1. Introduction - statistics & course
2. Background on the data sets
3. R / RStudio
4. Reproducible data analysis

History of Statistics

- ~ 300-400 yrs old
- Early stats was concerned w/ data for governments
- ~ 1750 "statistics" coined
- mean / median, graphic data, diff. b/w data and model "error"
- 1800s statisticians starting using probability

  Peirce → randomization & random sampling
- 1900's full integration of prob. & stats via study design and inference

  Ronald A. Fisher

- Axiomatic system for probability
  → mathematized statistics (mid-1900s)
- late 1900s (~1980s) personal computing
  → computational statistics
- Today: data collection is fast, cheap, and plentiful
  → modern statistics, ML & AI, Data Science

Definition of Statistics

statistics: the study of how to extract info from data, which includes how to

- collect
- organize
- analyze
- present

data

Applied Stats: the practical considerations and implementations needed to carry out a statistical analysis / study

Machine Learning: Interface of statistics
and computer science

Data Science: Broadening of statistics,
ML, and AI to capture
the data-driven ~~research~~
research and discovery era

genetics : genomics :: statistics :
data science

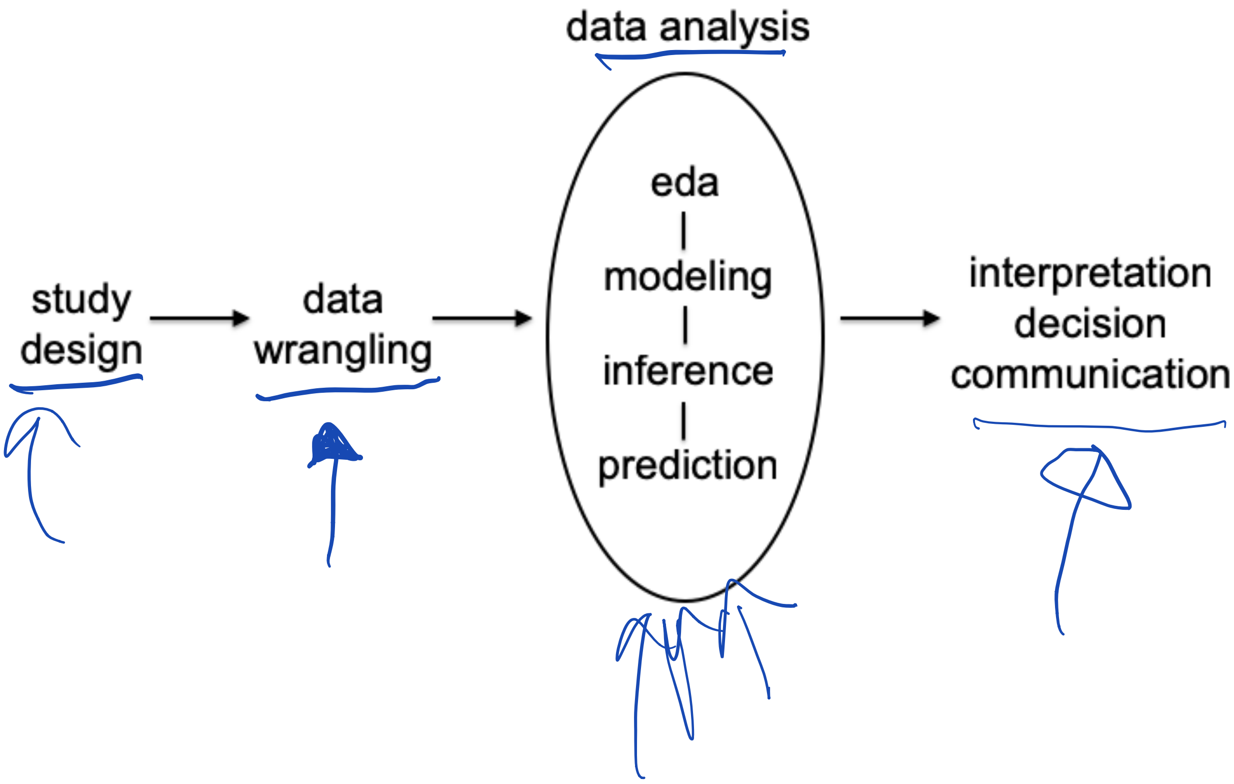
History of Data Science

John Tukey - 1962 paper "The Future of
Data Analysis"

Jeff Wu - Talk in 1997 called
"Statistics = Data Science?"

