assignment-4

Gage Clawson

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# read in the lobster traps dataset  
lob\_traps <- as.data.frame(read\_csv("lobster\_traps.csv"))

## Parsed with column specification:  
## cols(  
## YEAR = col\_integer(),  
## MONTH = col\_integer(),  
## DATE = col\_character(),  
## FISHING\_SEASON = col\_character(),  
## SITE = col\_character(),  
## SWATH\_START = col\_character(),  
## SWATH\_END = col\_character(),  
## TRAPS = col\_integer(),  
## OBSERVER = col\_integer(),  
## NOTES = col\_character()  
## )

# Read in the lobster size data set and make it tidy  
  
lob\_size <- read\_csv("lobster\_size\_abundance.csv")

## Parsed with column specification:  
## cols(  
## YEAR = col\_integer(),  
## MONTH = col\_integer(),  
## DATE = col\_character(),  
## SITE = col\_character(),  
## SBC\_LTER\_TRANSECT = col\_integer(),  
## LOBSTER\_TRANSECT = col\_character(),  
## SIZE = col\_integer(),  
## COUNT = col\_integer()  
## )

lob\_size1 <- as.data.frame(lob\_size)  
  
lob\_size2 <- expand.dft(lob\_size1, freq = "COUNT") ##expand.dft filters out all count = 0 rows and makes data tidy (each observation has it's own row)

Yes boss

lob\_size3 <- mutate(lob\_size2, DATE = as.Date(DATE, format = '%d-%b-%y')) # make date formats same for both datasets yyyy-mm-dd  
  
three\_sites <- c("AQUE", "CARP", "MOHK")  
  
lob\_traps1 <- mutate(lob\_traps, DATE = as.Date(DATE, format = '%m/%d/%y')) %>%  
 filter(SITE %in% three\_sites, TRAPS != 0) %>%  
 expand.dft(freq = "TRAPS")   
   
  
  
# make date formats the same and filter for only the 5 sites

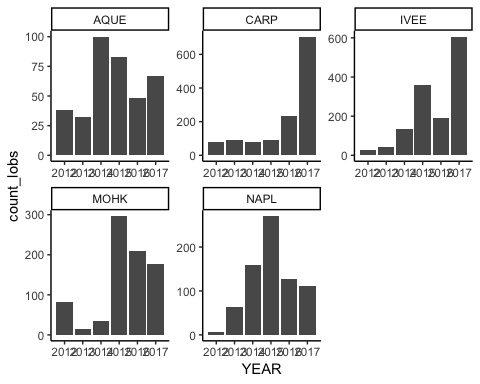
1. Lobster abundance and fishing pressure (2012 - 2017) Describe trends in lobster abundance (counts) and fishing pressure (trap buoys) at the five locations from 2012 - 2017. Ignore transect information - we are only interested in evaluating abundance and pressure on the order of SITE. Note: you are not expected to use regression here - just think of ways to clearly describe annual totals visually and in text, noting important trends, events and differences.

# find the counts of lobsters per each site per each year  
lob\_counts <- lob\_size3 %>%  
 group\_by(SITE, YEAR) %>%  
 dplyr::summarise(count\_lobs = length(SIZE))  
  
  
# find the counts of traps per each site per each year  
trap\_counts <- lob\_traps1 %>%  
 group\_by(SITE, YEAR) %>%  
 dplyr::summarise(count\_traps = length(OBSERVER))  
  
  
  
new\_lob\_traps <- left\_join(lob\_counts, trap\_counts, by = c("YEAR", "SITE"))

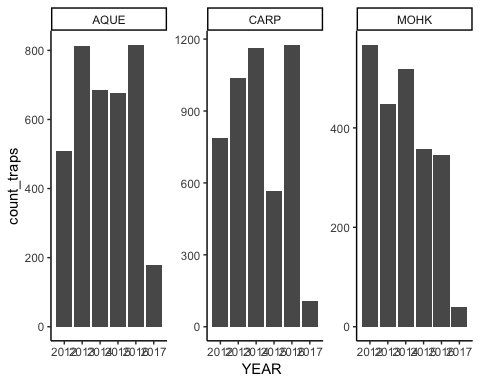
## Warning: Column `SITE` joining factors with different levels, coercing to  
## character vector

new\_lob\_traps[is.na(new\_lob\_traps)] <- 0 ## new\_lob\_traps is the final table for counts per each site per each year for number of lobsters and traps

