

Ants Seeds Removal Supplementary Material (S1)

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```
#May the Code be with You#
setwd('~/Dropbox/Seed Dispersal/Data')

library(vegan)

library(ggplot2)
library(lme4)

library(lmerTest)

library(gridExtra)
source("summary_se.R")
library(MASS)
library(car)
library("FactoMineR")
library("devtools")

library("ggbiplots")

#Load and subset datasets----
data_part<- read.csv('seed_depot_data_10_04_16.csv', header=T)
data_part$Elevation<-as.factor(data_part$Elevation)
data_part$seeds.removed<-as.numeric (data_part$seeds.removed)
str(data_part)

## 'data.frame': 2345 obs. of 15 variables:
## $ Depot.. : int 1 1 1 1 1 1 1 1 1 ...
## $ Site : Factor w/ 4 levels "CHI","CNF","LNF",...: 1 1 1 1 1
1 1 1 1 ...
## $ Elevation : Factor w/ 3 levels "1600","2200",...: 1 2 3 1 2 3 1
2 3 1 ...
## $ Seed : Factor w/ 4 levels "Datura","Iris",...: 1 1 1 2 2 2
3 3 3 4 ...
## $ X..of.seeds : Factor w/ 29 levels "0","1","10","11",...: 19 19 19
19 29 19 19 19 19 19 ...
## $ Time_cat : int 0 0 0 0 0 0 0 0 0 ...
## $ seeds.removed : num 0 0 0 0 0 0 0 0 0 ...
## $ hours : int 0 0 0 0 0 0 0 0 0 ...
## $ total.seeds.removed: int 0 0 0 NA NA NA NA NA NA ...
## $ Lat : num 31.9 31.9 31.9 31.9 31.9 ...
## $ Lon : num -109 -109 -109 -109 -109 ...
## $ Exact.Elevation : int 1602 2206 2787 1602 2206 2787 1602 2206 2787
1602 ...
```

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## $ bare.ground      : num  39.9 51.4 55.4 39.9 51.4 ...
## $ t.max            : num  47 43 30 47 43 30 47 43 30 47 ...
## $ t.min            : num  15 16 10.5 15 16 10.5 15 16 10.5 15 ...

#Partition the dataset by species
datura<-data_part[which(data_part$Seed=="Datura"),]
iris<-data_part[which(data_part$Seed=="Iris"),]
oat<-data_part[which(data_part$Seed=="Oat"),]
sumac<-data_part[which(data_part$Seed=="Sumac"),]

```

Table 1: Sampling site location information. Showing Elevation (m.a.s.l.), geographic coordinates and temperature ranges recorded during the sampling period. We recorded ground soil surface temperatures using iButton Thermochrons (iButtonLink LLC, Whitewater WI, USA).

Site	Elevation	Latitude	Longitude	Tmin	Tmax
Chiricahua Nat. Forest-Low	1602	31.884	-109.178	15	47
Chiricahua Nat. Forest-Mid	2206	31.924	-109.255	16	43
Chiricahua Nat. Forest-High	2787	31.888	-109.280	10.5	30
Coronado National Forest-Low	1585	32.668	-109.780	19.5	56
Coronado National Forest-Mid	2229	32.635	-109.821	13	44
Coronado National Forest-High	2828	32.693	-109.901	9	20
Gila National Forest-Low	1565	33.454	-108.928	23	50.5
Gila National Forest-Mid	2239	33.577	-108.728	7	41
Gila National Forest- High	2810	33.451	-108.656	4	28
Lincoln National Forest- Low	1595	32.962	-105.891	16	62
Lincoln National Forest-Mid	2241	32.926	-105.834	12	43
Lincoln National Forest-High	2834	32.889	-105.798	7	32

```

#GLMM function try with a poisson distribution for count data. Global model
data_part$id <- with(data_part, paste(Site, Elevation, Depot.., sep = "_"))
m1<- glmer(seeds.removed ~ hours + Elevation*Seed+ (1|Site) + (1+hours |id),
family= poisson, data_part)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.0114674 (tol =
## 0.001, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkCon
v, : Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

summary(m1)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: seeds.removed ~ hours + Elevation * Seed + (1 | Site) + (1 +
##         hours | id)
## Data: data_part
##
##      AIC      BIC  logLik deviance df.resid
## 12224.4 12322.4 -6095.2 12190.4     2328
##
## Scaled residuals:
##    Min     1Q   Median     3Q    Max
## -4.6083 -1.0842 -0.5188  0.4411 10.4508
##
## Random effects:
## Groups Name        Variance Std.Dev. Corr
## id     (Intercept) 1.7824165 1.33507
##       hours          0.0004083 0.02021 -0.91
## Site   (Intercept) 0.0364836 0.19101
## Number of obs: 2345, groups: id, 122; Site, 4
##
## Fixed effects:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -0.330973  0.185388 -1.785  0.074212 .
## hours                      0.056444  0.002139 26.384 < 2e-16 ***
## Elevation2200              -0.517718  0.144646 -3.579  0.000345 ***
## Elevation2800              -0.943020  0.166682 -5.658 1.54e-08 ***
## SeedIris                    -0.926290  0.050671 -18.281 < 2e-16 ***
## SeedOat                     0.149788  0.036815  4.069 4.73e-05 ***
## SeedSumac                  -1.091287  0.053828 -20.274 < 2e-16 ***
## Elevation2200:SeedIris     0.718974  0.074657  9.630 < 2e-16 ***
## Elevation2800:SeedIris     1.544175  0.087784 17.591 < 2e-16 ***
## Elevation2200:SeedOat      0.866704  0.056301 15.394 < 2e-16 ***
## Elevation2800:SeedOat      1.144818  0.075288 15.206 < 2e-16 ***
## Elevation2200:SeedSumac   0.362589  0.083611  4.337 1.45e-05 ***
## Elevation2800:SeedSumac   -0.207967  0.149030 -1.395 0.162873

