bacs_hw5

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Backstory

Verizon was an Incumbent Local Exchange Carrier (ILEC), responsible for maintaining land-line phone service in certain areas. Other competing providers, termed Competitive Local Exchange Carriers (CLEC), could also sell long-distance phone services in Verizon's areas. When something went wrong, Verizon would be responsible to respond and repair services as quickly for CLEC long-distance customers as for its own ILEC customers. The New York Public Utilities Commission (PUC) monitored fairness by comparing Verizon's response times for its ILEC customers versus CLEC customers. In each case, a hypothesis test was performed at the 1% significance level, to determine whether response times for CLEC customers were significantly slower than for Verizon's customers. If Verizon failed to provide fair treatment for CLEC customers, it would have to pay large penalties.

Verizon claims that mean response time for ILEC and CLEC customers are the same, but the PUC would like to test if CLEC customers were facing greater response times.

Question 1

The Verizon dataset this week is provided as a "wide" data frame. Let's practice reshaping it to a "long" data frame

Getting data ready

```
# Reading in the file
response_wide <- read.csv("verizon_wide.csv")
View(response_wide)
```

1a

Instruction

Pick a reshaping package – research them online and tell us why you picked it over others.

Answer

I chose tidyr over reshape2 for several reasons. For one thing, tidyr is more intuitive and integrated with tidyverse. For another, while reshape2 is powerful for more

complex reshaping tasks and works with a wider range of data types including matrices and arrays, this homework does not require such heavy data manipulation.

1b

Instruction

Show the code to reshape the verizon_wide.csv sample

```
# Reshaping the response_wide sample into response_long
library(tidyr)
response_long <- gather(response_wide, na.rm = TRUE, key = "host", valu
e = "response_time")
```

1c

Instruction

Show us the "head" and "tail" of the data to show that the reshaping worked

```
head(response_long)
```

```
##   host response_time
## 1 ILEC         17.50
## 2 ILEC          2.40
## 3 ILEC          0.00
## 4 ILEC          0.65
## 5 ILEC         22.23
## 6 ILEC          1.20
```

```
tail(response_long)
```

```
##      host response_time
## 1682 CLEC         24.20
## 1683 CLEC         22.13
## 1684 CLEC         18.57
## 1685 CLEC         20.00
## 1686 CLEC         14.13
## 1687 CLEC          5.80
```

