

# STATS 205: Homework Assignment 3

Brian Liu

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## Solution to Problem 1

(i)

```
library(bootstrap); data(law)
t(law)
```

```
##           1      2      3      4      5      6      7      8      9     10
## LSAT 576.00 635.0 558.00 578.00 666.00 580.00 555 661.00 651.00 605.00
## GPA   3.39   3.3   2.81   3.03   3.44   3.07   3   3.43   3.36   3.13
##           11     12     13     14     15
## LSAT 653.00 575.00 545.00 572.00 594.00
## GPA   3.12   2.74   2.76   2.88   2.96
```

```
theta.hat = cor(law$LSAT, law$GPA); theta.hat
```

```
## [1] 0.7763745
```

```
library(partitions)
```

```
n = 15
```

```
allCompositions = compositions(n, n); allCompositions[,1:5]
```

```
##           [,1] [,2] [,3] [,4] [,5]
## [1,]      15   14   13   12   11
## [2,]       0    1    2    3    4
## [3,]       0    0    0    0    0
## [4,]       0    0    0    0    0
## [5,]       0    0    0    0    0
## [6,]       0    0    0    0    0
## [7,]       0    0    0    0    0
## [8,]       0    0    0    0    0
## [9,]       0    0    0    0    0
## [10,]      0    0    0    0    0
## [11,]      0    0    0    0    0
## [12,]      0    0    0    0    0
## [13,]      0    0    0    0    0
## [14,]      0    0    0    0    0
## [15,]      0    0    0    0    0
```

```
allCompositions.sub = allCompositions[, sample(1:dim(allCompositions)[2], size=10000, replace=FALSE)]
```

```
draw.bootstrap.samples = function(df){
  n = dim(df)[1]
  ind = sample(n, replace = TRUE)
  cor.bootstrap.replicate = cor(df[ind, "LSAT"], df[ind, "GPA"])
  return(cor.bootstrap.replicate)
}
```

```
R = 10000
```

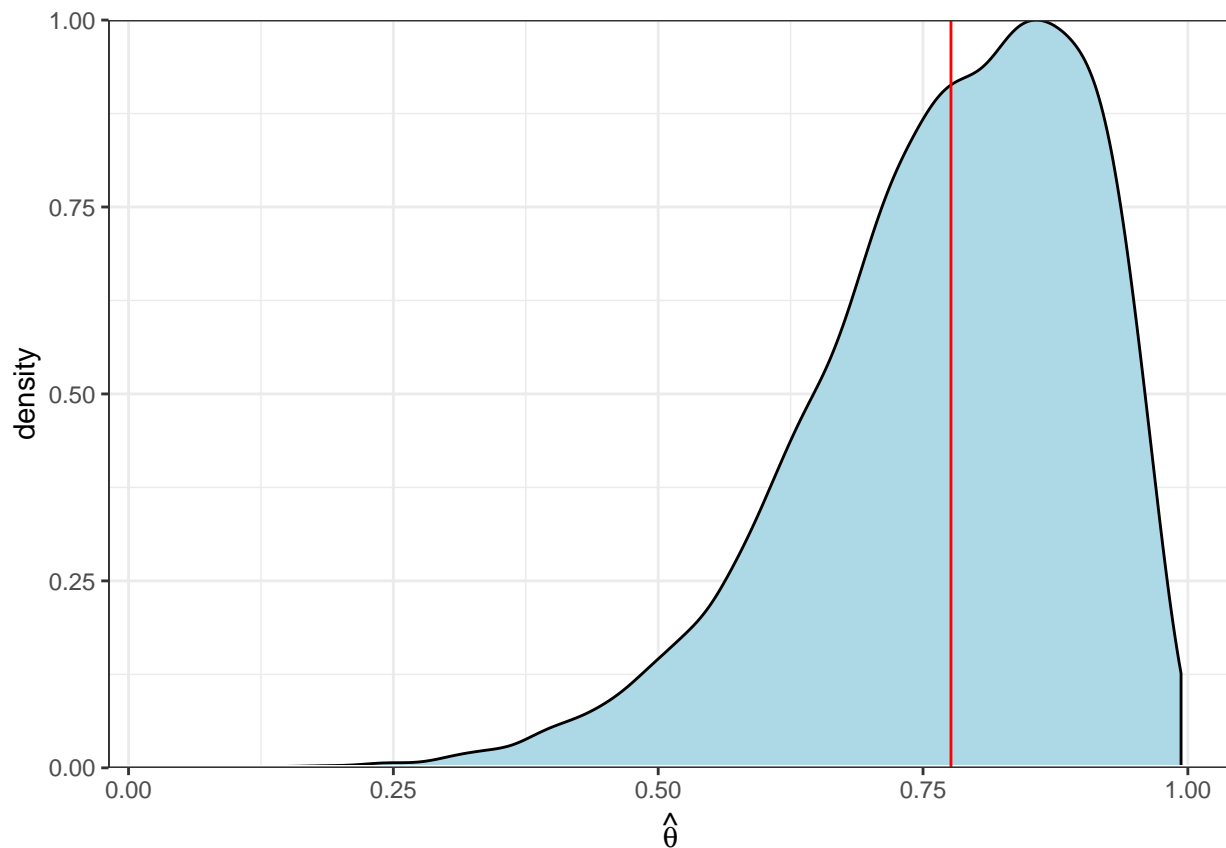
```

theta.hat.star = replicate(R, draw.bootstrap.samples(law))
# make a ggplot
library(ggplot2)

## Registered S3 methods overwritten by 'ggplot2':
##   method      from
##   [.quosures   rlang
##   c.quosures   rlang
##   print.quosures rlang

theta.hat.star.df = data.frame(theta.hat.star = theta.hat.star)
ggplot(theta.hat.star.df) +
  geom_density(aes(x = theta.hat.star, y = ..scaled..),
    fill = "lightblue") +
  geom_hline(yintercept=0, colour="white", size=1) +
  theme_bw() +
  ylab("density") +
  xlab(bquote(hat(theta))) +
  geom_vline(xintercept = theta.hat, col = "red")+
  scale_y_continuous(expand = c(0,0))

