R Markdown and RMD files

The most common way to use R in this class will be in R Markdown (.Rmd) files. These can combine LaTeX type setting, R code chunks, and visual outputs. For example, you can write the following true statement:

$$\forall w,b,n\in\mathbb{W} \text{ such that } w\geq n \text{ and } b\geq n, \sum_{k=0}^n \frac{\binom{w}{k}\binom{b}{n-k}}{\binom{w+b}{n}}=1$$

(Why is this true?)

1. Write a true statement with an integral.

TODO: Write a true statement.

R with flow control

While loops

If you doubted the first statement, you can verify it by adding an R chunk with code. To add a chunk, click on the green +C button up top and select R (or just type out the three ticks).

[1] 1

To run the chunk, either hit Command-Shift-Enter (Mac) or hit the green arrow in the top right of the chunk.

2. Write a loop that prints the integers from -5 to 5 inclusive.

```
# TODO: Write a loop
```

Manuals

In the earlier chunk, choose is an R function that calculates a binomial coefficient. You can run ?choose to see more information about this function.

You can also type ?choose in the "Console" at the bottom of the screen to get the same effect without adding a chunk. In the console, you can also verify that variables outside of functions are stored in memory until explicitly removed or overwritten. For example, type total or print(total) into the console to see that it is still contains the value 1. This can be useful for debugging after running code chunks.

For loops, vectorization, and sapply

```
We can also evaluate this sum four other ways. First we'll use a for loop:
```

```
total <- 0
for (k in 0:n) { # For k = 0, then k = 1, ... finally k = n
 total <- total + (choose(w, k) * choose(b, n-k)) / choose(w + b, n)
}
print(total)
## [1] 1
```

A for loop automatically increments k without an extra line to explicitly do so.

Second, we'll use a while loop with an if statement:

```
total <- 0
k < 0
while (TRUE) { # Run forever until broken
  total <- total + (choose(w, k) * choose(b, n-k)) / choose(w + b, n)
  k < - k + 1
  if (k > n) { # Break the while loop when k > n
    break
  }
}
print(total)
```

[1] 1

Third, we'll use vectorization. This is the best way to loop in R.

```
k \leftarrow 0:n # Assign k to be a vector containing the elements 0 through n
print(k)
```

```
## [1] 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
print(k[1:10]) # Print a subvector of the first 10 elements (R uses 1-based indexing)
```

```
## [1] 0 1 2 3 4 5 6 7 8 9
# Use vectorization and sum over all the elements
total <- sum((choose(w, k) * choose(b, n-k)) / choose(w + b, n))
print(total)
```

[1] 1

Fourth, we'll create a function and apply it over a vector.

```
\# Create a function called single_hyper with k, w, b, and n as parameters
single_hyper <- function(k, w, b, n) {</pre>
  value_to_return <- (choose(w, k) * choose(b, n-k)) / choose(w + b, n)</pre>
  return (value_to_return) # Return the calculated value
}
```

```
# Apply the function single_hyper to each element in k and sum the result
total <- sum(sapply(k, single_hyper, w=w, b=b, n=n))

print(total)

## [1] 1

3. Use a for loop, vectorization, and sapply to calculate \( \sum_{i=1}^{1000} \frac{1}{i} \).

# TODO: Calculate the sum</pre>
```

R Functions and more vectorization

There are many other functions built in for R. For example, the function we just wrote already has a built-in version:

```
k <- 0:15
total <- sum(dhyper(k, w, b, n))
print(total)</pre>
```

[1] 1

This function calculates the probability mass function of a hypergeometric with parameters w, b, and n evaluated at k. Basic operations are also vectorized in R:

```
v1 <- c(2, 4, 6) # Create vector with 3 elements by hand
v2 <- seq(5, 6, 0.5) # All real numbers from 5 to 6 spaced by 0.5
print(v1 * v2)
```

```
## [1] 10 22 36
```

[1] 10 22 36 13 28 45 16

A convenient (or annoying) feature of R is that vectorized operations will duplicate the smaller vector elements to match the length of the larger vector.

```
# For example,
print(3 * 1:3)
## [1] 3 6 9
# And also
v3 \leftarrow seq(5, 9, 0.5)
print(v1)
## [1] 2 4 6
print(v3)
## [1] 5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5 9.0
print(v1 * v3)
## [1] 10 22 36 13 28 45 16 34 54
# But this throws a warning
v4 \leftarrow seq(5, 8, 0.5)
print(v1 * v4)
## Warning in v1 * v4: longer object length is not a multiple of shorter object
## length
```

There is some thought that vectorization in R is always faster...

```
now <- Sys.time() # Start timer</pre>
to_time <- 10^6
n <- 10
output <- vector(length = to_time)</pre>
for (i in 1:to_time) { # Multiply elements in a for loop
  output[i] <- i^2</pre>
print(difftime(Sys.time(), now))
```

