

PrefPlastic17Nov2017.R

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Fri Nov 17 09:01:44 2017

```
library(ggplot2)
library(data.table)
library(scales)
library(plyr)
library(dplyr)
```

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

```
## The following objects are masked from 'package:plyr':
##
##   arrange, count, desc, failwith, id, mutate, rename, summarise,
##   summarize
```

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

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

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

```
library(reshape2)
```

```
##
## Attaching package: 'reshape2'
```

```
## The following objects are masked from 'package:data.table':
##
##   dcast, melt
```

```
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 3.4.2
```

```
## Loading required package: Matrix
```

```
library(effects)
```

```
## Loading required package: carData
```

```
## lattice theme set by effectsTheme()  
## See ?effectsTheme for details.
```

```
library(multcomp)
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: survival
```

```
## Loading required package: TH.data
```

```
## Loading required package: MASS
```

```
##  
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':  
##  
##      select
```

```
##  
## Attaching package: 'TH.data'
```

```
## The following object is masked from 'package:MASS':  
##  
##      geyser
```

```
library(lmerTest)
```

```
##  
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':  
##  
##      lmer
```

```
## The following object is masked from 'package:stats':  
##  
##      step
```

```
library(piecewiseSEM)  
library(car)
```

```
##  
## Attaching package: 'car'
```

```
## The following objects are masked from 'package:carData':  
##  
##      Guyer, UN, Vocab
```

```
## The following object is masked from 'package:dplyr':  
##  
##      recode
```

```
library(gridExtra)
```

```
##  
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':  
##  
##      combine
```

```
library(cowplot)
```

```
##  
## Attaching package: 'cowplot'
```

```
## The following object is masked from 'package:ggplot2':  
##  
##      ggsave
```

```
library(Rmisc)
```

```
## Loading required package: lattice
```

```
library(heplots)  
library(Hmisc)
```

```
## Loading required package: Formula
```

```
##  
## Attaching package: 'Hmisc'
```

```
## The following object is masked from 'package:gridExtra':  
##  
##      combine
```

```
## The following objects are masked from 'package:dplyr':  
##  
##      combine, src, summarize
```

```
## The following objects are masked from 'package:plyr':  
##  
##      is.discrete, summarize
```

```
## The following objects are masked from 'package:base':  
##  
##      format.pval, round.POSIXt, trunc.POSIXt, units
```

```
library(RcmdrMisc)
```

```
## Loading required package: sandwich
```

```
##  
## Attaching package: 'RcmdrMisc'
```

```
## The following object is masked from 'package:Hmisc':  
##  
##      Dotplot
```

```
library(corrplot)
```

```
## Warning: package 'corrplot' was built under R version 3.4.2
```

```
## corrplot 0.84 loaded
```

```
setwd("~/Documents/Friesen lab/MedicagoHerbPopulation/HerbivoryCollabWSU/Data/Pro  
cessedData/ChoiceExpts/")  
  
PrefData <- read.csv("Corrected_FINAL_PreferenceData.csv")  
MPmaster <- read.csv("~/Documents/Friesen lab/MedicagoHerbPopulation/HerbivoryCol  
labWSU/Data/ProcessedData/WSUV_BulkingData_Final_ZCL.csv")  
  
# Preparing the dataset  
PrefData$Genotype_Plant1 <- MPmaster[match(PrefData$PlantID_1, MPmaster$Unique.ID  
, "MSU.Genotype")]  
PrefData$Population_Plant1 <- MPmaster[match(PrefData$PlantID_1, MPmaster$Unique.  
ID), "Site.ID"]  
  
PrefData$Genotype_Plant2 <- MPmaster[match(PrefData$PlantID_2, MPmaster$Unique.ID  
, "MSU.Genotype")]  
PrefData$Population_Plant2 <- MPmaster[match(PrefData$PlantID_2, MPmaster$Unique.  
ID), "Site.ID"]  
  
write.table(PrefData, file = "ModifiedPreferenceData16Nov2017.csv", sep = ",", ro  
w = F)  
  
# Running a glm binomial model to check for preference for invasive or native pop  
ulation  
mod1 <- glm(as.factor(Inv_1_Nat_0) ~ Herbivore*CatStage + Population_Plant1+Popul  
ation_Plant2, family = binomial(link = "logit"), data = PrefData)  
anova(mod1, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: as.factor(Inv_1_Nat_0)
##
## Terms added sequentially (first to last)
##
##
```