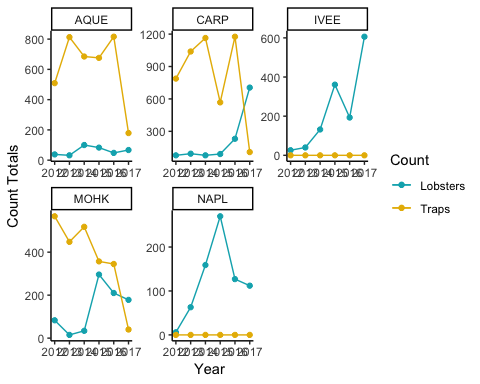
# graphs displaying trends  
  
ggplot(new\_lob\_traps, aes(x = YEAR, y = count\_lobs)) +  
 geom\_col() +   
 facet\_wrap(~SITE, scales = "free") +  
 theme\_classic() +  
 scale\_x\_continuous(breaks = seq(2012,2017, by = 1))



ggplot(trap\_counts, aes(x = YEAR, y = count\_traps)) +  
 geom\_col() +   
 facet\_wrap(~SITE, scales = "free") +   
 theme\_classic() +  
 scale\_x\_continuous(breaks = seq(2012,2017, by = 1))



## line graph of lobster vs trap counts per each year per each site  
lob\_vs\_trap\_counts <- ggplot(new\_lob\_traps, aes(x = YEAR)) +  
 geom\_line(aes(y = count\_lobs, color = "blue")) +  
 geom\_point(aes(y = count\_lobs, color = "blue")) +  
 geom\_line(aes(y = count\_traps, color = "red")) +  
 geom\_point(aes(y = count\_traps, color = "red")) +   
 facet\_wrap(~SITE, scales = "free") +  
 theme\_classic() +  
 scale\_color\_manual(values = c("#00AFBB", "#E7B800"), name = "Count", labels = c("Lobsters", "Traps")) +  
 labs(x = "Year", y = "Count Totals")  
  
lob\_vs\_trap\_counts



## add caption to graph to explain what is contained within it.

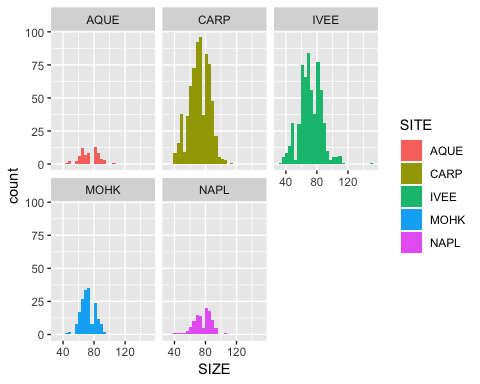
**Figure 1. Lobster abundance and fishing pressurein five Long-Term Ecological Research Sites (2012-2017).** The graphs show the trends in lobster counts and trap buoys at five locations Arroyo Quemado (AQUE), Carpinteria (CARP),Isla Vista (IVEE),Mohawk Reef (MOHK), Naples Reef(NAPL) in the Santa Barbara Channel between 2012 and 2017. Blue and yellow lines indicate lobster and trap buoy counts, respectively.

1. Compare mean lobster size by site in 2017 Compare mean lobster sizes (carapace length (mm)) across the five sites for lobster observations collected in
2. Warning: the size data are not in tidy format. There are rows that contain size information for multiple lobsters observed (e.g., if the researcher saw 3 lobsters all with carapace length ~ 60 mm, then they will have a single row where COUNT = 3 and SIZE = 60). You’ll want to get this into case format - where each lobster has its own row - before doing statistical analyses. There are many ways to do this. One hint: function expand.dft in the vcdExtra package (it doesn’t like tibbles, so you might need to coerce to data.frame first).

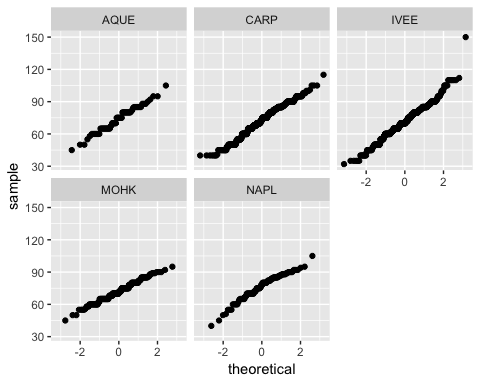
lob\_mean <- lob\_size3 %>%  
 filter(YEAR == 2017) %>%  
 group\_by(SITE) %>%  
 dplyr::summarise(mean\_size = mean(SIZE), sample\_size = length(SIZE), sd\_size = sd(SIZE))  
  
lob\_size\_2017 <- lob\_size3 %>%  
 filter(YEAR == 2017) %>%  
 select(YEAR, SITE, SIZE)

##exploratory graphs  
  
hists <- ggplot(lob\_size\_2017, aes(x = SIZE)) +  
 geom\_histogram(aes(fill = SITE)) +   
 facet\_wrap(~SITE)  
  
hists

## `stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.



qq <- ggplot(lob\_size\_2017, aes(sample = SIZE)) +  
 geom\_qq() +  
 facet\_wrap(~SITE)  
  
qq



## histogram and qqplots indicate normality  
  
# Levene's test for equal variances   
# We'll use the function leveneTest from the 'car' package  
  
# H0: Variances are equal  
# HA: Variances are unequal  
  
lobster\_levene <- leveneTest(SIZE ~ SITE, data = lob\_size\_2017)  
lobster\_levene

