

# HW 02

Due Thursday, October 15, 11:59 PM

Matthew Xiao

```
library(tidyverse)
licorice <- read_csv("data/licorice.csv")
```

## Exercise 1

```
c_licorice <- licorice %>% filter(!is.na(pacu30min_throatPain))

n_sims <- 1000
set.seed(1)
boot_dist = numeric(n_sims)

for (i in 1:n_sims){
  set.seed(i)
  indices <- sample(1:nrow(c_licorice), replace = TRUE)
  boot_mean <- c_licorice %>%
    slice(indices) %>%
    summarize(boot_meean = mean(pacu30min_throatPain)) %>% pull()
  boot_dist[i] = boot_mean
}

boot_means <- tibble(boot_dist)
boot_means %>% summarize(Lower = quantile(boot_dist, 0.025),
                        Upper = quantile(boot_dist, 0.975)) %>%
  knitr::kable()
```

Lower	Upper
0.4891631	0.8112661

```
t.test(c_licorice$pacu30min_throatPain, conf.level = .95)
```

```
##
## One Sample t-test
##
## data: c_licorice$pacu30min_throatPain
## t = 7.9287, df = 232, p-value = 9.291e-14
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.4870277 0.8091096
## sample estimates:
```

```
## mean of x
## 0.6480687
```

Both the clt- based approach and the simulation approach created similar bounds of around .49 for the lower bound and .81 for the upper bounds. The bounds for the simulation approach are slightly smaller as the lower bound is slightly higher as well as the upper bound is as well. In both cases the 95% constructed region creates bounds of the pain level of .487 to .809. If we would randomly sample the patient data for throat pain, following the same approach we would be 95% confident that 95% of the new constructed confidence intervals to encompass the true mean.

## Exercise 2

```
b_licorice <- licorice %>% summarize(mean_b = mean(preOp_calcBMI))

set.seed(2)
n_sims <- 2000
boot_dist = numeric(n_sims)
for(i in 1:n_sims){
  set.seed(i)
  indices <- sample(1:nrow(licorice), replace = T)
  boot_mean <- licorice %>%
    slice(indices) %>%
    summarize(boot_mean = mean(preOp_calcBMI)) %>%
    pull()

  boot_dist[i] <- boot_mean
}
mu_0 = 26
boot_means <- tibble(boot_dist)

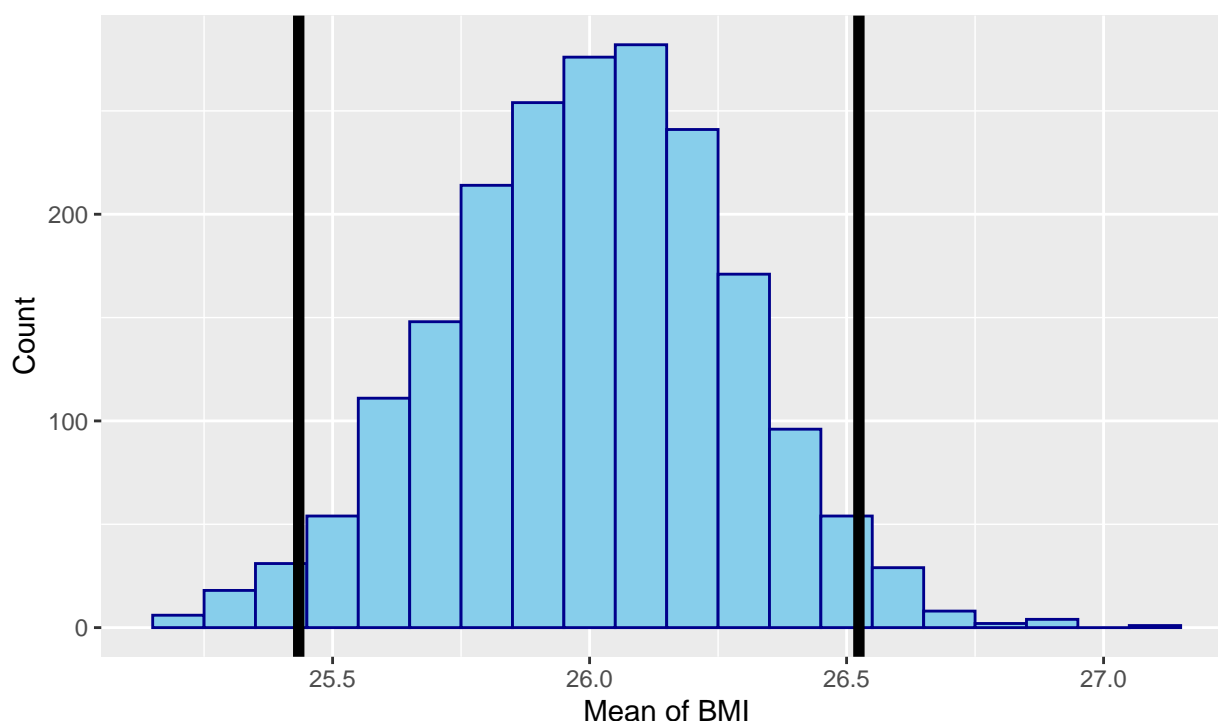
offset <- boot_means %>%
  summarize(mu_0 - mean(boot_dist)) %>% pull()
boot_means <- tibble(boot_dist)
boot_means %>% summarize(Lower = quantile(boot_dist, 0.025),
                          Upper = quantile(boot_dist, 0.975)) %>%
  knitr::kable()
```

