Your Title Here

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# Introduction

# Methods

## Study design

## Analysis

# Results

## Subsections are ok in the results section too

library("ggplot2")  
library("dplyr")

##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':  
##   
## filter, lag

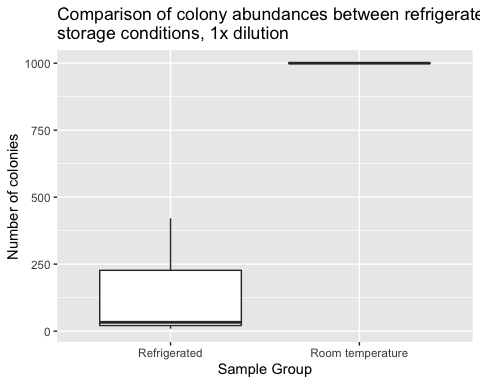
## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union

library("tidyr")  
library("readr")

# read in the culture data from csv  
culture\_data <- read\_csv(  
 "data/raw\_data/Raw\_culture\_count\_data/Culturing\_data.csv")

## Parsed with column specification:  
## cols(  
## student\_name = col\_character(),  
## sample\_id = col\_character(),  
## sample\_group = col\_character(),  
## dilution\_1\_10\_or\_100 = col\_double(),  
## year\_plated = col\_double(),  
## month\_plated = col\_double(),  
## day\_plated = col\_double(),  
## year\_observed = col\_double(),  
## month\_observed = col\_double(),  
## day\_observed = col\_double(),  
## number\_of\_colonies = col\_number(),  
## number\_of\_morphotypes = col\_character(),  
## notes = col\_character()  
## )

# filter out only my 100x dilutions and make a boxplot  
culture\_data %>%  
 filter(student\_name == "Kris Choi") %>%  
 filter(dilution\_1\_10\_or\_100 == "1") %>%  
 ggplot(aes(x = sample\_group,  
 y = number\_of\_colonies)) +  
 geom\_boxplot() +  
 ggtitle(paste("Comparison of colony abundances between refrigerated and",   
 "room temperature  
storage conditions, 1x dilution")) +  
 xlab("Sample Group") +  
 ylab("Number of colonies")



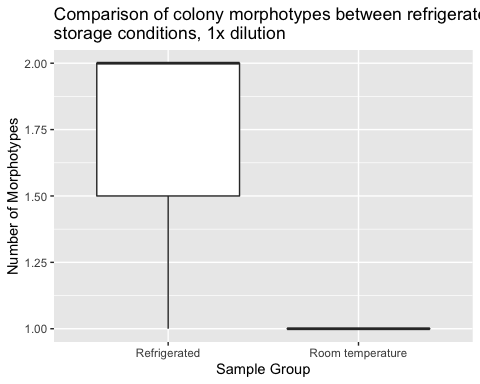
**Figure 1:** Boxplot of colony abundances at different storage conditions, 1x dilution. Despite a higher median number of colonies from room temperature samples, the mean numbers of colonies were not significantly different between the two storage conditions (Wilcox p = 0.0636).

# run a statistical test to compare the two groups of abundances  
culture\_data %>%  
 filter(student\_name == "Kris Choi") %>%  
 filter(dilution\_1\_10\_or\_100 == "1") %>%  
 wilcox.test(data = .,  
 number\_of\_colonies ~ sample\_group)

## Warning in wilcox.test.default(x = c(421, 33, 9), y = c(1000, 1000, 1000:  
## cannot compute exact p-value with ties

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: number\_of\_colonies by sample\_group  
## W = 0, p-value = 0.0636  
## alternative hypothesis: true location shift is not equal to 0

# filter out only my 100x dilutions and make a boxplot  
culture\_data %>%  
 filter(student\_name == "Kris Choi") %>%  
 filter(dilution\_1\_10\_or\_100 == "1") %>%  
 ggplot(aes(x = sample\_group,  
 y = as.numeric(number\_of\_morphotypes))) +  
 geom\_boxplot() +  
 ggtitle(paste("Comparison of colony morphotypes between refrigerated and",   
 "room temperature  
storage conditions, 1x dilution")) +  
 xlab("Sample Group") +  
 ylab("Number of Morphotypes")



**Figure 2:** Boxplot showing the number of morphotypes from the two different storage conditions. There was no difference in the mean number of morphotypes (Wilcox p=0.19).

# run a statistical test to compare the two groups of morphotypes  
culture\_data %>%  
 filter(student\_name == "Kris Choi") %>%  
 filter(dilution\_1\_10\_or\_100 == "1") %>%  
 wilcox.test(data = .,  
 as.numeric(number\_of\_morphotypes) ~ sample\_group)

## Warning in wilcox.test.default(x = c(1, 2, 2), y = c(1, 1, 1)): cannot  
## compute exact p-value with ties

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: as.numeric(number\_of\_morphotypes) by sample\_group  
## W = 7.5, p-value = 0.1876  
## alternative hypothesis: true location shift is not equal to 0

# Discussion

# Sources Cited