

Herbivory analysis

Exploración de la base de datos

The database on herbivory from six grasshopper species on meadow plants from mid-west France looks as follows:

NOTE: remember changing the directory when loading the database from a different computer.

```
herbivory <- read.table(file = "C:/Users/Granjel RR/Desktop/Nico Gross/Herbivory_2013.txt", header = TRUE)
herbivory <- cbind(herbivory[1:630, 1:9], (herbivory[1:630, 10:50] * 10))
head(herbivory)
```

```
##   block treatment datapoint Cb Cd Ci Ee Pg Pp ACHMIL AGREUP ARRELA BROERE
## 1      1         6sp        1 4 4 4 4 4 4      NA      NA      40      10
## 2      1         6sp        2 4 4 4 4 4 4      NA      NA      50      10
## 3      1         6sp        3 4 4 4 4 4 4      NA      NA      60      10
## 4      1         6sp        4 4 4 4 4 4 4      NA      NA      50      10
## 5      1         6sp        5 4 4 4 4 4 4      NA      NA      50      10
## 6      1         6sp        6 4 4 4 4 4 4      NA      NA      50      10
##   BROMOL CENJAC CONARV CREPIS DACGLO DAUCAR ELYREP ERYNGE FESARU FESRUB
## 1      NA      NA     50      NA      NA      0      NA      NA      NA      NA
## 2      NA      NA     50      NA     10      NA      NA      NA      NA      NA
## 3      NA      NA      NA      NA     10      0      NA      NA      NA      NA
## 4      NA      NA     10      NA     10     20      NA      NA      NA      NA
## 5      NA      NA      NA      NA     10     20      NA      NA      NA      NA
## 6      NA      NA      NA      NA     10      0      NA      NA      NA      NA
##   GARMOL GALVER GERDIS LEUVUL LOLPER LOTCOR MALSYL MEDARA ONOREP PICECH
## 1      NA      0      NA      NA      NA      NA      NA      NA      NA      0
## 2      NA     10      NA      0      NA      NA      NA      NA      NA      NA
## 3      NA     10      NA      NA      NA      NA      NA      NA      NA      NA
## 4      NA      0      NA      NA      NA      NA      NA      NA      NA      NA
## 5      NA      NA      NA     10      NA      NA      NA      NA      NA      NA
## 6      NA     10      NA      NA      NA      NA      NA      NA      NA      NA
##   PLALAN PLAMAJ POAANG POAPOI POAPRA POTREP RANACR RUBFRU RUMACE SALPRA
## 1      NA      NA      NA      NA      0      NA      NA      NA      NA      NA
## 2     20      NA      NA      NA      NA      NA      0      NA      NA      NA
## 3     50      NA      0      NA      NA      NA      0      NA      NA      NA
## 4     30      NA     10      NA      NA      NA      0      NA      NA      NA
## 5      NA      NA      0      NA      NA      NA      0      NA      NA      NA
## 6      NA      NA      NA      NA      NA      NA      0      NA      NA      NA
##   SENJAC SONCHU TAROFF TRIPRA TRIREP VERBOF Total
## 1      NA      0      NA     10      NA      NA    110
## 2      NA      NA      NA      NA      NA      NA    150
## 3      NA      NA      NA      NA      NA      NA    140
## 4      NA      NA      NA      0      NA      NA    140
## 5      NA      NA      NA     10      NA      NA    110
## 6      NA      NA      NA      NA      NA      NA     80
```

