

R Objects & Programmatic Data Manipulation

Fundamental Techniques in Data Science



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Outline

R Objects & Data Types

- Vectors & Matrices

- Lists & Data Frames

- Factors

Programmatic Data Manipulation

- Subsetting

- Transforming

- Pipes



R OBJECTS & DATA TYPES



Vectors

Vectors are the simplest kind of R object.

- There is no concept of a “scalar” in R.

Vectors come in one of six “atomic modes”:

- numeric/double
- logical
- character
- integer
- complex
- raw



Vectors

```
(v1 <- vector("numeric", 3))
```

```
[1] 0 0 0
```

```
(v2 <- vector("logical", 3))
```

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

```
(v3 <- vector("character", 3))
```

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

```
(v4 <- vector("integer", 3))
```

```
[1] 0 0 0
```

```
(v5 <- vector("complex", 3))
```

```
[1] 0+0i 0+0i 0+0i
```

```
(v6 <- vector("raw", 3))
```

```
[1] 00 00 00
```

Generating Vectors

We have many ways of generating vectors.

```
(y1 <- c(1, 2, 3))
```

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

```
(y2 <- c(TRUE, FALSE, TRUE, TRUE))
```

```
[1] TRUE FALSE TRUE TRUE
```

```
(y3 <- c("bob", "suzy", "danny"))
```

```
[1] "bob" "suzy" "danny"
```

```
1:5
```

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

```
1.2:5.3
```

```
[1] 1.2 2.2 3.2 4.2 5.2
```

Generating Vectors

```
rep(33, 4)
```

```
[1] 33 33 33 33
```

```
rep(1:3, 3)
```

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

```
rep(y3, each = 2)
```

```
[1] "bob"    "bob"    "suzy"   "suzy"   "danny"  "danny"
```

```
seq(0, 1, 0.25)
```

```
[1] 0.00 0.25 0.50 0.75 1.00
```



The Three Most Useful Data Types

Numeric

```
(a <- 1:5)
[1] 1 2 3 4 5
```

Character

```
(b <- c("foo", "bar"))
[1] "foo" "bar"
```

Logical

```
(c <- c(TRUE, FALSE))
[1] TRUE FALSE
```



Combining Data Types in Vectors

What happens if we try to concatenate different data types?

```
c(a, b)
```

```
[1] "1" "2" "3" "4" "5" "foo" "bar"
```

```
c(b, c)
```

```
[1] "foo" "bar" "TRUE" "FALSE"
```

```
c(a, c)
```

```
[1] 1 2 3 4 5 1 0
```



Matrices

Matrices generalize vectors by adding a dimension attribute.

```
(m1 <- matrix(a, nrow = 5, ncol = 2))
```

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

```
attributes(v1)
```

NULL

```
attributes(m1)
```

```
$dim  
[1] 5 2
```

Matrices

Matrices are populated in column-major order, by default.

```
(m2 <- matrix(1:9, 3, 3))
```

	[,1]	[,2]	[,3]
[1,]	1	4	7
[2,]	2	5	8
[3,]	3	6	9

The `byrow = TRUE` option allows us to fill by row-major order.

```
(m3 <- matrix(1:9, 3, 3, byrow = TRUE))
```

	[,1]	[,2]	[,3]
[1,]	1	2	3
[2,]	4	5	6
[3,]	7	8	9

Mixing Data Types in Matrices

Like vectors, matrices can only hold one type of data.

```
cbind(c, letters[1:5])
```

```
      c
[1,] "TRUE"  "a"
[2,] "FALSE" "b"
[3,] "TRUE"  "c"
[4,] "FALSE" "d"
[5,] "TRUE"  "e"
```

```
cbind(c, c(TRUE, TRUE, FALSE, FALSE, TRUE))
```

```
      c
[1,] TRUE TRUE
[2,] FALSE TRUE
[3,] TRUE FALSE
[4,] FALSE FALSE
[5,] TRUE TRUE
```

Lists

Lists are the workhorse of R data objects.

