

Benthamiana1

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12/30/2021

R Markdown

Bioassay data from **Benthamiana** project

```
##
## Attaching package: 'dplyr'

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

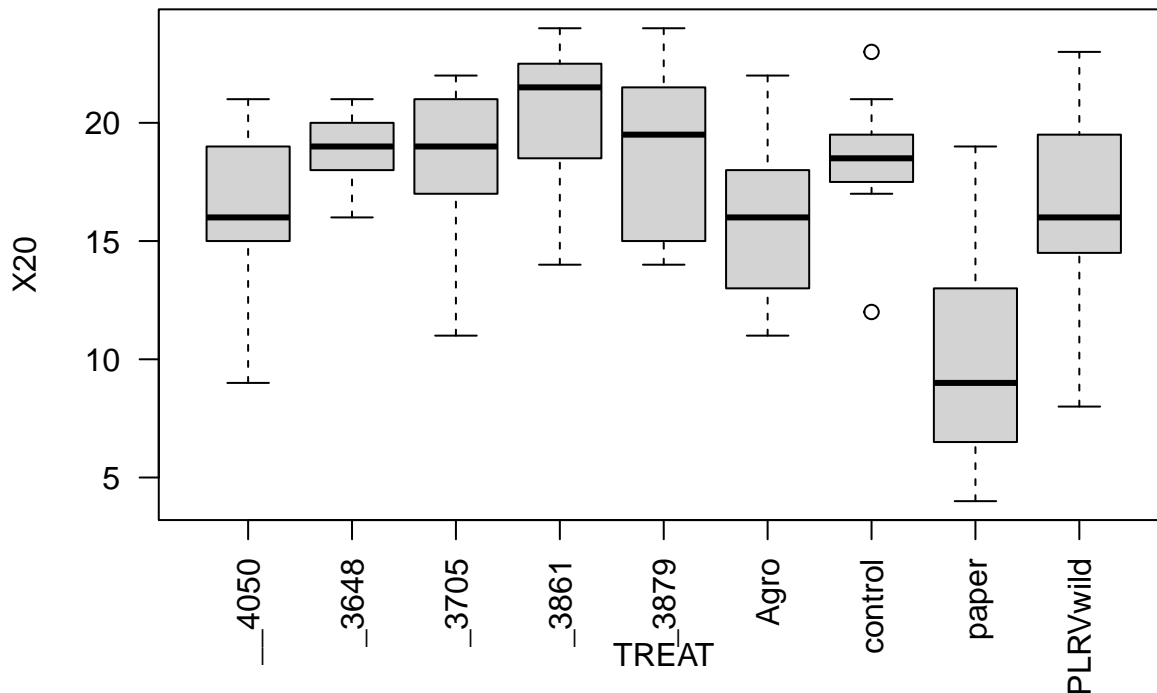
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

## 'data.frame':   137 obs. of  11 variables:
## $ PLANT   : int   1 2 3 4 5 6 7 8 9 10 ...
## $ ID      : Factor w/ 61 levels "##","#1","#10",...: 2 13 24 43 48 35 51 6 5 4 ...
## $ TREAT   : Factor w/ 9 levels "__4050","_3648",...: 6 6 6 6 6 6 6 6 6 ...
## $ TREAT.2 : Factor w/ 11 levels "__4050","_3648",...: 6 6 6 6 6 6 6 6 6 ...
## $ REP     : int   1 2 3 4 5 6 7 8 9 10 ...
## $ X10     : int  15 19 20 19 21 18 16 20 20 22 ...
## $ X20     : int  13 13 15 18 16 13 16 16 16 20 ...
## $ X30     : int  11 12 12 17 15 9 12 16 16 20 ...
## $ X40     : int   9 11 9 14 15 9 12 15 11 18 ...
## $ X50     : int   8 9 5 13 11 7 11 15 11 18 ...
## $ X60     : int   7 9 5 12 11 7 11 15 10 16 ...

##      PLANT      ID      TREAT      TREAT.2      REP
## Min.   : 1.00    #1      : 4    paper :23    paper :23    Min.   : 1.00
## 1st Qu.: 35.00   #13     : 4    PLRVwild:23   Agro  :16    1st Qu.: 2.00
## Median : 69.00   #14     : 4    Agro  :16    __4050 :15    Median : 3.00
## Mean   : 72.02   #17     : 4    __4050 :15    _3705  :15    Mean   : 3.65
## 3rd Qu.:112.00   #18     : 4    _3705  :15    PLRVwild:14   3rd Qu.: 5.00
## Max.   :146.00   #3      : 4    _3648  :13    _3648  :13    Max.   :13.00
##                (Other):113  (Other) :32  (Other) :41

##      X10      X20      X30      X40      X50
## Min.   : 6.00   Min.   : 4.00   Min.   : 3.00   Min.   : 3.00   Min.   : 2.0
## 1st Qu.:18.00   1st Qu.:14.00   1st Qu.:12.00   1st Qu.:10.00   1st Qu.: 9.0
## Median :20.00   Median :17.00   Median :16.00   Median :14.00   Median :13.0
## Mean   :19.45   Mean   :16.47   Mean   :14.82   Mean   :13.61   Mean   :12.5
## 3rd Qu.:22.00   3rd Qu.:20.00   3rd Qu.:18.00   3rd Qu.:17.00   3rd Qu.:16.0
## Max.   :26.00   Max.   :24.00   Max.   :23.00   Max.   :23.00   Max.   :23.0
##
```

```
##          X60
##  Min.    : 1.00
## 1st Qu.: 8.00
##  Median :12.00
##   Mean   :11.79
## 3rd Qu.:15.00
##   Max.   :23.00
##
##          Df Sum Sq Mean Sq F value    Pr(>F)
## TREAT      8   1287   160.90   13.49 4.93e-14 ***
## Residuals 128   1527    11.93
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
## Call:
## aov(formula = X20 ~ TREAT, data = bioassay9)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -8.4783 -2.2609  0.0625  2.2000  8.7391
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   17.02340    0.30799   55.272 <2e-16 ***
## TREATcontrast1 -0.09511    0.31157   -0.305  0.7607
## TREATcontrast2  0.13406    0.91809    0.146  0.8841
## TREATcontrast3  0.96608    0.09937    9.722 <2e-16 ***
## TREATcontrast4 -2.14583    1.11539   -1.924  0.0566 .
## TREAT         -1.77386    0.87532   -2.027  0.0448 *
## TREAT          0.75796    0.91429    0.829  0.4086
## TREAT          1.37012    1.11981    1.224  0.2234
```

```
## TREAT          1.45452    0.95506    1.523    0.1302
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.454 on 128 degrees of freedom
## Multiple R-squared:  0.4574, Adjusted R-squared:  0.4235
## F-statistic: 13.49 on 8 and 128 DF,  p-value: 4.926e-14
## [1] "__4050"    "_3648"      "_3705"      "_3861"      "_3879"      "Agro"       "control"
## [8] "paper"      "PLRVwild"
```