```



(ii)

```
sd(theta.hat.star)
```

```
## [1] 0.133341
```

## Solution to Problem 2

(i)

67 runs resulting in swallowing attempts  
58 successful  
9 failed

$H_0 : p = 0.6$

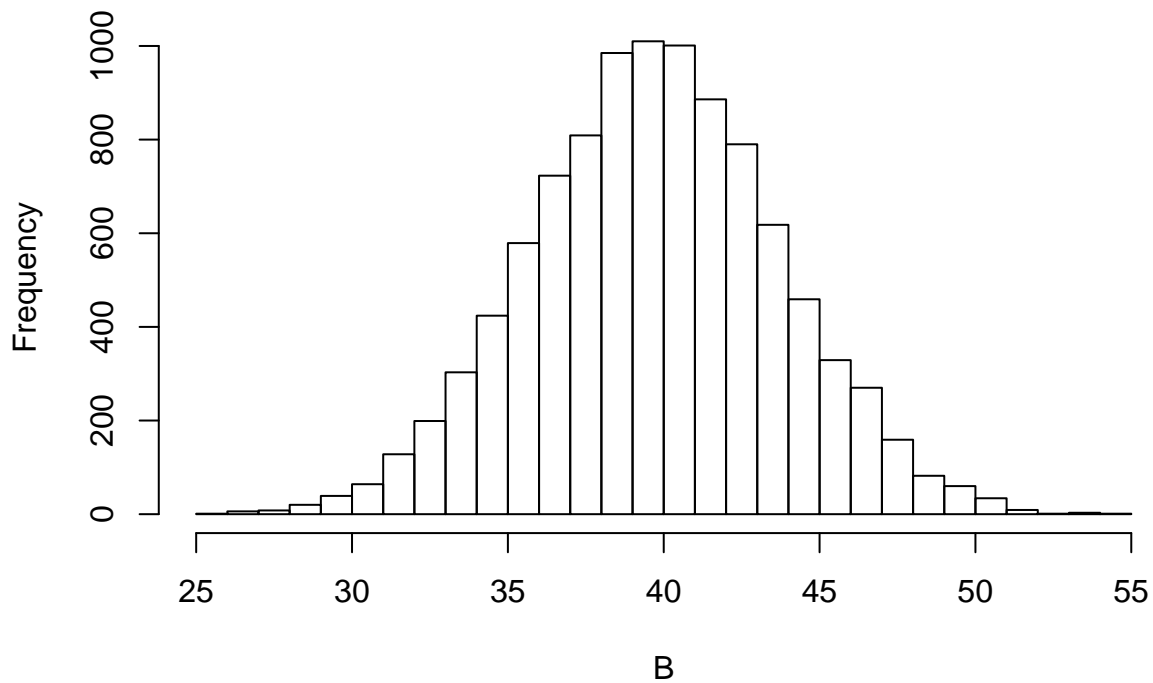
$H_A : p > 0.6$

```
n = 67
successes = 58
pbar = successes / n; pbar
```

```
## [1] 0.8656716
```

```
p0 = 0.6; nsim = 10000
B = rbinom(nsim, size = n, prob = p0)
hist(B, breaks = 30)
```

