Final Project: Patterns of Lemur Density in Ranomafana National Park, Madagascar

https://github.com/ag522/LemurProject_DeSisto_Gonzalez_Horn.git

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Contents

List of Tables

List of Figures

1 Rationale and Research Questions

Madagascar is one of Earth's biodiversity hotspots that harbors high levels of animal and plant endemism. Climate, land cover, and geography determine patterns of plant community structure throughout the island which, in turn, effects mammal diversity (Brown et al. 2015; Park & Razafindratsima 2019). Lemurs, Madagascar's most prominent group of frugivores by both biomass and species richness, play a critical role in seed dispersal and related processes and are important cultural icons (Wright et al. 2005). However, 91% of lemurs are threatened with extinction due to anthropogenic disturbances (Schwitzer et al. 2014; Razafindratsima et al. 2013).

Lemur habitat use is dependent on plant resource availability (Overdorff 1996), which is mediated by landscape-level characteristics such as roughness and slope. In fact, food trees are stronger predictors of lemur occurrence than climate (Herrera et al. 2017). Lemurs use trait-based cues to select fruits (Valenta et al. 2013; Overdorff 1996). For example, size matching, whereby large fruits are typically dispersed by large vertebrates, is an essential phenomenon in driving plant-frugivore interactions (Lim et al. 2020). Plant nutrient content may also be an important factor in influencing frugivory interactions in tropical forests. FOr example, Madagascar is the only region where there is a significant relationship between fruit protein and the degree of frugivory among primate communities (Donati et al. 2017). Additionally, the average percentage of fruit nitrogen content in Madagascar is lower than the minimum nitrogen requirement for primates, suggesting that the low protein availability in Malagasy fruits is particularly important in shaping lemur communities (Donati et al. 2017).

In this project, we examine a suite of environmental factors in relation to lemur densities in Ranomafana National Park, Madagascar. We seek to identify patterns in lemur densities throughout the park and examine potential causes of these patterns. Because different lemur species have specific responses to environmental cues based on their life history traits, we hypothesize that lemur densities among different sites and species are significantly different. Additionally, we expect that both landscape-level characteristics and plant functional traits act together to drive lemur densities throughout a national park in Madagascar. Specifically, we predict that a) lemur densities are negatively related to landscape roughness and slope and b) reward regulation causes positive relationships between animal densities and fruit nutrient contents.

2 Dataset Information

Data for this project were collected by James Herrera and Camille DeSisto, as a part of a larger project aimed at investigating plant-animal interactions in Madagascar's eastern rainforests. Field data were collected by James Herrera and his colleagues in the montane evergreen rainforest of Ranomafana National Park in southwestern Madagascar. They conducted diurnal and nocturnal lemur surveys at five sites (Ampatsoana, Maharira, Miaranony, Valohoaka, and Vohiparara) between 2011 and 2014. Diurnal lemur surveys were conducted at 31 transects among these five sites, whereas nocturnal lemur surveys were conducted at 26 of these sites due to logistical constraints. Habitat variables (slope, roughness, location, topogaphic position index, elevation, flow direction, and aspect) were collected along each transects. Additionally, vegetation data were collected from botanical surveys every 100 m along each transect. Camille DeSisto calculated lemur densities using a distance sampling and model averaging approach that jointly modeled for detection and density, using the R packages "unmarked" and "MuMln" (Fiske & Chandler 201; Barton 2020; Figure 1). Trait data were previously collected from the literature and mean trait values were calculated for each transect as part of the larger research project. Upon the start of this final project, the dataset was already clean and did not require additional wrangling to be used for our spatial visualization or linear models. However, we did use data wangling to summarise the transects by group in order to conduct the analysis of variance. In total, there are 11 plant functional trait variables and 5 habitat variables per transect, in addition to the predicted densities per lemur species (Table 1). Additionally information on the variables is available in the metedata file in the Github repository. We also created a Transect Map App to better visualize the data by species and site as well as allowing the user to select a variable and visualize it's relationship with population density for a particular species per site.

3 Exploratory Analysis

```
head(lemur_data)
```

```
##   X Transect_Site        WD logFruitLength logFruitWidth logSeedLength
## 1 1  Ampatsoana_A 0.5728243       2.548112      2.406191      2.032618
## 2 2  Ampatsoana_A 0.5728243       2.548112      2.406191      2.032618
## 3 3  Ampatsoana_A 0.5728243       2.548112      2.406191      2.032618
## 4 4  Ampatsoana_A 0.5728243       2.548112      2.406191      2.032618
## 5 5  Ampatsoana_A 0.5728243       2.548112      2.406191      2.032618
## 6 6  Ampatsoana_A 0.5728243       2.548112      2.406191      2.032618
##   logSeedWidth  logSugar   logFat logProtein logNitrogen logTannins   logSLA
## 1     1.812605 2.531025 1.766225   3.836518     0.75253  0.1496482 2.379374
## 2     1.812605 2.531025 1.766225   3.836518     0.75253  0.1496482 2.379374
## 3     1.812605 2.531025 1.766225   3.836518     0.75253  0.1496482 2.379374
## 4     1.812605 2.531025 1.766225   3.836518     0.75253  0.1496482 2.379374
## 5     1.812605 2.531025 1.766225   3.836518     0.75253  0.1496482 2.379374
## 6     1.812605 2.531025 1.766225   3.836518     0.75253  0.1496482 2.379374
##                   Species Predicted    tpi roughness    slope   aspect flowdir
## 1           Avahi_laniger 0.4788704 29.625        45 0.880696 99.65233       1
## 2 Cheirogaleus_crossleyi 0.6386449 29.625        45 0.880696 99.65233       1
## 3     Eulemur_rubriventer 3.8046858 29.625        45 0.880696 99.65233       1
## 4   Propithecus_edwardsi 2.8629977 29.625        45 0.880696 99.65233       1
## 5      Lepilemur_microdon 0.3100273 29.625        45 0.880696 99.65233       1
## 6       Hapalemur_griseus 1.1441688 29.625        45 0.880696 99.65233       1
##       lat   long
## 1 -20.992 47.402
## 2 -20.992 47.402
## 3 -20.992 47.402
## 4 -20.992 47.402
## 5 -20.992 47.402
## 6 -20.992 47.402
```

```
dim(lemur_data)
```

```
## [1] 259  22
```

```
str(lemur_data)
```

```
## 'data.frame':    259 obs. of  22 variables:
##  $ X            : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ Transect_Site : Factor w/ 31 levels "Ampatsoana_A",..: 1 1 1 1 1 1 1 1 1 2 ...
##  $ WD           : num  0.573 0.573 0.573 0.573 0.573 ...
##  $ logFruitLength: num  2.55 2.55 2.55 2.55 2.55 ...
##  $ logFruitWidth : num  2.41 2.41 2.41 2.41 2.41 ...
##  $ logSeedLength : num  2.03 2.03 2.03 2.03 2.03 ...
```

```
##  $ logSeedWidth  : num  1.81 1.81 1.81 1.81 1.81 ...
##  $ logSugar      : num  2.53 2.53 2.53 2.53 2.53 ...
##  $ logFat        : num  1.77 1.77 1.77 1.77 1.77 ...
##  $ logProtein    : num  3.84 3.84 3.84 3.84 3.84 ...
##  $ logNitrogen   : num  0.753 0.753 0.753 0.753 0.753 ...
##  $ logTannins    : num  0.15 0.15 0.15 0.15 0.15 ...
##  $ logSLA        : num  2.38 2.38 2.38 2.38 2.38 ...
##  $ Species       : Factor w/ 9 levels "Avahi_laniger",..: 1 2 3 8 6 5 4 9 7 1 ...
##  $ Predicted     : num  0.479 0.639 3.805 2.863 0.31 ...
##  $ tpi           : num  29.6 29.6 29.6 29.6 29.6 ...
##  $ roughness     : int  45 45 45 45 45 45 45 45 45 34 ...
##  $ slope         : num  0.881 0.881 0.881 0.881 0.881 ...
##  $ aspect        : num  99.7 99.7 99.7 99.7 99.7 ...
##  $ flowdir       : int  1 1 1 1 1 1 1 1 1 16 ...
##  $ lat           : num  -21 -21 -21 -21 -21 ...
##  $ long          : num  47.4 47.4 47.4 47.4 47.4 ...
```

summary(lemur_data)

```
##        X              Transect_Site         WD           logFruitLength
##  Min.   :  1.0   Ampatsoana_A:  9   Min.   :0.5414   Min.   :2.548
##  1st Qu.: 65.5   Ampatsoana_B:  9   1st Qu.:0.5756   1st Qu.:2.731
##  Median :130.0   Ampatsoana_C:  9   Median :0.5809   Median :2.811
##  Mean   :130.0   Ampatsoana_D:  9   Mean   :0.5805   Mean   :2.788
##  3rd Qu.:194.5   Ampatsoana_G:  9   3rd Qu.:0.5884   3rd Qu.:2.858
##  Max.   :259.0   Maharira_A  :  9   Max.   :0.5986   Max.   :3.037
##                  (Other)     :205
##  logFruitWidth   logSeedLength    logSeedWidth      logSugar
##  Min.   :2.406   Min.   :1.844   Min.   :1.574   Min.   :2.085
##  1st Qu.:2.577   1st Qu.:2.128   1st Qu.:1.874   1st Qu.:2.327
##  Median :2.640   Median :2.215   Median :1.981   Median :2.427
##  Mean   :2.642   Mean   :2.222   Mean   :1.953   Mean   :2.397
##  3rd Qu.:2.730   3rd Qu.:2.335   3rd Qu.:2.070   3rd Qu.:2.471
##  Max.   :2.874   Max.   :2.462   Max.   :2.137   Max.   :2.629
##
##      logFat        logProtein     logNitrogen       logTannins
##  Min.   :1.526   Min.   :3.237   Min.   :0.7243   Min.   :0.06874
##  1st Qu.:1.649   1st Qu.:3.554   1st Qu.:0.7502   1st Qu.:0.12004
##  Median :1.681   Median :3.754   Median :0.7995   Median :0.14729
##  Mean   :1.683   Mean   :3.734   Mean   :0.8043   Mean   :0.14192
##  3rd Qu.:1.743   3rd Qu.:3.875   3rd Qu.:0.8308   3rd Qu.:0.16534
##  Max.   :1.846   Max.   :4.269   Max.   :0.9160   Max.   :0.19137
##
##      logSLA                      Species      Predicted
##  Min.   :2.213   Eulemur_rubriventer :31   Min.   : 0.05666
```

```
##   1st Qu.:2.332   Eulemur_rufifrons    :31   1st Qu.: 0.50004
##   Median :2.363   Hapalemur_griseus    :31   Median : 1.10970
##   Mean   :2.368   Propithecus_edwardsi:31   Mean   : 1.78485
##   3rd Qu.:2.413   Varecia_variegata    :31   3rd Qu.: 2.76320
##   Max.   :2.468   Avahi_laniger        :26   Max.   :17.97175
##                   (Other)              :78
##       tpi               roughness        slope            aspect
##   Min.   :-206.7500   Min.   : 34   Min.   : 0.3905   Min.   :  9.781
##   1st Qu.: -32.8750   1st Qu.: 74   1st Qu.: 1.0238   1st Qu.: 70.045
##   Median :  10.7500   Median :168   Median : 2.8305   Median :122.482
##   Mean   :  -0.3528   Mean   :205   Mean   : 4.2638   Mean   :135.951
##   3rd Qu.:  35.5000   3rd Qu.:264   3rd Qu.: 6.6430   3rd Qu.:190.581
##   Max.   :  73.7500   Max.   :529   Max.   :13.5006   Max.   :280.187
##
##      flowdir             lat              long
##   Min.   : 1.000   Min.   :-21.34   Min.   :47.38
##   1st Qu.: 1.000   1st Qu.:-21.29   1st Qu.:47.40
##   Median : 1.000   Median :-21.23   Median :47.44
##   Mean   : 6.236   Mean   :-21.19   Mean   :47.44
##   3rd Qu.: 8.000   3rd Qu.:-21.15   3rd Qu.:47.45
##   Max.   :64.000   Max.   :-20.99   Max.   :47.55
##
```

```r
length(unique(lemur_data$Transect_Site))
```

```
## [1] 31
```

```r
length(unique(lemur_data$Species))
```

```
## [1] 9
```

```r
#make a heat map to visualize the densities
lemur_data$cuts <- cut(lemur_data$Predicted, breaks=c(0,0.25,0.5,0.75, 1,2,5,10,15,20,25

density_plot <- ggplot(lemur_data, aes(x = Species, y =Transect_Site))+
  geom_tile(aes(fill=cuts)) +
  theme_classic()+
  scale_fill_viridis_d(direction=-1, option="inferno")+
  theme(axis.text.x=element_text(angle = 30, hjust=1))+
  ylab("Transect")+
  labs(fill="Individual Density")

density_plot
```

```r
transect_variables_mean <- lemur_data %>%
  summarise(LogFruitLength = mean(logFruitLength),
            LogFruitWidth = mean(logFruitWidth),
```
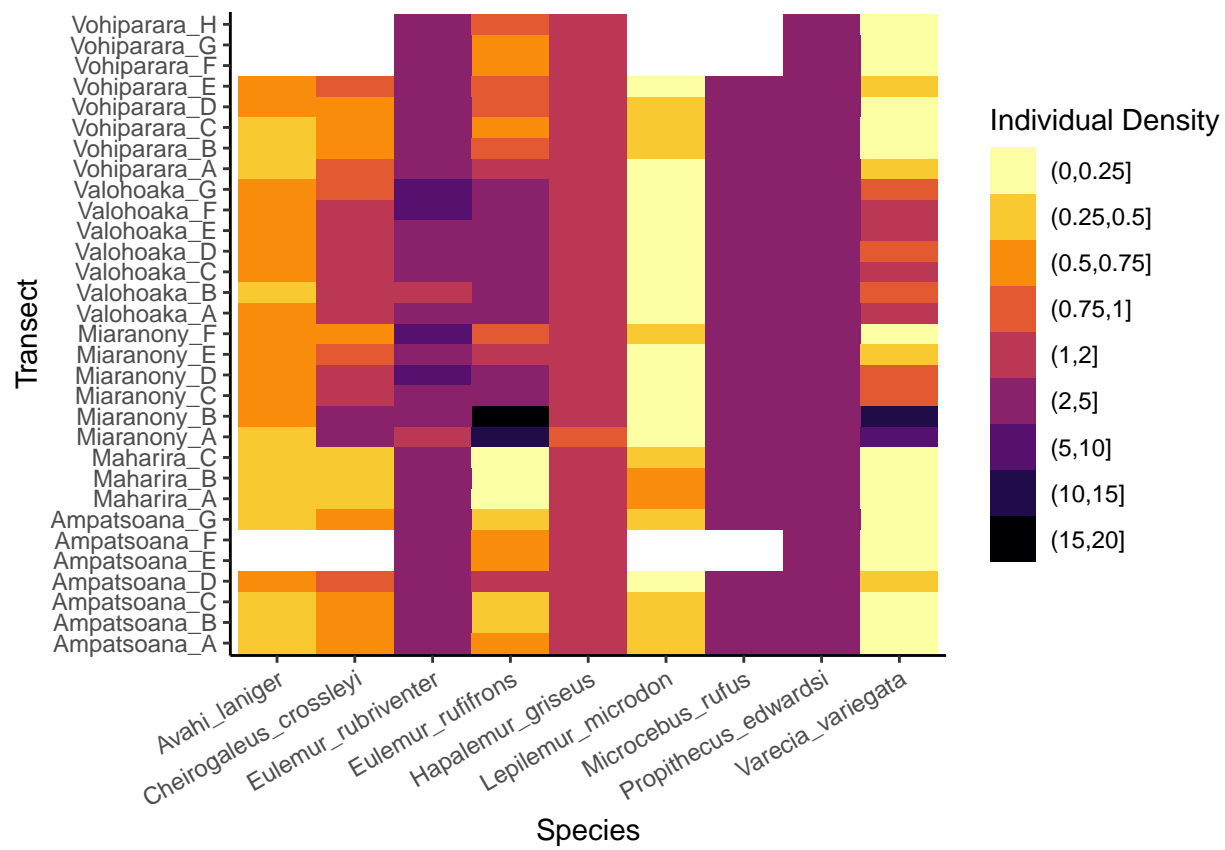
Figure 1: Figure 1. Heat map of lemur densities at each project transect site

```r
           LogSeedLength = mean(logSeedLength),
          LogSeedWidth = mean(logSeedWidth),
           LogSugar = mean(logSugar),
           LogFat = mean(logFat),
           LogProtein = mean(logProtein),
           LogNitrogen = mean(logNitrogen),
           LogTannins = mean(logTannins),
           SLA= mean(logSLA),
           WD= mean(WD),
           Tpi= mean(tpi),
           Roughness = mean(roughness),
           Slope = mean(slope),
           Aspect = mean(aspect),
           Flowdir = mean(flowdir),
          Density = mean(Predicted)
             )

transect_variables_max <- lemur_data %>%
  summarise(LogFruitLength = max(logFruitLength),
           LogFruitWidth = max(logFruitWidth),
           LogSeedLength = max(logSeedLength),
           LogSeedWidth = max(logSeedWidth),
           LogSugar = max(logSugar),
           LogFat = max(logFat),
           LogProtein = max(logProtein),
         LogNitrogen = max(logNitrogen),
           LogTannins = max(logTannins),
           SLA= max(logSLA),
           WD= max(WD),
           Tpi=max(tpi),
           Roughness = max(roughness),
           Slope = max(slope),
           Aspect = max(aspect),
           Flowdir =max(flowdir),
          Density = max(Predicted)
             )

transect_variables_min <- lemur_data %>%
  summarise(LogFruitLength = min(logFruitLength),
           LogFruitWidth = min(logFruitWidth),
           LogSeedLength = min(logSeedLength),
           LogSeedWidth = min(logSeedWidth),
         LogSugar = min(logSugar),
           LogFat = min(logFat),
```

```r
          LogProtein = min(logProtein),
          LogNitrogen = min(logNitrogen),
          LogTannins = min(logTannins),
          SLA= min(logSLA),
          WD= min(WD),
          Tpi=min(tpi),
          Roughness = min(roughness),
          Slope = min(slope),
          Aspect = min(aspect),
          Flowdir =min(flowdir),
         Density = min(Predicted)
          )

transect_variables_sd <- lemur_data %>%
  summarise(LogFruitLength = sd(logFruitLength),
          LogFruitWidth = sd(logFruitWidth),
          LogSeedLength = sd(logSeedLength),
          LogSeedWidth = sd(logSeedWidth),
          LogSugar = sd(logSugar),
          LogFat = sd(logFat),
          LogProtein = sd(logProtein),
          LogNitrogen = sd(logNitrogen),
          LogTannins = sd(logTannins),
          SLA= sd(logSLA),
          WD= sd(WD),
          Tpi=sd(tpi),
          Roughness = sd(roughness),
          Slope = sd(slope),
          Aspect = sd(aspect),
          Flowdir =sd(flowdir),
         Density = sd(Predicted)
          )

transect_variables_summary <- rbind(transect_variables_max, transect_variables_min, tran
stats <- c("Maximum", "Minimum", "Mean", "Standard Deviation")
transect_variables_summary<- cbind(stats, transect_variables_summary)
transect_variables_summary <- data.frame(t(transect_variables_summary[-1]))
colnames(transect_variables_summary) <- c("Maximum", "Minimum", "Mean", "Standard Deviat

kable(transect_variables_summary, caption ="Table 1. Summary Statistics for Transect-Lev
```

Table 1: Table 1. Summary Statistics for Transect-Level Variables

	Maximum	Minimum	Mean	Standard Deviation
LogFruitLength	3.0367699	2.5481124	2.7884419	0.1078722
LogFruitWidth	2.8735245	2.4061911	2.6418949	0.1105788
LogSeedLength	2.4618778	1.8435241	2.2224035	0.1463275
LogSeedWidth	2.1370075	1.5738239	1.9532329	0.1329052
LogSugar	2.6292634	2.0849150	2.3969571	0.1121973
LogFat	1.8455284	1.5255786	1.6830810	0.0767810
LogProtein	4.2689341	3.2368227	3.7342967	0.2510554
LogNitrogen	0.9160242	0.7243437	0.8042614	0.0578926
LogTannins	0.1913672	0.0687408	0.1419214	0.0294709
SLA	2.4679473	2.2134377	2.3677036	0.0578060
WD	0.5986437	0.5414205	0.5804747	0.0101335
Tpi	73.7500000	-206.7500000	-0.3527992	60.5243149
Roughness	529.0000000	34.0000000	205.0308880	151.3989769
Slope	13.5005877	0.3904947	4.2638428	3.6935512
Aspect	280.1872004	9.7805570	135.9507256	67.2499763
Flowdir	64.0000000	1.0000000	6.2355212	10.1291339
Density	17.9717477	0.0566592	1.7848451	2.0068795

4 Analysis

«««< HEAD ## Question 1: Are there significant differences in lemur densities among the different sites and among the different species? If so, how can the sites and species be grouped to reflect the patterns in densities? =======

