# Hao-HW6

```
#setwd("~/Google Drive/CUNY/git/DATA606/Lab6")
library(dplyr)
library(ggplot2)

# a function to return confidence interval for a proportion based on p, n and cl
prop.ci = function(p, n, cl) {
    moe = qnorm(mean(c(cl, 1))) * sqrt(p * (1 - p) / n)
    return(paste("(", round(p - moe, 4), ",", round(p + moe, 4), ")"))
}

# a function to return confidence interval for the difference between two proportions based on p, n and
prop.diff.ci = function(p1, n1, p2, n2, cl) {
    moe = qnorm(mean(c(cl, 1))) * sqrt(p1 * (1 - p1) / n1 + p2 * (1 - p2) / n2)
    return(paste("(", round(p1 - p2 - moe, 4), ",", round(p1 - p2 + moe, 4), ")"))
}
```

### 6.6

- a) False. The CI is constructed to estimate the population proportion, not the sample proportion.
- b) True.
- c) True.
- d) False. At a 90% confidence level, the margin of error would decrease.

### 6.12

- a) 48% is a sample statistic because it is calculated based on the sample; the population parameter would require surveying the entire population of Americans.
- b) (0.4524, 0.5076)
- c) Assuming that the sample was representative of the general population, then the CI should be accurate as the sample size is large and the central limit theorem should apply.
- d) No, the confidence interval straddles 50%, so it is unclear whether a majority support or do not support the legalization of marijuana.

```
prop.ci(0.48, 1259, 0.95)
## [1] "( 0.4524 , 0.5076 )"
6.20
599 people would need to be sampled.
p = 0.48
moe = 0.02
cl = 0.95
n = (p * (1-p))^2 / moe^2 * qnorm(mean(c(cl, 1)))^2
n
```

## [1] 598.3087

#### 6.28

6.43 Practice

The 95% CI is (-0.0175, 0.0015) which includes zero. As such, at the 95% confidence level, we cannot be sure if there is a difference between the two proportions.

```
prop.diff.ci(0.08, 11545, 0.088, 4691, 0.95)
## [1] "( -0.0175 , 0.0015 )"
```

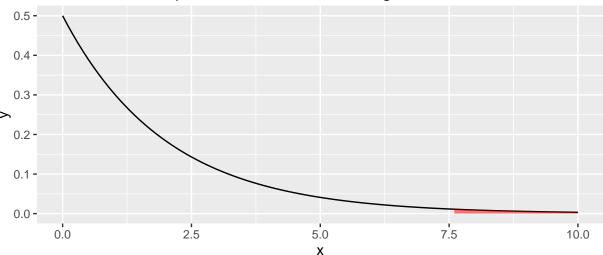
H<sub>0</sub>: No option is favored above any others

H<sub>A</sub>: At least one option is favored above one or more others

Since the p-value is below 5%, we reject the null hypothesis and accept the alternative that at least one option is favored above one or more others.

```
# create data frame to house actual and expected results
rps = data.frame(actual = c(43, 21, 35), expected = c((43 + 21 + 35)/3, (43 + 21 + 35)/3, (43 + 21 + 35)/3
                 row.names = c('Rock', 'Paper', 'Scissor'))
chi.sq = as.numeric(rps %>% mutate(Z2 = (actual - expected)^2 / expected) %>%
  summarise(chi.sq = sum(Z2)))
df = nrow(rps) - 1
1 - pchisq(chi.sq, df)
## [1] 0.02334025
chisq.test(rps$actual)
##
## Chi-squared test for given probabilities
##
## data: rps$actual
## X-squared = 7.5152, df = 2, p-value = 0.02334
chi.sq.stat = chisq.test(rps$actual)
x = seq(0, 10, 0.1)
xy = data.frame(x = x, y = dchisq(x, df))
shade = xy[x > chi.sq.stat$statistic, ]
xy \%>\% ggplot(aes(x = x, y = y)) +
 geom line() +
  geom_ribbon(data = shade, aes(ymax = y, ymin= 0), fill = 'red', alpha = 0.5) +
 ggtitle(paste('Chi-Square Distribution with', df, 'Degrees of Freedom'))
```

## Chi-Square Distribution with 2 Degrees of Freedom



#### 6.44

- a) H<sub>0</sub>: Barking deer have no preference as it relates to foraging in certain habitats H<sub>A</sub>: Barking deer do have a preference as it relates to foraging in certain habitats
- b) Chi-square test for one-way table

mutate(total = no.new + new) %>%

mutate(total = no.new + new) %>%

algo2 = algo %>%

- c) Independence: Met, the type of habitat for one site should not affect the others Sample size / distribution: Met, each habitat type has at least 5 expected cases
- d) The p-value is essentially zero, so we can reject the null hypothesis and accept the alternative that Barking deer do indeed have a preference as it relates to foraging in certain habitats

```
habitat = data.frame(actual = c(4, 16, 61, 345), expected = 426 * c(0.048, 0.147, 0.396, (1-0.048-0.147))
                     row.names = c('Woods', 'Cultivatd grassplot', 'Deciduous forests', 'Other'))
chi.sq = habitat %>% mutate(Z2 = (actual - expected)^2 / expected) %>%
  summarise(chi.sq = sum(Z2))
df = nrow(habitat) - 1
1 - pchisq(as.numeric(chi.sq), df)
## [1] 0
chisq.test(habitat\alpha, p = c(0.048, 0.147, 0.396, 1-0.048-0.147-0.396))
##
   Chi-squared test for given probabilities
##
##
## data: habitat$actual
## X-squared = 284.06, df = 3, p-value < 2.2e-16
6.47 Practice
# first reproduce example on pg 298 in book
algo = data.frame(no.new = c(3511, 1749, 1818), new = c(1489, 751, 682), row.names = c('current', 'test
algo.expected.prop = algo %>%
```