**Histogram of B**



Test statistic  $Z$ :

$$Z_0 = \frac{B - 67(0.6)}{(67(0.6)(0.4))^{\frac{1}{2}}}$$

```
qnorm((1-0.05), mean = 0, sd = 1)
```

```
## [1] 1.644854
```

Rejection region:  $Z \geq z_{0.05} = 1.645$

Observed test statistic  $Z_o$ :

$$Z_o = \frac{58 - 67(0.6)}{(67(0.6)(0.4))^{\frac{1}{2}}} = 4.44$$

```
numerator = successes - (n * p0)
denominator = sqrt(n * p0 * (1.0 - p0))
Z.obs = numerator / denominator; Z.obs
```

```
## [1] 4.438917
```

The large sample approximation value  $Z_o = 2.5 > 1.645$  and thus we reject  $H_0 : p = 0.6$  in favor of  $p > 0.6$  at the approximate  $\alpha = 0.05$  level. Thus there is evidence that the success rate of swallowing attempts is greater than 0.6.

(ii)

Power is the probability of rejecting  $H_0$  when  $H_A$  is true. We found that test reject  $H_0$  is  $Z \geq z_{0.05} = 1.645$ . Therefore, if  $p = 0.7$ ,

$$Z_o = \frac{58 - 67(0.6)}{(67(0.6)(0.4))^{\frac{1}{2}}} = 4.44$$

is no longer standard normal.

We have

$$Z_{o7} = \frac{58 - 67(0.7)}{(67(0.7)(0.3))^{\frac{1}{2}}} = 2.96$$

```
p1 = 0.7
numerator = successes - (n * p1)
denominator = sqrt(n * p1 * (1.0 - p1))
Z.obs.seven = numerator / denominator; Z.obs.seven
```

```
## [1] 2.959211
```

$$Power = P(Z \geq 1.645 | p = 0.7)$$

$$= P_{p=0.7} \left( \frac{B - 67(0.6)}{(67(0.6)(0.4))^{\frac{1}{2}}} \geq 1.645 \right)$$

$$= P_{p=0.7} (B \geq 1.645(67(0.6)(0.4))^{\frac{1}{2}} + 67(0.6))$$

$$= P_{p=0.7} \left( \frac{B - 67(0.7)}{(67(0.7)(0.3))^{\frac{1}{2}}} \geq \frac{1.645(67(0.6)(0.4))^{\frac{1}{2}} + 67(0.6) - 67(0.7)}{(67(0.7)(0.3))^{\frac{1}{2}}} \right)$$

```
triple_product = n * p0 * (1.0 - p0)
first_term = 1.645 * sqrt(triple_product)
second_term = n * p0
third_term = n * p1
bottom_term = n * p1 * (1.0 - p1)
```

```
p7_numerator = first_term + second_term - third_term
p7_denominator = sqrt(bottom_term)
Pp_7_zvalue = p7_numerator / p7_denominator; Pp_7_zvalue
```

```
## [1] -0.02761144
```

$$P(Z^* \geq -0.0276) = 0.4890$$

```
pvalue = pnorm(Pp_7_zvalue); pvalue
```

```
## [1] 0.488986
```

If  $p = 0.8$ ,

$$Power = P(Z \geq 1.645 | p = 0.8)$$

$$= P_{p=0.8} \left( \frac{B - 67(0.8)}{(67(0.8)(0.2))^{\frac{1}{2}}} \geq \frac{1.645(67(0.6)(0.4))^{\frac{1}{2}} + 67(0.6) - 67(0.8)}{(67(0.8)(0.2))^{\frac{1}{2}}} \right)$$

```
p2 = 0.8
triple_product = n * p0 * (1.0 - p0)
first_term = 1.645 * sqrt(triple_product)
second_term = n * p0
third_term = n * p2
bottom_term = n * p2 * (1.0 - p2)
p8_numerator = first_term + second_term - third_term
p8_denominator = sqrt(bottom_term)
Pp_8_zvalue = p8_numerator / p8_denominator; Pp_8_zvalue
```

```
## [1] -2.077971
```

$$P(Z^* \geq -2.078) = 0.01886$$

```
# pvalue = pnorm(-abs(Pp_7_zvalue)); pvalue
pvalue = pnorm(Pp_8_zvalue); pvalue
```

```
## [1] 0.01885601
```