## Levene's Test for Homogeneity of Variance (center = median)  
## Df F value Pr(>F)   
## group 4 8.3893 1.065e-06 \*\*\*  
## 1663   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# we reject the null hypothesis of equal variances (p < 0.05)  
  
var\_table <- lob\_size\_2017 %>%  
 group\_by(SITE) %>%  
 dplyr::summarise(variance = var(SIZE))  
  
# since largest variance < 4X larger than the smallest variance, can still use ANOVA

lobster\_aov <- aov(SIZE ~ SITE, data = lob\_size\_2017)  
new\_lobster\_aov <- summary(lobster\_aov)  
  
  
# H0: Mean sizes across all sites are equal  
# HA: There is at least one significant difference in means between the 5 sites  
  
# reject the null  
  
# At least two samples were taken from populations with different means. Which ones are different? All three are different from eachother? Or something else?  
  
  
# Post hoc testing using Tukey's HSD  
  
lobster\_ph <- TukeyHSD(lobster\_aov)  
lobster\_ph

## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##   
## Fit: aov(formula = SIZE ~ SITE, data = lob\_size\_2017)  
##   
## $SITE  
## diff lwr upr p adj  
## CARP-AQUE -1.6657352 -6.24294710 2.911477 0.8582355  
## IVEE-AQUE -2.4433772 -7.05292315 2.166169 0.5968998  
## MOHK-AQUE -1.8955224 -7.02720717 3.236162 0.8514711  
## NAPL-AQUE 2.3366205 -3.19311600 7.866357 0.7775633  
## IVEE-CARP -0.7776420 -2.76097123 1.205687 0.8216104  
## MOHK-CARP -0.2297872 -3.23309697 2.773523 0.9995765  
## NAPL-CARP 4.0023556 0.36042398 7.644287 0.0228728  
## MOHK-IVEE 0.5478548 -2.50450730 3.600217 0.9882889  
## NAPL-IVEE 4.7799976 1.09751057 8.462485 0.0037001  
## NAPL-MOHK 4.2321429 -0.08607271 8.550358 0.0579286

tukey\_data <- as.data.frame(lobster\_ph$SITE)   
  
  
## only significant differences between Naples and Carp, and Naples and IV

The mean lobster size (mm) differed significantly in five Long-Term Ecological Research (LTER) Sites in the Santa Barbara Channel:Arroyo Quemado (n= 67 , Naples Reef (n= 112 ), Mohawk Reef (n= 178), Isla Vista (n= 606), Carpinteria(n= 705 ) studied (one-way ANOVA, F(4,1663) = r, *p* < 0.001, *alpha*= 0.5; Table …). Post-hoc analysis by Tukey’s HSD revealed that the mean lobster size in Naples Reef differed significantly from Carpinteria and Isla Vista (pairwise *p* < 0.001).

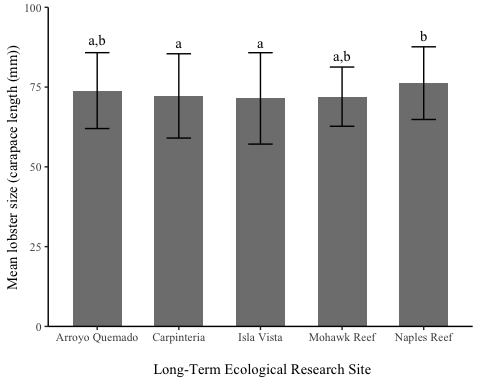
Ilayda: needs referencing for F value.

Lobster size ANOVA results summary.

Ilayda: I tried to make a table as in the example but it doesn’t work. Maybe you can fix this Gage.

Gage: Figured it out. If we knit to pdf in the file “xtable\_code.Rmd”, we can get the table. I also took a screenshot of the table and put it in our project file. All we need to do is add the screenshot of the table for our final word document.

ggplot(lob\_mean, aes(x = SITE, y = mean\_size)) +  
 geom\_col(colour = NA, fill = "gray50", width = 0.6) +  
 geom\_errorbar(aes(ymin =mean\_size - sd\_size, ymax = mean\_size + sd\_size), color = "gray0", width = .3) +  
 scale\_y\_continuous(expand = c(0,0), limits = c(0,100)) +  
 scale\_x\_discrete(labels = c("Arroyo Quemado","Carpinteria","Isla Vista","Mohawk Reef","Naples Reef")) +  
 annotate("text", x = 1, y = 90, label = "a,b", family = "Times New Roman") +  
 annotate("text", x = 2, y = 89, label = "a", family = "Times New Roman") +  
 annotate("text", x = 3, y = 89, label = "a", family = "Times New Roman") +  
 annotate("text", x = 4, y = 85, label = "a,b", family = "Times New Roman") +  
 annotate("text", x = 5, y = 91, label = "b", family = "Times New Roman") +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank(),  
 panel.background = element\_blank(), axis.line = element\_line(colour = "black"),text = element\_text(family = "Times New Roman"))+  
 xlab("\n Long-Term Ecological Research Site")+  
 ylab("Mean lobster size (carapace length (mm))") #we can change this title