William Cleveland - paper in 2001 extends
stats into data science

Central Dogma of Statistics



data analysis

study design

data wrangling

eda

modeling

inference

prediction

interpretation
decision
communication

scientific question

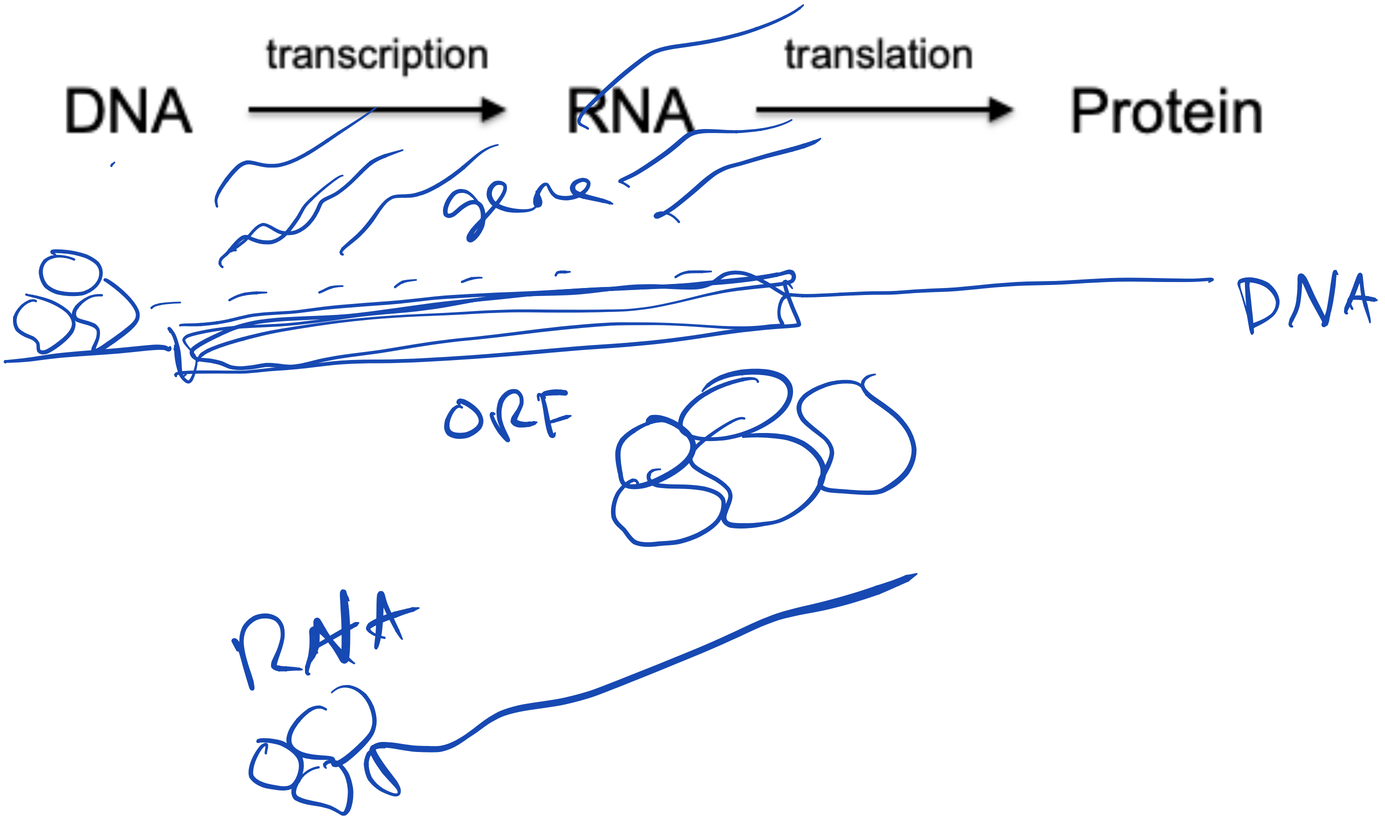
study designs:

- census
- randomized study
- observational
- sample survey
- case / control

Data Sets

- Available in R
- General interest
- Genomics data sets

Central Dogma of Molecular Biology:



DNA: sequence of ATGC

RNA: complementary sequence of its DNA (AUGC)

Problem: 3-letter codons are translated into amino acids (20 total)

Two types of genomic data:

(1) Genetic variation

Humans: ~3B bp's

categorical

People are different at different locations (loci) → genetic variation

HGDP: Human Genome Diversity Panel (Project)

~1000 individuals measured at ~650K locations

SNPs: single nucleotide polymorphisms

② Gene Expression:

Measuring RNA abundance for each gene

- Know RNA sequence for a given gene
- Measure gene-by-gene how much RNA is present (bulk cells, single cells)

Ex: Humans will have ~20K genes w/ expression measurements

Two types:

① Microarray - continuous

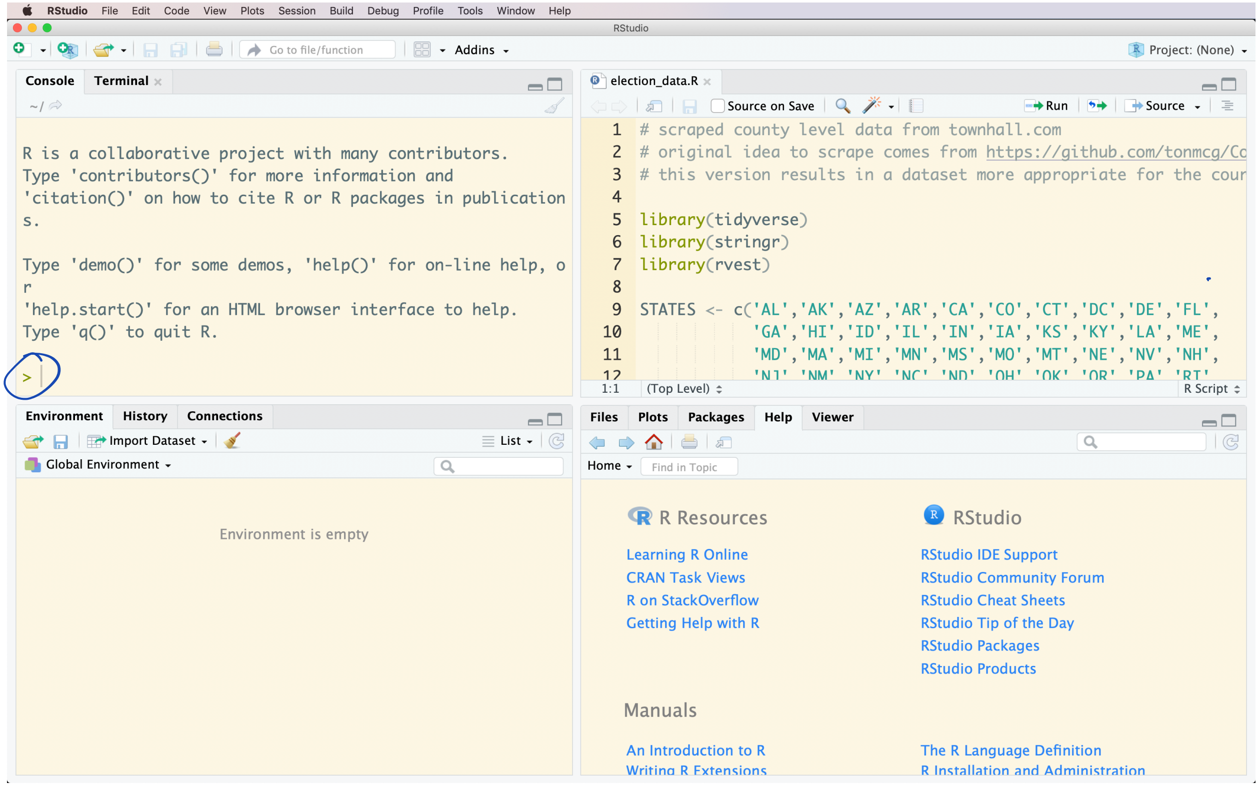
② RNA-seq - count

R

statistical programming language

R Studio

IDE - integrated dev. environ.



```
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publication
s.

Type 'demo()' for some demos, 'help()' for on-line help, o
r
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 
```

```
# scraped county level data from townhall.com
# original idea to scrape comes from https://github.com/tonmcg/Co
# this version results in a dataset more appropriate for the cour

library(tidyverse)
library(stringr)
library(rvest)

STATES <- c('AL','AK','AZ','AR','CA','CO','CT','DC','DE','FL',
            'GA','HI','ID','IL','IN','IA','KS','KY','LA','ME',
            'MD','MA','MI','MN','MS','MO','MT','NE','NV','NH',
            'NJ','NM','NY','NC','ND','OH','OK','OR','PA','RI',
```

Calculator

Operations on numbers: `+ - * / ^`

```
> 2+1
[1] 3
```

```
> 6+3*4-2^3
[1] 10
```

```
> 6+(3*4)-(2^3)
[1] 10
```

Atomic Classes

There are five atomic classes (or modes) of objects in R:

1. character
2. complex
3. integer
4. logical
5. numeric (real number)

There is a sixth called "raw" that we will not discuss.

Assigning Values to Variables

```
> x <- "qcb508" # character
> x <- 2+1i     # complex
> x <- 4L       # integer
> x <- TRUE     # logical
> x <- 3.14159  # numeric
```

Note: Anything typed after the # sign is not evaluated. The # sign allows you to add comments to your code.

More Ways to Assign Values

```
> x <- 1   ✓
> 1 -> x   X
> x = 1    ?
```

Evaluation

When a complete expression is entered at the prompt, it is evaluated and the result of the evaluated expression is returned. The result may be auto-printed.

```
> x <- 1
> x+2
[1] 3
> print(x)
[1] 1
> print(x+2)
[1] 3
```

Functions

log(x , base)

There are many useful functions included in R. “Packages” (covered later) can be loaded as libraries to provide additional functions. You can also write your own functions in any R session.