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
## NULL			137	182.845	
## Herbivore	1	0.123	136	182.721	0.7253140
## CatStage	3	3.585	133	179.137	0.3099669
## Population_Plant1	14	32.445	119	146.692	0.0034618 **
## Population_Plant2	27	33.221	92	113.471	0.1898645
## Herbivore:CatStage	3	16.727	89	96.744	0.0008044 ***

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

```
summary(mod1)
```

```
##
## Call:
## glm(formula = as.factor(Inv_1_Nat_0) ~ Herbivore * CatStage +
##      Population_Plant1 + Population_Plant2, family = binomial(link = "logit"),
##      data = PrefData)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.78096  -0.63199  -0.00013   0.37025   2.20529
##
## Coefficients:
##
##              Estimate Std. Error z value
## (Intercept)         4.22236    2.14303   1.970
## HerbivoreVelvetbean Caterpillar -0.80339    0.74259  -1.082
## CatStageB          -0.12602    1.46256  -0.086
## CatStageC          -4.86279    2.17581  -2.235
## CatStageD          -1.87606    1.09613  -1.712
## Population_Plant1BHI    0.55134    1.45346   0.379
## Population_Plant1DCR   -6.03345    2.30984  -2.612
## Population_Plant1EMO   -1.81948    1.60280  -1.135
## Population_Plant1MAG   16.52472  7487.98758   0.002
## Population_Plant1MEL   -3.77986    1.90791  -1.981
## Population_Plant1MLR   -0.76753    1.38419  -0.555
## Population_Plant1MP-PI566876 -0.35530    2.35581  -0.151
## Population_Plant1MP-PI577391 -3.62972  9861.38086   0.000
## Population_Plant1MP-PI577392 -21.53281  6317.24184  -0.003
## Population_Plant1PAL   22.59089  4207.62622   0.005
## Population_Plant1PEA   -1.36080    1.51582  -0.898
## Population_Plant1RIV   42.20474  8589.18345   0.005
## Population_Plant1SDS   -2.20745    1.71875  -1.284
## Population_Plant1STA   -2.08440    2.63975  -0.790
## Population_Plant2AUR   -2.19923    2.74809  -0.800
## Population_Plant2AZN   -4.11635    1.98537  -2.073
## Population_Plant2BOL   20.96344  6317.24198   0.003
## Population_Plant2CAM   -1.81131    2.33171  -0.777
## Population_Plant2CAR   -3.85828    2.49052  -1.549
## Population_Plant2COS   -1.13646    3.13763  -0.362
## Population_Plant2CRG    0.15933    1.81907   0.088
## Population_Plant2CVD  -20.76865  7572.27111  -0.003
## Population_Plant2DEB   -2.14758    1.55349  -1.382
## Population_Plant2FUR   -4.35782    2.13826  -2.038
## Population_Plant2FUS  -19.10335  4826.51382  -0.004
## Population_Plant2HIG   -4.15118    2.04150  -2.033
## Population_Plant2HUE   -0.09158    2.19265  -0.042
## Population_Plant2LDS  -16.09600  7572.27119  -0.002
## Population_Plant2LIS   -1.51750    2.19587  -0.691
## Population_Plant2MIR   -3.51610    2.31541  -1.519
## Population_Plant2MP-PI250782 -3.05313    2.41411  -1.265
```

