Rbootcamp/Workshop

Michael Kleinsasser

8/27/2019

Mike's Personal Introduction

- R programmer for the Department of Biostatistics
- Write and mantain R packages for faculty and students
- Consult faculty and students on writing R packages, optimization

Rbootcamp Introduction

Goals (roughly):

- Day 1: Setting up and using R interactively, syntax and data types, creating viewing and removing objects, on-line help, writing functions, how most statistical procedures are implemented in R
- Day 2: Non-interactive R and the cluster. How to write optimized code, including vectorization and loops, and introduction to data manipulation with dplyr, and visualization with ggplot2
- Day 3: Finally we combine our knowledge and apply it to a series of simulation problems

Materials

- All bootcamp materials online at https://github.com/umich-biostatistcs/Rbootcamp
  - Handouts with examples to work through
  - R scripts of our examples (.Rmd slides, .R scripts)
- Go to link and download zip archive, extract

Setup

Go to Rstudio cloud to follow along:

- Enter username, etc. for free account
- Follow along by typing commands in my slides
- If you have Rstudio/R, open that
- Recommended: Install R/Rstudio for days 2, 3
- See course materials for download instructions

R Basics: Big Picture

- R is a sophisticated calculator for statistics

Chambers (2016) Extending R:

- Everything that exists in R is an object
- Everything that happens in R is a function call

Obtain a basic working knowledge of R objects and functions,

- Google the rest!

R Basics: a basic schematic view

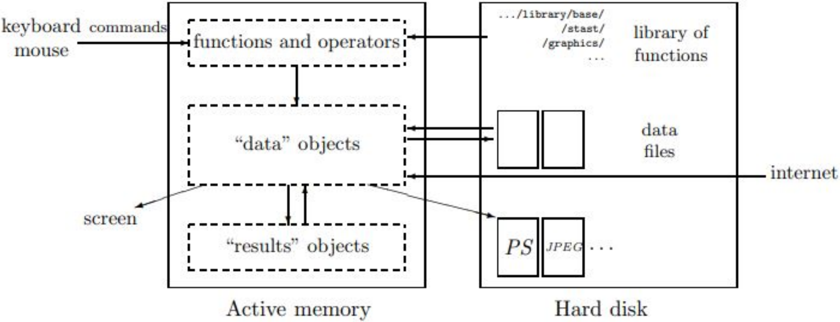


Figure 1: A schematic view of how R works.

R Basics: Goals

- Data types and functions
  - Create object having data types
  - Combine those into data structures
  - Write basic R function
- Learn parts of R most useful to statisticians
  - How do most modeling functions work in R, and
  - How to inspect structure and content of objects
  - Data manipulation and visualization
- Apply knowledge to simulation
  - Set up, draw from various distributions
  - Summarise, visualize

Ways to run R

Either "interactively" or "non-interactively"

- Interactive R:
- For line by line code execution
- Open the Rgui.exe or
- Open Rstudio.exe (recommended) - integrated developement environment for R

Non-interactively:

- For running entire scripts at once
- Desired for allocating large jobs on the cluster (return to later)

Use R as a calculator

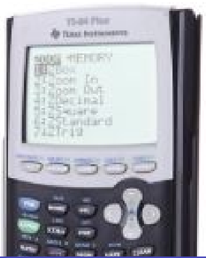
Standard operations:

```
# multiply *, divide /, add + subtract -
18056.983 - 1005.118 + 22.53
```

```
## [1] 17074.4
```

```
( (pi - 3.14) / (3.14) )  * 100
```

```
## [1] 0.05072145
```



Operators: arithmetic and logical

Operator	Description
+	addition
−	subtraction
/	division
^	exponential
%%	modulus (x mod y)
%/%	integer division

Table 1: Arithmetic Operators

Operator	Description
<	less than
<=	less than or equal
>	greater than
>=	greater than or equal
==	exactly equal to
!=	not equal to
!x	not x (x logical)
x|y	x OR y
x&y	x AND y
isTRUE(x)	is x TRUE

Table 2: Logical Operators

Operators: an example

Test if these two expressions are equivalent in R:

```r
A = c(TRUE, TRUE, FALSE); B = c(FALSE, FALSE, TRUE)
# Expression 1:
A | B

# Expression 2:
!(A == B)

# test equality:
all.equal(A | B, !(A == B))
```

Operators and vectorization

Arithmetic/logical operators are **vectorized**:

Given these vectors:

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

```
## [1]  4  8 16
```

```
x + y
```

```
## [1]  5 10 19
```

```
x * y
```

```
## [1]  4 16 48
```

```
y <= x
```

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

Create, list, delete objects

Create object with "assign" operator

- arrow then minus sign <-
- single equal sign =

```
# x gets the number 3.14
x <- 3.14
x      # print x
```

```
## [1] 3.14
```

```
# equivalently
x = 3.14
x      # print x
```

```
## [1] 3.14
```

Create, list, delete objects

Objects we create are stored in memory, e.g.:

```r
name = "Carmen"
n1 = 10
n2 = 100
m = 0.5
```

Use ls() function to list all objects in memory:

```r
ls()
```

```
## [1] "m"    "n1"   "n2"   "name" "x"    "y"
```

Notice: I created x before, it's still in memory.

Create, list, delete objects

Use ls() function to list all objects in memory:

```r
ls()
```

```
## [1] "m"    "n1"   "n2"   "name" "x"    "y"
```

The function ls.str() displays some details about objects in memory:

```r
ls.str()
```

```
## m :  num 0.5
## n1 :  num 10
## n2 :  num 100
## name :  chr "Carmen"
## x :  num 3.14
## y :  num [1:3] 4 8 16
```

Create, list, delete objects

To delete objects in memory, use rm() function

```
rm(x) # delets object named x
ls()  # which objects remain in memory?
```

```
## [1] "m"    "n1"   "n2"   "name" "y"
```

```
rm(m, n2, name) # remove multiple objects
ls()
```

```
## [1] "n1" "y"
```

```
rm(list = ls()) # remove everything from memory
ls()
```

```
## character(0)
```

The on-line help

R has structured help pages providing “how-to”

- **Description:** what function does
- **Usage:** name with arguments and options
- **Arguments:** how each argument should be structured
- **Details:** more detailed description
- **Value:** How the output is structured/ what it contains
- **Examples:** examples of the function in use

```r
?rm             # help documentation for rm function
help("rm")      # alternately
```

The on-line help

remove {base} R Documentation

Remove Objects from a Specified Environment

Description

`remove` and `rm` can be used to remove objects. These can be specified successively as character strings, or in the character vector `list`, or through a combination of both. All objects thus specified will be removed.