### Solution to Problem 3

**Summary:** Estimate for  $\hat{p} = 0.8615$  and estimate for standard deviation of  $\hat{p} = 0.04284$ .

Estimate for  $p$  using binomial confidence interval, `binom.confint()`:

```
library(binom)
binom.confint(x=56, n=65, conf.level=.95, methods = "asymptotic")
```

```
##      method x  n      mean      lower      upper
## 1 asymptotic 56 65 0.8615385 0.7775744 0.9455025
```

$$\hat{p} = (0.7776, 0.9455)$$

Estimate for  $p$  using 1-sample proportions test without continuity correction, `prop.test()`:

```
prop.test(x=56, n=65, p = 0.6, conf.level=0.95, alternative = c("greater"))
```

```
##
## 1-sample proportions test with continuity correction
##
## data: 56 out of 65, null probability 0.6
## X-squared = 17.452, df = 1, p-value = 1.473e-05
## alternative hypothesis: true p is greater than 0.6
## 95 percent confidence interval:
## 0.7676875 1.0000000
## sample estimates:
## p
## 0.8615385
```

$$p = 0.8615$$

Estimate for  $p$  using Exact Binomial Test:

```
binom.test(x=56, n=65, p = 0.6, alternative = c("greater"), conf.level = 0.95)
```

```
##
## Exact binomial test
##
## data: 56 and 65
## number of successes = 56, number of trials = 65, p-value =
## 4.096e-06
## alternative hypothesis: true probability of success is greater than 0.6
## 95 percent confidence interval:
## 0.7708174 1.0000000
## sample estimates:
## probability of success
## 0.8615385
```

Standard error of  $\hat{p}$  is:

$$\begin{aligned} & \sqrt{\frac{p(1-p)}{n}} \\ &= \sqrt{\frac{(0.6)(0.4)}{65}} \\ &= 0.06076 \end{aligned}$$

```
p = 0.6
n = 65
numerator = p * (1 - p)
denominator = n
answer = sqrt(numerator/denominator); answer
```

```
## [1] 0.06076436
```

and estimate is:

$$\sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$$

$$= \sqrt{\frac{(0.8615)(1 - 0.8615)}{65}}$$

$$= 0.04284$$

```
p.hat = 0.8615
n = 65
numerator = p.hat * (1 - p.hat)
denominator = n
answer = sqrt(numerator/denominator); answer

## [1] 0.04284458
```

## Solution to Problem 4

```
binom.confint(x = 56, n = 65, conf.level = 0.96, methods = "all")
```

```
##           method x  n      mean      lower      upper
## 1  agresti-coull 56 65 0.8615385 0.7488973 0.9301180
## 2    asymptotic 56 65 0.8615385 0.7735567 0.9495202
## 3         bayes 56 65 0.8560606 0.7655984 0.9375798
## 4      cloglog 56 65 0.8615385 0.7439982 0.9276404
## 5         exact 56 65 0.8615385 0.7480632 0.9371740
## 6         logit 56 65 0.8615385 0.7484912 0.9286194
## 7        probit 56 65 0.8615385 0.7545841 0.9312980
## 8        profile 56 65 0.8615385 0.7589798 0.9334925
## 9           lrt 56 65 0.8615385 0.7589836 0.9335307
## 10      prop.test 56 65 0.8615385 0.7483484 0.9308913
## 11         wilson 56 65 0.8615385 0.7514483 0.9275670
```

Here are the rows relevant to our problem:

```
##           method x  n      mean      lower      upper
## 1  agresti-coull 56 65 0.8615385 0.7488973 0.9301180
## 2    asymptotic 56 65 0.8615385 0.7735567 0.9495202
## 5         exact 56 65 0.8615385 0.7480632 0.9371740
## 11         wilson 56 65 0.8615385 0.7514483 0.9275670
```

where `asymptotic` is Laplace-Wald, `agresti-coull` is Agresti-Coull, `exact` is Clopper-Pearson, and `wilson` is Wilson.

It looks like `agresti-coull` and `exact` are fairly similar in terms of the location of the interval, while `asymptotic` is skewed towards the “right” side of the intervals, and `wilson` has the smallest range.