- An R list can hold an arbitrary set of other R objects.

We create lists using the `list()` function

```
(l1 <- list(1, 2, 3))
```

```
[[1]]
```

```
[1] 1
```

```
[[2]]
```

```
[1] 2
```

```
[[3]]
```

```
[1] 3
```

Lists

```
(l2 <- list("bob", TRUE, 33, 42+3i))
```

```
[[1]]
```

```
[1] "bob"
```

```
[[2]]
```

```
[1] TRUE
```

```
[[3]]
```

```
[1] 33
```

```
[[4]]
```

```
[1] 42+3i
```



Lists

List elements have no default names, but we can define our own

```
(l3 <- list(name = "bob",  
            alive = TRUE,  
            age = 33,  
            relationshipStatus = 42+3i)  
)  
  
$name  
[1] "bob"  
  
$alive  
[1] TRUE  
  
$age  
[1] 33  
  
$relationshipStatus  
[1] 42+3i
```

Lists

We can also assign post hoc names via the 'names()' function

```
names(l1) <- c("first", "second", "third")  
l1  
  
$first  
[1] 1  
  
$second  
[1] 2  
  
$third  
[1] 3
```



Lists

We can append new elements onto an existing list:

```
(l4 <- list())  
  
list()  
  
l4$grass <- "green"  
l4$money <- 0  
l4$logical <- FALSE  
l4  
  
$grass  
[1] "green"  
  
$money  
[1] 0  
  
$logical  
[1] FALSE
```

Lists

The elements inside a list don't really know that they live in a list; they'll pretty much behave as normal

```
14$money - 42
```

```
[1] -42
```



Data Frames

Data frames are R's way of storing rectangular data sets.

- Each column of a data frame is a vector.
- Each of these vectors can have a different type.

We create data frames using the `data.frame()` function

```
(d1 <- data.frame(1:10, c(-1, 1), seq(0.1, 1, 0.1)))
```

	X1.10	c..1..1.	seq.0.1..1..0.1.
1	1	-1	0.1
2	2	1	0.2
3	3	-1	0.3
4	4	1	0.4
5	5	-1	0.5
6	6	1	0.6
7	7	-1	0.7
8	8	1	0.8
9	9	-1	0.9
10	10	1	1.0

Data Frames

```
(d2 <- data.frame(x = 1:10, y = c(-1, 1), z = seq(0.1, 1, 0.1)))
```

	x	y	z
1	1	-1	0.1
2	2	1	0.2
3	3	-1	0.3
4	4	1	0.4
5	5	-1	0.5
6	6	1	0.6
7	7	-1	0.7
8	8	1	0.8
9	9	-1	0.9
10	10	1	1.0



Data Frames

```
(d3 <- data.frame(a = sample(c(TRUE, FALSE), 10, replace = TRUE),  
                  b = sample(c("foo", "bar"), 10, replace = TRUE),  
                  c = runif(10)  
                  )
```

```
)
```

	a	b	c
1	FALSE	foo	0.4708232
2	TRUE	foo	0.2701596
3	TRUE	bar	0.6199154
4	FALSE	bar	0.2078104
5	TRUE	bar	0.4912943
6	FALSE	bar	0.1840306
7	FALSE	bar	0.5438698
8	TRUE	bar	0.5755350
9	FALSE	bar	0.7557042
10	FALSE	bar	0.8405729

Data Frames

```
(d4 <- data.frame(matrix(NA, 10, 3)))
```

	X1	X2	X3
1	NA	NA	NA
2	NA	NA	NA
3	NA	NA	NA
4	NA	NA	NA
5	NA	NA	NA
6	NA	NA	NA
7	NA	NA	NA
8	NA	NA	NA
9	NA	NA	NA
10	NA	NA	NA



Data Frames

Data frames are actually lists of vectors (representing the columns)

```
is.data.frame(d3)
```

```
[1] TRUE
```

```
is.list(d3)
```

```
[1] TRUE
```

Although they look like rectangular "matrices", from R's perspective a data frame IS NOT a matrix

```
is.matrix(d3)
```

```
[1] FALSE
```

We cannot treat a data frame like a matrix. E.g., matrix algebra doesn't work with data frames

```
d1 %*% t(d2)
```

```
Error in d1 %*% t(d2): requires numeric/complex matrix/vector arguments
```

Factors

Factors are R's way of representing nominal variables.

