

Code Library

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Notes taken from Johns Hopkins University Coursera course series Data Science Specialization.

R Data Types

- Basic object is vector of same class except list.
- Atomic classes of objects: character, numeric (real), integer, complex, logical.
- Attributes can include names, dimnames, dimensions, class, length.

Atomic Data

```
# numeric Vector
x <- 5 # numeric vector of 1 element

# integer vector
x <- 5L # integer vector of len 1

x <- Inf # special number infinity, +/-
x <- NaN # special number undefined, usually hijacks operations

# character vector
msg <- "hello" # char vector of len 1

# logical vector
tf <- TRUE # logical vector of value true
# TRUE = 1 = T, FALSE = 0 = F, num > 0 = TRUE

# complex vector
x <- 1+4i # vector of complex num of len 1
```

complex Data Types

```
# vector
vector("numeric", length = 10) # create vector of one type, args: class, length

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

```
c(1,2,3,4) # creates vector of common denominator class with given values
```

```
## [1] 1 2 3 4
```

```
1:20 # vector sequence of 20 elements 1-20
```

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

```
pi:10 # will not exceed 10, start from pi, increment by 1
```

```
## [1] 3.141593 4.141593 5.141593 6.141593 7.141593 8.141593 9.141593
```

```
15:1 # increment -1
```

```
## [1] 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
```

```
seq(1,20) # same as :
```

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

```
seq(0,10,by=0.5) # to change increment
```

```
## [1] 0.0 0.5 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0 5.5 6.0 6.5 7.0  
## [16] 7.5 8.0 8.5 9.0 9.5 10.0
```

```
seq(5,10,length=30) # to not set increment but number of numbers
```

```
## [1] 5.000000 5.172414 5.344828 5.517241 5.689655 5.862069 6.034483  
## [8] 6.206897 6.379310 6.551724 6.724138 6.896552 7.068966 7.241379  
## [15] 7.413793 7.586207 7.758621 7.931034 8.103448 8.275862 8.448276  
## [22] 8.620690 8.793103 8.965517 9.137931 9.310345 9.482759 9.655172  
## [29] 9.827586 10.000000
```

```
seq_along(x) # vector of same length 1:length(x)
```

```
## [1] 1
```

```
rep(10, times = 4) # repeats 10 4 times in vector
```

```
## [1] 10 10 10 10
```

```
rep(c(0, 1, 2), times = 10) # repeats sequence of vector 10 times. Arg each can be used to repeat first
```

```
## [1] 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2 0 1 2
```

```

# lists
# vector capable of carrying different classes
x <- list(1, "a", TRUE, 1+4i) # vector of vectors

# Matrix
# vector of single class with rectangular dimensions (attribute of integer vector len 2)
x <- matrix(nrow=2,ncol=3) # empty matrix of given dimensions
x <- matrix(1:8, nrow = 4, ncol = 2) # creates matrix of given dimensions with values assigned, created
y <- matrix(rep(10,4),2,2) # creates matrix of 4 10s

x <- 1:10
dim(x) <- c(2,5) # creates matrix out of vector with dimension 2 rows x 5 columns

cbind(1:3,10:12) # creates matrix out of values in vector args, adding by column (1st arg = 1st col)

```

```

##      [,1] [,2]
## [1,]    1   10
## [2,]    2   11
## [3,]    3   12

```

```

rbind(1:3,10:12) # same but using rows

```

```

##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]   10   11   12

```

```

# factors
# self-describing type of vector representing categorical data, ordered or unordered (labels)
x <- factor(c("male","female","female","female","male")) # character vector with specific linear model
f <- gl(3,10) # factor 3 levels, 10 times each
table(x) # prints counts of each factor

```

```

## x
## female    male
##      3      2

```

Data Frames

```

# stores tabular/rectangular data, stored as lists of same length where each element is a column, length
x <- data.frame(foo=1:4, bar=c(T,T,F,F)) # creates data frame 2 columns foo and bar, 4 rows unnamed. Ca
x <- read.table(file = "hw1_data.csv", header = TRUE, sep = ",") # read in data from file
x <- read.csv("hw1_data.csv") # same

```

Date and Time Data Types

```

# useful for time-series data (temporal changes) or other temporal info
# lubridate package by Hadley Wickham

```

```
# Dates and Times
birthday <- as.Date("1970-01-01") # dates are date class defined by converting character string, year-m
today <- Sys.Date()

currentTime <- Sys.time() # time by POSIXct (large integer vector, useful in dataframe) or POSIXlt (list,
timedefined <- as.POSIXct("2012-10-25 06:00:00") # convert char vector, can define timezone
cTConvert <- as.POSIXlt(currentTime) # reclass, works other way
cTConvert$min # to subset list
```

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

```
datestring <- c("January 10, 2012 10:40", "December 9, 2011 9:10")
x <- strptime(datestring, "%B %d, %Y %H:%M") # Convert character vector to POSIXlt by defining format (
x
```

```
## [1] "2012-01-10 10:40:00 EST" "2011-12-09 09:10:00 EST"
```

```
weekdays(birthday) # return day of week, date or time classes
```

```
## [1] "Thursday"
```

```
months(birthday) # return month on date or time
```

```
## [1] "January"
```

```
quarters(birthday) # return quarter of date or time
```

```
## [1] "Q1"
```

```
# Operations
# CANNOT MIX CLASSES - convert
# add and subtract dates, compare dates
currentTime - timedefined # time difference, track of discrepancies (i.e. daylight savings, timezones, l
```

```
## Time difference of 4468.5 days
```

```
difftime(currentTime, timedefined, units = "days") # to specify unit
```

```
## Time difference of 4468.5 days
```

Basic R Functions

Functions and Operations

```
# Input and Evaluation  
x <- 1 # assignment operator, evaluates and returns  
print(x) # print value as vector
```

```
## [1] 1
```

```
x # auto-prints
```

```
## [1] 1
```

```
# in console, press Tab for auto-completion  
LETTERS # predefined character vector of capital letters
```

```
## [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J" "K" "L" "M" "N" "O" "P" "Q" "R" "S"  
## [20] "T" "U" "V" "W" "X" "Y" "Z"
```

```
# <- operator can be used to assign a value to an object in an environment that is different from the
```

```
# Mathematical and Statistical Functions
```

```
5 + 7 # basic arithmetic operations all work +, -, *, /, ^, %% (modulus). NA affects operation.
```

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

```
sqrt(4) # square root
```

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

```
abs(-1:2) # absolute value
```

```
## [1] 1 0 1 2
```

```
mean(c(3,4,5,6,7)) # return mean of numeric vector
```

```
## [1] 5
```

```
sd(c(3,4,5,6,7)) # returns standard deviation of numeric vector
```

```
## [1] 1.581139
```

```
cor(c(3,4,5,6,7), c(61,47,18,18,5)) # correlation of x and y vectors make sure to set arg use for NAs
```

```
## [1] -0.9587623
```

```
range(c(3,4,5,6,7)) # returns min and max as numeric vector of 2
```

```
## [1] 3 7
```

```
quantile(c(3,4,5,6,7), probs = 0.25) # returns 25th percentile
```

```
## 25%  
## 4
```

```
-c(0.5,0.8,10) # distributes the negative to all elements of vector
```

```
## [1] -0.5 -0.8 -10.0
```

```
# vectorized operations
```

```
x <- 1:4; y <- 6:9 # different length vectors
```

```
x + y # add the elements of the vectors, all operators work
```

```
## [1] 7 9 11 13
```

```
x > 2 # returns logical vector, >= or == or any of the logical expressions work
```

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

```
# Matrix Operations
```

```
x <- matrix(1:4,2,2); y <- matrix(rep(10,4),2,2)
```

```
x * y # element wise multiplication, for all operators
```

```
##      [,1] [,2]  
## [1,] 10 30  
## [2,] 20 40
```

```
x %*% y # matrix multiplication
```

```
##      [,1] [,2]  
## [1,] 40 40  
## [2,] 60 60
```

```
x <- matrix(rnorm(200), 20, 10)
```

```
rowSums(x) # vector of sum of rows
```

```
## [1] -6.3316009 -6.6495434 -1.2813142 -0.2217270 -3.6640599 -1.0261292  
## [7] 0.3375764 3.7790590 1.8566828 0.6749861 0.8494894 1.8734949  
## [13] 1.3157204 3.5022710 -2.2227177 -0.4010233 -3.7152519 -3.5178804  
## [19] -2.0278859 0.3957245
```

```
rowMeans(x) # vector of mean of rows
```

```
## [1] -0.63316009 -0.66495434 -0.12813142 -0.02217270 -0.36640599 -0.10261292  
## [7] 0.03375764 0.37790590 0.18566828 0.06749861 0.08494894 0.18734949  
## [13] 0.13157204 0.35022710 -0.22227177 -0.04010233 -0.37152519 -0.35178804  
## [19] -0.20278859 0.03957245
```

```
colSums(x) # vector of sum of cols
```

```
## [1] -5.2263256 -2.3423348 -0.8762161 2.4044422 0.7734381 3.0442012
## [7] -2.2558674 -1.1484339 -3.9528874 -6.8941457
```

```
colMeans(x) # vector of mean of cols
```

```
## [1] -0.26131628 -0.11711674 -0.04381080 0.12022211 0.03867190 0.15221006
## [7] -0.11279337 -0.05742169 -0.19764437 -0.34470729
```

```
x <- matrix(rnorm(100), 10, 10)
```

```
solve(x) # returns inverse of matrix if invertible
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.05350867 -0.001741815 -0.188655957 0.18574772 -0.60861903 -0.25720053
## [2,] 0.07919372 -0.047465321 0.069178122 -0.27971353 0.24965145 -0.40624997
## [3,] -0.30273861 0.167973244 -0.612458457 0.05176097 0.08376747 -0.32301449
## [4,] -0.03517739 0.338326998 -0.074427989 0.19128278 0.15108549 0.12319132
## [5,] -0.04545426 -0.100915811 -0.097779730 0.15294882 -0.01930548 -0.42432307
## [6,] -0.42783645 -0.182337425 -0.668522464 0.47335878 -1.13940117 -1.21363279
## [7,] -0.23582533 0.556391102 -0.239103842 -0.13509752 -0.20734603 0.12691557
## [8,] 0.19098635 0.366889679 0.006303534 -0.15938399 0.53425667 0.07329431
## [9,] -0.24686676 -0.237472002 -0.079471728 0.06711153 -0.81176856 -0.95141210
## [10,] -0.09121557 -0.194091932 -0.522422778 0.52638805 -0.70031253 -0.69411914
##           [,7]      [,8]      [,9]      [,10]
## [1,] 0.07189596 0.03314431 -0.05571443 -0.08698749
## [2,] -0.47373829 -0.09057521 -0.19083815 0.12121518
## [3,] 0.15521025 -0.12218794 -0.22173631 0.43545304
## [4,] 0.01869120 0.04659789 -0.08832634 -0.24440017
## [5,] 0.04883267 -0.01036752 -0.22085702 0.20490199
## [6,] 0.37347386 -0.31498091 0.03161104 0.68501206
## [7,] 0.04481330 0.16288178 0.23608576 0.34977611
## [8,] 0.01109651 0.13984494 0.34846857 -0.23352451
## [9,] 0.01150042 -0.28887809 -0.32292093 0.19714605
## [10,] 0.41640741 -0.45723714 -0.39972846 0.23862659
```

```
# Logical operators
```

```
5 >= 2 # returns logical. <, >, <=, >=, ==, !=. NA in expression returns NA. Can also use to compare lo
```

```
## [1] TRUE
```

```
TRUE | FALSE # OR A/B union, AND A&B intersection, NOT !A negation. & operates across vector, && evalua
```

```
## [1] TRUE
```

```
isTRUE(6 > 4) # also evaluates logical expression
```

```
## [1] TRUE
```

```
xor(5 == 6, !FALSE) # only returns TRUE if one is TRUE, one is FALSE
```

```
## [1] TRUE
```

```
which(c(1,2,3,4,5,6) < 2) # returns indices of logical vector where element is TRUE
```

```
## [1] 1
```

```
any(c(1,2,3,4,5,6) < 2) # returns TRUE if any of the logical index values are TRUE
```

```
## [1] TRUE
```

```
all(c(1,2,3,4,5,6) < 2) # returns TRUE only if all the elements of vector are TRUE
```

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

```
# Character functions
```

```
paste(c("My","name","is"),collapse = " ") # join elements into one element, can join multiple vectors w
```

```
## [1] "My name is"
```

```
c (c("My","name","is"), "Bob") # add to the vector
```

```
## [1] "My" "name" "is" "Bob"
```

```
# Factors functions
```

```
x <- factor(c("male","female","female","female","male")) # can include levels argument to set order (ba
```

```
x # prints values in vector and levels
```

```
## [1] male female female female male
```

```
## Levels: female male
```

```
table(x) # prints labels and counts present
```

```
## x
```

```
## female male
```

```
## 3 2
```

```
unclass(x) # strips class to integer with levels of labels
```

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

