

Introduction to R

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Topics to be Covered

- R Language Basics
- Vectors and Selections
- Matrices and Data Frames
- Writing and Reading Data
- Plotting
- Control Flows
 - for Loops
 - if Statements
- Using Packages
 - Installing
 - Loading
 - Viewing Help
- Additional Common Functions

Basics

- From: https://github.com/DataCamp/introduction_to_R/blob/master/chapter1.Rmd

Simple calculations

```
2 + 2
```

```
[1] 4
```

Commenting Code

```
# This is a comment  
2 + 2
```

```
[1] 4
```

```
# Addition  
5 + 5
```

```
[1] 10
```

```
# Subtraction  
5 - 5
```

```
[1] 0
```

```
# Multiplication  
3 * 5
```

```
[1] 15
```

```
# Division  
(5 + 5) / 2
```

```
[1] 5
```

Variable Assignments

```
my_variable <- 4  
my_variable
```

```
[1] 4
```

Basic Data Types

```
# What is the answer to the universe?  
my_numeric <- 42  
  
# The quotation marks indicate that the  
variable is of type character  
my_character <- "some text"  
  
# Change the value of my_logical  
my_logical <- TRUE
```

Help

?mean

Vectors

- From: https://github.com/Data-Camp/introduction_to_R/blob/master/chapter2.Rmd

Creating a vector

```
numeric_vector <- c(1, 2, 3)
character_vector <- c("a", "b", "c")
boolean_vector <- c(TRUE, FALSE, FALSE)
```

Selection by index

```
numeric_vector[c(1, 3)]
```

```
[1] 1 3
```

Selection by logical

```
my_variable <- 2
result <- numeric_vector[numERIC_vector > my_variable]
result
```

```
[1] 3
```

Matrices

- From: https://github.com/DataCamp/introduction_to_R/blob/master/chapter3.Rmd

Matrices from vectors

```
first_row <- c(6,8,7,9,9,10)
second_row <- c(6,8,7,5,9,6)
third_row <- c(5,4,6,6,7,8)
fourth_row <- c(4,5,3,4,6,8)

# Combine multiple vectors to form a matrix
theater <- rbind(first_row, second_row,
                  third_row, fourth_row)
row_scores <- rowSums(theater)
scores <- cbind(theater, row_scores)
```

Naming a Matrix

```
rownames(scores) <- c("row1", "row2", "row3", "row4")
colnames(scores) <- c("col1", "col2", "col3", "col4",
"col5", "col6", "total")
scores
```

	col1	col2	col3	col4	col5	col6	total
row1	6	8	7	9	9	10	49
row2	6	8	7	5	9	6	41
row3	5	4	6	6	7	8	36
row4	4	5	3	4	6	8	30

Size of Matrix

```
ncol(scores)
```

```
[1] 7
```

```
nrow(scores)
```

```
[1] 4
```

```
dim(scores)
```

```
[1] 4 7
```

Selecting Elements

Select rows and columns

```
i <- 1  
j <- 1
```

```
scores[i,]
```

col1	col2	col3	col4	col5	col6	total
6	8	7	9	9	10	49

```
scores[,j]
```

row1	row2	row3	row4
6	6	5	4

```
scores[i,j]
```

```
[1] 6
```

Data Frames

```
data(iris)
```

```
# See the first 6 rows of a data.frame  
head(iris)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Species				
1	5.1	3.5	1.4	0.2
setosa				
2	4.9	3.0	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	5.0	3.6	1.4	0.2
setosa				
6	5.4	3.9	1.7	0.4
setosa				

```
# See the last 6 rows of a data.frame  
tail(iris)
```

Rename data.frame Columns

```
numeric_vector <- c(1, 2, 3)
character_vector <- c("a", "b", "c")
boolean_vector <- c(TRUE, FALSE, FALSE)

df <- data.frame(numbers=numeric_vector,
                  characters=character_vector, boolean=boolean_vector)

df
```

	numbers	characters	boolean
1	1	a	TRUE
2	2	b	FALSE
3	3	c	FALSE

Selecting Columns by Name