First, we conducted a one-way analysis of variance (ANOVA) on lemur population density by site using the "aov" function in the R general interface. Next, we completed a post-hoc Tukey HSD test to determine pairwise differences between the sites. Then, we conducted a HSD post-hoc test from the R package "agricolae" (de Mendiburu 2020) to categorize the sites into groups based on their lemur densities. After these analyses of the sites, we repeated the process between lemur species rather than sites to determine if there are significant differences in densities depending on the particular species. Visualizations were conducted using the "ggplot2" package (Wockham 2016).

```
trait_data2 <- lemur_data %>%
  mutate(Transect_Site2 = Transect_Site)%>%
  separate(col= Transect_Site2, into="Site", sep ="_")
```

```
## Warning: Expected 1 pieces. Additional pieces discarded in 259 rows [1, 2, 3, 4,
## 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...].
```

```
#write.csv(trait_data2, "C:/ENV872/LemurProject_DeSisto_Gonzalez_Horn/Data/Processed/t
```

```
density_anova <- aov(data= trait_data2, Predicted ~ Site)
summary(density_anova)
```

```
##               Df Sum Sq Mean Sq F value  Pr(>F)
## Site           4   53.8  13.455   3.469 0.00884 **
## Residuals    254  985.3   3.879
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#I reject the null hypothesis and conclude that there is a significant difference in l
TukeyHSD(density_anova)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Predicted ~ Site, data = trait_data2)
##
## $Site
##                            diff         lwr        upr      p adj
## Maharira-Ampatsoana  -0.24434525 -1.51592352  1.02723302 0.9844326
## Miaranony-Ampatsoana  1.11175034  0.07509492  2.14840576 0.0287003
## Valohoaka-Ampatsoana  0.49076493 -0.50782868  1.48935854 0.6599856
```

```
## Vohiparara-Ampatsoana   0.06169045 -0.94847230   1.07185319 0.9998214
## Miaranony-Maharira       1.35609559  0.08064645   2.63154473 0.0308715
## Valohoaka-Maharira       0.73511018 -0.50960073   1.97982109 0.4843107
## Vohiparara-Maharira      0.30603570 -0.94797580   1.56004719 0.9625640
## Valohoaka-Miaranony     -0.62098541 -1.62450343   0.38253261 0.4356786
## Vohiparara-Miaranony    -1.05005989 -2.06509092  -0.03502886 0.0385856
## Vohiparara-Valohoaka    -0.42907448 -1.40520087   0.54705191 0.7469374
```

```r
# There is a significant difference in lemur densities between Miaranony and Ampatsoan
#and Miaranony and Vohiparara

anova_groups <- HSD.test(density_anova, "Site", group=TRUE)
# the predicted groups according to their lemur densities are Miaranony and Valohoaka
# and Valohoaka, Vohiparara, Ampatsoana, and Maharira in group b


density_aov_plot <- ggplot(data = trait_data2, aes(x = Site, y = Predicted))+
  geom_boxplot()+
  ylab("Lemur Density (N Individuals/"~(Km^2))+
  theme_classic()
#based on the plot it looks like it might be outliers that are driving the pattern we
# in Miaranony and Valohoaka
```

```r
density_anova2 <- aov(data= trait_data2, Predicted ~ Species)
summary(density_anova2)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Species       8  363.2    45.4   16.79 <2e-16 ***
## Residuals   250  675.9     2.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#I reject the null hypothesis and conclude that there is a significant difference in l

TukeyHSD(density_anova2)
```

```
##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = Predicted ~ Species, data = trait_data2)
##
## $Species
##                                               diff        lwr
## Cheirogaleus_crossleyi-Avahi_laniger    0.41233752 -1.01469480
## Eulemur_rubriventer-Avahi_laniger       3.30306813  1.93478684
## Eulemur_rufifrons-Avahi_laniger         1.81868377  0.45040247
```

```
## Hapalemur_griseus-Avahi_laniger                        0.62028125 -0.74800004
## Lepilemur_microdon-Avahi_laniger                      -0.25848688 -1.68551919
## Microcebus_rufus-Avahi_laniger                         2.22014703  0.79311471
## Propithecus_edwardsi-Avahi_laniger                     2.53047986  1.16219857
## Varecia_variegata-Avahi_laniger                        0.50347344 -0.86480786
## Eulemur_rubriventer-Cheirogaleus_crossleyi             2.89073061  1.52244932
## Eulemur_rufifrons-Cheirogaleus_crossleyi               1.40634625  0.03806496
## Hapalemur_griseus-Cheirogaleus_crossleyi               0.20794373 -1.16033756
## Lepilemur_microdon-Cheirogaleus_crossleyi             -0.67082440 -2.09785671
## Microcebus_rufus-Cheirogaleus_crossleyi                1.80780951  0.38077720
## Propithecus_edwardsi-Cheirogaleus_crossleyi            2.11814235  0.74986105
## Varecia_variegata-Cheirogaleus_crossleyi               0.09113592 -1.27714537
## Eulemur_rufifrons-Eulemur_rubriventer                 -1.48438436 -2.79127617
## Hapalemur_griseus-Eulemur_rubriventer                 -2.68278688 -3.98967868
## Lepilemur_microdon-Eulemur_rubriventer                -3.56155501 -4.92983631
## Microcebus_rufus-Eulemur_rubriventer                  -1.08292111 -2.45120240
## Propithecus_edwardsi-Eulemur_rubriventer              -0.77258827 -2.07948007
## Varecia_variegata-Eulemur_rubriventer                 -2.79959469 -4.10648650
## Hapalemur_griseus-Eulemur_rufifrons                   -1.19840252 -2.50529432
## Lepilemur_microdon-Eulemur_rufifrons                  -2.07717065 -3.44545194
## Microcebus_rufus-Eulemur_rufifrons                     0.40146326 -0.96681804
## Propithecus_edwardsi-Eulemur_rufifrons                 0.71179610 -0.59509571
## Varecia_variegata-Eulemur_rufifrons                   -1.31521033 -2.62210213
## Lepilemur_microdon-Hapalemur_griseus                  -0.87876813 -2.24704943
## Microcebus_rufus-Hapalemur_griseus                     1.59986577  0.23158448
## Propithecus_edwardsi-Hapalemur_griseus                 1.91019861  0.60330681
## Varecia_variegata-Hapalemur_griseus                   -0.11680781 -1.42369962
## Microcebus_rufus-Lepilemur_microdon                    2.47863390  1.05160159
## Propithecus_edwardsi-Lepilemur_microdon                2.78896674  1.42068545
## Varecia_variegata-Lepilemur_microdon                   0.76196032 -0.60632098
## Propithecus_edwardsi-Microcebus_rufus                  0.31033284 -1.05794846
## Varecia_variegata-Microcebus_rufus                    -1.71667359 -3.08495488
## Varecia_variegata-Propithecus_edwardsi                -2.02700643 -3.33389823
##                                                              upr       p adj
## Cheirogaleus_crossleyi-Avahi_laniger                   1.839369830 0.9925947
## Eulemur_rubriventer-Avahi_laniger                      4.671349428 0.0000000
## Eulemur_rufifrons-Avahi_laniger                        3.186965064 0.0014338
## Hapalemur_griseus-Avahi_laniger                        1.988562546 0.8898724
## Lepilemur_microdon-Avahi_laniger                       1.168545434 0.9997365
## Microcebus_rufus-Avahi_laniger                         3.647179338 0.0000692
## Propithecus_edwardsi-Avahi_laniger                     3.898761160 0.0000008
## Varecia_variegata-Avahi_laniger                        1.871754734 0.9654778
## Eulemur_rubriventer-Cheirogaleus_crossleyi             4.259011910 0.0000000
## Eulemur_rufifrons-Cheirogaleus_crossleyi               2.774627546 0.0387346
## Hapalemur_griseus-Cheirogaleus_crossleyi               1.576225029 0.9999300
```

16

```
## Lepilemur_microdon-Cheirogaleus_crossleyi    0.756207916 0.8679449
## Microcebus_rufus-Cheirogaleus_crossleyi      3.234841821 0.0030530
## Propithecus_edwardsi-Cheirogaleus_crossleyi  3.486423642 0.0000773
## Varecia_variegata-Cheirogaleus_crossleyi     1.459417217 0.9999999
## Eulemur_rufifrons-Eulemur_rubriventer       -0.177492560 0.0132340
## Hapalemur_griseus-Eulemur_rubriventer       -1.375895078 0.0000000
## Lepilemur_microdon-Eulemur_rubriventer      -2.193273716 0.0000000
## Microcebus_rufus-Eulemur_rubriventer         0.285360189 0.2485246
## Propithecus_edwardsi-Eulemur_rubriventer     0.534303535 0.6487500
## Varecia_variegata-Eulemur_rubriventer       -1.492702890 0.0000000
## Hapalemur_griseus-Eulemur_rufifrons          0.108489286 0.1013056
## Lepilemur_microdon-Eulemur_rufifrons        -0.708889352 0.0001180
## Microcebus_rufus-Eulemur_rufifrons           1.769744553 0.9917960
## Propithecus_edwardsi-Eulemur_rufifrons       2.018687899 0.7434653
## Varecia_variegata-Eulemur_rufifrons         -0.008318526 0.0472010
## Lepilemur_microdon-Hapalemur_griseus         0.489513165 0.5380854
## Microcebus_rufus-Hapalemur_griseus           2.968147070 0.0092519
## Propithecus_edwardsi-Hapalemur_griseus       3.217090417 0.0002567
## Varecia_variegata-Hapalemur_griseus          1.190083991 0.9999989
## Microcebus_rufus-Lepilemur_microdon          3.905666217 0.0000046
## Propithecus_edwardsi-Lepilemur_microdon      4.157248039 0.0000000
## Varecia_variegata-Lepilemur_microdon         2.130241614 0.7195202
## Propithecus_edwardsi-Microcebus_rufus        1.678614134 0.9986281
## Varecia_variegata-Microcebus_rufus          -0.348392291 0.0035252
## Varecia_variegata-Propithecus_edwardsi      -0.720114622 0.0000741
```

```r
anova_groups2 <- HSD.test(density_anova2, "Species", group=TRUE)
# the lemur species fall into four groups according to their densities
#What is interesting is that the groups do not seem to be organized by taxonomic famil

density_aov_plot2 <- ggplot(data = trait_data2, aes(x = reorder(Species, Predicted, FUN
  geom_boxplot()+
  ylab("Lemur Density (N Individuals/"~(Km^2))+
  xlab("Species")+
  theme_classic()+
  scale_x_discrete(labels= c("V. variegata", "L. microdon", "A. laniger", "C. crossleyi"
  theme(axis.text.x = element_text(angle = 45, vjust=0.5))
```

4.1 Question 2: What variables are related to differences in lemur densities?

Next, weanalyzed what transect-level habitat variables are significantly related to lemur densities. After an exploratory correlation plot to determine the correlations between the habitat variables, we conducted linear mixed effects models using the "lmer" function in the R package "lme4" (Bates et al. 2015). We used lemur density as the dependent variable, site-level

habitat characteristics (log fruit length, log fruit width, log seed length, log seed width, log fruit nitrogen content, log tree tannin content, log fruit sugar content, log fruit sugar content, log fruit protein content, latitude, longitude, aspect, slope, and roughness) as the independent variables. We conducted these models with both the transect and the lemur species as random variables. In the first set of models we included site as an independent variable, and in a second set of models we included it as a random variable. We used a backward stepwise approach to reduce the models and conducted model selection via comparison of their Akaike Information Criterion (AIC) values using the "lrtest" function in the R package "lmtest" (Zeileis & Horton 2002). Additionally, we identified the R-squared values of the models using the "r.squaredGLMM" function in the R package "MuMln" (Barton 2020).

4.2 Question 3: Which landscape-level characteristics and plant functional traits influence density of individual lemur species?

