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| title: “RC RC 159-5 Analysis of control of rec bacterial contamination by 3 antibiotics” |
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# Introduction

Tissue culture tube with callus in Bldg. 001, Rm. 331 after six months are beginning to be contaminated with a red slime. Consequently, it became imperitive that we find a way to control the bacteria. Evidently PPm wasn’t working. Maybe at a higher concenation. A series of experiments were planned to evaluate different antibiotics that we have used in the past ro control the bacteria. The first group of Antibiotic’s used are Tetracycline HCl, mg Streptomycin Sulfate, and Chloramphenicol. They will be used at the same rates from prior experiments: 25 mg/liter. This is for the first experimental replicate.

### 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 antibiotic -4 17.2  
## 2 antibiotic -3 81.2  
## 3 noantibiotic -4 26.8  
## 4 noantibiotic -3 90   
## 5 noantibiotic 0 0

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\_5Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -28.000 -3.875 0.000 3.000 33.000   
##   
## Coefficients: (1 not defined because of singularities)  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 17.250 6.543 2.637 0.0187 \*   
## Trtnoantibiotic 9.500 9.252 1.027 0.3208   
## concBac-3 64.000 9.252 6.917 4.92e-06 \*\*\*  
## concBac0 -26.750 9.252 -2.891 0.0112 \*   
## Trtnoantibiotic:concBac-3 -0.750 13.085 -0.057 0.9550   
## Trtnoantibiotic:concBac0 NA NA NA NA   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 13.08 on 15 degrees of freedom  
## Multiple R-squared: 0.9094, Adjusted R-squared: 0.8853   
## F-statistic: 37.66 on 4 and 15 DF, p-value: 1.175e-07

## 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 333.1 1 1.9453 0.1834   
## concBac 25279.6 2 73.8234 1.723e-08 \*\*\*  
## Trt:concBac 0.6 1 0.0033 0.9550   
## Residuals 2568.2 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\_5Data$count and RC159\_5Data$Trt   
##   
## antibiotic  
## noantibiotic 0.57   
##   
## 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\_5Data$count and RC159\_5Data$concBac   
##   
## -4 -3   
## -3 4.6e-08 -   
## 0 0.014 1.7e-08  
##   
## 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 antibiotic -4 17.2  
## 2 antibiotic -3 81.2  
## 3 noantibiotic -4 26.8  
## 4 noantibiotic -3 90

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

##   
## Call:  
## lm(formula = count ~ Trt + concBac + Trt \* concBac, data = RC159\_5Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -28.000 -4.625 -2.125 4.750 33.000   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 17.250 7.315 2.358 0.0362 \*   
## Trtnoantibiotic 9.500 10.345 0.918 0.3765   
## concBac-3 64.000 10.345 6.187 4.68e-05 \*\*\*  
## Trtnoantibiotic:concBac-3 -0.750 14.630 -0.051 0.9600   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 14.63 on 12 degrees of freedom  
## Multiple R-squared: 0.8655, Adjusted R-squared: 0.8319   
## F-statistic: 25.74 on 3 and 12 DF, p-value: 1.633e-05

## Anova Table (Type II tests)  
##   
## Response: count  
## Sum Sq Df F value Pr(>F)   
## Trt 333.1 1 1.5562 0.236   
## concBac 16192.6 1 75.6588 1.58e-06 \*\*\*  
## Trt:concBac 0.6 1 0.0026 0.960   
## Residuals 2568.3 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\_5Data$count and RC159\_5Data$Trt   
##   
## antibiotic  
## noantibiotic 0.63   
##   
## 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\_5Data$count and RC159\_5Data$concBac   
##   
## -4   
## -3 4.2e-07  
##   
## P value adjustment method: holm