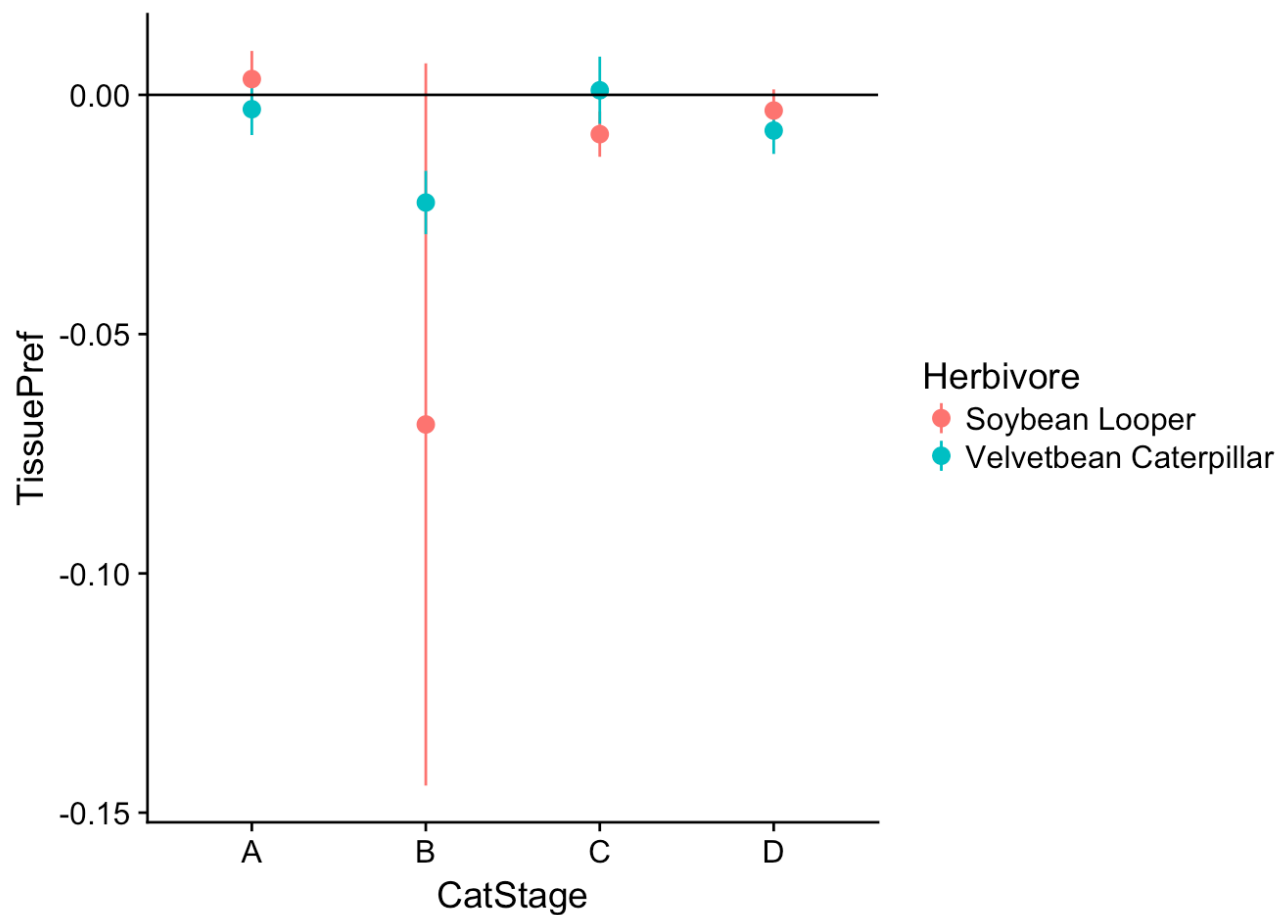
```
## Population_Plant2MP-PI319029      17.87759 7487.98773    0.002
## Population_Plant2MP-PI493291      18.59262 6317.24196    0.003
## Population_Plant2MP-W65435       -46.02541 8589.18367   -0.005
## Population_Plant2MUS              -0.73153    1.92861   -0.379
## Population_Plant2NAR             -26.41155 4207.62707   -0.006
## Population_Plant2ORB             -23.01112 7167.76548   -0.003
## Population_Plant2RHA             -22.19092 6317.24187   -0.004
## Population_Plant2RTM              0.23691    1.66626    0.142
## Population_Plant2SAN             -2.86556    1.80491   -1.588
## Population_Plant2SCA             -3.50874    2.19340   -1.600
## HerbivoreVelvetbean Caterpillar:CatStageB -0.94758    1.63465   -0.580
## HerbivoreVelvetbean Caterpillar:CatStageC  7.33867    2.66553    2.753
## HerbivoreVelvetbean Caterpillar:CatStageD  1.21279    1.17442    1.033
##                                     Pr(>|z|)
## (Intercept)                      0.0488 *
## HerbivoreVelvetbean Caterpillar    0.2793
## CatStageB                        0.9313
## CatStageC                        0.0254 *
## CatStageD                        0.0870 .
## Population_Plant1BHI              0.7044
## Population_Plant1DCR              0.0090 **
## Population_Plant1EMO              0.2563
## Population_Plant1MAG              0.9982
## Population_Plant1MEL              0.0476 *
## Population_Plant1MLR              0.5792
## Population_Plant1MP-PI566876      0.8801
## Population_Plant1MP-PI577391      0.9997
## Population_Plant1MP-PI577392      0.9973
## Population_Plant1PAL              0.9957
## Population_Plant1PEA              0.3693
## Population_Plant1RIV              0.9961
## Population_Plant1SDS              0.1990
## Population_Plant1STA              0.4297
## Population_Plant2AUR              0.4235
## Population_Plant2AZN              0.0381 *
## Population_Plant2BOL              0.9974
## Population_Plant2CAM              0.4373
## Population_Plant2CAR              0.1213
## Population_Plant2COS              0.7172
## Population_Plant2CRG              0.9302