```
## attr("levels")
```

```
## [1] "female" "male"
```



```
# Display Data Functions
```

```
print(data.frame(foo = 1:20, rar = 301:320)) # print whole object
```

```
##      foo rar
## 1      1 301
## 2      2 302
## 3      3 303
## 4      4 304
## 5      5 305
## 6      6 306
## 7      7 307
## 8      8 308
## 9      9 309
## 10     10 310
## 11     11 311
## 12     12 312
## 13     13 313
## 14     14 314
## 15     15 315
## 16     16 316
## 17     17 317
## 18     18 318
## 19     19 319
## 20     20 320
```

```
head(data.frame(foo = 1:20, rar = 301:320)) # prints preview of first 6 lines
```

```
##      foo rar
## 1      1 301
## 2      2 302
## 3      3 303
## 4      4 304
## 5      5 305
## 6      6 306
```

```
tail(data.frame(foo = 1:20, rar = 301:320)) # prints preview of last 6 lines
```

```
##      foo rar
## 15     15 315
## 16     16 316
## 17     17 317
## 18     18 318
## 19     19 319
## 20     20 320
```

```
table(c(1,1,1,2,2,2,2,2,2,2,2,2,3,3,3,3,4,4,5)) # returns table of counts
```

```
##
## 1 2 3 4 5
## 3 9 4 2 1
```

```
summary(c(3,4,5,6,7)) # result summaries of the results of various model fitting functions based on cla
```

```
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##         3         4         5         5         6         7
```

```
unique(c(3,4,5,6,7,3,3,5,7,2,8,3,5,6)) # returns only unique elements, duplicates removed
```

```
## [1] 3 4 5 6 7 2 8
```

```
# str function - compactly display internal structure of R object (esp large lists). Diagnostic, altern
str(unclass(as.POSIXlt(Sys.time()))) # prints list clearly
```

```
## List of 11
##  $ sec   : num 32
##  $ min   : int 0
##  $ hour  : int 17
##  $ mday  : int 18
##  $ mon   : int 0
##  $ year  : int 125
##  $ wday  : int 6
##  $ yday  : int 17
##  $ isdst : int 0
##  $ zone  : chr "EST"
##  $ gmtoff: int -18000
##  - attr(*, "tzname")= chr [1:3] "" "EST" "EDT"
##  - attr(*, "balanced")= logi TRUE
```

```
str(lm) # list of function arguments
```

```
## function (formula, data, subset, weights, na.action, method = "qr", model = TRUE,
##      x = FALSE, y = FALSE, qr = TRUE, singular.ok = TRUE, contrasts = NULL,
##      offset, ...)
```

```
str(rnorm(100,2,4)) # type of vector, length, first 5 elements
```

```
## num [1:100] -3.067 0.736 9.068 8.216 2.228 ...
```

```
str(gl(40,10)) # for factors
```

```
## Factor w/ 40 levels "1","2","3","4",...: 1 1 1 1 1 1 1 1 1 1 ...
```

```
# Missing Values
# represented as NA (missing, with specified class) or NaN (missing or undefined)
# NaN is NA but NA not always NaN
is.na(c(1,2,NA,5,6,NA, NA,3, NaN)) # output logical vector of length of input
```

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

```
is.nan(c(1,2,NaN,5,6,NA, NaN,3)) # output logical vector of length of input
```

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

Attributes of objects

```
x <- c(0.5,105,10,0.1,2)
class(x) # determine class of object
```

```
## [1] "numeric"
```

```
attributes(x) # function to return or modify attributes of object
```

```
## NULL
```

```
identical(x,x) # returns logical for if two objects are identical
```

```
## [1] TRUE
```

```
length(x) # to specifically get the length of vector
```

```
## [1] 5
```

```
dim(x) # to get dimensions of matrix, data frame (row, column)
```

```
## NULL
```

```
object.size(x) # return memory occupied in bytes
```

```
## 96 bytes
```

```
as.numeric(0:6) # explicit coercion, works on all atomic classes, if not possible converts to NA and wa
```

```
## [1] 0 1 2 3 4 5 6
```

```
# data frames
```

```
row.names(x) # get and set row names (attributes). Can also use rownames(x)
```

```
colnames(x) # get and set row names
```

```
## NULL
```

```
nrow(x) # number of rows
```

```
## NULL
```

```
ncol(x) # number of columns
```

```
## NULL
```

```
data.matrix(x) # converts data frame to matrix, coercion
```

```
##      [,1]  
## [1,]  0.5  
## [2,] 105.0  
## [3,]  10.0  
## [4,]   0.1  
## [5,]   2.0
```

```
dim(x) # (row, column) dimensions of data frame
```

```
## NULL
```

```
# names attribute  
x <- 1:3  
names(x) # is null
```

```
## NULL
```

```
names(x) <- c("foo","bar","norf") #now not numbered vector but named, print x and names(x) with names  
vect <- c(foo = 11, bar = 2, norf = NA) # adds elements with names to vector directly  
# also for lists, names vectors not items  
m <- matrix(1:4,nrow = 2, ncol = 2)  
dimnames(m) <- list(c("a","b"),c("c","d")) # each dimension has a name for matrices, rows names then co
```

Indexing, Subsetting, and Dealing with NAs

```
# Subsetting R Objects  
x <- c("a","b","c","c","d","a")  
x[1] # more than one element extracted, returns same class as the original, numeric/logical index
```

```
## [1] "a"
```

```
x[1:4] # sequence of num index
```

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

```
x[x>"a"] # logical indexing, returns vector where logical is true
```

```
## [1] "b" "c" "c" "d"
```

```
u <- x > "a" # create logical vector
x[u] # same as x[x>"a"]
```

```
## [1] "b" "c" "c" "d"
```

```
x[!is.na(x) & x > 0] # returns only positive, non NA values
```

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

```
x[c(-2, -10)] # returns vector with 2nd and 10th elements removed
```

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

```
x <- data.frame(foo = 1:6, bar = c("g","h","i","j","k","l"))
x[which(x$bar == "h"), "foo"] # get or set foo in the same row as bar of "h"
```

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

```
x <- list(foo = 1:4, bar = 0.6, baz = "hello")
x[1] # list containing first element
```

```
## $foo
## [1] 1 2 3 4
```

```
x[[1]] # extract from list/data frame, single element, class can change. Ex, numerical vector returned
```

```
## [1] 1 2 3 4
```

```
x$bar # like [[]] but by name. Ex, return num vector 0.6. Equivalent to x[["bar"]]. Expression x["bar"]
```

```
## [1] 0.6
```

```
x[c(1,3)] # multiple object extraction from list, returns list
```

```
## $foo
## [1] 1 2 3 4
##
## $baz
## [1] "hello"
```

```
name = "foo"
x[[name]] # must be used if using computed index
```

```
## [1] 1 2 3 4
```

```
x[1][3] # return element in element in object
```

```
## $<NA>  
## NULL
```

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

```
## [1] 3
```

```
# Subsetting Matrix  
x <- matrix(1:6, 2, 3)  
x[1,2] # returns vector len 1, different that x[2,1]. Get matrix using arg drop = FALSE.
```

```
## [1] 3
```

```
x[1,] # get num vector of first row, can also get col x[,2]. drop = FALSE also works
```

```
## [1] 1 3 5
```

```
# Removing NA values  
x <- c(1,2,NA,4,NA,5)  
bad <- is.na(x) # logical vector indicating presence of NA  
x[!bad] # removes NA values
```

```
## [1] 1 2 4 5
```

```
x[!is.na(x)] # simplified returns vector removing NA values
```

```
## [1] 1 2 4 5
```

```
x <- c(1,2,NA,4,NA,5) # for two vectors  
y <- c("a","b",NA,"d",NA,"f")  
good <- complete.cases(x,y) # logical vectors where there is no NA in either list  
x[good]
```

```
## [1] 1 2 4 5
```

```
y[good]
```

```
## [1] "a" "b" "d" "f"
```

```
# Sum of NA values  
my_na <- is.na(x)  
sum(my_na)
```

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

```
x <- read.csv("hw1_data.csv") # for data frames
goodVals <- complete.cases(x) # complete rows in the data frame
x[goodVals,]
```

##	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
## 7	23	299	8.6	65	5	7
## 8	19	99	13.8	59	5	8
## 9	8	19	20.1	61	5	9
## 12	16	256	9.7	69	5	12
## 13	11	290	9.2	66	5	13
## 14	14	274	10.9	68	5	14
## 15	18	65	13.2	58	5	15
## 16	14	334	11.5	64	5	16
## 17	34	307	12.0	66	5	17
## 18	6	78	18.4	57	5	18
## 19	30	322	11.5	68	5	19
## 20	11	44	9.7	62	5	20
## 21	1	8	9.7	59	5	21
## 22	11	320	16.6	73	5	22
## 23	4	25	9.7	61	5	23
## 24	32	92	12.0	61	5	24
## 28	23	13	12.0	67	5	28
## 29	45	252	14.9	81	5	29
## 30	115	223	5.7	79	5	30
## 31	37	279	7.4	76	5	31
## 38	29	127	9.7	82	6	7
## 40	71	291	13.8	90	6	9
## 41	39	323	11.5	87	6	10
## 44	23	148	8.0	82	6	13
## 47	21	191	14.9	77	6	16
## 48	37	284	20.7	72	6	17
## 49	20	37	9.2	65	6	18
## 50	12	120	11.5	73	6	19
## 51	13	137	10.3	76	6	20
## 62	135	269	4.1	84	7	1
## 63	49	248	9.2	85	7	2
## 64	32	236	9.2	81	7	3
## 66	64	175	4.6	83	7	5
## 67	40	314	10.9	83	7	6
## 68	77	276	5.1	88	7	7
## 69	97	267	6.3	92	7	8
## 70	97	272	5.7	92	7	9
## 71	85	175	7.4	89	7	10
## 73	10	264	14.3	73	7	12
## 74	27	175	14.9	81	7	13
## 76	7	48	14.3	80	7	15
## 77	48	260	6.9	81	7	16
## 78	35	274	10.3	82	7	17
## 79	61	285	6.3	84	7	18

## 80	79	187	5.1	87	7	19
## 81	63	220	11.5	85	7	20
## 82	16	7	6.9	74	7	21
## 85	80	294	8.6	86	7	24
## 86	108	223	8.0	85	7	25
## 87	20	81	8.6	82	7	26
## 88	52	82	12.0	86	7	27
## 89	82	213	7.4	88	7	28
## 90	50	275	7.4	86	7	29
## 91	64	253	7.4	83	7	30
## 92	59	254	9.2	81	7	31
## 93	39	83	6.9	81	8	1
## 94	9	24	13.8	81	8	2
## 95	16	77	7.4	82	8	3
## 99	122	255	4.0	89	8	7
## 100	89	229	10.3	90	8	8
## 101	110	207	8.0	90	8	9
## 104	44	192	11.5	86	8	12
## 105	28	273	11.5	82	8	13
## 106	65	157	9.7	80	8	14
## 108	22	71	10.3	77	8	16
## 109	59	51	6.3	79	8	17
## 110	23	115	7.4	76	8	18
## 111	31	244	10.9	78	8	19
## 112	44	190	10.3	78	8	20
## 113	21	259	15.5	77	8	21
## 114	9	36	14.3	72	8	22
## 116	45	212	9.7	79	8	24
## 117	168	238	3.4	81	8	25
## 118	73	215	8.0	86	8	26
## 120	76	203	9.7	97	8	28
## 121	118	225	2.3	94	8	29
## 122	84	237	6.3	96	8	30
## 123	85	188	6.3	94	8	31
## 124	96	167	6.9	91	9	1
## 125	78	197	5.1	92	9	2
## 126	73	183	2.8	93	9	3
## 127	91	189	4.6	93	9	4
## 128	47	95	7.4	87	9	5
## 129	32	92	15.5	84	9	6
## 130	20	252	10.9	80	9	7
## 131	23	220	10.3	78	9	8
## 132	21	230	10.9	75	9	9
## 133	24	259	9.7	73	9	10
## 134	44	236	14.9	81	9	11
## 135	21	259	15.5	76	9	12
## 136	28	238	6.3	77	9	13
## 137	9	24	10.9	71	9	14
## 138	13	112	11.5	71	9	15
## 139	46	237	6.9	78	9	16
## 140	18	224	13.8	67	9	17
## 141	13	27	10.3	76	9	18
## 142	24	238	10.3	68	9	19
## 143	16	201	8.0	82	9	20


```
## 144    13    238 12.6   64     9  21
## 145    23     14  9.2   71     9  22
## 146    36    139 10.3   81     9  23
## 147     7     49 10.3   69     9  24
## 148    14     20 16.6   63     9  25
## 149    30    193  6.9   70     9  26
## 151    14    191 14.3   75     9  28
## 152    18    131  8.0   76     9  29
## 153    20    223 11.5   68     9  30
```

Random Numbers