1d

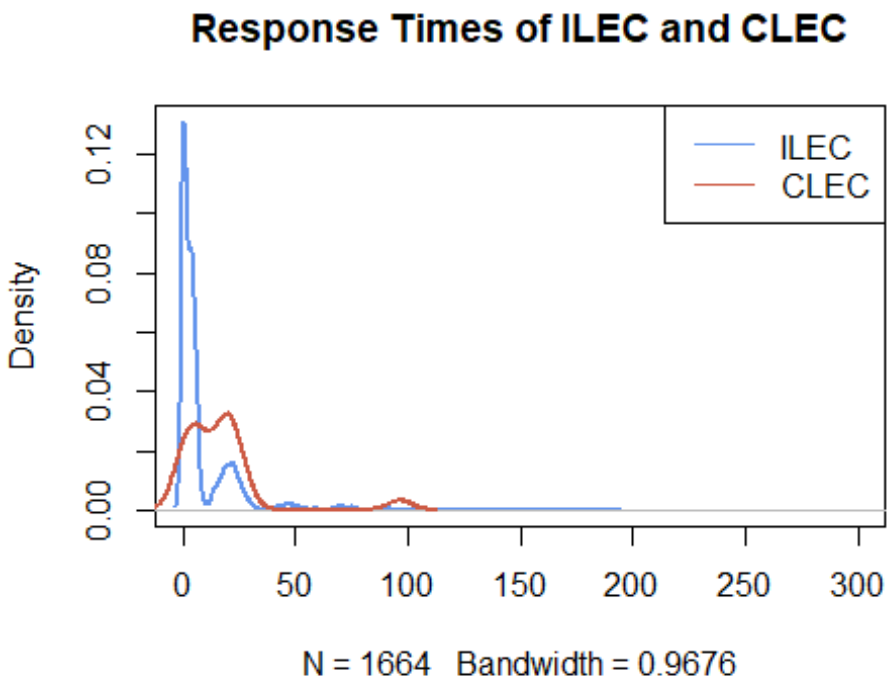
Instruction

Visualize Verizon's response times for ILEC vs. CLEC customers

```
hosts <- split(x = response_long$response_time, f = response_long$host)

plot(density(hosts$ILEC), col = "cornflowerblue", lwd = 2, xlim= c(0,30
0), main = "Response Times of ILEC and CLEC")
lines(density(hosts$CLEC), col = "coral3", lwd = 2)
```

```
legend("topright", lty = 1, c("ILEC","CLEC"), col = c("cornflowerblue",
"coral3"))
```



Question 2

Let's test if the mean of response times for CLEC customers is greater than for ILEC customers

2a

Instruction

State the appropriate null and alternative hypotheses (one-tailed)

Answer

Null Hypothesis H0: Mean of CLEC customers' response times is equal or less compared to that of ILEC customers' response times

Alternative Hypothesis H1: Mean of CLEC customers' response times is greater than that of ILEC customers' response times

2b

Instruction

Use the appropriate form of the t.test() function to test the difference between the mean of ILEC versus CLEC response times at 1% significance. For each of the following tests, show us the results and tell us whether you would reject the null hypothesis.

(i)

Conduct the test assuming variances of the two populations are equal

```
t.test(response_wide$CLEC, response_wide$ILEC, alt="greater", var.equal
 = TRUE, conf.level = 0.99)
```

```
##  Two Sample t-test
##
## data:  response_wide$CLEC and response_wide$ILEC
## t = 2.6125, df = 1685, p-value = 0.004534
## alternative hypothesis: true difference in means is greater than 0
## 99 percent confidence interval:
##  0.8801387       Inf
## sample estimates:
## mean of x mean of y
## 16.509130  8.411611
```

(ii)

Conduct the test assuming variances of the two populations are not equal

```
t.test(response_wide$CLEC, response_wide$ILEC, alt="greater", var.equal
 = FALSE, conf.level = 0.99)
```

```
##  Welch Two Sample t-test
##
## data:  response_wide$CLEC and response_wide$ILEC
## t = 1.9834, df = 22.346, p-value = 0.02987
## alternative hypothesis: true difference in means is greater than 0
## 99 percent confidence interval:
##  -2.130858       Inf
## sample estimates:
## mean of x mean of y
## 16.509130  8.411611
```

2c

Instruction

Use a permutation test to compare the means of ILEC vs. CLEC response times

(i)

Visualize the distribution of permuted differences, and indicate the observed difference as well.