Here are some examples of built-in functions:

log(x=10, base=2)

```
> x <- 2
> print(x)
[1] 2
> sqrt(x)
[1] 1.414214
> log(x)
[1] 0.6931472
> class(x)
[1] "numeric"
> is.vector(x)
[1] TRUE
```

Accessing Help in R

You can open the help file for any function by typing `?` with the functions name. Here is an example:

```
> ?sqrt
```

There’s also a function `help.search` that can do general searches for help. You can learn about it by typing:

```
> ?help.search
```

It’s also useful to use Google: for example, “r help square root”. The R help files are also on the web.

help("log") help(log)

Variable Names

In the previous examples, we used x as our variable name. Do not use the following variable names, as they have special meanings in R:

✗ c, q, s, t, C, D, F, I, T

When combining two words for a given variable, we recommend one of these options:

```
> my_variable <- 1
> myVariable <- 1
```

Variable names such as my.variable are problematic because of the special use of "." in R.

my.variable

Vectors

The vector is the most basic object in R. You can create vectors in a number of ways.

```
> x <- c(1, 2, 3, 4, 5)
> x
[1] 1 2 3 4 5
>
> y <- 1:20
> y
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
>
> z <- seq(from=0, to=100, by=10)
> z
 [1]   0  10  20  30  40  50  60  70  80  90 100
> length(z)
[1] 11
```

- Programmers: vectors are indexed starting at 1, not 0
- A vector can only contain elements of a single class:

```
> x <- "a"
> x[0]
character(0)
> x[1]
[1] "a"
>
> y <- 1:3
> z <- c(x, y, TRUE, FALSE)
> z
[1] "a"     "1"     "2"     "3"     "TRUE"  "FALSE"
```

Matrices

Like vectors, matrices are objects that can contain elements of only one class.

```
> m <- matrix(1:6, nrow=2, ncol=3)
> m
     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6
>
> m <- matrix(1:6, nrow=2, ncol=3, byrow=TRUE)
> m
     [,1] [,2] [,3]
[1,]    1    2    3
```

```
[2,]    4    5    6
```

Factors

In statistics, factors encode categorical data.

```
> paint <- factor(c("red", "white", "blue", "blue", "red",
+                   "red"))
> paint
[1] red   white blue  blue  red   red
Levels: blue red white
>
> table(paint)
paint
 blue   red white
    2     3     1
> unclass(paint)
[1] 2 3 1 1 2 2
attr(,"levels")
[1] "blue"  "red"   "white"
```

Lists

Lists allow you to hold different classes of objects in one variable.

```
> x <- list(1:3, "a", c(TRUE, FALSE))
> x
[[1]]
[1] 1 2 3

[[2]]
[1] "a"

[[3]]
[1]  TRUE FALSE
>
> ## access any element of the list
> x[[2]]
[1] "a"
> x[[3]][2]
[1] FALSE
```

Lists with Names

The elements of a list can be given names.

```
> x <- list(counting=1:3, char="a", logic=c(TRUE, FALSE))
> x
$counting
[1] 1 2 3

$char
[1] "a"

$logic
[1]  TRUE FALSE
>
> ## access any element of the list
> x$char
[1] "a"
> x$logic[2]
[1] FALSE
```

Missing Values

In data analysis and model fitting, we often have missing values. `NA` represents missing values and `NaN` means "not a number", which is a special type of missing value.

```
> m <- matrix(nrow=3, ncol=3)
> m
     [,1] [,2] [,3]
[1,]   NA   NA   NA
[2,]   NA   NA   NA
[3,]   NA   NA   NA
> 0/1
[1] 0
> 1/0
[1] Inf
> 0/0
[1] NaN
```

`NULL`

`NULL` is a special type of reserved value in R.

```
> x <- vector(mode="list", length=3)
> x
```

```
[[1]]
NULL

[[2]]
NULL

[[3]]
NULL
```

Coercion

We saw earlier that when we mixed classes in a vector they were all coerced to be of type character:

```
> c("a", 1:3, TRUE, FALSE)
[1] "a"     "1"     "2"     "3"     "TRUE"  "FALSE"
```

You can directly apply coercion with functions `as.numeric()`, `as.character()`, `as.logical()`, etc.

This doesn't always work out well:

```
> x <- 1:3
> as.character(x)
[1] "1" "2" "3"
>
> y <- c("a", "b", "c")
> as.numeric(y)
Warning: NAs introduced by coercion
[1] NA NA NA
```

Data Frames

The data frame is one of the most important objects in R. Data sets very often come in tabular form of mixed classes, and data frames are constructed exactly for this.

Data frames are lists where each element has the same length.

```
> df <- data.frame(counting=1:3, char=c("a", "b", "c"),
+                  logic=c(TRUE, FALSE, TRUE))
> df
  counting char logic
1        1    a  TRUE
2        2    b FALSE
3        3    c  TRUE
>
> nrow(df)
[1] 3
> ncol(df)
[1] 3
```

```
> dim(df)
[1] 3 3
>
> names(df)
[1] "counting" "char"     "logic"
>
> attributes(df)
$names
[1] "counting" "char"     "logic"

$class
[1] "data.frame"

$row.names
[1] 1 2 3
```

Attributes

Attributes give information (or meta-data) about R objects. The previous slide shows `attributes(df)`, the attributes of the data frame `df`.

```
> x <- 1:3
> attributes(x) # no attributes for a standard vector
NULL
>
> m <- matrix(1:6, nrow=2, ncol=3)
> attributes(m)
$dim
[1] 2 3
```

```
> paint <- factor(c("red", "white", "blue", "blue", "red",
+                    "red"))
> attributes(paint)
$levels
[1] "blue"  "red"   "white"

$class
[1] "factor"
```

Names

Names can be assigned to columns and rows of vectors, matrices, and data frames. This makes your code easier to write and read.

```
> names(x) <- c("Princeton", "Rutgers", "Penn")
> x
Princeton   Rutgers      Penn
        1         2         3
>
> colnames(m) <- c("NJ", "NY", "PA")
> rownames(m) <- c("East", "West")
> m
     NJ NY PA
East  1  3  5
West  2  4  6
> colnames(m)
[1] "NJ" "NY" "PA"
```

Accessing Names

Displaying or assigning names to these three types of objects does not have consistent syntax.