```
# Random number generation
# Probability distribution functions have 4 functions associated: d- density, r- random number generation, p- probability, q- quantile
set.seed(1) # set sequence of random number generation. set.seed(1); rnorm(5) always results in the same sequence
y <- rnorm(1000) # generate vector of 1000 numbers that are standard normal distribution. Args: n, mean, sd
y <- dnorm(c(0.25,0.5,0.75)) # evaluate Normal probability density, (given mean,sd) at point or vector
y <- pnorm(0.5) # evaluate cumulative distribution function for normal distribution. Args: q, mean=0, sd=1, lower.tail=TRUE, log.p=FALSE
y <- qnorm(0.5) # evaluates quantiles for normal distribution. Args: p, mean=0, sd=1, lower.tail=TRUE, log.p=FALSE
y <- sample(1:6,3) # random selection of 3 elements from array
ints <- sample(10) # random sample all integers from 1 to 10 without replacement. Permutation
nums <- sample(1:10, replace = TRUE) # with replacement
let <- sample(LETTERS) # sample all letters without replacement
flips <- sample(c(0,1), 100, replace = TRUE, prob = c(0.3,0.7)) # unfair coin
coin <- rbinom(1,1,0.5) # simulating coin flip
unfairflip <- rbinom(1, size = 100, prob = 0.7) # sum of flips above
flips2 <- rbinom(100,1,0.7) # flips above
y <- rpois(10, 1) # generate random poisson variates with given rate. Args: n (count), rate (mean)
pois_mat <- replicate(100, rpois(5, 10))

# Simulate Linear Model Ex
# y = B(0) + B(1) * x + e
# e ~ N(0,2^2) assume x ~ N(0,1^2), B(0) = 0.5, B(1) = 2.
set.seed(20)
x <- rnorm(100)
e <- rnorm(100,0,2)
y <- 0.5 + 2 * x + e
# can combine different distributions
# Poisson: Y ~ Poisson(mu)
# log(mu) = B(0) + B(1)x
# B(0) = 0.5 and B(1) = 0.3
set.seed(1)
x <- rnorm(100)
log.mu <- 0.5 + 0.3 * x
y <- rpois(100, exp(log.mu))
```

Control Functions and Loop Functions

Control Functions

```
# control execution of program
```

```
x = 2
# if,else loops
y <- if(x > 3){ # testing condition
  10
} else if(x > 0 & x <= 3) { # can not have or multiple
  5
} else{ # can not have, at end
  0
}
```

```
if(x-5 == 0){
  y <- 0
} else{
  y <- 2
}
```

```
# for loops
```

```
for(i in 1:10) {# execute loop fixed number of times. Args iterator variable and vector(inc seq) or lis
  print(i)
}
```

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

```
x <- c("a","b","c","d")
for(i in 1:4){
  print(x[i])
}
```

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

```
for(i in seq_along(x)){
  print(x[i])
}
```

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

```
for(letter in x){
  print(letter)
}
```

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

```
for(i in 1:4) print(x[i])
```

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

```
x <- matrix(1:6,2,3)
for(i in seq_len(nrow(x))) { # nested, don't use more than 2-3 for readability
  for(j in seq_len(ncol(x))) {
    print(x[i,j])
  }
}
```

```
## [1] 1
## [1] 3
## [1] 5
## [1] 2
## [1] 4
## [1] 6
```

```
# while loops
count <- 0
while(count < 10){ # loop while condition is true
  print(count)
  count <- count + 1
} # be wary of infinite loops!! when condition cannot be true
```

```
## [1] 0
## [1] 1
## [1] 2
## [1] 3
## [1] 4
## [1] 5
## [1] 6
## [1] 7
## [1] 8
## [1] 9
```

```

z <- 5
while(z >= 3 & z <= 10){
  print(z)
  coin <- rbinom(1,1,0.5)

  if (coin == 1) z <- z+1
  else z <- z-1
}

```

```

## [1] 5
## [1] 6
## [1] 5
## [1] 4
## [1] 3

```

```

# Repeat loop
x0 <- 0.01; tol <- 1e-3
repeat { # infinite loop
  x1 <- rnorm(1)
  if(abs(x1 - x0) < tol) {
    break # break execution of any loop
  }
  else x0 <- x1
}

# control a loop
for(i in 1:100) {
  if(i <= 20) next # skip next iteration of loop
  else {
    if (i > 50) break # exit for loop
  }
}

# return to exit a function, will end control structure inside function

```

Loop Functions

```

# Loop functions - useful for looping in the command line
# Hadley Wickham's Journal of Statistical Software paper titled 'The Split-Apply-Combine Strategy for D

# lapply - loop over a list and evaluate on each element. args: X (list or coercion), FUN (function or .
x <- list(a = 1:5, b = rnorm(10))
lapply(x, mean) # returns list of 2 numerics

```

```

## $a
## [1] 3
##
## $b
## [1] 0.3985388

```

```
x <- 1:4
lapply(x, runif, min = 0, max = 10) # passes subsequent args to function
```

```
## [[1]]
## [1] 4.180447
##
## [[2]]
## [1] 5.3804163 0.7510495
##
## [[3]]
## [1] 3.049216 2.719333 8.182229
##
## [[4]]
## [1] 0.8832537 3.4918707 8.5187127 9.8035107
```

```
x <- list(a = matrix(1:4, 2, 2), b = matrix(1:6, 3, 2))
lapply(x, function(elt) elt[,1]) # define an anonymous function inside lapply
```

```
## $a
## [1] 1 2
##
## $b
## [1] 1 2 3
```

```
# sapply - same as lapply but simplify, i.e. will make list of 1 element vectors a vector, multiple ele
x <- list(a = 1:5, b = rnorm(10))
lapply(x, mean) # now returns vector length 2
```

```
## $a
## [1] 3
##
## $b
## [1] 0.3902621
```

```
# mean only operates on single element numeric/logical, so need to use loop
```

```
# vapply - pre-specify type of return value, safer and faster. Args: X, FUN, FUN.VALUE (generalized vec
vapply(x, mean, numeric(1)) # same as sapply(x, mean)
```

```
##           a           b
## 3.0000000 0.3902621
```

```
# apply - apply function over margins of array (good for summary of matrices or higher level array). No
x <- matrix(rnorm(200), 20, 10)
apply(x, 2, mean) # mean of each column by collapsing 1st dimension, returns num vector length of ncol.
```

```
## [1] 0.39576926 0.39693829 -0.29548099 -0.30587580 0.31690617 -0.24744022
## [7] 0.26027330 0.07700510 -0.04652335 -0.23800285
```

```
rowSums(x) # equivalent to apply(x, 1, sum)
```

```
## [1] 0.7609383 -4.1967248 5.0584592 0.5808195 -3.3859346 8.2206313
## [7] 1.3595547 -0.1567391 2.1183256 2.2432819 3.0644650 1.3968116
## [13] 5.4715183 -2.0890661 -0.7462932 0.6588537 -2.3037316 -3.9577417
## [19] -4.5847842 -3.2412655
```

```
rowMeans(x) # equivalent to apply(x, 1, mean)
```

```
## [1] 0.07609383 -0.41967248 0.50584592 0.05808195 -0.33859346 0.82206313
## [7] 0.13595547 -0.01567391 0.21183256 0.22432819 0.30644650 0.13968116
## [13] 0.54715183 -0.20890661 -0.07462932 0.06588537 -0.23037316 -0.39577417
## [19] -0.45847842 -0.32412655
```

```
colSums(x) # apply(x, 2, sum)
```

```
## [1] 7.9153853 7.9387658 -5.9096198 -6.1175160 6.3381234 -4.9488043
## [7] 5.2054659 1.5401019 -0.9304669 -4.7600570
```

```
colMeans(x) # apply(x, 2, mean)
```

```
## [1] 0.39576926 0.39693829 -0.29548099 -0.30587580 0.31690617 -0.24744022
## [7] 0.26027330 0.07700510 -0.04652335 -0.23800285
```

```
apply(x, 1, quantile, probs = c(0.25, 0.75)) # runs quantile with 2 args for every element in list, returns list
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## 25% -0.7571352 -0.7008243 -0.2473744 -0.6418233 -0.5553241 0.4407991 0.1330451
## 75% 1.0018439 -0.1354330 1.4629405 0.7853807 0.1146551 1.2413891 1.0496289
##           [,8]      [,9]     [,10]     [,11]     [,12]     [,13]
## 25% -0.7121101 -0.2189623 -0.1192721 -0.1532343 -0.1754369 -0.2377421
## 75% 0.2584542 0.7632128 1.0476237 0.7373560 0.4873948 1.1822437
##           [,14]     [,15]     [,16]     [,17]     [,18]     [,19]     [,20]
## 25% -0.7463529 -0.3586825 -0.7882050 -0.7254670 -0.8275423 -0.799203 -0.8441518
## 75% 0.2985215 0.1503075 0.7323559 0.3109353 0.7182965 0.290152 -0.3795045
```

```
a <- array(rnorm(2 * 2 * 10), c(2, 2, 10)) # array in 3D
```

```
apply(a, c(1,2), mean) # collapses only 3rd dimension, returns 2x2 matrix. Equivalent rowMeans(a, dims = 3)
```

```
##           [,1]      [,2]
## [1,] -0.3294688 0.1786066
## [2,] -0.1456898 -0.2877835
```

```
# tapply - apply function over subset of a vector. args: X is vector, INDEX is factor/list factors vector
```

```
x <- c(rnorm(10), runif(10), rnorm(10,1))
f <- gl(3,10) # factor 3 levels, 10 times each
tapply(x,f,mean)
```

```
##           1           2           3
## 0.2233750 0.3445618 0.4956007
```

```
# mapply - multivariate version of lapply. args: FUN as above, ... (arguments to apply over), MoreArgs
list(rep(1,4), rep(2,3), rep(3,2), rep(4,1))
```

```
## [[1]]
## [1] 1 1 1 1
##
## [[2]]
## [1] 2 2 2
##
## [[3]]
## [1] 3 3
##
## [[4]]
## [1] 4
```

```
mapply(rep, 1:4, 4:1) # equivalent
```

```
## [[1]]
## [1] 1 1 1 1
##
## [[2]]
## [1] 2 2 2
##
## [[3]]
## [1] 3 3
##
## [[4]]
## [1] 4
```

```
noise <- function(n,mean,sd){rnorm(n,mean,sd)}
noise(1:5,1:5,2) # gives vector of 5, same as single num args
```

```
## [1] 0.5569244 1.6755360 3.6736906 6.1633545 7.0603864
```

```
mapply(noise,1:5,1:5,2) # applies function for each pair, list of 5 of length i
```

```
## [[1]]
## [1] 0.2931417
##
## [[2]]
## [1] 4.150763 1.569355
##
## [[3]]
## [1] 3.367118 4.901136 5.167102
##
## [[4]]
## [1] 1.010141 2.712134 6.857595 3.225181
##
## [[5]]
## [1] 4.858346 4.861672 4.799808 5.668715 2.350646
```

```
# split - in conjunction with lapply to split objects into subpieces. Args: x (any object), f (factor),
x <- c(rnorm(10), runif(10), rnorm(10,1))
f <- gl(3,10) # factor 3 levels, 10 times each
split(x,f) # tapply without function, sorts into list based on levels, can then use lapply or sapply.
```

```
## $'1'
## [1] 0.78002347 -0.78709697 -0.58691682 -0.54546587 0.76247880 0.06403316
## [7] 0.12819144 0.60560030 0.39492984 -0.53621606
##
## $'2'
## [1] 0.61128364 0.50431157 0.49886556 0.15303652 0.58167801 0.05305581
## [7] 0.08354486 0.19449867 0.50655472 0.80669924
##
## $'3'
## [1] 1.1065169 1.2236401 0.7009779 1.8481351 2.4935228 0.3468278
## [7] -0.3368842 1.8210809 0.5114539 1.2572268
```

```
lapply(split(x,f), mean) # in this case can use tapply
```

```
## $'1'
## [1] 0.02795613
##
## $'2'
## [1] 0.3993529
##
## $'3'
## [1] 1.09725
```

```
# can do data frames
data <- read.csv("hw1_data.csv")
s <- split(data, data$Month)
sapply(s, function(x) colMeans(x[,c("Ozone", "Solar.R", "Wind")], na.rm = TRUE)) # data$Month coerced into
```

```
##           5           6           7           8           9
## Ozone    23.61538  29.44444  59.115385  59.961538  31.44828
## Solar.R  181.29630 190.16667 216.483871 171.857143 167.43333
## Wind     11.62258  10.26667   8.941935   8.793548  10.18000
```

```
# Multi-level split
x <- rnorm(10)
f1 <- gl(2,5); f2 <- gl(5,2) # ex. race and gender 2 factors
interaction(f1,f1) # combine each pair, 10 factors
```

```
## [1] 1.1 1.1 1.1 1.1 1.1 2.2 2.2 2.2 2.2 2.2
## Levels: 1.1 2.1 1.2 2.2
```

```
split(x, list(f1,f2)) # interaction called, list returned for combination sort, drop = TRUE to remove u
```

```
## $'1.1'
## [1] 0.1165892 -0.1194990
```



```
##
## $'2.1'
## numeric(0)
##
## $'1.2'
## [1] 0.4679266 -1.4368877
##
## $'2.2'
## numeric(0)
##
## $'1.3'
## [1] 0.5310122
##
## $'2.3'
## [1] -0.8627139
##
## $'1.4'
## numeric(0)
##
## $'2.4'
## [1] -1.2451944 0.6457308
##
## $'1.5'
## numeric(0)
##
## $'2.5'
## [1] -0.3394378 -0.2064004
```

Defining Functions

stored in txt or R script, functions are R objects. Can pass functions as arguments for other functions