If `envir` is NULL then the currently active environment is searched first.

If `inherits` is `TRUE` then parents of the supplied directory are searched until a variable with the given name is encountered. A warning is printed for each variable that is not found.

Usage

```
remove(..., list = character(), pos = -1,
       envir = as.environment(pos), inherits = FALSE)

rm    (..., list = character(), pos = -1,
       envir = as.environment(pos), inherits = FALSE)
```

Other R help

Many package writers create Vignettes and READMEs

How to view vignettes?

```
vignette(all = TRUE) # list vignettes for installed packages
vignette(all = FALSE)  # vignettes from attached packages
```

How to view READMEs?

Other help. . .

Objects in R

Objects (data, model output, functions)

- Characterized by their **names** and **content**
- attributes - specify the kind of data represented
    - e.g. mode, length

```
x = 25
mode(x)
```

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

```
length(x)
```

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

Basic data "modes" in R

The mode is the basic type of the elements of an object

The four main modes:

- numeric, comes in two flavors: integer, numeric
- character
- logical
- complex

```
num = 15.533; name = "Mike"; isStudent = TRUE
```

```
mode(num); mode(name); mode(isStudent)
```

```
## [1] "numeric"

## [1] "character"

## [1] "logical"
```

Atomic vectors

Fundamental data structure in R:

- atomic vector - vector in which every element is of same mode

To create an atomic vector, use c() function:

```
c(3.145, 2.18, 9.98e3, 0.05)
```

```
## [1]    3.145    2.180 9980.000    0.050
```

Example: create empty character vector of length 3 and story your full name

```
vector(mode = "character", length = 3)
```

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

Data types examples

3 ways to create numeric vector:

```r
# empty numeric vector
y1 <- numeric(6)
y1      # print y1
```

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

```r
y2 <- vector(mode = "numeric", length = 6)
y2      # print y2
```

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

```r
y3 <- c(5, 13.222, 2, 0.001, 77.4, 31.9)
y3      # print y3
```

```
## [1]  5.000 13.222  2.000  0.001 77.400 31.900
```

Objects in R: NA

NA means "Not Available" and it denotes missing data

```
c(3, 5, 9, NA, 18, 25, NA)
```

```
## [1]  3  5  9 NA 18 25 NA
```

Example: Store the vector above and remove the missing values.

```
#incomplete.data =
#complete.data = incomplete.data[complete.cases(incomplete.data)]
```

R data types/structures

Four fundamental data types:

- character, numeric (numeric or integer), logical, complex

Combine to form data structures

- atomic vector (atomic - vector of single type)
- list
- matrix
- data.frame
- factor

We will focus on matrices and data.frames

Matrices

Matrices are the natural extension of atomic vectors into 2 dimensions

- any mode can be used, but numeric most common:

Syntax:

```
m = matrix(data, nrow, ncol, byrow, dimnames)
```

- **data** is the input vector which becomes the data elements of the matrix
- **nrow, ncol** is the number of rows/columns to be created
- **byrow** is T/F. If TRUE then the input vector elements are arranged by row
- **dimnames** is the names assigned to the rows and columns

Matrix examples:

Identity matrix:

```
dat = c(1,0,0,0,1,0,0,0,1)  # data
iden = matrix(data = dat, nrow = 3, byrow = T)
iden  # print matrix
```

```
##       [,1] [,2] [,3]
## [1,]    1    0    0
## [2,]    0    1    0
## [3,]    0    0    1
```

Easier:

```
iden = diag(rep(1,3))
iden
```

access elements of a matrix

- single brackets used to access elements

Access individual elements:

```r
# 2x5 matrix of numbers 1 to 10
P = matrix(data = 1:10, nrow = 2)
P[1,3] # row 1, column 3
```

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

```r
P[nrow(P),ncol(P)] # row 2, column 5 (bottom right position)
```

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

Access entire rows/columns:

```r
P[,3];
```

```
## [1] 5 6
```

The data.frame

The **data.frame** is the most common way to store and work with data in R

- Not surprising: they are designed for this purpose
- Most modeling functions work on data.frames

Composed of a list of equal length atomic vectors (can be of any type)

Exercise:

The following are data on students in the class:

- Has Master's (logical): TRUE FALSE FALSE TRUE
- GPA (numeric): 3.1 4.0 2.9 3.6
- First Name (character): Mike Dan Sara Karen

Convert to three atomic vectors of appropriate type.

```
#insert solution
```

data.frame examples

Create a data.frame out of the following “class” data:

- Has Master’s (logical): TRUE FALSE FALSE TRUE
- GPA (numeric): 3.1 4.0 2.9 3.6
- First Name (character): Mike Dan Sara Karen

```r
# store data
has_ms <- c(TRUE, FALSE, FALSE, TRUE)
gpa <- c(3.1, 4.0, 2.9, 3.6)
name <- c("Mike", "Dan", "Sara", "Karen")
# Create data.frame
dat <- data.frame(has_MS = has_ms, GPA = gpa, Name = name)
dat    # print data.frame
```

```
##   has_MS GPA  Name
## 1   TRUE 3.1  Mike
## 2  FALSE 4.0   Dan
## 3  FALSE 2.9  Sara
## 4   TRUE 3.6 Karen
```

access elements of a data.frame

Each vector of a data.frame contains the values of a variable

Access each vector with the dollar sign $

Ex: Extract the GPA column and print it

```
dat$GPA
```

```
## [1] 3.1 4.0 2.9 3.6
```

Another example: ToothGrowth data.

```
ToothGrowth$len
```

Exercise: Add a new column to the data.frame dat with NAs

```
# Hint: = NA will recycle NA to the appropriate length
```

Preview data.frame

Preview head (first few rows) of data.frame:

```
head(ToothGrowth)
```

```
##    len supp dose
## 1  4.2   VC  0.5
## 2 11.5   VC  0.5
## 3  7.3   VC  0.5
## 4  5.8   VC  0.5
## 5  6.4   VC  0.5
## 6 10.0   VC  0.5
```

View tail of data.frame:

```
tail(dat)
```

View entire data.frame in new window:

```
View(ToothGrowth)
```

Inspect an object

- class() - what kind of object is it (high-level)?
- typeof() - what is the data type (low-level)?
- length() - how long is it?
- attributes() - does it have meta-data?