Object	Column Names	Row Names
vector	`names()`	N/A
data frame	`names()`	`row.names()`
data frame	`colnames()`	`rownames()`
matrix	`colnames()`	`rownames()`

R + Markdown + knitr

R Markdown was developed by the RStudio team to allow one to write reproducible research documents using Markdown and `knitr`. This is contained in the `rmarkdown` package, but can easily be carried out in RStudio.

Markdown was originally developed as a very simply text-to-html conversion tool. With Pandoc, Markdown is a very simply text-to-`X` conversion tool where `X` can be many different formats: html, LaTeX, PDF, Word, etc.

R Markdown Files

.Rmd

R Markdown documents begin with a metadata section, the YAML header, that can include information on the title, author, and date as well as options for customizing output.

```
title: "QCB 508 -- Homework 1"
author: "Your Name"
date: February 23, 2017
output: pdf_document
```

Many options are available. See http://rmarkdown.rstudio.com for full documentation.

Markdown

Markdown

Headers:

```
# Header 1
## Header 2
### Header 3
```

Emphasis:

```
*italic* **bold**
_italic_ __bold__
```

Tables:

```
First Header  | Second Header
------------- | -------------
Content Cell  | Content Cell
Content Cell  | Content Cell
```

Unordered list:

```
- Item 1
- Item 2
    - Item 2a
    - Item 2b
```

Ordered list:

```
1. Item 1
2. Item 2
3. Item 3
    - Item 3a
    - Item 3b
```

Links:

```
http://example.com

[linked phrase](http://example.com)
```

Blockquotes:

```
Florence Nightingale once said:

> For the sick it is important
> to have the best.
```

Plain code blocks:

~~~
```
This text is displayed verbatim with no formatting.
```
~~~

Inline Code:

```
We use the `print()` function to print the contents
of a variable in R.
```

Additional documentation and examples can be found at http://rmarkdown.rstudio.com/authoring_basics.html and http://daringfireball.net/projects/markdown/basics.

LaTeX

LaTeX is a markup language for technical writing, especially for mathematics. It can be include in R Markdown files.

For example,

```
$y = a + bx + \epsilon$
```

produces

$y = a + bx + \epsilon$

For more help with LaTeX…

https://www.artofproblemsolving.com/wiki/index.php/LaTeX

is an introduction to LaTeX and

http://www.stat.cmu.edu/~cshalizi/rmarkdown/#math-in-r-markdown

is a primer on LaTeX for R Markdown.

knitr

The `knitr` R package allows one to execute R code within a document, and to display the code itself and its output (if desired). This is particularly easy to do in the R Markdown setting. For example…

Placing the following text in an R Markdown file

`The sum of 2 and 2 is `r 2+2`.`

produces in the output file

The sum of 2 and 2 is 4.

knitr Chunks

Chunks of R code separated from the text. In R Markdown:

~~~~
```{r}
x <- 2
x + 1
print(x)
```
~~~~

Output in file:

```
> x <- 2
> x + 1
[1] 3
> print(x)
[1] 2
```

Chunk Option: `echo`

In R Markdown:

~~~~
```{r, echo=FALSE}
x <- 2
x + 1
print(x)
```
~~~~

Output in file:

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

Chunk Option: `results`

In R Markdown:

~~~
```{r, results="hide"}
x <- 2
x + 1
print(x)
```
~~~

Output in file:

```
> x <- 2
> x + 1
> print(x)
```

Chunk Option: `include`

In R Markdown:

~~~
```{r, include=FALSE}
x <- 2
x + 1
print(x)
```
~~~

Output in file:

(nothing)

Chunk Option: `eval`

In R Markdown:

~~~
```{r, eval=FALSE}
x <- 2
x + 1
print(x)
```
~~~

Output in file:

```
> x <- 2
> x + 1
> print(x)
```

Chunk Names

Naming your chunks can be useful for identifying them in your file and during the execution, and also to denote dependencies among chunks.

~~~
```{r my_first_chunk}
~~~

```
x <- 2
x + 1
print(x)
```
```

knitr Option: cache

Sometimes you don't want to run chunks over and over, especially for large calculations. You can "cache" them.

````
```{r chunk1, cache=TRUE, include=FALSE}
x <- 2
```

```{r chunk2, cache=TRUE, dependson="chunk1"}
y <- 3
z <- x + y
```
````

This creates a directory called `cache` in your working directory that stores the objects created or modified in these chunks. When `chunk1` is modified, it is re-run. Since `chunk2` depends on `chunk1`, it will also be re-run.