Within this database, the final variable ('Total') represents the sum of the damage of all the plant species in the row.

```
summary(herbivory)
```

```

##      block      treatment      datapoint      Cb      Cd
## Min.   :1 6sp      : 45 Min.   :1 Min.   : 0.000 Min.   : 0.000
## 1st Qu.:2 Cb      : 45 1st Qu.:3 1st Qu.: 0.000 1st Qu.: 0.000
## Median :3 Cb.Cd.Pg: 45 Median :5 Median : 0.000 Median : 0.000
## Mean   :3 Cb.Ci.Pg: 45 Mean   :5 Mean   : 3.143 Mean   : 3.143
## 3rd Qu.:4 Cd      : 45 3rd Qu.:7 3rd Qu.: 4.000 3rd Qu.: 4.000
## Max.   :5 Cd.Pp.Ee: 45 Max.   :9 Max.   :24.000 Max.   :24.000
##      (Other) :360
##      Ci      Ee      Pg      Pp
## Min.   : 0.000 Min.   : 0.000 Min.   : 0.000 Min.   : 0.000
## 1st Qu.: 0.000 1st Qu.: 0.000 1st Qu.: 0.000 1st Qu.: 0.000
## Median : 0.000 Median : 0.000 Median : 0.000 Median : 0.000
## Mean   : 4.286 Mean   : 3.714 Mean   : 4.286 Mean   : 3.714
## 3rd Qu.: 8.000 3rd Qu.: 8.000 3rd Qu.: 8.000 3rd Qu.: 8.000
## Max.   :24.000 Max.   :24.000 Max.   :24.000 Max.   :24.000
##
##      ACHMIL      AGREUP      ARRELA      BROERE
## Min.   : 0.00 Min.   : 0.0 Min.   : 0.00 Min.   : 0.00
## 1st Qu.: 0.00 1st Qu.: 0.0 1st Qu.:10.00 1st Qu.: 0.00
## Median : 0.00 Median : 0.0 Median :30.00 Median :10.00
## Mean   :18.82 Mean   : 2.5 Mean   :28.08 Mean   :10.38
## 3rd Qu.:40.00 3rd Qu.: 2.5 3rd Qu.:50.00 3rd Qu.:15.00
## Max.   :80.00 Max.   :10.0 Max.   :80.00 Max.   :50.00
## NA's   :592 NA's   :626 NA's   :174 NA's   :162
##      BROMOL      CENJAC      CONARV      CREPIS
## Min.   : 0.00 Min.   : 0.00 Min.   : 0.00 Min.   : 0.000
## 1st Qu.: 0.00 1st Qu.: 0.00 1st Qu.: 0.00 1st Qu.: 0.000
## Median : 0.00 Median : 10.00 Median : 0.00 Median : 0.000
## Mean   :13.33 Mean   : 18.79 Mean   :11.33 Mean   : 2.935
## 3rd Qu.:20.00 3rd Qu.: 30.00 3rd Qu.:20.00 3rd Qu.: 0.000
## Max.   :40.00 Max.   :100.00 Max.   :70.00 Max.   :50.000
## NA's   :627 NA's   :597 NA's   :510 NA's   :584
##      DACGLO      DAUCAR      ELYREP      ERYNGE
## Min.   : 0.00 Min.   : 0.000 Min.   : 0.00 Min.   : 0.000
## 1st Qu.: 0.00 1st Qu.: 0.000 1st Qu.:30.00 1st Qu.: 0.000
## Median :10.00 Median : 0.000 Median :50.00 Median : 0.000
## Mean   :11.52 Mean   : 7.337 Mean   :45.98 Mean   : 4.261
## 3rd Qu.:20.00 3rd Qu.:10.000 3rd Qu.:60.00 3rd Qu.: 0.000
## Max.   :40.00 Max.   :70.000 Max.   :90.00 Max.   :40.000
## NA's   :300 NA's   :247 NA's   :564 NA's   :542
##      FESARU      FESRUB      GARMOL      GALVER
## Min.   : 0.0 Min.   : 0.00 Min.   : 0 Min.   : 0.000
## 1st Qu.:20.0 1st Qu.:10.00 1st Qu.: 0 1st Qu.: 0.000
## Median :30.0 Median :20.00 Median : 0 Median : 0.000
## Mean   :26.4 Mean   :18.53 Mean   :10 Mean   : 7.421
## 3rd Qu.:30.0 3rd Qu.:30.00 3rd Qu.: 0 3rd Qu.:10.000
## Max.   :50.0 Max.   :50.00 Max.   :70 Max.   :70.000
## NA's   :605 NA's   :538 NA's   :623 NA's   :440
##      GERDIS      LEUVUL      LOLPER      LOTCOR
## Min.   :0 Min.   : 0.000 Min.   :0 Min.   :10.00
## 1st Qu.:0 1st Qu.: 0.000 1st Qu.:0 1st Qu.:22.50
## Median :0 Median : 0.000 Median :0 Median :35.00
## Mean   :0 Mean   : 4.607 Mean   :0 Mean   :31.67
## 3rd Qu.:0 3rd Qu.:10.000 3rd Qu.:0 3rd Qu.:40.00