```
iris[, "Sepal.Length"]
```

```
[1] 5.1 4.9 4.7 4.6 5.0 5.4 4.6 5.0 4.4 4.9 5.4 4.8 4.8 4.3 5.8 5.7 5.4  
[18] 5.1 5.7 5.1 5.4 5.1 4.6 5.1 4.8 5.0 5.0 5.2 5.2 4.7 4.8 5.4 5.2 5.5  
[35] 4.9 5.0 5.5 4.9 4.4 5.1 5.0 4.5 4.4 5.0 5.1 4.8 5.1 4.6 5.3 5.0 7.0  
[52] 6.4 6.9 5.5 6.5 5.7 6.3 4.9 6.6 5.2 5.0 5.9 6.0 6.1 5.6 6.7 5.6 5.8  
[69] 6.2 5.6 5.9 6.1 6.3 6.1 6.4 6.6 6.8 6.7 6.0 5.7 5.5 5.5 5.8 6.0 5.4  
[86] 6.0 6.7 6.3 5.6 5.5 5.5 6.1 5.8 5.0 5.6 5.7 5.7 6.2 5.1 5.7 6.3 5.8  
[103] 7.1 6.3 6.5 7.6 4.9 7.3 6.7 7.2 6.5 6.4 6.8 5.7 5.8 6.4 6.5 7.7 7.7  
[120] 6.0 6.9 5.6 7.7 6.3 6.7 7.2 6.2 6.1 6.4 7.2 7.4 7.9 6.4 6.3 6.1 7.7  
[137] 6.3 6.4 6.0 6.9 6.7 6.9 5.8 6.8 6.7 6.7 6.3 6.5 6.2 5.9
```

```
iris$Sepal.Length
```

```
[1] 5.1 4.9 4.7 4.6 5.0 5.4 4.6 5.0 4.4 4.9 5.4 4.8 4.8 4.3 5.8 5.7 5.4  
[18] 5.1 5.7 5.1 5.4 5.1 4.6 5.1 4.8 5.0 5.0 5.2 5.2 4.7 4.8 5.4 5.2 5.5  
[35] 4.9 5.0 5.5 4.9 4.4 5.1 5.0 4.5 4.4 5.0 5.1 4.8 5.1 4.6 5.3 5.0 7.0  
[52] 6.4 6.9 5.5 6.5 5.7 6.3 4.9 6.6 5.2 5.0 5.9 6.0 6.1 5.6 6.7 5.6 5.8  
[69] 6.2 5.6 5.9 6.1 6.3 6.1 6.4 6.6 6.8 6.7 6.0 5.7 5.5 5.5 5.8 6.0 5.4  
[86] 6.0 6.7 6.3 5.6 5.5 5.5 6.1 5.8 5.0 5.6 5.7 5.7 6.2 5.1 5.7 6.3 5.8  
[103] 7.1 6.3 6.5 7.6 4.9 7.3 6.7 7.2 6.5 6.4 6.8 5.7 5.8 6.4 6.5 7.7 7.7  
[120] 6.0 6.9 5.6 7.7 6.3 6.7 7.2 6.2 6.1 6.4 7.2 7.4 7.9 6.4 6.3 6.1 7.7  
[137] 6.3 6.4 6.0 6.9 6.7 6.9 5.8 6.8 6.7 6.7 6.3 6.5 6.2 5.9
```

Exporting Data

Writing files