knitr Options: figures

You can add chunk options regarding the placement and size of figures. Examples include:

- `fig.width`
- `fig.height`
- `fig.align`

Changing Default Chunk Settings

If you will be using the same options on most chunks, you can set default options for the entire document. Run something like this at the beginning of your document with your desired chunk options.

````
```{r my_opts, cache=FALSE, echo=FALSE}
library("knitr")
opts_chunk$set(fig.align="center", fig.height=4, fig.width=6)
```
````

Documentation and Examples

- http://yihui.name/knitr/
````

- http://kbroman.org/knitr_knutshell/pages/Rmarkdown.html
- https://github.com/jdstorey/asdslectures

## Common Control Structures

- `if` and `else`: testing a condition and acting on it
- `for`: execute a loop a fixed number of times
- `while`: execute a loop while a condition is true
- `repeat`: execute an infinite loop (must break out of it to stop)
- `break`: break the execution of a loop
- `next`: skip an interation of a loop

From *R Programming for Data Science*, by Roger Peng

## Some Boolean Logic

R has built-in functions that produce `TRUE` or `FALSE` such as `is.vector` or `is.na`. You can also do the following:

- `x == y` : does x equal y?
- `x > y` : is x greater than y? (also `<` less than)
- `x >= y` : is x greater than or equal to y?
- `x && y` : are both x and y true?
- `x || y` : is either x or y true?
- `!is.vector(x)` : this is `TRUE` if x is not a vector

## `if`

Idea:

```
if(<condition>) {
        ## do something
}
# Continue with rest of code
```

Example:

```
> x <- c(1,2,3)
> if(is.numeric(x)) {
+   x+2
+ }
[1] 3 4 5
```

## `if-else`

Idea:

```
if(<condition>) {
        ## do something
}
```

```
else {
        ## do something else
}
```

Example:

```
> x <- c("a", "b", "c")
> if(is.numeric(x)) {
+   print(x+2)
+ } else {
+   class(x)
+ }
[1] "character"
```

### for Loops

Example:

```
> for(i in 1:10) {
+   print(i)
+ }
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
[1] 7
[1] 8
[1] 9
[1] 10
```

Examples:

```
> 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"
```

### Nested for Loops

Example:

```
> m <- matrix(1:6, nrow=2, ncol=3, byrow=TRUE)
>
> for(i in seq_len(nrow(m))) {
+   for(j in seq_len(ncol(m))) {
+     print(m[i,j])
+   }
+ }
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
```

### while

Example:

```
> x <- 1:10
> idx <- 1
>
> while(x[idx] < 4) {
+   print(x[idx])
+   idx <- idx + 1
+ }
[1] 1
[1] 2
[1] 3
>
> idx
[1] 4
```

Repeats the loop until while the condition is `TRUE`.

### repeat

Example:

```
> x <- 1:10
> idx <- 1
>
> repeat {
+   print(x[idx])
+   idx <- idx + 1
+   if(idx >= 4) {
+     break
+   }
+ }
[1] 1
[1] 2
[1] 3
>
> idx
[1] 4
```

Repeats the loop until `break` is executed.

### break and next

`break` ends the loop. `next` skips the rest of the current loop iteration.

Example:

```
> x <- 1:1000
> for(idx in 1:1000) {
+   # %% calculates division remainder
+   if((x[idx] %% 2) > 0) {
+     next
+   } else if(x[idx] > 10) { # an else-if!!
+     break
+   } else {
+     print(x[idx])
+   }
+ }
[1] 2
[1] 4
[1] 6
[1] 8
[1] 10
```

## Calculations on Vectors

R is usually smart about doing calculations with vectors. Examples:

```
>
> x <- 1:3
> y <- 4:6
>
> 2*x      # same as c(2*x[1], 2*x[2], 2*x[3])
[1] 2 4 6
> x + 1    # same as c(x[1]+1, x[2]+1, x[3]+1)
[1] 2 3 4
> x + y    # same as c(x[1]+y[1], x[2]+y[2], x[3]+y[3])
[1] 5 7 9
> x*y      # same as c(x[1]*y[1], x[2]*y[2], x[3]*y[3])
[1]  4 10 18
```

## A Caveat

If two vectors are of different lengths, R tries to find a solution for you (and doesn't always tell you).

```
> x <- 1:5
> y <- 1:2
> x+y
Warning in x + y: longer object length is not a multiple of shorter object
length
[1] 2 4 4 6 6
```

## Vectorized Matrix Operations

Operations on matrices are also vectorized. Example:

```
> x <- matrix(1:4, nrow=2, ncol=2, byrow=TRUE)
> y <- matrix(1:4, nrow=2, ncol=2)
>
> x+y
     [,1] [,2]
[1,]    2    5
[2,]    5    8
>
> x*y
     [,1] [,2]
```

```
[1,]    1    6
[2,]    6   16
```

### Mixing Vectors and Matrices

What happens when we do calculations involving a vector and a matrix? Example:

```
> x <- matrix(1:6, nrow=2, ncol=3, byrow=TRUE)
> z <- 1:2
>
> x + z
     [,1] [,2] [,3]
[1,]    2    3    4
[2,]    6    7    8
>
> x * z
     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    8   10   12
```

### Mixing Vectors and Matrices

Another example:

```
> x <- matrix(1:6, nrow=2, ncol=3, byrow=TRUE)
> z <- 1:3
>
> x + z
     [,1] [,2] [,3]
[1,]    2    5    5
[2,]    6    6    9
>
> x * z
     [,1] [,2] [,3]
[1,]    1    6    6
[2,]    8    5   18
```

What happened this time?

### Vectorized Boolean Logic

We saw `&&` and `||` applied to pairs of logical values. We can also vectorize these operations.