The final step of our analyses was exploring the effects of habitat variables for specific lemur species. To do this, we subset the data by species and conducted linear models for four lemur species (*Avahi laniger, Eulemur rubriventer, Propithecus edwardsi*, and *Lepilemur microdon*) using the function "lm" from the R general interface. We used density as the dependent variable and the aforementioned habitat variables as independent variables. We chose to focus on these four lemur species as case studies because we identified them as having distinct densities based on the ANOVA and exploratory data analysis. Further, we identified *Avahi laniger* and *Lepilemur microdon* as having the two lowest mean densities of all species included in our data, and we identified *Propithecus edwardsi* and *Eulemur rubriventer* as having the two highest mean densities of all species included in our data. Therefore, analyzing these four species individually could provide us with insights into drivers of high and low densities.

```
#More analyses using linear models
traitdata_subset <- select(trait_data2, logFruitLength:logSLA, Predicted, slope, aspect,
lemur_density_Corr <- cor(traitdata_subset)
corrplot(lemur_density_Corr, method = "ellipse")
```
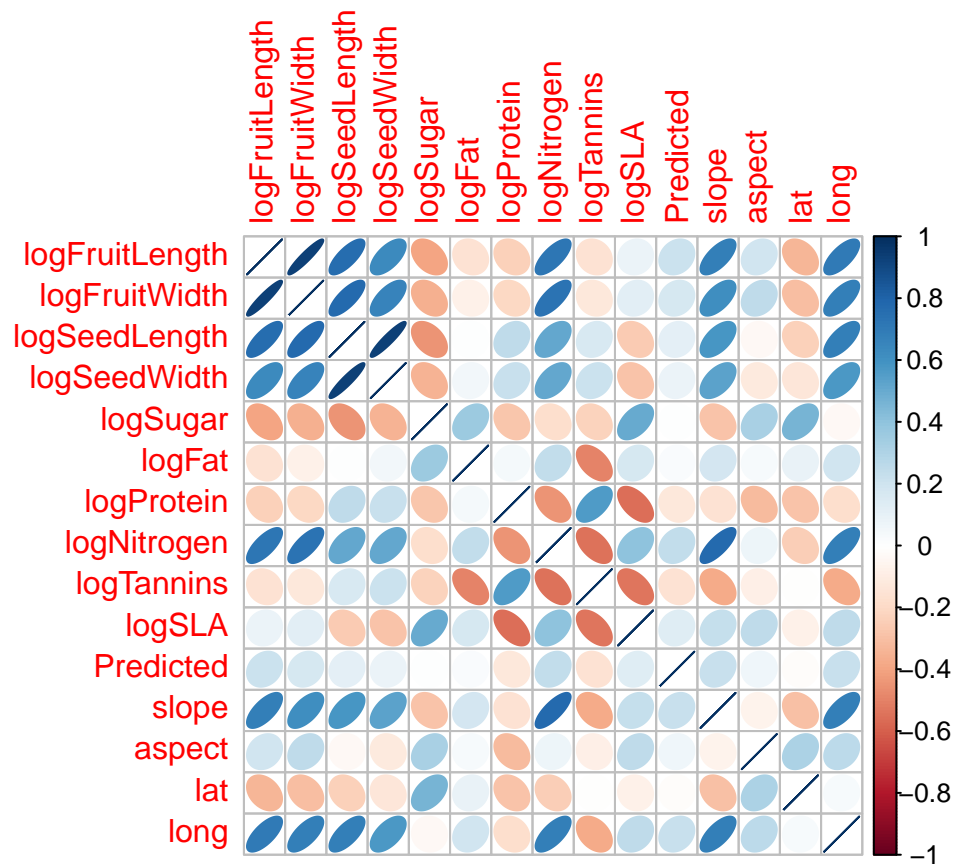
```
#The correlation plot matrix indicates that there are slight correlations between our
```

```
Fruit_trait_plot <- ggplot(traitdata_subset, aes(x = logFruitLength, y = Predicted, colo
  geom_point()
print(Fruit_trait_plot)
```
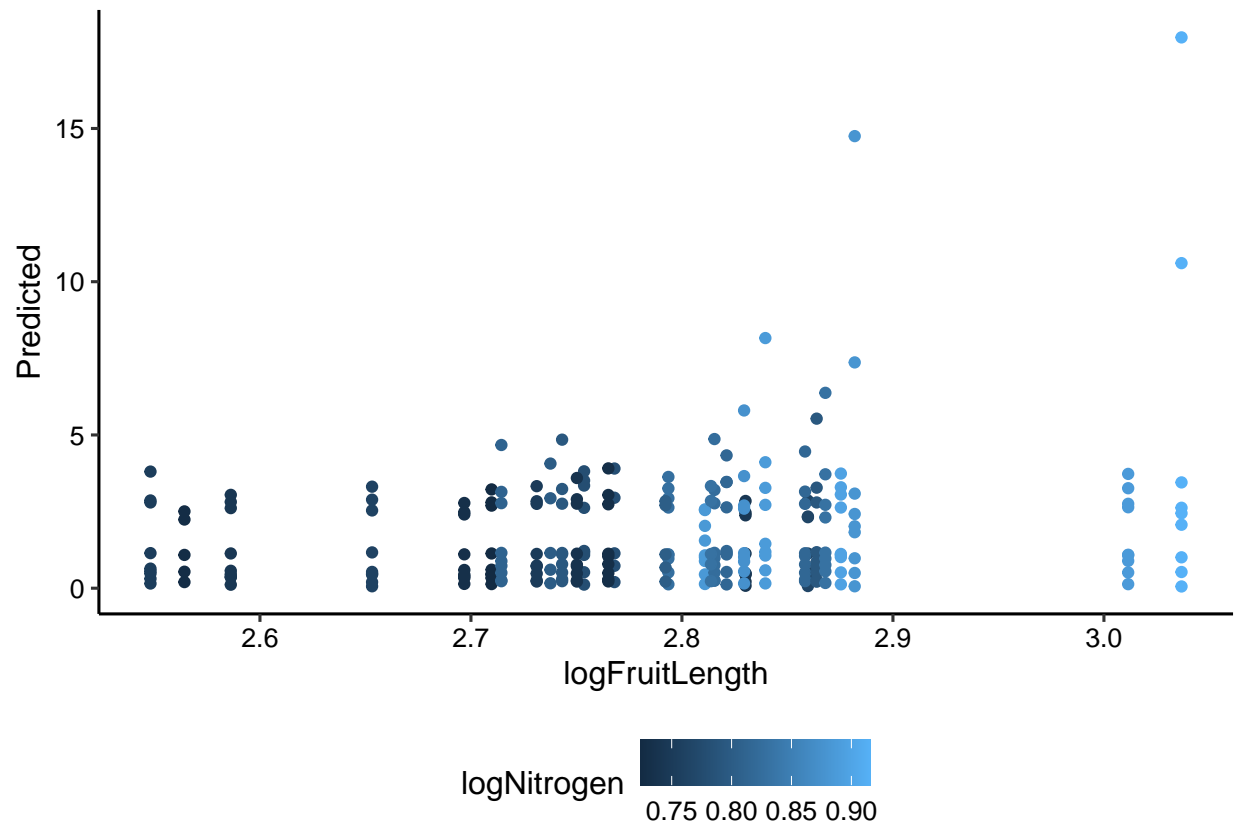
```
# plot to visually explore the relationship between some of fruit trait variables that

Fruit_trait_nutrient_plot2 <- ggplot(traitdata_subset, aes(x = logProtein, y = Predicted
  geom_point()
print(Fruit_trait_nutrient_plot2)
```
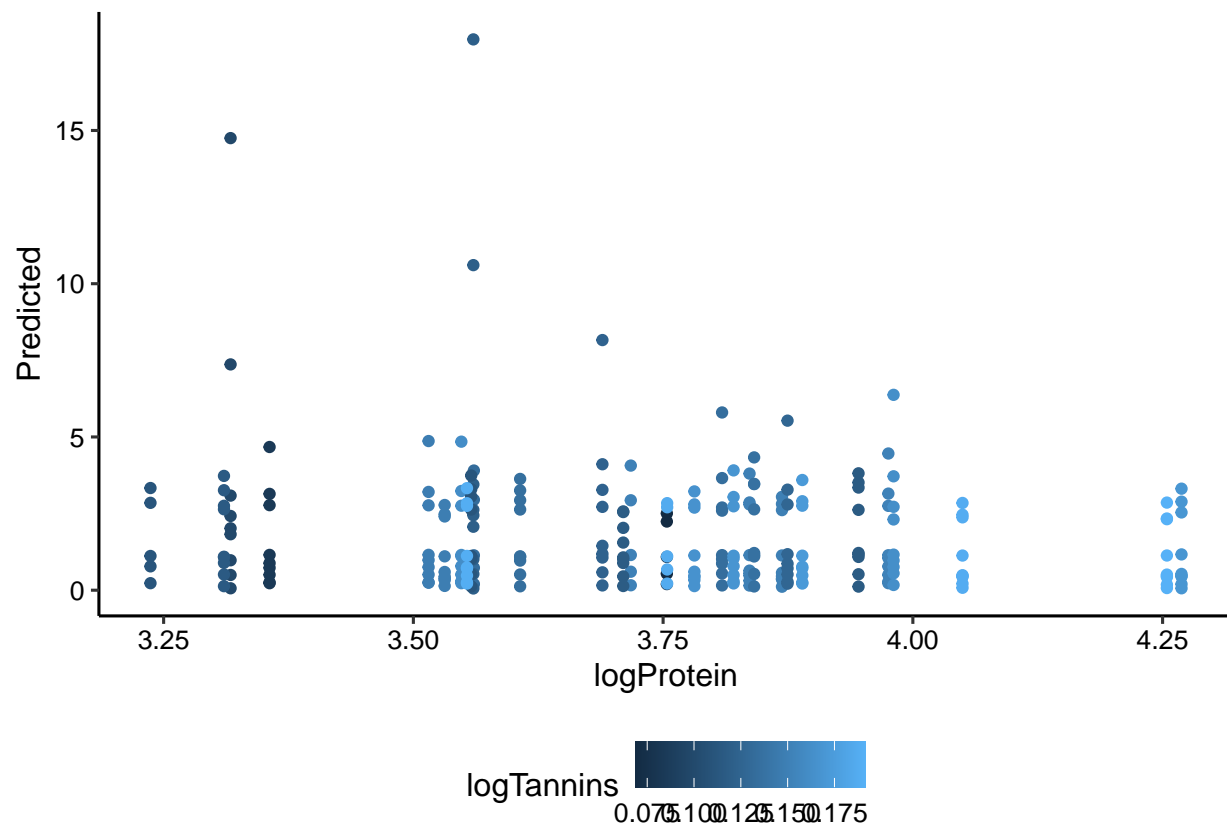
```
# plot to visually explore the relationship between two other fruit trait variables th
```

```
#Creating a linear model with random effects (transect site and species as random effe
lemur_dens_lmer1 <- lmer(data = trait_data2, Predicted ~ logSeedLength + logNitrogen + l
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logSeedLength + logNitrogen + lat + logSeedWidth +
##     logTannins + roughness + long + logSugar + logSLA + slope +
##     Site + logFruitLength + logFat + aspect + logFruitWidth +
##     logProtein + (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
```

```
## REML criterion at convergence: 942.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4001 -0.2993 -0.0091  0.2590  8.5591
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 1.125e-11 3.354e-06
##  Species       (Intercept) 1.563e+00 1.250e+00
##  Residual                  2.374e+00 1.541e+00
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)    -18.771085 616.337417 230.883243  -0.030  0.97573
## logSeedLength    0.564743   4.280281 231.037733   0.132  0.89515
## logNitrogen     15.507459   5.807085 230.997034   2.670  0.00811 **
## lat            -25.853124  12.960069 231.092886  -1.995  0.04724 *
## logSeedWidth    -2.666833   4.783737 231.003118  -0.557  0.57774
## logTannins       5.047217  10.863562 231.085231   0.465  0.64265
## roughness       -0.006877   0.003449 230.994197  -1.994  0.04733 *
## long           -11.359045  13.294831 230.946483  -0.854  0.39377
## logSugar         2.601340   2.692910 230.997313   0.966  0.33506
## logSLA           0.162660   4.549210 231.028321   0.036  0.97151
## slope            0.239327   0.136268 230.991674   1.756  0.08036 .
## SiteMaharira    -7.968357   4.513314 231.058902  -1.766  0.07880 .
## SiteMiaranony   -1.419236   2.010303 230.942810  -0.706  0.48091
## SiteValohoaka   -7.237059   3.725982 231.041098  -1.942  0.05331 .
## SiteVohiparara  -6.154208   2.893724 231.079496  -2.127  0.03450 *
## logFruitLength   8.252693   4.542446 230.992059   1.817  0.07054 .
## logFat          -1.431096   2.397225 231.044363  -0.597  0.55111
## aspect          -0.001160   0.002815 230.997184  -0.412  0.68067
## logFruitWidth   -8.690045   4.130924 231.002929  -2.104  0.03649 *
## logProtein       0.764685   1.130087 231.013454   0.677  0.49930
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
```
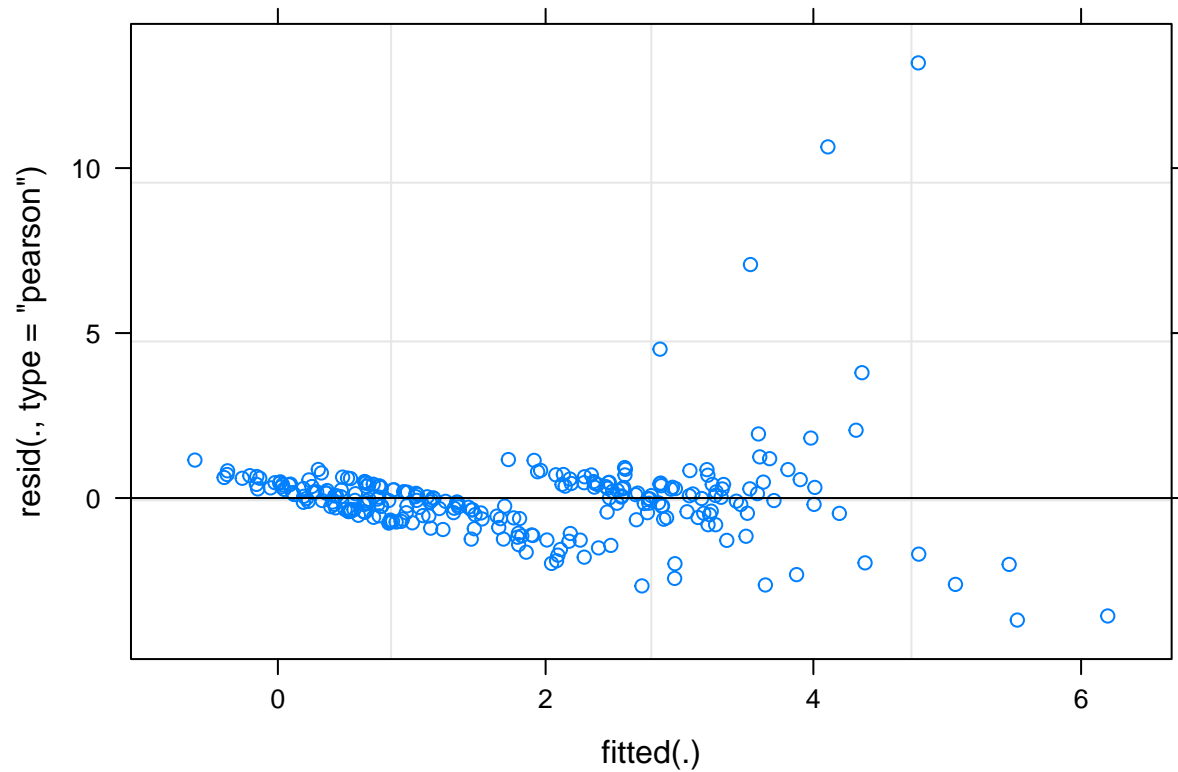
```
## boundary (singular) fit: see ?isSingular
```

```
#Checking whether the linear model conforms to the assumptions of linear models
par(mfrow = c(2,2), mar=c(4,4,4,4))
plot(lemur_dens_lmer1)
```



```
par(mfrow = c(1,1))
#There appears to be a balance of positive and negative residuals, which is a good sig

qqnorm(trait_data2$Predicted); qqline(trait_data2$Predicted)
```
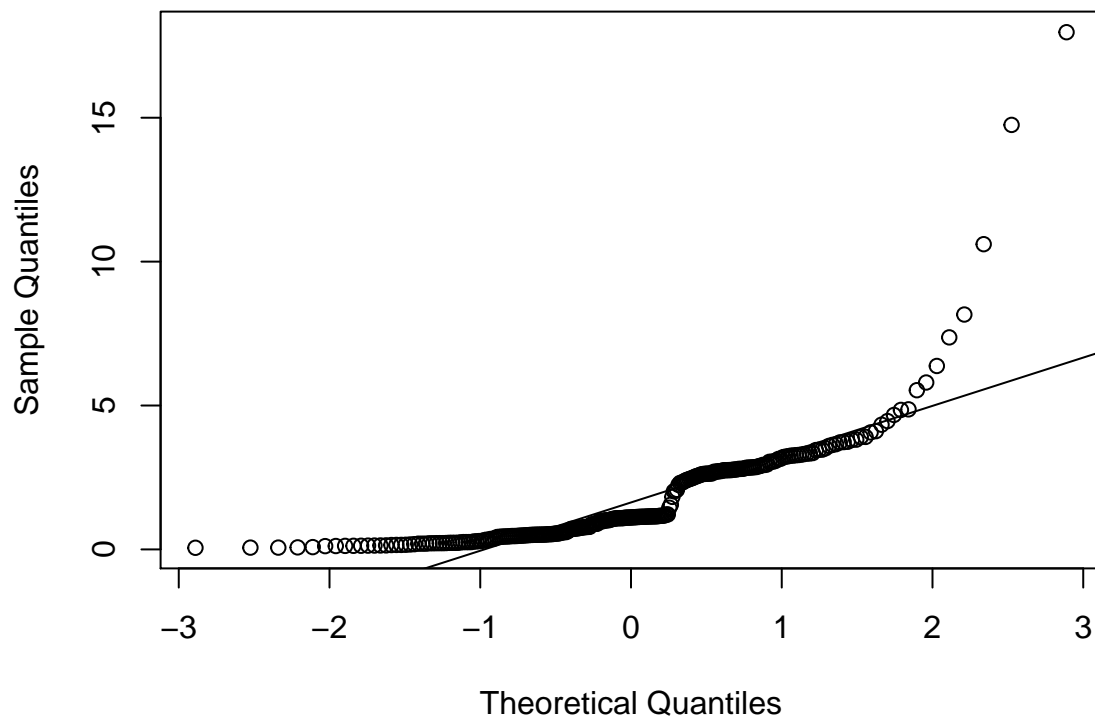
Normal Q–Q Plot


```
#This qqplot provides information on the normality of the response variable. The data


#Reducing the linear model manually
lemur_dens_lmer2 <- update(lemur_dens_lmer1,~.-logSLA)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer2)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logSeedLength + logNitrogen + lat + logSeedWidth +
##     logTannins + roughness + long + logSugar + slope + Site +
##     logFruitLength + logFat + aspect + logFruitWidth + logProtein +
##     (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
```

```
##
## REML criterion at convergence: 947
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4045 -0.2986 -0.0093  0.2604  8.5760
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 1.945e-10 1.395e-05
##  Species       (Intercept) 1.563e+00 1.250e+00
##  Residual                  2.364e+00 1.537e+00
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)    -26.674315 573.799178 232.157724  -0.046  0.96296
## logSeedLength    0.546642   4.241875 232.036918   0.129  0.89757
## logNitrogen     15.571900   5.508461 232.014680   2.827  0.00511 **
## lat            -25.771740  12.724015 232.110126  -2.025  0.04397 *
## logSeedWidth    -2.683522   4.750223 232.007443  -0.565  0.57267
## logTannins       5.113201  10.686930 232.084293   0.478  0.63278
## roughness       -0.006896   0.003400 232.000108  -2.028  0.04369 *
## long           -11.148195  11.873011 232.230010  -0.939  0.34873
## logSugar         2.653271   2.260511 232.043294   1.174  0.24170
## slope            0.240850   0.129138 232.002284   1.865  0.06344 .
## SiteMaharira    -7.924850   4.333427 232.084895  -1.829  0.06872 .
## SiteMiaranony   -1.420115   2.005797 232.056658  -0.708  0.47965
## SiteValohoaka   -7.211115   3.645078 232.051760  -1.978  0.04908 *
## SiteVohiparara  -6.123724   2.756602 232.116146  -2.221  0.02728 *
## logFruitLength   8.222066   4.450877 232.003527   1.847  0.06598 .
## logFat          -1.436903   2.386225 232.060435  -0.602  0.54765
## aspect          -0.001166   0.002804 232.016796  -0.416  0.67799
## logFruitWidth   -8.681959   4.115650 232.005736  -2.109  0.03597 *
## logProtein       0.751625   1.067410 232.009721   0.704  0.48204
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
```

```
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer3 <- update(lemur_dens_lmer2,~.-logSeedLength)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer3)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## Predicted ~ logNitrogen + lat + logSeedWidth + logTannins + roughness +
##     long + logSugar + slope + Site + logFruitLength + logFat +
##     aspect + logFruitWidth + logProtein + (1 | Species) + (1 |
##     Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 951.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4137 -0.2998 -0.0048  0.2553  8.5962
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Transect_Site (Intercept) 0.000    0.000
##  Species       (Intercept) 1.564    1.251
##  Residual                  2.354    1.534
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    -39.767482 563.486415 233.087642  -0.071  0.94380
## logNitrogen     15.357836   5.240647 233.008258   2.931  0.00372 **
## lat            -25.812878  12.693337 233.110665  -2.034  0.04313 *
## logSeedWidth    -2.220452   3.099731 233.011508  -0.716  0.47450
## logTannins       4.917120  10.554481 233.104427   0.466  0.64174
## roughness       -0.006886   0.003392 232.998728  -2.030  0.04350 *
## long           -10.896234  11.684317 233.219473  -0.933  0.35202
## logSugar         2.583951   2.191114 233.018059   1.179  0.23949
## slope            0.240445   0.128827 233.001730   1.866  0.06324 .
```

```
## SiteMaharira       -7.929625    4.324114 233.088837  -1.834   0.06796 .
## SiteMiaranony      -1.424570    2.001240 232.997595  -0.712   0.47727
## SiteValohoaka      -7.247266    3.626744 233.048813  -1.998   0.04685 *
## SiteVohiparara     -6.110012    2.748611 233.127341  -2.223   0.02718 *
## logFruitLength      8.483533    3.952993 232.999605   2.146   0.03290 *
## logFat             -1.337441    2.253533 233.034956  -0.593   0.55343
## aspect             -0.001276    0.002667 233.009703  -0.478   0.63285
## logFruitWidth      -8.709550    4.101411 233.005554  -2.124   0.03476 *
## logProtein          0.789655    1.023521 233.025080   0.772   0.44119
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer4 <- update(lemur_dens_lmer3,~.-aspect)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer4)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## Predicted ~ logNitrogen + lat + logSeedWidth + logTannins + roughness +
##     long + logSugar + slope + Site + logFruitLength + logFat +
##     logFruitWidth + logProtein + (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 942
##
## Scaled residuals:
##     Min       1Q  Median      3Q      Max
## -2.4083 -0.3137 -0.0025  0.2473  8.6144
##
```

```
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Transect_Site (Intercept) 0.000    0.000
##  Species       (Intercept) 1.564    1.251
##  Residual                  2.346    1.532
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                 Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    -1.403e+02  5.219e+02 2.341e+02  -0.269   0.7883
## logNitrogen     1.484e+01  5.121e+00 2.340e+02   2.899   0.0041 **
## lat            -2.573e+01  1.267e+01 2.341e+02  -2.030   0.0435 *
## logSeedWidth   -2.350e+00  3.083e+00 2.340e+02  -0.762   0.4467
## logTannins      5.167e+00  1.052e+01 2.341e+02   0.491   0.6239
## roughness      -7.112e-03  3.354e-03 2.340e+02  -2.121   0.0350 *
## long           -8.687e+00  1.071e+01 2.343e+02  -0.811   0.4183
## logSugar        2.532e+00  2.185e+00 2.340e+02   1.159   0.2477
## slope           2.512e-01  1.266e-01 2.340e+02   1.983   0.0485 *
## SiteMaharira   -7.779e+00  4.305e+00 2.341e+02  -1.807   0.0721 .
## SiteMiaranony  -1.632e+00  1.950e+00 2.339e+02  -0.837   0.4034
## SiteValohoaka  -7.101e+00  3.608e+00 2.341e+02  -1.968   0.0502 .
## SiteVohiparara -6.122e+00  2.744e+00 2.342e+02  -2.231   0.0266 *
## logFruitLength  7.926e+00  3.771e+00 2.340e+02   2.102   0.0366 *
## logFat         -1.583e+00  2.191e+00 2.340e+02  -0.723   0.4706
## logFruitWidth  -8.542e+00  4.080e+00 2.340e+02  -2.094   0.0374 *
## logProtein      6.972e-01  1.003e+00 2.340e+02   0.695   0.4879
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 17 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer5 <- update(lemur_dens_lmer4,~.-logTannins)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
```

```
## rescaling
```

```
summary(lemur_dens_lmer5)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logNitrogen + lat + logSeedWidth + roughness + long +
##     logSugar + slope + Site + logFruitLength + logFat + logFruitWidth +
##     logProtein + (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 948.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4055 -0.3170 -0.0098  0.2495  8.6196
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 3.129e-11 5.593e-06
##  Species       (Intercept) 1.560e+00 1.249e+00
##  Residual                  2.339e+00 1.529e+00
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)    -72.561704 502.586079 235.077393  -0.144  0.88533
## logNitrogen     14.485665   5.060587 235.003476   2.862  0.00458 **
## lat            -26.774374  12.470277 235.133587  -2.147  0.03281 *
## logSeedWidth    -1.159255   1.901018 235.089092  -0.610  0.54258
## roughness       -0.006954   0.003333 234.997920  -2.087  0.03801 *
## long           -10.594842   9.968675 235.330322  -1.063  0.28896
## logSugar         2.570350   2.179957 235.010831   1.179  0.23956
## slope            0.249734   0.126409 235.000398   1.976  0.04937 *
## SiteMaharira    -8.147535   4.232928 235.108060  -1.925  0.05546 .
## SiteMiaranony   -1.764698   1.928517 234.956075  -0.915  0.36110
## SiteValohoaka   -7.563403   3.476956 235.078626  -2.175  0.03061 *
## SiteVohiparara  -6.258400   2.725627 235.135247  -2.296  0.02255 *
## logFruitLength   8.299771   3.687833 234.997712   2.251  0.02534 *
## logFat          -2.011861   2.005758 235.001941  -1.003  0.31687
## logFruitWidth   -9.178807   3.861854 235.034704  -2.377  0.01827 *
## logProtein       0.888857   0.922900 234.999547   0.963  0.33648
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)         if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer6 <- update(lemur_dens_lmer5,~.-logSeedWidth)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## boundary (singular) fit: see ?isSingular

## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer6)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logNitrogen + lat + roughness + long + logSugar +
##     slope + Site + logFruitLength + logFat + logFruitWidth +
##     logProtein + (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 952.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4321 -0.3178 -0.0073  0.2546  8.6591
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 9.920e-13 9.960e-07
##  Species       (Intercept) 1.566e+00 1.251e+00
##  Residual                  2.332e+00 1.527e+00
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                Estimate Std. Error          df t value Pr(>|t|)
## (Intercept)  -68.887752 501.855688 236.152027  -0.137  0.89094
## logNitrogen   14.392694   5.051285 236.003023   2.849  0.00477 **
## lat          -28.372314  12.175612 236.166011  -2.330  0.02064 *
## roughness     -0.006971   0.003328 235.999206  -2.094  0.03730 *
## long         -11.353927   9.877391 236.293131  -1.149  0.25152
```

```
## logSugar          2.404177   2.159881 236.016257   1.113  0.26680
## slope             0.251844   0.126187 236.001143   1.996  0.04710 *
## SiteMaharira     -8.536007   4.179072 236.151312  -2.043  0.04221 *
## SiteMiaranony    -1.832956   1.922595 236.067749  -0.953  0.34137
## SiteValohoaka    -8.011145   3.393986 236.124443  -2.360  0.01907 *
## SiteVohiparara   -6.412735   2.710162 236.179854  -2.366  0.01878 *
## logFruitLength    8.389868   3.679773 235.999461   2.280  0.02350 *
## logFat           -1.652913   1.914781 236.001166  -0.863  0.38888
## logFruitWidth   -10.344726   3.350771 236.001571  -3.087  0.00226 **
## logProtein        0.648009   0.832938 236.008191   0.778  0.43736
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 15 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer7 <- update(lemur_dens_lmer6,~.-logProtein)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## boundary (singular) fit: see ?isSingular

## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer7)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logNitrogen + lat + roughness + long + logSugar +
##     slope + Site + logFruitLength + logFat + logFruitWidth +
##     (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 954.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4629 -0.3217 -0.0249  0.2614  8.7084
##
```

```
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 1.607e-12 1.268e-06
##  Species       (Intercept) 1.564e+00 1.250e+00
##  Residual                  2.328e+00 1.526e+00
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)    -98.911092 499.963808 237.069953  -0.198  0.84334
## logNitrogen     12.360405   4.319870 237.002434   2.861  0.00460 **
## lat            -27.438830  12.106512 237.128548  -2.266  0.02433 *
## roughness       -0.007768   0.003164 236.997884  -2.455  0.01480 *
## long           -10.243573   9.765794 237.288983  -1.049  0.29528
## logSugar         2.825153   2.089304 237.001623   1.352  0.17760
## slope            0.279581   0.120947 236.999392   2.312  0.02166 *
## SiteMaharira    -7.732801   4.046244 237.107903  -1.911  0.05720 .
## SiteMiaranony   -1.584268   1.894299 236.975809  -0.836  0.40381
## SiteValohoaka   -7.504780   3.328287 237.073410  -2.255  0.02506 *
## SiteVohiparara  -6.209522   2.695356 237.153253  -2.304  0.02210 *
## logFruitLength   7.668334   3.558092 236.998648   2.155  0.03216 *
## logFat          -1.569764   1.910246 236.997609  -0.822  0.41204
## logFruitWidth   -9.668936   3.233596 236.998560  -2.990  0.00308 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 14 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer8 <- update(lemur_dens_lmer7,~.-logFat)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## boundary (singular) fit: see ?isSingular

## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer8)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logNitrogen + lat + roughness + long + logSugar +
##     slope + Site + logFruitLength + logFruitWidth + (1 | Species) +
##     (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 958.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4465 -0.3214 -0.0322  0.2786  8.7317
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Transect_Site (Intercept) 0.000    0.000
##  Species       (Intercept) 1.564    1.250
##  Residual                  2.325    1.525
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    -1.789e+02  4.901e+02 2.379e+02  -0.365  0.71547
## logNitrogen     1.131e+01  4.125e+00 2.380e+02   2.743  0.00656 **
## lat            -2.803e+01  1.208e+01 2.381e+02  -2.321  0.02115 *
## roughness      -7.185e-03  3.081e-03 2.380e+02  -2.332  0.02054 *
## long           -8.865e+00  9.614e+00 2.381e+02  -0.922  0.35740
## logSugar        2.251e+00  1.968e+00 2.380e+02   1.144  0.25381
## slope           2.594e-01  1.184e-01 2.380e+02   2.192  0.02935 *
## SiteMaharira   -8.080e+00  4.021e+00 2.381e+02  -2.009  0.04564 *
## SiteMiaranony  -1.996e+00  1.826e+00 2.379e+02  -1.093  0.27542
## SiteValohoaka  -7.845e+00  3.300e+00 2.380e+02  -2.377  0.01824 *
## SiteVohiparara -6.291e+00  2.692e+00 2.381e+02  -2.337  0.02026 *
## logFruitLength  8.711e+00  3.322e+00 2.380e+02   2.622  0.00930 **
## logFruitWidth  -1.007e+01  3.194e+00 2.380e+02  -3.153  0.00182 **
## ---
## 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
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
```

```
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer9 <- update(lemur_dens_lmer8,~.-logSugar)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer9)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logNitrogen + lat + roughness + long + slope + Site +
##       logFruitLength + logFruitWidth + (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 962.7
##
## Scaled residuals:
##     Min       1Q  Median      3Q     Max
## -2.3503 -0.3031 -0.0432  0.2659  8.7576
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 2.365e-13 4.864e-07
##  Species       (Intercept) 1.566e+00 1.251e+00
##  Residual                  2.328e+00 1.526e+00
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)    -3.455e+02  4.682e+02  2.389e+02  -0.738  0.46121
## logNitrogen     9.642e+00  3.860e+00  2.390e+02   2.498  0.01316 *
## lat            -3.110e+01  1.178e+01  2.391e+02  -2.640  0.00884 **
## roughness      -6.218e-03  2.965e-03  2.390e+02  -2.097  0.03702 *
## long           -6.506e+00  9.396e+00  2.391e+02  -0.692  0.48932
## slope           2.256e-01  1.147e-01  2.390e+02   1.967  0.05032 .
## SiteMaharira   -9.693e+00  3.768e+00  2.391e+02  -2.572  0.01071 *
## SiteMiaranony  -2.517e+00  1.769e+00  2.389e+02  -1.423  0.15612
## SiteValohoaka  -8.689e+00  3.219e+00  2.391e+02  -2.700  0.00744 **
## SiteVohiparara -6.845e+00  2.649e+00  2.391e+02  -2.584  0.01037 *
## logFruitLength  6.916e+00  2.930e+00  2.390e+02   2.361  0.01904 *
## logFruitWidth  -9.344e+00  3.132e+00  2.390e+02  -2.983  0.00315 **
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) lgNtrg lat    rghnss long   slope  StMhrr StMrnn StVlhk
## logNitrogen  0.190
## lat          0.360 -0.067
## roughness    0.211 -0.275  0.155
## long        -0.856 -0.239  0.175 -0.139
## slope       -0.195  0.044 -0.018 -0.884  0.199
## SiteMaharir  0.351 -0.017  0.992  0.087  0.180  0.029
## SiteMiarnny  0.827  0.112  0.736  0.071 -0.463 -0.050  0.750
## SiteValohok  0.423 -0.076  0.989  0.159  0.103 -0.046  0.987  0.799
## SiteVohiprr  0.307 -0.071  0.991  0.118  0.226  0.022  0.991  0.716  0.984
## logFrtLngth  0.024  0.190  0.129 -0.201  0.043  0.098  0.135  0.062  0.100
## logFrutWdth  0.155 -0.438  0.023  0.457 -0.151 -0.335 -0.022  0.039  0.046
##             StVhpr lgFrtL
## logNitrogen
## lat
## roughness
## long
## slope
## SiteMaharir
## SiteMiarnny
## SiteValohok
## SiteVohiprr
## logFrtLngth  0.127
## logFrutWdth -0.009 -0.812
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer10 <- update(lemur_dens_lmer9,~.-long)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer10)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
```

```
## Formula:
## Predicted ~ logNitrogen + lat + roughness + slope + Site + logFruitLength +
##      logFruitWidth + (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 969.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3171 -0.2926 -0.0750  0.2852  8.7793
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 2.052e-11 4.530e-06
##  Species       (Intercept) 1.556e+00 1.247e+00
##  Residual                  2.324e+00 1.524e+00
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    -6.229e+02  2.421e+02 2.401e+02  -2.572  0.01070 *
## logNitrogen     9.003e+00  3.744e+00 2.400e+02   2.404  0.01695 *
## lat            -2.967e+01  1.159e+01 2.401e+02  -2.561  0.01106 *
## roughness      -6.503e-03  2.934e-03 2.400e+02  -2.217  0.02758 *
## slope           2.413e-01  1.123e-01 2.400e+02   2.150  0.03257 *
## SiteMaharira   -9.222e+00  3.703e+00 2.401e+02  -2.490  0.01343 *
## SiteMiaranony  -3.083e+00  1.567e+00 2.400e+02  -1.968  0.05022 .
## SiteValohoaka  -8.460e+00  3.198e+00 2.401e+02  -2.645  0.00871 **
## SiteVohiparara -6.430e+00  2.578e+00 2.401e+02  -2.494  0.01331 *
## logFruitLength  7.003e+00  2.924e+00 2.400e+02   2.395  0.01740 *
## logFruitWidth  -9.671e+00  3.093e+00 2.400e+02  -3.126  0.00199 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) lgNtrg lat    rghnss slope  StMhrr StMrnn StVlhk StVhpr
## logNitrogen -0.029
## lat          1.000 -0.027
## roughness    0.180 -0.321  0.184
## slope       -0.049  0.096 -0.055 -0.882
## SiteMaharir  0.992  0.027  0.992  0.115 -0.008
## SiteMiarnny  0.939  0.002  0.936  0.007  0.048  0.956
## SiteValohok  0.992 -0.053  0.992  0.176 -0.068  0.990  0.959
## SiteVohiprr  0.993 -0.018  0.993  0.155 -0.024  0.992  0.950  0.991
## logFrtLngth  0.116  0.206  0.124 -0.197  0.091  0.129  0.092  0.096  0.121
```

```
## logFrutWdth  0.051 -0.494  0.051  0.446 -0.314  0.005 -0.035  0.062  0.027
##             lgFrtL
## logNitrogen
## lat
## roughness
## slope
## SiteMaharir
## SiteMiarnny
## SiteValohok
## SiteVohiprr
## logFrtLngth
## logFrutWdth -0.816
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lemur_dens_lmer11 <- update(lemur_dens_lmer10,~.-SiteMiaranony)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lemur_dens_lmer11)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## Predicted ~ logNitrogen + lat + roughness + slope + Site + logFruitLength +
##     logFruitWidth + (1 | Species) + (1 | Transect_Site)
##    Data: trait_data2
##
## REML criterion at convergence: 969.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3171 -0.2926 -0.0750  0.2852  8.7793
##
## Random effects:
##  Groups        Name        Variance  Std.Dev.
##  Transect_Site (Intercept) 2.052e-11 4.530e-06
##  Species       (Intercept) 1.556e+00 1.247e+00
##  Residual                  2.324e+00 1.524e+00
```

```
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9
##
## Fixed effects:
##                  Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    -6.229e+02  2.421e+02  2.401e+02  -2.572  0.01070 *
## logNitrogen     9.003e+00  3.744e+00  2.400e+02   2.404  0.01695 *
## lat            -2.967e+01  1.159e+01  2.401e+02  -2.561  0.01106 *
## roughness      -6.503e-03  2.934e-03  2.400e+02  -2.217  0.02758 *
## slope           2.413e-01  1.123e-01  2.400e+02   2.150  0.03257 *
## SiteMaharira   -9.222e+00  3.703e+00  2.401e+02  -2.490  0.01343 *
## SiteMiaranony  -3.083e+00  1.567e+00  2.400e+02  -1.968  0.05022 .
## SiteValohoaka  -8.460e+00  3.198e+00  2.401e+02  -2.645  0.00871 **
## SiteVohiparara -6.430e+00  2.578e+00  2.401e+02  -2.494  0.01331 *
## logFruitLength  7.003e+00  2.924e+00  2.400e+02   2.395  0.01740 *
## logFruitWidth  -9.671e+00  3.093e+00  2.400e+02  -3.126  0.00199 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) lgNtrg lat    rghnss slope  StMhrr StMrnn StVlhk StVhpr
## logNitrogen -0.029
## lat          1.000 -0.027
## roughness    0.180 -0.321  0.184
## slope       -0.049  0.096 -0.055 -0.882
## SiteMaharir  0.992  0.027  0.992  0.115 -0.008
## SiteMiarnny  0.939  0.002  0.936  0.007  0.048  0.956
## SiteValohok  0.992 -0.053  0.992  0.176 -0.068  0.990  0.959
## SiteVohiprr  0.993 -0.018  0.993  0.155 -0.024  0.992  0.950  0.991
## logFrtLngth  0.116  0.206  0.124 -0.197  0.091  0.129  0.092  0.096  0.121
## logFrutWdth  0.051 -0.494  0.051  0.446 -0.314  0.005 -0.035  0.062  0.027
##             lgFrtL
## logNitrogen
## lat
## roughness
## slope
## SiteMaharir
## SiteMiarnny
## SiteValohok
## SiteVohiprr
## logFrtLngth
## logFrutWdth -0.816
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
lrtest(lemur_dens_lmer6, lemur_dens_lmer7, lemur_dens_lmer8, lemur_dens_lmer9, lemur_den
```

```
## Likelihood ratio test
##
## Model 1: Predicted ~ logNitrogen + lat + roughness + long + logSugar +
##     slope + Site + logFruitLength + logFat + logFruitWidth +
##     logProtein + (1 | Species) + (1 | Transect_Site)
## Model 2: Predicted ~ logNitrogen + lat + roughness + long + logSugar +
##     slope + Site + logFruitLength + logFat + logFruitWidth +
##     (1 | Species) + (1 | Transect_Site)
## Model 3: Predicted ~ logNitrogen + lat + roughness + long + logSugar +
##     slope + Site + logFruitLength + logFruitWidth + (1 | Species) +
##     (1 | Transect_Site)
## Model 4: Predicted ~ logNitrogen + lat + roughness + long + slope + Site +
##     logFruitLength + logFruitWidth + (1 | Species) + (1 | Transect_Site)
## Model 5: Predicted ~ logNitrogen + lat + roughness + slope + Site + logFruitLength +
##     logFruitWidth + (1 | Species) + (1 | Transect_Site)
##    #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   18 -476.14
## 2   17 -477.18 -1 2.0772   0.149512
## 3   16 -479.08 -1 3.8074   0.051026 .
## 4   15 -481.33 -1 4.4998   0.033899 *
## 5   14 -484.73 -1 6.7974   0.009129 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
AIC(lemur_dens_lmer6, lemur_dens_lmer7, lemur_dens_lmer8, lemur_dens_lmer9, lemur_dens_l
```

```
##                  df      AIC
## lemur_dens_lmer6  18 988.2770
## lemur_dens_lmer7  17 988.3543
## lemur_dens_lmer8  16 990.1617
## lemur_dens_lmer9  15 992.6615
## lemur_dens_lmer10 14 997.4588
```

```
#models 6 and 7 seem to have the lowest AICs
#Lemur_dens_lmer8 is the best linear model
#the significant variables of lemur_dens_8 are logNitrogen, lat, roughness, slope, Sit
```

```
r.squaredGLMM(lemur_dens_lmer8)
```

```
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.
```

```
##          R2m       R2c
## [1,] 0.10867 0.4670399
```

```
#lemur_dens_lmer8 explains 46.7% of density

#now creating a linear model using more random effects (site is now a random effect) t
#Testing linear models with site as a random variable
test <- lmer(data = trait_data2, Predicted ~ logSeedLength + logNitrogen + lat + logSeed
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(test)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logSeedLength + logNitrogen + lat + logSeedWidth +
##     logTannins + roughness + long + logSugar + logSLA + slope +
##     logFruitLength + logFat + aspect + logFruitWidth + logProtein +
##     (1 | Species) + (1 | Transect_Site) + (1 | Site)
##    Data: trait_data2
##
## REML criterion at convergence: 959.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1953 -0.3105 -0.0424  0.2115  8.6241
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Transect_Site (Intercept) 0.0000   0.0000
##  Species       (Intercept) 1.5358   1.2393
##  Site          (Intercept) 0.0927   0.3045
##  Residual                  2.3997   1.5491
## Number of obs: 259, groups:  Transect_Site, 31; Species, 9; Site, 5
##
## Fixed effects:
##                 Estimate Std. Error         df t value Pr(>|t|)
## (Intercept)    -3.038e+02  3.432e+02  2.990e+00  -0.885   0.4414
## logSeedLength   6.232e-01  3.993e+00  8.237e+01   0.156   0.8764
## logNitrogen     1.446e+01  5.674e+00  2.161e+02   2.548   0.0115 *
## lat             9.902e-02  2.361e+00  6.220e-01   0.042   0.9760
## logSeedWidth   -5.051e+00  3.582e+00  5.002e+00  -1.410   0.2175
## logTannins      1.068e+01  9.212e+00  2.331e+01   1.159   0.2581
```

```
## roughness       -5.204e-03  2.955e-03  1.591e+01  -1.761   0.0974 .
## long             6.338e+00  6.878e+00  3.001e+00   0.921   0.4248
## logSugar         2.637e+00  1.965e+00  6.122e+00   1.342   0.2272
## logSLA          -2.830e+00  4.076e+00  1.452e+02  -0.694   0.4886
## slope            2.343e-01  1.183e-01  2.928e+01   1.980   0.0572 .
## logFruitLength   7.312e+00  4.081e+00  3.672e+01   1.792   0.0814 .
## logFat          -1.220e+00  2.344e+00  2.191e+02  -0.520   0.6034
## aspect          -4.123e-04  2.335e-03  1.383e+01  -0.177   0.8624
## logFruitWidth   -6.797e+00  3.448e+00  1.554e+01  -1.971   0.0668 .
## logProtein       6.502e-01  9.955e-01  4.356e+01   0.653   0.5171
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)          if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

r.squaredGLMM(test)