**Figure 2. Lobster size in five Long-Term Ecological Research Sites.** Mean lobster sizes (mm) for sites Arroyo Quemado, Carpinteria,Isla Vista,Mohawk Reef,Naples Reef in the Santa Barbara Channel. Error bars indicate +/- 1 standard deviation. Like letters indicate values that do not differ significantly (by one-way ANOVA with Tukey’s HSD; F(4,1663) = 3.424, *p* < 0.001), with = 0.05 for all post-hoc pairwise comparisons).

1. Changes in lobster size at MPA and non-MPA sites (comparing only 2012 and 2017 sizes) From the data description (<http://sbc.lternet.edu/cgi-bin/showDataset.cgi?docid=knb-lter-sbc.77>): “Data on abundance, size and fishing pressure of California spiny lobster (Panulirus interruptus) are collected along the mainland coast of the Santa Barbara Channel. Spiny lobsters are an important predator in giant kelp forests off southern California. Two SBC LTER study reefs are located in or near the California Fish and Game Network of Marine Protected Areas (MPA), Naples and Isla Vista, both established as MPAs on 2012-01-01. MPAs provide a unique opportunity to investigate the effects of fishing on kelp forest community dynamics. Sampling began in 2012 and is ongoing.” At Isla Vista and Naples Reef, the two protected MPA sites (with zero fishing pressure), how do lobster sizes in 2012 and 2017 compare? At the non-MPA sites?

mpa <- c("IVEE", "NAPL")   
  
'%!in%' <- function(x,y)!('%in%'(x,y))  
  
## filter for mpa sites and 2017 or 2012  
  
mpa\_site <- lob\_size3 %>%  
 filter(SITE %in% mpa, YEAR == 2012|YEAR == 2017) %>%  
 select(SITE,YEAR,SIZE)  
  
## filter for non mpa sites and 2017 or 2012  
non\_mpa\_site <- lob\_size3 %>%  
 filter(SITE %!in% mpa, YEAR==2012|YEAR==2017) %>%  
 select(SITE,YEAR,SIZE)

# sandro talked to allison and apparently we have to do 5 different t tests for EACH SITE, instead of only one ttest for MPA and non mpa   
  
# these are datasets for our five different t-tests  
  
mpa\_2012 <- lob\_size3 %>%  
 filter(SITE %in% mpa, YEAR == 2012) %>%  
 select(SITE,YEAR,SIZE) %>%  
 mutate( i = row\_number()) %>%  
 spread(SITE,SIZE) %>%  
 select(-i)  
  
mpa\_2017 <- lob\_size3 %>%  
 filter(SITE %in% mpa, YEAR == 2017) %>%  
 select(SITE,YEAR,SIZE) %>%  
 mutate( i = row\_number()) %>%  
 spread(SITE,SIZE) %>%  
 select(-i)  
  
non\_mpa\_2012 <- lob\_size3 %>%  
 filter(SITE %!in% mpa, YEAR == 2012) %>%  
 select(SITE,YEAR,SIZE) %>%  
 mutate( i = row\_number()) %>%  
 spread(SITE,SIZE) %>%  
 select(-i)  
  
non\_mpa\_2017 <- lob\_size3 %>%  
 filter(SITE %!in% mpa, YEAR == 2017) %>%  
 select(SITE,YEAR,SIZE) %>%  
 mutate( i = row\_number()) %>%  
 spread(SITE,SIZE) %>%  
 select(-i)

############### MPA SITE IVEE ################  
  
####### F test for equal variances for IVEE 2012 vs 2017 #######  
  
# H0: The variances are equal (ratio of variances = 1)  
# HA: The variances are not equal (ratio of variances != 1)  
  
IVEE\_ftest <- var.test(mpa\_2012$IVEE, mpa\_2017$IVEE)  
  
IVEE\_ftest

##   
## F test to compare two variances  
##   
## data: mpa\_2012$IVEE and mpa\_2017$IVEE  
## F = 0.71311, num df = 25, denom df = 605, p-value = 0.307  
## alternative hypothesis: true ratio of variances is not equal to 1  
## 95 percent confidence interval:  
## 0.4322948 1.3698611  
## sample estimates:  
## ratio of variances   
## 0.713111

# retain the null hypothesis of equal variances  
  
# We can override the default setting in t.test() function of var.equal = FALSE, because the variances are actually likely equal.  
  