Inspect an object

- class() - what kind of object is it (high-level)?

```
class(ToothGrowth)
```

```
## [1] "data.frame"
```

- typeof() - what is the data type (low-level)?

```
typeof(ToothGrowth$supp)
```

```
## [1] "integer"
```

Inspect an object

- length() - how long is it?

```
length(ToothGrowth$dose)
```

```
## [1] 60
```

- attributes() - does it have meta-data?

```
attributes(ToothGrowth)
```

```
## $names
## [1] "len"  "supp" "dose"
##
## $class
## [1] "data.frame"
##
## $row.names
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18
```

R functions

R function syntax:

NAME <- function(ARG1, ARG2, ARG3) {
    DO SOMETHING
    STORE RESULT
    return(RESULT)
}

```r
pow <- function(base, expon) { # power function
  prod(rep(base, expon)) # base^(expon)
}
# Use power function
pow(5, 2)
```

```
## [1] 25
```

```r
pow(10, 3)
```

```
## [1] 1000
```

R functions:

R function syntax:

NAME <- function(ARG1, ARG2, ARG3) {
    DO SOMETHING
    STORE RESULT
    return(RESULT)
}

Exercise: Write a function that calls the pow() function and returns a list of base taken to the powers 2, 4, and 8.

```
# Hint: create list with list(pow2 = , pow4 = , pow8 = )
```

Common R functions

R has a huge collection of packages:

- 6,000+ packages for data analysis build (on CRAN alone)

Example: lm (linear models)

- Use ?lm to read help documentation

lm {stats} R Documentation

Fitting Linear Models

Description

`lm` is used to fit linear models. It can be used to carry out regression, single stratum analysis of variance and analysis of covariance (although `aov` may provide a more convenient interface for these).

Usage

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

Arguments

`formula`	an object of class "`formula`" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
`data`	an optional data frame, list or environment (or object coercible by `as.data.frame` to a data frame) containing the variables in the model. If not found in `data`, the variables are taken from `environment(formula)`, typically the environment from which `lm` is called.

Fit a linear model with lm

- Use built-in data set ToothGrowth
- ?ToothGrowth for help:

The Effect of Vitamin C on Tooth Growth in Guinea Pigs

Description

The response is the length of odontoblasts (cells responsible for tooth growth) in 60 guinea pigs. Each animal received one of three dose levels of vitamin C (0.5, 1, and 2 mg/day) by one of two delivery methods, orange juice or ascorbic acid (a form of vitamin C and coded as `VC`).

Usage

```
ToothGrowth
```

Format

A data frame with 60 observations on 3 variables.

[,1]	len	numeric	Tooth length
[,2]	supp	factor	Supplement type (VC or OJ).
[,3]	dose	numeric	Dose in milligrams/day

View the data

View data in new window:

```
View(ToothGrowth)
```

Or use head to view only first 6 rows:

```
head(ToothGrowth)
```

```
##    len supp dose
## 1  4.2   VC  0.5
## 2 11.5   VC  0.5
## 3  7.3   VC  0.5
## 4  5.8   VC  0.5
## 5  6.4   VC  0.5
## 6 10.0   VC  0.5
```

How big is the data?

```
dim(ToothGrowth)
```

```
## [1] 60  3
```

Using lm() function for linear models

Call lm on the data and formula, store result "lm" object:

```
tooth_fit = lm(formula = len ~ supp + dose,
               data = ToothGrowth)
```

Formulas in R:

```
len ~       # Response column name, ~ for "="
  supp +    # First predictor name + for "+"
  dose      # second predictor name
```

Many R functions use the formula argument.

Getting detailed information

Basic "print" of model:

```r
print(tooth_fit)     # equivalent to tooth_fit
```

```
##
## Call:
## lm(formula = len ~ supp + dose, data = ToothGrowth)
##
## Coefficients:
## (Intercept)       suppVC         dose
##       9.272       -3.700        9.764
```

Detailed summary:

```r
summary(tooth_fit)
```

```
##
## Call:
## lm(formula = len ~ supp + dose, data = ToothGrowth)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.600 -3.700  0.373  2.116  8.800
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   9.2725     1.2824   7.231 1.31e-09 ***
## suppVC       -3.7000     1.0936  -3.383   0.0013 **
## dose          9.7636     0.8768  11.135 6.31e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

Understanding R classes

- What is this thing?

```
class(tooth_fit)
```

- What are the methods for this object?

```
methods(class = "lm")
```

- What is its structure? (i.e., what's in it)

```
str(tooth_fit)
```

Understanding R classes

- What is this thing?

```r
class(tooth_fit)
```

```
## [1] "lm"
```

Understanding R classes

- What are the methods for this object?

```
methods(class = "lm")
```

```
##  [1] add1           alias          anova          case.names
##  [5] coerce         confint        cooks.distance deviance
##  [9] dfbeta         dfbetas        drop1          dummy.coef
## [13] effects        extractAIC     family         formula
## [17] hatvalues      influence      initialize     kappa
## [21] labels         logLik         model.frame    model.matrix
## [25] nobs           plot           predict        print
## [29] proj           qr             residuals      rstandard
## [33] rstudent       show           simulate       slotsFromS3
## [37] summary        variable.names vcov
## see '?methods' for accessing help and source code
```

Understanding R classes

- What is its structure? (i.e., what's in it)

```
str(tooth_fit)
```

```
## List of 13
##  $ coefficients : Named num [1:3] 9.27 -3.7 9.76
##   ..- attr(*, "names")= chr [1:3] "(Intercept)" "suppVC" "dose"
##  $ residuals    : Named num [1:60] -6.25 1.05 -3.15 -4.65 -4.05 ...
##   ..- attr(*, "names")= chr [1:60] "1" "2" "3" "4" ...
##  $ effects      : Named num [1:60] -145.73 14.33 47.16 -3.86 -3.26 ...
##   ..- attr(*, "names")= chr [1:60] "(Intercept)" "suppVC" "dose" "" ...
##  $ rank         : int 3
##  $ fitted.values: Named num [1:60] 10.5 10.5 10.5 10.5 10.5 ...
##   ..- attr(*, "names")= chr [1:60] "1" "2" "3" "4" ...
##  $ assign       : int [1:3] 0 1 2
##  $ qr           :List of 5
##   ..$ qr   : num [1:60, 1:3] -7.746 0.129 0.129 0.129 0.129 ...
##   .. ..- attr(*, "dimnames")=List of 2
##   .. .. ..$ : chr [1:60] "1" "2" "3" "4" ...
##   .. .. ..$ : chr [1:3] "(Intercept)" "suppVC" "dose"
##   .. ..- attr(*, "assign")= int [1:3] 0 1 2
##   .. ..- attr(*, "contrasts")=List of 1
##   .. .. ..$ supp: chr "contr.treatment"
##   ..$ qraux: num [1:3] 1.13 1.11 1.11
##   ..$ pivot: int [1:3] 1 2 3
##   ..$ tol  : num 1e-07
##   ..$ rank : int 3
##   ..- attr(*, "class")= chr "qr"
##  $ df.residual  : int 57
##  $ contrasts    :List of 1
##   ..$ supp: chr "contr.treatment"
##  $ xlevels      :List of 1
```

Understanding R classes

- Pull something out of the "lm" fit object:

```
tooth_fit$fitted.values        # y_hat's for the linear model
```

```
##        1        2        3        4        5        6        7        8
## 10.45429 10.45429 10.45429 10.45429 10.45429 10.45429 10.45429 10.45429
##        9       10       11       12       13       14       15       16
## 10.45429 10.45429 15.33607 15.33607 15.33607 15.33607 15.33607 15.33607
##       17       18       19       20       21       22       23       24
## 15.33607 15.33607 15.33607 15.33607 25.09964 25.09964 25.09964 25.09964
##       25       26       27       28       29       30       31       32
## 25.09964 25.09964 25.09964 25.09964 25.09964 25.09964 14.15429 14.15429
##       33       34       35       36       37       38       39       40
## 14.15429 14.15429 14.15429 14.15429 14.15429 14.15429 14.15429 14.15429
##       41       42       43       44       45       46       47       48
## 19.03607 19.03607 19.03607 19.03607 19.03607 19.03607 19.03607 19.03607
##       49       50       51       52       53       54       55       56
## 19.03607 19.03607 28.79964 28.79964 28.79964 28.79964 28.79964 28.79964
##       57       58       59       60
## 28.79964 28.79964 28.79964 28.79964
```

Extracting data from model objects

Some generic extraction methods:

```
coef(tooth_fit)              # model coefficients

coef(summary(tooth_fit))     # adds test statistics, p-values

vcov(tooth_fit)              # variance/covariance matrix
```

Note: depending on implementation, these may not be available - Check methods with “methods(object)” before attempting

Extracting data from model objects (in detail)

Extract coefficients, test stats, and p-values

```
coef(summary(tooth_fit))   # adds test statistics, p-values
```

```
##              Estimate Std. Error   t value     Pr(>|t|)
## (Intercept)  9.272500  1.2823649  7.230781 1.312335e-09
## suppVC      -3.700000  1.0936045 -3.383307 1.300662e-03
## dose         9.763571  0.8768343 11.135025 6.313519e-16
```

Predict new values

- predict() function is generic and works with many models
- Pass in a new data.frame with the same column names:

```
to_predict = data.frame(dose = 0.5, supp = "VC")
```

```
predict(tooth_fit, newdata = to_predict)
```

```
##        1
## 10.45429
```

Predict new values (example 2)

- predict() function is generic and works with many models
- Pass in a new data.frame with the same column names:

```
to_predict = data.frame(dose = seq(0,1,0.1), supp = "OJ")
```

```
predict(tooth_fit, newdata = to_predict)
```

```
##        1        2        3        4        5        6        7 
##  9.27250 10.24886 11.22521 12.20157 13.17793 14.15429 15.13064 16
##        9       10       11
## 17.08336 18.05971 19.03607
```

Day 2

- Non-interactive R and the cluster (Instructed by Dan Barker)
- How to write optimized code, including vectorization and loops, and
- introduction to data manipulation with dplyr, and visualization with ggplot2

Packages to install for today

Run the following chunk to install packages:

```r
install.packages("tidyverse")
```

Load into memory:

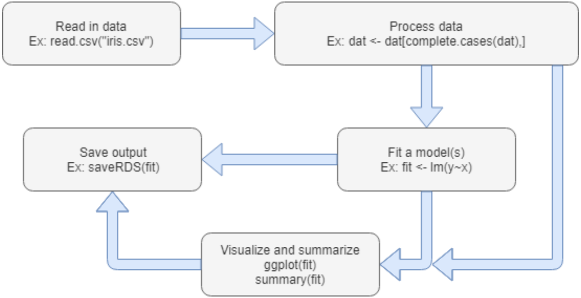
```r
library(tidyverse) # actually a set of packages
```

R on cluster (non-interactive R)

Cluster Computation

- Dan Barker danbarke at umich.edu
- Cluster System Administrator

Basic workflow for statistical analysis



What is the tidyverse?

- collection of (very useful) R packages for doing “data science”
- ggplot2 - for plotting, visualizing data
- dplyr - for data manipulation/processing
- tidyr, readr (read data), purrr (better loops), tibble (improved data.frame), stringr, forcats
- Learn: R for Data Science, Grolemund and Wickham (free online)

Advanced control structures

Common misconception: "loops in R are slow"

- Many commenters say loops in R are a bad idea,
- But, sometimes difficult (or impossible) to write vectorized code, or vectorized code consumes too much memory.

- We discuss:
  - How to improve loops when they are necessary
  - Eliminate them when possible

Loops: often not necessary

- Many R functions are "vectorized" (vector in, vector out)
- While most other languages require loops, R does not:

```
a = c(5, 2, 4, 12, 1)
b = c(2, 0, 3, -1, 2)

a + b      # vector + vector = vector
```

```
## [1]  7  2  7 11  3
```

Takehome: When possible, operate on vectors and matrices, don't loop over each row/position index

Problem: not all functions are vectorized

- Some functions, like read.table() for reading a table of data into R, are not vectorized
- But what if we have a list of files to read in? "data1.txt", "data2.txt", "data3.txt", . . . , "data50.txt"

```
  # the 50 data set names
file_names = paste0("data", 1:50, ".txt")
```

Attempt it, will cause error:

```
read.table(file_names)  # error!
```

map() from purrr package to avoid loop

- map() allows you to apply a function to each element of a vector
- faster, easier to read than a loop

```
read.table(file_names)  # error!
```

```
    # list of 50 data sets
my_dat_list = map(file_names, read.table)
    # results from reading data1.txt
my_dat_list[[1]]
    # results from reading data50.txt
my_dat_list[[50]]
```

Create your own functions for map

Generate random samples from a Normal with different variances