```
##              R2m        R2c
## [1,] 0.09654791 0.4617936
```

step(test)

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## boundary (singular) fit: see ?isSingular

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.3e+04
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
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```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
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```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
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```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
```

```
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

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## rescaling

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## rescaling

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## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Backward reduced random-effect table:
##
##                     Eliminated npar  logLik     AIC    LRT Df Pr(>Chisq)
## <none>                          20 -479.64  999.28
## (1 | Transect_Site)          1  19 -479.64  997.28  0.000  1     1.0000
## (1 | Site)                   2  18 -479.66  995.33  0.045  1     0.8313
## (1 | Species)                0  17 -524.97 1083.94 90.614  1     <2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                 Eliminated  Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## logSeedLength            1  0.0786  0.0786     1 235.09  0.0327 0.856717
## aspect                   2  0.1368  0.1368     1 236.00  0.0571 0.811333
## lat                      3  0.3069  0.3069     1 237.13  0.1287 0.720149
## logFat                   4  0.6825  0.6825     1 238.05  0.2872 0.592535
## logProtein               5  1.0376  1.0376     1 239.00  0.4379 0.508756
## logSLA                   6  2.2553  2.2553     1 240.14  0.9541 0.329653
## logSugar                 7  0.9067  0.9067     1 241.01  0.3836 0.536283
## logTannins               8  7.6842  7.6842     1 242.02  3.2592 0.072264 .
## logSeedWidth             9  4.9347  4.9347     1 243.09  2.0735 0.151168
## roughness               10  4.0023  4.0023     1 244.00  1.6747 0.196860
## slope                   11  0.5541  0.5541     1 245.09  0.2312 0.631038
## long                    12  4.8277  4.8277     1 246.00  2.0207 0.156433
## logNitrogen              0 23.3110 23.3110     1 247.00  9.7163 0.002043 **
## logFruitLength           0 19.4009 19.4009     1 247.09  8.0865 0.004833 **
## logFruitWidth            0 15.4624 15.4624     1 247.06  6.4449 0.011742 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## Predicted ~ logNitrogen + logFruitLength + logFruitWidth + (1 | Species)
```

```
#the model below was created by the step function
step_test_model <- lmer(data = trait_data2, Predicted ~ logNitrogen + logFruitLength + l
summary(step_test_model)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Predicted ~ logNitrogen + logFruitLength + logFruitWidth + (1 |
##     Species)
##    Data: trait_data2
##
## REML criterion at convergence: 975.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.0505 -0.3962 -0.0497  0.2565  9.3116
##
## Random effects:
```

```
##  Groups    Name          Variance Std.Dev.
##  Species  (Intercept) 1.531    1.237
##  Residual                2.399    1.549
## Number of obs: 259, groups:  Species, 9
##
## Fixed effects:
##               Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)     -7.843     2.622 254.776  -2.991  0.00305 **
## logNitrogen      7.758     2.489 247.002   3.117  0.00204 **
## logFruitLength   7.367     2.591 247.095   2.844  0.00483 **
## logFruitWidth   -6.512     2.565 247.061  -2.539  0.01174 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) lgNtrg lgFrtL
## logNitrogen  0.259
## logFrtLngth -0.402 -0.154
## logFrutWdth -0.025 -0.231 -0.865
```

```
r.squaredGLMM(step_test_model)
```

```
##               R2m        R2c
## [1,] 0.07570071 0.4357929
```

```
AIC(step_test_model, lemur_dens_lmer8, lemur_dens_lmer7)
```

```
##                  df      AIC
## step_test_model   6 987.2448
## lemur_dens_lmer8 16 990.1617
## lemur_dens_lmer7 17 988.3543
```

```
#based off of the results of the AIC, the step_test_model appears to explain the data
#the significant variables of the best linear model for the entire data set (step_test
#the significant variables of the next best model (lemur_dens_lmer8) are logNitrogen,
#Therefore, lat, roughness, slope, and site are interesting variables

#checking the residuals of the final linear model for the entire data set (step_test_m
par(mfrow = c(2,2), mar=c(4,4,4,4))
plot(step_test_model)
```
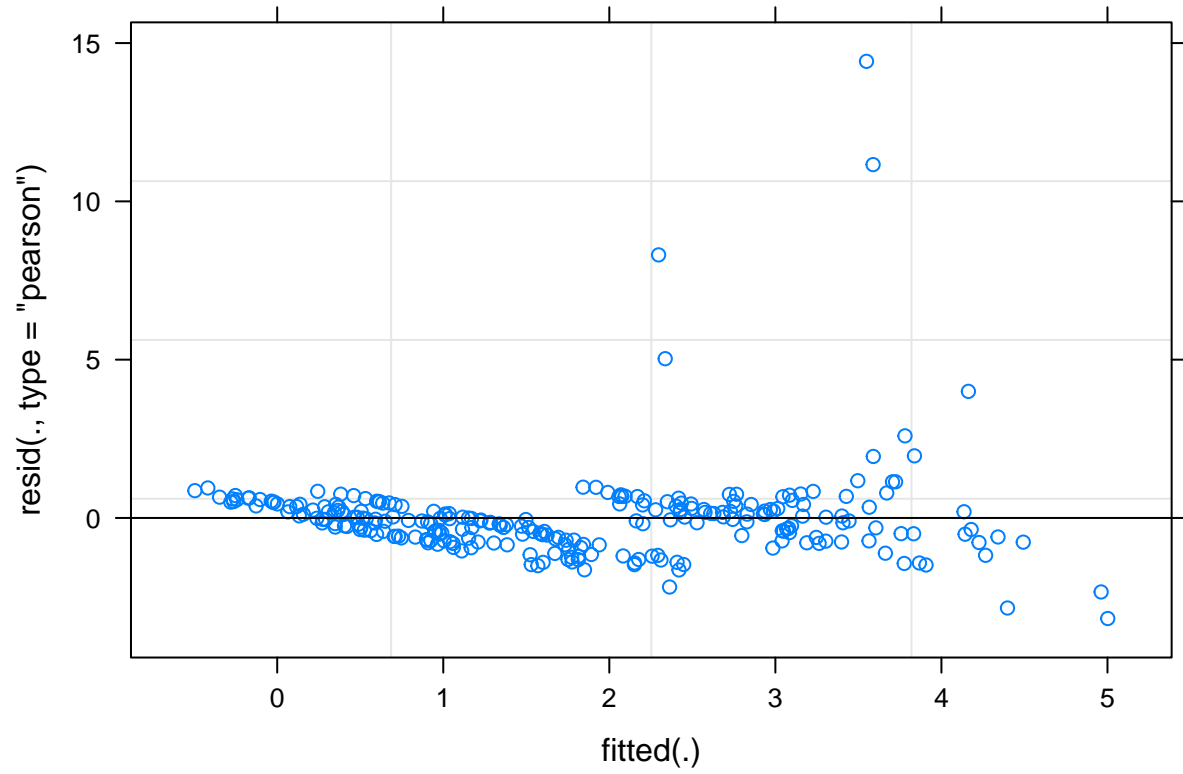
```
par(mfrow = c(1,1))
```

«««< HEAD ## Question 3: Which landscape-level characteristics and plant functional traits influence density of individual lemur species?

```r
#Exploring drivers of density for individual species though the use of linear models
#I will explore the drivers of density for the two species with the greatest densities

checking_lemur_densities <-
  trait_data2 %>%
  group_by(Species) %>%
  summarize(mean(Predicted))

#Avahi_laniger and Lepilemur_microdon are the species with the lowest predicted densit
#I will create linear models for each of these four species to analyze species specifi

AL_subset <- filter(trait_data2, Species == "Avahi_laniger")

AL_lm_1 <- lm(data = AL_subset, Predicted ~ logSeedLength + logNitrogen + lat + logSeedW
summary(AL_lm_1)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + logTannins + roughness + long + logSugar +
##     logSLA + slope + Site + logFruitLength + logFat + aspect +
##     logFruitWidth + logProtein, data = AL_subset)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -0.0183628 -0.0078726 -0.0004125  0.0075975  0.0227697
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5.266e+01  2.869e+01  -1.836   0.1161
## logSeedLength  3.733e-01  2.846e-01   1.312   0.2375
## logNitrogen   -1.254e-02  2.884e-01  -0.043   0.9667
## lat           -9.978e-01  6.246e-01  -1.597   0.1613
## logSeedWidth  -4.049e-01  2.956e-01  -1.370   0.2199
## logTannins    -6.037e-03  8.544e-01  -0.007   0.9946
## roughness      4.225e-05  1.734e-04   0.244   0.8157
## long           6.657e-01  6.591e-01   1.010   0.3515
## logSugar      -1.034e-03  1.692e-01  -0.006   0.9953
## logSLA         2.716e-01  2.210e-01   1.229   0.2650
## slope         -1.946e-03  6.547e-03  -0.297   0.7763
## SiteMaharira  -4.377e-01  2.183e-01  -2.005   0.0918 .
## SiteMiaranony -2.544e-01  1.001e-01  -2.542   0.0440 *
```