```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 13 > 12.
## Use print(x, correlation=TRUE)  or
##   vcov(x)      if you need it

## convergence code: 0
## Model failed to converge with max|grad| = 0.0114674 (tol = 0.001, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

Anova(m1)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: seeds.removed
##              Chisq Df Pr(>Chisq)
## hours        696.1079  1     <2e-16 ***
## Elevation     0.2412  2      0.8864
## Seed         2652.5547  3     <2e-16 ***
## Elevation:Seed 561.5954  6     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

###Figure 1 Global model of total number of seeds removed over time.
M1<- summarySE(data_part, measurevar="seeds.removed", groupvars=c("hours","Elevation"))
total.seeds.graph<-ggplot(M1, aes(x=hours , y=seeds.removed, group = Elevation)) +
  geom_errorbar (aes(ymin=seeds.removed-se, ymax=seeds.removed+se), size = 1,
width=.3, position=position_dodge(.01)) + theme_bw() +
  geom_line(aes(), size = 1) +
  geom_point(aes(shape = Elevation), size = 6) +
  theme(legend.position=("none")) + theme(text = element_text(size=20)) +
  xlab ("Time") +ylab("Seeds removed")
total.seeds.graph

```

Figure 1 (part of main manuscript): Mean seed removal rates per bait station along the elevation gradient over a 48 hour period. Squares=1600 m.a.s.l., circles= 2200 m.a.s.l. and triangles= 2800 m.a.s.l. Bars indicate standard error about the mean.

```

tiff (filename = "Figure1.tiff", height= 4, width= 4, units= "in", res=300)
total.seeds.graph
dev.off()

```

```

## quartz_off_screen
##                         2

####ANOVA Table
datura$id <- with(datura, paste(Site, Elevation, Depot.., sep = " "))
Datura.lmer<- glmer (seeds.removed ~ hours + Elevation + Site + (1|Site) + (1 +hours|id), family= poisson, datura)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model failed to converge with max|grad| = 0.250013 (tol = 0.001, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

summary(Datura.lmer)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: seeds.removed ~ hours + Elevation + Site + (1 | Site) + (1 +
##           hours | id)
## Data: datura
##
##      AIC      BIC  logLik deviance df.resid
##  2544.4   2592.7  -1261.2    2522.4      584
##
## Scaled residuals:
##      Min      1Q  Median      3Q     Max
## -3.2959 -0.7556 -0.3386  0.4532  4.9111
##
## Random effects:
## Groups Name        Variance Std.Dev. Corr
## id      (Intercept) 2.830e+00 1.682284
##          hours       3.490e-04 0.018682 -0.87
## Site    (Intercept) 8.433e-06 0.002904
## Number of obs: 595, groups: id, 122; Site, 4
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.176861  0.295864 -0.598  0.550
## hours       0.056864  0.003281 17.329 < 2e-16 ***
## Elevation2200 -1.040578  0.238428 -4.364 1.28e-05 ***
## Elevation2800 -1.209831  0.267477 -4.523 6.09e-06 ***
## SiteCNF      -0.556682  0.284072 -1.960  0.050 .
## SiteLNF       -0.454353  0.294173 -1.545  0.122
## SiteMOG       0.159441  0.276310  0.577  0.564
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##

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## Correlation of Fixed Effects:
##          (Intr) hours El2200 El2800 SitCNF SitLNF
## hours     -0.633
## Elevatn2200 -0.429  0.146
## Elevatn2800 -0.460  0.291  0.431
## SiteCNF     -0.460 -0.011  0.033 -0.043
## SiteLNF      -0.389 -0.061 -0.084 -0.088  0.492
## SiteMOG      -0.403 -0.104 -0.003 -0.130  0.515  0.516
## convergence code: 0
## Model failed to converge with max|grad| = 0.250013 (tol = 0.001, component
## 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

