

## start\_2\_R\_basics

In R, an object is anything that can be assigned to a variable. This includes constants, data structures, functions, and even graphs. Objects have a mode (which describes how the object is stored) and a class (which tells generic functions like print how to handle it).

Vectors are one-dimensional arrays that can hold numeric data, character data, or logical data. The combine function `c()` is used to form the vector.

```
x <- c(1,2,4) #The "c" stands for "concatenate."
x
```

```
## [1] 1 2 4
```

```
q <- c(x,x,8)
q
```

```
## [1] 1 2 4 1 2 4 8
```

```
#
a <- c(1, 2, 5, 3, 6, -2, 4)
b <- c("one", "two", "three")
c <- c(TRUE, TRUE, TRUE, FALSE, TRUE, FALSE)
```

Seen Above -- a is numeric vector, b is a character vector, and c is a logical vector. Note that the data in a vector must only be one type or mode (numeric, character, or logical). You can't mix modes in the same vector.

Indexing vectors -

```
#
a_idx_1_3 <- a[c(1:3)]
```

```
a_idx_1_3 <- a[c(1:3)]
a_idx_1_3
```

```
## [1] 1 2 5
print(a_idx_1_3)

## [1] 1 2 5
# x <- c(1,3,4) #The "c" stands for "concatenate."
# x
# q <- c(x,x,8)
# q
```

A matrix is a two-dimensional array where each element has the same mode (numeric, character, or logical). Matrices are created with the matrix function

```
#
The option byrow indicates whether the matrix should be filled in
by row ( byrow=TRUE ) or by column ( byrow=FALSE ). The default is by column.
```

```
myymatrix <- matrix(vector, nrow=number_of_rows, ncol=number_of_columns,
byrow=logical_value, dimnames=list(
char_vector_rownames, char_vector_colnames))

matrx_y <- matrix(1:20, nrow=5, ncol=4)
matrx_y
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    6   11   16
## [2,]    2    7   12   17
## [3,]    3    8   13   18
## [4,]    4    9   14   19
## [5,]    5   10   15   20
```

## Read CSV

```
library(readr)
df_iris <- read_csv("~/temp/11_22/#Rstats/RStudio_Nov22/git_up/rstats_nov22/iris.csv")

## Rows: 150 Columns: 5
## -- Column specification -----
## Delimiter: ","
## chr (1): Species
## dbl (4): Sepal.Length, Sepal.Width, Petal.Length, Petal.Width
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
df_iris_1 <- read_csv("~/temp/11_22/#Rstats/RStudio_Nov22/git_up/rstats_nov22/iris_1.csv") ## Dummy IRI

## Rows: 150 Columns: 5
## -- Column specification -----
## Delimiter: ","
## chr (1): Species
## dbl (4): Sepal.Length, Sepal.Width, Petal.Length, Petal.Width
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
View(df_iris)
```

```
print(df_iris$Species)
```

Get DF Cols

```
## [1] "setosa" "setosa" "setosa" "setosa" "setosa"
## [6] "setosa" "setosa" "setosa" "setosa" "setosa"
## [11] "setosa" "setosa" "setosa" "setosa" "setosa"
## [16] "setosa" "setosa" "setosa" "setosa" "setosa"
## [21] "setosa" "setosa" "setosa" "setosa" "setosa"
## [26] "setosa" "setosa" "setosa" "setosa" "setosa"
## [31] "setosa" "setosa" "setosa" "setosa" "setosa"
## [36] "setosa" "setosa" "setosa" "setosa" "setosa"
## [41] "setosa" "setosa" "setosa" "setosa" "setosa"
## [46] "setosa" "setosa" "setosa" "setosa" "setosa"
## [51] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [56] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [61] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [66] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [71] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [76] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [81] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [86] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [91] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [96] "versicolor" "versicolor" "versicolor" "versicolor" "versicolor"
## [101] "virginica" "virginica" "virginica" "virginica" "virginica"
## [106] "virginica" "virginica" "virginica" "virginica" "virginica"
## [111] "virginica" "virginica" "virginica" "virginica" "virginica"
## [116] "virginica" "virginica" "virginica" "virginica" "virginica"
## [121] "virginica" "virginica" "virginica" "virginica" "virginica"
## [126] "virginica" "virginica" "virginica" "virginica" "virginica"
## [131] "virginica" "virginica" "virginica" "virginica" "virginica"
## [136] "virginica" "virginica" "virginica" "virginica" "virginica"
## [141] "virginica" "virginica" "virginica" "virginica" "virginica"
## [146] "virginica" "virginica" "virginica" "virginica" "virginica"
```

```
vector_species <- df_iris$Species
print(class(vector_species))
```

```
## [1] "character"
```

```
print(class(vector_species))
```