Treatments in order

__4050, _3648, 3705, 3861, 3879, Agro, control, paper, PLRVwild

Contrast coefficients (revise based on script)

```
contrast1 = c(1,1,1,1,1,0,0,-5)
contrast2 = c(0,0,0,0,0,0,1,0,-1)
contrast3 = c(1,1,1,1,1,1,1,-7,1)
contrast4 = c(0,0,0,-1,0,0,0,0,1)
```

EMIGRATION MODEL

```
str(bioassaymod)
```

```
## 'data.frame':    1022 obs. of  8 variables:
## $ PLANT      : int   1 2 3 4 5 6 7 8 9 10 ...
## $ ID        : Factor w/ 61 levels "##","#1","#10",...: 2 13 24 43 48 35 51 6 5 4 ...
## $ TREAT     : Factor w/ 10 levels "__4050","_3648",...: 7 7 7 7 7 7 7 7 7 ...
## $ TREAT.2   : Factor w/ 12 levels "__4050","_3648",...: 7 7 7 7 7 7 7 7 7 ...
## $ REP       : int   1 2 3 4 5 6 7 8 9 10 ...
## $ Time      : int  10 10 10 10 10 10 10 10 10 10 ...
## $ Remaining : int  15 19 20 19 21 18 16 20 20 22 ...
## $ Emigrating: int  15 11 10 11 9 12 14 10 10 8 ...
```

```
#plot(bioassaymod$Time, bioassaymod$Emigrating, xlab = "seconds", ylab= "number emigrating/30")
#title("Scatter Plot of Emigration by Time")
```

```
attach (bioassaymod)
```

```
#bioassaymod
```

```
plot(Time,Remaining, col = TREAT, pch = 1, xlab = "seconds", ylab= "number Remaining/30",xlim = c(0,75),
```

```
title("Scatter Plot of Emigration by Time")
```

```
legend("topright",c("__4050", "_3648", "3705", "3861", "3879", "Agro", "control", "paper", "PLRVwild"),
```

```
emmod<-lm(log(Remaining+0.1)~Time)
```

```
summary(emmod)
```

```
##
```

```
## Call:
```

```
## lm(formula = log(Remaining + 0.1) ~ Time)
```

```
##
```

```
## Residuals:
```

```
##      Min      1Q  Median      3Q      Max
## -2.1977 -0.1476  0.1018  0.2109  0.8468
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.1935956  0.0211026  151.34  <2e-16 ***
## Time        -0.0150101  0.0005853  -25.65  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3742 on 1020 degrees of freedom
## Multiple R-squared:  0.392, Adjusted R-squared:  0.3914
## F-statistic: 657.7 on 1 and 1020 DF, p-value: < 2.2e-16
```

```
factor<-emmod$coefficients["Time"]
factor
```