Anova(Datura.lmer)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: seeds.removed
##           Chisq Df Pr(>Chisq)
## hours      300.2924  1 < 2.2e-16 ***
## Elevation   27.6155  2 1.008e-06 ***
## Site        9.2486  3  0.02616 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

iris$id <- with(iris, paste(Site, Elevation, Depot.., sep = "_"))
Iris.lmer<- glmer (seeds.removed ~ hours + Elevation + Site + (1|Site) + (1+hours|id), family= poisson, iris)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkCon
v, : Model failed to converge with max|grad| = 0.106386 (tol = 0.001, compone
nt 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkCon
v, : Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

summary(Iris.lmer)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: seeds.removed ~ hours + Elevation + Site + (1 | Site) + (1 +
##         hours | id)
## Data: iris
##
##          AIC      BIC      logLik deviance df.resid
## 2042.8  2090.7 -1010.4    2020.8      568
##
## Scaled residuals:
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##      Min     1Q   Median     3Q    Max
## -3.2673 -0.6467 -0.2989  0.3945  3.5108
##
## Random effects:
## Groups Name        Variance Std.Dev. Corr
## id      (Intercept) 3.165e+00 1.7789534
##          hours         3.301e-04 0.0181676 -0.87
## Site    (Intercept) 4.862e-07 0.0006973
## Number of obs: 579, groups: id, 122; Site, 4
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.396030  0.325164 -7.369 1.72e-13 ***
## hours        0.056787  0.003552 15.988 < 2e-16 ***
## Elevation2200 0.297268  0.272854  1.089 0.275943
## Elevation2800 0.944890  0.270009  3.499 0.000466 ***
## SiteCNF      0.427219  0.321055  1.331 0.183297
## SiteLNF      0.539972  0.342598  1.576 0.115001
## SiteMOG      0.962483  0.320468  3.003 0.002670 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) hours El2200 El2800 SitCNF SitLNF
## hours       -0.421
## Elevatn2200 -0.413 -0.042
## Elevatn2800 -0.446 -0.010  0.502
## SiteCNF     -0.497 -0.081 -0.014 -0.008
## SiteLNF      -0.477 -0.154 -0.016  0.030  0.529
## SiteMOG      -0.515 -0.151  0.052  0.022  0.554  0.576
## convergence code: 0
## Model failed to converge with max|grad| = 0.106386 (tol = 0.001, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

```

Anova(Iris.lmer)

```

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: seeds.removed
##              Chisq Df Pr(>Chisq)
## hours      255.6289  1  < 2.2e-16 ***
## Elevation  12.8429  2   0.001626 **
## Site       9.1843  3   0.026938 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

oat$id <- with(oat, paste(Site, Elevation, Depot.., sep = "_"))
Oat.lmer<- glmer (seeds.removed ~ hours + Elevation + Site + (1|Site) + (1+hours|id), family= poisson, oat)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model failed to converge with max|grad| = 0.0569292 (tol = 0.001, component 1)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?

summary(Oat.lmer)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: seeds.removed ~ hours + Elevation + Site + (1 | Site) + (1 +
##         hours | id)
## Data: oat
##
##      AIC      BIC  logLik deviance df.resid
## 3731.7  3780.0 -1854.8    3709.7     587
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -3.2998 -1.0421 -0.4423  0.6945  5.8378
##
## Random effects:
##   Groups Name        Variance Std.Dev. Corr
##   id      (Intercept) 2.975e+00 1.724884
##          hours       7.346e-04 0.027103 -0.95
##   Site    (Intercept) 1.207e-06 0.001099
## Number of obs: 598, groups: id, 122; Site, 4
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.635645  0.221411 -2.871  0.00409 **
## hours        0.062189  0.003065 20.287 < 2e-16 ***
## Elevation2200 0.478369  0.144480  3.311  0.00093 ***
## Elevation2800 0.088926  0.170463  0.522  0.60190
## SiteCNF      0.398293  0.168404  2.365  0.01803 *
## SiteLNF      -0.302216  0.186289 -1.622  0.10474
## SiteMOG      0.496245  0.167671  2.960  0.00308 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) hours  El2200 El2800 SitCNF SitLNF
## hours      -0.747

```

```

## Elevatn2200 -0.316 -0.012
## Elevatn2800 -0.375  0.100  0.458
## SiteCNF     -0.334 -0.051 -0.042 -0.092
## SiteLNF      -0.344  0.005 -0.075 -0.047  0.491
## SiteMOG      -0.379 -0.023  0.022 -0.030  0.525  0.477
## convergence code: 0
## Model failed to converge with max|grad| = 0.0569292 (tol = 0.001, component 1)
## Model is nearly unidentifiable: very large eigenvalue
##   - Rescale variables?