```
myfunction <- function(){ #create a function
  x <- rnorm(100)
  mean(x)
}
myfunction() #call created function
```

```
## [1] -0.1028367
```

myfunction # prints source code for function

```
## function ()
## {
##   x <- rnorm(100)
##   mean(x)
## }
```

```
args(myfunction) # returns arguments for passed function
```

```
## function ()  
## NULL
```

```
myaddedfunction <- function(x,y){ #create a function with formal arguments x and y  
  x + y + rnorm(100) # implicit return last expression  
}  
myaddedfunction(5,3)
```

```
## [1] 7.647769 6.334089 7.593286 6.268142 9.548806 9.191841 8.190586  
## [8] 8.226173 8.766742 9.634012 9.245233 5.921075 6.841281 7.993894  
## [15] 6.722897 9.420619 8.915033 7.623340 8.032766 8.883314 9.142204  
## [22] 8.000106 7.991077 7.685731 6.878269 7.864682 7.372188 8.462985  
## [29] 8.260722 6.964953 8.243108 8.238265 7.603194 7.843892 8.568631  
## [36] 9.067935 7.573488 9.495201 7.325929 6.319661 7.007791 6.507580  
## [43] 9.482838 9.262762 9.473943 7.560676 7.166530 7.353693 9.219610  
## [50] 8.611367 6.644443 8.048528 6.539457 8.539169 7.676676 8.584478  
## [57] 8.233269 7.799053 7.504200 7.847320 6.365965 10.249351 9.269278  
## [64] 6.715166 8.497680 8.015868 6.417507 7.669606 7.323856 8.684615  
## [71] 6.486430 8.711168 8.226389 7.602351 7.960909 5.829723 6.282247  
## [78] 7.605290 7.147546 7.433600 7.803719 7.836636 8.618066 8.022089  
## [85] 8.608157 8.589619 8.760178 9.216551 6.242489 8.209841 8.268497  
## [92] 5.898325 7.066211 7.331588 8.012126 7.676726 9.810349 7.364054  
## [99] 6.261003 7.979133
```

```
myaddedfunction(4:10,2)
```

```
## Warning in x + y + rnorm(100): longer object length is not a multiple of  
## shorter object length
```

```
## [1] 6.409714 6.341150 8.912148 8.792755 11.154946 12.277935 12.926515  
## [8] 5.939344 4.986605 9.444333 8.014862 10.204588 10.538864 13.736550  
## [15] 4.563040 8.080383 8.684333 8.388580 11.043038 10.504557 12.941534  
## [22] 6.405706 5.874937 8.759100 8.274475 9.002475 10.189102 12.813112  
## [29] 8.025275 9.588654 7.999254 7.269448 10.570705 13.922480 13.380562  
## [36] 6.301785 7.219056 8.360819 9.090101 10.532460 10.865300 11.339198  
## [43] 5.243282 6.518864 7.321305 8.387538 10.510045 12.148739 11.287710  
## [50] 5.292170 5.165806 7.699683 8.664981 9.362315 10.495106 14.330201  
## [57] 6.509956 6.178560 7.865012 9.993201 9.207881 9.523909 12.187720  
## [64] 5.027184 7.545402 9.329583 9.364413 9.260397 10.757635 11.208893  
## [71] 6.239572 6.448273 9.943164 8.470355 8.911138 12.665069 11.722099  
## [78] 4.015922 5.826076 7.836202 10.036603 9.776626 11.550650 11.751905  
## [85] 7.533689 5.243682 7.060479 8.798539 10.764209 10.285979 9.854701  
## [92] 5.259725 8.486536 7.838495 9.715276 8.769817 11.769759 11.175956  
## [99] 7.670140 7.005200
```

```
# function with default argument if left unspecified, for common cases  
above <- function(x, n = 10){  
  use <- x > n  
  x[use]  
}  
above(1:20) # n is default set to 10
```

```
## [1] 11 12 13 14 15 16 17 18 19 20
```

```
above(1:20, 12) # n set at 12
```

```
## [1] 13 14 15 16 17 18 19 20
```

```
columnmean <- function(y, removeNA = TRUE) {  
  nc <- ncol(y)  
  means <- numeric(nc)  
  for(i in 1:nc) means[i] <- mean(y[,i], na.rm = removeNA)  
  invisible(means) # auto-return blocks auto-print  
}  
  
# Lazy Evaluation: R evaluated statements and arguments as they come  
f <- function (a,b,c){  
  print(a)  
  #print(b) # error  
}  
f(3) # prints a, error for b, no rxn to not having c
```

```
## [1] 3
```

```
# ways to call functions  
# positional matching and naming can be mixed. Partial matching also allowed, if not found uses position  
# named helps for long arg list where most defaults are maintained or if order is hard to remember.  
mydata <- rnorm(100)  
sd(mydata) # default to first argument
```

```
## [1] 1.001767
```

```
sd(x = mydata)
```

```
## [1] 1.001767
```

```
sd(x = mydata, na.rm = FALSE)
```

```
## [1] 1.001767
```

```
sd(na.rm = FALSE, x = mydata)
```

```
## [1] 1.001767
```

```
sd(na.rm = FALSE, mydata) # remove argument from list, default works on first unspecified arg
```

```
## [1] 1.001767
```

```

# Variable Arguments
# to extend another function without copying arg list of OG function
simon_says <- function(...){
  paste("Simon says:", ...)
}
# or for generic functions passed to methods
# unpacking an ellipses
mad_libs <- function(...){
  args <- list(...)
  place <- args$place
  adjective <- args$adjective
  noun <- args$noun
  paste("News from", place, "today where", adjective, "students took to the streets in protest of the n
}
# or when number of args unknown in advance (if at beginning, no positional or partial matching)
args(paste) # operates on unknown sets of character vectors

```

```

## function (... , sep = " ", collapse = NULL, recycle0 = FALSE)
## NULL

```

```

# function as an argument
some_function <- function(func){
  func(2, 4) # returns result of function with 2,4 arguments
}
some_function(mean) # returns mean of 2,4

```

```

## [1] 2

```

```

# Anonymous function (chaos)
evaluate <- function(func, dat){
  func(dat)
}
evaluate(function(x){x+1}, 6) # creates a function when calling evaluate to add 1

```

```

## [1] 7

```

```

# create a binary operation
"%mult_add_one%" <- function(left, right){
  left * right + 1
}
4 %mult_add_one% 5

```

```

## [1] 21

```

Lexical Scoping

```

make.power <- function(n) {
  pow <- function(x) {
    x^n
  }
}

```

```

}
  pow
}

cube <- make.power(3)
square <- make.power(2)
cube(3)

```

```
## [1] 27
```

```
square(3)
```

```
## [1] 9
```

```

# Scoping - environments
search() # provides list of environments

```

```

## [1] ".GlobalEnv"      "package:stats"    "package:graphics"
## [4] "package:grDevices" "package:utils"    "package:datasets"
## [7] "package:methods"  "Autoloads"       "package:base"

```

```
ls(environment(cube)) # object names in function environment, same for square
```

```
## [1] "n"    "pow"
```

```
get("n",environment(cube)) # values in function environment, changes for square
```

```
## [1] 3
```

R Packages

- Repositories: CRAN, BioConductor (bioinformatics), GitHub
- Search: <https://www.rdocumentation.org/>
- Base packages: utils, stats, datasets, graphics, grDevices, grid, methods, tools, parallel, compiler, splines, tcltk, stats4.
- Recommended packages: boot, class, cluster, codetools, foreign, KernSmooth, lattice, mgcv, nime, rpart, survival, MASS, spatial, nnet, Matrix.

```

# Install from CRAN:
#   install.packages("ggplot2", repos = "http://cran.us.r-project.org") #install
#   install.packages(c("labeling","tibble"), repos = "http://cran.us.r-project.org") #multiple

# Install from Bioconductor
#   install.packages("BiocManager", repos = "https://bioconductor.org/biocLite.R")

```

```

# BiocManager::install(c("GenomicFeatures", "AnnotationDbi")) #install package

# Install from GitHub (need package, author name)
# install.packages("devtools", repos = "http://cran.us.r-project.org") #only once
# library(devtools)
# install_github("author/package") #installs package

# library(ggplot2) # Load package, careful of dependencies
# installed.packages() #check installed packages
# library() #alternate
# old.packages(repos = "http://cran.us.r-project.org") #check packages to update
# update.packages(repos = "http://cran.us.r-project.org") #update all packages
# install.packages("ggplot2") #to update single package
# detach("package:ggplot2", unload=TRUE) #unload function
# remove.packages("ggplot2") #remove package
# help(package = "ggplot2") #package info
# browseVignettes("ggplot2") #extended help files

```

Working With Data

Defining Workspace or directory

```

x <- getwd() # find working directory
x

```

```
## [1] "C:/Users/Owner/OneDrive/Documents/CompSci/CourseraDS/CourseraDataScience"
```

```
dir.create("testdir") # create a directory if doesn't exist, args: dir name, for nested recursive = TRUE

```

```
## Warning in dir.create("testdir"): 'testdir' already exists
```

```

setwd("testdir") # set working dir
file.create("mytest.R") # create file in wd

```

```
## [1] TRUE
```

```
file.exists("mytest.R") # check if file or directory exists in wd
```

```
## [1] TRUE
```

```
file.info("mytest.R") # file metadata, use $ operator to grab specific items
```

```

##           size isdir mode                mtime                ctime
## mytest.R    0 FALSE  666 2025-01-18 17:00:32 2025-01-18 17:00:32
##                                     atime exe
## mytest.R 2025-01-18 17:00:32  no

```

```
file.rename("mytest.R","mytest2.R") # rename
```

```
## [1] TRUE
```

```
file.copy("mytest2.R","mytest3.R") # copy file
```

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

```
file.remove("mytest2.R") # remove file
```

```
## [1] TRUE
```

```
file.path("mytest3.R") # relative path
```

```
## [1] "mytest3.R"
```

```
setwd(x) # could use relative setwd("../") to move up one, setwd("./data"), or absolute path directly u
```

```
dir() # output files in directory. Also list.files()
```

```
## [1] "Code-Library.pdf"      "Code-Library.Rmd"
## [3] "Code Library.Rmd"      "coded.R"
## [5] "complete.R"            "corr.R"
## [7] "Course-Notes.pdf"      "Course Notes.Rmd"
## [9] "CourseraDataScience.Rproj" "hw1_data.csv"
## [11] "pollutantmean.R"       "Programming 2.3"
## [13] "Rprof.out"             "rprog_data_ProgAssignment3"
## [15] "specdata"              "specdata.zip"
## [17] "testdir"
```

```
files_full <- list.files("specdata", full.names=TRUE) # pull all file names from a directory
ls() # prints the objects in work space
```

```
## [1] "%mult_add_one%" "a" "above" "bad"
## [5] "birthday" "coin" "columnmean" "count"
## [9] "cTConvert" "cube" "currentTime" "data"
## [13] "datestring" "e" "evaluate" "f"
## [17] "f1" "f2" "files_full" "flips"
## [21] "flips2" "good" "goodVals" "i"
## [25] "ints" "j" "let" "letter"
## [29] "log.mu" "m" "mad_libs" "make.power"
## [33] "msg" "my_na" "myaddedfunction" "mydata"
## [37] "myfunction" "name" "noise" "nums"
## [41] "pois_mat" "s" "simon_says" "some_function"
## [45] "square" "tf" "timedefined" "today"
## [49] "tol" "u" "unfairflip" "vect"
## [53] "x" "x0" "x1" "y"
## [57] "z"
```

```
rm(list=ls()) # clear workspace
rm(list=setdiff(ls(), "x")) # clear workspace except x
version #R info version
```

```
##
## platform      x86_64-w64-mingw32
## arch          x86_64
## os            mingw32
## crt           ucrt
## system        x86_64, mingw32
## status
## major         4
## minor         4.1
## year          2024
## month         06
## day           14
## svn rev       86737
## language      R
## version.string R version 4.4.1 (2024-06-14 ucrt)
## nickname      Race for Your Life
```

```
sessionInfo() #R info version, packages
```

```
## R version 4.4.1 (2024-06-14 ucrt)
## Platform: x86_64-w64-mingw32/x64
## Running under: Windows 11 x64 (build 22631)
##
## Matrix products: default
##
##
## locale:
## [1] LC_COLLATE=English_United States.utf8
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## loaded via a namespace (and not attached):
## [1] compiler_4.4.1    fastmap_1.2.0     cli_3.6.3        tools_4.4.1
## [5] htmltools_0.5.8.1 rstudioapi_0.17.1 yaml_2.3.10      rmarkdown_2.29
## [9] knitr_1.49        xfun_0.49         digest_0.6.37    rlang_1.1.4
## [13] evaluate_1.0.1
```

```
source("coded.R") # load code into console
```

```
## [1] "Hello World"
```



```
args(ls()) # get arguments for a function
```

```
## NULL
```

```
help(ls) # access documentation on ls() function
```

```
## starting httpd help server ... done
```

```
?ls # same. for operator use ?`:`
```

Reading and Writing Data

```
# Download data from website
```

```
fileUrl <- "https://stg-arcgisazurecdataprodl.az.arcgis.com/exportfiles-1506-24014/Part1_Crime_Beta_596"
if(!file.exists("./testdir/crimedata.csv")) download.file(fileUrl, destfile = "./testdir/crimedata.csv")
dateDownloaded <- date() # Keep track of date downloaded for file
```