```
write.table(iris, file="iris.txt", sep="\t",
row.names=TRUE, col.names=TRUE, quote=FALSE)
```

Reading files

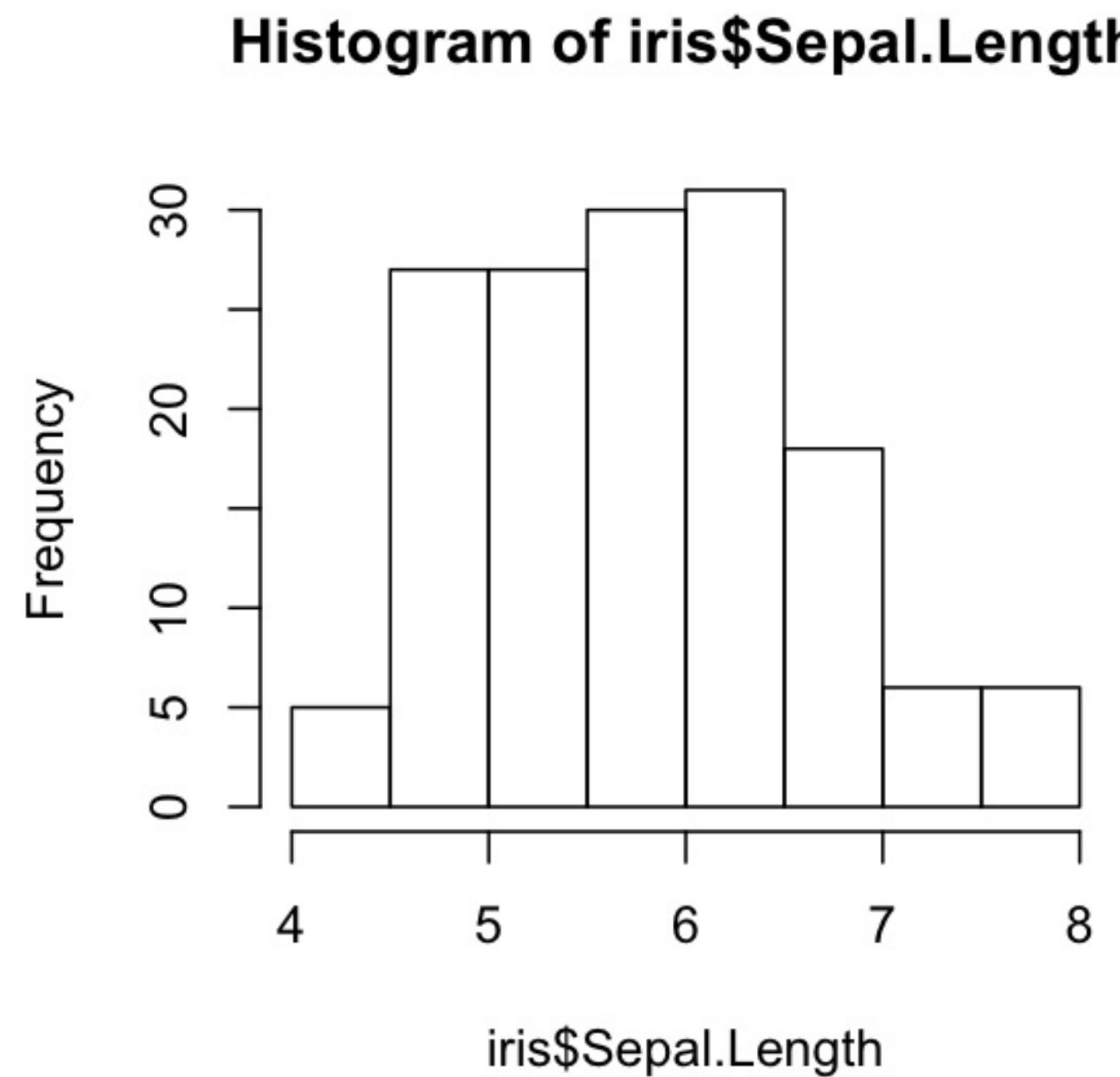
```
df <- read.table("iris.txt", sep="\t",