## Population_Plant2CVD              0.9978
## Population_Plant2DEB              0.1668
## Population_Plant2FUR              0.0415 *
## Population_Plant2FUS              0.9968
## Population_Plant2HIG              0.0420 *
## Population_Plant2HUE              0.9667
## Population_Plant2LDS              0.9983
## Population_Plant2LIS              0.4895
## Population_Plant2MIR              0.1289
```



```
## Population_Plant2MP-PI250782      0.2060
## Population_Plant2MP-PI319029      0.9981
## Population_Plant2MP-PI493291      0.9977
## Population_Plant2MP-W65435        0.9957
## Population_Plant2MUS               0.7045
## Population_Plant2NAR               0.9950
## Population_Plant2ORB               0.9974
## Population_Plant2RHA               0.9972
## Population_Plant2RTM               0.8869
## Population_Plant2SAN               0.1124
## Population_Plant2SCA               0.1097
## HerbivoreVelvetbean Caterpillar:CatStageB 0.5621
## HerbivoreVelvetbean Caterpillar:CatStageC 0.0059 **
## HerbivoreVelvetbean Caterpillar:CatStageD 0.3018
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 182.845  on 137  degrees of freedom
## Residual deviance:  96.744  on   89  degrees of freedom
## AIC: 194.74
##
## Number of Fisher Scoring iterations: 18
```

```
# Trying a visualization of results (sig interaction between herb and cat)
PrefData$HerbStage <- interaction(PrefData$Herbivore, PrefData$CatStage, sep = ".")

PrefData$TissuePref <- PrefData$AmtPlant1Consumed - PrefData$AmtPlant2Consumed
ggplot(PrefData, aes(CatStage, TissuePref, colour = Herbivore)) + stat_summary(fun.data = "mean_se") + geom_hline(yintercept = 0, colour = "black")
```



```
# Drop neg final weight consumeds and then rerunning data
PrefData2 <- subset(PrefData, AmtPlant1Consumed > 0)
PrefData2 <- subset(PrefData2, AmtPlant2Consumed > 0)
mod2 <- glm(as.factor(Inv_1_Nat_0) ~ Herbivore*CatStage + Population_Plant1, fami
ly = binomial(link = "logit"), data = PrefData2)
anova(mod2, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: as.factor(Inv_1_Nat_0)
##
## Terms added sequentially (first to last)
##
##
```