Lower	Upper
25.01972	26.10958

```
boot_means <- boot_means %>%
  mutate(shifted_means = boot_dist+offset)
ggplot(data = boot_means, aes(x = shifted_means)) +
  geom_histogram(binwidth = 0.1, color = "darkblue", fill = "skyblue") +
  labs(x = "Mean of BMI",
       y = "Count",
       title = "The graph displays the null distribution for
the mean BMI of the Preoperation Patients with the assumption that the
mean BMI is 26.") +
  geom_vline(xintercept = quantile(boot_means$shifted_means, 0.025),
            lwd = 2,
            color = "black") +
  geom_vline(xintercept = quantile(boot_means$shifted_means, 0.975),
```

```
lwd= 2,
color = "black")
```

The graph displays the null distribution for the mean BMI of the Preoperation Patients with the assumption that the mean BMI is 26.



```
obs <- licorice %>%
  summarize(mean(preOp_calcBMI)) %>%
  pull()
dif <- mu_0 - obs
boot_means <- boot_means %>%
  mutate(shifted_means = boot_dist + offset)

boot_means1 <- boot_means %>%
  mutate(extreme = ifelse(shifted_means <= obs |
    shifted_means >= mu_0 + dif, 1, 0)) %>%
  count(extreme) %>%
  mutate(prob = n / sum(n)) %>%
  select(prob) %>%
  slice(2)
boot_means1 %>% knitr::kable()
```

prob
0.144

Based on the simulated data. It seems as if that the probability that the mean of sampled patients' BMI have a 25.59 or more extreme BMI is 14.4%. This is above the general pvalue of .05 which means that we have insufficient evidence to reject the null hypothesis (that the BMI of patients is the same as the rest of the German population. )

### Exercise 3

```
B_pain <- c_licorice %>%
  mutate(asapain = ifelse(pacu30min_throatPain >0, 1, 0))

t.test(B_pain$preOp_asa ~ asapain,
  data = B_pain,
  mu = 0,
  var.equal = FALSE,
  alternative = "two.sided",
  conf.level = 0.95)

##
## Welch Two Sample t-test
##
## data: B_pain$preOp_asa by asapain
## t = -1.2976, df = 124.15, p-value = 0.1968
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.29954887 0.06230774
## sample estimates:
## mean in group 0 mean in group 1
## 2.053254 2.171875
```

### Exercise 4

```
t.test(pacu30min_throatPain ~ treat,
  data = c_licorice,
  mu = 0,
  var.equal = FALSE,
  alternative = "greater",
  conf.level = 0.95)

##
## Welch Two Sample t-test
##
## data: pacu30min_throatPain by treat
## t = 4.8035, df = 157.3, p-value = 1.804e-06
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
## 0.4932019 Inf
## sample estimates:
## mean in group 0 mean in group 1
## 1.0258621 0.2735043
```

Those that were treated with sugar (treat 0) had a higher incidence of having throat pain 30 after. We recieved a pvalue of 1.8e-06 which is much smaller than 0.05 thus we can reject the null hypothesis and state that we have evidence that licorice decreases the incidence of having throat pain 30 min after the operation.

### Exercise 5

```
set.seed(5)
cc_licorice <- c_licorice %>%
  mutate(pain = ifelse(pacu30min_throatPain >0 | pacu30min_swallowPain >0, 1, 0))
```

```

sugar <- cc_licorice %>%
  filter(treat == 0 )
licorice_l <- cc_licorice %>%
  filter(treat == 1 )
n_sims <- 2000
boot_diffs <- numeric(n_sims)

for(i in 1:n_sims){
  # create indices
  indices_h <- sample(1:nrow(sugar), replace = T)
  indices_p <- sample(1:nrow(licorice_l), replace = T)
  # bootstrap est. group means
  temp_h <- sugar %>%
    slice(indices_h) %>%
    summarize(mean1 = mean(pain)) %>%
    select(mean1) %>%
    pull()
  temp_p <- licorice_l %>%
    slice(indices_p) %>%
    summarize(mean_jitter = mean(pain)) %>%
    select(mean_jitter) %>%
    pull()

  boot_diffs[i] <- temp_h - temp_p
}
boot_diffs <- tibble(diffs = boot_diffs)
boot_diffs %>%
  summarize(lower = quantile(diffs, 0.025),
            upper = quantile(diffs, 0.975))

## # A tibble: 1 x 2
##   lower upper
##   <dbl> <dbl>
## 1 0.0446 0.277

obs_diff <- boot_diffs %>%
  summarize(obs_diff = mean(diffs)) %>%
  pull()
offset <- boot_diffs %>%
  summarize(offset = 0 - mean(diffs)) %>%
  pull()
null_dist <- boot_diffs %>%
  mutate(centered_diffs = diffs + offset) %>%
  select(centered_diffs)
null_dist %>%
  mutate(extreme = ifelse(centered_diffs > abs(obs_diff), 1, 0)) %>%
  summarize(p_val = mean(extreme))

## # A tibble: 1 x 1
##   p_val
##   <dbl>
## 1 0.0055

```

The pvalue created is 0.0055 which is much smaller than the alpha level of 0.05. thus we have evidence that

to reject the null hypothesis and conclude that those who take licorice in general will less likely have pain 30 minutes after.

**Exercise 6**

We do have enough evidence. we only know that 30 minutes after that a licorice gargle will reduce pain. However we can not tell if that hold true 90 minutes or 4 hours or at 1 am. That would require further extrapolation of the data in which then we can conclude with the data we collected that a licorice gargle will reduce the pain that a patient felt in general.

**Exercise 7**

TRUE

**Exercise 8**

FALSE. Our p-value can not be evidence for, but rather it would only be evidence that does not reject it can not support.

**Exercise 9**

True

**Exercise 10**

TRUE

**Exercise 11**

FALSE we can not know for sure

**Exercise 12**

TRUE