```

| | | | | | | | | |
|----|----------|---------|----------|---------|----------|---------|----------|----------|
| ## | Max. | :0 | Max. | :30.000 | Max. | :0 | Max. | :50.00 |
| ## | NA's | :626 | NA's | :541 | NA's | :629 | NA's | :624 |
| ## | MALSYL | | MEDARA | | ONOREP | | PICECH | |
| ## | Min. | : 0.0 | Min. | :0 | Min. | : 0.00 | Min. | : 0.00 |
| ## | 1st Qu.: | 0.0 | 1st Qu.: | 0 | 1st Qu.: | 0.00 | 1st Qu.: | 0.00 |
| ## | Median : | 0.0 | Median : | 0 | Median : | 20.00 | Median : | 0.00 |
| ## | Mean | :12.5 | Mean | :0 | Mean | :23.75 | Mean | :10.99 |
| ## | 3rd Qu.: | 12.5 | 3rd Qu.: | 0 | 3rd Qu.: | 40.00 | 3rd Qu.: | 10.00 |
| ## | Max. | :50.0 | Max. | :0 | Max. | :80.00 | Max. | :80.00 |
| ## | NA's | :626 | NA's | :628 | NA's | :546 | NA's | :509 |
| ## | PLALAN | | PLAMAJ | | POAANG | | POAPOI | |
| ## | Min. | : 0.00 | Min. | : 0.00 | Min. | : 0.000 | Min. | : 0.000 |
| ## | 1st Qu.: | 20.00 | 1st Qu.: | 0.00 | 1st Qu.: | 0.000 | 1st Qu.: | 0.000 |
| ## | Median : | 30.00 | Median : | 10.00 | Median : | 5.000 | Median : | 5.000 |
| ## | Mean | : 30.93 | Mean | :20.91 | Mean | : 6.861 | Mean | : 7.143 |
| ## | 3rd Qu.: | 50.00 | 3rd Qu.: | 35.00 | 3rd Qu.: | 10.000 | 3rd Qu.: | 10.000 |
| ## | Max. | :100.00 | Max. | :80.00 | Max. | :40.000 | Max. | :30.000 |
| ## | NA's | :349 | NA's | :619 | NA's | :329 | NA's | :616 |
| ## | POAPRA | | POTREP | | RANACR | | RUBFRU | |
| ## | Min. | : 0.0 | Min. | : 0.00 | Min. | : 0.000 | Min. | :30 |
| ## | 1st Qu.: | 0.0 | 1st Qu.: | 10.00 | 1st Qu.: | 0.000 | 1st Qu.: | 30 |
| ## | Median : | 10.0 | Median : | 20.00 | Median : | 0.000 | Median : | 30 |
| ## | Mean | : 6.8 | Mean | :22.94 | Mean | : 1.623 | Mean | :30 |
| ## | 3rd Qu.: | 10.0 | 3rd Qu.: | 40.00 | 3rd Qu.: | 0.000 | 3rd Qu.: | 30 |
| ## | Max. | :20.0 | Max. | :50.00 | Max. | :30.000 | Max. | :30 |
| ## | NA's | :605 | NA's | :613 | NA's | :285 | NA's | :627 |
| ## | RUMACE | | SALPRA | | SENJAC | | SONCHU | |
| ## | Min. | : 0.00 | Min. | : 0.00 | Min. | : 0 | Min. | : 0.0000 |
| ## | 1st Qu.: | 0.00 | 1st Qu.: | 5.00 | 1st Qu.: | 10 | 1st Qu.: | 0.0000 |
| ## | Median : | 0.00 | Median : | 10.00 | Median : | 15 | Median : | 0.0000 |
| ## | Mean | :10.75 | Mean | :24.41 | Mean | :20 | Mean | : 0.7407 |
| ## | 3rd Qu.: | 20.00 | 3rd Qu.: | 40.00 | 3rd Qu.: | 35 | 3rd Qu.: | 0.0000 |
| ## | Max. | :50.00 | Max. | :80.00 | Max. | :40 | Max. | :20.0000 |
| ## | NA's | :590 | NA's | :469 | NA's | :624 | NA's | :603 |
| ## | TAROFF | | TRIPRA | | TRIREP | | VERBOF | |
| ## | Min. | : 0.000 | Min. | : 0 | Min. | :10 | Min. | : 0.00 |
| ## | 1st Qu.: | 0.000 | 1st Qu.: | 0 | 1st Qu.: | 10 | 1st Qu.: | 0.00 |
| ## | Median : | 0.000 | Median : | 10 | Median : | 10 | Median : | 5.00 |
| ## | Mean | : 4.294 | Mean | :10 | Mean | :10 | Mean | :14.38 |
| ## | 3rd Qu.: | 0.000 | 3rd Qu.: | 10 | 3rd Qu.: | 10 | 3rd Qu.: | 22.50 |
| ## | Max. | :50.000 | Max. | :50 | Max. | :10 | Max. | :50.00 |
| ## | NA's | :545 | NA's | :427 | NA's | :629 | NA's | :614 |
| ## | Total | | | | | | | |
| ## | Min. | : 0.00 | | | | | | |
| ## | 1st Qu.: | 50.00 | | | | | | |
| ## | Median : | 90.00 | | | | | | |
| ## | Mean | : 91.77 | | | | | | |
| ## | 3rd Qu.: | 125.00 | | | | | | |
| ## | Max. | :310.00 | | | | | | |
| ## | | | | | | | | |

Plot total damage ~ grasshoppers:

I'm plotting now the total damage versus the amount of grasshoppers for each grasshopper species.

```
# Installing the ggplot2 package for cool graphics and gridExtra for grids
# install.packages("ggplot2")
# install.packages("gridExtra")
```

```
library(gridExtra)
```