summarise(no.new.prop = sum(no.new)/sum(total), new.prop = sum(new)/sum(total))

```
mutate(no.new.expected = algo.expected.prop$no.new.prop * total, new.expected = algo.expected.prop$ne
chi.sq = algo2 %>% mutate(Z2a = (no.new - no.new.expected)^2 / no.new.expected, Z2b = (new - new.expect
  summarise(chi.sq = sum(Z2a) + sum(Z2b))
df = (nrow(algo) - 1) * (ncol(algo) - 1)
1 - pchisq(as.numeric(chi.sq), df)
## [1] 0.04688013
chisq.test(t(algo))
##
   Pearson's Chi-squared test
##
## data: t(algo)
## X-squared = 6.1203, df = 2, p-value = 0.04688
# attempt 6.47 using the same logic
offshore = data.frame(support = c(154, 132), oppose = c(180, 126), unsure = c(104, 131),
                      row.names = c('grad', 'notGrad'))
offshore.expected.prop = offshore %>%
  mutate(total = support + oppose + unsure) %>%
  summarise(support.prop = sum(support)/sum(total), oppose.prop = sum(oppose)/sum(total), unsure.prop =
offshore2 = offshore %>%
  mutate(total = support + oppose + unsure) %>%
  mutate(support.expected = offshore.expected.prop$support.prop * total,
         oppose.expected = offshore.expected.prop$oppose.prop * total,
         unsure.expected = offshore.expected.prop$unsure.prop * total)
chi.sq = offshore2 %% mutate(Z2a = (support - support.expected)^2 / support.expected,
                              Z2b = (oppose - oppose.expected)^2 / oppose.expected,
                              Z2c = (unsure - unsure.expected)^2 / unsure.expected) %>%
  summarise(chi.sq = sum(Z2a) + sum(Z2b) + sum(Z2c))
chi.sq
##
       chi.sq
## 1 11.46082
df = (nrow(offshore) -1)* (ncol(offshore) - 1)
1 - pchisq(as.numeric(chi.sq), df)
## [1] 0.003245752
chisq.test(t(offshore))
##
## Pearson's Chi-squared test
##
## data: t(offshore)
## X-squared = 11.461, df = 2, p-value = 0.003246
6.48
  a) Chi-square test for two-way table
```

b)  $H_0$ : There is no association between coffee intake and clinical depression  $H_A$ : There is an association between coffee intake and clinical depression

- c) 5.13% of women in the study suffer from depression; 94.86% do not
- d) The expected counts appear under the yes.exp and no.exp columns in the data frame below
- e) The p-value is 0.0003
- f) The conclusion of the hypothesis test is to reject the null and accept the alternative that there is an association between coffee intake and clinical depression
- g) Yes, because this was an observational study, no causal relationship can be established. As such, the observed association does not necessarily imply causation.

```
coffee = data.frame('1perWeek' = c(670, 11545), '2-6perWeek' = c(373, 6244), '1perDay' = c(905, 16329),
                    '2-3perDay' = c(564, 11726), '4perDay' = c(95, 2288), row.names = c('yes', 'no'))
coffee.expected.prop = coffee %>%
  mutate(total = X1perWeek + X2.6perWeek + X1perDay + X2.3perDay + X4perDay) %>%
  mutate(prop = total / sum(total)) %>%
  select(prop)
coffee.expected.prop
           prop
## 1 0.05138059
## 2 0.94861941
coffee2 = data.frame(intake = colnames(coffee), t(coffee)) %>%
  mutate(total = yes + no) %>%
  mutate(yes.exp = coffee.expected.prop$prop[1] * total, no.exp = coffee.expected.prop$prop[2] * total)
coffee2
##
          intake yes
                        no total yes.exp
## 1
      X1perWeek 670 11545 12215 627.6140 11587.386
## 2 X2.6perWeek 373 6244 6617 339.9854 6277.015
       X1perDay 905 16329 17234 885.4932 16348.507
## 4 X2.3perDay 564 11726 12290 631.4675 11658.532
       X4perDay 95 2288 2383 122.4400 2260.560
## 5
chi.sq = coffee2 %% mutate(Z2a = (yes - yes.exp)^2 / yes.exp, Z2b = (no - no.exp)^2 / no.exp) %>%
  summarise(chi.sq = sum(Z2a) + sum(Z2b))
chi.sq
##
       chi.sq
## 1 20.93161
df = (nrow(coffee) - 1) * (ncol(coffee) -1)
1 - pchisq(as.numeric(chi.sq), df)
## [1] 0.0003267104
chisq.test(coffee)
##
   Pearson's Chi-squared test
##
##
## data: coffee
## X-squared = 20.932, df = 4, p-value = 0.0003267
chi.sq.stat = chisq.test(coffee)
x = seq(0, 50, 0.2)
```

```
xy = data.frame(x = x, y = dchisq(x, df))
shade = xy[x > chi.sq.stat$statistic, ]
xy %>% ggplot(aes(x = x, y = y)) +
  geom_line() +
  geom_ribbon(data = shade, aes(ymax = y, ymin= 0), fill = 'red', alpha = 0.5) +
  ggtitle(paste('Chi-Square Distribution with', df, 'Degrees of Freedom'))
```

# Chi-Square Distribution with 4 Degrees of Freedom

