RC 159-5: Evaluation of three differents to coltrol red slime

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# Introduction

## Contains Control

### load required packages

## Loading required package: carData

##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:data.table':  
##   
## between, first, last

## The following object is masked from 'package:car':  
##   
## recode

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

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

### input

### convert class of dataframeRC159\_1Data variables

### summary

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

### analysi of variance for total area

##   
## 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 diff vs PlantId

##   
## 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

## Control removed from dataframe

RC159\_5Data <- RC159\_5Data %>%  
 filter(concBac != 0)

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

### 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   
## -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

##   
## 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

##   
## 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