Time difference of 0.029459 secs

```
now <- Sys.time()</pre>
output <- (1:to time)^2 # Do vectorized multiplication of elements (in a good way)
print(difftime(Sys.time(), now))
```

Time difference of 0.002475977 secs

```
now <- Sys.time()</pre>
# Do vectorized multiplication of elements (in a bad way)
output <- sapply(1:to_time, `^`, 2)</pre>
print(difftime(Sys.time(), now))
```

Time difference of 0.3816531 secs

But using the apply functions doesn't give you much speed up. Unless there's a built-in vectorized method (which there usually is), it might be clearer to just use a for loop.

4. Print the average of $1, 1/2, 1/3, \ldots, 1/10^8$ in the fastest way you can. What is the limit of the mean of $1, 1/2, 1/3, ..., 1/n \text{ as } n \to \infty$?

```
# TODO: Print the average
```

TODO: Find the limit.

Knitting

Now is a good point to knit your code. Press Command-Shift-K or the blue knit button at the top.

Setting headers in your chunk can have helpful effects. For example, cache=T stores the chunk outputs when knitting so they don't have to run again unless you change the code. The option warning=F prevents ugly warning messages from appearing in your output. The option echo=F includes the code output but not the code. The option eval=F includes the code but not the output. The option include=F skips the chunk when knitting (no code or output).

[1] "Chunk was here"

Importing data, working with data, and plotting

Importing data

You can import data from a CSV (comma separated values) file to a data.frame as follows. If the data cannot be found, make sure you're in the right directory by right clicking Nickols_R_Bootcamp.Rmd at the top left and selecting "Set Working Directory."

```
countries <- read.csv("data/country_stats.csv", check.names = F)</pre>
```

This section will deal with a data set of country-level statistics from UNdata and Varieties of Democracy.

A few columns will be useful for the following questions:

- GDP: GDP per capita in 2010 US dollars
- EducExpend: Public expenditure on education (% of GDP)
- Doctors: Physicians (per 1000 population)

Selecting rows and columns

You can select columns by name or by index:

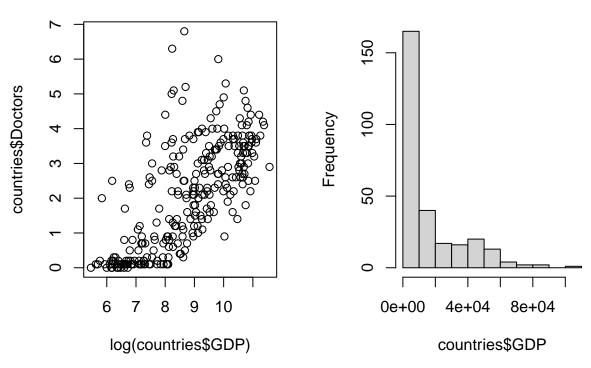
```
print(countries$GDP[1:10]) # Print the first 10 GDP per capitas
## [1]
          504
                544
                      497 40065 35748 14971 1753 3432 3607 37710
print(countries[,3][1:10]) # Same thing
                544
                      497 40065 35748 14971 1753 3432 3607 37710
    [1]
          504
The comma in the second line above is important. You can select rows by putting the number before the
print(countries[1,][1:3]) # First 3 columns of row 1
         Country Year GDP
## 1 Afghanistan 2010 504
print(countries[1:5,1:3]) # First 3 columns of rows 1-5
##
         Country Year
                         GDP
## 1 Afghanistan 2010
                        504
## 2 Afghanistan 2015
                        544
## 3 Afghanistan 2019
                         497
## 4
         Andorra 2005 40065
## 5
         Andorra 2015 35748
You can also select rows by a condition.
print(dim(countries)) # Original dimensions
## [1] 280
# Subset the data frame to only countries with GDPs per capita of over $10000
print(dim(countries[countries$GDP > 10000,]))
## [1] 115
```

Base R plots

The following code plots the relationship between log GDP and the number of doctors:

```
par(mfrow = c(1,2)) # Place two plots side by side (1 row, 2 columns)
plot(log(countries$GDP), countries$Doctors)
hist(countries$GDP)
```

Histogram of countries\$GDP



These are quite ugly, but we can make them prettier in ggplot.

GGplot

The following chunk installs and loads the package ggplot. You'll need to install packages only once but load them in each file.

```
if(!"ggplot2" %in% rownames(installed.packages())) {
   install.packages("ggplot2")
}
library(ggplot2)

if(!"gridExtra" %in% rownames(installed.packages())) {
   install.packages("gridExtra")
}
library(gridExtra)
```

The following code creates the earlier plots, but prettier.