# H0: mean Lobster size at IVEE site in 2012 is equal to mean lobster size at IVEE site in 2017  
# HA: mean Lobster size at IVEE site in 2012 is NOT equal to mean lobster size at IVEE site in 2017  
  
IVEE\_ttest <- t.test(mpa\_2012$IVEE, mpa\_2017$IVEE, var.equal = TRUE)  
  
IVEE\_ttest # retain null they are equal, p =0.0599

##   
## Two Sample t-test  
##   
## data: mpa\_2012$IVEE and mpa\_2017$IVEE  
## t = -1.885, df = 630, p-value = 0.0599  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -10.9750916 0.2246473  
## sample estimates:  
## mean of x mean of y   
## 66.07692 71.45215

#calculate the difference in means at IVEE 2012 and 2017  
  
IVEE\_mean\_2012 <- mean(mpa\_2012$IVEE, na.rm = TRUE)  
  
IVEE\_mean\_2017 <- mean(mpa\_2017$IVEE, na.rm = TRUE)  
  
IVEE\_mean\_2012 - IVEE\_mean\_2017

## [1] -5.375222

## difference in means is -5.375222 mm  
  
   
# calculate effect size  
IVEE\_cohen\_d <- cohen.d(mpa\_2012$IVEE, mpa\_2017$IVEE, na.rm = TRUE)  
IVEE\_cohen\_d

##   
## Cohen's d  
##   
## d estimate: -0.3775177 (small)  
## 95 percent confidence interval:  
## inf sup   
## -0.77136540 0.01633002

sd(mpa\_2012$IVEE, na.rm = TRUE)

## [1] 12.09272

# IVEE 2012 sd: 12.09272  
length(mpa\_2012$IVEE[!is.na(mpa\_2012$IVEE)])

## [1] 26

# IVEE 2012 n: 26  
  
sd(mpa\_2017$IVEE, na.rm = TRUE)

## [1] 14.32008

# IVEE 2012 sd: 14.32008  
length(mpa\_2017$IVEE[!is.na(mpa\_2017$IVEE)])

## [1] 606

# IVEE 2012 n: 606  
  
## effect size is small (d = -0.3775177) which indicates that there likely is NOT a significant difference in mean lobster size between the two years.

The mean lobster size at Isla Vista (Marine Protected Area) in 2012 (66.08 ± 12.09 mm [mean±sd], n=26 ) and 2017 (71.45 ± 14.32 mm [mean±sd], n=606 ) did not differ significantly based on a two-sample Student’s t-test (t(630) = -1.89, p = 0.060, α = 0.05). Also, the effect size is small (Cohen’s d = -0.38) and the absolute difference in mean lobster size between the two years is 5.38 mm.

############### MPA SITE NAPL ################  
  
####### F test for equal variances for NAPL 2012 vs 2017 #######  
  
# H0: The variances are equal (ratio of variances = 1)  
# HA: The variances are not equal (ratio of variances != 1)  
  
NAPL\_ftest <- var.test(mpa\_2012$NAPL, mpa\_2017$NAPL)  
  
NAPL\_ftest

##   
## F test to compare two variances  
##   
## data: mpa\_2012$NAPL and mpa\_2017$NAPL  
## F = 1.064, num df = 5, denom df = 111, p-value = 0.7685  
## alternative hypothesis: true ratio of variances is not equal to 1  
## 95 percent confidence interval:  
## 0.3966019 6.4626426  
## sample estimates:  
## ratio of variances   
## 1.064048

# retain the null hypothesis of equal variances  
  
# We can override the default setting in t.test() function of var.equal = FALSE, because the variances are actually likely equal.  
  
# H0: mean Lobster size at NAPL site in 2012 is equal to mean lobster size at NAPL site in 2017  
# HA: mean Lobster size at NAPL site in 2012 is NOT equal to mean lobster size at NAPL site in 2017  
  
NAPL\_ttest <- t.test(mpa\_2012$NAPL, mpa\_2017$NAPL, var.equal = TRUE)  
  
NAPL\_ttest # retain null they are equal, p =0.5002

##   
## Two Sample t-test  
##   
## data: mpa\_2012$NAPL and mpa\_2017$NAPL  
## t = -0.67636, df = 116, p-value = 0.5002  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -12.697051 6.232765  
## sample estimates:  
## mean of x mean of y   
## 73.00000 76.23214

#calculate the difference in means at NAPL 2012 and 2017  
  
NAPL\_mean\_2012 <- mean(mpa\_2012$NAPL, na.rm = TRUE)  
  
NAPL\_mean\_2017 <- mean(mpa\_2017$NAPL, na.rm = TRUE)  
  