Anova(Oat.lmer)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: seeds.removed
##             Chisq Df Pr(>Chisq)
## hours      411.559  1 < 2.2e-16 ***
## Elevation  12.218  2  0.002223 **
## Site       25.426  3  1.258e-05 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

sumac$id <- with(sumac, paste(Site, Elevation, Depot.., sep = "_"))
Sumac.lmer<- glmer (seeds.removed ~ hours + Elevation + Site + (1|Site) + (1+hours|id), family= poisson, sumac)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.416955 (tol =
## 0.001, component 1)

summary(Sumac.lmer)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: seeds.removed ~ hours + Elevation + Site + (1 | Site) + (1 +
##   hours | id)
## Data: sumac
##
##          AIC      BIC  logLik deviance df.resid
## 1361.6  1409.4 -669.8   1339.6      562
##
## Scaled residuals:
##    Min     1Q  Median     3Q    Max
## -3.2298 -0.4507 -0.2007 -0.0682  7.4200
##
## Random effects:
## Groups Name        Variance Std.Dev. Corr
## id     (Intercept) 6.356e+00 2.521146
##         hours       1.174e-03 0.034263 -0.83

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```

## Site  (Intercept) 1.515e-05 0.003893
## Number of obs: 573, groups: id, 117; Site, 4
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.748144  0.594260 -6.307 2.84e-10 ***
## hours        0.076572  0.008818  8.683 < 2e-16 ***
## Elevation2200 0.218711  0.391421  0.559  0.5763
## Elevation2800 -0.924223  0.434182 -2.129  0.0333 *
## SiteCNF      0.108332  0.483896  0.224  0.8229
## SiteLNF       0.937997  0.461903  2.031  0.0423 *
## SiteMOG      0.512381  0.454140  1.128  0.2592
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) hours El2200 El2800 SitCNF SitLNF
## hours     -0.728
## Elevatn2200 -0.440  0.163
## Elevatn2800 -0.442  0.162  0.456
## SiteCNF    -0.398 -0.003 -0.022  0.120
## SiteLNF     -0.422  0.016 -0.004  0.093  0.496
## SiteMOG    -0.379 -0.034  0.022  0.010  0.486  0.508
## convergence code: 0
## Model failed to converge with max|grad| = 0.416955 (tol = 0.001, component 1)

```

Anova(Sumac.lmer)

```

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: seeds.removed
##             Chisq Df Pr(>Chisq)
## hours      75.4027  1   < 2e-16 ***
## Elevation  7.4850  2    0.02369 *
## Site       5.1113  3    0.16382
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#####Figure 2 in the paper (4 panel with each species)
Datura<- summarySE(datura, measurevar="seeds.removed", groupvars=c("hours","Elevation"))
head (Datura)

##   hours Elevation N seeds.removed      sd      se      ci
## 1     0      1600 40 0.0000000 0.0000000 0.0000000 0.000000
## 2     0      2200 48 0.0000000 0.0000000 0.0000000 0.000000
## 3     0      2800 46 0.0000000 0.0000000 0.0000000 0.000000
## 4    12      1600 40 3.2250000 4.1786239 0.66069845 1.336389
## 5    12      2200 44 3.2954545 6.2266477 0.93870246 1.893074
## 6    12      2800 38 0.2894737 0.5651068 0.09167242 0.185746

```

```

datura.graph<-ggplot(Datura, aes(x=hours , y=seeds.removed, group = Elevation
)) +
  geom_errorbar (aes(ymin=seeds.removed-se, ymax=seeds.removed+se), size = 1,
width=.3, position=position_dodge(.01)) + theme_bw() +
  geom_line(aes(), size = 1) +
  geom_point(aes(shape = Elevation, colour = Elevation), size = 6) +
  theme(legend.position=("none")) + theme(text = element_text(size=20)) +
  xlab ("Time") +ylab("Seeds removed") +
  annotate("text", x = 22, y = 22, label = "Datura")
datura.graph

```

```

Iris<- summarySE(iris, measurevar="seeds.removed", groupvars=c("hours","Elevation"))
Iris

##      hours Elevation   N seeds.removed        sd        se         ci
## 1       0       1600 40 0.0000000 0.0000000 0.0000000 0.0000000
## 2       0       2200 41 0.0000000 0.0000000 0.0000000 0.0000000
## 3       0       2800 47 0.0000000 0.0000000 0.0000000 0.0000000
## 4      12       1600 40 1.950000 4.744497 0.7501709 1.5173639
## 5      12       2200 39 2.564103 5.729861 0.9175121 1.8574061
## 6      12       2800 39 1.384615 2.335260 0.3739409 0.7570039
## 7      24       1600 40 3.200000 6.068836 0.9595672 1.9409079
## 8      24       2200 39 3.564103 5.825510 0.9328282 1.8884120
## 9      24       2800 38 3.263158 4.104607 0.6658551 1.3491506
## 10     36       1600 40 3.875000 6.649417 1.0513651 2.1265867
## 11     36       2200 38 4.236842 5.961290 0.9670490 1.9594274
## 12     36       2800 24 3.916667 4.042348 0.8251409 1.7069340
## 13     48       1600 40 4.450000 6.946499 1.0983379 2.2215981
## 14     48       2200 38 5.078947 5.915539 0.9596271 1.9443892
## 15     48       2800 36 7.361111 5.909570 0.9849283 1.9995108