```
draws = map(2:20, function(x) rnorm(25, mean=0, sd=x))
# returns a list with vectors of draws
str(draws)
# first vector of draws:
draws[[1]]

# last vector of draws:
draws[[19]]
```

Create your own functions for map

Now, estimate the standard error:

```r
map(draws, sd)  # sd() is standard deviation in R

map_dbl(draws, sd) # numeric vector
```

For loop vs map() version

- Standard for loop:

```
sdvs = 2:20; result.list = list(length = 19)
for (i in 1:19) {
  result.list[[i]] = rnorm(25, mean=0, sd=sdvs[i])
}
```

- map():

```
map(2:20, function(x) rnorm(25, mean=0, sd=x))
```

Advice: If you're tracking indexes (like with the for loop), consider re-writing so you no longer have to depend on correct indexing

Sometimes loops are required

Sometime you just need loops:

- Growth model, new values depend on previous values

```
N = 20
for (i in 2:30) {
  f = rpois(1, 0.15*N[i-1])    # births
  d = rbinom(1, N[i-1], 0.1)  # deaths
  N[i] = N[i-1] + f - d
}

plot(seq_along(N), N)
```

Execute the code to see our simulated growth curve

Problem: Growing objects is slow

```
N = 20
for (i in 2:30) {
  f = rpois(1, 0.15*N[i-1])    # births
  d = rbinom(1, N[i-1], 0.1)  # deaths
  N[i] = N[i-1] + f - d        # alive
}

plot(seq_along(N), N)
```

- Our growth model loop is slow because we are growing a vector at each iteration
- Solution pre-allocate vector (or any data type), then fill with loop

Efficient memory usage

Improved code:

```
# Pre-allocate to correct size
N = vector(mode = "numeric", length = 30)
N[1] = 20
for (i in 2:30) {
  f = rpois(1, 0.15*N[i-1])   # births
  d = rbinom(1, N[i-1], 0.1)  # deaths
  N[i] = N[i-1] + f - d       # alive
}

plot(seq_along(N), N)
```

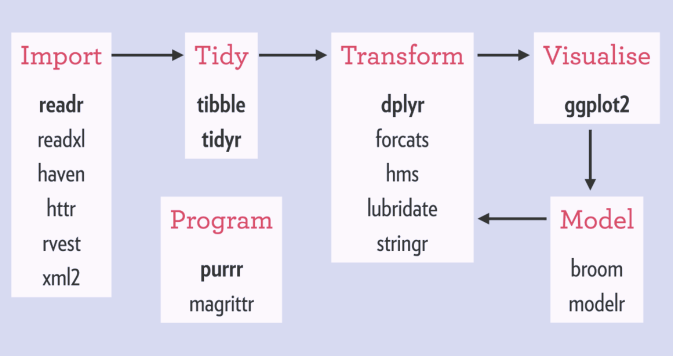
- In this simple example, does not make a difference
- With real-world, it will make a difference

overview of loops

- Do not do things inside a loop that can be done outside
- Use vectorized functions whenever possible
- Map when function is not vectorized
    - Avoids the need to track indexes
    - Does the pre-allocation for you
- If you use loops, avoid growing lists/collections/data.frames
    - pre-allocate memory

tidyverse

Brief introduction to programming with tidyverse



dplyr

Motivation:

- Analysts spend a lot of time manipulating and summarizing data
- Base R provides many functions for this, BUT:
  - the syntax is ugly
  - the functions can be slow/inefficient
- dplyr exists to make data manipulation easy to follow/correct/fast

Install and load dplyr

- ggplot is included in the tidyverse package. To load the tidyverse package, run

```
library(tidyverse)
```

- If you get the message “there is no package ‘tidyverse’ ” you must install it first:

```
install.packages("tidyverse")
library(tidyverse) # now load the tidyverse package
```

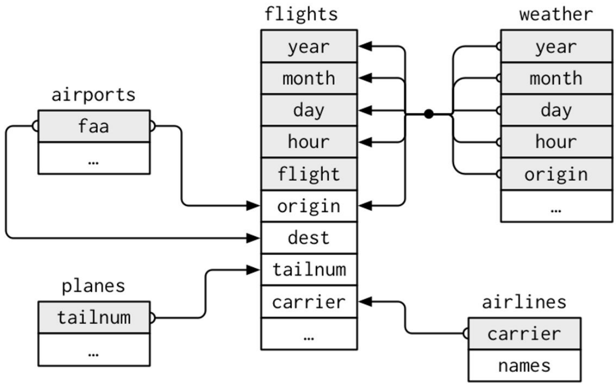
Sample data set

- We will be using a data set containing all out-bound flights from NYC in 2013
- Available as an R package

```r
#install.packages("nycflights13")
library(nycflights13)
#View(flights)
```

nycflights13 tables

Multiple data sets in this "package" of data related to the NYCflights:



"flights" table

Preview the flights data:

```
## # A tibble: 336,776 x 19
##     year month   day dep_time sched_dep_time dep_delay arr_time
##    <int> <int> <int>    <int>          <int>     <dbl>    <int>
##  1  2013     1     1      517            515         2      830
##  2  2013     1     1      533            529         4      850
##  3  2013     1     1      542            540         2      923
##  4  2013     1     1      544            545        -1     1004
##  5  2013     1     1      554            600        -6      812
##  6  2013     1     1      554            558        -4      740
##  7  2013     1     1      555            600        -5      913
##  8  2013     1     1      557            600        -3      709
##  9  2013     1     1      557            600        -3      838
## 10  2013     1     1      558            600        -2      753
## # ... with 336,766 more rows, and 12 more variables: sched_arr_time <int>,
## #   arr_delay <dbl>, carrier <chr>, flight <int>, tailnum <chr>,
## #   origin <chr>, dest <chr>, air_time <dbl>, distance <dbl>, hour <dbl>,
## #   minute <dbl>, time_hour <dttm>
```

dplyr verbs

dplyr provides a cogent, systematic way to carry out most data manipulation tasks:

These functions, called "verbs" are:

- filter() - keep rows matching desired properties
- select() - choose which columns you want to extract
- arrange() - sort rows
- mutate() - create new columns
- summarize() - collapse rows into summaries
- group_by() - operate on subsets of rows at a time

dplyr verb properties

- Always take data set as the first parameter
- Returns a new data object, never updates/replaces original
- Specify columns as unquotes strings (symbols)
- use “pipes” (%>%) to pass result of one call on to the next
    - %>% operator passes the result of the left side to the first arg. on right
    - a(b(c(x))) equals x %>% c() %>% b() %>% a()

Example:

```
flights %>%                     # data
  filter(carrier == "AA")       # apply verb
```

Filtering rows

- Find all flights to Detroit (DTW) in June (2013)
- Use filter() to complete the task

```
flights %>%                              # data
  filter(carrier == "AA" & month == 6)    # filter DTW as dest.
```

Equivalently:

```
flights %>%                              # data
  filter(carrier == "AA") %>%   # filter DTW as dest.
  filter(month == 6)            # On the DTW data, filter only
```

Selecting columns

- To select specific columns, send a comma separated list of unquoted names

Select specific columns:

```
flights %>%
  select(dep_time, arr_time, carrier)
```

Exclude specific columns:

```
flights %>%
  select(-year, -tailnum)
```

Select range of columns:

```
flights %>%
  select(month:dep_delay)
```

Selecting columns: Part 2

```
flights %>% select(starts_with("d"))

flights %>% select(ends_with("time"))

flights %>% select(contains("arr"))

flights %>% select(-starts_with("d"))
```

See “?select” for complete list and examples

Sort data

- Use arrange() to sort your rows

```
flights %>% arrange(sched_dep_time)
```

- Use desc() to reverse the sort order of a column

```
flights %>% arrange(month, desc(day))
```

- You can sort on functions of variables

```
flights %>% arrange(desc(dep_time-sched_dep_time))
```

Create new variables

- Mutate allows you to create columns using existing values

```
flights %>%
  mutate(speed = distance/(air_time/60)) %>%
  arrange(desc(speed)) %>%
  select(flight, speed)
```

- Remember, changes are not saved to “flights”, be sure to save the result if you want to use it later

```
new_flights <- flights %>% mutate(...)
```

Use new variables right away

- The parameters to mutate are processed in the order they appear
    - You can use new variables right away

```
flights %>%
  mutate( dist_km = distance * 1.61,
          hours = air_time / 60,
          kph = dist_km/hours ) %>%
  select(flight, kph)
```

- Be careful! You can overwrite existing variables

Summarize data

- You generally use summarize() to reduce the number of rows in your data by specifying summary functions for each of the columns

```
flights %>%
  filter(!is.na(arr_delay)) %>%
  summarize(avg_arr_delay = mean(arr_delay))
```

- Most useful summary functions:
  - mean(), median(), var(), sd(), min(), max(), first(), last(), n(), n_distinct()

Summarize data

- Most useful summary functions:
  - mean(), median(), var(), sd(), min(), max(), first(), last(), n(), n_distinct()
- exercise: create one statement to calculate the mean and standard deviation for the departure delay (dep_delay()) column

Grouping data

- Often you want to perform summaries for groups of rows at a time
- group_by() function allow you to specify columns that define groups
- Functions like mutate() and summarize() are then performed for each group

group_by() + summarize() example

- Find the average arrival delay for each carrier, where all the missings are removed from arr_delay

```
flights %>%
  filter(!is.na(arr_delay)) %>%
  group_by(carrier) %>%
  summarize(avg_arr_delay = mean(arr_delay))
```

- Exercise: Improve the summary above to only include airlines with a negative mean arrival delay, i.e. the flights are early, on average

Some special shortcuts

- count()
  - count number of rows with unique values of selected columns

```
flights %>% count(carrier)
```

- summarize_all()/mutate_all()
  - apply function to all columns

```
flights %>%
  summarize_all(mean, na.rm=T)
```

- summarize_at()/mutate_at()
  - apply function to chosen columns

```
flights %>%
  summarize_at(vars(ends_with("time")), mean, na.rm=T)
```

Summarization exercises

- What month received the most number of flights to your home/favorite airport?
- What is the average airspeed for all flights?
- What was the average departure delay (for flights that actually had a departure)?
- What was the longest delay for each carrier (which carrier had the longest delay for a single flight)?

Combining data frames

- bind_rows()
  - Stack two data frames on top of each other (should have the same number of columns)
- bind_columns()
  - Place two data frames next to each other (should have the same number of rows) – no merge-able columns
- intersect(), union(), setdiff()
  - For rows shared or exclusive to data frames

ggplot2

- Even though the package is sometimes just referred to as “ggplot”, the package name is “ggplot2”
- ggplot is included in the tidyverse package. To load the tidyverse package, run

```
library(tidyverse)
```

- If you get the message “there is no package ‘tidyverse’ ” you must install it first:

```
install.packages("tidyverse")
library(tidyverse) # now load the tidyverse package
```

ggplot2 help

- Use the R help with

```
?ggplot
```

- Use the website: http://ggplot2.tidyverse.org/reference/
- Read Hadley's book (ggplot2: Elegant graphics for data analysis)

Gapminder Data

- Dataset tracking life expectancy and per-capita GDP of 142 countries
- Data reported every five years from 1952-2007
- Data set is available in R package on CRAN:
    - install.packages("gapminder")

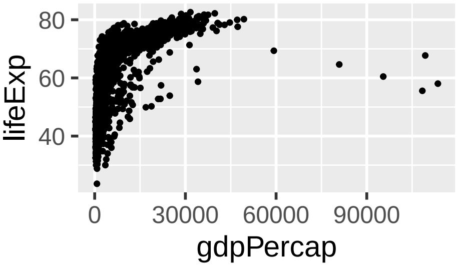
```
#install.packages("gapminder")
library(gapminder)
#View(gapminder)    # check out the data, scroll through it
```

Create scatterplot

- Interest in how life expectancy relates to GDP per capita
    - Does life expectancy increase with per capita GDP?

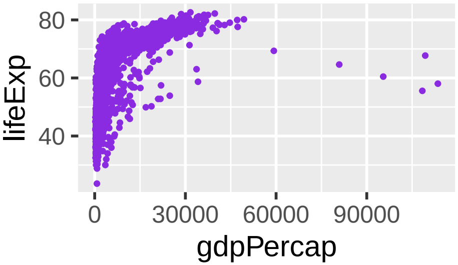
- Create a scatterplot of gdpPercap (Y-axis) vs lifeExp (X-axis)

```
ggplot(data = gapminder, aes(x=gdpPercap, y=lifeExp)) +
  geom_point(size = 0.5)
```



Add some color