47

```
## SiteValohoaka  -2.773e-01  1.839e-01  -1.508    0.1822
## SiteVohiparara -2.588e-01  1.371e-01  -1.888    0.1079
## logFruitLength -3.823e-01  2.540e-01  -1.505    0.1830
## logFat         -1.116e-01  1.237e-01  -0.902    0.4016
## aspect         -9.069e-07  2.848e-04  -0.003    0.9976
## logFruitWidth   4.008e-01  1.874e-01   2.139    0.0763 .
## logProtein      4.985e-02  7.744e-02   0.644    0.5436
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02236 on 6 degrees of freedom
## Multiple R-squared:  0.9173, Adjusted R-squared:  0.6556
## F-statistic: 3.504 on 19 and 6 DF,  p-value: 0.06328
```

```
AL_lm_2 <- update(AL_lm_1,~.-logSugar)
summary(AL_lm_2)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + logTannins + roughness + long + logSLA + slope +
##     Site + logFruitLength + logFat + aspect + logFruitWidth +
##     logProtein, data = AL_subset)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -0.0183629 -0.0078610 -0.0004582  0.0075967  0.0227761
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.268e+01  2.647e+01  -1.990   0.0869 .
## logSeedLength   3.735e-01  2.608e-01   1.432   0.1951
## logNitrogen    -1.205e-02  2.568e-01  -0.047   0.9639
## lat            -9.967e-01  5.526e-01  -1.804   0.1143
## logSeedWidth   -4.049e-01  2.737e-01  -1.479   0.1826
## logTannins     -7.318e-03  7.669e-01  -0.010   0.9927
## roughness       4.202e-05  1.568e-04   0.268   0.7964
## long            6.664e-01  5.985e-01   1.113   0.3023
## logSLA          2.710e-01  1.793e-01   1.512   0.1744
## slope          -1.931e-03  5.602e-03  -0.345   0.7404
## SiteMaharira   -4.371e-01  1.822e-01  -2.399   0.0475 *
## SiteMiaranony  -2.545e-01  9.230e-02  -2.757   0.0282 *
## SiteValohoaka  -2.771e-01  1.669e-01  -1.660   0.1409
## SiteVohiparara -2.586e-01  1.207e-01  -2.143   0.0694 .
## logFruitLength -3.823e-01  2.351e-01  -1.626   0.1480
```

```
## logFat            -1.120e-01   9.755e-02  -1.149    0.2885
## aspect            -1.133e-06   2.615e-04  -0.004    0.9967
## logFruitWidth      4.009e-01   1.731e-01   2.316    0.0537 .
## logProtein         4.980e-02   7.130e-02   0.699    0.5074
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0207 on 7 degrees of freedom
## Multiple R-squared:  0.9173, Adjusted R-squared:  0.7048
## F-statistic: 4.316 on 18 and 7 DF,  p-value: 0.02804
```

```
AL_lm_3 <- update(AL_lm_2,~.-logTannins)
summary(AL_lm_3)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + roughness + long + logSLA + slope + Site +
##     logFruitLength + logFat + aspect + logFruitWidth + logProtein,
##     data = AL_subset)
##
## Residuals:
##         Min         1Q      Median         3Q         Max
## -0.0184039 -0.0078313 -0.0004705  0.0075981  0.0228028
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -5.274e+01  2.400e+01  -2.197   0.0592 .
## logSeedLength    3.738e-01  2.423e-01   1.543   0.1614
## logNitrogen     -1.076e-02  2.041e-01  -0.053   0.9592
## lat             -9.959e-01  5.104e-01  -1.951   0.0869 .
## logSeedWidth    -4.066e-01  1.951e-01  -2.084   0.0707 .
## roughness        4.147e-05  1.364e-04   0.304   0.7688
## long             6.682e-01  5.316e-01   1.257   0.2442
## logSLA           2.702e-01  1.490e-01   1.814   0.1073
## slope           -1.918e-03  5.088e-03  -0.377   0.7159
## SiteMaharira    -4.365e-01  1.602e-01  -2.724   0.0261 *
## SiteMiaranony   -2.541e-01  7.869e-02  -3.229   0.0121 *
## SiteValohoaka   -2.763e-01  1.366e-01  -2.023   0.0777 .
## SiteVohiparara  -2.584e-01  1.117e-01  -2.314   0.0494 *
## logFruitLength  -3.833e-01  1.971e-01  -1.944   0.0877 .
## logFat          -1.118e-01  8.871e-02  -1.261   0.2430
## aspect           4.339e-07  1.903e-04   0.002   0.9982
## logFruitWidth    4.012e-01  1.595e-01   2.514   0.0361 *
## logProtein       4.935e-02  5.010e-02   0.985   0.3534
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01936 on 8 degrees of freedom
## Multiple R-squared:  0.9173, Adjusted R-squared:  0.7417
## F-statistic: 5.222 on 17 and 8 DF,  p-value: 0.01142
```

```
AL_lm_4 <- update(AL_lm_3,~.-aspect)
summary(AL_lm_4)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + roughness + long + logSLA + slope + Site +
##     logFruitLength + logFat + logFruitWidth + logProtein, data = AL_subset)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -0.0184061 -0.0078314 -0.0004696  0.0075889  0.0228034
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -5.274e+01  2.263e+01  -2.331  0.04469 *
## logSeedLength    3.735e-01  1.892e-01   1.974  0.07979 .
## logNitrogen     -1.078e-02  1.922e-01  -0.056  0.95651
## lat             -9.958e-01  4.792e-01  -2.078  0.06748 .
## logSeedWidth    -4.064e-01  1.629e-01  -2.495  0.03415 *
## roughness        4.158e-05  1.197e-04   0.347  0.73623
## long             6.683e-01  5.012e-01   1.333  0.21516
## logSLA           2.702e-01  1.402e-01   1.927  0.08603 .
## slope           -1.922e-03  4.524e-03  -0.425  0.68094
## SiteMaharira    -4.366e-01  1.507e-01  -2.897  0.01767 *
## SiteMiaranony   -2.541e-01  7.419e-02  -3.425  0.00757 **
## SiteValohoaka   -2.764e-01  1.277e-01  -2.164  0.05872 .
## SiteVohiparara  -2.584e-01  1.051e-01  -2.458  0.03625 *
## logFruitLength  -3.831e-01  1.555e-01  -2.463  0.03598 *
## logFat          -1.118e-01  7.941e-02  -1.407  0.19288
## logFruitWidth    4.012e-01  1.470e-01   2.729  0.02326 *
## logProtein       4.941e-02  3.960e-02   1.248  0.24353
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01826 on 9 degrees of freedom
## Multiple R-squared:  0.9173, Adjusted R-squared:  0.7704
## F-statistic: 6.242 on 16 and 9 DF,  p-value: 0.004282
```

```
AL_lm_5 <- update(AL_lm_4,~.-logNitrogen)
summary(AL_lm_5)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     roughness + long + logSLA + slope + Site + logFruitLength +
##     logFat + logFruitWidth + logProtein, data = AL_subset)
##
## Residuals:
##        Min        1Q     Median        3Q        Max
## -0.0183122 -0.0075201 -0.0005731  0.0073756  0.0225534
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.242e+01  2.078e+01  -2.522   0.0303 *
## logSeedLength   3.747e-01  1.785e-01   2.099   0.0622 .
## lat            -9.977e-01  4.534e-01  -2.200   0.0524 .
## logSeedWidth   -4.070e-01  1.541e-01  -2.641   0.0247 *
## roughness       4.141e-05  1.135e-04   0.365   0.7228
## long            6.606e-01  4.576e-01   1.444   0.1794
## logSLA          2.691e-01  1.317e-01   2.042   0.0684 .
## slope          -1.948e-03  4.270e-03  -0.456   0.6580
## SiteMaharira   -4.376e-01  1.420e-01  -3.082   0.0116 *
## SiteMiaranony  -2.537e-01  7.012e-02  -3.619   0.0047 **
## SiteValohoaka  -2.772e-01  1.204e-01  -2.301   0.0441 *
## SiteVohiparara -2.588e-01  9.955e-02  -2.599   0.0265 *
## logFruitLength -3.819e-01  1.463e-01  -2.610   0.0260 *
## logFat         -1.129e-01  7.288e-02  -1.549   0.1524
## logFruitWidth   3.979e-01  1.275e-01   3.121   0.0108 *
## logProtein      5.031e-02  3.437e-02   1.464   0.1739
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01732 on 10 degrees of freedom
## Multiple R-squared:  0.9173, Adjusted R-squared:  0.7933
## F-statistic: 7.395 on 15 and 10 DF,  p-value: 0.001486
```

```
AL_lm_6 <- update(AL_lm_5,~.-roughness)
summary(AL_lm_6)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     long + logSLA + slope + Site + logFruitLength + logFat +
```

```
##        logFruitWidth + logProtein, data = AL_subset)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -0.0186348 -0.0075396 -0.0007129  0.0065590  0.0221233
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.267e+01  1.994e+01  -2.642  0.02292 *
## logSeedLength   3.807e-01  1.706e-01   2.232  0.04733 *
## lat            -1.027e+00  4.281e-01  -2.400  0.03525 *
## logSeedWidth   -4.113e-01  1.475e-01  -2.788  0.01764 *
## long            6.535e-01  4.388e-01   1.489  0.16449
## logSLA          2.720e-01  1.262e-01   2.155  0.05413 .
## slope          -5.606e-04  1.863e-03  -0.301  0.76910
## SiteMaharira   -4.407e-01  1.360e-01  -3.241  0.00786 **
## SiteMiaranony  -2.509e-01  6.689e-02  -3.751  0.00320 **
## SiteValohoaka  -2.824e-01  1.148e-01  -2.460  0.03168 *
## SiteVohiparara -2.637e-01  9.463e-02  -2.787  0.01768 *
## logFruitLength -3.814e-01  1.404e-01  -2.716  0.02007 *
## logFat         -1.098e-01  6.946e-02  -1.580  0.14238
## logFruitWidth   3.814e-01  1.144e-01   3.333  0.00668 **
## logProtein      4.586e-02  3.084e-02   1.487  0.16505
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01663 on 11 degrees of freedom
## Multiple R-squared:  0.9162, Adjusted R-squared:  0.8096
## F-statistic: 8.591 on 14 and 11 DF,  p-value: 0.0005089
```

```
AL_lm_7 <- update(AL_lm_6,~.-slope)
summary(AL_lm_7)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     long + logSLA + Site + logFruitLength + logFat + logFruitWidth +
##     logProtein, data = AL_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.018766 -0.007359 -0.001678  0.005595  0.023094
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)      -53.59434   18.93478  -2.830   0.01516 *
## logSeedLength      0.37747    0.16363   2.307   0.03970 *
## lat               -1.00638    0.40608  -2.478   0.02905 *
## logSeedWidth      -0.40820    0.14146  -2.886   0.01369 *
## long               0.68351    0.41076   1.664   0.12198
## logSLA             0.25729    0.11180   2.301   0.04010 *
## SiteMaharira      -0.43526    0.12957  -3.359   0.00568 **
## SiteMiaranony     -0.25252    0.06411  -3.939   0.00197 **
## SiteValohoaka     -0.27893    0.10980  -2.540   0.02592 *
## SiteVohiparara    -0.25684    0.08826  -2.910   0.01308 *
## logFruitLength    -0.38817    0.13323  -2.914   0.01300 *
## logFat            -0.11118    0.06663  -1.669   0.12102
## logFruitWidth      0.38066    0.10999   3.461   0.00471 **
## logProtein         0.04671    0.02952   1.582   0.13954
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01598 on 12 degrees of freedom
## Multiple R-squared:  0.9155, Adjusted R-squared:  0.824
## F-statistic:    10 on 13 and 12 DF,  p-value: 0.000159
```

```
AL_lm_8 <- update(AL_lm_7,~.-logProtein)
summary(AL_lm_8)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     long + logSLA + Site + logFruitLength + logFat + logFruitWidth,
##     data = AL_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.021608 -0.008082 -0.001649  0.008836  0.027191
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -48.96124   19.75957  -2.478   0.02772 *
## logSeedLength    0.49371    0.15444   3.197   0.00701 **
## lat             -1.11014    0.42330  -2.623   0.02108 *
## logSeedWidth    -0.45543    0.14605  -3.118   0.00816 **
## long             0.54806    0.42435   1.292   0.21901
## logSLA           0.20917    0.11363   1.841   0.08860 .
## SiteMaharira    -0.44741    0.13662  -3.275   0.00603 **
## SiteMiaranony   -0.24035    0.06723  -3.575   0.00339 **
## SiteValohoaka   -0.29196    0.11565  -2.524   0.02539 *
```

```
## SiteVohiparara  -0.26653     0.09300  -2.866   0.01325 *
## logFruitLength  -0.47527     0.12816  -3.709   0.00263 **
## logFat          -0.07757     0.06670  -1.163   0.26577
## logFruitWidth    0.34529     0.11376   3.035   0.00957 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01688 on 13 degrees of freedom
## Multiple R-squared:  0.8979, Adjusted R-squared:  0.8036
## F-statistic: 9.526 on 12 and 13 DF,  p-value: 0.0001391
```

```r
AL_lm_9 <- update(AL_lm_8,~.-logFat)
summary(AL_lm_9)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     long + logSLA + Site + logFruitLength + logFruitWidth, data = AL_subset)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -0.0278399 -0.0059317 -0.0006755  0.0065675  0.0242129
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -48.65563   20.00492  -2.432  0.02902 *
## logSeedLength    0.48554    0.15621   3.108  0.00771 **
## lat             -1.15117    0.42710  -2.695  0.01742 *
## logSeedWidth    -0.44093    0.14734  -2.993  0.00969 **
## long             0.51948    0.42893   1.211  0.24590
## logSLA           0.20199    0.11489   1.758  0.10055
## SiteMaharira    -0.45539    0.13815  -3.296  0.00530 **
## SiteMiaranony   -0.24668    0.06784  -3.636  0.00270 **
## SiteValohoaka   -0.30835    0.11622  -2.653  0.01891 *
## SiteVohiparara  -0.27027    0.09411  -2.872  0.01231 *
## logFruitLength  -0.40120    0.11260  -3.563  0.00312 **
## logFruitWidth    0.29131    0.10516   2.770  0.01503 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01709 on 14 degrees of freedom
## Multiple R-squared:  0.8873, Adjusted R-squared:  0.7987
## F-statistic: 10.02 on 11 and 14 DF,  p-value: 7.534e-05
```

```r
AL_lm_10 <- update(AL_lm_9,~.-long)
summary(AL_lm_10)
```

```
## 
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logSLA + Site + logFruitLength + logFruitWidth, data = AL_subset)
## 
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.024985 -0.008192 -0.001441  0.009811  0.025280
## 
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -26.78267    8.73649  -3.066  0.00785 **
## logSeedLength   0.54270    0.15121   3.589  0.00269 **
## lat            -1.27377    0.42134  -3.023  0.00856 **
## logSeedWidth   -0.47180    0.14736  -3.202  0.00594 **
## logSLA          0.26009    0.10600   2.454  0.02685 *
## SiteMaharira   -0.49563    0.13617  -3.640  0.00242 **
## SiteMiaranony  -0.20344    0.05858  -3.473  0.00341 **
## SiteValohoaka  -0.32752    0.11692  -2.801  0.01343 *
## SiteVohiparara -0.30482    0.09107  -3.347  0.00441 **
## logFruitLength -0.41023    0.11409  -3.596  0.00265 **
## logFruitWidth   0.29228    0.10678   2.737  0.01527 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.01736 on 15 degrees of freedom
## Multiple R-squared:  0.8755, Adjusted R-squared:  0.7924
## F-statistic: 10.54 on 10 and 15 DF,  p-value: 4.189e-05

AIC(AL_lm_2, AL_lm_3, AL_lm_4, AL_lm_5, AL_lm_6, AL_lm_7, AL_lm_8, AL_lm_9, AL_lm_10)

##           df       AIC
## AL_lm_2   20 -121.9668
## AL_lm_3   19 -123.9664
## AL_lm_4   18 -125.9664
## AL_lm_5   17 -127.9573
## AL_lm_6   16 -129.6135
## AL_lm_7   15 -131.4004
## AL_lm_8   14 -128.4729
## AL_lm_9   13 -127.8998
## AL_lm_10  12 -127.3093

#AL_lm_7 has the lowest AIC, and explains 82% of the variation of Avahi laniger densit
#AL_lm_10 has only significant variables, and explains 79% of the variation of Avahi l
#I selected model AL_lm_10
#logSeedLength, lat, logSeedWidth, logSLA, SiteMaharira, SiteMiaranony, SiteValohoaka,
```

```
ER_subset <- filter(trait_data2, Species == "Eulemur_rubriventer")

ER_lm_1 <- lm(data = ER_subset, Predicted ~ logSeedLength + logNitrogen + lat + logSeedW
summary(ER_lm_1)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + logTannins + roughness + long + logSugar +
##     logSLA + slope + Site + logFruitLength + logFat + aspect +
##     logFruitWidth + logProtein, data = ER_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.11606 -0.44945 -0.09879  0.35030  1.53307
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.452e+03  1.276e+03  -1.922  0.08083 .
## logSeedLength   7.417e+00  8.321e+00   0.891  0.39185
## logNitrogen    -3.880e+00  1.197e+01  -0.324  0.75191
## lat            -6.441e+01  2.641e+01  -2.439  0.03288 *
## logSeedWidth   -1.668e+01  9.670e+00  -1.725  0.11250
## logTannins      3.481e+01  2.128e+01   1.636  0.13019
## roughness       3.789e-03  7.127e-03   0.532  0.60557
## long            2.350e+01  2.710e+01   0.867  0.40426
## logSugar       -5.728e+00  5.113e+00  -1.120  0.28645
## logSLA          6.004e+00  9.273e+00   0.647  0.53059
## slope          -3.554e-01  2.810e-01  -1.265  0.23215
## SiteMaharira   -2.492e+01  9.215e+00  -2.704  0.02052 *
## SiteMiaranony  -1.006e+01  4.175e+00  -2.410  0.03459 *
## SiteValohoaka  -1.539e+01  7.614e+00  -2.021  0.06827 .
## SiteVohiparara -1.609e+01  5.927e+00  -2.715  0.02011 *
## logFruitLength -2.781e+01  9.286e+00  -2.995  0.01219 *
## logFat         -5.819e-01  4.860e+00  -0.120  0.90686
## aspect          4.942e-04  5.139e-03   0.096  0.92511
## logFruitWidth   2.947e+01  8.582e+00   3.433  0.00559 **
## logProtein      8.693e-01  2.203e+00   0.395  0.70074
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.075 on 11 degrees of freedom
## Multiple R-squared:  0.7795, Adjusted R-squared:  0.3986
## F-statistic: 2.047 on 19 and 11 DF,  p-value: 0.1123
```

```
ER_lm_2 <- update(ER_lm_1,~.-aspect)
summary(ER_lm_2)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + logTannins + roughness + long + logSugar +
##     logSLA + slope + Site + logFruitLength + logFat + logFruitWidth +
##     logProtein, data = ER_subset)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.1168 -0.4553 -0.1004  0.3480  1.5300
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.420e+03  1.180e+03  -2.052  0.06269 .
## logSeedLength   7.208e+00  7.694e+00   0.937  0.36731
## logNitrogen    -3.657e+00  1.125e+01  -0.325  0.75070
## lat            -6.433e+01  2.528e+01  -2.544  0.02573 *
## logSeedWidth   -1.648e+01  9.054e+00  -1.821  0.09369 .
## logTannins      3.483e+01  2.038e+01   1.709  0.11315
## roughness       3.846e-03  6.802e-03   0.565  0.58220
## long            2.285e+01  2.512e+01   0.910  0.38098
## logSugar       -5.690e+00  4.883e+00  -1.165  0.26652
## logSLA          5.912e+00  8.835e+00   0.669  0.51603
## slope          -3.585e-01  2.673e-01  -1.341  0.20477
## SiteMaharira   -2.490e+01  8.826e+00  -2.822  0.01541 *
## SiteMiaranony  -9.961e+00  3.868e+00  -2.575  0.02431 *
## SiteValohoaka  -1.541e+01  7.291e+00  -2.113  0.05620 .
## SiteVohiparara -1.604e+01  5.654e+00  -2.837  0.01498 *
## logFruitLength -2.752e+01  8.404e+00  -3.274  0.00665 **
## logFat         -4.411e-01  4.439e+00  -0.099  0.92248
## logFruitWidth   2.938e+01  8.171e+00   3.595  0.00368 **
## logProtein      8.973e-01  2.092e+00   0.429  0.67560
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.03 on 12 degrees of freedom
## Multiple R-squared:  0.7793, Adjusted R-squared:  0.4483
## F-statistic: 2.354 on 18 and 12 DF,  p-value: 0.06708
```

```
ER_lm_3 <- update(ER_lm_2,~.-logFat)
summary(ER_lm_3)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##      logSeedWidth + logTannins + roughness + long + logSugar +
##      logSLA + slope + Site + logFruitLength + logFruitWidth +
##      logProtein, data = ER_subset)
##
## Residuals:
##        Min      1Q   Median       3Q      Max
## -1.12655 -0.44307 -0.08421  0.35848  1.55283
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.455e+03  1.082e+03  -2.270  0.04088 *
## logSeedLength   7.001e+00  7.118e+00   0.983  0.34332
## logNitrogen    -3.987e+00  1.033e+01  -0.386  0.70572
## lat            -6.442e+01  2.428e+01  -2.653  0.01991 *
## logSeedWidth   -1.636e+01  8.621e+00  -1.898  0.08017 .
## logTannins      3.546e+01  1.864e+01   1.903  0.07945 .
## roughness       3.947e-03  6.464e-03   0.611  0.55195
## long            2.354e+01  2.320e+01   1.014  0.32891
## logSugar       -5.854e+00  4.418e+00  -1.325  0.20800
## logSLA          5.994e+00  8.455e+00   0.709  0.49094
## slope          -3.624e-01  2.542e-01  -1.426  0.17746
## SiteMaharira   -2.495e+01  8.474e+00  -2.944  0.01141 *
## SiteMiaranony  -1.005e+01  3.611e+00  -2.784  0.01551 *
## SiteValohoaka  -1.546e+01  6.991e+00  -2.211  0.04555 *
## SiteVohiparara -1.605e+01  5.434e+00  -2.953  0.01120 *
## logFruitLength -2.726e+01  7.679e+00  -3.549  0.00356 **
## logFruitWidth   2.929e+01  7.815e+00   3.748  0.00243 **
## logProtein      8.636e-01  1.984e+00   0.435  0.67054
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9898 on 13 degrees of freedom
## Multiple R-squared:  0.7791, Adjusted R-squared:  0.4903
## F-statistic: 2.698 on 17 and 13 DF,  p-value: 0.03779
```

```
ER_lm_4 <- update(ER_lm_3,~.-logNitrogen)
summary(ER_lm_4)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##      logTannins + roughness + long + logSugar + logSLA + slope +
```

```
##     Site + logFruitLength + logFruitWidth + logProtein, data = ER_subset)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -1.12981 -0.45212 -0.05761  0.40728  1.49928
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.415e+03  1.043e+03  -2.314  0.03635 *
## logSeedLength  7.771e+00  6.622e+00   1.174  0.26012
## lat           -6.397e+01  2.351e+01  -2.721  0.01655 *
## logSeedWidth  -1.753e+01  7.825e+00  -2.240  0.04183 *
## logTannins     3.765e+01  1.720e+01   2.189  0.04605 *
## roughness      3.572e-03  6.193e-03   0.577  0.57329
## long           2.286e+01  2.242e+01   1.020  0.32525
## logSugar      -5.329e+00  4.074e+00  -1.308  0.21192
## logSLA         5.133e+00  7.905e+00   0.649  0.52660
## slope         -3.578e-01  2.460e-01  -1.454  0.16797
## SiteMaharira  -2.477e+01  8.200e+00  -3.020  0.00918 **
## SiteMiaranony -9.962e+00  3.492e+00  -2.853  0.01279 *
## SiteValohoaka -1.539e+01  6.772e+00  -2.272  0.03940 *
## SiteVohiparara -1.597e+01 5.263e+00  -3.035  0.00891 **
## logFruitLength -2.695e+01 7.403e+00  -3.641  0.00267 **
## logFruitWidth  2.837e+01  7.213e+00   3.934  0.00150 **
## logProtein     9.784e-01  1.901e+00   0.515  0.61488
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9592 on 14 degrees of freedom
## Multiple R-squared:  0.7766, Adjusted R-squared:  0.5213
## F-statistic: 3.042 on 16 and 14 DF,  p-value: 0.02123
```

```
ER_lm_5 <- update(ER_lm_4,~.-logProtein)
summary(ER_lm_5)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + roughness + long + logSugar + logSLA + slope +
##     Site + logFruitLength + logFruitWidth, data = ER_subset)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -1.10261 -0.46309 -0.00053  0.32655  1.51726
##
```

```
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -2.515e+03  9.999e+02  -2.515 0.023802 *
## logSeedLength    8.582e+00  6.272e+00   1.368 0.191354
## lat             -6.195e+01  2.260e+01  -2.741 0.015163 *
## logSeedWidth    -1.874e+01  7.277e+00  -2.575 0.021108 *
## logTannins       4.203e+01  1.458e+01   2.883 0.011379 *
## roughness        2.408e-03  5.622e-03   0.428 0.674543
## long             2.603e+01  2.103e+01   1.238 0.234724
## logSugar        -4.363e+00  3.526e+00  -1.237 0.234956
## logSLA           3.518e+00  7.075e+00   0.497 0.626198
## slope           -3.113e-01  2.232e-01  -1.395 0.183404
## SiteMaharira    -2.344e+01  7.592e+00  -3.088 0.007505 **
## SiteMiaranony   -9.578e+00  3.327e+00  -2.879 0.011475 *
## SiteValohoaka   -1.443e+01  6.350e+00  -2.272 0.038226 *
## SiteVohiparara  -1.542e+01  5.023e+00  -3.069 0.007794 **
## logFruitLength  -2.867e+01  6.448e+00  -4.446 0.000472 ***
## logFruitWidth    2.886e+01  6.973e+00   4.139 0.000875 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9354 on 15 degrees of freedom
## Multiple R-squared:  0.7724, Adjusted R-squared:  0.5448
## F-statistic: 3.393 on 15 and 15 DF,  p-value: 0.01187
```

```
ER_lm_6 <- update(ER_lm_5,~.-roughness)
summary(ER_lm_6)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + long + logSugar + logSLA + slope + Site + logFruitLength +
##     logFruitWidth, data = ER_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.18733 -0.42150  0.01556  0.28845  1.53172
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2600.3392   954.2845  -2.725 0.014987 *
## logSeedLength      7.8139     5.8545   1.335 0.200667
## lat              -62.4887    21.9861  -2.842 0.011770 *
## logSeedWidth     -18.2158     6.9875  -2.607 0.019071 *
## logTannins        41.7733    14.1894   2.944 0.009529 **
```

```
## long             27.5933   20.1727    1.368 0.190264
## logSugar         -4.0510    3.3607   -1.205 0.245565
## logSLA            3.6538    6.8851    0.531 0.602926
## slope            -0.2269    0.1020   -2.224 0.040885 *
## SiteMaharira    -23.2783    7.3865   -3.151 0.006176 **
## SiteMiaranony    -9.5938    3.2409   -2.960 0.009213 **
## SiteValohoaka   -14.5673    6.1777   -2.358 0.031432 *
## SiteVohiparara  -15.4960    4.8902   -3.169 0.005956 **
## logFruitLength  -27.8168    5.9762   -4.655 0.000264 ***
## logFruitWidth    28.0591    6.5438    4.288 0.000565 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9112 on 16 degrees of freedom
## Multiple R-squared:  0.7696, Adjusted R-squared:  0.568
## F-statistic: 3.817 on 14 and 16 DF,  p-value: 0.006109
```

```
ER_lm_7 <- update(ER_lm_6,~.-logSLA)
summary(ER_lm_7)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + long + logSugar + slope + Site + logFruitLength +
##     logFruitWidth, data = ER_subset)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -1.13432 -0.42182 -0.09341  0.34694  1.64062
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.846e+03  8.168e+02  -3.484 0.002841 **
## logSeedLength   6.595e+00  5.270e+00   1.251 0.227743
## lat            -6.092e+01  2.132e+01  -2.857 0.010907 *
## logSeedWidth   -1.778e+01  6.791e+00  -2.618 0.017984 *
## logTannins      4.099e+01  1.381e+01   2.968 0.008624 **
## long            3.364e+01  1.629e+01   2.066 0.054425 .
## logSugar       -3.353e+00  3.027e+00  -1.108 0.283342
## slope          -2.001e-01  8.674e-02  -2.307 0.033917 *
## SiteMaharira   -2.261e+01  7.121e+00  -3.174 0.005546 **
## SiteMiaranony  -9.905e+00  3.119e+00  -3.175 0.005537 **
## SiteValohoaka  -1.420e+01  6.009e+00  -2.364 0.030245 *
## SiteVohiparara -1.482e+01  4.619e+00  -3.208 0.005161 **
## logFruitLength -2.805e+01  5.833e+00  -4.809 0.000164 ***
```

```
## logFruitWidth    2.841e+01  6.370e+00    4.460 0.000344 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8918 on 17 degrees of freedom
## Multiple R-squared:  0.7655, Adjusted R-squared:  0.5862
## F-statistic:  4.27 on 13 and 17 DF,  p-value: 0.003106
```

```r
ER_lm_8 <- update(ER_lm_7,~.-logSugar)
summary(ER_lm_8)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + long + slope + Site + logFruitLength + logFruitWidth,
##     data = ER_subset)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.2881 -0.4963 -0.1182  0.3891  1.8263
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.528e+03  7.697e+02  -3.285 0.004118 **
## logSeedLength   6.542e+00  5.303e+00   1.234 0.233205
## lat            -5.366e+01  2.042e+01  -2.628 0.017055 *
## logSeedWidth   -1.851e+01  6.802e+00  -2.722 0.013988 *
## logTannins      4.091e+01  1.390e+01   2.943 0.008689 **
## long            2.985e+01  1.602e+01   1.863 0.078866 .
## slope          -1.933e-01  8.707e-02  -2.220 0.039490 *
## SiteMaharira   -1.951e+01  6.591e+00  -2.960 0.008386 **
## SiteMiaranony  -8.809e+00  2.977e+00  -2.959 0.008405 **
## SiteValohoaka  -1.208e+01  5.731e+00  -2.108 0.049284 *
## SiteVohiparara -1.356e+01  4.505e+00  -3.009 0.007535 **
## logFruitLength -2.568e+01  5.461e+00  -4.703 0.000177 ***
## logFruitWidth   2.911e+01  6.379e+00   4.564 0.000240 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8974 on 18 degrees of freedom
## Multiple R-squared:  0.7486, Adjusted R-squared:  0.581
## F-statistic: 4.467 on 12 and 18 DF,  p-value: 0.002246
```

```r
ER_lm_9 <- update(ER_lm_8,~.-logSeedLength)
summary(ER_lm_9)
```

```
##
## Call:
## lm(formula = Predicted ~ lat + logSeedWidth + logTannins + long +
##     slope + Site + logFruitLength + logFruitWidth, data = ER_subset)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.1818 -0.4380 -0.1329  0.4505  1.8942
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.597e+03  7.782e+02  -3.337 0.003463 **