iris.graph<-ggplot(Iris, aes(x=hours , y=seeds.removed, group = Elevation)) +
  geom_errorbar (aes(ymin=seeds.removed-se, ymax=seeds.removed+se), size = 1,
width=.3, position=position_dodge(.01)) + theme_bw() +
  geom_line(aes(), size = 1) +
  geom_point(aes(shape = Elevation, colour = Elevation), size = 6) +
  theme(legend.position=("none")) + theme(text = element_text(size=20)) +
  xlab ("Time") +ylab("Seeds removed") +
  annotate("text", x = 22, y = 22, label = "Iris")
iris.graph

```

```

Oat<- summarySE(oat, measurevar="seeds.removed", groupvars=c("hours","Elevation"))
Oat

```

```

##   hours Elevation N seeds.removed      sd      se      ci
## 1     0      1600 40    0.0000000 0.000000 0.0000000 0.0000000
## 2     0      2200 48    0.0000000 0.000000 0.0000000 0.0000000
## 3     0      2800 47    0.0000000 0.000000 0.0000000 0.0000000
## 4    12      1600 40  5.5750000 6.830878 1.0800567 2.1846208
## 5    12      2200 44  5.7727273 9.258217 1.3957288 2.8147553
## 6    12      2800 39  0.5897436 1.185836 0.1898858 0.3844037
## 7    24      1600 40  8.9750000 8.483733 1.3413959 2.7132293
## 8    24      2200 44 11.4318182 9.458349 1.4258997 2.8756008
## 9    24      2800 39  6.3589744 9.232344 1.4783581 2.9927796
## 10   36      1600 40 10.8000000 8.629704 1.3644760 2.7599133
## 11   36      2200 38 15.1578947 8.011904 1.2997025 2.6334474
## 12   36      2800 25  9.1200000 9.812067 1.9624135 4.0502224
## 13   48      1600 40 14.1750000 8.711582 1.3774221 2.7860992
## 14   48      2200 38 19.0263158 7.674059 1.2448967 2.5224004
## 15   48      2800 36 14.8888889 9.970751 1.6617918 3.3736167

oat.graph<-ggplot(Oat, aes(x=hours , y=seeds.removed, group = Elevation)) +
  geom_errorbar (aes(ymin=seeds.removed-se, ymax=seeds.removed+se), size = 1,
width=.3, position=position_dodge(.01)) + theme_bw() +
  geom_line(aes(), size = 1) +
  geom_point(aes(shape = Elevation, colour = Elevation), size = 6) +
  theme(legend.position=("none")) + theme(text = element_text(size=20)) +
  xlab ("Time") +ylab("Seeds removed") +
  annotate("text", x = 22, y = 22, label = "Oat")
oat.graph

```

```

Sumac<- summarySE(sumac, measurevar="seeds.removed", groupvars=c("hours","Elevation"))
Sumac

##   hours Elevation N seeds.removed      sd      se      ci
## 1     0      1600 40    0.0000000 0.0000000 0.0000000 0.0000000
## 2     0      2200 48    0.0000000 0.0000000 0.0000000 0.0000000
## 3     0      2800 41    0.0000000 0.0000000 0.0000000 0.0000000
## 4    12      1600 40  1.5750000 4.9711346 0.78600540 1.5898460
## 5    12      2200 44  1.0909091 3.9462563 0.59492052 1.1997716
## 6    12      2800 34  0.1764706 0.4586270 0.07865387 0.1600225
## 7    24      1600 40  2.5250000 5.7154200 0.90368725 1.8278800
## 8    24      2200 44  1.7727273 4.2199065 0.63617484 1.2829688
## 9    24      2800 34  0.3529412 0.6911717 0.11853497 0.2411612
## 10   36      1600 40  3.4750000 6.8086954 1.07654927 2.1775264
## 11   36      2200 38  1.9736842 5.4549102 0.88490329 1.7929844
## 12   36      2800 20  0.5500000 0.8255779 0.18460484 0.3863824
## 13   48      1600 40  3.8500000 6.8296112 1.07985635 2.1842156
## 14   48      2200 38  4.1578947 6.5079009 1.05572093 2.1390938
## 15   48      2800 32  1.0312500 1.4024029 0.24791215 0.5056202

```