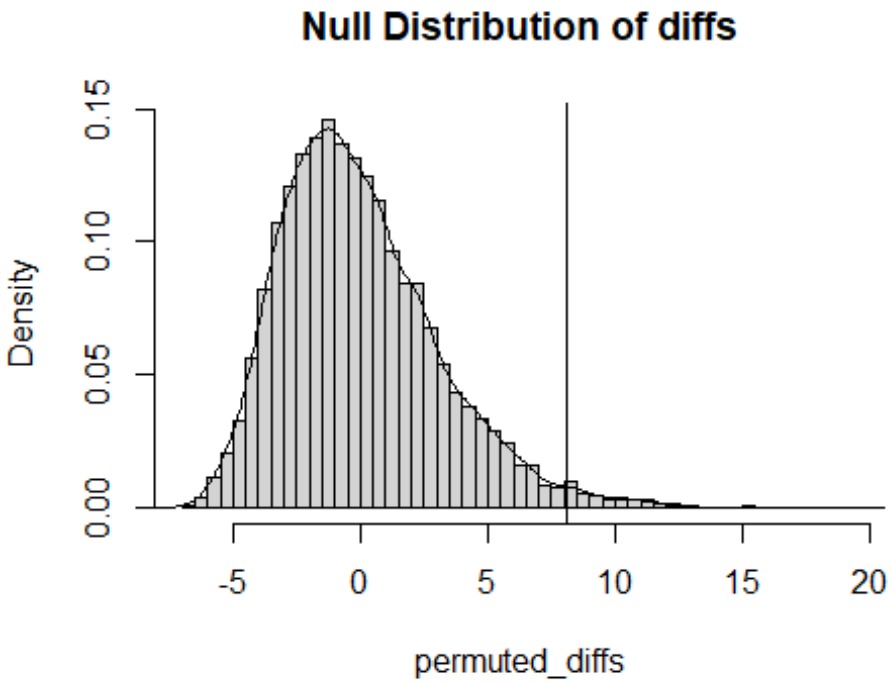
```
# Setting seed
set.seed(123123)

# Observed difference
observed_diff <- mean(hosts$CLEC) - mean(hosts$ILEC)


# Getting the function ready for permutation
permute_diff <- function(values, groups){
  permuted <- sample(values, replace = FALSE)
  grouped <- split(permuted, groups)
  permute_diff <- mean(grouped$CLEC) - mean(grouped$ILEC)
}

# Visualize after 10000 permutations
nperms = 10000
permuted_diffs <- replicate(nperms, permute_diff(response_long$response
_time, response_long$host))
hist(permuted_diffs, breaks = "fd", probability = TRUE, main = "Null Di
stribution of diffs")
lines(density(permuted_diffs))

# Displaying observed difference
abline(v = observed_diff)
```



(ii)

What are the one-tailed and two-tailed p-values of the permutation test ?

```
# one-tailed p-value
p_1tailed <- sum(permuted_diffs > observed_diff)/ nperms
p_1tailed

## [1] 0.0172

# two-tailed p-value
p_2tailed <- sum(abs(permuted_diffs) > observed_diff)/ nperms
p_2tailed

## [1] 0.0172
```

(iii)

Question

Would you reject the null hypothesis at 1% significance in a one-tailed test ?

Answer

No, we would not reject H0 since p-value > 0.01

Question 3

Let's use the Wilcoxon test to see if the response times for CLEC are different than ILEC.

3a

Instruction

Compute the W statistic comparing the values. You may use either the permutation approach (try the functional form) or the rank sum approach

```
# Define gt_eq() for comparing values from two groups
gt_eq <- function(a,b){
  ifelse(a > b, 1, 0) + ifelse(a ==b, 0.5, 0)
}

# W statistic
W <- sum(outer(hosts$CLEC , hosts$ILEC, FUN = gt_eq))
W

## [1] 26820
```

3b

Instruction

Compute the one-tailed p-value for W

```
# Lengths of the CLEC and ILEC groups to be used in the p-value calcula
tion
n1 <- length(hosts$CLEC)
n2 <- length(hosts$ILEC)

wilcox_p_1tail<- 1 - pwilcox(W,n1,n2)
wilcox_p_2tail <- 2 * wilcox_p_1tail
wilcox_p_1tail

## [1] 0.0003688341
```

3c

Instruction

Run the Wilcoxon Test again using the wilcox.test() function in R

```
wilcox.test(hosts$CLEC, hosts$ILEC, alternative = "greater")


##  Wilcoxon rank sum test with continuity correction
##
## data:  hosts$CLEC and hosts$ILEC
```

```
## W = 26820, p-value = 0.0004565
## alternative hypothesis: true location shift is greater than 0
```

3d

Question

At 1% significance, and one-tailed, would you reject the null hypothesis that the values of CLEC and ILEC are similar?

Answer

Yes, we would reject H0 since p-value < 0.01

Question 4

One of the assumptions of some classical statistical tests is that our population data should be roughly normal. Let's explore one way of visualizing whether a sample of data is normally distributed.

