R Objects & Programmatic Data Manipulation

Fundamental Techniques in Data Science



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Outline

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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

5 of 64

```
(v1 <- vector("numeric", 3))</pre>
[1] 0 0 0
(v2 <- vector("logical", 3))</pre>
[1] FALSE FALSE FALSE
(v3 <- vector("character", 3))</pre>
[1] "" "" ""
(v4 <- vector("integer", 3))</pre>
[1] 0 0 0
(v5 <- vector("complex", 3))</pre>
[1] 0+0i 0+0i 0+0i
(v6 <- vector("raw", 3))</pre>
[1] 00 00 00
```

Generating Vectors

We have many ways of generating vectors.

```
(y1 \leftarrow 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 \leftarrow matrix(a, nrow = 5, ncol = 2))
     [,1] [,2]
[1,]
[2,] 2
[3,] 3 3
[4,] 4 4
[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])
     С
[1.] "TRUE"
             "a"
[2,] "FALSE" "b"
[3.] "TRUE"
              " c "
[4,] "FALSE" "d"
[5.] "TRUE"
             اا ۾ اا
cbind(c, c(TRUE, TRUE, FALSE, FALSE, TRUE))
         С
[1,]
     TRUE
           TRUE
[2.] FALSE TRUE
[3,] TRUE FALSE
[4,] FALSE FALSE
[5,] TRUE TRUE
```

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
```

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

[[1]]
[1] "bob"

[[2]]
[1] TRUE

[[3]]
[1] 33

[[4]]
[1] 42+3i
```

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

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

We can also assign post hoc names via the <code>names()</code> function.

```
names(11) <- c("first", "second", "third")
11

$first
[1] 1

$second
[1] 2

$third
[1] 3</pre>
```

We can append new elements onto an existing list.

```
(14 <- list())
list()
14$people <- c("Bob", "Alice", "Suzy")
14$money <- 0
14$logical <- FALSE
14
$people
[1] "Bob" "Alice" "Suzy"
$money
[1] 0
$logical
[1] FALSE
```

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

```
14$money + 42
[1] 42
paste0("Hello, ", 14$people, "!\n") %>% cat()
Hello, Bob!
Hello, Alice!
Hello, Suzy!
```

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.

```
(d2 <- data.frame(x = 1:6, y = c(-1, 1), z = seq(0.1, 0.6, 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
```

```
(d3 <- data.frame(a = sample(c(TRUE, FALSE), 8, replace = TRUE),</pre>
                  b = sample(c("foo", "bar"), 8, replace = TRUE),
                  c = runif(8)
1 FALSE bar 0.3218011
  TRUE bar 0.5110387
  TRUE foo 0.8472829
4 FALSE foo 0.1928677
  TRUE bar 0.4708232
6 FALSE bar 0.2701596
7 FALSE bar 0.6199154
  TRUE bar 0.2078104
```

```
(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

8 NA NA NA

9 NA NA NA

10 NA NA NA
```

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

as.matrix(d1) %*% t(as.matrix(d2))

[1,1] [,2] [,3] [,4] [,5] [,6]
[1,1] 2.01 1.02 4.03 3.04 6.05 5.06
[2,1] 1.02 5.04 5.06 9.08 9.10 13.12
[3,1] 4.03 5.06 10.09 11.12 16.15 17.18
[4,1] 3.04 9.08 11.12 17.16 19.20 25.24
[5,1] 6.05 9.10 16.15 19.20 26.25 29.30
[6,1] 5.06 13.12 17.18 25.24 29.30 37.36
```

Factors

Factors are R's way of repesenting nominal variables.

• We can create a factor using the factor() function.

```
(f1 <- factor(sample(1:3, 15, TRUE), labels = c("red", "yellow", "blue")))
[1] yellow red blue yellow red yellow blue red
[9] blue blue yellow red red yellow
Levels: red yellow blue</pre>
```

Factors

Factors are integer vectors with a levels attribute and a factor class.

```
typeof(f1)
[1] "integer"
attributes(f1)
$levels
[1] "red" "yellow" "blue"
$class
[1] "factor"
```

The levels are just group labels.

```
levels(f1)
[1] "red" "yellow" "blue"
```

Factors

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

```
is.numeric(f1)
[1] FALSE
is.integer(f1)
[1] FALSE
```

Factors represent nominal variables, so we cannot do math with factors.

DATA MANIPULATION

tibble is a tidyverse dataframe



Base R Subsetting

In Base R, we typically use three operators to subset objects:

- []
- [[]]
- \$

Which of these operators we choose to use (and how we implement the chosen operator) will depend on two criteria:

- What type of object are we trying to subset?
- How much of the original typing do we want to keep in the subset?

To subset vectors and matrices, we can use either <code>[] or [[]] .</code>

```
(x \leftarrow rnorm(8))
[1]
   1.17766957 -0.16448325 0.94412165 2.07070102
[5] 1.10427674 0.39615080 -0.09361605 0.13621028
x[1:3]
[1] 1.1776696 -0.1644832 0.9441216
x [2]
[1] -0.1644832
x[c(2, 5, 7)]
[1] -0.16448325 1.10427674 -0.09361605
x[c(TRUE, FALSE)]
[1] 1.17766957 0.94412165 1.10427674 -0.09361605
```

double bracket only selects a single element

The [[]] operator can only select a single element.

```
x[[2]]
[1] -0.1644832
x[[1:3]]
Error in x[[1:3]]: attempt to select more than one element in vectorIndex
```

To subset matrices, we need to differentiate the dimensions.

```
(y \leftarrow matrix(x, 6, 4))
           Γ.17
                      [,2]
                                  [,3]
                                             [,4]
[1.] 1.1776696 -0.09361605 1.10427674 0.94412165
[2,] -0.1644832 0.13621028
                            0.39615080 2.07070102
[3,] 0.9441216 1.17766957 -0.09361605 1.10427674
[4,] 2.0707010 -0.16448325 0.13621028 0.39615080
[5,] 1.1042767 0.94412165 1.17766957 -0.09361605
[6.] 0.3961508 2.07070102 -0.16448325
                                        0.13621028
y[2, 2]
[1] 0.1362103
y[1:3, 1]
[1]
   1.1776696 -0.1644832 0.9441216
```

We can select sub-matrices and mix different indexing styles.

```
y[1:2, c(2, 4)]

[,1] [,2]

[1,] -0.09361605 0.9441216

[2,] 0.13621028 2.0707010

y[c(1:3, 5), c(FALSE, TRUE, TRUE, FALSE)]

[,1] [,2]

[1,] -0.09361605 1.10427674

[2,] 0.13621028 0.39615080

[3,] 1.17766957 -0.09361605

[4,] 0.94412165 1.17766957
```

Leaving the rows or columns section empty will return all rows or columns, respectively.

The [[]] operator can still select only a single element.

```
y[[2, 2]]
[1] 0.1362103
y[[1:3, 2]]
Error in y[[1:3, 2]]: attempt to select more than one element in get1index
```

We can use all three operators to subset lists.

```
14$people

[1] "Bob" "Alice" "Suzy"

14[1]

$people
[1] "Bob" "Alice" "Suzy"

14[["people"]]

[1] "Bob" "Alice" "Suzy"
```

Lists

As expected, we cannot select multiple list elements with <code>[[]]</code> .

```
14[1:2]

$people
[1] "Bob" "Alice" "Suzy"

$money
[1] 0

14[[1:2]]
[1] "Alice"
```

Lists

The relative behavior of [] and [[]] is more important for lists.

```
(tmp1 < - 14[1])
$people
[1] "Bob" "Alice" "Suzy"
class(tmp1)
[1] "list"
(tmp2 <- 14[[1]])
[1] "Bob" "Alice" "Suzy"
class(tmp2)
[1] "character"
```

We can subset the columns of a data frame using list semantics.

```
d3$a
[1] FALSE TRUE TRUE FALSE TRUE FALSE FALSE TRUE
d3[1]
      а
1 FALSE
  TRUE
  TRUE
4 FALSE
  TRUE
6 FALSE
7 FALSE
  TRUE
```

```
d3["a"]
1 FALSE
  TRUE
 TRUE
4 FALSE
  TRUE
6 FALSE
7 FALSE
  TRUE
d3[["a"]]
[1] FALSE TRUE TRUE FALSE TRUE FALSE FALSE TRUE
```

We can also use matrix-style subsetting.

```
d3[1:5, 1:2]
1 FALSE bar
2 TRUE bar
3 TRUE foo
4 FALSE foo
5 TRUE bar
d3[c(1, 3, 5, 7), letters[2:3]]
    b
1 bar 0.3218011
3 foo 0.8472829
5 bar 0.4708232
7 bar 0.6199154
```

The list-style subsetting can have advantages.

```
(tmp1 \leftarrow d3[, 2])
[1] "bar" "bar" "foo" "foo" "bar" "bar" "bar" "bar"
(tmp2 <- d3[2])
    b
1 bar
2 bar
3 foo
4 foo
5 bar
6 bar
7 bar
8 bar
```

Single columns are returned as $N \times \mathbf{1}$ data frames, rather than N-element vectors.

```
class(tmp1)
[1] "character"
class(tmp2)
[1] "data.frame"
```

Overwriting Values

We also use subsetting syntax to overwrite values in an R object.

```
x[2:3] \leftarrow NA
x
[1]
   1.17766957
                        NΑ
                            NA 2.07070102
[5] 1.10427674 0.39615080 -0.09361605 0.13621028
14$people <- "None"
14
$people
[1] "None"
$money
[1] 0
$logical
[1] FALSE
```

Overwriting Values

```
y[1:3, 2:4] <- -1
print(y, digits = 3)

[,1] [,2] [,3] [,4]
[1,] 1.178 -1.000 -1.000 -1.0000
[2,] -0.164 -1.000 -1.000 -1.0000
[3,] 0.944 -1.000 -1.000 -1.0000
[4,] 2.071 -0.164 0.136 0.3962
[5,] 1.104 0.944 1.178 -0.0936
[6,] 0.396 2.071 -0.164 0.1362
```

```
d4 <- d3

d4[1:2] <- rgamma(nrow(d4) * 2, 10)

print(d4, digits = 3)

a b c

1 9.99 11.53 0.322

2 10.35 10.23 0.511

3 16.20 5.39 0.847

4 16.81 8.01 0.193

5 15.30 8.24 0.471

6 12.66 8.96 0.270

7 9.95 10.17 0.620

8 11.74 12.88 0.208
```

Tidyverse Subsetting

The **dplyr** package provides many ways to subset data, but two functions are most frequently useful.

```
select() : subset columns
```

```
• filter() : subset rows
```

```
library(dplyr)
```

Subsetting Columns: select()

The dplyr::select() function provides a very intuitive syntax for variable selection and column-wise subsetting.

```
select(d3, a, b)
                                         select(d3, -a)
                                                 C
1 FALSE bar
                                         1 bar 0.3218011
 TRUE bar
                                         2 bar 0.5110387
 TRUE foo
                                         3 foo 0.8472829
4 FALSE foo
                                         4 foo 0.1928677
  TRUE bar
                                         5 bar 0.4708232
6 FALSE bar
                                         6 bar 0.2701596
7 FALSE bar
                                         7 bar 0.6199154
8 TRUE bar
                                         8 bar 0.2078104
```

Subsetting Rows

The dplyr::filter() function provides easy row subsetting:

```
filter(d3, c > 0.5)

a b c

1 TRUE bar 0.5110387

2 TRUE foo 0.8472829

3 FALSE bar 0.6199154
```

```
filter(d3, c > 0.15, b == "foo")

a b c

1 TRUE foo 0.8472829

2 FALSE foo 0.1928677
```

We can achieve the same effect via logical indexing in Base R:

```
d3[d3$c > 0.5, ]

a b c
2 TRUE bar 0.5110387
3 TRUE foo 0.8472829
7 FALSE bar 0.6199154
```

```
d3[d3$c > 0.15 & d3$b == "foo", ]

a b c
3 TRUE foo 0.8472829
4 FALSE foo 0.1928677
```

Base R Variable Transformations

There is nothing very special about the process of transforming variables in Base R.

```
<- d3
                                              <- d3
d4
d4$d \leftarrow scale(d4$c)
                                         d4$c <- scale(d4$c, scale = FALSE)
                                         d4$a <- as.numeric(d4$a)
d4$e <- !d4$a
d4
                                         d4
                                               b
1 FALSE bar 0.3218011 -0.4771996
                                  TRIIF
                                         1 0 bar -0.10841126
  TRUE bar 0.5110387 0.3557774 FALSE
                                         2 1 bar 0.08082628
  TRUE foo 0.8472829 1.8358417 FALSE
                                         3 1 foo 0.41707055
 FALSE foo 0.1928677 -1.0447329
                                         4 0 foo -0.23734472
                                 TRUE
  TRUE bar 0.4708232 0.1787590 FALSE
                                         5 1 bar 0.04061085
6 FALSE bar 0.2701596 -0.7045129
                                 TRUE
                                         6 0 bar -0.16005280
7 FALSE bar 0.6199154 0.8350260
                                  TRUE
                                         7 0 bar 0.18970305
 TRUE bar 0.2078104 -0.9789586 FALSE
                                         8 1 bar -0.22240197
```

Tidyverse Variable Transformations

The mutate() function from **dplyr** is the workhorse of Tidyverse transformation functions.

```
mutate(d3, d = rbinom(nrow(d3), 1, c))

a b c d

1 FALSE bar 0.3218011 0

2 TRUE bar 0.5110387 1

3 TRUE foo 0.8472829 1

4 FALSE foo 0.1928677 0

5 TRUE bar 0.4708232 1

6 FALSE bar 0.2701596 0

7 FALSE bar 0.6199154 1

8 TRUE bar 0.2078104 0
```

Sorting & Ordering

To sort a single vector, the best option is the Base R sort() function.

```
sort(d3$c)
[1] 0.1928677 0.2078104 0.2701596 0.3218011 0.4708232
[6] 0.5110387 0.6199154 0.8472829
sort(d3$c, decreasing = TRUE)
[1] 0.8472829 0.6199154 0.5110387 0.4708232 0.3218011
[6] 0.2701596 0.2078104 0.1928677
```

To sort the rows of a data frame according to the order of one of its columns, the dplyr::arrange() works best.

- You can use the Base R order() function to achieve similar results.
- The behavior of order() is (extremely) unintuitive.

Tidyverse Ordering

Using dplyr::arrange() could not be simpler.

```
arrange(d3, -c)
                                                       arrange(d3, -a, c)
arrange(d3, a)
      а
          b
                                     b
                                                                 b
 FALSE bar 0.3218011
                              TRUE foo 0.8472829
                                                          TRUE bar 0.2078104
2 FALSE foo 0.1928677
                           2 FALSE bar 0.6199154
                                                          TRUE bar 0.4708232
3 FALSE bar 0.2701596
                              TRUE bar 0.5110387
                                                          TRUE bar 0.5110387
4 FALSE bar 0.6199154
                              TRUE bar 0.4708232
                                                          TRUE foo 0.8472829
  TRUE bar 0.5110387
                             FALSE bar 0.3218011
                                                         FALSE foo 0.1928677
  TRUE foo 0.8472829
                             FALSE bar 0.2701596
                                                         FALSE bar 0.2701596
  TRUE bar 0.4708232
                              TRUE bar 0.2078104
                                                         FALSE bar 0.3218011
  TRUE bar 0.2078104
                           8 FALSE foo 0.1928677
                                                       8 FALSE bar 0.6199154
```

PIPES



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 <-
  readRDS("boys.rds") %>%
  head()
```

This pipeline replaces the following code.

```
firstBoys <- head(readRDS("boys.rds"))</pre>
```

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:

```
library(dplyr)

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

Why are pipes useful?

With the pipe, we could do something like this:

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

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 instead of 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] 0.05223587
rnorm(10) %>% mean()
[1] 0.04802827
```

What do pipes do?

Multiple function arguments are fine.

```
• f(x, y) becomes x %>% f(y)
```

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

hgt wgt bmi
hgt 1.0000000 0.6100784 0.1758781
wgt 0.6100784 1.0000000 0.8841304
bmi 0.1758781 0.8841304 1.0000000

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

hgt wgt bmi
hgt 1.0000000 0.6100784 0.1758781
wgt 0.6100784 1.0000000 0.8841304
bmi 0.1758781 0.8841304 1.0000000
```

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)))
[1] 117.4
boys %>%
    subset(select = wgt) %>%
    na.omit() %>%
    max()
[1] 117.4
```

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 = "MASS")
cats %>% plot(Hwt ~ Bwt)

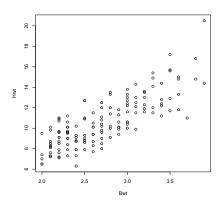
Error in text.default(x, y, txt, cex = cex, font = font): invalid
mathematical annotation
```

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 = .)
```



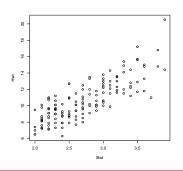


Exposition Pipe: %\$%

There are several different flavors of pipe. The *exposition pipe*, %\$%, is a particularly useful variant.

• The exposition pipe *exposes* the contents of an object to the next function in the pipeline.

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





Performing a T-Test in a Pipeline

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

```
Welch Two Sample t-test

data: Hwt by Sex

t = -6.5179, df = 140.61, p-value = 1.186e-09

alternative hypothesis: true difference in means between group F and group M is not equal to 0

95 percent confidence interval:

-2.763753 -1.477352

sample estimates:

mean in group F mean in group M

9.202128

11.322680
```

The above is equivalent to either of the following.

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