```
sumac.graph<-ggplot(Sumac, aes(x=hours , y=seeds.removed, group = Elevation)) +  
  geom_errorbar (aes(ymin=seeds.removed-se, ymax=seeds.removed+se), size = 1,  
width=.3, position=position_dodge(.01)) + theme_bw() +  
  geom_line(aes(), size = 1) +  
  geom_point(aes(shape = Elevation), size = 6) +  
  theme(legend.position=c(.8, 0.8)) + theme(text = element_text(size=20)) +  
  xlab ("Time") +ylab("Seeds removed") +  
  annotate("text", x = 22, y = 22, label = "Sumac")  
sumac.graph
```

```

## <bytecode: 0x7ff6e2c80b80>
## <environment: namespace:grDevices>

grid.arrange(datura.graph, iris.graph, oat.graph, sumac.graph, ncol=2)

dev.off()

## null device
##           1

df<-read.csv("Genera_Abundance.csv", header=TRUE)
genera.env<-(df[, c(1:2)])
ant_abund<-df[, c(1,2,18)]
genera<-df[, c(3:17)]
str(genera)

## 'data.frame':   12 obs. of  15 variables:
## $ Pogo      : int  16 3 0 15 0 0 10 6 0 2 ...
## $ Formica   : int  5 7 0 3 3 0 3 6 4 3 ...
## $ Camponotus: int  0 1 0 0 0 0 0 0 0 0 ...
## $ Crematogaster: int  2 0 0 0 0 0 2 1 0 0 ...
## $ Myrmecocystus: int  12 1 0 0 0 0 9 6 2 1 ...
## $ Tetramorium : int  2 0 0 0 1 0 3 0 0 0 ...
## $ Dorymyrmex : int  15 0 0 0 4 0 9 0 0 0 ...
## $ Forelius   : int  2 0 0 0 0 0 3 0 0 0 ...
## $ Pheidole   : int  2 0 0 0 2 0 0 0 0 0 ...
## $ Liometopum : int  0 2 0 0 0 0 0 3 0 0 ...
## $ Myrmica    : int  0 0 5 0 0 0 0 0 1 0 ...
## $ Aphaenogaster: int  0 0 0 13 0 0 0 0 0 0 ...
## $ Tapinoma   : int  0 0 0 0 3 0 0 0 0 0 ...
## $ Monomorium : int  0 0 0 0 3 0 0 0 0 0 ...
## $ Lasius     : int  0 0 0 0 0 2 0 0 0 0 ...
#relationship between abundance and number of seeds removed
whisker1<-ggplot(ant_abund, aes(Elevation, Abundance)) +
  geom_boxplot() + theme_bw() +
  scale_y_continuous("Abundance (# of of traps with ants)")

```

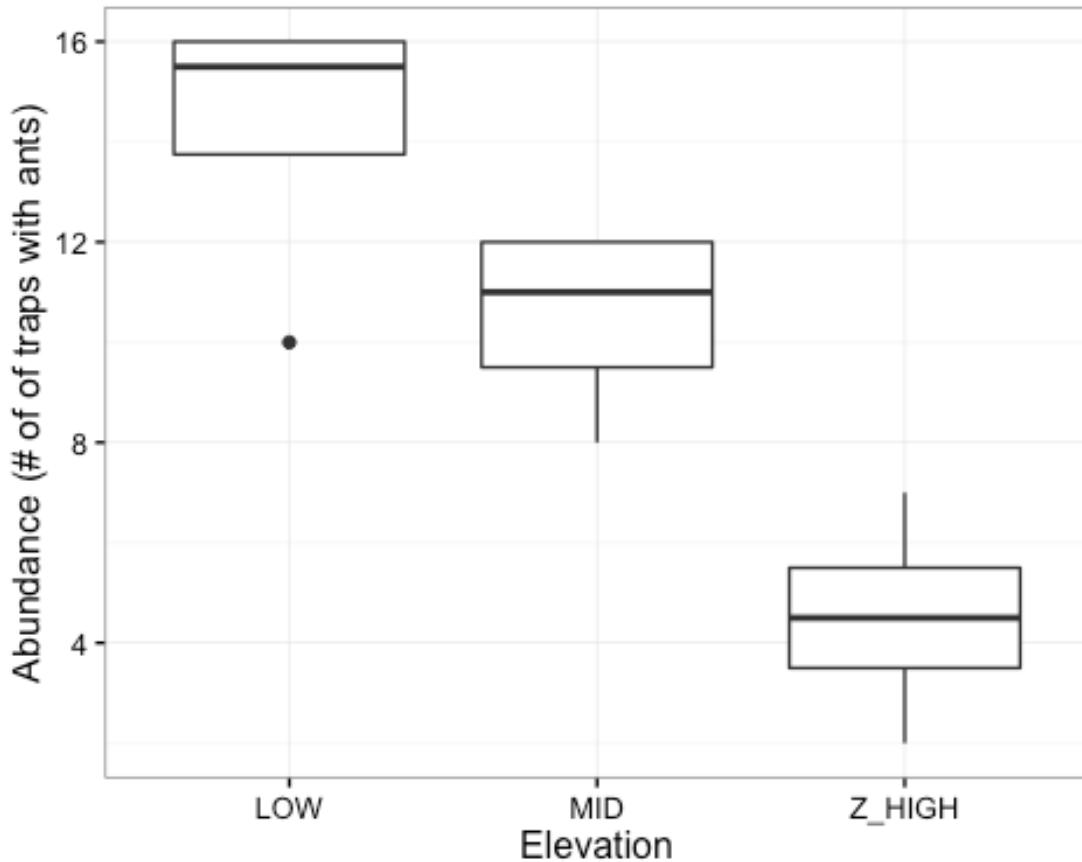


Figure S1: Box and whisker plot of abundance (incidence) of ants at pitfall trap arrays across the three elevations of interest (low~1600 m.a.s.l, mid~2200 m.a.s.l. and high~2800 m.a.s.l.).

PCA

