2
## $ y: int [1:3, 1:3] 43 14 25 90 91 69 96 57 92
## $ z: int [1:3] 9 9 3
```

The sapply() function sapply(our_list, max)

```
## w x y z
## 6 3 96 9
```

```
sapply(our_list, min)
...
```

```
## w x y z
## 1 2 14 3
sapply(our_list, class)
```

```
## $w
## [1] "integer"
```

```
## $x
## [1] "integer"
```

##

##

```
## $y
## [1] "matrix" "array"
```

```
How many numbers are there inside each element of our_list? sapply(our_list, length)
```

```
## w x y z
## 6 4 9 3
```

```
set.seed(123)
our list 2 <- list(
 w = 1:6,
 x = sample(1:5, 4, replace = TRUE),
 y = airquality
sapply(our_list_2, class)
##
     "integer" "integer" "data.frame"
##
dim(airquality)
## [1] 153 6
```

How many numbers are there inside each element of our_list_2?

The length of a data frame is the number of columns, and hence sapply(our_list_2, length) won't do the trick.

```
our_fum <- function(x){
  if(class(x) == "data.frame"){
    nrow(x) * ncol(x)
  }else{
    length(x)
  }
}</pre>
```

```
## w x y
## 6 4 918
```

sapply() vs for loop

The same but with a for loop:

```
res <- vector()

for(i in seq_along(our_list_2)){
   res[i] <- our_fun(our_list_2[[i]])
   names(res)[i] <- names(our_list_2)[i]
}
res</pre>
```

```
## w x y
## 6 4 918
```



mapply() is a generalization of sapply(). It applies a multivariate function over multiple vectors of arguments.

Suppose we want 3 samples of different sizes from a Normal(0,1) distribution:

```
set.seed(123)
rnorm(n = 1)
## [1] -0.5604756
rnorm(n = 2)
## [1] -0.2301775 1.5587083
rnorm(n = 3)
## [1] 0.07050839 0.12928774 1.71506499
```

The same result can be obtained more compactly with mapply():

```
set.seed(123)
sample_size <- 1:3</pre>
mapply(FUN = rnorm, n = sample_size)
## [[1]]
## [1] -0.5604756
##
## [[2]]
## [1] -0.2301775 1.5587083
##
## [[3]]
## [1] 0.07050839 0.12928774 1.71506499
```

Since we only iterated over one vector, we could have used sapply():

```
set.seed(123)
sample_size <- 1:3</pre>
sapply(FUN = rnorm, X = sample_size)
## [[1]]
## [1] -0.5604756
##
## [[2]]
## [1] -0.2301775 1.5587083
##
## [[3]]
   [1] 0.07050839 0.12928774 1.71506499
```

But what if we want to sample from normal distributions with different means, while still having samples of different sizes?

```
set.seed(123)
rnorm(n = 1, mean = 5)
## [1] 4.439524
rnorm(n = 2, mean = 10)
## [1] 9.769823 11.558708
rnorm(n = 3, mean = -3)
## [1] -2.929492 -2.870712 -1.284935
```

In this case we need to iterate over two vectors, one for sample sizes and one for means:

```
set.seed(123)
sample size <- 1:3
mu \leftarrow c(5, 10, -3)
mapply(rnorm, n = sample size, mean = mu)
## [[1]]
## [1] 4.439524
##
## [[2]]
## [1] 9.769823 11.558708
##
## [[3]]
   [1] -2.929492 -2.870712 -1.284935
```

Now suppose we also want each sample to have a different standard deviation:

```
set.seed(123)
rnorm(n = 1, mean = 5, sd = 1)
## [1] 4.439524
rnorm(n = 2, mean = 10, sd = 3)
## [1] 9.309468 14.676125
rnorm(n = 3, mean = -3, sd = 5)
## [1] -2.647458 -2.353561 5.575325
```

```
set.seed(123)
sample_size <- 1:3</pre>
mu < -c(5, 10, -3)
sigma \leftarrow c(1, 3, 5)
mapply(rnorm, mean = mu, sd = sigma, n = sample_size)
## [[1]]
## [1] 4.439524
##
## [[2]]
## [1] 9.309468 14.676125
##
## [[3]]
## [1] -2.647458 -2.353561 5.575325
```

Now suppose we wanted our results with two decimal places only: set.seed(123) results <- mapply(rnorm, mean = mu, sd = sigma, n = sample size)sapply(results, FUN = round, 2) ## [[1]] ## [1] 4.44 ## ## [[2]] ## [1] 9.31 14.68 ## ## [[3]] ## [1] -2.65 -2.35 5.58

mapply() vs for loop

```
set.seed(123)
sample_size <- 1:3</pre>
mu < -c(5, 10, -3)
sigma \leftarrow c(1, 3, 5)
res <- vector(mode = "list")
for (i in 1:3) {
  res[[i]] <- round(rnorm(mean = mu[i],
                              sd = sigma[i],
                             n = \text{sample size}[i]),
                       2)
```

mapply() vs for loop

res

```
## [[1]]
## [1] 4.44
##
## [[2]]
## [1] 9.31 14.68
##
## [[3]]
## [1] -2.65 -2.35 5.58
```