- We can create a factor using the `factor()` function

```
(f1 <- factor(sample(1:3, 10, TRUE), labels = c("red", "yellow", "blue")))  
  
[1] red    yellow blue   red    blue   blue   yellow red  
[9] red    red  
Levels: red yellow blue
```

Factors are stored as integer vectors with a *levels* attribute and a special *factor* class.

```
typeof(f1)  
  
[1] "integer"  
  
attributes(f1)
```

```
$levels  
[1] "red"    "yellow" "blue"
```

```
$class  
[1] "factor"
```


Factors

Even though a factor's data are represented by an integer vector, R does not consider factors to be integer/numeric data.

```
is.numeric(f1)
```

```
[1] FALSE
```

```
is.integer(f1)
```

```
[1] FALSE
```

Since factors represent nominal variables, we cannot do math with factors

```
f1 + 1
```

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

```
mean(f1)
```

```
[1] NA
```

PROGRAMMATIC DATA MANIPULATION



Tidyverse Solutions: **dplyr**

The **dplyr** package provides two principle subsetting functions

- `select()` : subset columns
- `filter()` : subset rows

```
library(dplyr)
```



What are pipes?

The %>% symbol represents the *pipe* operator.

- We use the pipe operator to compose functions into a *pipeline*.

The following code represents a pipeline.

```
firstBoys <-  
  read_sav("../data/boys.sav") %>%  
  head()
```

This pipeline replaces the following code.

```
firstBoys <- head(read_sav("../data/boys.sav"))
```



Why are pipes useful?

Let's assume that we want to:

1. Load data
2. Transform a variable
3. Filter cases
4. Select columns

Without a pipe, we may do something like this:

```
boys <- read_sav("../data/boys.sav")
```

```
Error in read_sav("../data/boys.sav"): could not find function "read_sav"
```

```
boys <- transform(boys, hgt = hgt / 100)
```

```
Error in transform(boys, hgt = hgt/100): object 'boys' not found
```

```
boys <- filter(boys, age > 15)
```

```
Error in filter(boys, age > 15): object 'boys' not found
```

```
boys <- subset(boys, select = c(hgt, wgt, bmi))
```

```
Error in subset(boys, select = c(hgt, wgt, bmi)): object 'boys' not found
```

Why are pipes useful?

Let's assume that we want to:

1. Load data
2. Transform a variable
3. Filter cases
4. Select columns

With the pipe, we could do something like this:

```
library(magrittr)

boys <-
  read_sav("../data/boys.sav") %>%
  transform(hgt = hgt / 100) %>%
  filter(age > 15) %>%
  subset(select = c(hgt, wgt, bmi))
```

```
Error in read_sav("../data/boys.sav"): could not find function "read_sav"
```

With a pipeline, our code more clearly represents the sequence of steps in our analysis.

Benefits of Pipes

When you use pipes, your code becomes more readable.

- Operations are structured from left-to-right and not from in-to-out
- You can avoid many nested function calls
- You don't have to keep track of intermediate objects
- It's easy to add steps to the sequence

In RStudio, you can use a keyboard shortcut to insert the `%>%` symbol.

- Windows/Linux: *ctrl + shift + m*
- Mac: *cmd + shift + m*



What do pipes do?

Pipes compose R functions without nesting.

- `f(x)` becomes `x %>% f()`

```
mean(rnorm(10))
```

```
[1] -0.4294987
```

```
rnorm(10) %>% mean()
```

```
[1] -0.04373715
```



What do pipes do?

Multiple function arguments are fine.