```
cor(genera)
```

	Pogo	Formica	Camponotus	Crematogaster
## Pogo	1.000000000	0.37649156	-0.09750562	0.6550739
## Formica	0.376491560	1.00000000	0.51796977	0.2742768
## Camponotus	-0.097505623	0.51796977	1.00000000	-0.1654758
## Crematogaster	0.655073924	0.27427676	-0.16547585	1.0000000
## Myrmecocystus	0.665630835	0.41303316	-0.13614280	0.9700062
## Tetramorium	0.506654081	0.08155909	-0.15745916	0.8598377
## Dorymyrmex	0.638557341	0.23257195	-0.17522216	0.8292580
## Forelius	0.583073804	0.09551475	-0.13171584	0.9110641
## Pheidole	0.249805456	0.13968606	-0.13483997	0.3436165
## Liometopum	-0.002568607	0.62766839	0.50052020	0.1054916
## Myrmica	-0.416748436	-0.58527141	-0.14738264	-0.2682709

## Aphaenogaster	0.540713002	-0.04708816	-0.09090909	-0.1654758	
## Tapinoma	-0.257060280	-0.04708816	-0.09090909	-0.1654758	
## Monomorium	-0.257060280	-0.04708816	-0.09090909	-0.1654758	
## Lasius	-0.257060280	-0.47088161	-0.09090909	-0.1654758	
##	Myrmecocystus	Tetramorium	Dorymyrmex	Forelius	Pheidole
## Pogo	0.6656308	0.50665408	0.63855734	0.58307380	0.2498055
## Formica	0.4130332	0.08155909	0.23257195	0.09551475	0.1396861
## Camponotus	-0.1361428	-0.15745916	-0.17522216	-0.13171584	-0.1348400
## Crematogaster	0.9700062	0.85983773	0.82925803	0.91106405	0.3436165
## Myrmecocystus	1.0000000	0.77479198	0.84813886	0.83973763	0.3750173
## Tetramorium	0.7747920	1.00000000	0.85357600	0.95818183	0.4670994
## Dorymyrmex	0.8481389	0.85357600	1.00000000	0.83144024	0.6659847
## Forelius	0.8397376	0.95818183	0.83144024	1.00000000	0.2735126
## Pheidole	0.3750173	0.46709937	0.66598470	0.27351263	1.0000000
## Liometopum	0.1408956	-0.22813853	-0.25387488	-0.19083969	-0.1953662
## Myrmica	-0.3188119	-0.25527421	-0.28407175	-0.21353891	-0.2186038
## Aphaenogaster	-0.2139387	-0.15745916	-0.17522216	-0.13171584	-0.1348400
## Tapinoma	-0.2139387	0.15745916	0.08761108	-0.13171584	0.6741999
## Monomorium	-0.2139387	0.15745916	0.08761108	-0.13171584	0.6741999
## Lasius	-0.2139387	-0.15745916	-0.17522216	-0.13171584	-0.1348400
##	Liometopum	Myrmica	Aphaenogaster	Tapinoma	
## Pogo	-0.002568607	-0.4167484	0.54071300	-0.25706028	
## Formica	0.627668387	-0.5852714	-0.04708816	-0.04708816	
## Camponotus	0.500520201	-0.1473826	-0.09090909	-0.09090909	
## Crematogaster	0.105491627	-0.2682709	-0.16547585	-0.16547585	
## Myrmecocystus	0.140895576	-0.3188119	-0.21393869	-0.21393869	
## Tetramorium	-0.228138531	-0.2552742	-0.15745916	0.15745916	
## Dorymyrmex	-0.253874883	-0.2840717	-0.17522216	0.08761108	
## Forelius	-0.190839695	-0.2135389	-0.13171584	-0.13171584	
## Pheidole	-0.195366166	-0.2186038	-0.13483997	0.67419986	
## Liometopum	1.000000000	-0.2135389	-0.13171584	-0.13171584	
## Myrmica	-0.213538908	1.0000000	-0.14738264	-0.14738264	
## Aphaenogaster	-0.131715842	-0.1473826	1.00000000	-0.09090909	
## Tapinoma	-0.131715842	-0.1473826	-0.09090909	1.00000000	
## Monomorium	-0.131715842	-0.1473826	-0.09090909	1.00000000	
## Lasius	-0.131715842	-0.1473826	-0.09090909	-0.09090909	
##	Monomorium	Lasius			
## Pogo	-0.25706028	-0.25706028			
## Formica	-0.04708816	-0.47088161			
## Camponotus	-0.09090909	-0.09090909			
## Crematogaster	-0.16547585	-0.16547585			
## Myrmecocystus	-0.21393869	-0.21393869			
## Tetramorium	0.15745916	-0.15745916			
## Dorymyrmex	0.08761108	-0.17522216			
## Forelius	-0.13171584	-0.13171584			
## Pheidole	0.67419986	-0.13483997			
## Liometopum	-0.13171584	-0.13171584			
## Myrmica	-0.14738264	-0.14738264			
## Aphaenogaster	-0.09090909	-0.09090909			
## Tapinoma	1.00000000	-0.09090909			