```
# Read table or csv data into R
```

```
x <- read.table("hw1_data.csv", header = TRUE, sep = ",") # reading tabular data from text files, return
head(x)
```

```
##      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
```

```
x <- read.csv("hw1_data.csv") # Same but default separator is ", " and header = TRUE
# write.table(x)
```

```
# help read.table with colClasses with smaller sample
```

```
initial <- read.table("hw1_data.csv", header = TRUE, sep = ",", nrows = 100)
classes <- sapply(initial, class)
tabAll <- read.table("hw1_data.csv", header = TRUE, sep = ",", colClasses = classes)
```

```
# Read Excel file into R
```

```
x <- "https://stg-arcgisazurecdataprodl.az.arcgis.com/exportfiles-1506-24014/Part1_Crime_Beta_383480701"
if(!file.exists("./testdir/crimexl.xlsx")) {
  download.file(x, destfile = "./testdir/crimexl.xlsx", method = "curl") # improve
  dateXl <- date()
}
library(readxl) # xlsx, XLConnect other options
```

```
## Warning: package 'readxl' was built under R version 4.4.2
```

```
cameraData <- read_excel("./testdir/crimexl.xlsx", sheet = 1, col_types = "text", n_max = 100)
head(cameraData)
```

```
## # A tibble: 6 x 23
##   RowID CCNumber CrimeDateTime CrimeCode Description Inside_Outside Weapon Post
##   <chr> <chr>      <chr>          <chr>      <chr>          <chr>      <chr>
## 1 1      14I10336 41880.5          5A        BURGLARY      <NA>        NA      835
## 2 2      14H13075 41880.989583~ 4E        COMMON ASS~ <NA>        NA      515
## 3 3      14H13066 41880.965277~ 6G        LARCENY      <NA>        NA      114
## 4 4      14I00593 41880.291666~ 6J        LARCENY      <NA>        NA      732
## 5 5      14H13360 41880.979166~ 6G        LARCENY      <NA>        NA      213
## 6 6      14H12804 41880.475694~ 4E        COMMON ASS~ <NA>        NA      412
## # i 15 more variables: Gender <chr>, Age <chr>, Race <chr>, Ethnicity <chr>,
## #   Location <chr>, Old_District <chr>, New_District <chr>, Neighborhood <chr>,
## #   Latitude <chr>, Longitude <chr>, GeoLocation <chr>, PremiseType <chr>,
## #   Total_Incidents <chr>, x <chr>, y <chr>
```

```
# write also works
```

```
lines <- readLines("coded.R") # reading lines of text file, return character vector
```

```
## Warning in readLines("coded.R"): incomplete final line found on 'coded.R'
```

```
writeLines("coded.R")
```

```
## coded.R
```

```
# editable textual format retains metadata, helpful for version control, corruption fixable, memory cos
dget("coded.R") # reading R objects deparsed into text files
```

```
## [1] "Hello World"
```

```
dput("coded.R") # takes R object, create R code to reconstruct object saving attributes, names
```

```
## "coded.R"
```

```
source("coded.R") # reading in R code files
```

```
## [1] "Hello World"
```

```
#dump() # multiple R objects
```

```
# load() # read in saved workspace read binary objects into R
```

```
# save()
```

```
# unserialize() # read single R objects in binary form
```

```
# serialize()
```

```
# Interface to outside world
```

```
file(description = "hw1_data.csv") # open connection to standard, uncompressed file. Helps for partial
```

```
## A connection with
## description "hw1_data.csv"
## class      "file"
## mode       "r"
## text       "text"
## opened     "closed"
## can read   "yes"
## can write  "yes"

# gzfile() # connection to file w compression gzip
# bzfile() # connection to file w compression bzip2
jh <- url("http://www.jhsph.edu", "r") # connection to webpage
close(jh) # to end connection
```

Just XML stuff

- XML (extensible markup language)
- <http://en.wikipedia.org/wiki/XML>
- store structured data in internet applications. From web scraping, API
- Components: markup (labels for structure) and content (text)
- Tags (labels): start
end
empty
- Elements: example of tag Hello, world
- Attributes: component of label
- XPath language: <http://www.stat.berkeley.edu/~statcur/Workshop2/Presentations/XML.pdf>
- /node (top level node), //node (node any level), node[@attr-name] node w attr name, node[@attr-name='bob']
- XML Short Intro: <https://www.omegahat.net/RXML/shortIntro.pdf>
- XML Long Intro: <https://www.omegahat.net/RXML/Tour.pdf>

```
# Reading file
library(XML)
```

```
## Warning: package 'XML' was built under R version 4.4.2
```

```
library(httr)
```

```
## Warning: package 'httr' was built under R version 4.4.2
```

```
fileUrl <- "https://www.w3schools.com/xml/simple.xml"
doc <- xmlTreeParse(rawToChar(GET(fileUrl)$content),useInternalNodes = TRUE) # read file into R to parse
rootNode <- xmlRoot(doc) # wrapper for structured element

# Access Data
xmlName(rootNode) # name of xml
```

```
## [1] "breakfast_menu"
```

```
names(rootNode) # names of root node
```

```
## food food food food food
## "food" "food" "food" "food" "food"
```

```
rootNode[[1]] # first food element, get first subelement of element using [[1]][[1]]
```

```
## <food>
## <name>Belgian Waffles</name>
## <price>$5.95</price>
## <description>Two of our famous Belgian Waffles with plenty of real maple syrup</description>
## <calories>650</calories>
## </food>
```

```
xmlSApply(rootNode,xmlValue) # give xml value of each root node
```

```
##
## "Belgian Waffles$5.95Two of our famous Belgian Waffles with plenty of 1
##
## "Strawberry Belgian Waffles$7.95Light Belgian waffles covered with strawberries and
##
## "Berry-Berry Belgian Waffles$8.95Light Belgian waffles covered with an assortment of fresh berries and
##
## "French Toast$4.50Thick slices made from our homemade
##
## "Homestyle Breakfast$6.95Two eggs, bacon or sausage, toast, and our ever-popular
```

```
xpathSApply(rootNode,"//name",xmlValue) # get node xmlValue for each names
```

```
## [1] "Belgian Waffles" "Strawberry Belgian Waffles"
## [3] "Berry-Berry Belgian Waffles" "French Toast"
## [5] "Homestyle Breakfast"
```

```
xpathSApply(rootNode,"//price",xmlValue)
```

```
## [1] "$5.95" "$7.95" "$8.95" "$4.50" "$6.95"
```

```
# Pokemon
library(rvest)
```

```
## Warning: package 'rvest' was built under R version 4.4.2
```

```
fileUrlBase <- "https://pokeмонdb.net/pokedex/stats/gen"
generations <- 1:8
# Scrape Data
pokemonList <- lapply(generations,function(x){
  html <- read_html(paste0(fileUrlBase,x)) # create URL
  tableNode <- html_node(html,xpath="//*[(@id = 'pokedex')]") # read HTML, extract node using xpath sel
  data <- html_table(html,header=TRUE)[[1]] # convert to data frame
  colnames(data)[1] <- "ID"
  data$Generation <- x # add generation ID
  data # return data frame to list
})
thePokemon <- do.call(rbind,pokemonList) # one data frame
# Cleaning
types <- strsplit(gsub('[a-z]\\K(?:[A-Z])', ' ',thePokemon$Type, perl=T)," ") # split Type column
thePokemon$Type1 <- unlist(lapply(types,function(x) x[1])) # Type1 column
thePokemon$Type2 <- unlist(lapply(types,function(x) ifelse(is.na(x[2])," ",x[2]))) # Type2 column
pokemonNames <- strsplit(gsub('[a-z]\\K(?:[A-Z])', '--', thePokemon$Name, perl=T),"--") # split Name
thePokemon$Name <- unlist(lapply(pokemonNames,function(x) x[1]))
thePokemon$Form <- unlist(lapply(pokemonNames,function(x) ifelse(is.na(x[2])," ",x[2])))
thePokemon <- thePokemon[,c(1,2,14,12,13,4,5,6,7,8,9,10,11)] # reorder and remove unnecessary
thePokemon[29,"Name"] <- "Nidoran" # cleaning gender
thePokemon[29,"Form"] <- "Female"
thePokemon[32,"Name"] <- "Nidoran"
thePokemon[32,"Form"] <- "Male"
```

Just JSON Stuff

- Javascript Object Notation- light weight data storage, common format from APIs, similar to XML but different syntax/format.
- Data stored as: number(double), strings(double quoted), boolean, array(ordered, comma sep, [] enclosed), objects(unordered, comma sep, {} enclosed, key:value pairs).
- <http://en.wikipedia.org/wiki/JSON>
- <http://www.json.org/>
- jsonlite vignette
- <http://www.r-bloggers.com/new-package-jsonlite-a-smarter-json-encoderdecoder/>

```
library(jsonlite)
```

```
## Warning: package 'jsonlite' was built under R version 4.4.2
```

```
jsonData <- fromJSON("https://api.github.com/users/jtleek/repos") # can pass any format
names(jsonData) # names of data frame
```

```
## [1] "id" "node_id"
## [3] "name" "full_name"
## [5] "private" "owner"
## [7] "html_url" "description"
## [9] "fork" "url"
## [11] "forks_url" "keys_url"
## [13] "collaborators_url" "teams_url"
## [15] "hooks_url" "issue_events_url"
## [17] "events_url" "assignees_url"
## [19] "branches_url" "tags_url"
## [21] "blobs_url" "git_tags_url"
## [23] "git_refs_url" "trees_url"
## [25] "statuses_url" "languages_url"
## [27] "stargazers_url" "contributors_url"
## [29] "subscribers_url" "subscription_url"
## [31] "commits_url" "git_commits_url"
## [33] "comments_url" "issue_comment_url"
## [35] "contents_url" "compare_url"
## [37] "merges_url" "archive_url"
## [39] "downloads_url" "issues_url"
## [41] "pulls_url" "milestones_url"
## [43] "notifications_url" "labels_url"
## [45] "releases_url" "deployments_url"
## [47] "created_at" "updated_at"
## [49] "pushed_at" "git_url"
## [51] "ssh_url" "clone_url"
## [53] "svn_url" "homepage"
## [55] "size" "stargazers_count"
## [57] "watchers_count" "language"
## [59] "has_issues" "has_projects"
## [61] "has_downloads" "has_wiki"
## [63] "has_pages" "has_discussions"
## [65] "forks_count" "mirror_url"
## [67] "archived" "disabled"
## [69] "open_issues_count" "license"
## [71] "allow_forking" "is_template"
## [73] "web_commit_signoff_required" "topics"
## [75] "visibility" "forks"
## [77] "open_issues" "watchers"
## [79] "default_branch"
```

```
names(jsonData$owner) # names of column
```

```
## [1] "login" "id" "node_id"
## [4] "avatar_url" "gravatar_id" "url"
## [7] "html_url" "followers_url" "following_url"
## [10] "gists_url" "starred_url" "subscriptions_url"
## [13] "organizations_url" "repos_url" "events_url"
## [16] "received_events_url" "type" "user_view_type"
## [19] "site_admin"
```

```
jsonData$owner$login # who logged in
```

```
## [1] "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek"
## [9] "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek"
## [17] "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek"
## [25] "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek"
```

```
# write data frame to JSON
```

```
myjson <- toJSON(iris, pretty = TRUE)
cat(myjson)
```

```
## [
##   {
##     "Sepal.Length": 5.1,
##     "Sepal.Width": 3.5,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
##   },
##   {
##     "Sepal.Length": 4.9,
##     "Sepal.Width": 3,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
##   },
##   {
##     "Sepal.Length": 4.7,
##     "Sepal.Width": 3.2,
##     "Petal.Length": 1.3,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
##   },
##   {
##     "Sepal.Length": 4.6,
##     "Sepal.Width": 3.1,
##     "Petal.Length": 1.5,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
##   },
##   {
##     "Sepal.Length": 5,
##     "Sepal.Width": 3.6,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
##   },
##   {
##     "Sepal.Length": 5.4,
##     "Sepal.Width": 3.9,
##     "Petal.Length": 1.7,
##     "Petal.Width": 0.4,
##     "Species": "setosa"
##   }
## ]
```

```

## },
## {
##     "Sepal.Length": 4.6,
##     "Sepal.Width": 3.4,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.3,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5,
##     "Sepal.Width": 3.4,
##     "Petal.Length": 1.5,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.4,
##     "Sepal.Width": 2.9,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.9,
##     "Sepal.Width": 3.1,
##     "Petal.Length": 1.5,
##     "Petal.Width": 0.1,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5.4,
##     "Sepal.Width": 3.7,
##     "Petal.Length": 1.5,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.8,
##     "Sepal.Width": 3.4,
##     "Petal.Length": 1.6,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.8,
##     "Sepal.Width": 3,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.1,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.3,
##     "Sepal.Width": 3,
##     "Petal.Length": 1.1,

```