```
ggplot(data = gapminder, aes(x=gdpPercap, y=lifeExp)) +
  geom_point(size = 0.5, color = "blueviolet")
```



- Check out the color names that R knows:

```
colors()
```

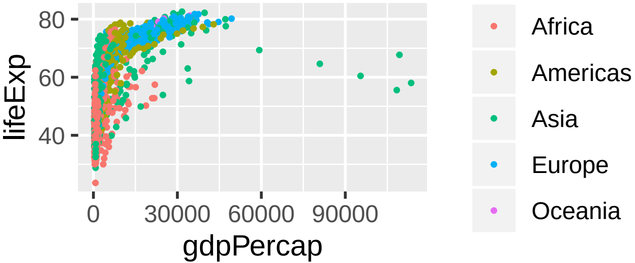
- Can also take HEX values, e.g. “#8A2BE2”

Color by the data

Incorporate color into the plot in a useful way:

- Color by continent to see trends by region of the world

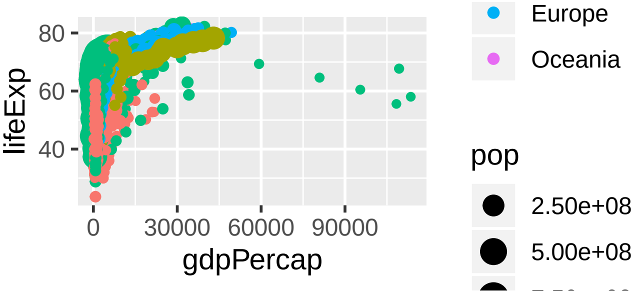
```
ggplot(data = gapminder, aes(x=gdpPercap, y=lifeExp, color = continent)) +
  geom_point(size = 0.5)
```



Scale point size by data

- Make countries with larger populations have larger dots
  - How big are the high GDP countries?

```r
ggplot(data = gapminder, aes(x=gdpPercap, y=lifeExp, color = continent, size = pop)) +
  geom_point()
```

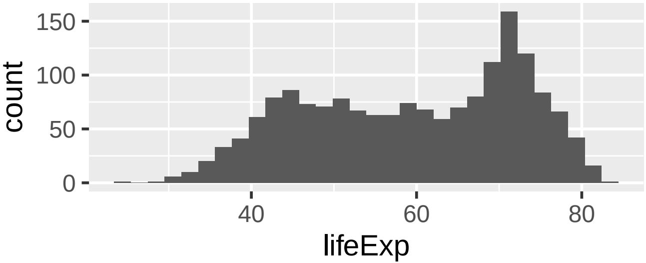


Geometries

- geom_point() is just one of many geometries:
  - Used to make scatter plots
  - Works best with two continuous variables
- What if we wanted to look at a distribution of a single continuous variable?

```
ggplot(data = gapminder, aes(x=lifeExp)) +
  geom_histogram()  # function for histograms
```

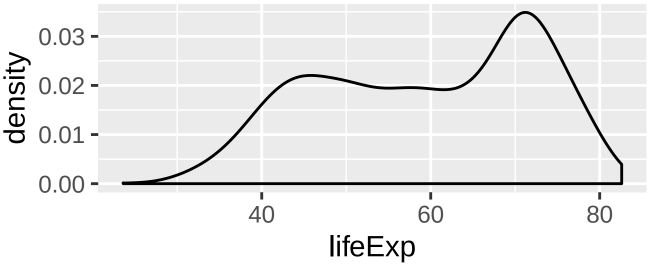
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Geometries

- geom_point() is just one of many geometries:
  - Used to make scatter plots
  - Works best with two continuous variables
- What if we wanted to look at a distribution of a single continuous variable?

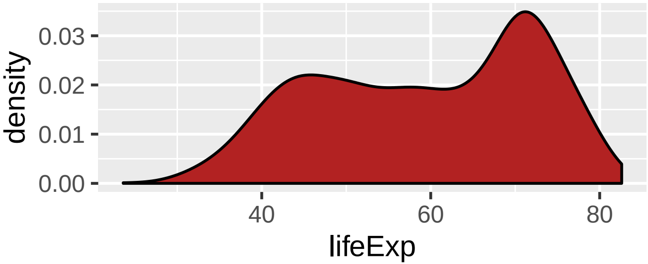
```
ggplot(data = gapminder, aes(x=lifeExp)) +
  geom_density()  # function for smoothed density
```



Density plot with custom aesthetics

- Add color fill

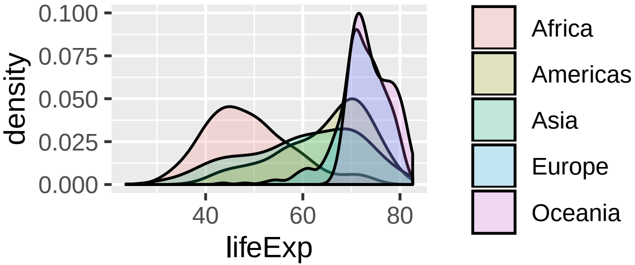
```
ggplot(data = gapminder, aes(x=lifeExp)) +
  geom_density(fill = "firebrick")  # function for smoothed density
```



Single variable across groups

- Plot density over life expectancies by continent
  - Fill contients with their own color to distinguish them

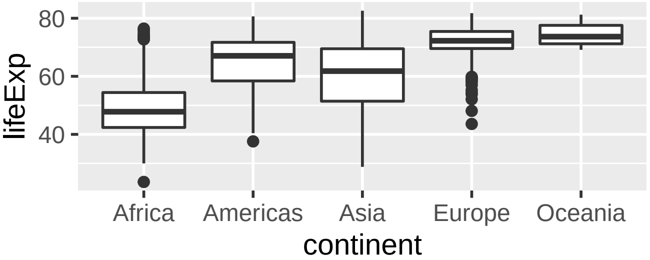
```
ggplot(data = gapminder, aes(x=lifeExp, fill = continent)) +
  geom_density(alpha = 0.2)  # function for smoothed density
```



Single variable across groups

- Another approach to the same problem:
  - Use boxplots to characterize differences across groups

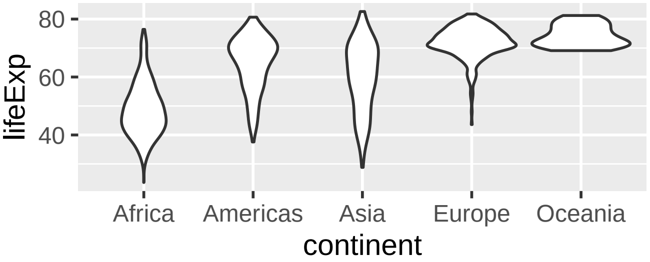
```r
# Notice how aes change
ggplot(data = gapminder, aes(x=continent, y = lifeExp)) +
  geom_boxplot()
```



Single variable across groups

- Violin plot:

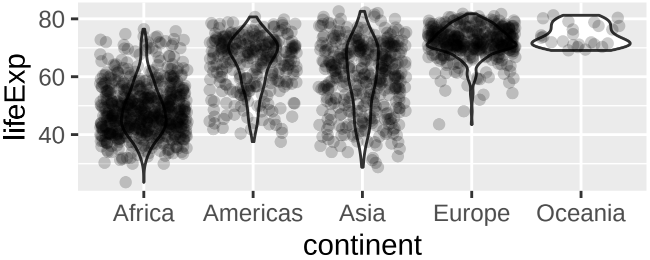
```
# Notice how aes change
ggplot(data = gapminder, aes(x=continent, y = lifeExp)) +
  geom_violin()
```



Stack geometries in layers

- How can we display the plot with data overlay?