```

## Monomorium      1.00000000  -0.09090909
## Lasius        -0.09090909  1.00000000

pca.data= genera
genera.pca = PCA(genera, scale.unit=TRUE, ncp=5, graph=T)

#PCA for coordinate plots
pca <- prcomp(genera, scale. = TRUE)

#PCA with ellipses for Elevation and points for sites.
pca.total.elev <- ggbiplots(pca, obs.scale = 1, var.scale = 1, group=df$Elevation, ellipse = T) +
  scale_colour_manual(values = c("dark green", "blue", "orange")) + scale_shape_manual(values = c(15, 16, 17, 18))+
  geom_point(size = 3, aes(colour=df$Elevation,shape=df$Elevation)) + theme_bw() + theme(panel.grid.minor=element_blank(), panel.grid.major=element_blank()) +
  theme(legend.position="none") + theme(text=element_text(size = 18, colour="black"))
pca.total.elev

```

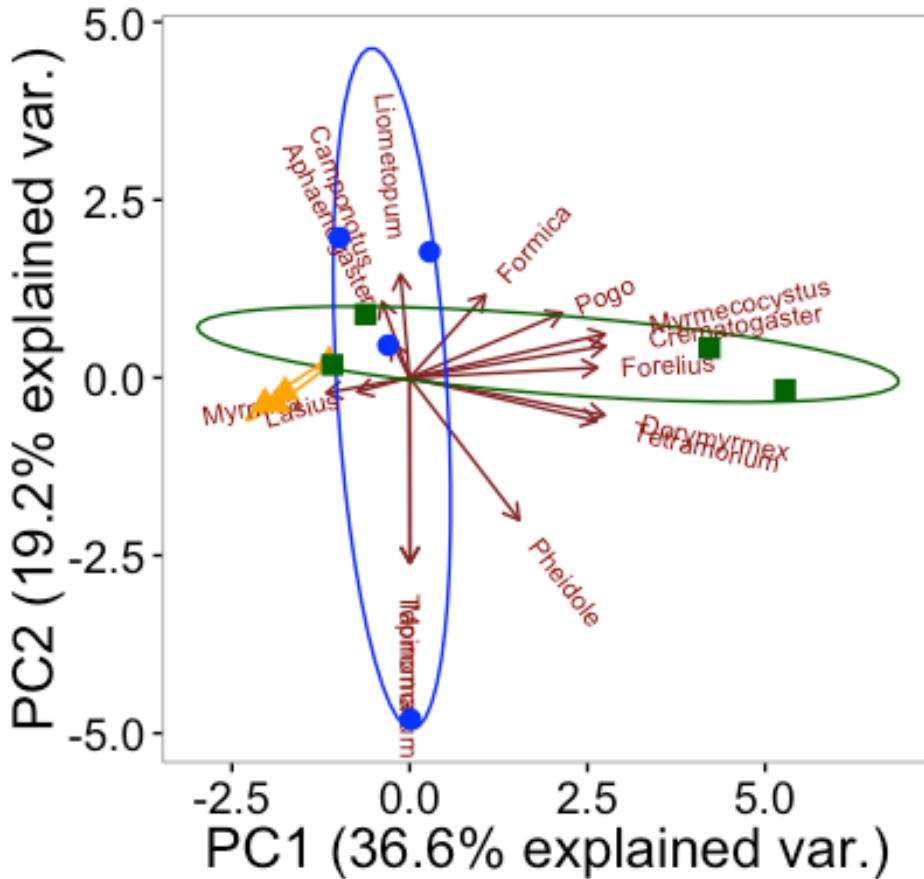


Figure S2: Principal component analysis showing the genera differences in community composition at low elevation sites (green), mid elevation sites (blue) and high elevation sites (yellow).