RC RC 159-5.3a Analysis of control of rec bacterial contamination by 3 times concentration of two antibiotics antibiotics

Ron Collins

2020-09-29

# Introduction

The first group of Antibiotic’s used are Tetracycline HCl, mg Streptomycin Sulfate, and Chloramphenicol. They did not control the red bacteria. Consequently, two other antibiotics, Penicillin G and Vancomycin at 150 mg per liter will be evaluated.

### summary with background control included

The following is a summary of the treatments ( antibiotics and no antibiotics) by bacterial concentration.

## `summarise()` regrouping output by 'Trt' (override with `.groups` argument)

## # A tibble: 5 x 3  
## # Groups: Trt [2]  
## Trt concBac Total\_mean  
## <fct> <fct> <dbl>  
## 1 antibiotics -4 111   
## 2 antibiotics -3 448   
## 3 noantibiotics -4 116.   
## 4 noantibiotics -3 433.   
## 5 noantibiotics 0 0.25

From looking at the counts, it appears that the only difference is between bacteria concentration.

### analysis of variance for bacterial count as a result of antibiotics with background control.

##   
## Call:  
## lm(formula = count ~ Trt + concBac + Trt \* concBac, data = RC159\_5.3Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -141.00 -15.12 -0.25 13.19 151.00   
##   
## Coefficients: (1 not defined because of singularities)  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 111.00 30.77 3.608 0.00259 \*\*   
## Trtnoantibiotics 5.50 43.51 0.126 0.90110   
## concBac-3 337.00 43.51 7.745 1.28e-06 \*\*\*  
## concBac0 -116.25 43.51 -2.672 0.01742 \*   
## Trtnoantibiotics:concBac-3 -20.25 61.54 -0.329 0.74665   
## Trtnoantibiotics:concBac0 NA NA NA NA   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 61.54 on 15 degrees of freedom  
## Multiple R-squared: 0.9222, Adjusted R-squared: 0.9015   
## F-statistic: 44.45 on 4 and 15 DF, p-value: 3.81e-08

## Note: model has aliased coefficients  
## sums of squares computed by model comparison

## Anova Table (Type II tests)  
##   
## Response: count  
## Sum Sq Df F value Pr(>F)   
## Trt 86 1 0.0226 0.8825   
## concBac 628506 2 82.9857 7.738e-09 \*\*\*  
## Trt:concBac 410 1 0.1083 0.7467   
## Residuals 56802 15   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### pair wise t test Count vs trt with background control included

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: RC159\_5.3Data$count and RC159\_5.3Data$Trt   
##   
## antibiotics  
## noantibiotics 0.29   
##   
## P value adjustment method: holm

The results are skewed because of the background control. I do not put much faith in the results.

### pair wise t test count vs concBac with background control included

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: RC159\_5.3Data$count and RC159\_5.3Data$concBac   
##   
## -4 -3   
## -3 5.3e-09 -   
## 0 0.0053 1.9e-09  
##   
## P value adjustment method: holm

The results are skewed because of the background control. I do not put much faith in the results.

### summary with background control removed

## `summarise()` regrouping output by 'Trt' (override with `.groups` argument)

## # A tibble: 4 x 3  
## # Groups: Trt [2]  
## Trt concBac Total\_mean  
## <fct> <fct> <dbl>  
## 1 antibiotics -4 111   
## 2 antibiotics -3 448   
## 3 noantibiotics -4 116.  
## 4 noantibiotics -3 433.

### analysi of variance for colony count with background control removed

##   
## Call:  
## lm(formula = count ~ Trt + concBac + Trt \* concBac, data = RC159\_5.3Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -141.00 -20.25 -4.25 19.81 151.00   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 111.00 34.40 3.227 0.00726 \*\*   
## Trtnoantibiotics 5.50 48.65 0.113 0.91186   
## concBac-3 337.00 48.65 6.927 1.59e-05 \*\*\*  
## Trtnoantibiotics:concBac-3 -20.25 68.80 -0.294 0.77353   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 68.8 on 12 degrees of freedom  
## Multiple R-squared: 0.8828, Adjusted R-squared: 0.8535   
## F-statistic: 30.13 on 3 and 12 DF, p-value: 7.205e-06

## Anova Table (Type II tests)  
##   
## Response: count  
## Sum Sq Df F value Pr(>F)   
## Trt 86 1 0.0181 0.8953   
## concBac 427389 1 90.2907 6.201e-07 \*\*\*  
## Trt:concBac 410 1 0.0866 0.7735   
## Residuals 56802 12   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### pair wise t test count vs Trt with background control removed.

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: RC159\_5.3Data$count and RC159\_5.3Data$Trt   
##   
## antibiotics  
## noantibiotics 0.96   
##   
## P value adjustment method: holm

### pair wise t test count vs concBac with background control removed

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: RC159\_5.3Data$count and RC159\_5.3Data$concBac   
##   
## -4   
## -3 7.1e-08  
##   
## P value adjustment method: holm