## lat            -5.330e+01  2.069e+01  -2.575 0.018530 *
## logSeedWidth   -1.284e+01  5.082e+00  -2.527 0.020530 *
## logTannins      3.917e+01  1.401e+01   2.795 0.011557 *
## long            3.146e+01  1.619e+01   1.944 0.066895 .
## slope          -2.095e-01  8.725e-02  -2.401 0.026742 *
## SiteMaharira   -1.865e+01  6.643e+00  -2.807 0.011250 *
## SiteMiaranony  -8.371e+00  2.996e+00  -2.794 0.011578 *
## SiteValohoaka  -1.190e+01  5.807e+00  -2.049 0.054512 .
## SiteVohiparara -1.326e+01  4.560e+00  -2.907 0.009029 **
## logFruitLength -2.411e+01  5.383e+00  -4.480 0.000257 ***
## logFruitWidth   2.872e+01  6.458e+00   4.448 0.000276 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9096 on 19 degrees of freedom
## Multiple R-squared:  0.7274, Adjusted R-squared:  0.5695
## F-statistic: 4.608 on 11 and 19 DF,  p-value: 0.0018
```

```r
ER_lm_10 <- update(ER_lm_9,~.-long)
summary(ER_lm_10)
```

```
##
## Call:
## lm(formula = Predicted ~ lat + logSeedWidth + logTannins + slope +
##     Site + logFruitLength + logFruitWidth, data = ER_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.39714 -0.46323 -0.02793  0.50480  1.67159
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1322.5869   447.4299  -2.956 0.007812 **
```

```
## lat                 -63.3686     21.3807  -2.964 0.007675 **
## logSeedWidth          -8.5481      4.8839  -1.750 0.095398 .
## logTannins            27.3007     13.4626   2.028 0.056104 .
## slope                 -0.2114      0.0931  -2.271 0.034368 *
## SiteMaharira         -21.7962      6.8758  -3.170 0.004815 **
## SiteMiaranony         -6.5317      3.0339  -2.153 0.043715 *
## SiteValohoaka        -14.5118      6.0295  -2.407 0.025877 *
## SiteVohiparara       -15.4614      4.7133  -3.280 0.003741 **
## logFruitLength       -23.0551      5.7153  -4.034 0.000650 ***
## logFruitWidth         27.3213      6.8487   3.989 0.000721 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9708 on 20 degrees of freedom
## Multiple R-squared:  0.6731, Adjusted R-squared:  0.5097
## F-statistic: 4.119 on 10 and 20 DF,  p-value: 0.003431
```

```
ER_lm_11 <- update(ER_lm_10,~.-logSeedWidth)
summary(ER_lm_11)
```

```
##
## Call:
## lm(formula = Predicted ~ lat + logTannins + slope + Site + logFruitLength +
##     logFruitWidth, data = ER_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.11036 -0.56636 -0.00057  0.53954  1.75513
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.432e+03  4.643e+02  -3.084  0.00562 **
## lat            -6.851e+01  2.219e+01  -3.087  0.00559 **
## logTannins      7.525e+00  7.672e+00   0.981  0.33779
## slope          -1.989e-01  9.728e-02  -2.044  0.05368 .
## SiteMaharira   -2.295e+01  7.173e+00  -3.199  0.00431 **
## SiteMiaranony  -7.960e+00  3.062e+00  -2.600  0.01673 *
## SiteValohoaka  -1.699e+01  6.142e+00  -2.767  0.01155 *
## SiteVohiparara -1.540e+01  4.939e+00  -3.117  0.00521 **
## logFruitLength -1.923e+01  5.535e+00  -3.475  0.00226 **
## logFruitWidth   1.862e+01  4.934e+00   3.773  0.00112 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.017 on 21 degrees of freedom
```

```
## Multiple R-squared:  0.6231, Adjusted R-squared:  0.4615
## F-statistic: 3.857 on 9 and 21 DF,  p-value: 0.005161
```

```
ER_lm_12 <- update(ER_lm_11,~.-logTannins)
summary(ER_lm_12)
```

```
##
## Call:
## lm(formula = Predicted ~ lat + slope + Site + logFruitLength +
##     logFruitWidth, data = ER_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.19232 -0.45601  0.06244  0.50266  1.68377
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.417e+03  4.636e+02  -3.056 0.005787 **
## lat            -6.772e+01  2.216e+01  -3.056 0.005791 **
## slope          -2.167e-01  9.548e-02  -2.270 0.033374 *
## SiteMaharira   -2.250e+01  7.152e+00  -3.146 0.004688 **
## SiteMiaranony  -8.144e+00  3.054e+00  -2.667 0.014089 *
## SiteValohoaka  -1.697e+01  6.136e+00  -2.765 0.011304 *
## SiteVohiparara -1.536e+01  4.935e+00  -3.113 0.005070 **
## logFruitLength -1.855e+01  5.486e+00  -3.381 0.002693 **
## logFruitWidth   1.888e+01  4.923e+00   3.835 0.000902 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.016 on 22 degrees of freedom
## Multiple R-squared:  0.6058, Adjusted R-squared:  0.4625
## F-statistic: 4.226 on 8 and 22 DF,  p-value: 0.003409
```

```
#all variables are significant
```

```
AIC(ER_lm_1, ER_lm_2, ER_lm_3, ER_lm_4, ER_lm_5, ER_lm_6, ER_lm_7, ER_lm_8, ER_lm_9, ER_
```

```
##          df       AIC
## ER_lm_1  21 102.34611
## ER_lm_2  20 100.37216
## ER_lm_3  19  98.39766
## ER_lm_4  18  96.75100
## ER_lm_5  17  95.33182
## ER_lm_6  16  93.70858
## ER_lm_7  15  92.24948
## ER_lm_8  14  92.41058
```

```
## ER_lm_9  13  92.92663
## ER_lm_10 12  96.54857
## ER_lm_11 11  98.96660
## ER_lm_12 10  98.35546
```

```
#7, 8, and 9 have has the lowest AIC
summary(ER_lm_7)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + long + logSugar + slope + Site + logFruitLength +
##     logFruitWidth, data = ER_subset)
##
## Residuals:
##     Min      1Q   Median      3Q     Max
## -1.13432 -0.42182 -0.09341  0.34694  1.64062
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.846e+03  8.168e+02  -3.484 0.002841 **
## logSeedLength   6.595e+00  5.270e+00   1.251 0.227743
## lat            -6.092e+01  2.132e+01  -2.857 0.010907 *
## logSeedWidth   -1.778e+01  6.791e+00  -2.618 0.017984 *
## logTannins      4.099e+01  1.381e+01   2.968 0.008624 **
## long            3.364e+01  1.629e+01   2.066 0.054425 .
## logSugar       -3.353e+00  3.027e+00  -1.108 0.283342
## slope          -2.001e-01  8.674e-02  -2.307 0.033917 *
## SiteMaharira   -2.261e+01  7.121e+00  -3.174 0.005546 **
## SiteMiaranony  -9.905e+00  3.119e+00  -3.175 0.005537 **
## SiteValohoaka  -1.420e+01  6.009e+00  -2.364 0.030245 *
## SiteVohiparara -1.482e+01  4.619e+00  -3.208 0.005161 **
## logFruitLength -2.805e+01  5.833e+00  -4.809 0.000164 ***
## logFruitWidth   2.841e+01  6.370e+00   4.460 0.000344 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8918 on 17 degrees of freedom
## Multiple R-squared:  0.7655, Adjusted R-squared:  0.5862
## F-statistic:  4.27 on 13 and 17 DF,  p-value: 0.003106
```

```
summary(ER_lm_8)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
```

```
##      logTannins + long + slope + Site + logFruitLength + logFruitWidth,
##      data = ER_subset)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.2881 -0.4963 -0.1182  0.3891  1.8263
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.528e+03  7.697e+02  -3.285 0.004118 **
## logSeedLength   6.542e+00  5.303e+00   1.234 0.233205
## lat            -5.366e+01  2.042e+01  -2.628 0.017055 *
## logSeedWidth   -1.851e+01  6.802e+00  -2.722 0.013988 *
## logTannins      4.091e+01  1.390e+01   2.943 0.008689 **
## long            2.985e+01  1.602e+01   1.863 0.078866 .
## slope          -1.933e-01  8.707e-02  -2.220 0.039490 *
## SiteMaharira   -1.951e+01  6.591e+00  -2.960 0.008386 **
## SiteMiaranony  -8.809e+00  2.977e+00  -2.959 0.008405 **
## SiteValohoaka  -1.208e+01  5.731e+00  -2.108 0.049284 *
## SiteVohiparara -1.356e+01  4.505e+00  -3.009 0.007535 **
## logFruitLength -2.568e+01  5.461e+00  -4.703 0.000177 ***
## logFruitWidth   2.911e+01  6.379e+00   4.564 0.000240 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8974 on 18 degrees of freedom
## Multiple R-squared:  0.7486, Adjusted R-squared:  0.581
## F-statistic: 4.467 on 12 and 18 DF,  p-value: 0.002246
```

```
summary(ER_lm_9)
```

```
##
## Call:
## lm(formula = Predicted ~ lat + logSeedWidth + logTannins + long +
##      slope + Site + logFruitLength + logFruitWidth, data = ER_subset)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.1818 -0.4380 -0.1329  0.4505  1.8942
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.597e+03  7.782e+02  -3.337 0.003463 **
## lat            -5.330e+01  2.069e+01  -2.575 0.018530 *
## logSeedWidth   -1.284e+01  5.082e+00  -2.527 0.020530 *
```

```
## logTannins       3.917e+01  1.401e+01   2.795 0.011557 *
## long             3.146e+01  1.619e+01   1.944 0.066895 .
## slope           -2.095e-01  8.725e-02  -2.401 0.026742 *
## SiteMaharira    -1.865e+01  6.643e+00  -2.807 0.011250 *
## SiteMiaranony   -8.371e+00  2.996e+00  -2.794 0.011578 *
## SiteValohoaka   -1.190e+01  5.807e+00  -2.049 0.054512 .
## SiteVohiparara  -1.326e+01  4.560e+00  -2.907 0.009029 **
## logFruitLength  -2.411e+01  5.383e+00  -4.480 0.000257 ***
## logFruitWidth    2.872e+01  6.458e+00   4.448 0.000276 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9096 on 19 degrees of freedom
## Multiple R-squared:  0.7274, Adjusted R-squared:  0.5695
## F-statistic: 4.608 on 11 and 19 DF,  p-value: 0.0018
```

```
summary(ER_lm_10)
```

```
##
## Call:
## lm(formula = Predicted ~ lat + logSeedWidth + logTannins + slope +
##      Site + logFruitLength + logFruitWidth, data = ER_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.39714 -0.46323 -0.02793  0.50480  1.67159
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1322.5869   447.4299  -2.956 0.007812 **
## lat              -63.3686    21.3807  -2.964 0.007675 **
## logSeedWidth      -8.5481     4.8839  -1.750 0.095398 .
## logTannins        27.3007    13.4626   2.028 0.056104 .
## slope             -0.2114     0.0931  -2.271 0.034368 *
## SiteMaharira     -21.7962     6.8758  -3.170 0.004815 **
## SiteMiaranony     -6.5317     3.0339  -2.153 0.043715 *
## SiteValohoaka    -14.5118     6.0295  -2.407 0.025877 *
## SiteVohiparara   -15.4614     4.7133  -3.280 0.003741 **
## logFruitLength   -23.0551     5.7153  -4.034 0.000650 ***
## logFruitWidth     27.3213     6.8487   3.989 0.000721 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9708 on 20 degrees of freedom
## Multiple R-squared:  0.6731, Adjusted R-squared:  0.5097
```

```
## F-statistic: 4.119 on 10 and 20 DF,  p-value: 0.003431
```

```
#Propithecus_edwardsi has the second highest density
PE_subset <- filter(trait_data2, Species == "Propithecus_edwardsi")

PE_lm_1<- lm(data = PE_subset, Predicted ~ logSeedLength + logNitrogen + lat + logSeedWi
summary(PE_lm_1)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##      logSeedWidth + logTannins + roughness + long + logSugar +
##      logSLA + slope + Site + logFruitLength + logFat + aspect +
##      logFruitWidth + logProtein, data = PE_subset)
##
## Residuals:
##        Min        1Q     Median        3Q        Max
## -0.257675 -0.092568 -0.007372  0.135958  0.293599
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.792e+02  3.054e+02  -1.896   0.0845 .
## logSeedLength   2.066e+00  1.992e+00   1.037   0.3220
## logNitrogen     7.657e-01  2.866e+00   0.267   0.7943
## lat            -1.586e+01  6.323e+00  -2.508   0.0291 *
## logSeedWidth   -4.613e+00  2.315e+00  -1.992   0.0717 .
## logTannins      9.282e+00  5.095e+00   1.822   0.0958 .
## roughness       4.721e-04  1.706e-03   0.277   0.7872
## long            5.220e+00  6.488e+00   0.805   0.4381
## logSugar       -1.140e+00  1.224e+00  -0.931   0.3719
## logSLA          2.029e+00  2.220e+00   0.914   0.3804
## slope          -3.954e-02  6.728e-02  -0.588   0.5686
## SiteMaharira   -6.367e+00  2.206e+00  -2.886   0.0148 *
## SiteMiaranony  -2.412e+00  9.996e-01  -2.413   0.0344 *
## SiteValohoaka  -3.783e+00  1.823e+00  -2.075   0.0622 .
## SiteVohiparara -3.980e+00  1.419e+00  -2.804   0.0171 *
## logFruitLength -3.932e+00  2.223e+00  -1.768   0.1047
## logFat         -1.920e-01  1.164e+00  -0.165   0.8720
## aspect          1.493e-04  1.231e-03   0.121   0.9056
## logFruitWidth   4.601e+00  2.055e+00   2.239   0.0468 *
## logProtein      2.933e-01  5.276e-01   0.556   0.5894
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2574 on 11 degrees of freedom
## Multiple R-squared:  0.8635, Adjusted R-squared:  0.6277
## F-statistic: 3.662 on 19 and 11 DF,  p-value: 0.01588
```

```
PE_lm_2 <- update(PE_lm_1,~.-aspect)
summary(PE_lm_2)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + logTannins + roughness + long + logSugar +
##     logSLA + slope + Site + logFruitLength + logFat + logFruitWidth +
##     logProtein, data = PE_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.25789 -0.09303 -0.00336  0.13867  0.29269
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.696e+02  2.825e+02  -2.016   0.0668 .
## logSeedLength   2.003e+00  1.843e+00   1.087   0.2984
## logNitrogen     8.332e-01  2.694e+00   0.309   0.7624
## lat            -1.583e+01  6.055e+00  -2.615   0.0226 *
## logSeedWidth   -4.554e+00  2.168e+00  -2.100   0.0575 .
## logTannins      9.290e+00  4.881e+00   1.903   0.0813 .
## roughness       4.895e-04  1.629e-03   0.300   0.7690
## long            5.023e+00  6.016e+00   0.835   0.4201
## logSugar       -1.128e+00  1.169e+00  -0.965   0.3537
## logSLA          2.001e+00  2.116e+00   0.946   0.3629
## slope          -4.049e-02  6.403e-02  -0.632   0.5390
## SiteMaharira   -6.364e+00  2.114e+00  -3.011   0.0109 *
## SiteMiaranony  -2.381e+00  9.264e-01  -2.571   0.0245 *
## SiteValohoaka  -3.789e+00  1.746e+00  -2.170   0.0508 .
## SiteVohiparara -3.964e+00  1.354e+00  -2.928   0.0127 *
## logFruitLength -3.843e+00  2.013e+00  -1.910   0.0804 .
## logFat         -1.494e-01  1.063e+00  -0.141   0.8905
## logFruitWidth   4.574e+00  1.957e+00   2.337   0.0376 *
## logProtein      3.017e-01  5.010e-01   0.602   0.5583
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.2466 on 12 degrees of freedom
## Multiple R-squared:  0.8633, Adjusted R-squared:  0.6583
## F-statistic: 4.211 on 18 and 12 DF,  p-value: 0.007305
```

```
PE_lm_3 <- update(PE_lm_2,~.-logFat)
summary(PE_lm_3)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##     logSeedWidth + logTannins + roughness + long + logSugar +
##     logSLA + slope + Site + logFruitLength + logFruitWidth +
##     logProtein, data = PE_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.26120 -0.08857 -0.01069  0.13935  0.30040
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.815e+02  2.592e+02  -2.243  0.04293 *
## logSeedLength   1.933e+00  1.705e+00   1.133  0.27754
## logNitrogen     7.214e-01  2.475e+00   0.292  0.77527
## lat            -1.586e+01  5.818e+00  -2.726  0.01730 *
## logSeedWidth   -4.512e+00  2.066e+00  -2.185  0.04783 *
## logTannins      9.502e+00  4.465e+00   2.128  0.05303 .
## roughness       5.238e-04  1.549e-03   0.338  0.74063
## long            5.256e+00  5.560e+00   0.945  0.36168
## logSugar       -1.184e+00  1.059e+00  -1.118  0.28374
## logSLA          2.029e+00  2.026e+00   1.001  0.33487
## slope          -4.181e-02  6.089e-02  -0.687  0.50437
## SiteMaharira   -6.378e+00  2.030e+00  -3.141  0.00780 **
## SiteMiaranony  -2.412e+00  8.652e-01  -2.788  0.01537 *
## SiteValohoaka  -3.806e+00  1.675e+00  -2.272  0.04070 *
## SiteVohiparara -3.966e+00  1.302e+00  -3.047  0.00936 **
## logFruitLength -3.756e+00  1.840e+00  -2.041  0.06207 .
## logFruitWidth   4.547e+00  1.872e+00   2.428  0.03043 *
## logProtein      2.903e-01  4.754e-01   0.611  0.55196
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2371 on 13 degrees of freedom
## Multiple R-squared:  0.8631, Adjusted R-squared:  0.6841
## F-statistic: 4.821 on 17 and 13 DF,  p-value: 0.003163
```

```
PE_lm_4 <- update(PE_lm_3,~.-logNitrogen)
summary(PE_lm_4)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + roughness + long + logSugar + logSLA + slope +
##     Site + logFruitLength + logFruitWidth + logProtein, data = PE_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.26061 -0.10071 -0.01784  0.13681  0.31009
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.888e+02  2.494e+02  -2.361  0.03327 *
## logSeedLength   1.793e+00  1.583e+00   1.133  0.27616
## lat            -1.594e+01  5.619e+00  -2.838  0.01317 *
## logSeedWidth   -4.301e+00  1.870e+00  -2.300  0.03735 *
## logTannins      9.105e+00  4.111e+00   2.215  0.04387 *
## roughness       5.917e-04  1.480e-03   0.400  0.69537
## long            5.379e+00  5.360e+00   1.004  0.33261
## logSugar       -1.278e+00  9.737e-01  -1.313  0.21030
## logSLA          2.185e+00  1.889e+00   1.156  0.26691
## slope          -4.265e-02  5.880e-02  -0.725  0.48018
## SiteMaharira   -6.411e+00  1.960e+00  -3.271  0.00557 **
## SiteMiaranony  -2.429e+00  8.347e-01  -2.910  0.01142 *
## SiteValohoaka  -3.819e+00  1.619e+00  -2.359  0.03337 *
## SiteVohiparara -3.980e+00  1.258e+00  -3.164  0.00690 **
## logFruitLength -3.811e+00  1.769e+00  -2.154  0.04919 *
## logFruitWidth   4.713e+00  1.724e+00   2.734  0.01614 *
## logProtein      2.695e-01  4.544e-01   0.593  0.56253
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2293 on 14 degrees of freedom
## Multiple R-squared:  0.8622, Adjusted R-squared:  0.7047
## F-statistic: 5.475 on 16 and 14 DF,  p-value: 0.001326
```

```
PE_lm_5 <- update(PE_lm_4,~.-roughness)
summary(PE_lm_5)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
```

```
##      logTannins + long + logSugar + logSLA + slope + Site + logFruitLength +
##      logFruitWidth + logProtein, data = PE_subset)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.27681 -0.09093 -0.01362  0.13810  0.31439
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -613.82134  234.54381  -2.617  0.01943 *
## logSeedLength    1.68479    1.51480   1.112  0.28355
## lat            -15.92105    5.45871  -2.917  0.01063 *
## logSeedWidth    -4.27186    1.81560  -2.353  0.03270 *
## logTannins       9.34760    3.95071   2.366  0.03187 *
## long             5.92625    5.03443   1.177  0.25748
## logSugar        -1.14654    0.89004  -1.288  0.21720
## logSLA           2.10392    1.82509   1.153  0.26704
## slope           -0.02153    0.02505  -0.859  0.40368
## SiteMaharira    -6.28613    1.87993  -3.344  0.00444 **
## SiteMiaranony   -2.40596    0.80911  -2.974  0.00947 **
## SiteValohoaka   -3.78344    1.57032  -2.409  0.02929 *
## SiteVohiparara  -3.95896    1.22102  -3.242  0.00547 **
## logFruitLength  -3.74551    1.71189  -2.188  0.04492 *
## logFruitWidth    4.57577    1.64113   2.788  0.01378 *
## logProtein       0.20320    0.41102   0.494  0.62819
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2228 on 15 degrees of freedom
## Multiple R-squared:  0.8606, Adjusted R-squared:  0.7212
## F-statistic: 6.175 on 15 and 15 DF,  p-value: 0.0005424
```

```
PE_lm_6 <- update(PE_lm_5,~.-logProtein)
summary(PE_lm_6)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##      logTannins + long + logSugar + logSLA + slope + Site + logFruitLength +
##      logFruitWidth, data = PE_subset)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.26266 -0.10602 -0.04387  0.13888  0.31668
##
```

```
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -625.88954  227.69558  -2.749  0.01427 *
## logSeedLength      1.93027    1.39691   1.382  0.18602
## lat              -15.44855    5.24596  -2.945  0.00951 **
## logSeedWidth      -4.57619    1.66724  -2.745  0.01439 *
## logTannins        10.28271    3.38563   3.037  0.00785 **
## long               6.42791    4.81328   1.335  0.20042
## logSugar          -0.97721    0.80187  -1.219  0.24064
## logSLA             1.75489    1.64280   1.068  0.30127
## slope             -0.02036    0.02434  -0.836  0.41527
## SiteMaharira      -6.02734    1.76244  -3.420  0.00351 **
## SiteMiaranony     -2.32467    0.77330  -3.006  0.00837 **
## SiteValohoaka     -3.57052    1.47403  -2.422  0.02766 *
## SiteVohiparara    -3.83591    1.16682  -3.287  0.00464 **
## logFruitLength    -4.18674    1.42595  -2.936  0.00969 **
## logFruitWidth      4.75715    1.56137   3.047  0.00769 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2174 on 16 degrees of freedom
## Multiple R-squared:  0.8584, Adjusted R-squared:  0.7344
## F-statistic: 6.925 on 14 and 16 DF,  p-value: 0.0002179
```

```
PE_lm_7 <- update(PE_lm_6,~.-slope)
summary(PE_lm_7)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + long + logSugar + logSLA + Site + logFruitLength +
##     logFruitWidth, data = PE_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.26273 -0.11441 -0.01438  0.12357  0.36278
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -649.2846   223.9647  -2.899  0.00998 **
## logSeedLength     1.8431     1.3806   1.335  0.19951
## lat             -14.2011     4.9848  -2.849  0.01110 *
## logSeedWidth     -4.5692     1.6524  -2.765  0.01324 *
## logTannins       10.2645     3.3555   3.059  0.00710 **
## long              7.5086     4.5954   1.634  0.12065
```

```
## logSugar          -0.8093      0.7694  -1.052   0.30761
## logSLA             1.0744      1.4145   0.760   0.45791
## SiteMaharira      -5.6225      1.6796  -3.347   0.00382 **
## SiteMiaranony     -2.3254      0.7664  -3.034   0.00749 **
## SiteValohoaka     -3.3010      1.4256  -2.316   0.03334 *
## SiteVohiparara    -3.4842      1.0788  -3.230   0.00492 **
## logFruitLength    -4.3215      1.4042  -3.077   0.00683 **
## logFruitWidth      4.7768      1.5473   3.087   0.00669 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2155 on 17 degrees of freedom
## Multiple R-squared:  0.8522, Adjusted R-squared:  0.7391
## F-statistic: 7.538 on 13 and 17 DF,  p-value: 0.0001024
```

```
PE_lm_8 <- update(PE_lm_7,~.-logSLA)
summary(PE_lm_8)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth +
##     logTannins + long + logSugar + Site + logFruitLength + logFruitWidth,
##     data = PE_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.27923 -0.12564 -0.00001  0.12339  0.38155
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -732.9258   192.7193  -3.803  0.00130 **
## logSeedLength     1.4129     1.2443   1.136  0.27105
## lat             -14.2290     4.9257  -2.889  0.00978 **
## logSeedWidth     -4.4037     1.6186  -2.721  0.01402 *
## logTannins        9.9684     3.2934   3.027  0.00725 **
## long              9.3117     3.8883   2.395  0.02772 *
## logSugar         -0.6236     0.7209  -0.865  0.39844
## SiteMaharira     -5.5682     1.6583  -3.358  0.00350 **
## SiteMiaranony    -2.4462     0.7409  -3.302  0.00397 **
## SiteValohoaka    -3.2980     1.4087  -2.341  0.03094 *
## SiteVohiparara   -3.4004     1.0604  -3.207  0.00489 **
## logFruitLength   -4.3436     1.3873  -3.131  0.00577 **
## logFruitWidth     4.9052     1.5199   3.227  0.00467 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## 
## Residual standard error: 0.2129 on 18 degrees of freedom
## Multiple R-squared:  0.8471, Adjusted R-squared:  0.7452
## F-statistic: 8.313 on 12 and 18 DF,  p-value: 4.364e-05
```

```
PE_lm_9 <- update(PE_lm_8,~.-logSugar)
summary(PE_lm_9)
```

```
## 
## Call:
## lm(formula = Predicted ~ logSeedLength + lat + logSeedWidth + 
##       logTannins + long + Site + logFruitLength + logFruitWidth, 
##       data = PE_subset)
## 
## Residuals:
##       Min       1Q    Median       3Q       Max
## -0.26752 -0.11826 -0.03062  0.13223  0.41413
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -675.4097   179.6813  -3.759  0.00133 **
## logSeedLength     1.3915     1.2358   1.126  0.27418
## lat             -12.9520     4.6680  -2.775  0.01207 *
## logSeedWidth     -4.5343     1.6009  -2.832  0.01064 *
## logTannins        9.9425     3.2714   3.039  0.00675 **
## long              8.6058     3.7764   2.279  0.03441 *
## SiteMaharira     -5.0124     1.5185  -3.301  0.00376 **
## SiteMiaranony    -2.2461     0.6992  -3.212  0.00459 **
## SiteValohoaka    -2.9182     1.3296  -2.195  0.04081 *
## SiteVohiparara   -3.1832     1.0234  -3.110  0.00576 **
## logFruitLength   -3.8933     1.2774  -3.048  0.00662 **
## logFruitWidth     5.0400     1.5018   3.356  0.00332 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.2115 on 19 degrees of freedom
## Multiple R-squared:  0.8408, Adjusted R-squared:  0.7486
## F-statistic: 9.122 on 11 and 19 DF,  p-value: 1.918e-05
```

```
PE_lm_10 <- update(PE_lm_9,~.-logSeedLength)
summary(PE_lm_10)
```

```
## 
## Call:
## lm(formula = Predicted ~ lat + logSeedWidth + logTannins + long + 
##       Site + logFruitLength + logFruitWidth, data = PE_subset)
```

```
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.34149 -0.11743 -0.01979  0.12201  0.43437
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -686.0190   180.6319  -3.798  0.00113 **
## lat             -12.6711     4.6925  -2.700  0.01377 *
## logSeedWidth     -3.3152     1.1872  -2.793  0.01124 *
## logTannins        9.5931     3.2784   2.926  0.00835 **
## long              8.9559     3.7887   2.364  0.02832 *
## SiteMaharira     -4.7688     1.5131  -3.152  0.00502 **
## SiteMiaranony    -2.1405     0.6975  -3.069  0.00606 **
## SiteValohoaka    -2.8374     1.3366  -2.123  0.04644 *
## SiteVohiparara   -3.0696     1.0252  -2.994  0.00717 **
## logFruitLength   -3.5793     1.2549  -2.852  0.00985 **
## logFruitWidth     4.9420     1.5093   3.274  0.00379 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.2129 on 20 degrees of freedom
## Multiple R-squared:  0.8302, Adjusted R-squared:  0.7452
## F-statistic: 9.776 on 10 and 20 DF,  p-value: 1.024e-05
```

```
AIC(PE_lm_1, PE_lm_2, PE_lm_3, PE_lm_4, PE_lm_5, PE_lm_6, PE_lm_7, PE_lm_8, PE_lm_9, PE_
```

```
##           df       AIC
## PE_lm_1   21 13.718151
## PE_lm_2   20 11.759641
## PE_lm_3   19  9.810641
## PE_lm_4   18  8.012610
## PE_lm_5   17  6.364464
## PE_lm_6   16  4.865534
## PE_lm_7   15  4.192017
## PE_lm_8   14  3.226645
## PE_lm_9   13  2.489078
## PE_lm_10  12  2.491676
```

```
#PE_lm 9 and 10 have the lowest and therefore the best AIC scores
#I decided that PE_lm_10 is the best model, because it only contains significant varia
summary(PE_lm_10)
```

```
## 
## Call:
## lm(formula = Predicted ~ lat + logSeedWidth + logTannins + long +
```

```
##      Site + logFruitLength + logFruitWidth, data = PE_subset)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -0.34149 -0.11743 -0.01979  0.12201  0.43437
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -686.0190   180.6319  -3.798  0.00113 **
## lat            -12.6711     4.6925  -2.700  0.01377 *
## logSeedWidth    -3.3152     1.1872  -2.793  0.01124 *
## logTannins       9.5931     3.2784   2.926  0.00835 **
## long             8.9559     3.7887   2.364  0.02832 *
## SiteMaharira    -4.7688     1.5131  -3.152  0.00502 **
## SiteMiaranony   -2.1405     0.6975  -3.069  0.00606 **
## SiteValohoaka   -2.8374     1.3366  -2.123  0.04644 *
## SiteVohiparara  -3.0696     1.0252  -2.994  0.00717 **
## logFruitLength  -3.5793     1.2549  -2.852  0.00985 **
## logFruitWidth    4.9420     1.5093   3.274  0.00379 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2129 on 20 degrees of freedom
## Multiple R-squared:  0.8302, Adjusted R-squared:  0.7452
## F-statistic: 9.776 on 10 and 20 DF,  p-value: 1.024e-05

#lat, logseedwidth, logtannins, long, siteMaharira, SiteMiaranony, SiteValohoaka, Site

#Lepilemur_microdon has the lowest average density of all of the lemurs analyzed
LM_subset <- filter(trait_data2, Species == "Lepilemur_microdon")

LM_lm_1<- lm(data = LM_subset, Predicted ~ logSeedLength + logNitrogen + lat + logSeedWi
summary(LM_lm_1)


##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##      logSeedWidth + logTannins + roughness + long + logSugar +
##      logSLA + slope + Site + logFruitLength + logFat + aspect +
##      logFruitWidth + logProtein, data = LM_subset)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -0.0180194 -0.0093517 -0.0007755  0.0102822  0.0195459
##
```