NAPL\_mean\_2012 - NAPL\_mean\_2017

## [1] -3.232143

## difference in means is -3.232143 mm  
  
   
# calculate effect size  
NAPL\_cohen\_d <- cohen.d(mpa\_2012$NAPL, mpa\_2017$NAPL, na.rm = TRUE)  
NAPL\_cohen\_d

##   
## Cohen's d  
##   
## d estimate: -0.2834216 (small)  
## 95 percent confidence interval:  
## inf sup   
## -1.1141889 0.5473456

## effect size is small (d = -0.2834216) which indicates that there likely is NOT a significant difference in mean lobster size between the two years.  
  
sd(mpa\_2012$NAPL, na.rm = TRUE)

## [1] 11.74734

# NAPL 2012 sd: 11.74734  
length(mpa\_2012$NAPL[!is.na(mpa\_2012$NAPL)])

## [1] 6

# NAPL 2012 n: 6  
  
sd(mpa\_2017$NAPL, na.rm = TRUE)

## [1] 11.3883

# NAPL 2012 sd: 11.3883  
length(mpa\_2017$NAPL[!is.na(mpa\_2017$NAPL)])

## [1] 112

# NAPL 2012 n: 112

The mean lobster size at Naples Reef (Marine Protected Area) in 2012 (73.00 ± 11.74 mm [mean±sd], n= 6 ) and 2017 ( 76.23± 11.39 mm [mean±sd], n= 112) did not differ significantly based on a two-sample Student’s t-test (t(116) = -0.68, p = 0.500, α = 0.05).Also,the effect size is small (Cohen’s d = -0.28) and the absolute difference in mean lobster size between two years is only 3.232 mm.

############### NON MPA SITE AQUE ################  
  
####### F test for equal variances for AQUE 2012 vs 2017 #######  
  
# H0: The variances are equal (ratio of variances = 1)  
# HA: The variances are not equal (ratio of variances != 1)  
  
AQUE\_ftest <- var.test(non\_mpa\_2012$AQUE, non\_mpa\_2017$AQUE)  
  
AQUE\_ftest

##   
## F test to compare two variances  
##   
## data: non\_mpa\_2012$AQUE and non\_mpa\_2017$AQUE  
## F = 0.72863, num df = 37, denom df = 66, p-value = 0.2986  
## alternative hypothesis: true ratio of variances is not equal to 1  
## 95 percent confidence interval:  
## 0.419142 1.327868  
## sample estimates:  
## ratio of variances   
## 0.7286314

# retain the null hypothesis of equal variances  
  
# We can override the default setting in t.test() function of var.equal = FALSE, because the variances are actually likely equal.  
  
# H0: mean Lobster size at AQUE site in 2012 is equal to mean lobster size at AQUE site in 2017  
# HA: mean Lobster size at AQUE site in 2012 is NOT equal to mean lobster size at AQUE site in 2017  
  
AQUE\_ttest <- t.test(non\_mpa\_2012$AQUE, non\_mpa\_2017$AQUE, var.equal = TRUE)  
  
AQUE\_ttest # retain null they are equal, p =0.2097

##   
## Two Sample t-test  
##   
## data: non\_mpa\_2012$AQUE and non\_mpa\_2017$AQUE  
## t = -1.2622, df = 103, p-value = 0.2097  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -7.445357 1.654312  
## sample estimates:  
## mean of x mean of y   
## 71.00000 73.89552

#calculate the difference in means at AQUE 2012 and 2017  
  
AQUE\_mean\_2012 <- mean(non\_mpa\_2012$AQUE, na.rm = TRUE)  
  
AQUE\_mean\_2017 <- mean(non\_mpa\_2017$AQUE, na.rm = TRUE)  
  
AQUE\_mean\_2012 - AQUE\_mean\_2017

## [1] -2.895522

## difference in means is -2.895522 mm  
  
   
# calculate effect size  
AQUE\_cohen\_d <- cohen.d(non\_mpa\_2012$AQUE, non\_mpa\_2017$AQUE, na.rm = TRUE)  
AQUE\_cohen\_d

##   
## Cohen's d  
##   
## d estimate: -0.2563169 (small)  
## 95 percent confidence interval:  
## inf sup   
## -0.6606014 0.1479675

## effect size is small (d = -0.2563169) which indicates that there likely is NOT a significant difference in mean lobster size between the two years.  
  
sd(non\_mpa\_2012$AQUE, na.rm = TRUE)

## [1] 10.15022

# AQUE 2012 sd: 10.15022  
length(non\_mpa\_2012$AQUE[!is.na(non\_mpa\_2012$AQUE)])

## [1] 38

# AQUE 2012 n: 38  
  
sd(non\_mpa\_2017$AQUE, na.rm = TRUE)

## [1] 11.89109

# AQUE 2012 sd: 11.89109  
length(non\_mpa\_2017$AQUE[!is.na(non\_mpa\_2017$AQUE)])

## [1] 67

# AQUE 2012 n: 67

The mean lobster size at Arroyo Quemado(non-Marine Protected Area) in 2012 (71.00 ± 10.15 mm [mean±sd], n= 38) and 2017 (73.90 ± 11.89 mm [mean±sd], n=67 ) did not differ significantly based on a two-sample Student’s t-test (t(103) = -1.26, p = 0.210, α = 0.05). Also,the effect size is small (Cohen’s d = -0.26) and the absolute difference in mean lobster size between the two years is only 2.90 mm.