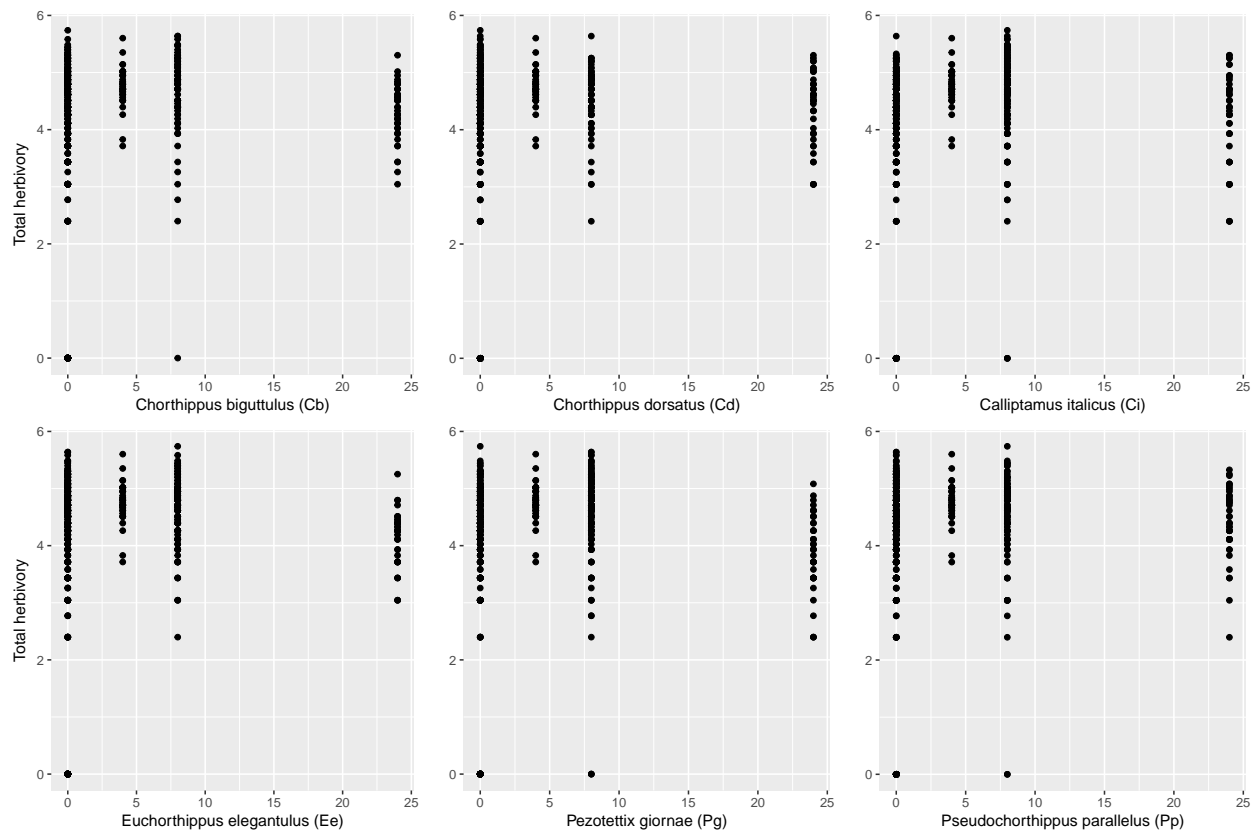
```
## Warning: package 'gridExtra' was built under R version 3.4.4
```

```
library(grid)
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.4.4
```

```
library(lattice)
```

```
Cb_plot <- qplot(x = Cb, y = log(Total+1), xlab = "Chorthippus biguttulus (Cb)", ylab = "Total herbivory", data = herbivory_grasshoppers)
Cd_plot <- qplot(x = Cd, y = log(Total+1), xlab = "Chorthippus dorsatus (Cd)", ylab = " ", data = herbivory_grasshoppers)
Ci_plot <- qplot(x = Ci, y = log(Total+1), xlab = "Calliptamus italicus (Ci)", ylab = " ", data = herbivory_grasshoppers)
Ee_plot <- qplot(x = Ee, y = log(Total+1), xlab = "Euchorthippus elegantulus (Ee)", ylab = "Total herbivory", data = herbivory_grasshoppers)
Pg_plot <- qplot(x = Pg, y = log(Total+1), xlab = "Pezotettix giornae (Pg)", ylab = " ", data = herbivory_grasshoppers)
Pp_plot <- qplot(x = Pp, y = log(Total+1), xlab = "Pseudochorthippus parallelus (Pp)", ylab = " ", data = herbivory_grasshoppers)
herbivory_grasshoppers <- grid.arrange(Cb_plot, Cd_plot, Ci_plot, Ee_plot, Pg_plot, Pp_plot, nrow = 2, ncol = 3)
```



Trying different models - all the grasshopper species together

Now I'm trying 4 different models and selecting the one that better fits the data (total herbivory ~ all grasshoppers together).

Linear (a + bx)

```
library(nlme)
Grasshoppers_linear <- lme(log(Total+1) ~ 0 + Cb + Cd + Ci + Ee + Pg + Pp, data = herbivory, random = ~
summary(Grasshoppers_linear)

## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 1353.321 1388.81 -668.6604
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:   0.1120645 0.6686181
##
## Fixed effects: log(Total + 1) ~ 0 + Cb + Cd + Ci + Ee + Pg + Pp
##      Value Std.Error DF t-value p-value
## Cb 0.1882492 0.004236922 620 44.43065      0
## Cd 0.1880142 0.004219223 620 44.56133      0
## Ci 0.1867353 0.004070111 620 45.87966      0
## Ee 0.1815923 0.004126281 620 44.00871      0
## Pg 0.1741710 0.004054725 620 42.95508      0
## Pp 0.1883173 0.004126281 620 45.63851      0
## Correlation:
##      Cb      Cd      Ci      Ee      Pg
## Cd 0.117
## Ci 0.151 0.233
## Ee 0.210 0.131 0.099
## Pg 0.078 0.144 0.043 0.174
## Pp 0.210 0.131 0.099 0.088 0.174
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -6.6988382 -0.3690315 0.1484255 0.6128491 1.9798392
##
## Number of Observations: 630
## Number of Groups: 5
```

