R Crash Course for STAT111

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I use Windows, so I may get some MacOS shortcuts wrong.

To get the most mileage from this document, I suggest having both the R Markdown file open alongside the PDF. By default, the chunks are set to not evaluate using `eval = F` (see the source). If you want to see results from each chunk, remove `eval = F` from the very first chunk in the source `.Rmd` file and recompile the document.

If you have additional questions, email me at axin@college.harvard.edu.

Want to skip to practice problems? Click here.

What is R Markdown?

R Markdown is a file format that integrates text editing and R code evaluation. Using R Markdown, you can create reports with formatted text, LaTeX and R.

R Markdown files have the extension `.Rmd`. You can view the contents within any text editor (not necessarily RStudio). However, RStudio provides convenient integration of R with the files.

R code in `.Rmd` lives in chunks, which are sandwiched by three grave accents. You can create a chunk by going to the menu bar and selecting Code > Insert Chunk, using the drop down next to Insert at the top right of the file and selecting R, or using the shortcut Ctrl + Alt + I in Windows or Ctrl + Option + I in MacOS.

To run the code in a single chunk, press the green play button in the upper right of the chunk. You can also use Ctrl + Shift + Enter (Windows) or Cmd + Shift + Return (MacOS). To run a single line, select the line and use Ctrl + Enter or Cmd + Return.

In RStudio, you can "knit" R Markdown files to produce documents that execute the code within all the chunks, and incorporates it into a single document along with the text and LaTeX. You can knit the file using the button in the top right or using the keyboard shortcut Ctrl + Shift + K or Cmd + Shift + K in MacOS.

LaTEX

To use LaTEX in R Markdown, you need to install a compatible LaTEX engine. ∞

```r
install.packages("tinytex")
tinytex::install_tinytex()
```

$$\frac{1}{2}$$

1 R Basics

Some features of R:

- R is case-sensitive
- Indexing begins with 1
- Comments start with pound signs `#`

1.1 Arithmetic

Arithmetic in R automatically follows order of operations. Symbols are consistent with most other coding languages.

```
# Demonstration of arithmetic
# This equals 111
11 + 4 * 5 ^ 2
# Modulo (remainder) in R
139560 %% 2021
```

1.2 Data types

The most important data types we'll use are:

- Logical: `TRUE`, `FALSE`, `T`, `F`
- Integer: `110`, `111`
- Numeric: `6.036`
- Character: `"Conditioning is the soul of statistics"`

R does type assignment automatically; just assign whatever value you need to a variable name. Assignment is accomplished using an arrow, i.e., `<-`. Standard practice is to use left arrows (as demonstrated), though right arrows also work. It is possible to assign using `=`, but it is discouraged.

You can check data type with the function `class()`.

```
# Create a numeric variable approximately equal to sqrt(2)
x <- 1.41421
x = 1.41421 # discouraged, but possible
# This is equivalent to 1.41421 -> x
class(x)
```

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

1.3 Vectors

R's most useful data structures are vectors. These are finite ordered sequences of elements of a single data type (similar to tuples in Python).

Create vectors using the function `c()`. Index a vector to obtain its components using square brackets. Recall that indexing in R begins with 1, not 0. You can also modify the vector's components using indexing.

Remove elements of a vector through indexing with negative integers.

```r
x <- c("hydrogen", 1, 1.01, "gas")
x[1]

# Notice that 1, 1.001, and x are coerced to "character"
class(x)
class(x[2])

# Modify components
x[3] <- 1.008
x

# Delete components
x <- x[-4]
x

# Insert components
x <- c(x, "helium")

# Insert components in the middle
x <- c(x[1:2], "third", x[3:5])
x
```

You can also name the components of a vector and index based on name, though this is also rarely used in STAT 111.

```r
names(x) <- c("name", "number", "mass")
x["number"]
```

1.3.1 Vector arithmetic Vectors in R support element-wise operations, which is best illustrated through examples.

```r
# Arithmetic of vectors of the same length
c(50, 51, 61) + c(110, 111, 139)

# Arithmetic with vectors of differing lengths
# Shortest vector is recycled (warning if not whole multiple)
c(121, 124) + c(110, 111, 139)
c(121, 124) + c(104, 110, 111, 139)

# Arithmetic with constants
2 * c(110, 111, 139)
c(1, 2, 3) * c(110, 111, 139)
100 + c(10, 11, 39)
```

1.4 Equality

Standard practice in R is to use `<-` when assigning a value to a variable. When checking for equality, use `==`, i.e., `x == 2`. When assigning arguments, use single equals signs. For example, `mean(c(1, 2, 3, NA), na.rm = T)`.

```
c(110, 51, 61) == c(110, 111, 139)
```

1.5 Lists

For more flexibility, we can use lists, which are ordered collections of elements that can contain more than one data type (including other lists).

Create lists using `list()`. The components of lists can also be named. Index lists with double square brackets.

```
# Instead of using names(), you can create lists with components already named
# The same applies for vectors
x <- list(
  name = "hydrogen",
  number = 1,
  mass = 1.008
)

x[[1]]
x[["number"]]
# Here, 1 is not coerced to a character
class(x[["number"]])
```

1.6 Exercise 1: Variance of a vector

Create a vector `temp` and return its sample variance.

Sample variance can be calculated for a vector using the function `var()`. Check the results of your calculation against `var(temp)`.

Recall that sample variance is calculated as

$$\mathrm{Var}(\mathbf{x}) = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2.$$

If you look at the `.Rmd` source here, you'll see a good example of how to format LaTeX in the file. For display style equations, use double dollar signs; for inline style equations, use single dollar signs.

```
set.seed(111)
x <- rnorm(11234)
1/(length(x) - 1) * sum((x - mean(x))^2)
var(x)
cat(
  "Our function:", 1/(length(x) - 1) * sum((x - mean(x))^2), "\n",
  "Built-in var():", var(x)
)
```

1.7 Packages

To install R packages, use the function `install.packages()` with the package name in quotes. After a package has been installed, you can use its functions using double colon notation. For example, if we wanted to use `str_detect()` from `stringr` to find patterns of characters, we could write `stringr::str_detect()`. This can become a hassle, so you can load all the functions in a package with `library(stringr)`.

2. Probability distributions in R

R has built-in functions for working with many probability distributions covered in STAT 111. For any family of distributions in R (Binomial, Normal, etc.), there are four functions. For example, with Normal distributions, we have:

- `dnorm(x, mean = mu, sd = sigma)`: Returns the probability density evaluated at `x` for a Normal distribution with mean `mu` and standard deviation `sigma`. Be careful to specify the standard deviation, *not* the variance.
  - This is equivalent to $\phi((x - \mu)/\sigma)$
- `pnorm(q, mean = mu, sd = sigma)`: Returns the CDF evaluated at `q`.
  - Equivalent to $\Phi((x - \mu)/\sigma)$
- `qnorm(p, mu, sigma)`: Returns the value corresponding to pth quantile.
- `rnorm(n, my, sigma)`: Returns n i.i.d. observations from the Normal r.v.

The prefixes `d`, `p`, `q`, and `r` and the first arguments are consistent between probability distributions. However, different distributions require additional arguments to be specified. For example, to generate 10 i.i.d. observations with distribution `\text{Bin}(n, p)`, we would use the function call `rbinom(10, size = n, prob = p)`.

```r
# What are the outputs for each of these?
dnorm(0)
pnorm(0)
qnorm(0)
rnorm(10)
```

2.1 Exercise 2: Law of large numbers

Recall that the Law of Large Numbers (LLN) states that the sample mean of i.i.d. observations approaches the expected value as the sample size increases.

Choose a distribution and generate samples of various sizes to observe the LLN.

```r
x <- lapply(
  c(10 * c(1:10), 1000, 10000, 100000),
  rexp,
  rate = 1
)

y <- lapply(x, mean)
```

3. Tabular data

3.1 Matrices

Matrices in R can be created using `matrix()`. The first argument is a vector containing the data for the matrix. The second argument is the number of rows or columns and whether the data should be read by row or by column. Default behavior is to read data by columns.

```r
X <- matrix(c(1, 1, 0, 1, 1, 1, 1, 3, 9), nrow = 3, byrow = T)
X
```

```
##      [,1] [,2] [,3]
## [1,]    1    1    0
## [2,]    1    1    1
## [3,]    1    3    9
```

R can handle various matrix operations. First, indexing can be accomplished using single square brackets. First element is row, and second element is column.

```r
# Get a row of the matrix
X[1, ]

# Get a column of the matrix
X[, 1]

# Get the dimensions of X (row, col)
dim(X)

# Create the transpose of X
Xt <- t(X)

# Matrix multiplication
XtX <- Xt %*% X

# Find the inverse of a matrix
XtX_inverse <- solve(XtX)

# Sanity check (notice zero can sometimes be a very small number)
XtX %*% XtX_inverse
```

Matrices can be modified like vectors, though indexing for a single element requires both the row and column coordinate.

```r
# Change a single element at the [2,2] position
X[2, 2] <- 5

# Replace the first row
X[1, ] <- c(2, 2, 3)

# Remove the last column
X <- X[, -3]

# Reset the matrix
X <- matrix(c(1, 1, 0, 1, 1, 1, 1, 3, 9), nrow = 3, byrow = T)
```

3.2 Data frames

Data frames are more flexible than matrices. They can be created from matrices or created by supplying the columns. The two methods shown below create the same data frame.

```
Y <- data.frame(X)
names(Y) <- c("Q", "W", "E")
Y
```

```
##   Q W E
## 1 1 1 0
## 2 1 1 1
## 3 1 3 9
```

```
X
```

```
##      [,1] [,2] [,3]
## [1,]    1    1    0
## [2,]    1    1    1
## [3,]    1    3    9
```

```
Y <- data.frame(
  Q = c(1, 1, 1),
  W = c(1, 1, 3),
  E = c(0, 1, 9)
)
Y
```

```
##   Q W E
## 1 1 1 0
## 2 1 1 1
## 3 1 3 9
```

Structurally, data frames are lists of vectors, where each vector corresponds to a column. So, while a data frame can contain many data types, each column corresponds to only one data type. We can access the columns of a data frame by name using the dollar sign, double brackets, or single brackets. Rows can also be retrieved and modified with similar operations.

By supplying elements to a new index, you can also add elements to the data frame.

```
# The following commands return the same element: the first column of Y
Y[["Q"]]
Y[[1]]
Y$Q
Y[, "Q"]

# Rows can also be named and indexed that way
# Rows cannot use dollar sign notation or double brackets
# The following all return the first row of Y
rownames(Y) <- c("A", "S", "D")
Y["A", ]
Y[1, ]

# The following both return the middle element of Y
Y[2, 2]
Y["S", "W"]
```

```r
# Either of the following would add the the column `R`
# This is added to the end of the data frame
Y[, 4] <- c("Joe", "Joe and Neil", "Kevin")
names(Y)[4] <- "R"

Y$R <- c("Joe", "Joe and Neil", "Kevin")

# Remove the column
Y <- Y[, -4]
```

We can filter data frames by supplying Boolean vectors when indexing. Additionally, because of the helpful element-wise properties of R vectors, we can use this property to sort data frames.

```r
# We want rows of the data frame where the second element is 1
Y[Y$W == 1, ]
```

```
##   Q W E
## 1 1 1 0
## 2 1 1 1
```

3.3 Exercise 3: Datasets in R

R has a variety of example data sets that you can look through using the function `data()`. Take a look at the data set `iris`, which you can view by entering `iris`. (Think of the data set as an "invisible" variable that contains the data frame.)

Which of the flower species has the widest petals, on average?

3.4 Miscellaneous useful commands

To view the first few rows of a data frame or first few elements of a vector/list, use `head()`. To view the last elements, use `tail()`. You can supply an optional second argument specifying the number of elements you want to see.

```r
head(iris, 3)
```

3.5 Further reading

There are more advanced (and convenient, if you want to put time into learning) ways of sorting data frames using the packages `tibble`, `dplyr`, and `tidyr`. These will largely not be necessary for STAT 111, though reach out if you want any tips!

For example, we can use `dplyr` to solve Exercise 3 with:

```r
library(dplyr)
iris %>%
  group_by(Species) %>%
  summarize(petal_width_avg = mean(Petal.Width), .groups = "drop") %>%
  top_n(1, petal_width_avg) %>%
  .$Species
```

4 Iteration

4.1 For loops

For loops are common in STAT 111. They allow you to run some code for every element in a collection. For example:

```r
my_vector <- c(110, 111, 139) # Numbers 1 through 10
for (i in my_vector) {
  print(i %% 17)
}
```

```
## [1] 8
## [1] 9
## [1] 3
```

4.2 Vectorized operations

For loops can be useful but are usually not the most efficient solution. For example, we could accomplish the same task as the example in 4.1 with a single vector operation.

```r
my_vector %% 17
```

4.3 Replicate

The function `replicate` repeatedly evaluates an expression. This is useful for simulations. For example, if our experiment was to observe 10 i.i.d. r.v.s with an Exponential distribution with $\lambda = 1$, we can replicate the experiment 100 times using the following:

```r
# run the code to see how simplify changes the result
result <- replicate(100, rexp(10, 1), simplify = F)
result <- replicate(100, rexp(10, 1), simplify = T)
```

4.4 Exercise 4: Central Limit Theorem (CLT)

Observe the CLT in action with simulations!

Generate 500 trials of observing 5 i.i.d. Exponential r.v.s with $\lambda = 1$. Find the mean of each trial and plot the histogram of the sample means using hist(vector.name).

Repeat the above with 50 and 1000 r.v.s (not replications).

Hint: Define a separate vector to store the means.

```r
trial <- function() {
 x <- rexp(50, 1)
 mean(x)
}
result <- replicate(500, trial())
hist(result)
```

5 Functions and control flow

5.1 Creating functions

Replication is most useful when combined with custom functions. We can define a function to find the element with the highest magnitude in a vector like so:

```r
# We can set default values to arguments in functions, like na.rm here
max_magnitude <- function(vec, na.rm = T) {
  max(abs(vec), na.rm = na.rm)
}
max_magnitude(c(NA, -50, 51, -61, 121, -124))
```

5.2 Control flow

R uses fairly intuitive control flow with notation for `if`, `else if`, and `else`. Additionally, a value of 0 evaluates to `FALSE` and any other value evaluates to `TRUE`.

```r
for (i in 1:5) {
  if (i %% 2) {
    message(i, " is odd")
  } else {
    message(i, " is even")
  }
}
```

R also has switch-case capabilities, though it is unlikely to be used in this class.

5.3 Exercise 5: CLT Revisited

Instead of a for loop, can you get the vector of means using a single call to `replicate`?

6 Plotting

R has base functions for plotting, but I personally dislike them. Instead, we'll be using `ggplot2`.

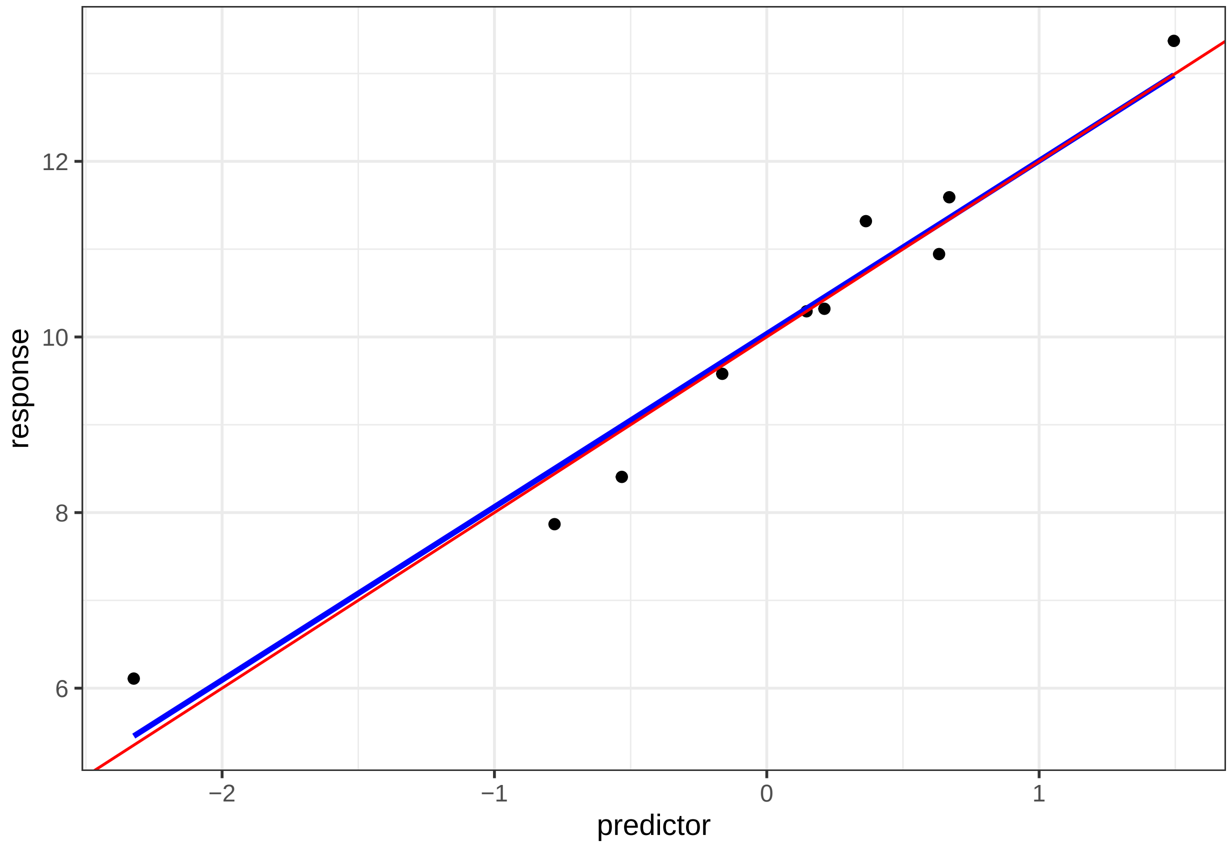
6.1 Creating a scatterplot

```r
# install ggplot2 if you haven't already
# install.packages(ggplot2)
library(ggplot2)

# Let's generate some example data
predictor <- rnorm(10)
response <- 10 + 2*predictor + rnorm(10, 0, .5)
# Create a data frame of data
df <- data.frame(predictor, response)

ggplot(data = df, aes(x = predictor, y = response)) +
  geom_point() + # create points with x and y
  # create blue linear regression line
  geom_smooth(method = "lm", se = F, color = "blue") +
  # create red true regression line
  geom_abline(slope = 2, intercept = 10, color = "red") +
  # make it pretty (optional)
  theme_bw()
```

```
## `geom_smooth()` using formula 'y ~ x'
```



6.2 Creating a histogram

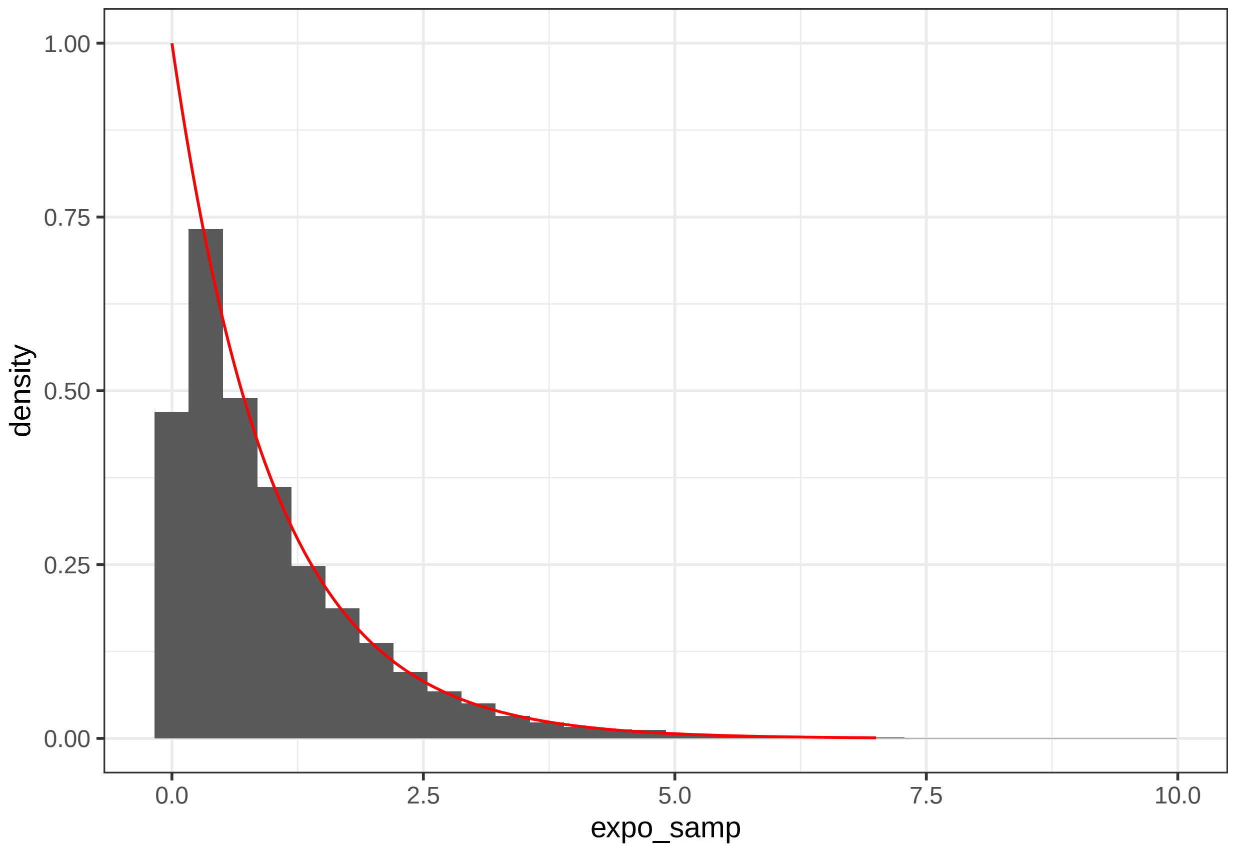
We can generate 400 samples from an Exponential distribution with $\lambda = 1$ and see how the histogram compared to the known PDF of the distribution.

```r
# Generate samples of data
expo_samp <- rexp(10000, 1)
expo_samp_df <- data.frame(expo_samp)

# Generate known PDF
x <- seq(0, 7, by = 0.01)
expo_pdf <- dexp(x, 1)
expo_df <- data.frame(x, expo_pdf)
```

```
ggplot(data = expo_samp_df, aes(x = expo_samp)) +
  # An ordinary histogram would not have the additional aes() arg
  geom_histogram(aes(y = ..density..)) +
  # Add a line for the PDF (use different data)
  geom_line(data = expo_df, aes(x = x, y = expo_pdf), color = "red") +
  theme_bw()
```

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

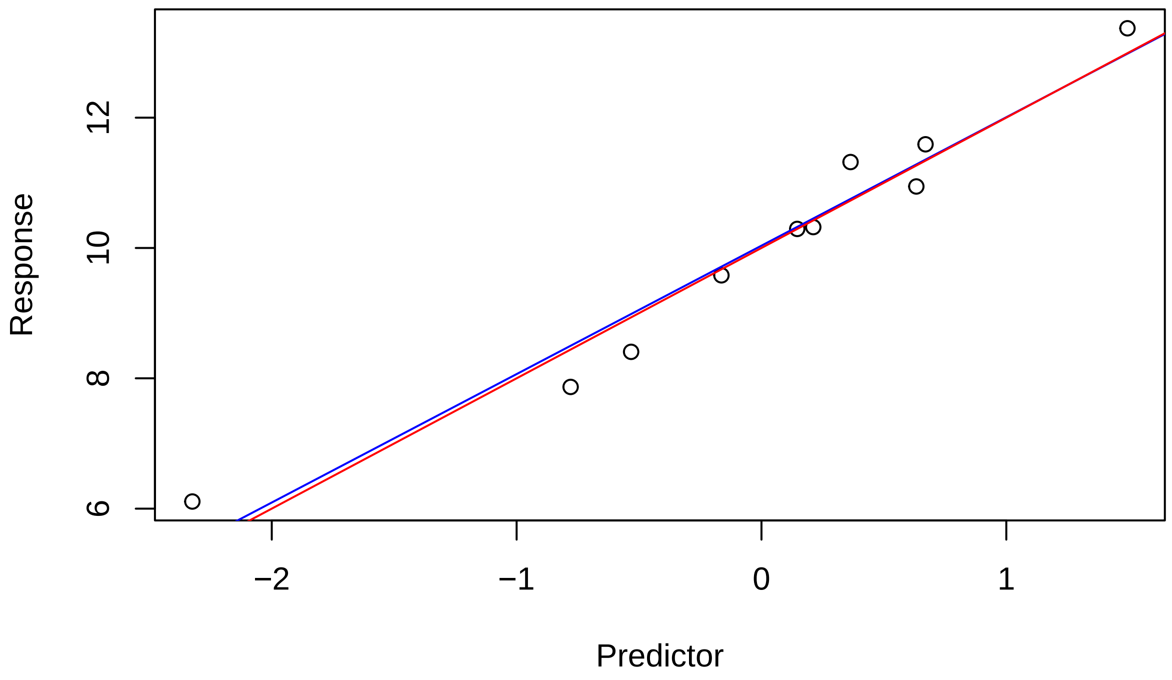


6. Equivalent functions in base R

If you're curious about how to do the same things using base R (without needing to install `ggplot2`) here's a brief summary.

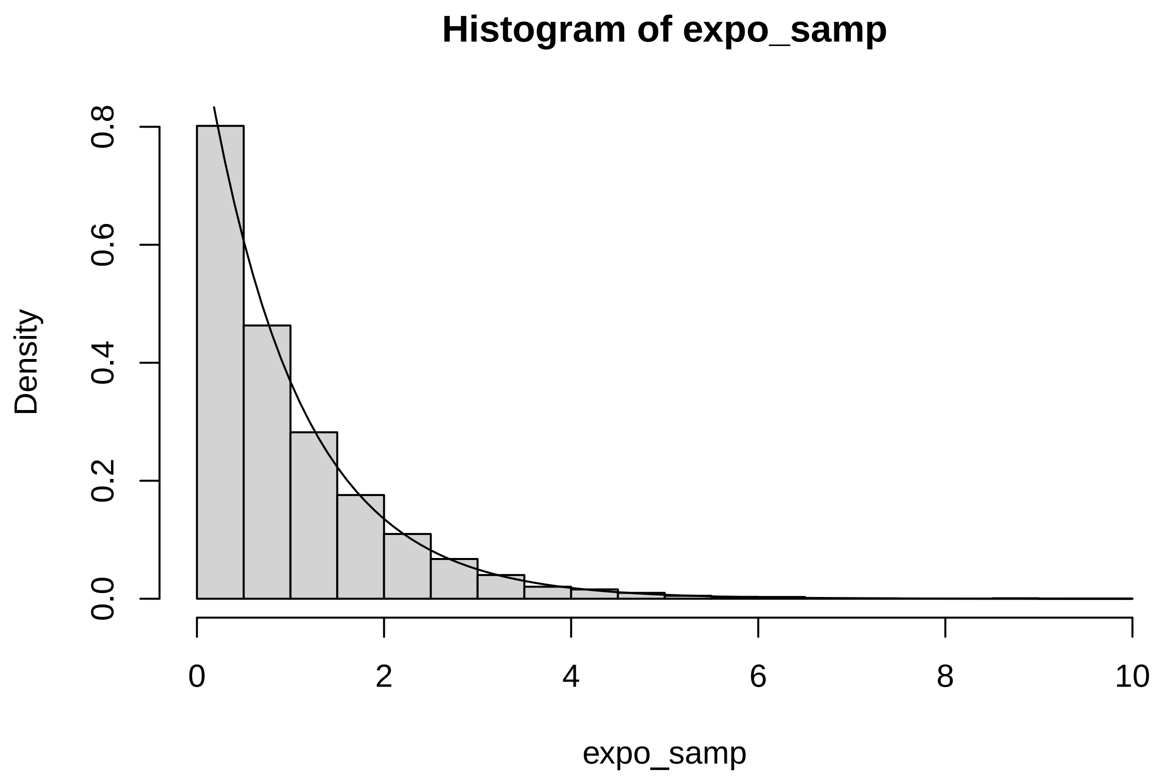
```
# Make a scatter plot with the same data
plot(
 predictor,
 response,
 xlab = "Predictor",
 ylab = "Response"
) +
# Add calculated linear regression line
abline(lm(response ~ predictor), col = "blue") +
```

```r
# Add true regression line
abline(10, 2, col = "red")
```



```
## integer(0)
```

```r
# Make a histogram with the same data
# To make a normal histogram, set freq = T
hist(expo_samp, freq = F)
curve(dexp, add = T)
```


Histogram of expo_samp
Density
0.0
0.2
0.4
0.6
0.8
0
2
4
6
8
10
expo_samp

Practice problems

1 Maximum likelihood estimator

We're often concerned with finding the value of a parameter that maximizes the probability of observing the data that we did. This is called a *maximum likelihood estimate* or MLE. Let's use an example to visualize maximum likelihood.

1.1 Create 20 random observations from a Pois(3) r.v. Suppose we know that the data are i.i.d. Pois observations but we don't know that $\lambda = 3$. (Consider: is this a realistic scenario?)

For each λ in $\{0.01, 0.02, 0.03, \ldots, 4.99, 5\}$, find the likelihood of your data. I.e. for each λ, find $P(Y_1 = y_1, Y_2 = y_2, \ldots, Y_{100} = y_{100}|\lambda)$. Save these likelihoods in some vector.

Solution:

```r
set.seed(111)
x <- rpois(10000, 3)
lambdavec <- seq(0.01, 5, 0.01)

get_poislik <- function(xvec, lambda) sum(dpois(xvec, lambda))

poislik <- sapply(
    lambdavec,
    get_poislik,
    xvec = x
)
```

1.2 Now, make a line plot of the λs versus the likelihoods. What appears to be the value of λ that maximizes the likelihood? Plot a vertical line at the peak of the likelihood.