header=TRUE)
```

Plotting

- From: https://github.com/DataCamp/introduction_to_R/blob/master/chapter7.Rmd

Histogram

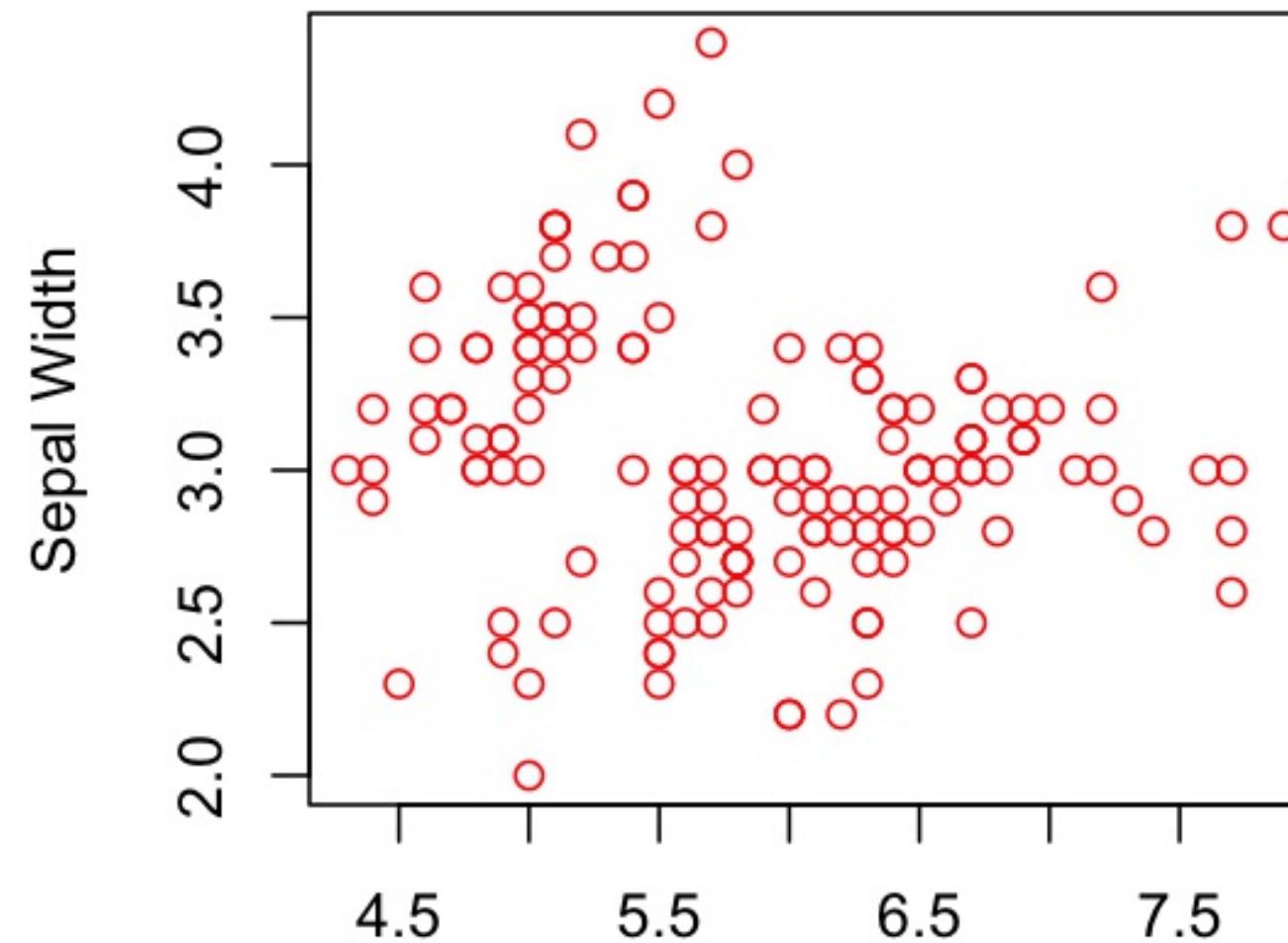
```
hist(iris$Sepal.Length)
```



Scatterplot