Quadratic model (a + x²)

```
Grasshoppers_quadratic <- lme(log(Total+1) ~ 0 + (Cb)^2 + (Cd)^2 + (Ci)^2 + (Ee)^2 + (Pg)^2 + (Pp)^2, d
summary(Grasshoppers_quadratic)

## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
```

```
##    1353.321 1388.81 -668.6604
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:    0.1120645 0.6686181
##
## Fixed effects: log(Total + 1) ~ 0 + (Cb)^2 + (Cd)^2 + (Ci)^2 + (Ee)^2 + (Pg)^2 +      (Pp)^2
##      Value Std.Error DF t-value p-value
## Cb 0.1882492 0.004236922 620 44.43065      0
## Cd 0.1880142 0.004219223 620 44.56133      0
## Ci 0.1867353 0.004070111 620 45.87966      0
## Ee 0.1815923 0.004126281 620 44.00871      0
## Pg 0.1741710 0.004054725 620 42.95508      0
## Pp 0.1883173 0.004126281 620 45.63851      0
## Correlation:
##      Cb      Cd      Ci      Ee      Pg
## Cd 0.117
## Ci 0.151 0.233
## Ee 0.210 0.131 0.099
## Pg 0.078 0.144 0.043 0.174
## Pp 0.210 0.131 0.099 0.088 0.174
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -6.6988382 -0.3690315 0.1484255 0.6128491 1.9798392
##
## Number of Observations: 630
## Number of Groups: 5
```

Neperian log model ($a + \log(x+1)$)

```
Grasshoppers_log <- lme(log(Total+1) ~ 0 + log(Cb+1) + log(Cd+1) + log(Ci+1) + log(Ee+1) + log(Pg+1) + log(Pp+1),
summary(Grasshoppers_log)

## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 1925.345 1960.834 -954.6724
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      2.45384 1.05448
##
## Fixed effects: log(Total + 1) ~ 0 + log(Cb + 1) + log(Cd + 1) + log(Ci + 1) +      log(Ee + 1) + log(Pg + 1) + log(Pp + 1)
##      Value Std.Error DF t-value p-value
## log(Cb + 1) 0.4013827 0.04211872 620 9.529793      0
## log(Cd + 1) 0.3731241 0.04152234 620 8.986106      0
## log(Ci + 1) 0.3552545 0.03972156 620 8.943618      0
## log(Ee + 1) 0.3268466 0.03917033 620 8.344239      0
## log(Pg + 1) 0.2526926 0.03861795 620 6.543399      0
## log(Pp + 1) 0.3478211 0.03917033 620 8.879708      0
```

```
## Correlation:
##      lg(Cb+1) lg(Cd+1) log(C+1) l(E+1) lg(Pg+1)
## log(Cd + 1) -0.069
## log(Ci + 1)  0.057    0.344
## log(Ee + 1)  0.227   -0.029   -0.077
## log(Pg + 1) -0.117    0.017   -0.219    0.155
## log(Pp + 1)  0.227   -0.029   -0.077   -0.060  0.155
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -4.5285514 -0.4089328  0.1890195  0.6957243  1.7069750
##
## Number of Observations: 630
## Number of Groups: 5
```

Exponential model ($a + \exp(-x)$)

```
Grasshoppers_exp <- lme(log(Total+1) ~ 0 + exp(Cb) + exp(Cd) + exp(Ci) + exp(Ee) + exp(Pg) + exp(Pp), d
summary(Grasshoppers_exp)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2482.108 2517.597 -1233.054
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:    4.017722 1.323407
##
## Fixed effects: log(Total + 1) ~ 0 + exp(Cb) + exp(Cd) + exp(Ci) + exp(Ee) +      exp(Pg) + exp(Pp)
##      Value Std.Error DF   t-value p-value
## exp(Cb)  1.090261e-11 7.89877e-12 620  1.3802929  0.1680
## exp(Cd)  1.341049e-11 7.89877e-12 620  1.6977943  0.0900
## exp(Ci)  6.881246e-12 7.89877e-12 620  0.8711795  0.3840
## exp(Ee)  4.503353e-12 7.89877e-12 620  0.5701335  0.5688
## exp(Pg) -4.547091e-12 7.89877e-12 620 -0.5756707  0.5650
## exp(Pp)  1.416871e-11 7.89877e-12 620  1.7937865  0.0733
## Correlation:
##      exp(Cb) exp(Cd) exp(Ci) exp(E) exp(Pg)
## exp(Cd) 0.111
## exp(Ci) 0.111  0.111
## exp(Ee) 0.111  0.111  0.111
## exp(Pg) 0.111  0.111  0.111  0.111
## exp(Pp) 0.111  0.111  0.111  0.111  0.111
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1161042 -0.1451159  0.2760755  0.5661609  1.3399764
##
## Number of Observations: 630
## Number of Groups: 5
```

Trying different models - each grasshopper species separately

Now I'm trying the same 4 different models for each grasshopper species separately.