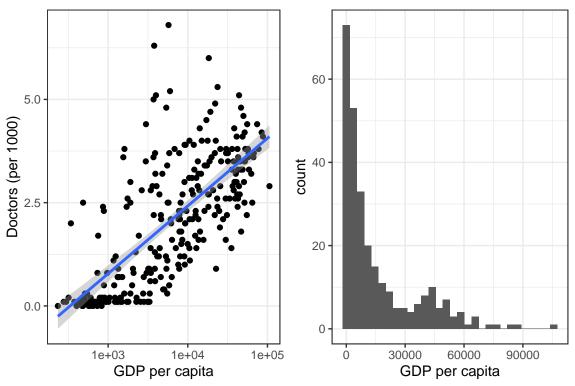
```
# GDP per capita is x, OSPI is y
p1 <- ggplot(countries, aes(x = GDP, y = Doctors)) +
    geom_point() + # Plot points
    geom_smooth(method = 'lm', formula = "y~x") + # Plot line
    # Log transform x axis and set break points
    scale_x_continuous(trans = 'log10', breaks = c(1000, 10000, 100000)) +
    ylab("Doctors (per 1000)") + # Rename y axis
    xlab("GDP per capita") + # Rename x axis</pre>
```

```
theme_bw() # Change background

p2 <- ggplot(countries, aes(x = GDP)) +
    geom_histogram(bins = 30) +
    xlab("GDP per capita") +
    theme_bw()

# You can display individual plots by not assigning them to p1 or p2

grid.arrange(p1, p2, ncol=2) # Put plots side by side</pre>
```



5. Plot the relationship between education expenditures and doctors in countries with GDPs per capita of at least \$20,000.

```
# TODO: Subset and plot
```

Random number usage

One of the main benefits of R is its ability to generate and manipulate random numbers easily. Most common distributions are already ready to go. Make sure to set a seed so your code is reproducible. For example:

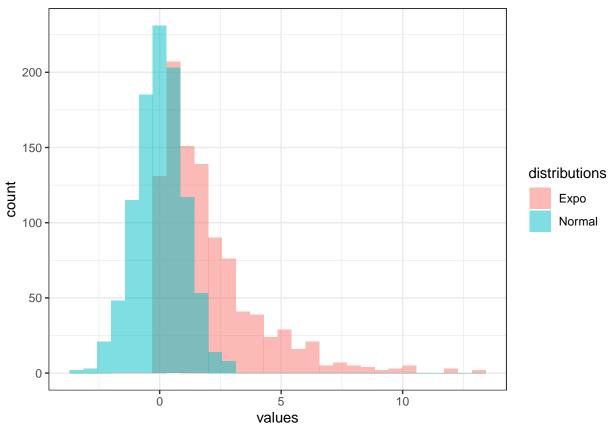
```
set.seed(111)

n <- 1000
normals <- rnorm(n, 0, 1) # Generate 1000 standard normals
expos <- rexp(n, 1/2) # 1000 exponentials with rate 1/2 (mean 2)

# Create a data frame with the normal and expontials in one column
# and the names in another column
df <- data.frame("values" = c(normals, expos),</pre>
```

```
"distributions" = rep(c("Normal", "Expo"), each = n))

ggplot(df, aes(x = values, fill = distributions)) +
  geom_histogram(alpha = 0.5, position="identity", bins = 30) +
  theme_bw()
```



You can also calculate summary statistics for the distributions:

```
print(c(mean(normals), median(normals)))
```

```
## [1] 0.01080923 0.01967487
```

print(summary(normals))

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## -3.32334 -0.65366 0.01968 0.01081 0.67559 2.92603
```

There are also quantile functions (they start with "q"), density functions (they start with "d"), and cumulative density functions (they start with "p").

```
print(pnorm(-3:3))
```

```
## [1] 0.001349898 0.022750132 0.158655254 0.500000000 0.841344746 0.977249868
## [7] 0.998650102
print(qnorm(c(1 - (1-0.997)/2, 1 - (1-0.95)/2, 1 - (1-0.68)/2)))
```

```
## [1] 2.9677379 1.9599640 0.9944579
```

(Which rule does the line above show?)

The functions **rep** is useful for repeating values, and the function **replicate** is useful for replicating computations.

```
print(rep(10, 5))
## [1] 10 10 10 10 10
print(replicate(10, mean(rnorm(100, mean = 1, sd = 2))))
## [1] 0.8934618 1.0457099 0.9842224 1.2385490 1.1066039 0.5112138 1.0136824
## [8] 1.2919768 1.2427886 0.9372874
6. Show visually the law of large numbers applying to draws from $\mathcal{N}(0,1)$.
# TODO: Show the LLN
```

This concludes the instructional material. One last thing is that you can include a picture (e.g., of handwritten math) like this:

