STAT 231: Problem Set 9B

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due by 5 PM on Friday, November 13

This homework assignment is designed to help you further ingest, practice, and expand upon the material covered in class over the past week(s). You are encouraged to work with other students, but all code and text must be written by you, and you must indicate below who you discussed the assignment with (if anyone).

Steps to proceed:

1. In RStudio, go to File > Open Project, navigate to the folder with the course-content repo, select the course-content project (course-content.Rproj), and click "Open"
2. Pull the course-content repo (e.g. using the blue-ish down arrow in the Git tab in upper right window)
3. Copy ps9B.Rmd from the course repo to your repo (see page 6 of the GitHub Classroom Guide for Stat231 if needed)
4. Close the course-content repo project in RStudio
5. Open YOUR repo project in RStudio
6. In the ps9B.Rmd file in YOUR repo, replace "YOUR NAME HERE" with your name
7. Add in your responses, committing and pushing to YOUR repo in appropriate places along the way
8. Run "Knit PDF"
9. Upload the pdf to Gradescope. Don't forget to select which of your pages are associated with each problem. *You will not get credit for work on unassigned pages (e.g., if you only selected the first page but your solution spans two pages, you would lose points for any part on the second page that the grader can't see).*

If you discussed this assignment with any of your peers, please list who here:

ANSWER:

1. MDSR Exercise 9.5

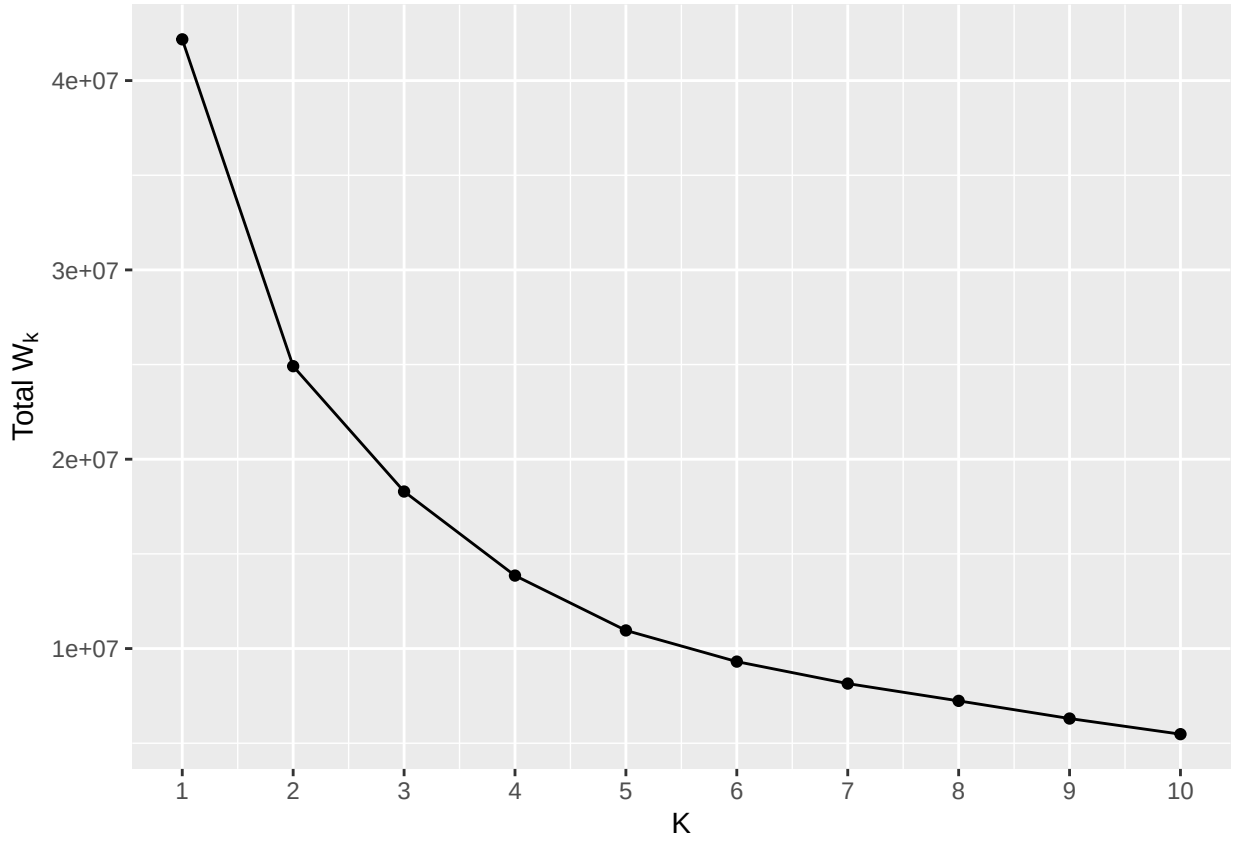
Baseball players are voted into the Hall of Fame by the members of the Baseball Writers of America Association. Quantitative criteria are used by the voters, but they are also allowed wide discretion. The following code identifies the position players who have been elected to the Hall of Fame and tabulates a few basic statistics, include their number of career hits (`tH`), home runs (`tHR`), runs batted in (`tRBI`), and stolen bases (`tSB`). Use the `kmeans()` function to perform a cluster analysis on these players. Describe the properties that seem common to each cluster.

ANSWER:

```
##### PLEASE DO NOT CHANGE THIS SEED NUMBER
##### keep set.seed(75)
set.seed(75)

hof <- Batting %>%
  group_by(playerID) %>%
  inner_join(HallOfFame, by = "playerID") %>%
  filter(inducted == "Y" & votedBy == "BBWAA") %>%
  summarize(tH = sum(H), tHR = sum(HR), tRBI = sum(RBI), tSB = sum(SB)) %>%
  filter(tH > 1000)
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
# Elbow plot to determine best number of clusters
fig <- matrix(NA, nrow=10, ncol=2)
for (i in 1:10){
  fig[i,1] <- i
  fig[i,2] <- kmeans(hof[, 2:ncol(hof)],
                     centers=i,
                     nstart=20)$tot.withinss
}

ggplot(data = as.data.frame(fig), aes(x = V1, y = V2)) +
  geom_point() +
  geom_line() +
  scale_x_continuous(breaks=c(1:10)) +
  labs(x = "K", y = expression("Total W"[k]))
```




```
# K-means algorithm w/ k = 5
km <- kmeans(hof[, 2:ncol(hof)], centers = 5, nstart = 20)
km$centers
```

```
##         tH      tHR     tRBI      tSB
## 1 1531.500 211.0000  917.000  69.5000
## 2 2920.105 144.9474 1085.421 511.1053
## 3 2808.913 444.9565 1683.087 125.7826
## 4 3524.889 362.5556 1857.444 373.8889
## 5 2238.640 358.4800 1365.320  96.4800
```

2. MDSR Exercise 10.6

Equal variance assumption: What is the impact of the violation of the equal variance assumption for linear regression models? Repeatedly generate data from a "true" model given by the following code. (Note that the standard deviation is dependent upon x2, which is random; i.e., the equal variance assumption is violated. The Ys are *not* generated from a distribution with the same variance.)

For each simulation, fit the linear regression model and display the distribution of 1,000 estimates of the β_1 parameter. Does the distribution of the estimates follow a normal distribution?

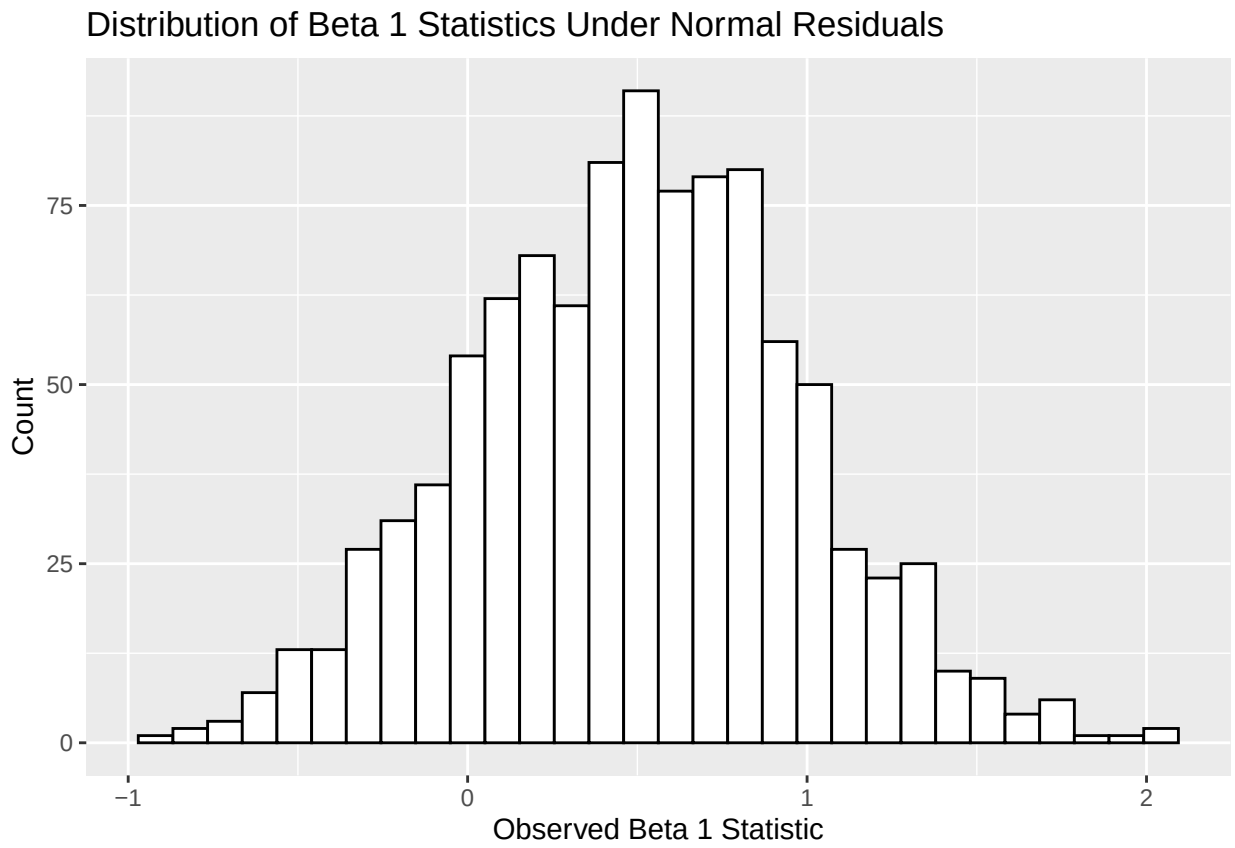
> ANSWER: Yes, the distribution of β_1 estimates seems to follow a normal distribution. The qqplot also shows the majority of points falling on the expected line.

```
# number of observations in each sample
n_obs <- 250

# parameters held constant
rmse <- 1
beta0 <- -1
beta1 <- 0.5
beta2 <- 1.5

# how to generate data
x1 <- rep(c(0,1), each=n_obs/2)
x2 <- runif(n_obs, min=0, max=5)
y <- beta0 + beta1*x1 + beta2*x2 + rnorm(n=n_obs, mean=0, sd=rmse + x2)

# fit model
mod <- lm(y ~ x1 + x2)

# extract beta1 coefficient
summary(mod)$coeff["x1","Estimate"]
```

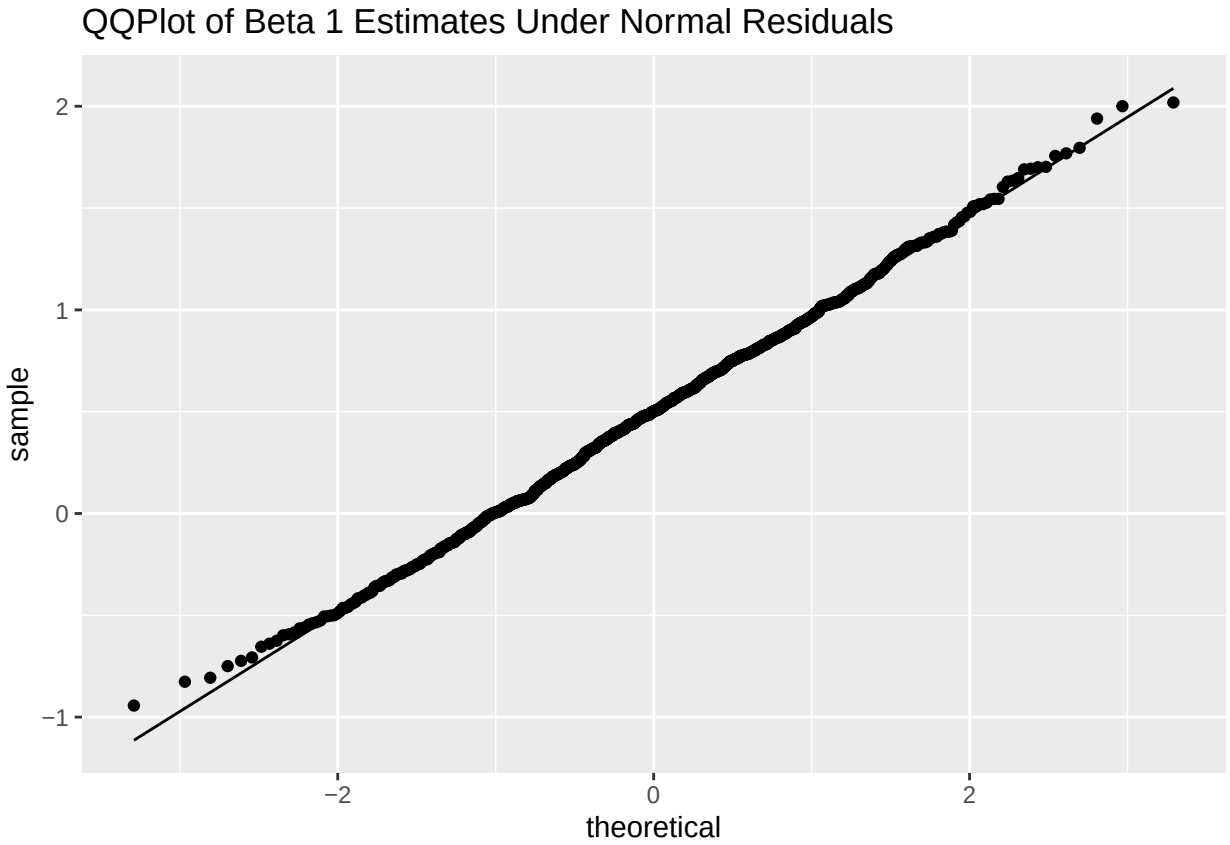
```
## [1] 1.242598
```

```
# now, write code to repeatedly generate data, fit the model, and extract the beta coefficient (1,000 t
set.seed(523)

runsim <- function() {
  x1 <- rep(c(0, 1), each = n_obs/2)
  x2 <- runif(n_obs, min = 0, max = 5)
  y <- beta0 + beta1*x1 + beta2*x2 + rnorm(n = n_obs, mean = 0, sd = rmse + x2)
  mod <- lm(y ~ x1 + x2)
  return(tibble(beta1_est = summary(mod)$coeff["x1", "Estimate"]))
}

# number of simulations
n_sim <- 1000
beta1_values <- mosaic::do(n_sim) * runsim()

# visualize sampling distribution for beta1 (e.g. with histogram or density plot)
ggplot(data = beta1_values, aes(x = beta1_est)) +
  geom_histogram(color = "black", fill = "white") +
```

```
  labs(x = "Observed Beta 1 Statistic", y = "Count") +
  ggtitle("Distribution of Beta 1 Statistics Under Normal Residuals")
```




```
# can also check normality with qqplot
ggplot(data = beta1_values, aes(sample = beta1_est)) +
  stat_qq() +
  stat_qq_line() +
  ggtitle("QQPlot of Beta 1 Estimates Under Normal Residuals")
```


QQPlot of Beta 1 Estimates Under Normal Residuals
sample
theoretical
2
1
0
−1
−2
0
2

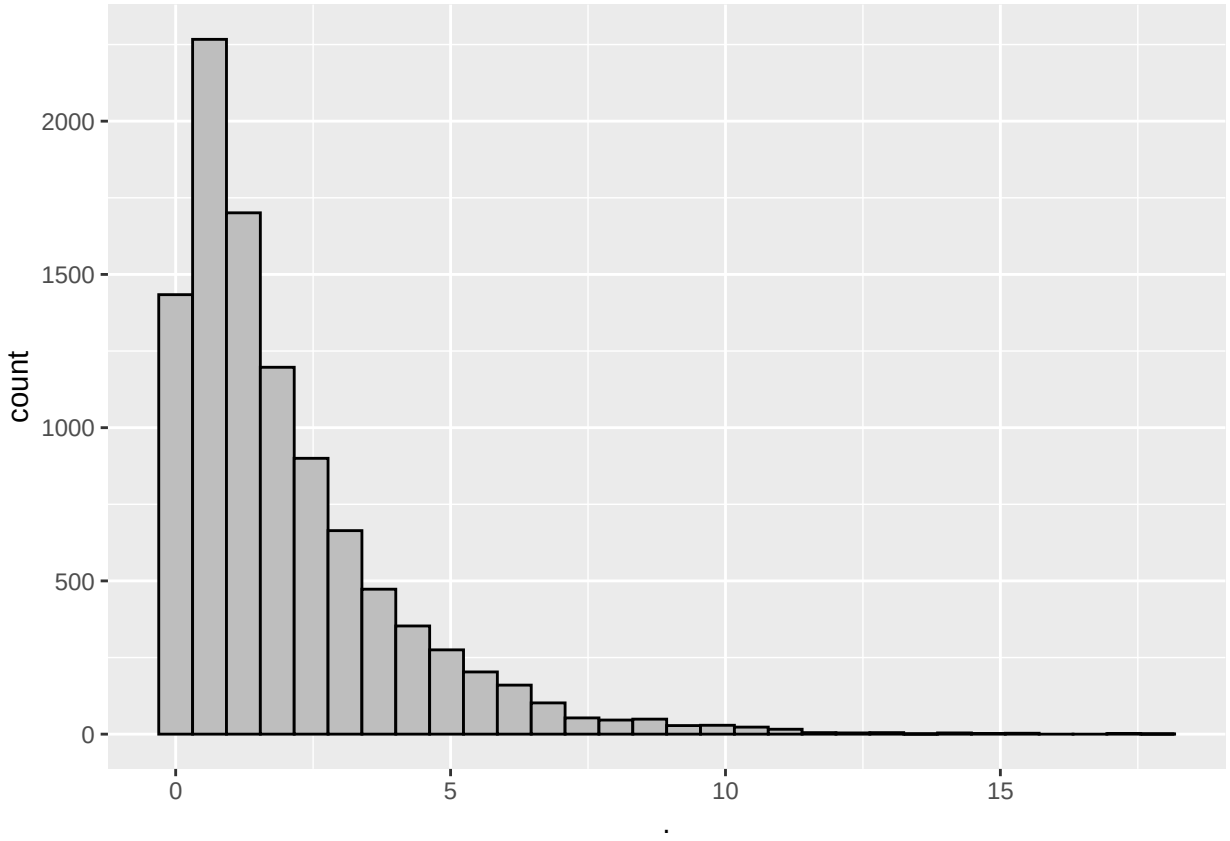
3. MDSR Exercise 10.7

Skewed residuals: What is the impact if the residuals from a linear regression model are skewed (and not from a normal distribution)? Repeatedly generate data from a "true" model given by the parameters below.

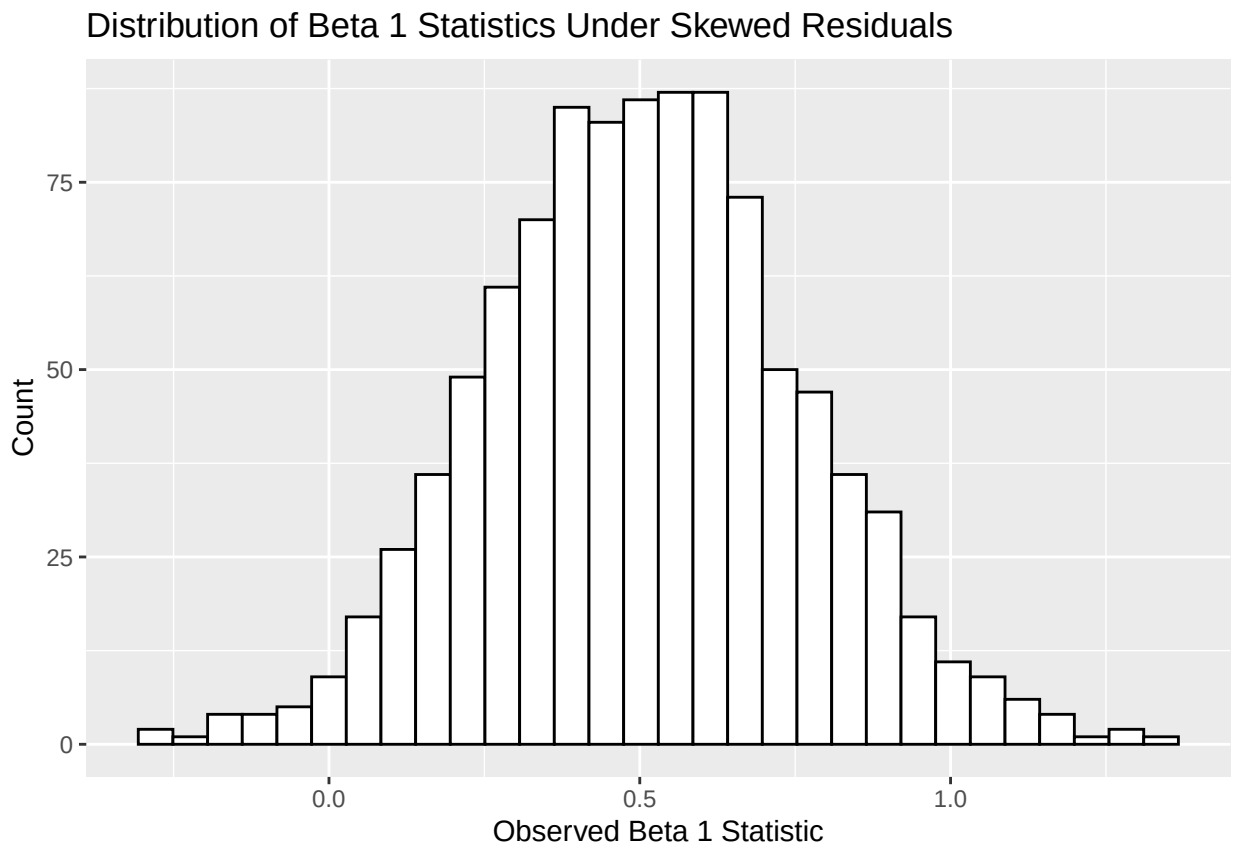
For each simulation, fit the linear regression model and display the distribution of 1,000 estimates of the β_1 parameter.

> ANSWER: Even with skewed residuals the distribution of the β_1 estimates appear to follow a normal distribution. This is also evident in the qqplot, where the majority of points still fall on the expected line.