4a

Instruction

Make a function called norm_qq_plot() that takes a set of values

```
norm_qq_plot <- function(values) {
  # (i) Create a sequence of probability numbers from 0 to 1, with ~100
0 probabilities in between
  probs1000 <- seq(0, 1, 0.001)
  # (ii) Calculate ~1000 quantiles of our values
  q_vals <- quantile(values, probs = probs1000)
  # (iii) Calculate ~1000 quantiles of a perfectly normal distribution
with the same mean and standard deviation as our values
  q_norm <- qnorm(p = probs1000, mean = mean(values), sd = sd(values))
  # (iv) Create a scatterplot comparing the quantiles of a normal distr
ibution versus quantiles of values
  plot(q_norm, q_vals, xlab="normal quantiles", ylab="values quantiles")
  # (v) Draw a red line with intercept of 0 and slope of 1, comparing t
hese two sets of quantiles
  abline(a = 0, b = 1, col="red", lwd=2) # a:intercept, b:slope
}
```

4b

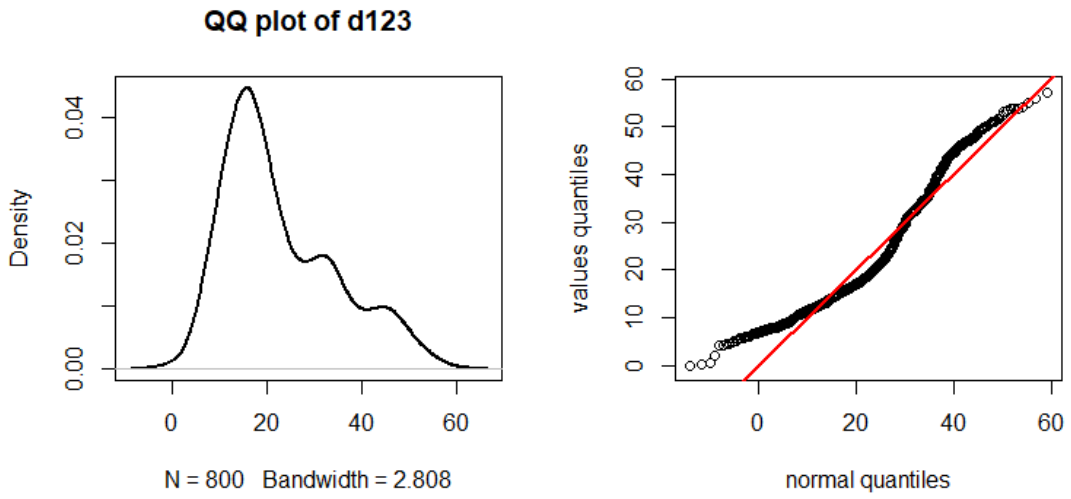
Instruction

Confirm that your function works by running it against the values of our d123 distribution from week 3 and checking that it looks like the given plot

```r
set.seed(123123)

d1 <- rnorm(n=500, mean=15, sd=5)
d2 <- rnorm(n=200, mean=30, sd=5)
d3 <- rnorm(n=100, mean=45, sd=5)
d123 <- c(d1, d2, d3)

par(mfrow = c(1,2))
plot(density(d123), main = "QQ plot of d123", lwd = 2)
norm_qq_plot(d123)
```