############### NON MPA SITE CARP ################  
  
####### F test for equal variances for CARP 2012 vs 2017 #######  
  
# H0: The variances are equal (ratio of variances = 1)  
# HA: The variances are not equal (ratio of variances != 1)  
  
CARP\_ftest <- var.test(non\_mpa\_2012$CARP, non\_mpa\_2017$CARP)  
  
CARP\_ftest

##   
## F test to compare two variances  
##   
## data: non\_mpa\_2012$CARP and non\_mpa\_2017$CARP  
## F = 1.2244, num df = 77, denom df = 704, p-value = 0.2043  
## alternative hypothesis: true ratio of variances is not equal to 1  
## 95 percent confidence interval:  
## 0.896208 1.750406  
## sample estimates:  
## ratio of variances   
## 1.224405

# retain the null hypothesis of equal variances  
  
# We can override the default setting in t.test() function of var.equal = FALSE, because the variances are actually likely equal.  
  
# H0: mean Lobster size at CARP site in 2012 is equal to mean lobster size at CARP site in 2017  
# HA: mean Lobster size at CARP site in 2012 is NOT equal to mean lobster size at CARP site in 2017  
  
CARP\_ttest <- t.test(non\_mpa\_2012$CARP, non\_mpa\_2017$CARP, var.equal = TRUE)  
  
CARP\_ttest # retain null they are equal, p =0.1819

##   
## Two Sample t-test  
##   
## data: non\_mpa\_2012$CARP and non\_mpa\_2017$CARP  
## t = 1.3361, df = 781, p-value = 0.1819  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.998958 5.257332  
## sample estimates:  
## mean of x mean of y   
## 74.35897 72.22979

#calculate the difference in means at CARP 2012 and 2017  
  
CARP\_mean\_2012 <- mean(non\_mpa\_2012$CARP, na.rm = TRUE)  
  
CARP\_mean\_2017 <- mean(non\_mpa\_2017$CARP, na.rm = TRUE)  
  
CARP\_mean\_2012 - CARP\_mean\_2017

## [1] 2.129187

## difference in means is 2.129187 mm  
  
   
# calculate effect size  
CARP\_cohen\_d <- cohen.d(non\_mpa\_2012$CARP, non\_mpa\_2017$CARP, na.rm = TRUE)  
CARP\_cohen\_d

##   
## Cohen's d  
##   
## d estimate: 0.1594364 (negligible)  
## 95 percent confidence interval:  
## inf sup   
## -0.07493682 0.39380971

## effect size is small (d = 0.1594364) which indicates that there likely is NOT a significant difference in mean lobster size between the two years.  
  
sd(non\_mpa\_2012$CARP, na.rm = TRUE)

## [1] 14.61628

# CARP 2012 sd: 14.61628  
length(non\_mpa\_2012$CARP[!is.na(non\_mpa\_2012$CARP)])

## [1] 78

# CARP 2012 n: 78  
  
sd(non\_mpa\_2017$CARP, na.rm = TRUE)

## [1] 13.20913

# CARP 2012 sd: 13.20913  
length(non\_mpa\_2017$CARP[!is.na(non\_mpa\_2017$CARP)])

## [1] 705

# CARP 2012 n: 705

The mean lobster size at Carpinteria (non-Marine Protected Area) in 2012 (74.36 ± 14.62 mm [mean±sd], n= 78) and 2017 ( 72.23± 13.21 mm [mean±sd], n= 705 ) did not differ significantly based on a two-sample Student’s t-test (t(781) = 1.34, p = 0.182, α = 0.05).Also,the effect size is small (Cohen’s d = 0.16) and the absolute difference in mean lobster size between the two years is only 2.13 mm.

############### NON MPA SITE MOHK ################  
  
####### F test for equal variances for MOHK 2012 vs 2017 #######  
  
# H0: The variances are equal (ratio of variances = 1)  
# HA: The variances are not equal (ratio of variances != 1)  
  
MOHK\_ftest <- var.test(non\_mpa\_2012$MOHK, non\_mpa\_2017$MOHK)  
  
MOHK\_ftest

##   
## F test to compare two variances  
##   
## data: non\_mpa\_2012$MOHK and non\_mpa\_2017$MOHK  
## F = 1.3015, num df = 82, denom df = 177, p-value = 0.1509  
## alternative hypothesis: true ratio of variances is not equal to 1  
## 95 percent confidence interval:  
## 0.9085131 1.9131403  
## sample estimates:  
## ratio of variances   
## 1.301535

# retain the null hypothesis of equal variances  
  
# We can override the default setting in t.test() function of var.equal = FALSE, because the variances are actually likely equal.  
  