Cb (*Chorthippus biguttulus*)

Cb - Linear (a + bx)

```
Cb_linear <- lme(log(Total+1) ~ 0 + Cb, data = herbivory, random = ~ 1 | block)
summary(Cb_linear)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2180.395 2193.727 -1087.197
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.016189 1.314326
##
## Fixed effects: log(Total + 1) ~ 0 + Cb
##      Value Std.Error DF t-value p-value
## Cb 0.0277221 0.008122658 625 3.412935 7e-04
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.3053577 -0.1885465 0.3088276 0.5864990 1.3502487
##
## Number of Observations: 630
## Number of Groups: 5
```

Cb - Quadratic model (a + x²)

```
Cb_quadratic <- lme(log(Total+1) ~ 0 + (Cb)^2, data = herbivory, random = ~ 1 | block)
summary(Cb_quadratic)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2180.395 2193.727 -1087.197
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.016189 1.314326
##
## Fixed effects: log(Total + 1) ~ 0 + (Cb)^2
##      Value Std.Error DF t-value p-value
## Cb 0.0277221 0.008122658 625 3.412935 7e-04
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.3053577 -0.1885465 0.3088276 0.5864990 1.3502487
```



```
##
## Number of Observations: 630
## Number of Groups: 5
```

Cb - Neperian log model ($a + \log(x+1)$)

```
Cb_log <- lme(log(Total+1) ~ 0 + log(Cb+1), data = herbivory, random = ~ 1 | block)
summary(Cb_log)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2162.042 2175.375 -1078.021
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.94071 1.299037
##
## Fixed effects: log(Total + 1) ~ 0 + log(Cb + 1)
##              Value Std.Error DF t-value p-value
## log(Cb + 1) 0.2469609 0.0476203 625 5.186043      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.5330933 -0.2012842  0.2810076  0.5704111  1.4242970
##
## Number of Observations: 630
## Number of Groups: 5
```

Cb - Exponential model ($a + \exp(x)$)

```
Cb_exp <- lme(log(Total+1) ~ 0 + exp(Cb), data = herbivory, random = ~ 1 | block)
summary(Cb_exp)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2232.358 2245.691 -1113.179
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.087617 1.325141
##
## Fixed effects: log(Total + 1) ~ 0 + exp(Cb)
##              Value Std.Error DF t-value p-value
## exp(Cb) 8.253147e-12 7.738679e-12 625 1.06648 0.2866
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1649888 -0.1546378  0.2909427  0.5664604  1.2852611
##
## Number of Observations: 630
```

```
## Number of Groups: 5
```

Cd (*Chorthippus dorsatus*)

Cd - Linear model (a + bx)

```
Cd_linear <- lme(log(Total+1) ~ 0 + Cd, data = herbivory, random = ~ 1 | block)
summary(Cd_linear)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2179.771 2193.104 -1086.886
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.01389 1.313676
##
## Fixed effects: log(Total + 1) ~ 0 + Cd
##      Value Std.Error DF t-value p-value
## Cd 0.02845401 0.008118638 625 3.504777 5e-04
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1364227 -0.1433511 0.2886844 0.5683298 1.3526672
##
## Number of Observations: 630
## Number of Groups: 5
```

Cd - Quadratic model (a + x²)

```
Cd_quadratic <- lme(log(log(Total+1)+1) ~ 0 + (Cd)^2, data = herbivory, random = ~ 1 | block)
summary(Cd_quadratic)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 860.5289 873.8613 -427.2644
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      1.525304 0.4600119
##
## Fixed effects: log(log(Total + 1) + 1) ~ 0 + (Cd)^2
##      Value Std.Error DF t-value p-value
## Cd 0.01036123 0.00284296 625 3.644524 3e-04
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.36147445 0.03045539 0.31531470 0.46547677 0.85687151
##
## Number of Observations: 630
```

```
## Number of Groups: 5
```

Cd - Neperian log model ($a + \log(x+1)$)

```
Cd_log <- lme(log(Total+1) ~ 0 + log(Cd+1), data = herbivory, random = ~ 1 | block)
summary(Cd_log)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2163.433 2176.765 -1078.716
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.944973 1.300474
##
## Fixed effects: log(Total + 1) ~ 0 + log(Cd + 1)
##              Value Std.Error DF t-value p-value
## log(Cd + 1) 0.2404842 0.04767298 625 5.044455      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1152126 -0.1386177  0.2713311  0.5596199  1.4194452
##
## Number of Observations: 630
## Number of Groups: 5
```

Cd - Exponential model ($a + \exp(x)$)

```
Cd_exp <- lme(log(Total+1) ~ 0 + exp(Cd), data = herbivory, random = ~ 1 | block)
summary(Cd_exp)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2231.492 2244.824 -1112.746
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.08251 1.324235
##
## Fixed effects: log(Total + 1) ~ 0 + exp(Cd)
##              Value Std.Error DF t-value p-value
## exp(Cd) 1.095391e-11 7.733384e-12 625 1.416445  0.1571
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1632973 -0.1508850  0.2950003  0.5611470  1.2899997
##
## Number of Observations: 630
## Number of Groups: 5
```

Ci (*Calliptamus italicus*)