Comment

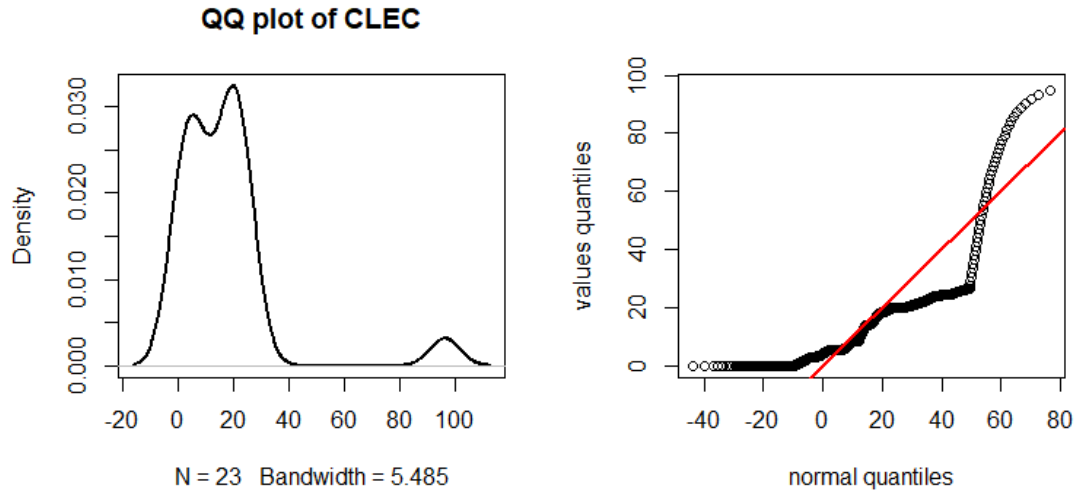
The QQplot of d123 suggests that it is not normally distributed. Rather, d123 appears to exhibit patterns of a bimodal distribution.

4c

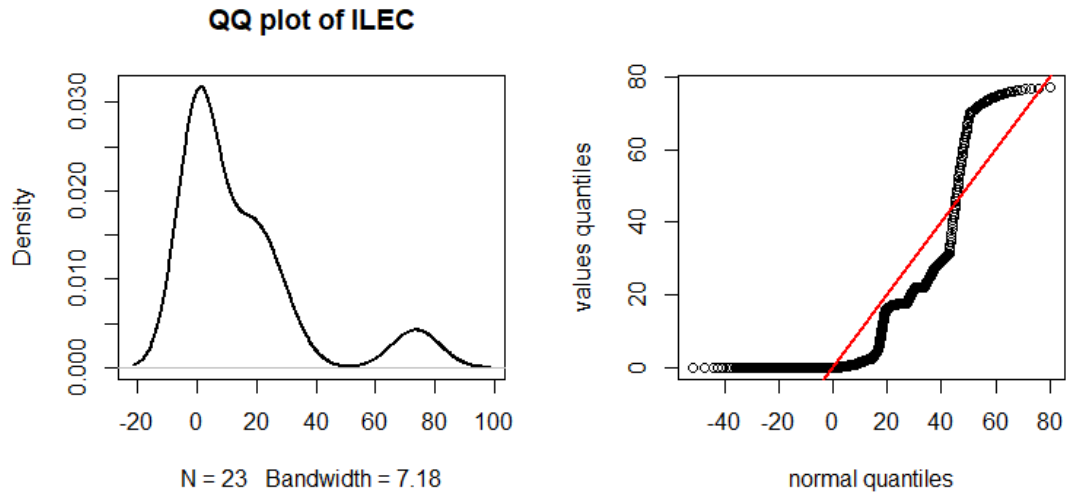
Instruction

Traditional statistical t-tests to compare the means of two populations require that the two populations are normally distributed. Use your normal Q-Q plot function, norm_qq_plot, to check if the values from each of the CLEC and ILEC samples we compared in question 2 could be normally distributed. What's your conclusion?

```r
# QQ-plotting for CLEC
par(mfrow = c(1,2))
response_wide <- response_wide[!is.na(response_wide$CLEC), ]
plot(density(response_wide$CLEC), main = "QQ plot of CLEC", lwd = 2)
norm_qq_plot(response_wide$CLEC)
```




```r
# QQ-plotting for ILEC
par(mfrow = c(1,2))
plot(density(response_wide$ILEC), main = "QQ plot of ILEC", lwd = 2)
norm_qq_plot(response_wide$ILEC)
```



Conclusion

As observed in the graphs above, there are many unaligned data points in both CLEC and ILEC's QQplots, so one could easily conclude that both are not normally distributed.