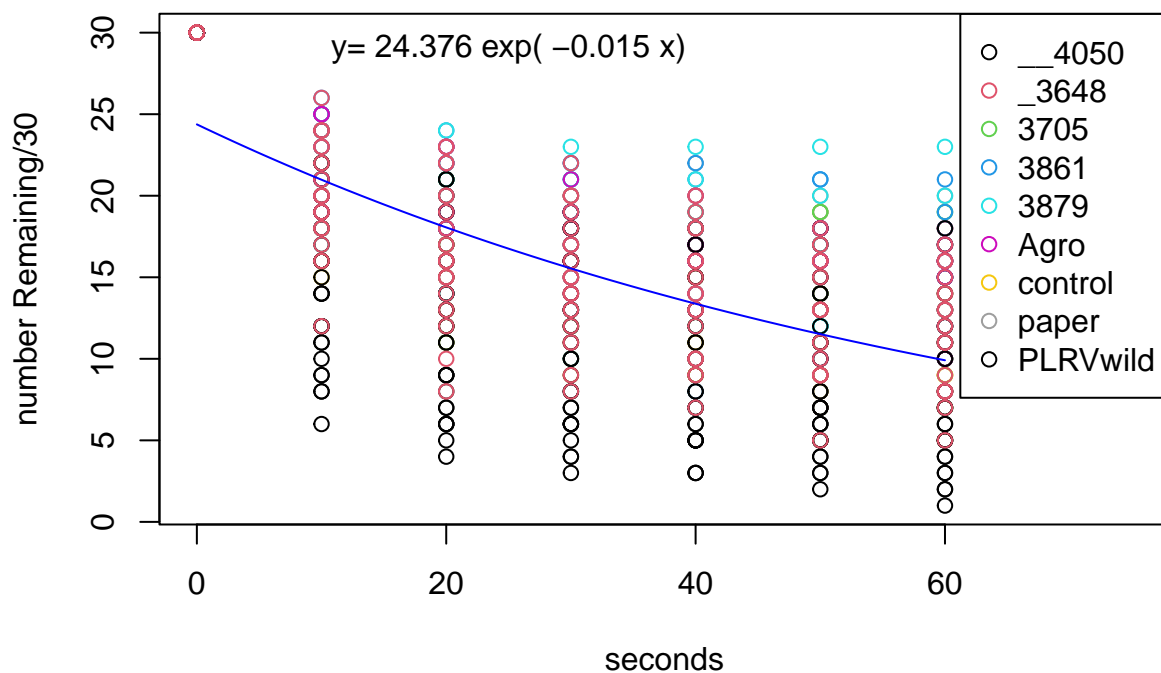
```
##      Time
## -0.01501009
```

```
coeff<-exp(emmod$coefficients["(Intercept)"])
coeff
```

```
## (Intercept)
##      24.37592
```

```
factor<-round(factor,3)
coeff<-round(coeff,3)
fit_eq=paste("y=",coeff,"exp(",factor,"x)")
text(25,29,fit_eq)
curve(coeff*exp(factor*x),0,60,add=TRUE,col="blue")
```