- `f(x, y)` becomes `x %>% f(y)`

```
cor(boys, use = "pairwise.complete.obs")
```

```
Error in is.data.frame(x): object 'boys' not found
```

```
boys %>% cor(use = "pairwise.complete.obs")
```

```
Error in is.data.frame(x): object 'boys' not found
```



What do pipes do?

Composing more than two functions is easy, too.

- `h(g(f(x)))` becomes `x %>% f %>% g %>% h`

```
max(na.omit(subset(boys, select = wgt)))
```

```
Error in subset(boys, select = wgt): object 'boys' not found
```

```
boys %>%  
  subset(select = wgt) %>%  
  na.omit() %>%  
  max()
```

```
Error in subset(., select = wgt): object 'boys' not found
```



The Role of `.` in a Pipeline

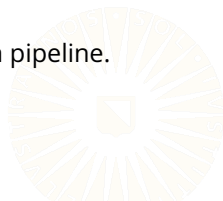
In the expression `a %>% f(arg1, arg2, arg3)`, `a` will be "piped into" `f()` as `arg1`.

```
data(cats, package = "mice")  
cats %>% plot(Hwt ~ Bwt)
```

```
Error in plot(., Hwt ~ Bwt): object 'cats' not found
```

Clearly, we have a problem if we pipe our data into the wrong argument.

- We can change this behavior with the `.` symbol.
- The `.` symbol acts as a placeholder for the data in a pipeline.



The Role of `.` in a Pipeline

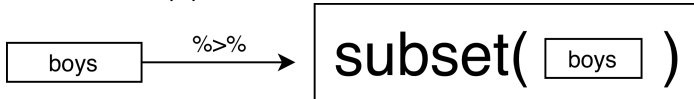
```
cats %>% plot(Hwt ~ Bwt, data = .)
```

```
Error in eval(m$data, eframe): object 'cats' not found
```

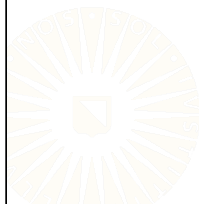
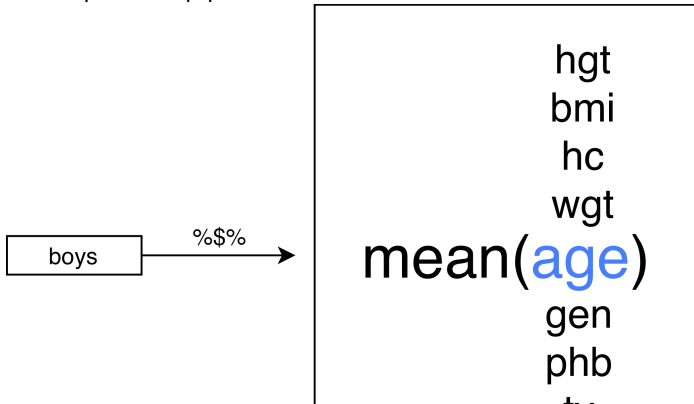


Different Flavors of Pipe

The standard pipe (%>%)



The exposition pipe (%\$%)



Using the Exposition Pipe: %\$%

The exposition pipe offers a more elegant way to solve our earlier problem.

```
cats %$% plot(Hwt ~ Bwt)
```

```
Error in base::with(., plot(Hwt ~ Bwt)): object 'cats' not found
```



Performing a T-Test in a Pipeline

```
cats %$% t.test(Hwt ~ Sex)
```

```
Error in base::with(., t.test(Hwt ~ Sex)): object 'cats' not found
```

The above is equivalent to either of the following.

```
cats %>% t.test(Hwt ~ Sex, data = .)
t.test(Hwt ~ Sex, data = cats)
```



Storing the Results

```
catsTest <- cats %$% t.test(Bwt ~ Sex)
```

```
Error in base::with(., t.test(Bwt ~ Sex)): object 'cats' not found
```

```
catsTest
```

```
Error in eval(expr, envir, enclos): object 'catsTest' not found
```



References