```

##      "Petal.Width": 0.1,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.8,
##      "Sepal.Width": 4,
##      "Petal.Length": 1.2,
##      "Petal.Width": 0.2,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.7,
##      "Sepal.Width": 4.4,
##      "Petal.Length": 1.5,
##      "Petal.Width": 0.4,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.4,
##      "Sepal.Width": 3.9,
##      "Petal.Length": 1.3,
##      "Petal.Width": 0.4,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.1,
##      "Sepal.Width": 3.5,
##      "Petal.Length": 1.4,
##      "Petal.Width": 0.3,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.7,
##      "Sepal.Width": 3.8,
##      "Petal.Length": 1.7,
##      "Petal.Width": 0.3,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.1,
##      "Sepal.Width": 3.8,
##      "Petal.Length": 1.5,
##      "Petal.Width": 0.3,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.4,
##      "Sepal.Width": 3.4,
##      "Petal.Length": 1.7,
##      "Petal.Width": 0.2,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.1,

```

```

##      "Sepal.Width": 3.7,
##      "Petal.Length": 1.5,
##      "Petal.Width": 0.4,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 4.6,
##      "Sepal.Width": 3.6,
##      "Petal.Length": 1,
##      "Petal.Width": 0.2,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.1,
##      "Sepal.Width": 3.3,
##      "Petal.Length": 1.7,
##      "Petal.Width": 0.5,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 4.8,
##      "Sepal.Width": 3.4,
##      "Petal.Length": 1.9,
##      "Petal.Width": 0.2,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5,
##      "Sepal.Width": 3,
##      "Petal.Length": 1.6,
##      "Petal.Width": 0.2,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5,
##      "Sepal.Width": 3.4,
##      "Petal.Length": 1.6,
##      "Petal.Width": 0.4,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.2,
##      "Sepal.Width": 3.5,
##      "Petal.Length": 1.5,
##      "Petal.Width": 0.2,
##      "Species": "setosa"
##    },
##    {
##      "Sepal.Length": 5.2,
##      "Sepal.Width": 3.4,
##      "Petal.Length": 1.4,
##      "Petal.Width": 0.2,
##      "Species": "setosa"
##    },
##  ],

```

```

## {
##   "Sepal.Length": 4.7,
##   "Sepal.Width": 3.2,
##   "Petal.Length": 1.6,
##   "Petal.Width": 0.2,
##   "Species": "setosa"
## },
## {
##   "Sepal.Length": 4.8,
##   "Sepal.Width": 3.1,
##   "Petal.Length": 1.6,
##   "Petal.Width": 0.2,
##   "Species": "setosa"
## },
## {
##   "Sepal.Length": 5.4,
##   "Sepal.Width": 3.4,
##   "Petal.Length": 1.5,
##   "Petal.Width": 0.4,
##   "Species": "setosa"
## },
## {
##   "Sepal.Length": 5.2,
##   "Sepal.Width": 4.1,
##   "Petal.Length": 1.5,
##   "Petal.Width": 0.1,
##   "Species": "setosa"
## },
## {
##   "Sepal.Length": 5.5,
##   "Sepal.Width": 4.2,
##   "Petal.Length": 1.4,
##   "Petal.Width": 0.2,
##   "Species": "setosa"
## },
## {
##   "Sepal.Length": 4.9,
##   "Sepal.Width": 3.1,
##   "Petal.Length": 1.5,
##   "Petal.Width": 0.2,
##   "Species": "setosa"
## },
## {
##   "Sepal.Length": 5,
##   "Sepal.Width": 3.2,
##   "Petal.Length": 1.2,
##   "Petal.Width": 0.2,
##   "Species": "setosa"
## },
## {
##   "Sepal.Length": 5.5,
##   "Sepal.Width": 3.5,
##   "Petal.Length": 1.3,
##   "Petal.Width": 0.2,

```

```

##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.9,
##     "Sepal.Width": 3.6,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.1,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.4,
##     "Sepal.Width": 3,
##     "Petal.Length": 1.3,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5.1,
##     "Sepal.Width": 3.4,
##     "Petal.Length": 1.5,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5,
##     "Sepal.Width": 3.5,
##     "Petal.Length": 1.3,
##     "Petal.Width": 0.3,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.5,
##     "Sepal.Width": 2.3,
##     "Petal.Length": 1.3,
##     "Petal.Width": 0.3,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.4,
##     "Sepal.Width": 3.2,
##     "Petal.Length": 1.3,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5,
##     "Sepal.Width": 3.5,
##     "Petal.Length": 1.6,
##     "Petal.Width": 0.6,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5.1,
##     "Sepal.Width": 3.8,

```

```

##     "Petal.Length": 1.9,
##     "Petal.Width": 0.4,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.8,
##     "Sepal.Width": 3,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.3,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5.1,
##     "Sepal.Width": 3.8,
##     "Petal.Length": 1.6,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 4.6,
##     "Sepal.Width": 3.2,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5.3,
##     "Sepal.Width": 3.7,
##     "Petal.Length": 1.5,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 5,
##     "Sepal.Width": 3.3,
##     "Petal.Length": 1.4,
##     "Petal.Width": 0.2,
##     "Species": "setosa"
## },
## {
##     "Sepal.Length": 7,
##     "Sepal.Width": 3.2,
##     "Petal.Length": 4.7,
##     "Petal.Width": 1.4,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 6.4,
##     "Sepal.Width": 3.2,
##     "Petal.Length": 4.5,
##     "Petal.Width": 1.5,
##     "Species": "versicolor"
## },
## {

```

```

##      "Sepal.Length": 6.9,
##      "Sepal.Width": 3.1,
##      "Petal.Length": 4.9,
##      "Petal.Width": 1.5,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.5,
##      "Sepal.Width": 2.3,
##      "Petal.Length": 4,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.5,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 4.6,
##      "Petal.Width": 1.5,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.7,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 4.5,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.3,
##      "Sepal.Width": 3.3,
##      "Petal.Length": 4.7,
##      "Petal.Width": 1.6,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 4.9,
##      "Sepal.Width": 2.4,
##      "Petal.Length": 3.3,
##      "Petal.Width": 1,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.6,
##      "Sepal.Width": 2.9,
##      "Petal.Length": 4.6,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.2,
##      "Sepal.Width": 2.7,
##      "Petal.Length": 3.9,
##      "Petal.Width": 1.4,
##      "Species": "versicolor"

```

```

## },
## {
##     "Sepal.Length": 5,
##     "Sepal.Width": 2,
##     "Petal.Length": 3.5,
##     "Petal.Width": 1,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.9,
##     "Sepal.Width": 3,
##     "Petal.Length": 4.2,
##     "Petal.Width": 1.5,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 6,
##     "Sepal.Width": 2.2,
##     "Petal.Length": 4,
##     "Petal.Width": 1,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 6.1,
##     "Sepal.Width": 2.9,
##     "Petal.Length": 4.7,
##     "Petal.Width": 1.4,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.6,
##     "Sepal.Width": 2.9,
##     "Petal.Length": 3.6,
##     "Petal.Width": 1.3,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 6.7,
##     "Sepal.Width": 3.1,
##     "Petal.Length": 4.4,
##     "Petal.Width": 1.4,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.6,
##     "Sepal.Width": 3,
##     "Petal.Length": 4.5,
##     "Petal.Width": 1.5,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.8,
##     "Sepal.Width": 2.7,
##     "Petal.Length": 4.1,

```

```

##      "Petal.Width": 1,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.2,
##      "Sepal.Width": 2.2,
##      "Petal.Length": 4.5,
##      "Petal.Width": 1.5,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.6,
##      "Sepal.Width": 2.5,
##      "Petal.Length": 3.9,
##      "Petal.Width": 1.1,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.9,
##      "Sepal.Width": 3.2,
##      "Petal.Length": 4.8,
##      "Petal.Width": 1.8,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.1,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 4,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.3,
##      "Sepal.Width": 2.5,
##      "Petal.Length": 4.9,
##      "Petal.Width": 1.5,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.1,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 4.7,
##      "Petal.Width": 1.2,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.4,
##      "Sepal.Width": 2.9,
##      "Petal.Length": 4.3,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.6,

```



```

##     "Sepal.Width": 3,
##     "Petal.Length": 4.4,
##     "Petal.Width": 1.4,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 6.8,
##     "Sepal.Width": 2.8,
##     "Petal.Length": 4.8,
##     "Petal.Width": 1.4,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 6.7,
##     "Sepal.Width": 3,
##     "Petal.Length": 5,
##     "Petal.Width": 1.7,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 6,
##     "Sepal.Width": 2.9,
##     "Petal.Length": 4.5,
##     "Petal.Width": 1.5,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.7,
##     "Sepal.Width": 2.6,
##     "Petal.Length": 3.5,
##     "Petal.Width": 1,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.5,
##     "Sepal.Width": 2.4,
##     "Petal.Length": 3.8,
##     "Petal.Width": 1.1,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.5,
##     "Sepal.Width": 2.4,
##     "Petal.Length": 3.7,
##     "Petal.Width": 1,
##     "Species": "versicolor"
## },
## {
##     "Sepal.Length": 5.8,
##     "Sepal.Width": 2.7,
##     "Petal.Length": 3.9,
##     "Petal.Width": 1.2,
##     "Species": "versicolor"
## },

```

```

## {
##   "Sepal.Length": 6,
##   "Sepal.Width": 2.7,
##   "Petal.Length": 5.1,
##   "Petal.Width": 1.6,
##   "Species": "versicolor"
## },
## {
##   "Sepal.Length": 5.4,
##   "Sepal.Width": 3,
##   "Petal.Length": 4.5,
##   "Petal.Width": 1.5,
##   "Species": "versicolor"
## },
## {
##   "Sepal.Length": 6,
##   "Sepal.Width": 3.4,
##   "Petal.Length": 4.5,
##   "Petal.Width": 1.6,
##   "Species": "versicolor"
## },
## {
##   "Sepal.Length": 6.7,
##   "Sepal.Width": 3.1,
##   "Petal.Length": 4.7,
##   "Petal.Width": 1.5,
##   "Species": "versicolor"
## },
## {
##   "Sepal.Length": 6.3,
##   "Sepal.Width": 2.3,
##   "Petal.Length": 4.4,
##   "Petal.Width": 1.3,
##   "Species": "versicolor"
## },
## {
##   "Sepal.Length": 5.6,
##   "Sepal.Width": 3,
##   "Petal.Length": 4.1,
##   "Petal.Width": 1.3,
##   "Species": "versicolor"
## },
## {
##   "Sepal.Length": 5.5,
##   "Sepal.Width": 2.5,
##   "Petal.Length": 4,
##   "Petal.Width": 1.3,
##   "Species": "versicolor"
## },
## {
##   "Sepal.Length": 5.5,
##   "Sepal.Width": 2.6,
##   "Petal.Length": 4.4,
##   "Petal.Width": 1.2,

```

```

##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.1,
##      "Sepal.Width": 3,
##      "Petal.Length": 4.6,
##      "Petal.Width": 1.4,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.8,
##      "Sepal.Width": 2.6,
##      "Petal.Length": 4,
##      "Petal.Width": 1.2,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5,
##      "Sepal.Width": 2.3,
##      "Petal.Length": 3.3,
##      "Petal.Width": 1,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.6,
##      "Sepal.Width": 2.7,
##      "Petal.Length": 4.2,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.7,
##      "Sepal.Width": 3,
##      "Petal.Length": 4.2,
##      "Petal.Width": 1.2,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.7,
##      "Sepal.Width": 2.9,
##      "Petal.Length": 4.2,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.2,
##      "Sepal.Width": 2.9,
##      "Petal.Length": 4.3,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.1,
##      "Sepal.Width": 2.5,

```

```

##      "Petal.Length": 3,
##      "Petal.Width": 1.1,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 5.7,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 4.1,
##      "Petal.Width": 1.3,
##      "Species": "versicolor"
##    },
##    {
##      "Sepal.Length": 6.3,
##      "Sepal.Width": 3.3,
##      "Petal.Length": 6,
##      "Petal.Width": 2.5,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 5.8,
##      "Sepal.Width": 2.7,
##      "Petal.Length": 5.1,
##      "Petal.Width": 1.9,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.1,
##      "Sepal.Width": 3,
##      "Petal.Length": 5.9,
##      "Petal.Width": 2.1,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.3,
##      "Sepal.Width": 2.9,
##      "Petal.Length": 5.6,
##      "Petal.Width": 1.8,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.5,
##      "Sepal.Width": 3,
##      "Petal.Length": 5.8,
##      "Petal.Width": 2.2,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.6,
##      "Sepal.Width": 3,
##      "Petal.Length": 6.6,
##      "Petal.Width": 2.1,
##      "Species": "virginica"
##    },
##    {

```

```

##      "Sepal.Length": 4.9,
##      "Sepal.Width": 2.5,
##      "Petal.Length": 4.5,
##      "Petal.Width": 1.7,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.3,
##      "Sepal.Width": 2.9,
##      "Petal.Length": 6.3,
##      "Petal.Width": 1.8,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.7,
##      "Sepal.Width": 2.5,
##      "Petal.Length": 5.8,
##      "Petal.Width": 1.8,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.2,
##      "Sepal.Width": 3.6,
##      "Petal.Length": 6.1,
##      "Petal.Width": 2.5,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.5,
##      "Sepal.Width": 3.2,
##      "Petal.Length": 5.1,
##      "Petal.Width": 2,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.4,
##      "Sepal.Width": 2.7,
##      "Petal.Length": 5.3,
##      "Petal.Width": 1.9,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.8,
##      "Sepal.Width": 3,
##      "Petal.Length": 5.5,
##      "Petal.Width": 2.1,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 5.7,
##      "Sepal.Width": 2.5,
##      "Petal.Length": 5,
##      "Petal.Width": 2,
##      "Species": "virginica"

```

```

## },
## {
##   "Sepal.Length": 5.8,
##   "Sepal.Width": 2.8,
##   "Petal.Length": 5.1,
##   "Petal.Width": 2.4,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.4,
##   "Sepal.Width": 3.2,
##   "Petal.Length": 5.3,
##   "Petal.Width": 2.3,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.5,
##   "Sepal.Width": 3,
##   "Petal.Length": 5.5,
##   "Petal.Width": 1.8,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 7.7,
##   "Sepal.Width": 3.8,
##   "Petal.Length": 6.7,
##   "Petal.Width": 2.2,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 7.7,
##   "Sepal.Width": 2.6,
##   "Petal.Length": 6.9,
##   "Petal.Width": 2.3,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6,
##   "Sepal.Width": 2.2,
##   "Petal.Length": 5,
##   "Petal.Width": 1.5,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.9,
##   "Sepal.Width": 3.2,
##   "Petal.Length": 5.7,
##   "Petal.Width": 2.3,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 5.6,
##   "Sepal.Width": 2.8,
##   "Petal.Length": 4.9,

```

```

##      "Petal.Width": 2,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.7,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 6.7,
##      "Petal.Width": 2,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.3,
##      "Sepal.Width": 2.7,
##      "Petal.Length": 4.9,
##      "Petal.Width": 1.8,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.7,
##      "Sepal.Width": 3.3,
##      "Petal.Length": 5.7,
##      "Petal.Width": 2.1,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.2,
##      "Sepal.Width": 3.2,
##      "Petal.Length": 6,
##      "Petal.Width": 1.8,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.2,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 4.8,
##      "Petal.Width": 1.8,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.1,
##      "Sepal.Width": 3,
##      "Petal.Length": 4.9,
##      "Petal.Width": 1.8,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.4,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 5.6,
##      "Petal.Width": 2.1,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.2,

```

```

##      "Sepal.Width": 3,
##      "Petal.Length": 5.8,
##      "Petal.Width": 1.6,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.4,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 6.1,
##      "Petal.Width": 1.9,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.9,
##      "Sepal.Width": 3.8,
##      "Petal.Length": 6.4,
##      "Petal.Width": 2,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.4,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 5.6,
##      "Petal.Width": 2.2,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.3,
##      "Sepal.Width": 2.8,
##      "Petal.Length": 5.1,
##      "Petal.Width": 1.5,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.1,
##      "Sepal.Width": 2.6,
##      "Petal.Length": 5.6,
##      "Petal.Width": 1.4,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 7.7,
##      "Sepal.Width": 3,
##      "Petal.Length": 6.1,
##      "Petal.Width": 2.3,
##      "Species": "virginica"
##    },
##    {
##      "Sepal.Length": 6.3,
##      "Sepal.Width": 3.4,
##      "Petal.Length": 5.6,
##      "Petal.Width": 2.4,
##      "Species": "virginica"
##    },
##  },

```



```

## {
##   "Sepal.Length": 6.4,
##   "Sepal.Width": 3.1,
##   "Petal.Length": 5.5,
##   "Petal.Width": 1.8,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6,
##   "Sepal.Width": 3,
##   "Petal.Length": 4.8,
##   "Petal.Width": 1.8,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.9,
##   "Sepal.Width": 3.1,
##   "Petal.Length": 5.4,
##   "Petal.Width": 2.1,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.7,
##   "Sepal.Width": 3.1,
##   "Petal.Length": 5.6,
##   "Petal.Width": 2.4,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.9,
##   "Sepal.Width": 3.1,
##   "Petal.Length": 5.1,
##   "Petal.Width": 2.3,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 5.8,
##   "Sepal.Width": 2.7,
##   "Petal.Length": 5.1,
##   "Petal.Width": 1.9,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.8,
##   "Sepal.Width": 3.2,
##   "Petal.Length": 5.9,
##   "Petal.Width": 2.3,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.7,
##   "Sepal.Width": 3.3,
##   "Petal.Length": 5.7,
##   "Petal.Width": 2.5,

```

```
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.7,
##   "Sepal.Width": 3,
##   "Petal.Length": 5.2,
##   "Petal.Width": 2.3,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.3,
##   "Sepal.Width": 2.5,
##   "Petal.Length": 5,
##   "Petal.Width": 1.9,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.5,
##   "Sepal.Width": 3,
##   "Petal.Length": 5.2,
##   "Petal.Width": 2,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 6.2,
##   "Sepal.Width": 3.4,
##   "Petal.Length": 5.4,
##   "Petal.Width": 2.3,
##   "Species": "virginica"
## },
## {
##   "Sepal.Length": 5.9,
##   "Sepal.Width": 3,
##   "Petal.Length": 5.1,
##   "Petal.Width": 1.8,
##   "Species": "virginica"
## }
## ]
```

```
# upload again
iris2 <- fromJSON(myjson)
head(iris2)
```

```
##   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
```

Data Tables (not Frames)

- Package, faster and more memory efficient
- Inherits from data.frame (all functions), written in C, faster at sub-setting, grouping, and updating
- <http://stackoverflow.com/questions/13618488/what-you-can-do-with-data-frame-that-you-cant-in-data-table>
- <https://github.com/Rdatatable/data.table>

```
library(data.table)
```

```
## Warning: package 'data.table' was built under R version 4.4.2
```

```
DF = data.frame(x=rnorm(9),y=rep(c("a","b","c"), each=3),z=rnorm(9))
head(DF,3)
```

```
##           x y           z
## 1 -0.6925349 a 0.7635296
## 2 -2.5337551 a 0.8789114
## 3 -1.0199867 a 0.6268136
```

```
DT = data.table(x=rnorm(9),y=rep(c("a","b","c"), each=3),z=rnorm(9))
head(DT,3)
```

```
##           x      y      z
##      <num> <char> <num>
## 1: -0.4413771      a -0.1214552
## 2:  0.2070986      a -0.4732344
## 3: -0.4314813      a -0.2022749
```

```
tables() # get all data tables in memory
```

```
##      NAME NROW NCOL MB  COLS  KEY
## 1:   DT      9    3  0 x,y,z [NULL]
## Total: OMB using type_size
```

```
# subsetting
DT[2,] # subset rows
```

```
##           x      y      z
##      <num> <char> <num>
## 1: 0.2070986      a -0.4732344
```

```
DT[DT$y=="a",] # subset where y is "a"
```

```
##           x      y      z
##      <num> <char> <num>
## 1: -0.4413771      a -0.1214552
## 2:  0.2070986      a -0.4732344
## 3: -0.4314813      a -0.2022749
```

```
DT[c(2,3)] # subset rows 2 & 3, one variable is assigned to rows
```

```
##           x           y           z
##      <num> <char>      <num>
## 1:  0.2070986      a -0.4732344
## 2: -0.4314813      a -0.2022749
```

```
# subset cols, DT[,c(2.3)] does not work bc uses expressions
DT[,list(mean(x),sum(z))] # pass list of functions applied by names of columns
```

```
##           V1           V2
##      <num>      <num>
## 1: -0.3562172 -0.5212528
```

```
DT[,table(y)] # get table of y values
```

```
## y
## a b c
## 3 3 3
```

```
DT[, w := z^2] # adds columns quickly
DT2 <- DT # does not make a copy in memory, change one changes all, pointing to same memory. Use copy f
DT[,m:= {tmp <- (x+z); log2(tmp+5)}] # multiple step function, returns last statement in evaluation
DT[,a:=x>0] # expression evaluates boolean for new variable
DT[,b:= mean(x+w),by=a] # grouping by boolean a into factors to evaluate expression
# special variable .N integer len 1 num times group appears
set.seed(123)
DT <- data.table(x=sample(letters[1:3], 1E5, TRUE))
DT[, .N, by=x] # count number of times grouped by x variable
```

```
##           x           N
##      <char> <int>
## 1:      c 33294
## 2:      b 33305
## 3:      a 33401
```

```
# data.table contains keys
DT <- data.table(x=rep(c("a","b","c"),each=100), y=rnorm(300))
setkey(DT, x)
DT["a"] # subset based on key x, faster
```

```
## Key: <x>
##           x           y
##      <char>      <num>
## 1:      a 0.88631257
## 2:      a 2.82858132
## 3:      a 2.03145429
## 4:      a 1.90675413
## 5:      a 0.21490826
## 6:      a -0.86273413
```

```
## 7:      a -2.20493863
## 8:      a  0.24105923
## 9:      a  1.83832419
## 10:     a  0.79205468
## 11:     a  0.65053469
## 12:     a -1.53912061
## 13:     a -0.60830053
## 14:     a  0.38195644
## 15:     a -1.07500044
## 16:     a  0.21994264
## 17:     a -0.78288781
## 18:     a -1.11003346
## 19:     a -1.65871456
## 20:     a -0.50147343
## 21:     a  1.91636375
## 22:     a  1.41236645
## 23:     a  0.92260986
## 24:     a  1.01106201
## 25:     a  0.57213026
## 26:     a -0.62843126
## 27:     a -0.36316140
## 28:     a -1.05858811
## 29:     a -0.42935803
## 30:     a  0.86941467
## 31:     a -0.54001647
## 32:     a -1.14647747
## 33:     a -0.17151840
## 34:     a -0.56368340
## 35:     a -0.42994346
## 36:     a -1.23723779
## 37:     a  0.15901329
## 38:     a -1.16711067
## 39:     a -0.08111944
## 40:     a -0.51667953
## 41:     a  0.99540703
## 42:     a  0.79752142
## 43:     a  0.53895224
## 44:     a -1.40405605
## 45:     a  0.40144065
## 46:     a -0.52432237
## 47:     a -0.83952146
## 48:     a  0.47556591
## 49:     a -0.01194696
## 50:     a  0.10319780
## 51:     a -0.38575415
## 52:     a  1.11726438
## 53:     a -0.49961390
## 54:     a -0.44735091
## 55:     a -0.23784512
## 56:     a -0.86939374
## 57:     a  1.14887678
## 58:     a  0.53864996
## 59:     a -0.10680992
## 60:     a  0.60053649
```

```
## 61:      a -1.47499445
## 62:      a  0.98126964
## 63:      a -0.61118738
## 64:      a  0.08938648
## 65:      a -0.01327227
## 66:      a -0.97219341
## 67:      a -0.57946225
## 68:      a  0.14963144
## 69:      a  0.47640689
## 70:      a  0.44729682
## 71:      a -0.19180956
## 72:      a  0.51712710
## 73:      a  0.40338273
## 74:      a  1.78411385
## 75:      a  0.27775645
## 76:      a  0.77394978
## 77:      a -2.08081928
## 78:      a -0.35920889
## 79:      a -0.45932217
## 80:      a  0.20181947
## 81:      a  0.62401138
## 82:      a -0.25722981
## 83:      a  0.94414021
## 84:      a  0.25074808
## 85:      a -0.72784257
## 86:      a  0.36881323
## 87:      a  0.44415068
## 88:      a -1.00535422
## 89:      a -0.33152471
## 90:      a -0.37039325
## 91:      a -0.79701529
## 92:      a  0.28148559
## 93:      a  0.33307250
## 94:      a  0.52690325
## 95:      a -0.78168949
## 96:      a -0.02793948
## 97:      a -1.74492339
## 98:      a  0.65284209
## 99:      a -0.93830821
## 100:     a  0.62753159
##          x          y
```

```
DT1 <- data.table(x=c("a","a","b","dt1"), y=1:4)
DT2 <- data.table(x=c("a","b","dt2"), z=5:7)
setkey(DT1,x); setkey(DT2,x)
merge(DT1,DT2) # uses keys to merge
```

```
## Key: <x>
##      x      y      z
##   <char> <int> <int>
## 1:     a      1      5
## 2:     a      2      5
## 3:     b      3      6
```

```
# fast reading in data.table
big_df <- data.frame(x=rnorm(1E6),y=rnorm(1E6))
file <- tempfile()
write.table(big_df, file=file, row.names=FALSE, col.names=TRUE, sep="\t", quote=FALSE)
system.time(fread(file)) # basically read.table for csv
```