Scatter Plot of Emigration by Time



second try

```
bioassaymod2<-data.frame(bioassaymod, group = TREAT)
#bioassaymod2
bioassaymodwt<-subset(bioassaymod2, group=="PLRVwild")
#bioassaymodpaper

attach (bioassaymodwt)

## The following objects are masked from bioassaymod:
##
##      Emigrating, ID, PLANT, Remaining, REP, Time, TREAT, TREAT.2

#bioassaymod
plot(Time,Remaining, col = TREAT, pch = 1, xlab = "seconds", ylab= "number Remaining/30",xlim = c(0,75),
title("Scatter Plot of Emigration by Time")
legend("topright",c("__4050", "_3648", "3705", "3861", "3879", "Agro", "control", "paper", "PLRVwild"),

emmod<-lm(log(Remaining+0.1)~Time)
summary(emmod)

##
## Call:
## lm(formula = log(Remaining + 0.1) ~ Time)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8311 -0.1894  0.0761  0.1900  0.5295
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.214574   0.038380  83.76  <2e-16 ***
## Time        -0.015084   0.001064 -14.17  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2701 on 159 degrees of freedom
## Multiple R-squared:  0.5581, Adjusted R-squared:  0.5553
## F-statistic: 200.8 on 1 and 159 DF,  p-value: < 2.2e-16

factor<-emmod$coefficients["Time"]
factor

##           Time
## -0.01508399

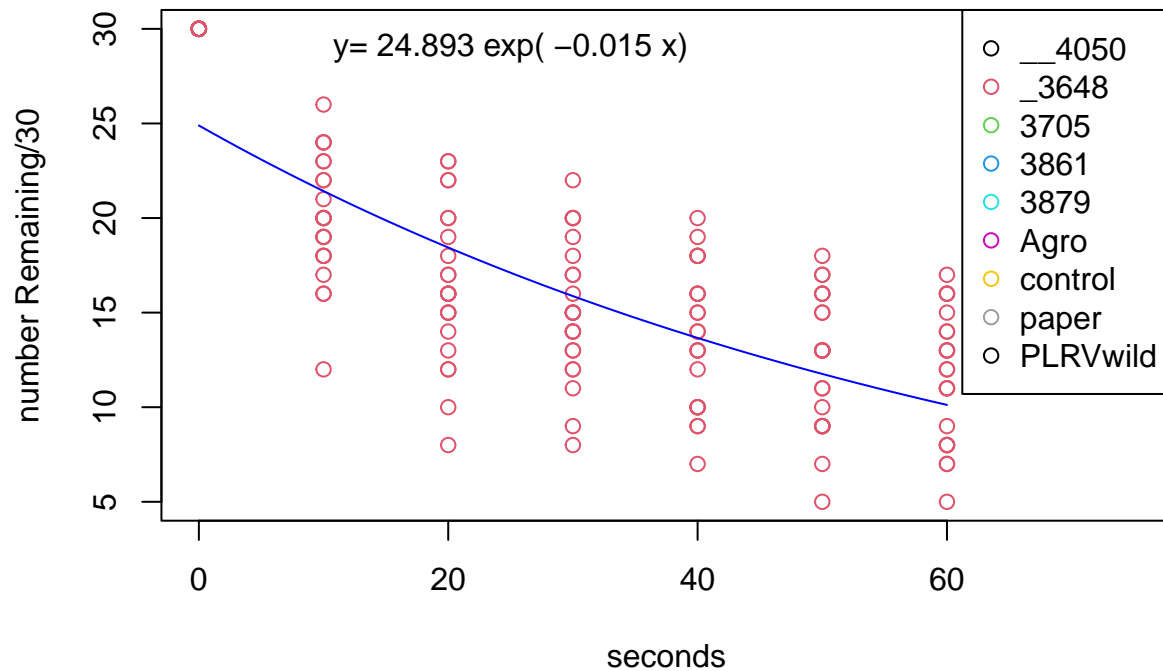
coeff<-exp(emmod$coefficients["(Intercept)"])
coeff

## (Intercept)
##      24.89269

factor<-round(factor,3)
coeff<-round(coeff,3)
fit_eq=paste("y=",coeff,"exp(",factor,"x)")
text(25,29,fit_eq)
```

```
curve(coeff*exp(factor*x),0,60,add=TRUE,col ="blue")
```

Scatter Plot of Emigration by Time



NOTES

MADE PROGRESS FITTING THE EMIGRATION DATA TO A MODEL AND PLOTTING. MODEL NEEDS WORK. NEED TO GET SOME ESTIMATE OF THE VARIANCE AROUND THE INTERCEPT AND SLOPE AND A WAY TO COMPARE THE LINES AMONG TREATMENTS. THE MODEL WORKS WELL FOR NUMBER OF SUBJECTS REMAINING, BUT WHEN I TRY TO WRITE FOR NUMBER EMIGRATING, SOMETHING DOESN'T WORK. MODEL BILL USED IS $N = Rm \times (1 - e^{-\beta t})$, AND THAT IS NOT WHAT I'M USING, YET. I HOPE I CAN USE THIS BASIC CODE BUT MAYBE NOT.