Solution:

```r
# install.packages("ggplot2") # if you haven't already
library(ggplot2)
q12 <- data.frame(lambda = lambdavec, lik = poislik)

ggplot(q12, aes(x = lambda, y = lik)) +
    geom_line() +
    geom_vline(xintercept = lambdavec[which.max(poislik)], color = "red") +
    theme_bw() +
    labs(
        x = "Lambda candidate values",
        y = "Log-likelihood"
    )
```

2 Biased sample variance

The sample variance of i.i.d. observations $X_1, \ldots, X_n$ with true variance σ^2 is given by $\hat{\sigma}^2_{n-1} = \frac{1}{n-1}\sum_{i=1}^n (X_i - \bar{X})^2$. $\hat{\sigma}^2$ is *unbiased* in that its expectation is the true variance, i.e. $E(\hat{\sigma}^2_{n-1}) = \sigma^2$. This problem shows that $\hat{\sigma}^2$ is unbiased while $\hat{\sigma}^2_n = \frac{1}{n}\sum_{i=1}^n (X_i - \bar{X})^2$ is.

2.1 Create a function that calculates $\hat{\sigma}_n^2$ for any vector of data.

Solution:

```
var_new <- function(x) var(x) * (length(x) - 1) / length(x)
```

2.2 Using 10000 iterations, run a for loop that generates $n = 10$ independent observations from a Standard Normal r.v. and calculates $\hat{\sigma}_{n-1}^2$ and $\hat{\sigma}_n^2$. On average, which estimator is closer to the true value, $\sigma^2 = 1$?

Solution: We can print a result that will be knitted in the PDF using the `cat` function to concatenate text and output.

Note that we're taking the matrix result of `replicate` and converting it to a `data.frame` to use `sapply`.

```
q22 <- data.frame(replicate(10000, rnorm(10)))
sigma_n1 <- sapply(q22, var)
sigma_n <- sapply(q22, var_new)

cat(
    "n:", mean(sigma_n - 1), "\n",
    "n - 1:", mean(sigma_n1 - 1)
)
```

2.3 (Challenge) Let's see how the bias of $\hat{\sigma}_n^2$ varies with the sample size n. Using $n = 2, 3, ..., 30$, do the following 100 times: generate n independent observations from a Standard Normal and calculate $\hat{\sigma}_n^2$. Then plot n vs. the average $\hat{\sigma}_n^2 - \sigma^2$ for each value n. (Note: we have two loops here: one for each size n and one inner-loop that calculates 100 samples of size n for each n).

Solution: Note that our inner loop is our solution from 2.2. So, let's convert that into a function. This function will take the argument for the number of observations in the sample.

Notice how the pipe operator `%>%` is used to send the output of a function to another function. This is clearer and requires less reassigning of variables.

```
library(dplyr) # gives us the pipe "%>%"
nsamp <- c(2:30)
get_n <- function(nsamp) {
    temp <- replicate(10000, rnorm(nsamp)) %>%
        data.frame() %>%
        sapply(var_new)
    mean(temp - 1)
}
q2_3 <- data.frame(nsamp, bias = sapply(nsamp, get_n))
ggplot(q2_3, aes(x = nsamp, y = bias)) +
    geom_line() +
    labs(
        x = "Number in sample",
        y = "Bias of variance estimator"
    )
```

As a bonus, we can also do the same calculations for the unbiased estimator and compare them. This code shows one of several ways you could combine the two lines on one graph.

```r
get_n1 <- function(nsamp) {
    temp <- replicate(10000, rnorm(nsamp)) %>%
        data.frame() %>%
        sapply(var)
    mean(temp - 1)
}
q2_3b <- data.frame(nsamp, bias = sapply(nsamp, get_n1)) %>%
    mutate(estimator = "unbiased")
q2_3 <- mutate(q2_3, estimator = "biased")
q2_3c <- rbind(q2_3b, q2_3)
ggplot(q2_3c, aes(x = nsamp, y = bias, color = estimator)) +
    geom_line() +
    labs(
        x = "Number in sample",
        y = "Bias of variance estimator",
        color = "Variance estimator"
    )
```

3 Universality of the uniform

Let's use the universality of the uniform to generate random observations from an Exponential distribution with rate parameter 1. Recall that $F_X(x) = 1 - e^{-x}$ for $X \sim \text{Expo}(1)$.

3.1 U of U says that if we plug a uniform into the inverse-CDF, we will observe draws from the desired distribution. First find the inverse CDF analytically (the function of the inverse CDF).

Solution: The default base of the `log` function in R is the natural log.

```r
invcdf <- function(x) -log(1 - x)
```

3.2 Now generate 10 000 draws from a uniform, plug them into the inverse-CDF, and plot them using a histogram.

Solution:

```r
x <- invcdf(runif(10000)) %>%
    data.frame(x = .) # names the column

ggplot(x, aes(x = x)) +
    geom_histogram()
```

3.3 Now overlay the density of a Expo(1) to your histogram. Does the observed data appear to match the theoretical distribution?

Solution: We can use the additional argument `aes(y = ..density)` in the call to `geom_histogram` to get a density plot.