```
##      user  system elapsed
##    0.08    0.00    0.08
```

```
system.time(read.table(file,header=TRUE,sep="\t"))
```

```
##      user  system elapsed
##    1.94    0.02    3.56
```

Cleaning Data

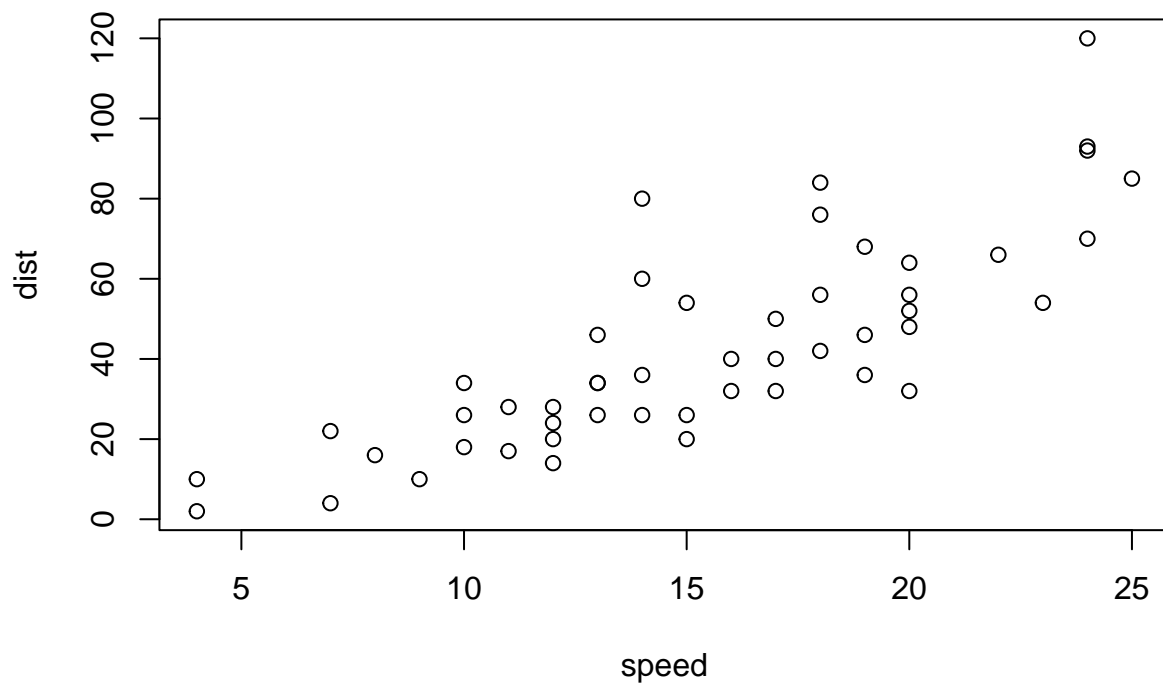
- End of process generate: raw data, tidy data set, code book (metadata) describing each variable and its values in the tidy data set, explicit and exact recipe used to convert raw data to tidy data set and code book.
- Raw Data: original source of data i.e. no processing, editing, summarizing. Must process for data analysis (merging, sub-setting, transforming, etc.), be mindful of processing standards. Colloquially may be later step i.e. genome seq but must use rawest.
- Processed Data: ready for analysis, steps to reach stage must be recorded. Must: one variable per column, each observation in a separate row, different tables for different types of variables, if multiple tables allow for linking. Useful: top row of variable names which are human readable, save one file per table.
- Code book: info about variables not contained in data incl. units called *Code book*, info about summary choices, info about experimental study design called *Study design*. Often word/text file.
- Instruction list: in a computer script where input is raw data and output is tidy data with no parameters to the script. If not possible, provide instructions in steps (incl. parameters, software versions, how to use software).

Graphics

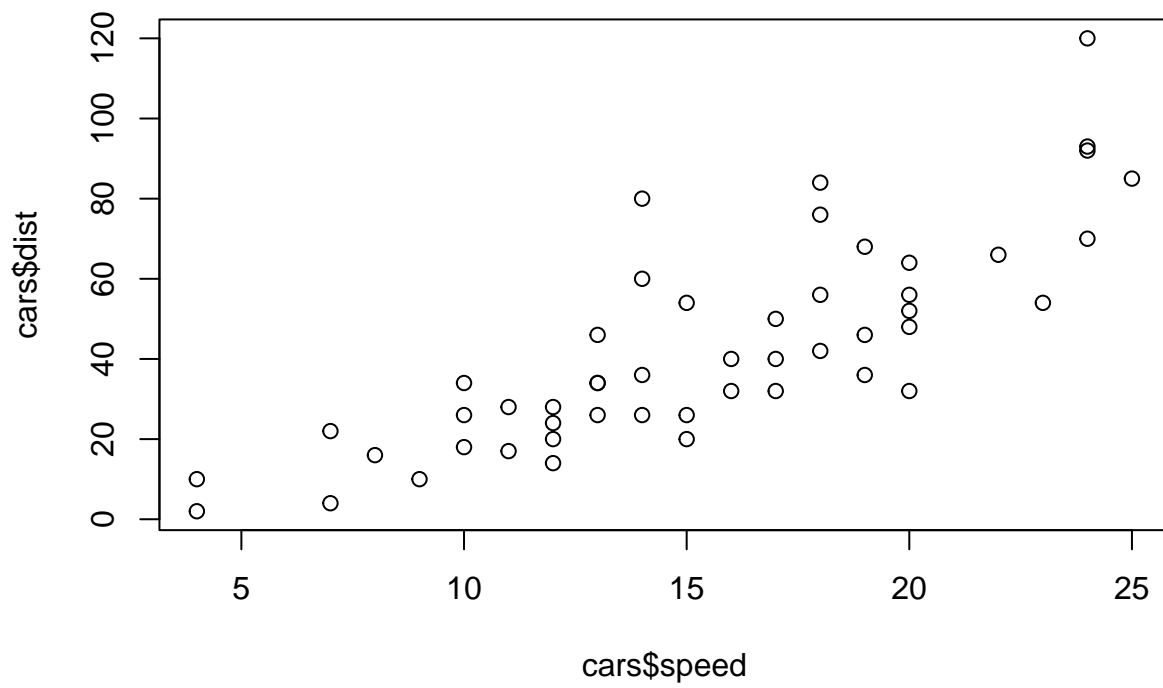
<http://www.ling.upenn.edu/~joseff/rstudy/week4.html>

```
# Start by getting sense of the data: dim(), names(), head(), tail() and summary().

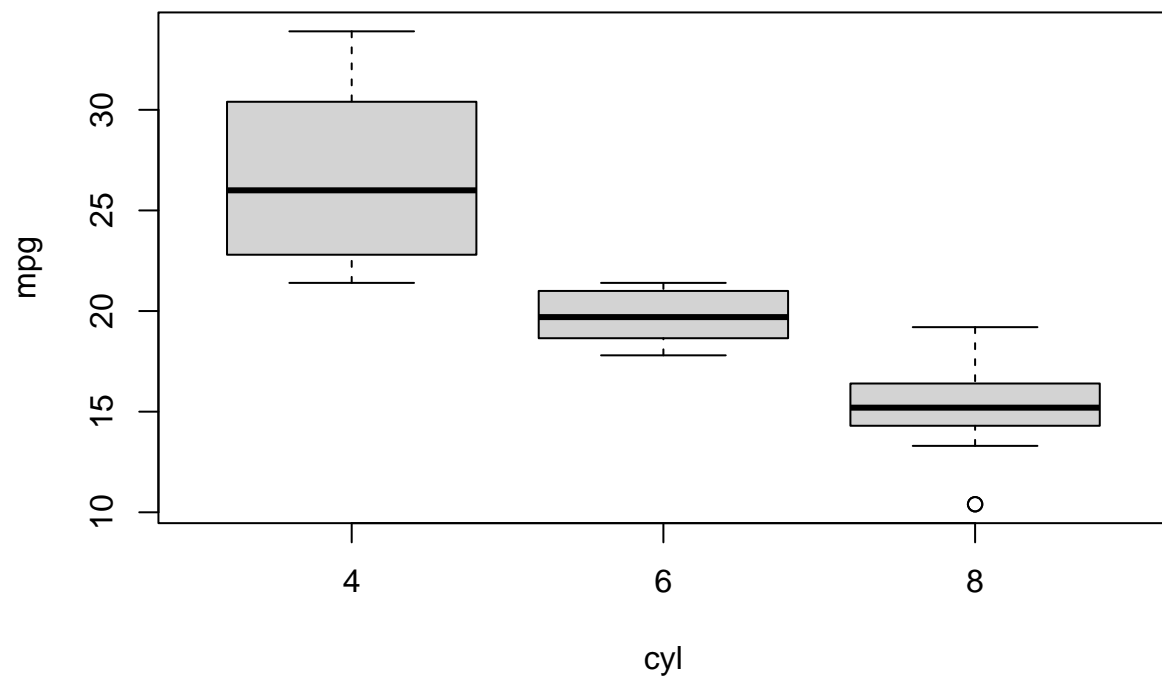
# Scatterplot
data(cars)
plot(cars) # generates scatterplot with two columns against each other
```



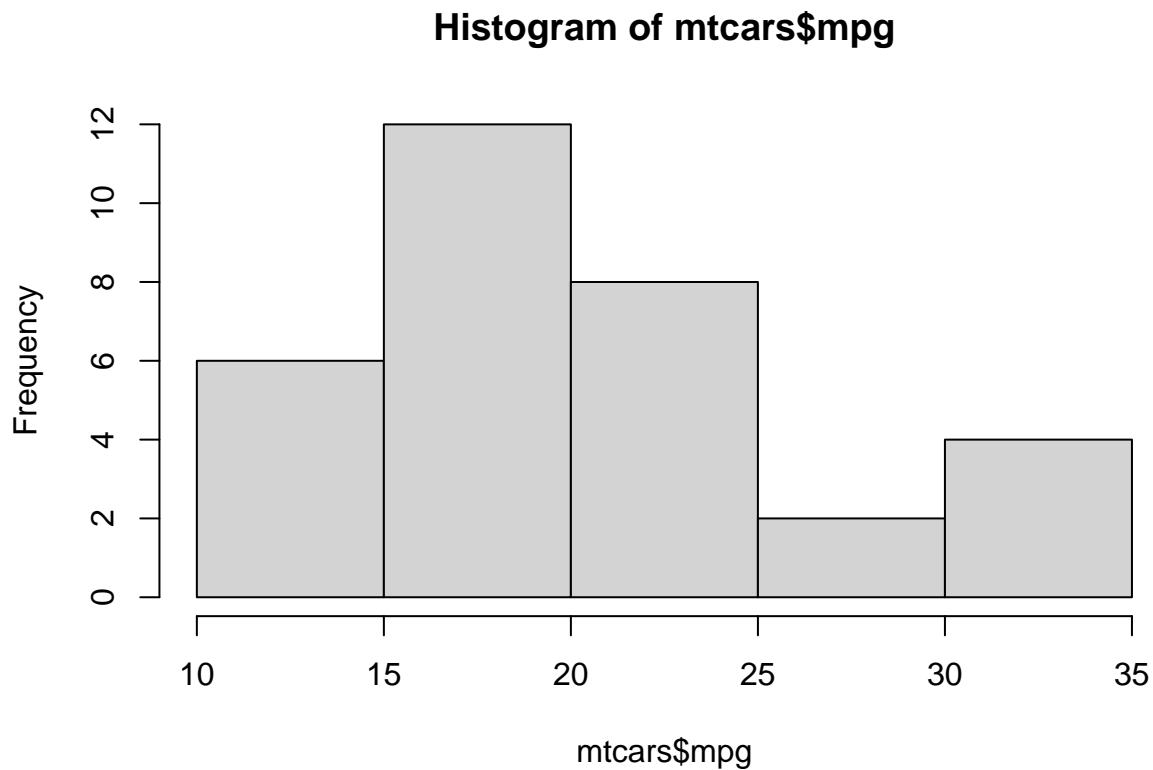
```
plot(x = cars$speed, y = cars$dist) # explicit, can also pass plot(dist ~ speed, cars). Args: x, y = NU
```

```
# Boxplot  
data(mtcars)  
boxplot(mpg ~ cyl, data = mtcars) # generate relationship between mpg(x) and cyl(y) from mtcars
```



```
# Histogram  
hist(mtcars$mpg) # generate a histogram of vector
```



R Profiler and Optimization

- Systematic way to examine time spent in various part of the program. Useful to optimize the code.
- DON'T PREMATURELY OPTIMIZE
- Measure, not guess, data on what needs to be optimized.
- User time: computer experienced, may be greater if multiple cores/processors (accessible in multi-threaded BLAS libraries). Elapsed time: wall-clock time, may be greater if other computing tasks.

```
system.time(read.csv("hw1_data.csv")) # returns seconds to execute, if error then seconds to error. Wrap
```

```
##      user  system elapsed
##         0         0         0
```

```
data(mtcars)
Rprof() # track function call stack at intervals (def = 0.02 sec), time spent in functions.

fit <- lm(mtcars$mpg ~ mtcars$cyl)

Rprof(NULL)

summaryRprof() # makes Rprof readable, tabulates, time in each function
```

```
## $by.self
## [1] self.time self.pct total.time total.pct
## <0 rows> (or 0-length row.names)
##
## $by.total
## [1] total.time total.pct self.time self.pct
## <0 rows> (or 0-length row.names)
##
## $sample.interval
## [1] 0.02
##
## $sampling.time
## [1] 0
```

```
# $by.total - divides time spent per function by total run time
```

```
# $by.self - same as by.total but first subtracts time spent in function above in call stack. Helps tar.
```