```
> a <- c(TRUE, TRUE, FALSE)
> b <- c(FALSE, TRUE, FALSE)
>
> a | b
[1]  TRUE  TRUE FALSE
> a & b
[1] FALSE  TRUE FALSE
```

### Subsetting Vectors

```
> x <- 1:8
>
> x[1]           # extract the first element
[1] 1
> x[2]           # extract the second element
[1] 2
>
> x[1:4]         # extract the first 4 elements
[1] 1 2 3 4
>
> x[c(1, 3, 4)]  # extract elements 1, 3, and 4
[1] 1 3 4
> x[-c(1, 3, 4)] # extract all elements EXCEPT 1, 3, and 4
[1] 2 5 6 7 8
```

### Subsetting Vectors

```
> names(x) <- letters[1:8]
> x
a b c d e f g h
1 2 3 4 5 6 7 8
>
> x[c("a", "b", "f")]
a b f
1 2 6
>
> s <- x > 3
> s
    a     b     c     d     e     f     g     h
FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
> x[s]
d e f g h
4 5 6 7 8
```

### Subsettng Matrices

```
> x <- matrix(1:6, nrow=2, ncol=3, byrow=TRUE)
> x
     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    4    5    6
```

```
>
> x[1,2]
[1] 2
> x[1, ]
[1] 1 2 3
> x[ ,2]
[1] 2 5
```

### Subsettng Matrices

```
> colnames(x) <- c("A", "B", "C")
>
> x[ , c("B", "C")]
     B C
[1,] 2 3
[2,] 5 6
>
> x[c(FALSE, TRUE), c("B", "C")]
B C
5 6
>
> x[2, c("B", "C")]
B C
5 6
```

### Subsettng Matrices

```
> s <- (x %% 2) == 0
> s
         A     B     C
[1,] FALSE  TRUE FALSE
[2,]  TRUE FALSE  TRUE
>
> x[s]
[1] 4 2 6
>
> x[c(2, 3, 6)]
[1] 4 2 6
```

### Subsetting Lists

```
> x <- list(my=1:3, favorite=c("a", "b", "c"),
+           course=c(FALSE, TRUE, NA))
>
> x[[1]]
[1] 1 2 3
> x[["my"]]
[1] 1 2 3
> x$my
[1] 1 2 3
```

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

```
> x[c(3,1)]
$course
[1] FALSE  TRUE    NA

$my
[1] 1 2 3
```

### Subsetting Data Frames

```
> x <- data.frame(my=1:3, favorite=c("a", "b", "c"),
+           course=c(FALSE, TRUE, NA))
>
> x[[1]]
[1] 1 2 3
> x[["my"]]
[1] 1 2 3
> x$my
[1] 1 2 3
```

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

```
> x[c(3,1)]
  course my
1  FALSE  1
2   TRUE  2
```

```
3     NA  3
```

### Subsetting Data Frames

```
> x <- data.frame(my=1:3, favorite=c("a", "b", "c"),
+            course=c(FALSE, TRUE, NA))
>
> x[1, ]
  my favorite course
1  1        a  FALSE
> x[ ,3]
[1] FALSE  TRUE    NA
> x[ ,"favorite"]
[1] a b c
Levels: a b c
```

```
> x[1:2, ]
  my favorite course
1  1        a  FALSE
2  2        b   TRUE
> x[ ,2:3]
  favorite course
1        a  FALSE
2        b   TRUE
3        c     NA
```

### Missing Values

```
> data("airquality", package="datasets")
> head(airquality)
  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
> dim(airquality)
[1] 153   6
```

```
> which(is.na(airquality$Ozone))
 [1]   5  10  25  26  27  32  33  34  35  36  37  39  42  43  45  46  52
[18]  53  54  55  56  57  58  59  60  61  65  72  75  83  84 102 103 107
```

```
[35] 115 119 150
> sum(is.na(airquality$Ozone))
[1] 37
```

### Subsetting by Matching

```
> letters
 [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q"
[18] "r" "s" "t" "u" "v" "w" "x" "y" "z"
> vowels <- c("a", "e", "i", "o", "u")
>
> letters %in% vowels
 [1]  TRUE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE  TRUE FALSE FALSE
[12] FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE
[23] FALSE FALSE FALSE FALSE
> which(letters %in% vowels)
[1]  1  5  9 15 21
>
> letters[which(letters %in% vowels)]
[1] "a" "e" "i" "o" "u"
```

## Defining a New Function

- Functions are defined using the `function()` directive
- They are stored as variables, so they can be passed to other functions and assigned to new variables
- Arguments and a final return object are defined

### Example 1