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
## NULL			125	166.46	
## Herbivore	1	0.0339	124	166.42	0.853841
## CatStage	3	4.1534	121	162.27	0.245370
## Population_Plant1	14	30.0114	107	132.26	0.007604 **
## Herbivore:CatStage	3	7.0476	104	125.21	0.070396 .

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

```
t.test(PrefData$TissuePref, mu = 0) # overall, but need to subset
```

```
##
## One Sample t-test
##
## data: PrefData$TissuePref
## t = -1.5423, df = 137, p-value = 0.1253
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -0.018587159 0.002297883
## sample estimates:
## mean of x
## -0.008144638
```

```
mod3 <- lm(TissuePref ~ Herbivore*CatStage + Population_Plant1*Population_Plant2,
data = PrefData)
anova(mod3)
```

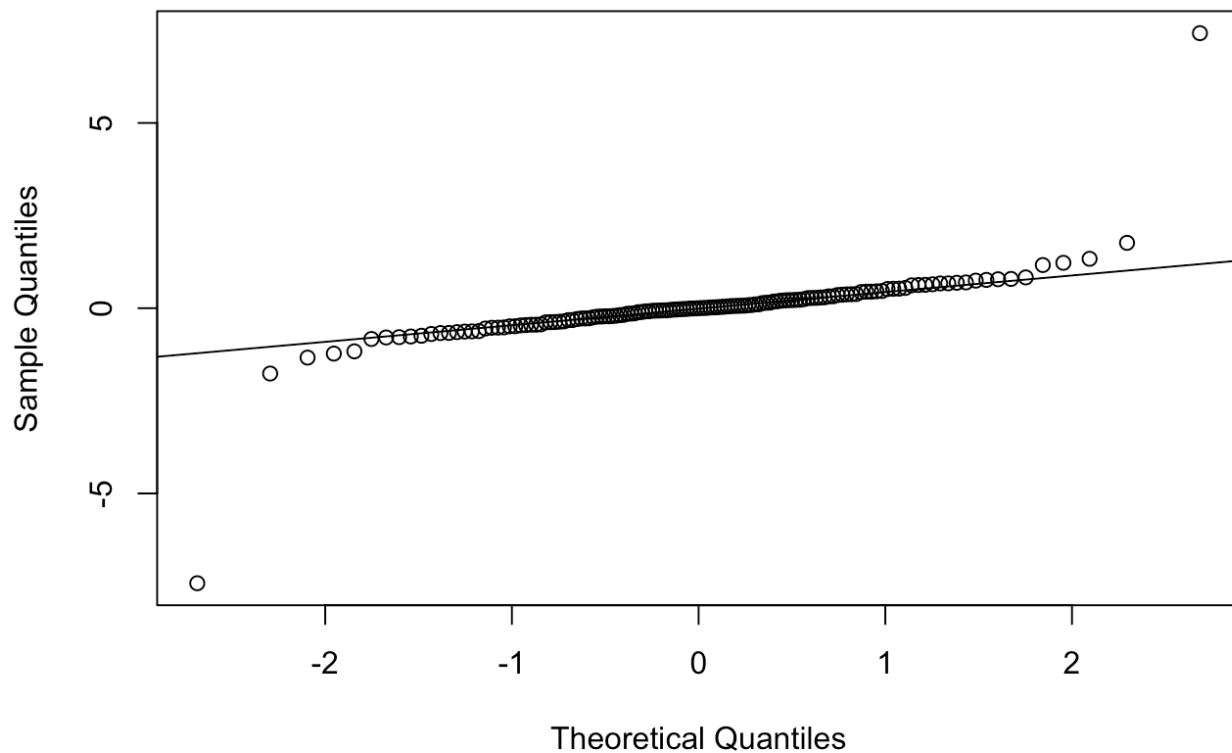
```
## Analysis of Variance Table
##
## Response: TissuePref
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## Herbivore	1	0.000975	0.0009755	0.3061	0.58198
## CatStage	3	0.029842	0.0099472	3.1209	0.03177
## Population_Plant1	14	0.067130	0.0047950	1.5044	0.13423
## Population_Plant2	27	0.064184	0.0023772	0.7458	0.79892
## Herbivore:CatStage	3	0.010139	0.0033798	1.0604	0.37199
## Population_Plant1:Population_Plant2	23	0.144606	0.0062872	1.9726	0.01688
## Residuals	66	0.210362	0.0031873		

```
##
## Herbivore
## CatStage *
## Population_Plant1
## Population_Plant2
## Herbivore:CatStage
## Population_Plant1:Population_Plant2 *
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
M3.res <- rstandard(mod3)
qqnorm(M3.res)
qqline(M3.res)
```

Normal Q-Q Plot



```
PrefData3 <- read.csv("Plant_PrefSep16Nov2017.csv")
mod4 <- lm(AmtConsumed ~ Range*Herbivore*CatStage , data = PrefData3)
anova(mod4)
```

```
## Analysis of Variance Table
##
## Response: AmtConsumed
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## Range	1	0.00458	0.0045771	2.2541	0.13447
## Herbivore	1	0.00627	0.0062727	3.0892	0.07999 .
## CatStage	3	0.02120	0.0070651	3.4794	0.01653 *
## Range:Herbivore	1	0.00049	0.0004877	0.2402	0.62447
## Range:CatStage	3	0.01492	0.0049736	2.4494	0.06405 .
## Herbivore:CatStage	3	0.01320	0.0043998	2.1668	0.09235 .
## Range:Herbivore:CatStage	3	0.00507	0.0016899	0.8322	0.47718
## Residuals	260	0.52794	0.0020305		