78

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      40.7625312 30.8494729   1.321  0.23454
## logSeedLength    -0.2750299  0.3059723  -0.899  0.40335
## logNitrogen      -0.5156004  0.3101388  -1.662  0.14748
## lat               0.4433133  0.6716103   0.660  0.53371
## logSeedWidth      0.3699227  0.3178761   1.164  0.28871
## logTannins       -1.5694754  0.9186961  -1.708  0.13843
## roughness         0.0002068  0.0001865   1.109  0.30986
## long             -0.6594290  0.7086504  -0.931  0.38800
## logSugar          0.1266086  0.1819044   0.696  0.51246
## logSLA           -0.2753776  0.2376048  -1.159  0.29050
## slope            -0.0124940  0.0070395  -1.775  0.12627
## SiteMaharira      0.2668631  0.2347306   1.137  0.29894
## SiteMiaranony     0.0162262  0.1076119   0.151  0.88509
## SiteValohoaka    -0.0743192  0.1977142  -0.376  0.71993
## SiteVohiparara    0.0425892  0.1473915   0.289  0.78234
## logFruitLength   -0.4608627  0.2731234  -1.687  0.14250
## logFat           -0.1319226  0.1330252  -0.992  0.35963
## aspect           -0.0006395  0.0003063  -2.088  0.08180 .
## logFruitWidth     0.7974165  0.2014771   3.958  0.00747 **
## logProtein        0.1367226  0.0832653   1.642  0.15170
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02404 on 6 degrees of freedom
## Multiple R-squared:  0.9916, Adjusted R-squared:  0.9648
## F-statistic: 37.11 on 19 and 6 DF,  p-value: 0.0001088
```

```
#Woa, this has an adjusted r squared value of 96.5!
step(LM_lm_1)
```

```
## Start:  AIC=-191.98
## Predicted ~ logSeedLength + logNitrogen + lat + logSeedWidth +
##     logTannins + roughness + long + logSugar + logSLA + slope +
##     Site + logFruitLength + logFat + aspect + logFruitWidth +
##     logProtein
##
##                   Df Sum of Sq       RSS     AIC
## - lat              1 0.0002518 0.0037197 -192.16
## <none>                         0.0034679 -191.98
## - logSugar         1 0.0002800 0.0037479 -191.96
## - logSeedLength    1 0.0004670 0.0039348 -190.69
## - long             1 0.0005005 0.0039683 -190.47
## - logFat           1 0.0005684 0.0040363 -190.03
```

```
## - roughness        1 0.0007109 0.0041788 -189.13
## - logSLA           1 0.0007763 0.0042442 -188.73
## - logSeedWidth     1 0.0007827 0.0042506 -188.69
## - logProtein       1 0.0015583 0.0050262 -184.33
## - logNitrogen      1 0.0015974 0.0050653 -184.13
## - logFruitLength   1 0.0016456 0.0051135 -183.88
## - logTannins       1 0.0016868 0.0051547 -183.67
## - slope            1 0.0018207 0.0052885 -183.01
## - aspect           1 0.0025204 0.0059883 -179.78
## - logFruitWidth    1 0.0090538 0.0125216 -160.60
## - Site             4 0.0191389 0.0226068 -151.24
##
## Step:  AIC=-192.16
## Predicted ~ logSeedLength + logNitrogen + logSeedWidth + logTannins +
##      roughness + long + logSugar + logSLA + slope + Site + logFruitLength +
##      logFat + aspect + logFruitWidth + logProtein
##
##                   Df Sum of Sq       RSS      AIC
## - logSugar         1 0.0001592 0.0038788 -193.07
## <none>                         0.0037197 -192.16
## - logSeedLength    1 0.0004144 0.0041341 -191.41
## - logFat           1 0.0004452 0.0041649 -191.22
## - logSLA           1 0.0006574 0.0043771 -189.93
## - roughness        1 0.0006676 0.0043873 -189.87
## - logSeedWidth     1 0.0008502 0.0045699 -188.81
## - long             1 0.0009244 0.0046440 -188.39
## - logProtein       1 0.0015487 0.0052684 -185.11
## - logNitrogen      1 0.0017413 0.0054610 -184.17
## - logFruitLength   1 0.0017489 0.0054686 -184.14
## - logTannins       1 0.0017946 0.0055143 -183.92
## - slope            1 0.0019057 0.0056254 -183.40
## - aspect           1 0.0025025 0.0062221 -180.78
## - logFruitWidth    1 0.0088578 0.0125775 -162.48
## - Site             4 0.0221579 0.0258776 -149.72
##
## Step:  AIC=-193.07
## Predicted ~ logSeedLength + logNitrogen + logSeedWidth + logTannins +
##      roughness + long + logSLA + slope + Site + logFruitLength +
##      logFat + aspect + logFruitWidth + logProtein
##
##                   Df Sum of Sq      RSS      AIC
## - logFat           1  0.000292 0.004171 -193.18
## <none>                         0.003879 -193.07
## - logSLA           1  0.000499 0.004378 -191.92
## - logSeedLength    1  0.000526 0.004405 -191.76
```

```
## - logSeedWidth     1  0.000825 0.004703 -190.06
## - roughness        1  0.000889 0.004767 -189.71
## - long             1  0.001009 0.004888 -189.06
## - logTannins       1  0.001636 0.005515 -185.92
## - logProtein       1  0.001684 0.005563 -185.69
## - logFruitLength   1  0.001710 0.005589 -185.57
## - logNitrogen      1  0.002167 0.006045 -183.53
## - aspect           1  0.002380 0.006259 -182.63
## - slope            1  0.002753 0.006632 -181.12
## - logFruitWidth    1  0.008868 0.012747 -164.13
## - Site             4  0.044143 0.048022 -135.65
##
## Step:  AIC=-193.18
## Predicted ~ logSeedLength + logNitrogen + logSeedWidth + logTannins +
##     roughness + long + logSLA + slope + Site + logFruitLength +
##     aspect + logFruitWidth + logProtein
##
##                   Df Sum of Sq      RSS      AIC
## <none>                         0.004171 -193.18
## - logSeedLength    1  0.000599 0.004770 -191.69
## - logSLA           1  0.000655 0.004826 -191.39
## - logSeedWidth     1  0.000790 0.004960 -190.67
## - roughness        1  0.000830 0.005001 -190.46
## - long             1  0.000960 0.005131 -189.79
## - logTannins       1  0.001398 0.005569 -187.66
## - logProtein       1  0.001434 0.005605 -187.50
## - logFruitLength   1  0.001479 0.005650 -187.29
## - logNitrogen      1  0.002320 0.006491 -183.68
## - aspect           1  0.002551 0.006722 -182.77
## - slope            1  0.002691 0.006862 -182.24
## - logFruitWidth    1  0.008584 0.012755 -166.12
## - Site             4  0.047476 0.051647 -135.76
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + logSeedWidth +
##     logTannins + roughness + long + logSLA + slope + Site + logFruitLength +
##     aspect + logFruitWidth + logProtein, data = LM_subset)
##
## Coefficients:
##    (Intercept)   logSeedLength    logNitrogen    logSeedWidth      logTannins
##     40.2891721      -0.3045140     -0.5953817       0.3701160      -1.3256810
##      roughness            long         logSLA           slope     SiteMaharira
##      0.0002160      -0.8435321     -0.2183913      -0.0140026       0.1110546
##   SiteMiaranony   SiteValohoaka   SiteVohiparara   logFruitLength          aspect
```

81

```
##      0.0022528       -0.1800685       -0.0496010       -0.4238395       -0.0006351
##   logFruitWidth        logProtein
##      0.7445719         0.1257439
```

```
LM_lm_2 <- update(LM_lm_1,~.-logSugar)
summary(LM_lm_2)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##       logSeedWidth + logTannins + roughness + long + logSLA + slope +
##       Site + logFruitLength + logFat + aspect + logFruitWidth +
##       logProtein, data = LM_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.027058 -0.009030  0.000284  0.008859  0.021018
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)    42.5353174 29.5903209   1.437  0.19374
## logSeedLength  -0.3054045  0.2914784  -1.048  0.32957
## logNitrogen    -0.5747048  0.2870921  -2.002  0.08539 .
## lat             0.3055318  0.6176879   0.495  0.63600
## logSeedWidth    0.3667815  0.3059154   1.199  0.26955
## logTannins     -1.4126995  0.8572288  -1.648  0.14335
## roughness       0.0002349  0.0001752   1.341  0.22194
## long           -0.7553176  0.6690416  -1.129  0.29612
## logSLA         -0.1956820  0.2003817  -0.977  0.36133
## slope          -0.0143648  0.0062620  -2.294  0.05548 .
## SiteMaharira    0.1961263  0.2036474   0.963  0.36759
## SiteMiaranony   0.0228324  0.1031696   0.221  0.83117
## SiteValohoaka  -0.1013079  0.1865984  -0.543  0.60403
## SiteVohiparara  0.0108326  0.1348919   0.080  0.93824
## logFruitLength -0.4578173  0.2628394  -1.742  0.12508
## logFat         -0.0833951  0.1090381  -0.765  0.46937
## aspect         -0.0006118  0.0002923  -2.093  0.07460 .
## logFruitWidth   0.7879081  0.1934694   4.073  0.00473 **
## logProtein      0.1428306  0.0796940   1.792  0.11620
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02314 on 7 degrees of freedom
## Multiple R-squared:  0.9909, Adjusted R-squared:  0.9674
## F-statistic: 42.26 on 18 and 7 DF,  p-value: 1.996e-05
```

```
LM_lm_2b <- update(LM_lm_2,~.-Site)
summary(LM_lm_2b)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + lat +
##      logSeedWidth + logTannins + roughness + long + logSLA + slope +
##      logFruitLength + logFat + aspect + logFruitWidth + logProtein,
##      data = LM_subset)
##
## Residuals:
##       Min        1Q     Median        3Q        Max
## -0.067832 -0.029507 -0.001111  0.019683  0.122162
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    29.8787490 47.0081671   0.636   0.5380
## logSeedLength   0.2205024  0.7160424   0.308   0.7639
## logNitrogen    -0.0587495  0.7293761  -0.081   0.9372
## lat             0.2836171  0.3663204   0.774   0.4551
## logSeedWidth   -0.5446463  0.4840781  -1.125   0.2845
## logTannins      0.2809909  1.4462475   0.194   0.8495
## roughness       0.0007370  0.0003927   1.877   0.0873 .
## long           -0.4583896  0.9293097  -0.493   0.6315
## logSLA         -0.7240697  0.5243772  -1.381   0.1947
## slope          -0.0297935  0.0160348  -1.858   0.0901 .
## logFruitLength -1.1272882  0.5515193  -2.044   0.0657 .
## logFat         -0.3162924  0.2931204  -1.079   0.3037
## aspect         -0.0003668  0.0004895  -0.749   0.4694
## logFruitWidth   1.2840497  0.4825329   2.661   0.0221 *
## logProtein      0.1938687  0.1544901   1.255   0.2355
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06434 on 11 degrees of freedom
## Multiple R-squared:  0.8892, Adjusted R-squared:  0.7482
## F-statistic: 6.305 on 14 and 11 DF,  p-value: 0.002042
```

```
LM_lm_3 <- update(LM_lm_2,~.-lat)
summary(LM_lm_3)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + logSeedWidth +
##      logTannins + roughness + long + logSLA + slope + Site + logFruitLength +
```

```
##      logFat + aspect + logFruitWidth + logProtein, data = LM_subset)
##
## Residuals:
##       Min       1Q    Median       3Q       Max
## -0.029173 -0.008715 -0.001060  0.009268  0.023847
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    41.3822521 28.0712660   1.474   0.1787
## logSeedLength  -0.2862881  0.2749281  -1.041   0.3282
## logNitrogen    -0.5774151  0.2731533  -2.114   0.0675 .
## logSeedWidth    0.3785118  0.2902396   1.304   0.2285
## logTannins     -1.4796778  0.8055157  -1.837   0.1035
## roughness       0.0002239  0.0001654   1.354   0.2128
## long           -0.8657510  0.6001791  -1.442   0.1871
## logSLA         -0.1934128  0.1906376  -1.015   0.3400
## slope          -0.0141719  0.0059475  -2.383   0.0443 *
## SiteMaharira    0.1005988  0.0614853   1.636   0.1404
## SiteMiaranony  -0.0046599  0.0827131  -0.056   0.9565
## SiteValohoaka  -0.1844208  0.0772258  -2.388   0.0440 *
## SiteVohiparara -0.0540842  0.0296621  -1.823   0.1057
## logFruitLength -0.4682733  0.2493134  -1.878   0.0972 .
## logFat         -0.0804141  0.1036044  -0.776   0.4600
## aspect         -0.0006159  0.0002780  -2.215   0.0576 .
## logFruitWidth   0.7655243  0.1790025   4.277   0.0027 **
## logProtein      0.1412182  0.0757751   1.864   0.0994 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02202 on 8 degrees of freedom
## Multiple R-squared:  0.9906, Adjusted R-squared:  0.9705
## F-statistic: 49.39 on 17 and 8 DF,  p-value: 3.045e-06
```

```
LM_lm_4 <- update(LM_lm_3,~.-logFat)
summary(LM_lm_4)
```

```
##
## Call:
## lm(formula = Predicted ~ logSeedLength + logNitrogen + logSeedWidth +
##      logTannins + roughness + long + logSLA + slope + Site + logFruitLength +
##      aspect + logFruitWidth + logProtein, data = LM_subset)
##
## Residuals:
##       Min       1Q    Median       3Q       Max
## -0.032389 -0.007740 -0.001133  0.010140  0.019265
```

```
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     40.2891721 27.4096918   1.470   0.17566
## logSeedLength   -0.3045140  0.2678049  -1.137   0.28487
## logNitrogen     -0.5953817  0.2660913  -2.238   0.05205 .
## logSeedWidth     0.3701160  0.2835595   1.305   0.22419
## logTannins      -1.3256810  0.7632604  -1.737   0.11642
## roughness        0.0002160  0.0001614   1.338   0.21364
## long            -0.8435321  0.5861054  -1.439   0.18395
## logSLA          -0.2183913  0.1837045  -1.189   0.26493
## slope           -0.0140026  0.0058107  -2.410   0.03926 *
## SiteMaharira     0.1110546  0.0586514   1.893   0.09083 .
## SiteMiaranony    0.0022528  0.0803954   0.028   0.97826
## SiteValohoaka   -0.1800685  0.0753015  -2.391   0.04047 *
## SiteVohiparara  -0.0496010  0.0284444  -1.744   0.11516
## logFruitLength  -0.4238395  0.2372317  -1.787   0.10765
## aspect          -0.0006351  0.0002707  -2.346   0.04358 *
## logFruitWidth    0.7445719  0.1730027   4.304   0.00198 **
## logProtein       0.1257439  0.0714724   1.759   0.11238
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02153 on 9 degrees of freedom
## Multiple R-squared:  0.9899, Adjusted R-squared:  0.9718
## F-statistic: 54.86 on 16 and 9 DF,  p-value: 5.229e-07
```

```
LM_lm_5 <- update(LM_lm_4,~.-logSeedLength)
summary(LM_lm_5)
```

```
##
## Call:
## lm(formula = Predicted ~ logNitrogen + logSeedWidth + logTannins +
##     roughness + long + logSLA + slope + Site + logFruitLength +
##     aspect + logFruitWidth + logProtein, data = LM_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.039313 -0.005687  0.001275  0.010570  0.021756
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     47.9161096 26.9627642   1.777   0.10592
## logNitrogen     -0.5492032  0.2667979  -2.058   0.06655 .
## logSeedWidth     0.1149899  0.1759103   0.654   0.52806
```

```
## logTannins     -1.1814790  0.7635954  -1.547  0.15284
## roughness       0.0001619  0.0001565   1.035  0.32518
## long           -0.9974038  0.5785619  -1.724  0.11544
## logSLA         -0.1838239  0.1838061  -1.000  0.34085
## slope          -0.0124309  0.0057260  -2.171  0.05508 .
## SiteMaharira    0.1311338  0.0567432   2.311  0.04343 *
## SiteMiaranony   0.0233732  0.0793577   0.295  0.77438
## SiteValohoaka  -0.1424759  0.0686395  -2.076  0.06466 .
## SiteVohiparara -0.0513998  0.0288134  -1.784  0.10476
## logFruitLength -0.5856430  0.1925762  -3.041  0.01244 *
## aspect         -0.0004780  0.0002362  -2.024  0.07052 .
## logFruitWidth   0.7210213  0.1742560   4.138  0.00202 **
## logProtein      0.0819899  0.0611056   1.342  0.20934
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02184 on 10 degrees of freedom
## Multiple R-squared:  0.9884, Adjusted R-squared:  0.971
## F-statistic: 56.77 on 15 and 10 DF,  p-value: 1.205e-07
```

