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| title: “RC RC 159-5.1a Analysis of control of rec bacterial contamination by 3 antibiotics” |
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| date: “2020-09-29” |
| output: |
| word\_document: default |
| html\_notebook: default |
| html\_document: default |
| pdf\_document: default |

# 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.

## # A tibble: 5 x 3  
## # Groups: Trt [2]  
## Trt concBac Total\_mean  
## <fct> <fct> <dbl>  
## 1 with anti -4 18   
## 2 with anti -3 57.2  
## 3 without anti -4 22.7  
## 4 without anti -3 181   
## 5 without anti 0 4.6

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\_5.1Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -83.000 -7.667 -1.000 4.583 162.000   
##   
## Coefficients: (1 not defined because of singularities)  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 18.000 26.105 0.690 0.5010   
## Trtwithout anti 4.667 39.876 0.117 0.9084   
## concBac-3 39.250 36.918 1.063 0.3045   
## concBac0 -18.067 38.129 -0.474 0.6424   
## Trtwithout anti:concBac-3 119.083 54.342 2.191 0.0446 \*  
## Trtwithout anti:concBac0 NA NA NA NA   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 52.21 on 15 degrees of freedom  
## Multiple R-squared: 0.6747, Adjusted R-squared: 0.588   
## F-statistic: 7.779 on 4 and 15 DF, p-value: 0.001331

## 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 17575 1 6.4476 0.0226779 \*   
## concBac 67330 2 12.3500 0.0006757 \*\*\*  
## Trt:concBac 13090 1 4.8021 0.0446247 \*   
## Residuals 40889 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\_5.1Data$count and RC159\_5.1Data$Trt   
##   
## with anti  
## without anti 0.43   
##   
## 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\_5.1Data$count and RC159\_5.1Data$concBac   
##   
## -4 -3   
## -3 0.02 -   
## 0 0.69 0.02  
##   
## 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 with anti -4 18   
## 2 with anti -3 57.2  
## 3 without anti -4 22.7  
## 4 without anti -3 181

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

##   
## Call:  
## lm(formula = count ~ Trt + concBac + Trt \* concBac, data = RC159\_5.1Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -83.000 -10.958 0.000 5.167 162.000   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 18.000 30.402 0.592 0.5658   
## Trtwithout anti 4.667 46.440 0.100 0.9218   
## concBac-3 39.250 42.995 0.913 0.3809   
## Trtwithout anti:concBac-3 119.083 63.288 1.882 0.0866 .  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 60.8 on 11 degrees of freedom  
## Multiple R-squared: 0.6235, Adjusted R-squared: 0.5208   
## F-statistic: 6.072 on 3 and 11 DF, p-value: 0.01081

## Anova Table (Type II tests)  
##   
## Response: count  
## Sum Sq Df F value Pr(>F)   
## Trt 17575 1 4.7537 0.05184 .  
## concBac 32967 1 8.9168 0.01238 \*  
## Trt:concBac 13090 1 3.5405 0.08660 .  
## Residuals 40669 11   
## ---  
## 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\_5.1Data$count and RC159\_5.1Data$Trt   
##   
## with anti  
## without anti 0.097   
##   
## 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\_5.1Data$count and RC159\_5.1Data$concBac   
##   
## -4   
## -3 0.023  
##   
## P value adjustment method: holm