Ci - Linear model (a + bx)

```
Ci_linear <- lme(log(Total+1) ~ 0 + Ci, data = herbivory, random = ~ 1 | block)
summary(Ci_linear)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2174.526 2187.858 -1084.263
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.958869 1.308294
##
## Fixed effects: log(Total + 1) ~ 0 + Ci
##      Value Std.Error DF t-value p-value
## Ci 0.03372382 0.008021876 625 4.203981      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.3134058 -0.1483863  0.3233436  0.5700448  1.2025105
##
## Number of Observations: 630
## Number of Groups: 5
```

Ci - Quadratic model (a + x²)

```
Ci_quadratic <- lme(log(Total+1) ~ 0 + (Ci)^2, data = herbivory, random = ~ 1 | block)
summary(Ci_quadratic)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2174.526 2187.858 -1084.263
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.958869 1.308294
##
## Fixed effects: log(Total + 1) ~ 0 + (Ci)^2
##      Value Std.Error DF t-value p-value
## Ci 0.03372382 0.008021876 625 4.203981      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.3134058 -0.1483863  0.3233436  0.5700448  1.2025105
##
## Number of Observations: 630
## Number of Groups: 5
```

Ci - Neperian log model ($a + \log(x+1)$)

```
Ci_log <- lme(log(Total+1) ~ 0 + log(Ci+1), data = herbivory, random = ~ 1 | block)
summary(Ci_log)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2146.694 2160.027 -1070.347
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.823008 1.283327
##
## Fixed effects: log(Total + 1) ~ 0 + log(Ci + 1)
##              Value Std.Error DF t-value p-value
## log(Ci + 1) 0.2884347 0.04385472 625 6.57705      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.5554978 -0.1446962  0.2954833  0.5759705  1.3318862
##
## Number of Observations: 630
## Number of Groups: 5
```

Ci - Exponential model ($a + \exp(x)$)

```
Ci_exp <- lme(log(Total+1) ~ 0 + exp(Ci), data = herbivory, random = ~ 1 | block)
summary(Ci_exp)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2233.238 2246.571 -1113.619
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.095809 1.326055
##
## Fixed effects: log(Total + 1) ~ 0 + exp(Ci)
##              Value Std.Error DF t-value p-value
## exp(Ci) 3.922355e-12 7.744013e-12 625 0.5065016 0.6127
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1689902 -0.1271839  0.3113492  0.5507000  1.2781951
##
## Number of Observations: 630
## Number of Groups: 5
```

Ee (*Euchorthippus elegantulus*)

Ee - Linear model (a + bx)

```
Ee_linear <- lme(log(Total+1) ~ 0 + Ee, data = herbivory, random = ~ 1 | block)
summary(Ee_linear)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2181.906 2195.238 -1087.953
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.007962 1.315923
##
## Fixed effects: log(Total + 1) ~ 0 + Ee
##      Value Std.Error DF t-value p-value
## Ee 0.02567923 0.00806905 625 3.182436 0.0015
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1265284 -0.1847147 0.3121670 0.5732359 1.2823213
##
## Number of Observations: 630
## Number of Groups: 5
```

Ee - Quadratic model (a + x²)

```
Ee_quadratic <- lme(log(Total+1) ~ 0 + (Ee)^2, data = herbivory, random = ~ 1 | block)
summary(Ee_quadratic)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2181.906 2195.238 -1087.953
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.007962 1.315923
##
## Fixed effects: log(Total + 1) ~ 0 + (Ee)^2
##      Value Std.Error DF t-value p-value
## Ee 0.02567923 0.00806905 625 3.182436 0.0015
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1265284 -0.1847147 0.3121670 0.5732359 1.2823213
##
## Number of Observations: 630
## Number of Groups: 5
```

Ee - Neperian log model ($a + \log(x+1)$)

```
Ee_log <- lme(log(Total+1) ~ 0 + log(Ee+1), data = herbivory, random = ~ 1 | block)
summary(Ee_log)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2160.627 2173.96 -1077.314
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.905713 1.297563
##
## Fixed effects: log(Total + 1) ~ 0 + log(Ee + 1)
##              Value Std.Error DF t-value p-value
## log(Ee + 1) 0.2424159 0.04543101 625 5.335912      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.0918860 -0.2075531  0.2948094  0.5939781  1.3793449
##
## Number of Observations: 630
## Number of Groups: 5
```

Ee - Exponential model ($a + \exp(x)$)

```
Ee_exp <- lme(log(Total+1) ~ 0 + exp(Ee), data = herbivory, random = ~ 1 | block)
summary(Ee_exp)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2233.464 2246.796 -1113.732
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.100654 1.326282
##
## Fixed effects: log(Total + 1) ~ 0 + exp(Ee)
##              Value Std.Error DF t-value p-value
## exp(Ee) 1.361431e-12 7.74534e-12 625 0.1757742  0.8605
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1721032 -0.1177728  0.3076402  0.5592001  1.2743206
##
## Number of Observations: 630
## Number of Groups: 5
```

Pg (*Pezotettix giornae*)