```r
# Notice how aes change
ggplot(data = gapminder, aes(x=continent, y = lifeExp)) +
  geom_violin() +
  geom_jitter(alpha = 0.2)  # jitter the points
```



Day 3

If you were not present for Days 1 and 2

- Go to https://github.com/mkleinsa/Rbootcamp
- Click Clone or download
- Download .zip archive
- extract to desktop, open slides/slides.Rmd to follow along
- Cntrl + f search "Day 3" to find today's slides

Simulation Basics

Why simulate?

- confirm model/method works by mimicking the real world
- Get intuition before writing a proof
- *Closed form solution does not exist, only option to simulate

Challenge in figuring out how to model real world processes with numbers and variables

Note: randomness in R is pseudo-random. The default random number generator depends on a seed which is some initial starting value where random numbers grow from. Always set a seed.

Simulation Basics

- Often interested in expected values of random variables or probability of events occuring

- Through simulation, we don't calculate these values directly.

Instead:

1. Create a sample with the given constraints
2. From sample, calculate the mean over the random draws to estimate expected value, or, calculate an observed frequency to estimate the probability.

Simulation Basics

Sampling in R from sets:

- Use the sample() function to sample from a discrete set

Example - Simulate a coin toss experiment:

- toss a coin ten times, record what side it lands on each time

```
set.seed(7794)
sample(c("H","T"), size = 10, replace = TRUE) # fair coin
```

```
##  [1] "H" "H" "H" "H" "T" "T" "T" "T" "T" "H"
```

```
sample(c("H","T"), size = 10, replace = TRUE,
                               prob = c(0.6, 0.4)) # weighted coin
```

```
##  [1] "H" "H" "H" "T" "H" "T" "T" "H" "T" "H"
```

Simulation Basics

Sampling in R from distributions:

- d____(x) returns the density of a probability distribution for a discrete value of x
- p____(q) returns the cumulative density function (CDF) up to q
- q____(p) returns the quantile from a cumulative probability
- r____(n) returns a random deviate (a simulation of random draw) of size n

Example:

```
qnorm(0.025); dnorm(0)
```

```
## [1] -1.959964
```

```
## [1] 0.3989423
```

?distributions for more information

Simulation

distribution	function
Normal	norm(n, mean=0, sd=1)
exponential	exp(n, rate=1)
uniform	unif(n, min=0, max=1)
gamma	gamma(n, shape, scale=1)
poisson	pois(n, lambda)
Weibull	weibull(n, shape, scale=1)
Cauchy	cauchy(n, location=0, scale=1)
beta	beta(n, shape1, shape2)
Student t	t(n, df)
binomial	binom(n, size, prob)
logistic	logis(n, location=0, scale=1)

Table 3: Built-in distributions

Simulation: sample from probability distributions

```
rnorm(6) # 6 standard normal deviates
rnorm(10, mean=50, sd=19) # set mean and spread
runif(10, min=0, max=1) # uniform distribution
rpois(10, lambda=15) # Poisson
```

Cointoss reframed: toss coin 8 times using binomial distribution

```
set.seed(7794)
rbinom(8, size=1, p=0.5) # 8 coin tosses
```

Some simple simulations

Problem: predict the number of girls in 400 births in a population where prob. of female birth is 48.8%

```
#set.seed()
n.girls = rbinom(n=1, size=400, prob=0.488)
n.girls
```

```
## [1] 199
```

- Get a distribution of the number of female births when prob. $= 0.488$

```
n.sims=1000
n.girls=rbinom(n.sims,400,0.488)
hist(n.girls)
```

Some simple simulations

- Exercise: calculate the expected number of girls born.

```
# estimate expected value by computing the mean over all
# draws
sum(n.girls)/n.sims
```

- Does your estimate of the expected number of girls born make sense? Check:

```
# expected value of a binomial r.v. is n*p
n.sims*0.488
```

- Exercise: calculate the probability that the number of girls born will exceed half the total population size.

```
# estimate the probability by calculculating the desired
# frequency
sum(n.girls > 200)/n.sims
```

Replicate for repeating simulations

Function to simulate the mean of 100 standard normal draws:

```
sim.mean = function() { mean(rnorm(100)) }
```

The following for loop repeats the simulation 1,000 times:

```
sims = vector(mode = "numeric", length = 1000L)
for(i in 1:1000) { sims[i] = sim.mean() }
```

We can avoid the for loop with **replicate()**:

```
sims = replicate(1000, sim.mean())
```

Replicate example

- Recommendation: for each solution you produce,

```
sim = replicate(1000,
                {
                  isert simulation code here
                })
```

Example: use the sample() function to draw a collection of M/F values where the probability of F is 0.75. What is the probability of getting more males than females in a set of 10 random people?

```
experiment = replicate(1000, {
                      mydraw = sample(c("M","F"), 10, replace = T,
                                     prob = c(0.25,0.75))
                      sum(mydraw=="M") > sum(mydraw == "F")
                    })
mean(experiment)
```

Simulation: Confidence intervals

Open simulations.R script in course files

Exercise: Is the coverage rate of confidence intervals for the mean accurate?

- Given conditions similar to ours, does our method for generating confidence intervals capture the true value 95% of the time?