## Solution to Problem 5

```
plant_vector <- c(926, 288, 293, 104)

expected = c(9/16, 3/16, 3/16, 1/16)

# goodness-of-fit test

res <- chisq.test(x = plant_vector, p = expected); res
```

```
##
## Chi-squared test for given probabilities
##
## data: plant_vector
## X-squared = 1.4687, df = 3, p-value = 0.6895
```

```
res$expected
```

```
## [1] 906.1875 302.0625 302.0625 100.6875
```

```
res$observed
```

```
## [1] 926 288 293 104
```

The **p-value** of the test is  $p = 0.6895$ , which is more than the significance level  $\alpha = 0.05$ . We cannot conclude that the data does *not* support Mendelian theory at the  $\alpha = 0.05$  level.

## Solution to Problem 6

```
df = data.frame(Low = c(0, 2), High = c(5, 1))
rownames(df) = c("Multiple attack", "Primary attack"); df
```

```
##              Low High
## Multiple attack    0    5
## Primary attack     2    1
```

```
fisher.test(df, alternative = "less")
```

```
##
## Fisher's Exact Test for Count Data
##
## data: df
## p-value = 0.1071
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
##  0.00000 1.75251
## sample estimates:
## odds ratio
##          0
```

There is *not enough evidence* that the unknown probability that a multiple-attack patient will have low reactivity is *less than* the unknown probability that a primary-attack patient will have low reactivity at the  $\alpha = 0.05$  level. The  $P$ -value achieved by these data if we use Fisher's exact test of  $H_0$  against the alternative  $p_1 < p_2$  is 0.1071.

```
df = data.frame(Low = c(0, 2), High = c(5, 1))
rownames(df) = c("Multiple attack", "Primary attack"); df
```

```
##              Low High
## Multiple attack    0    5
## Primary attack     2    1
```

```
fisher.test(df, alternative = "two.sided")
```

```
##
## Fisher's Exact Test for Count Data
##
## data: df
```



```
## p-value = 0.1071
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
## 0.00000 2.75184
## sample estimates:
## odds ratio
## 0
```

The  $P$ -value achieved when testing the null against a two-sided hypothesis is the same, 0.1071, and therefore, there is *not enough evidence* that the unknown probability that a multiple-attack patient will have low reactivity is *not equal* to the unknown probability that a primary-attack patient will have low reactivity.

## Solution to Problem 7

Since we want to find out if having tonsils reduces the rate of Hodgkin's, we want to see if there is a higher rate of tonsillectomy among Hodgkin's cases than among non-Hodgkin's cases. Therefore, we will test the null hypothesis that there is no difference in the rate of tonsillectomy between the two populations of Hodgkin's and non-Hodgkin's cases against the alternative hypothesis that there is higher rate of tonsillectomy among Hodgkin's cases.

$$H_0 : p_1 = p_2$$

$$H_A : p_1 > p_2$$

```
x = c(67, 43)
n = c(101, 107)
prop.test(x, n, alternative = c("greater"), conf.level = 0.99)

##
## 2-sample test for equality of proportions with continuity
## correction
##
## data:  x out of n
## X-squared = 13.229, df = 1, p-value = 0.0001379
## alternative hypothesis: greater
## 99 percent confidence interval:
## 0.09655707 1.00000000
## sample estimates:
## prop 1 prop 2
## 0.6633663 0.4018692
```

The 99% confidence interval for difference between rate of tonsillectomy in Hodgkin's cases and rate of tonsillectomy in non-Hodgkin's cases is between 9.66% and 100%.

The  $P$ -value achieved by these data if we use a 2-sample test for equality of proportions with continuity correction is 0.0001379. There is *strong evidence* at the  $\alpha = 0.05$  level that there is higher rate of tonsillectomy among Hodgkin's cases.

## Solution to Problem 8

```
elisa_matrix <- matrix(c(82, 13, 6, 0), nrow=2, ncol=2, byrow=TRUE, dimnames = list("ABC-ELISA" = c("+"
```

```
##           Standard ELISA
## ABC-ELISA  +   -
##           + 82 13
##           -  6  0
```

```
# prop.test(x = elisa_matrix)

mcnemar.test(x = elisa_matrix)
```

```
##
## McNemar's Chi-squared test with continuity correction
##
## data:  elisa_matrix
## McNemar's chi-squared = 1.8947, df = 1, p-value = 0.1687
```

The  $P$ -value for McNemar's test is 0.1687. What we can conclude concerning the hypothesis of equal proportions positive for both ELISA tests is that equal proportions may not be positive for both ELISA tests.

## Solution to Problem 9

```
ptsd_matrix <- matrix(c(29, 7, 21, 30), nrow = 2, ncol = 2, byrow = TRUE, dimnames = list(c("Yes", "No"),
```

```
##           Battered women
## Yes                29
## No                 21
## Maritally distressed women who had not experienced battering
## Yes                                7
## No                                30
```