# H0: mean Lobster size at MOHK site in 2012 is equal to mean lobster size at MOHK site in 2017  
# HA: mean Lobster size at MOHK site in 2012 is NOT equal to mean lobster size at MOHK site in 2017  
  
MOHK\_ttest <- t.test(non\_mpa\_2012$MOHK, non\_mpa\_2017$MOHK, var.equal = TRUE)  
  
MOHK\_ttest # REJECT null they are equal, p = 6.276e-05

##   
## Two Sample t-test  
##   
## data: non\_mpa\_2012$MOHK and non\_mpa\_2017$MOHK  
## t = 4.0689, df = 259, p-value = 6.276e-05  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 2.710776 7.795248  
## sample estimates:  
## mean of x mean of y   
## 77.25301 72.00000

#calculate the difference in means at MOHK 2012 and 2017  
  
MOHK\_mean\_2012 <- mean(non\_mpa\_2012$MOHK, na.rm = TRUE)  
  
MOHK\_mean\_2017 <- mean(non\_mpa\_2017$MOHK, na.rm = TRUE)  
  
MOHK\_mean\_2012 - MOHK\_mean\_2017

## [1] 5.253012

## difference in means is 5.253012 mm  
  
   
# calculate effect size  
MOHK\_cohen\_d <- cohen.d(non\_mpa\_2012$MOHK, non\_mpa\_2017$MOHK, na.rm = TRUE)  
MOHK\_cohen\_d

##   
## Cohen's d  
##   
## d estimate: 0.5408116 (medium)  
## 95 percent confidence interval:  
## inf sup   
## 0.2749635 0.8066597

## effect size is MEDIUM (d = 0.5408116) which indicates that there likely is a significant difference in mean lobster size between the two years.  
  
sd(non\_mpa\_2012$MOHK, na.rm = TRUE)

## [1] 10.58743

# MOHK 2012 sd: 10.58743  
length(non\_mpa\_2012$MOHK[!is.na(non\_mpa\_2012$MOHK)])

## [1] 83

# MOHK 2012 n: 83  
  
sd(non\_mpa\_2017$MOHK, na.rm = TRUE)

## [1] 9.280318

# MOHK 2012 sd: 9.280318  
length(non\_mpa\_2017$MOHK[!is.na(non\_mpa\_2017$MOHK)])

## [1] 178

# MOHK 2012 n: 178

The mean lobster size at Mohawk Reef (non-Marine Protected Area) in 2012 (77.25 ± 10.59 mm [mean±sd], n= 83) and 2017 ( 72.00 ± 9.28 mm [mean±sd], n= 178 ) differed significantly based on a two-sample Student’s t-test (t(259) = 4.07, p <0.05, α = 0.05).Also,the effect size is moderate (Cohen’s d = 0.54) and the absolute difference in mean lobster size between the two years is 5.25 mm.

1. Proportions of “legal” lobsters at the 5 sites in 2017 The legal minimum carapace size for lobster is 82.6 mm. What proportion of observed lobsters at each site are above the legal minimum? Does that proportion differ significantly across the 5 sites? Note: We’ll be doing chi-square in labs next week, or go ahead with maximum resourcefulness and check out the chisq.test() function on your own!

# filter for 2017  
# filter for above 82.6 mm  
  
  
legal\_min <- lob\_size3 %>%  
 filter(YEAR == 2017) %>%  
 mutate(above\_legal = case\_when(  
 SIZE >= 82.6 ~ 'yes',  
 SIZE < 82.6 ~ 'no'  
 )) %>%  
 count(SITE, above\_legal) %>%  
 spread(above\_legal, n) %>%  
 select(-SITE)  
   
rownames(legal\_min) <- c("AQUE", "CARP", "IVEE", "MOHK", "NAPL")

## Warning: Setting row names on a tibble is deprecated.

legal\_prop <- prop.table(as.matrix(legal\_min), 1)  
  
  
above\_x2 <- chisq.test(legal\_prop)

## Warning in chisq.test(legal\_prop): Chi-squared approximation may be  
## incorrect

above\_x2

##   
## Pearson's Chi-squared test  
##   
## data: legal\_prop  
## X-squared = 0.11095, df = 4, p-value = 0.9985

## The proportion does not differ significantly between each location.   
# there is no signficant association between legal lobster size and different test sites

Based on the obervations from five Long-Term Ecological Research (LTER) Sites in the Santa Barbara Channel:Arroyo Quemado (n= 67) , Naples Reef (n= 112 ), Mohawk Reef (n= 178), Isla Vista (n= 606), Carpinteria(n= 705 ),the proportion of observed lobsters that are above the legal minimum carapace size does not differ significantly by site.( (4)= 0.11095, *p*= 0.9985)