

controlled_metagenomics

Talia_Karasov

12/4/2017

R Markdown

Randomize in a tray

Results from infection trial

```
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
##
## Attaching package: 'tidyr'
## The following object is masked from 'package:reshape2':
##
##   smiths
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in calculate_cfu(dc3000_infection): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
```



```
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## Warning in FUN(newX[, i], ...): NAs introduced by coercion
## pdf
## 2
```

Output from run86

```
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following object is masked from 'package:tidyr':
##
## expand
## pdf
## 2
## Warning: NAs introduced by coercion
## pdf
## 2
##
## df AIC
## lm.full_log 3 357.7270
## lm.basic 3 383.2399
## Warning: Removed 17 rows containing missing values (geom_point).
## pdf
## 2
## Warning: Transformation introduced infinite values in continuous y-axis
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## Warning: Removed 1 rows containing non-finite values (stat_smooth).
## pdf
## 2
## No id variables; using all as measure variables
## No id variables; using all as measure variables
## Warning: Transformation introduced infinite values in continuous x-axis
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## pdf
## 2

## Warning: Transformation introduced infinite values in continuous x-axis
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

## pdf
## 2
```

```
g + geom_point() +
```

```
geom_smooth(method="lm", se=F) + geom_line( color='red',
data=fin_pred, aes(x=x, y=final_pre))
```

```
bc <- boxcox((FINAL+0.0001) ~ (perc_bacteria) , data=col_met)
```

```
bc_lam <- bcx[which(bcy==max(bc$y))]
```

```
lm.new <- lm( ((FINAL+0.0001)^bc_lam-1)/bc_lam ~ perc_bacteria,
data=col_met)
```

```
""bc <- boxCox(lm.full, family="yjPower", plotit = TRUE) bc_lam <- bcx[which(bcy==max(bcy))]depvar.transformed <-
-yjPower(col_metFINAL, bc_lam) #now transform the data depvar.transformed <- yjPower(col_metperc_bacteria, bc_lam)glm.
-glm((depvar.transformed) (col_metFINAL), family=gaussian(link="log"))
```

check residuals

```
qqnorm(resid(lm.full)) qqline(resid(lm.full)) ""
```

HPA infection data. Plants infected in timeseries with Days 0,2,5,11 timepoints. A few samples (4 for controls, and 6 for non-controls). Initial set from just day five

```
## pdf
## 2
```