```
> my_square <- function(x) {
+   x*x  # can also do return(x*x)
+ }
>
> my_square(x=2)
[1] 4
>
> my_fun2 <- my_square
> my_fun2(x=3)
[1] 9
```

### Example 2

```
> my_square_ext <- function(x) {
+   y <- x*x
+   return(list(x_original=x, x_squared=y))
+ }
>
> my_square_ext(x=2)
$x_original
[1] 2

$x_squared
[1] 4
>
> z <- my_square_ext(x=2)
```

### Example 3

```
> my_power <- function(x, e, say_hello) {
+   if(say_hello) {
+     cat("Hello World!")
+   }
+   x^e
+ }
>
> my_power(x=2, e=3, say_hello=TRUE)
Hello World!
[1] 8
>
> z <- my_power(x=2, e=3, say_hello=TRUE)
Hello World!
> z
[1] 8
```

### Default Function Argument Values

Some functions have default values for their arguments:

```
> str(matrix)
function (data = NA, nrow = 1, ncol = 1, byrow = FALSE, dimnames = NULL)
```

You can define a function with default values by the following:

```
f <- function(x, y=2) {
  x + y
}
```

If the user types `f(x=1)` then it defaults to `y=2`, but if the user types `f(x=1, y=3)`, then it executes with these assignments.

### The Ellipsis Argument

You will encounter functions that include as a possible argument the ellipsis: `...`

This basically holds arguments that can be passed to functions called within a function. Example:

```
> double_log <- function(x, ...) {
+   log((2*x), ...)
+ }
>
> double_log(x=1, base=2)
[1] 1
> double_log(x=1, base=10)
[1] 0.30103
```

### Argument Matching

R tries to automatically deal with function calls when the arguments are not defined explicity. For example:

```
x <- matrix(1:6, nrow=2, ncol=3, byrow=TRUE)  # versus
x <- matrix(1:6, 2, 3, TRUE)
```

I strongly recommend that you define arguments explcitly. For example, I can never remember which comes first in `matrix()`, `nrow` or `ncol`.

### Loading .RData Files

An .RData file is a binary file containing R objects. These can be saved from your current R session and also loaded into your current session.

```
> # generally...
> # to load:
> load(file="path/to/file_name.RData")
> # to save:
> save(file="path/to/file_name.RData")
```

```
> ## assumes file in working directory
> load(file="project_1_R_basics.RData")
```

```
> ## loads from our GitHub repository
> load(file=url("https://github.com/SML201/project1/raw/
+          master/project_1_R_basics.RData"))
```

### Listing Objects

The objects in your current R session can be listed. An environment can also be specificied in case you have objects stored in different environments.

```
> ls()
[1] "num_people_in_precept"     "SML201_grade_distribution"
[3] "some_ORFE_profs"
>
> ls(name=globalenv())
[1] "num_people_in_precept"     "SML201_grade_distribution"
[3] "some_ORFE_profs"
>
> ## see help file for other options
> ?ls
```

### Removing Objects

You can remove specific objects or all objects from your R environment of choice.

```
> rm("some_ORFE_profs") # removes variable some_ORFE_profs
>
> rm(list=ls()) # Removes all variables from environment
```

## Packages

"In R, the fundamental unit of shareable code is the package. A package bundles together code, data, documentation, and tests, and is easy to share with others. As of January 2015, there were over 6,000 packages available on the **C**omprehensive **R** **A**rchive **N**etwork, or CRAN, the public clearing house for R packages. This huge variety of packages is one of the reasons that R is so successful: the chances are that someone has already solved a problem that you're working on, and you can benefit from their work by downloading their package."

From http://r-pkgs.had.co.nz/intro.html by Hadley Wickham

## Contents of a Package

- R functions
- R data objects
- Help documents for using the package
- Information on the authors, dependencies, etc.
- Information to make sure it "plays well" with R and other packages

## Installing Packages

### From CRAN:

```
install.packages("dplyr")
```

### From GitHub (for advanced users):

```
library("devtools")
install_github("hadley/dplyr")
```

### From Bioconductor (basically CRAN for biology):

```
library("BiocManager")
BiocManager::install("qvalue")
```

Multiple packages:

```
install.packages(c("dplyr", "ggplot2"))
```

Install all dependencies:

```
install.packages(c("dplyr", "ggplot2"), dependencies=TRUE)
```

Updating packages:

```
update.packages()
```

### Loading Packages

Two ways to load a package:

```
library("dplyr")
library(dplyr)
```

I prefer the former.

### Getting Started with a Package

When you install a new package and load it, what's next? I like to look at the help files and see what functions and data sets a package has.

```
library("dplyr")
help(package="dplyr")
```

### Specifying a Function within a Package

You can call a function from a specific package. Suppose you are in a setting where you have two packages loaded that have functions with the same name.

```
dplyr::arrange(mtcars, cyl, disp)
```

This calls the `arrange` functin specifically from `dplyr`. The package `plyr` also has an `arrange` function.