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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.

### summary

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 64.1   
## 2 antibiotic -3 265.   
## 3 noantibiotic -4 71.6   
## 4 noantibiotic -3 262.   
## 5 noantibiotic 0 0.125

### analysi of variance forbacterial count as a result of antibiotics

##   
## Call:  
## lm(formula = count ~ Trt + concBac + Trt \* concBac, data = RC159\_5Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -199.62 -49.50 -0.12 46.37 334.37   
##   
## Coefficients: (1 not defined because of singularities)  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 64.12 46.20 1.388 0.17394   
## Trtnoantibiotic 7.50 65.34 0.115 0.90927   
## concBac-3 200.50 65.34 3.069 0.00414 \*\*  
## concBac0 -71.50 65.34 -1.094 0.28131   
## Trtnoantibiotic:concBac-3 -10.50 92.41 -0.114 0.91018   
## Trtnoantibiotic:concBac0 NA NA NA NA   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 130.7 on 35 degrees of freedom  
## Multiple R-squared: 0.4455, Adjusted R-squared: 0.3822   
## F-statistic: 7.031 on 4 and 35 DF, p-value: 0.0002899

## 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 40 1 0.0024 0.9614   
## concBac 452832 2 13.2582 5.174e-05 \*\*\*  
## Trt:concBac 220 1 0.0129 0.9102   
## Residuals 597711 35   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### pair wise t test Count vs trt

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: RC159\_5Data$count and RC159\_5Data$Trt   
##   
## antibiotic  
## noantibiotic 0.33   
##   
## P value adjustment method: holm

## Remove back ground control from analysis

### summary

## `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 64.1  
## 2 antibiotic -3 265.   
## 3 noantibiotic -4 71.6  
## 4 noantibiotic -3 262.

### analysi of variance for colony count

##   
## Call:  
## lm(formula = count ~ Trt + concBac + Trt \* concBac, data = RC159\_5Data,   
## na.action = na.omit)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -199.63 -73.00 -4.88 69.50 334.38   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 64.12 51.66 1.241 0.2248   
## Trtnoantibiotic 7.50 73.05 0.103 0.9190   
## concBac-3 200.50 73.05 2.745 0.0105 \*  
## Trtnoantibiotic:concBac-3 -10.50 103.31 -0.102 0.9198   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 146.1 on 28 degrees of freedom  
## Multiple R-squared: 0.338, Adjusted R-squared: 0.2671   
## F-statistic: 4.766 on 3 and 28 DF, p-value: 0.008298

## Anova Table (Type II tests)  
##   
## Response: count  
## Sum Sq Df F value Pr(>F)   
## Trt 40 1 0.0019 0.9655664   
## concBac 304980 1 14.2869 0.0007559 \*\*\*  
## Trt:concBac 220 1 0.0103 0.9197717   
## Residuals 597711 28   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### pair wise t test count vs Trt

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: RC159\_5Data$count and RC159\_5Data$Trt   
##   
## antibiotic  
## noantibiotic 0.97   
##   
## P value adjustment method: holm

### pair wise t test count vs concBac

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: RC159\_5Data$count and RC159\_5Data$concBac   
##   
## -4   
## -3 0.00049  
##   
## P value adjustment method: holm