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

```

# Plastic Data
PlasticData <- read.csv("Corrected_FINAL_PlasticityData.csv")

# Preparing the dataset
PlasticData$Genotype_Plant1 <- MPmaster[match(PlasticData$PlantID_1, MPmaster$Unique.ID), "MSU.Genotype"]
PlasticData$Population_Plant1 <- MPmaster[match(PlasticData$PlantID_1, MPmaster$Unique.ID), "Site.ID"]

PlasticData$Genotype_Plant2 <- MPmaster[match(PlasticData$PlantID_2, MPmaster$Unique.ID), "MSU.Genotype"]
PlasticData$Population_Plant2 <- MPmaster[match(PlasticData$PlantID_2, MPmaster$Unique.ID), "Site.ID"]

mod1 <- glm(as.factor(Con_1_Ind_0) ~ Herbivore*CatStage, family = binomial(link = "logit"), data = PlasticData)
anova(mod1, test = "Chisq")

```

```

## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: as.factor(Con_1_Ind_0)
##
## Terms added sequentially (first to last)
##
##

```

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
## NULL			79	106.82	
## Herbivore	1	0.47457	78	106.34	0.4909
## CatStage	3	2.36757	75	103.98	0.4997
## Herbivore:CatStage	3	1.02461	72	102.95	0.7953

```
summary(mod1)
```

```
##
## Call:
## glm(formula = as.factor(Con_1_Ind_0) ~ Herbivore * CatStage,
##      family = binomial(link = "logit"), data = PlasticData)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.1774  -1.0108  -0.8446   1.1774   1.7941
##
## Coefficients:
##                                Estimate Std. Error z value
## (Intercept)                   -0.8473     0.6901  -1.228
## HerbivoreVelvetbean Caterpillar -0.5390     1.0494  -0.514
## CatStageB                      0.8473     0.9361   0.905
## CatStageC                      0.8473     0.9361   0.905
## CatStageD                      0.4418     0.9449   0.468
## HerbivoreVelvetbean Caterpillar:CatStageB 0.1335     1.3849   0.096
## HerbivoreVelvetbean Caterpillar:CatStageC -0.3083     1.4062  -0.219
## HerbivoreVelvetbean Caterpillar:CatStageD 0.9445     1.3849   0.682
##                                Pr(>|z|)
## (Intercept)                   0.220
## HerbivoreVelvetbean Caterpillar 0.608
## CatStageB                     0.365
## CatStageC                     0.365
## CatStageD                     0.640
## HerbivoreVelvetbean Caterpillar:CatStageB 0.923
## HerbivoreVelvetbean Caterpillar:CatStageC 0.826
## HerbivoreVelvetbean Caterpillar:CatStageD 0.495
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 106.82  on 79  degrees of freedom
## Residual deviance: 102.95  on 72  degrees of freedom
## (24 observations deleted due to missingness)
## AIC: 118.95
##
## Number of Fisher Scoring iterations: 4
```

```
PlasticData$TissuePref <- PlasticData$AmtPlant1Consumed - PlasticData$AmtPlant2Consumed

mod3 <- lm(TissuePref ~ Herbivore*CatStage + Population_Plant1*Population_Plant2,
data = PlasticData)
anova(mod3)
```

```
## Analysis of Variance Table
##
## Response: TissuePref
##
##           Df Sum Sq Mean Sq F value Pr(>F)
## Herbivore    1 0.04883  0.048825   3.4944 0.06856 .
## CatStage     3 0.18784  0.062614   4.4812 0.00811 **
## Population_Plant1 22 0.27704  0.012593   0.9013 0.59350
## Population_Plant2  5 0.09079  0.018158   1.2996 0.28247
## Herbivore:CatStage  3 0.15035  0.050117   3.5868 0.02139 *
## Population_Plant1:Population_Plant2  1 0.08059  0.080589   5.7677 0.02083 *
## Residuals    42 0.58684  0.013972
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(PlasticData, aes(CatStage, TissuePref, colour = Herbivore)) + stat_summary
(fun.data = "mean_se") + geom_hline(yintercept = 0, colour = "black")
```

```
## Warning: Removed 24 rows containing non-finite values (stat_summary).
```