To plot the line of the Exponential density, we create a data frame `expodf`.

```r
expodf <- data.frame(
    x = seq(0, 10, 0.01),
    y = dexp(seq(0, 10, 0.01), 1)
)

ggplot(x, aes(x = x)) +
    geom_histogram(aes(y = ..density..)) +
    geom_line(data = expodf, aes(x = x, y = y), color = "red")
```

4 Linear regression

This problem explores *linear regression* using the `stats` package's `lm` command and via matrix operations. We will use the `iris` dataset.

4.1 Create a binary variable within `iris` for whether the species of each flower is `setosa` (i.e. it should be 1 if the flower is `setosa` and 0 otherwise). Call this variable `issetosa`.

Solution: This example demonstrates this operation in base R or with `dplyr`.

```
iris$issetosa <- c(iris$Species == "setosa")
# dplyr
iris_dplyr <- iris %>%
    mutate(issetosa = c(Species == "setosa"))
```

4.2 Use the `lm` command to run a regression of `setosa` on all variables within `iris` except the `Species` variable. Save the model by the name `lm1`. (Note: you can use the documentation for `lm` for help. View it by entering `?lm` in the console).

Solution:

```
lm1 <- lm(issetosa ~ . - Species, iris)
```

4.3 Find the "regression coefficients" by running `lm1$coefficients` or `coef(lm1)`.

Solution

```
coef(lm1)
```

4.4 Replicate the above with matrix operations.

Create a data frame called `X` which has our "predictor variables" (everything in `iris` except `Species` and `setosa`).

Add a column to `X` of all 1s (this should be to the left of all other columns). (Note: if you're stuck on how to do this with `data.frame()`, also try `cbind()`)

Make `X` into a matrix (hint: `as.matrix()`). Then, make a vector (which is just a 1D matrix) called `y` which has the response variable, `setosa`.

The following matrix operations should return the same coefficients as we found in 4.3. Check that this is the case

$$\left(\mathbf{X}^T\mathbf{X}\right)^{-1}\mathbf{X}^T\mathbf{y}.$$

```
iris_mat <- cbind(1, iris)
iris_mat <- iris_mat[1:5] %>% as.matrix()
x <- iris_mat

solve(t(x) %*% x) %*% t(x) %*% as.matrix(iris$issetosa)
```

Miscellaneous Advice

Everything you want to know about R Markdown can be found in this documentation: R Markdown Cookbook

A cheat sheet is also provided here: R Markdown Cheat Sheet

I've included some of the more important notes for STAT 111 here.

Setup for LaTeX

The easiest way to go about this is useing the `tinytex` package to install TinyTeX. You can do this with

```
# install.packages("tinytex")
tinytex::install_tinytex()
```

Replicating "random" variables

In order to set the RNG to be replicable, use `set.seed()`, where the argument is some number of your choosing.

Chunk options

When creating R chunks, you can alter the settings by adding additional fields to the header of the chunk. Here are some useful settings:

- `echo`: Set to `F` (equivalent to `FALSE`) to have the results of code chunks display in the output file while the code chunk is hidden.
- `include`: Set to `F` to hide a code chunk. The chunk will still evaluate, but will be hidden in the file. This is different from `echo = F` because `include = F` will not include graphs.
- `eval`: Set to `F` to have code be rendered in the output but not evaluated.
- `message`: Set to `F` to suppress messages from displaying. Works well with `include = F` when loading libraries.
- `warning`: Set to `F` to suppress warnings from displaying.
- `cache`: See Time-saving measures

For example, if I wanted to run a code chunk to disaply a graph without including all the code in the final document, I would change the content within the brackets starting the code chunk to be `{r, echo = F}`. The comma after `r` is important to include!

To globally alter chunk settings, use `knitr::opts_chunk$set(...)`, where the ellipses are replaced with the settings you want. A good example of this is found in the default R Markdown loaded when you create a new `.Rmd` file in RStudio.

Time-saving measures

When knitting R Markdown files, PDF files are processed more slowly than HTML files. When drafting homework, it's useful to check your LaTeX (e.g., making sure there aren't any formatting errors) using HTML as the output before finalizing the file as a PDF. You can do this by modifying the `output` field in the header of the R Markdown file. By changing the header to read `output: html_document` (or selecting HTML when creating the file), the file will knit as an HTML. To switch to a PDF, use `output: pdf_document`.

Additionally, some psets will require running simulations with many repetitions. To prevent the code from running these simulations every time you knit, you can adjust the header for R code chunks to cache the results of the chunk. This will prevent the chunk from executing in subsequent knits if it is detected that the contents of the file have not been modified.

```
# Check the R Markdown source to see how this is done!
```

However, it is also possible to manually save files. This is useful because using caching can come with caveats and you may invalidate your cache unexpectedly. To manually save R objects, use `saveRDS` and `readRDS`.

```
# Let `helium` be the R object of interest
# You can name the file anything you want
saveRDS(helium, file = "helium.RDS")
helium <- readRDS(file = "helium.RDS")
```

Help

For functions, you can get view documentation by using a question mark. For example, `?replicate`.

You can also view the contents of a function by entering only the function name, no parentheses. This is useful for troubleshooting custom functions.