## Check Duplicates

```
## [1] "character"
```

```
duplicated(vector_species)
```

```
## [1] FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [13] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [25] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [37] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [49] TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [61] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [73] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [85] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [97] TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [109] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [121] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [133] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [145] TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

## Merge 2 Data Sets

```
# df_merged_iris <- merge(df_iris, df_iris_1, by="Species", all.x=TRUE, all.y=TRUE)
# #View(df_merged_iris)
# print(nrow(df_merged_iris))## nrow
# print(ncol(df_merged_iris)) ## ncol
```

```
#order_iris <- df_iris[order(df_iris$Species)]
#Error in order(df_iris$Species) :
#object of type 'closure' is not subsettable

order_iris <- df_iris[order(df_iris$Species),]
order_iris_1 <- df_iris[order(df_iris$Species , df_iris$Sepal.Length),] #Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, Species
order_iris_2 <- df_iris[order(df_iris$Species , df_iris$Sepal.Width),]
print(class(order_iris)) #[1] "spec_tbl_df" "tbl_df"      "tbl"        "data.frame"

## [1] "tbl_df"      "tbl"        "data.frame"
print(head(order_iris))
```

```
## # A tibble: 6 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##   <dbl>         <dbl>         <dbl>         <dbl> <chr>
## 1         5.1         3.5         1.4         0.2 setosa
```

```
## 2      4.9      3      1.4      0.2 setosa
## 3      4.7      3.2      1.3      0.2 setosa
## 4      4.6      3.1      1.5      0.2 setosa
## 5      5       3.6      1.4      0.2 setosa
## 6      5.4      3.9      1.7      0.4 setosa
```

```
print(tail(order_iris))
```

```
## # A tibble: 6 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##   <dbl>         <dbl>         <dbl>         <dbl> <chr>
## 1      6.7      3.3      5.7      2.5 virginica
## 2      6.7      3       5.2      2.3 virginica
## 3      6.3      2.5      5       1.9 virginica
## 4      6.5      3       5.2      2   virginica
## 5      6.2      3.4      5.4      2.3 virginica
## 6      5.9      3       5.1      1.8 virginica
```

```
#
print(head(order_iris_1))
```

```
## # A tibble: 6 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##   <dbl>         <dbl>         <dbl>         <dbl> <chr>
## 1      4.3      3       1.1      0.1 setosa
## 2      4.4      2.9      1.4      0.2 setosa
## 3      4.4      3       1.3      0.2 setosa
## 4      4.4      3.2      1.3      0.2 setosa
## 5      4.5      2.3      1.3      0.3 setosa
## 6      4.6      3.1      1.5      0.2 setosa
```

```
print(tail(order_iris_1))
```

```
## # A tibble: 6 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##   <dbl>         <dbl>         <dbl>         <dbl> <chr>
## 1      7.6      3       6.6      2.1 virginica
## 2      7.7      3.8      6.7      2.2 virginica
## 3      7.7      2.6      6.9      2.3 virginica
## 4      7.7      2.8      6.7      2   virginica
## 5      7.7      3       6.1      2.3 virginica
## 6      7.9      3.8      6.4      2   virginica
```

```
#
print(head(order_iris_2))
```

```
## # A tibble: 6 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##   <dbl>         <dbl>         <dbl>         <dbl> <chr>
## 1      4.5      2.3      1.3      0.3 setosa
## 2      4.4      2.9      1.4      0.2 setosa
## 3      4.9      3       1.4      0.2 setosa
## 4      4.8      3       1.4      0.1 setosa
## 5      4.3      3       1.1      0.1 setosa
## 6      5       3       1.6      0.2 setosa
```

```
print(tail(order_iris_2))
```

```
## # A tibble: 6 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##   <dbl>         <dbl>         <dbl>         <dbl> <chr>
## 1         6.7         3.3         5.7         2.5 virginica
## 2         6.3         3.4         5.6         2.4 virginica
## 3         6.2         3.4         5.4         2.3 virginica
## 4         7.2         3.6         6.1         2.5 virginica
## 5         7.7         3.8         6.7         2.2 virginica
## 6         7.9         3.8         6.4         2   virginica
```

```
#
# print(nrow(df_merged_iris))## nrow
# print(ncol(df_merged_iris)) ## ncol
```

## Import CSV from WWW

```
# #https://www.rdocumentation.org/packages/utils/versions/3.6.2/topics/read.table
# www <- "http://www.massey.ac.nz/~pscowper/ts/cbe.dat"
# CBE <- read.table(www, header = T)
```

```
y <- matrix(1:20, nrow=5, ncol=4)
```

```
y <- matrix(1:20, nrow=5, ncol=4)
```

```
x <- c(1,7,4) #The "c" stands for "concatenate."
x
```

```
## [1] 1 7 4
```

```
q <- c(x,x,8)
q
```

```
## [1] 1 7 4 1 7 4 8
```

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