Pg - Linear model (a + bx)

```
Pg_linear <- lme(log(Total+1) ~ 0 + Pg, data = herbivory, random = ~ 1 | block)
summary(Pg_linear)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2185.377 2198.709 -1089.688
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.014211 1.319572
##
## Fixed effects: log(Total + 1) ~ 0 + Pg
##      Value Std.Error DF t-value p-value
## Pg 0.0208039 0.008091044 625 2.571225 0.0104
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.2487126 -0.1324631 0.3091630 0.5668141 1.3464433
##
## Number of Observations: 630
## Number of Groups: 5
```

Pg - Quadratic model (a + x²)

```
Pg_quadratic <- lme(log(Total+1) ~ 0 + (Pg)^2, data = herbivory, random = ~ 1 | block)
summary(Pg_quadratic)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2185.377 2198.709 -1089.688
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.014211 1.319572
##
## Fixed effects: log(Total + 1) ~ 0 + (Pg)^2
##      Value Std.Error DF t-value p-value
## Pg 0.0208039 0.008091044 625 2.571225 0.0104
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.2487126 -0.1324631 0.3091630 0.5668141 1.3464433
##
## Number of Observations: 630
## Number of Groups: 5
```


Pg - Neperian log model ($a + \log(x+1)$)

```
Pg_log <- lme(log(Total+1) ~ 0 + log(Pg+1), data = herbivory, random = ~ 1 | block)
summary(Pg_log)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2161.806 2175.139 -1077.903
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.877967 1.298813
##
## Fixed effects: log(Total + 1) ~ 0 + log(Pg + 1)
##              Value Std.Error DF t-value p-value
## log(Pg + 1) 0.2318901 0.04438398 625 5.224636      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.4597677 -0.1611661  0.2860970  0.5599534  1.4729814
##
## Number of Observations: 630
## Number of Groups: 5
```

Pg - Exponential model ($a + \exp(x)$)

```
Pg_exp <- lme(log(Total+1) ~ 0 + exp(Pg), data = herbivory, random = ~ 1 | block)
summary(Pg_exp)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2232.322 2245.654 -1113.161
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.1191 1.325021
##
## Fixed effects: log(Total + 1) ~ 0 + exp(Pg)
##              Value Std.Error DF t-value p-value
## exp(Pg) -8.386082e-12 7.737979e-12 625 -1.083756  0.2789
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.18905822 -0.09995077  0.31290870  0.54579612  1.26159829
##
## Number of Observations: 630
## Number of Groups: 5
```

Pp (*Pseudochorthippus parallelus*)

Pp - Linear model ($a + bx$)

```
Pp_linear <- lme(log(Total+1) ~ 0 + Pp, data = herbivory, random = ~ 1 | block)
summary(Pp_linear)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2175.313 2188.645 -1084.656
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.980928 1.309061
##
## Fixed effects: log(Total + 1) ~ 0 + Pp
##      Value Std.Error DF t-value p-value
## Pp 0.03296245 0.008026965 625 4.106465      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1222636 -0.1651918  0.2865117  0.5657018  1.3096990
##
## Number of Observations: 630
## Number of Groups: 5
```

Pp - Quadratic model ($a + x^2$)

```
Pp_quadratic <- lme(log(Total+1) ~ 0 + (Pp)^2, data = herbivory, random = ~ 1 | block)
summary(Pp_quadratic)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2175.313 2188.645 -1084.656
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.980928 1.309061
##
## Fixed effects: log(Total + 1) ~ 0 + (Pp)^2
##      Value Std.Error DF t-value p-value
## Pp 0.03296245 0.008026965 625 4.106465      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1222636 -0.1651918  0.2865117  0.5657018  1.3096990
##
## Number of Observations: 630
## Number of Groups: 5
```

Pp - Neperian log model ($a + \log(x+1)$)

```
Pp_log <- lme(log(Total+1) ~ 0 + log(Pp+1), data = herbivory, random = ~ 1 | block)
summary(Pp_log)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2156.335 2169.667 -1075.167
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      3.891388 1.293145
##
## Fixed effects: log(Total + 1) ~ 0 + log(Pp + 1)
##              Value Std.Error DF t-value p-value
## log(Pp + 1) 0.2599914 0.04527635 625 5.742322      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.2880638 -0.1753126  0.2756859  0.5519598  1.3951348
##
## Number of Observations: 630
## Number of Groups: 5
```

Pp - Exponential model ($a + \exp(x)$)

```
Pp_exp <- lme(log(Total+1) ~ 0 + exp(Pp), data = herbivory, random = ~ 1 | block)
summary(Pp_exp)
```

```
## Linear mixed-effects model fit by REML
## Data: herbivory
##      AIC      BIC    logLik
## 2231.181 2244.514 -1112.591
##
## Random effects:
## Formula: ~1 | block
##      (Intercept) Residual
## StdDev:      4.080966 1.32391
##
## Fixed effects: log(Total + 1) ~ 0 + exp(Pp)
##              Value Std.Error DF t-value p-value
## exp(Pp) 1.177044e-11 7.731485e-12 625 1.522404  0.1284
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.1629076 -0.1497554  0.2962394  0.5628096  1.2914832
##
## Number of Observations: 630
## Number of Groups: 5
```