```
plot(x=iris$Sepal.Length,  
      y=iris$Sepal.Width,  
      main = "Sepal Length versus Sepal Width",  
      xlab = "Sepal Length",  
      ylab = "Sepal Width",  
      col = "red")
```

Sepal Length versus Sepal Width



for Loops

```
hellos <- c("Hello World!",  
          "Hola Mundo",  
          "Ola Mundo!")  
  
for(hello in hellos) {  
  cat(hello, "\n")  
}
```

```
Hello World!  
Hola Mundo  
Ola Mundo!
```

if Statements

```
a <- 5

# Greater than or equal to
if(a >= 5) {
  cat("Greater than or equal to")
} else {
  cat("Not greater than or equal to")
}
```

Greater than or equal to

```
# Equivalent
if(a == 5) {
  cat("Equal")
```

Equal

```
# Not equivalent
if(a != "Hello World!") {
  cat("Not equal")
```

Not equal

R Packages

- From:
http://www.jkarreth.net/files/RPOS517_Day1_IntroR.pdf

Install packages from repositories

- NOTE: These commands are commented out since these packages are already installed

```
# From CRAN (for general packages)
install.packages("httr")

# From Bioconductor (for biology-related
# packages)
source("https://bioconductor.org/biocLite.R")

biocLite("rcellminer")
```

Load Package

```
library(rcellminer)  
  
# Check if package was loaded  
sessionInfo()
```

Package Help

```
help(package="rcellminer")
```

length Function

```
# Find the length of a vector  
my_variable <- runif(100)  
length(my_variable)
```

```
[1] 100
```

min, max, summary Functions

```
# Find the minimum  
min(my_variable)
```

```
[1] 0.001824665
```

```
# Find the maximum  
max(my_variable)
```

```
[1] 0.9447014
```

```
# Output a summary statistics of vector  
summary(my_variable)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.001825	0.173600	0.451800	0.448800	0.692900	0.944700

cat, paste Functions

```
hello <- c("hello", "hola", "ola")
world <- c("world", "mundo")

# Make a new string from multiple variable and
# separated by "sep"
helloWorld <- paste(hello[1], world[2], sep=" ")
cat(helloWorld)
```

```
hello mundo
```

names Function

```
indices <- 1:10  
  
randNum <- runif(max(indices))  
vectorNames <- letters[indices]  
  
# Name the randNum vector according to  
vectorNames  
names(randNum) <- vectorNames
```

list Function

```
# Make a list variable; each list element has a different  
length  
my_list <- list(a=1:5, b=1:10, c=1:100)  
  
names(my_list)
```

```
[1] "a" "b" "c"
```

```
my_list$a
```

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

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

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

```
my_list[["a"]]
```

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

```
length(my_list)
```

is.na, which Function and not Operator

```
my_vector <- c(1, 2, NA, 4, 5, 6, 7, 8, NA, 10)  
  
# Is each element in my_vector an NA  
is.na(my_vector)
```

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

```
# Which indices in my_vector are NA  
which(is.na(my_vector))
```

```
[1] 3 9
```

```
# Which indices in my_vector are not NA  
which(!is.na(my_vector))
```

```
[1] 1 2 4 5 6 7 8 10
```

is.null Function

```
# NULL variables have undefined values  
my_vector <- NULL  
my_vector
```

```
NULL
```

```
is.null(my_vector)
```

```
[1] TRUE
```

```
my_vector <- c(my_vector, 5)  
my_vector <- c(my_vector, 6)  
my_vector
```

```
[1] 5 6
```

```
is.null(my_vector)
```

```
[1] FALSE
```

```
is.vector(my_vector)
```

```
[1] TRUE
```

is.nan Function

```
my_variable <- NaN  
  
is.nan(my_variable)
```

```
[1] TRUE
```

unique Function

```
my_vector <- c(1, 1, 2, 3, 3, 4, 4, 5)  
  
# Find the unique values in a vector  
unique(my_vector)
```

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

sort Function

```
my_vector <- c(1, 4, 3, 6, 7, 10, 9, 5, 2,  
8)
```

```
# Sort values in vector  
sort(my_vector)
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```

```
sort(my_vector, decreasing=TRUE)
```

```
[1] 10 9 8 7 6 5 4 3 2 1
```

%in% Function

```
restaurant_foods <- c("mango", "chicken", "pork", "chips",
                      "cookies", "cake", "muffins",
                      "cupcakes")

favorite_foods <- c("mango", "orange", "cake", "chicken")

# Does the restaurant have my favorite foods?
restaurant_foods %in% favorite_foods
```

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

```
# What are the indicies of my favorite foods
which(restaurant_foods %in% favorite_foods)
```

```
[1] 1 2 6
```

```
# Return my favorite foods
restaurant_foods[which(restaurant_foods %in% favorite_foods)]
```

```
[1] "mango"   "chicken" "cake"
```

Getting Help

- Stack Overflow
 - <http://stackoverflow.com/>
- Cross-Validated Stats Exchange
 - Part of Stack Overflow
 - <http://stats.stackexchange.com/>
- Biostars
 - <https://www.biostars.org>