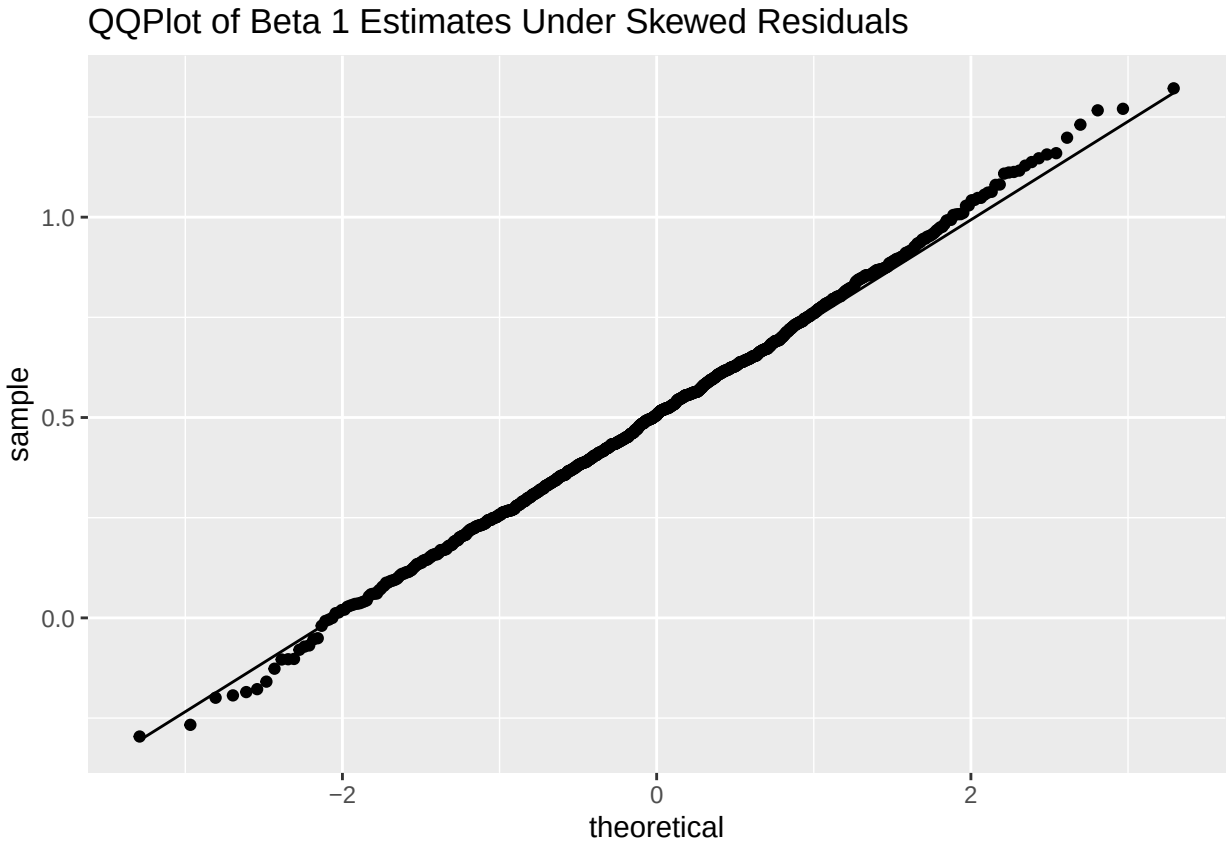
```
# number of observations in each sample
n_obs <- 250

# parameters held constant
rmse <- 1
beta0 <- -1
beta1 <- 0.5
beta2 <- 1.5

# how to generate data
x1 <- rep(c(0,1), each=n_obs/2)
x2 <- runif(n_obs, min=0, max=5)
y <- beta0 + beta1*x1 + beta2*x2 + rexp(n=n_obs, rate=1/2)

# what does an exponential dist'n with rate = 1/2 look like?
# very skewed!
rexp(n=10000, rate=1/2) %>%
  as.data.frame() %>%
  ggplot(aes(x=`.`)) +
    geom_histogram(color="black", fill="grey")
```




```r
# simulation
set.seed(523)

runsim2 <- function() {
  x1 <- rep(c(0, 1), each = n_obs/2)
  x2 <- runif(n_obs, min = 0, max = 5)
  y <- beta0 + beta1*x1 + beta2*x2 + rexp(n = n_obs, rate = 1/2)
  mod <- lm(y ~ x1 + x2)
  return(tibble(beta1_est = summary(mod)$coeff["x1", "Estimate"]))
}

n_sim <- 1000
beta1_values_skewed <- mosaic::do(n_sim) * runsim2()

ggplot(data = beta1_values_skewed, aes(x = beta1_est)) +
  geom_histogram(color = "black", fill = "white") +
  labs(x = "Observed Beta 1 Statistic", y = "Count") +
  ggtitle("Distribution of Beta 1 Statistics Under Skewed Residuals")
```




```
ggplot(data = beta1_values_skewed, aes(sample = beta1_est)) +
  stat_qq() +
  stat_qq_line() +
  ggtitle("QQPlot of Beta 1 Estimates Under Skewed Residuals")
```


QQPlot of Beta 1 Estimates Under Skewed Residuals
sample
1.0
0.5
0.0
−2
0
2
theoretical