```
LM_lm_6 <- update(LM_lm_5,~.-logSeedWidth)
summary(LM_lm_6)
```

```
##
## Call:
## lm(formula = Predicted ~ logNitrogen + logTannins + roughness +
##     long + logSLA + slope + Site + logFruitLength + aspect +
##     logFruitWidth + logProtein, data = LM_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.038937 -0.006791 -0.000514  0.009256  0.023038
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    41.9129355 24.6818487   1.698  0.11756
## logNitrogen    -0.4681992  0.2300407  -2.035  0.06664 .
## logTannins     -0.7466451  0.3650505  -2.045  0.06550 .
## roughness       0.0001298  0.0001446   0.897  0.38872
## long           -0.8638889  0.5270299  -1.639  0.12944
## logSLA         -0.2383968  0.1594328  -1.495  0.16297
## slope          -0.0117787  0.0054897  -2.146  0.05507 .
## SiteMaharira    0.1451866  0.0511279   2.840  0.01609 *
## SiteMiaranony   0.0355312  0.0751123   0.473  0.64543
## SiteValohoaka  -0.1114011  0.0482069  -2.311  0.04123 *
```

86

```
## SiteVohiparara -0.0565632  0.0269786  -2.097  0.05995 .
## logFruitLength -0.6487420  0.1622412  -3.999  0.00209 **
## aspect          -0.0003943  0.0001932  -2.041  0.06604 .
## logFruitWidth   0.7675966  0.1548287   4.958  0.00043 ***
## logProtein      0.0632472  0.0525376   1.204  0.25392
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02126 on 11 degrees of freedom
## Multiple R-squared:  0.9879, Adjusted R-squared:  0.9725
## F-statistic: 64.14 on 14 and 11 DF,  p-value: 1.773e-08
```

```
LM_lm_7 <- update(LM_lm_6,~.-roughness)
summary(LM_lm_7)
```

```
##
## Call:
## lm(formula = Predicted ~ logNitrogen + logTannins + long + logSLA +
##     slope + Site + logFruitLength + aspect + logFruitWidth +
##     logProtein, data = LM_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.039355 -0.007815  0.001196  0.009864  0.025295
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    39.8323796 24.3726138   1.634 0.128137
## logNitrogen    -0.4546580  0.2276760  -1.997 0.069023 .
## logTannins     -0.6818867  0.3549330  -1.921 0.078780 .
## long           -0.8152340  0.5199647  -1.568 0.142892
## logSLA         -0.2411413  0.1581054  -1.525 0.153125
## slope          -0.0073615  0.0024111  -3.053 0.010026 *
## SiteMaharira    0.1736610  0.0397648   4.367 0.000917 ***
## SiteMiaranony   0.0534859  0.0718091   0.745 0.470708
## SiteValohoaka  -0.0939140  0.0437339  -2.147 0.052889 .
## SiteVohiparara -0.0493131  0.0255310  -1.932 0.077379 .
## logFruitLength -0.6583225  0.1605712  -4.100 0.001473 **
## aspect         -0.0003357  0.0001804  -1.861 0.087408 .
## logFruitWidth   0.7090636  0.1392764   5.091 0.000266 ***
## logProtein      0.0436734  0.0474068   0.921 0.375071
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02109 on 12 degrees of freedom
```

```
## Multiple R-squared:  0.987,   Adjusted R-squared:  0.9729
## F-statistic: 70.15 on 13 and 12 DF,  p-value: 2.98e-09
```

```
LM_lm_8 <- update(LM_lm_7,~.-logProtein)
summary(LM_lm_8)
```

```
##
## Call:
## lm(formula = Predicted ~ logNitrogen + logTannins + long + logSLA +
##     slope + Site + logFruitLength + aspect + logFruitWidth, data = LM_subset)
##
## Residuals:
##       Min        1Q     Median        3Q        Max
## -0.040317 -0.009564   0.001203   0.008842   0.027429
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)     35.5897845 23.7938860    1.496 0.158595
## logNitrogen     -0.4918646  0.2227575   -2.208 0.045813 *
## logTannins      -0.4839877  0.2808956   -1.723 0.108572
## long            -0.7155416  0.5056110   -1.415 0.180516
## logSLA          -0.2946097  0.1462089   -2.015 0.065068 .
## slope           -0.0073181  0.0023966   -3.054 0.009236 **
## SiteMaharira     0.2032861  0.0232543    8.742 8.36e-07 ***
## SiteMiaranony    0.0662294  0.0700529    0.945 0.361686
## SiteValohoaka   -0.0642091  0.0293736   -2.186 0.047712 *
## SiteVohiparara  -0.0401553  0.0233790   -1.718 0.109584
## logFruitLength  -0.7486778  0.1263941   -5.923 5.04e-05 ***
## aspect          -0.0002436  0.0001493   -1.632 0.126671
## logFruitWidth    0.7196572  0.1379908    5.215 0.000167 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02097 on 13 degrees of freedom
## Multiple R-squared:  0.9861, Adjusted R-squared:  0.9733
## F-statistic: 76.81 on 12 and 13 DF,  p-value: 4.893e-10
```

```
LM_lm_9 <- update(LM_lm_8,~.-long)
summary(LM_lm_9)
```

```
##
## Call:
## lm(formula = Predicted ~ logNitrogen + logTannins + logSLA +
##     slope + Site + logFruitLength + aspect + logFruitWidth, data = LM_subset)
##
## Residuals:
```

```
##        Min        1Q    Median        3Q       Max
## -0.039923 -0.009305 -0.000107  0.011619  0.029678
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.9225655  0.4622099   4.160 0.000964 ***
## logNitrogen     -0.5577458  0.2255057  -2.473 0.026813 *
## logTannins      -0.5341104  0.2884610  -1.852 0.085291 .
## logSLA          -0.3480112  0.1462272  -2.380 0.032077 *
## slope           -0.0064561  0.0023995  -2.691 0.017575 *
## SiteMaharira     0.1987749  0.0238455   8.336 8.46e-07 ***
## SiteMiaranony   -0.0260644  0.0264790  -0.984 0.341654
## SiteValohoaka   -0.0863111  0.0257533  -3.351 0.004750 **
## SiteVohiparara  -0.0299286  0.0230167  -1.300 0.214497
## logFruitLength  -0.7779674  0.1290765  -6.027 3.11e-05 ***
## aspect          -0.0002188  0.0001535  -1.426 0.175815
## logFruitWidth    0.7214090  0.1428416   5.050 0.000177 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02171 on 14 degrees of freedom
## Multiple R-squared:  0.984,  Adjusted R-squared:  0.9713
## F-statistic: 78.03 on 11 and 14 DF,  p-value: 1.335e-10
```

```
LM_lm_10 <- update(LM_lm_9,~.-aspect)
summary(LM_lm_10)
```

```
##
## Call:
## lm(formula = Predicted ~ logNitrogen + logTannins + logSLA +
##     slope + Site + logFruitLength + logFruitWidth, data = LM_subset)
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -0.047895 -0.009684  0.000507  0.009117  0.027020
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)     1.958283   0.477161   4.104 0.000939 ***
## logNitrogen    -0.477762   0.225815  -2.116 0.051507 .
## logTannins     -0.409735   0.284268  -1.441 0.170032
## logSLA         -0.348304   0.151179  -2.304 0.035951 *
## slope          -0.006615   0.002478  -2.669 0.017497 *
## SiteMaharira    0.219426   0.019585  11.204 1.10e-08 ***
## SiteMiaranony  -0.024489   0.027352  -0.895 0.384746
```

```
## SiteValohoaka  -0.062570    0.020313  -3.080 0.007617 **
## SiteVohiparara -0.026888    0.023694  -1.135 0.274269
## logFruitLength -0.775461    0.133435  -5.812 3.43e-05 ***
## logFruitWidth   0.659863    0.140775   4.687 0.000292 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02244 on 15 degrees of freedom
## Multiple R-squared:  0.9816, Adjusted R-squared:  0.9694
## F-statistic: 80.11 on 10 and 15 DF,  p-value: 3.657e-11
```

```
LM_lm_11 <- update(LM_lm_10,~.-logTannins)
summary(LM_lm_11)
```

```
##
## Call:
## lm(formula = Predicted ~ logNitrogen + logSLA + slope + Site +
##     logFruitLength + logFruitWidth, data = LM_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.047689 -0.009712  0.000158  0.014724  0.028041
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.905131   0.491492   3.876 0.001339 **
## logNitrogen   -0.299725   0.195299  -1.535 0.144394
## logSLA        -0.346708   0.156183  -2.220 0.041223 *
## slope         -0.006858   0.002554  -2.685 0.016264 *
## SiteMaharira   0.215116   0.019997  10.758 9.85e-09 ***
## SiteMiaranony -0.014520   0.027340  -0.531 0.602646
## SiteValohoaka -0.058405   0.020772  -2.812 0.012534 *
## SiteVohiparara -0.022674  0.024292  -0.933 0.364481
## logFruitLength -0.762293  0.137532  -5.543 4.46e-05 ***
## logFruitWidth   0.587195   0.135792   4.324 0.000524 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02318 on 16 degrees of freedom
## Multiple R-squared:  0.9791, Adjusted R-squared:  0.9673
## F-statistic: 83.18 on 9 and 16 DF,  p-value: 1.005e-11
```

```
LM_lm_12 <- update(LM_lm_11,~.-logNitrogen)
summary(LM_lm_12)
```

```
##
```

```
## Call:
## lm(formula = Predicted ~ logSLA + slope + Site + logFruitLength +
##     logFruitWidth, data = LM_subset)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.042739 -0.011202  0.001897  0.014948  0.034419
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.176295   0.476566   4.567 0.000274 ***
## logSLA        -0.468250   0.139877  -3.348 0.003817 **
## slope         -0.007760   0.002583  -3.004 0.007979 **
## SiteMaharira   0.222237   0.020211  10.996 3.79e-09 ***
## SiteMiaranony -0.009928   0.028238  -0.352 0.729461
## SiteValohoaka -0.062951   0.021364  -2.947 0.009024 **
## SiteVohiparara -0.008559  0.023362  -0.366 0.718603
## logFruitLength -0.748885  0.142620  -5.251 6.50e-05 ***
## logFruitWidth  0.488035   0.124104   3.932 0.001073 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02409 on 17 degrees of freedom
## Multiple R-squared:  0.976,  Adjusted R-squared:  0.9647
## F-statistic: 86.39 on 8 and 17 DF,  p-value: 3.062e-12
```

```
#model 12 has the fewest non-significant variables

LM_lm_13 <- update(LM_lm_12,~.-Site)
summary(LM_lm_13)
```

```
##
## Call:
## lm(formula = Predicted ~ logSLA + slope + logFruitLength + logFruitWidth,
##     data = LM_subset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.08330 -0.06137 -0.01925  0.03721  0.20627
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.619227   0.968474   3.737  0.00122 **
## logSLA        -1.087907   0.307717  -3.535  0.00196 **
## slope         -0.009728   0.006489  -1.499  0.14868
```

```
## logFruitLength -0.882190   0.474771  -1.858  0.07723 .
## logFruitWidth   0.642035   0.422422   1.520  0.14345
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08391 on 21 degrees of freedom
## Multiple R-squared:  0.6402, Adjusted R-squared:  0.5717
## F-statistic: 9.343 on 4 and 21 DF,  p-value: 0.0001682
```

`AIC(LM_lm_1, LM_lm_2, LM_lm_2b, LM_lm_3, LM_lm_4, LM_lm_5, LM_lm_6, LM_lm_7, LM_lm_8, LM`

```
##           df        AIC
## LM_lm_1   21 -116.19538
## LM_lm_2   20 -116.17658
## LM_lm_2b  16  -59.24383
## LM_lm_3   19 -117.28334
## LM_lm_4   18 -117.39565
## LM_lm_5   17 -115.90558
## LM_lm_6   16 -116.81767
## LM_lm_7   15 -116.98058
## LM_lm_8   14 -117.20384
## LM_lm_9   13 -115.47838
## LM_lm_10  12 -113.95271
## LM_lm_11  11 -112.58016
## LM_lm_12  10 -111.00959
## LM_lm_13   6  -48.62531
```

#models 3, 4, and 8 have the best AIC values
#I choose LM_lm_9
#significant variables are logNitrogen, logTannins (marginally significant), logSLA, s
#this models explains about 97 of the variability in density (Adjusted R-squared = 0.9

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#Results

There is a significant difference in lemur densities between different sites ($F(4,254) = 3.469$, p = 0.009; Figure 2). In particular, a post-hoc Tukey HSD test revealed that there are significant differences in densities between Miaranony and Ampatsoana (p = 0.0287), Miaranony and Maharira (p = 0.031) and Vohiparara and Miaranony (p = 0.386) sites. However, visual analysis of lemur densities via boxplots boxplots (Figure 1) suggests that the higher lemur densities observed in Miaranony and Valohoaka are the result of outliers. An HSD post-hoc test from the R package "agricolae" (de Mendiburu 2020) indicates that the sites can be categorized into two main groups according to their lemur densities, with Miaranony in one group, Vohiparara, Ampatsona, and Maharira in another group, and Valohoaka in both groups. There is also a significant difference in lemur densities between different species (F

(8,250) = 16.79, p = <2e-16; Figure 3). The HSD post-hoc test indicates that lemur species can be categorized into four main groups according to their density (Table 2).

Group	Average population Density
- *Eulemur rubriventer,Propithecus edwardsi,Microcebus rufus*	2.72 - 3.80
- *Propithecus edwardsi,Microcebus rufus,Eulemur rufifrons*	2.31 - 3.03
- *Eulemur rufifrons ,Hapalemur griseus*	1.11 - 2.31
- *Hapalemur griseus,Varecia variegata ,Cheirogaleus crossleyi,Avahi laniger ,Lepilemur microdon*	0.24 - 1.11

Table 2. Groupings of lemur species according to their population densities.

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6   ## Question 2: What variables are related to differences in lemur densities?

```
print(density_aov_plot)
```

```
print(density_aov_plot2)
```

Our best model with site as an independent vaiable demonstrates that fruit nitrogen content, latitude, roughness, slope, fruit length, fruit width, and the sites were significantly related to lemur density. This model explains46.7% of the variance in lemur density. With every increase in one percentage of nitrogen on the log scale, lemur density increases by 11.310 individuals per square Km (p = 0.007). With every increase in one degree latitude, lemur density decreases by 28.030 individuals per square Km (p = 0.021). With every increase in one roughness unit, lemur density decreases by 0.007 individuals per square Km (p = 0.0.021). With every increase in one degree in slope, lemur density increases by 0.259 individuals per square Km (p = 0.0294). Site Maharira has 8.080 fewer lemurs per square Km (p =
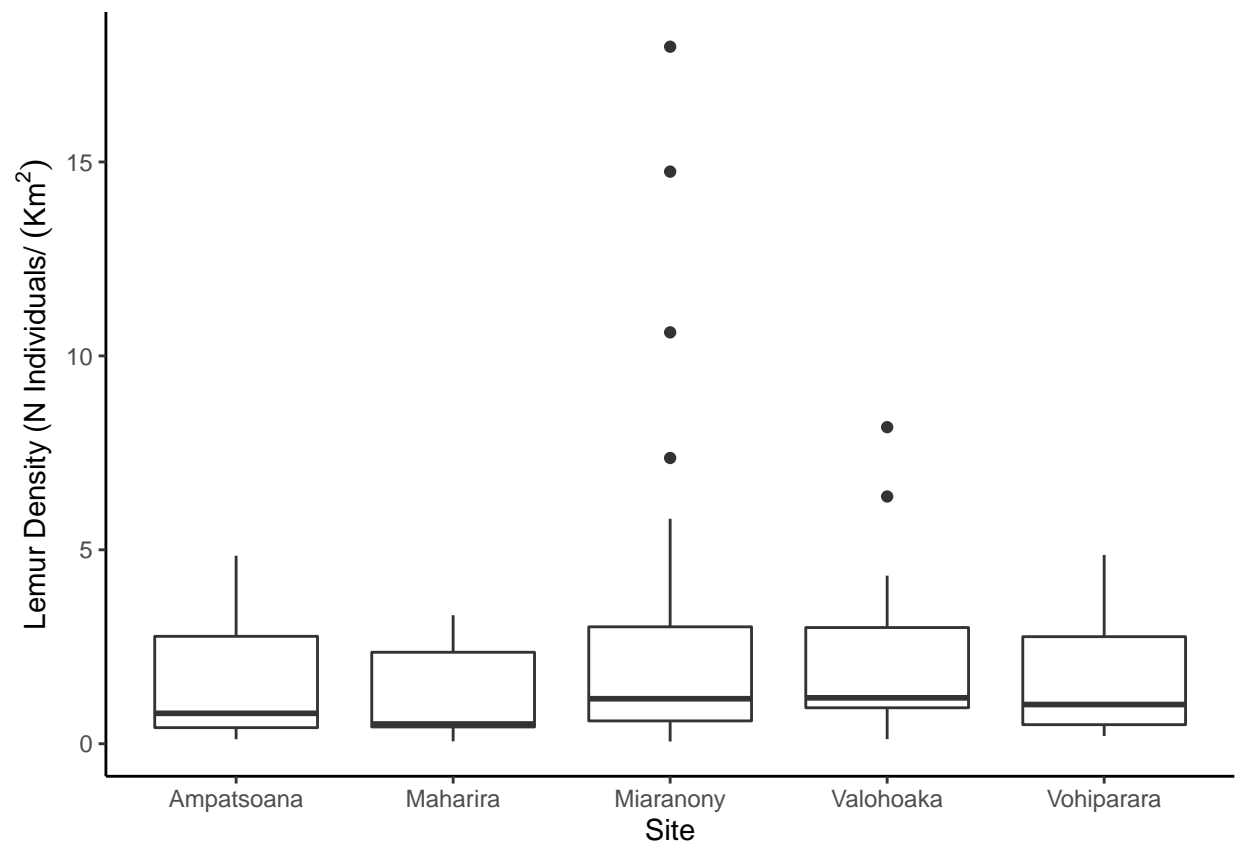
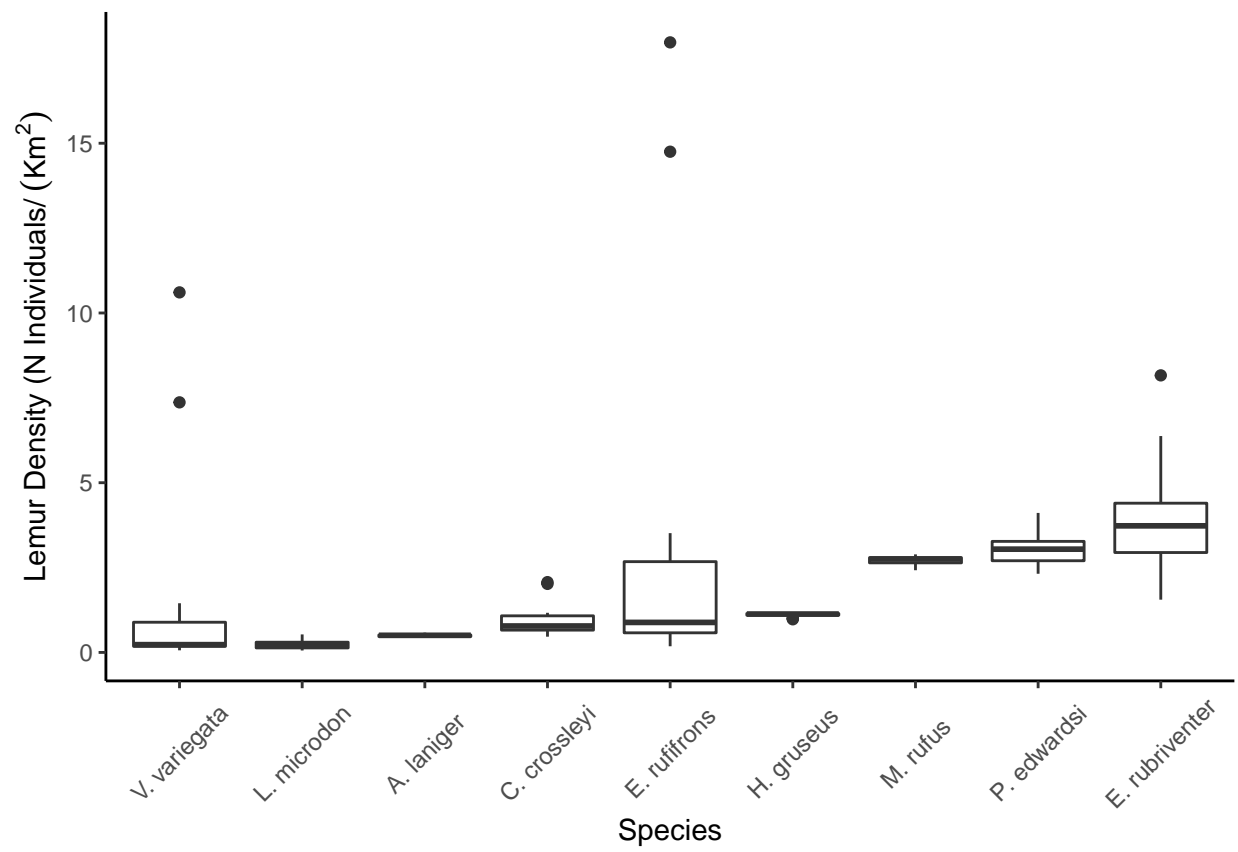Figure 2: Figure 2. Boxplot of lemur densities at each sampling site.

Figure 3: Figure 3. Boxplot of lemur densities for each species surveyed.

0.275) when compared to Ampatsona, whereas Valohoaka has 7.845 fewer (p = 0.0182) and Vohiparara has 6.291 fewer (0.02026). With every increase in one mm of mean fruit length on the log scale, lemur density increases by 8.711 individuals per square Km (p = 0.009). On the other hand, with every increase in one mm of mean fruit width on the log scale, lemur density decreases by 10.070 individuals per square Km (p = 0.002). When we included site as a random variable, only nitrogen content, fruit length, and fruit width were significantly related to lemur densities in the best model. However, this model explained less variation in lemur density (43.580%) than the model where it was included as an independent variable. With every increase in one percentage of mean nitrogen on the log scale, lemur density increases by 7.758 individuals per square Km (p = 0.002). With every increase in one mm of the mean fruit length, lemur density increases by 7.737 individuals per square Km (p = 0.00483). With every increase in one mm of the mean fruit width, lemur density decreases by 6.512 individuals per square Km (p = 0.0117).

In our species-specific models, we identified that lemur specis differ in their relationships to the habitat variables. Based on our best model for *Avahi laniger*, we found that log seed length, latitude, log seed width, log SLA, site Maharira, site Valohoaka, site Vohiparara, log fruit length, and log fruit width were related to the density of Avahi laniger (p < 0.001). This model explains 82.4% of variation in density. The model for the *Eulemur rubriventer* species indicated that log nitrogen, log SLA, slope, SiteMaharira, SiteMiaranony, SiteValohoaka (marginally), Site Vohiparara, log fruit length, and log fruit width are relevant to *Eulemur rubriventer* densities (p = 0.002). This model explains 56.95% of the variation in the density data. The model for Lepilemur microdon indicated that log nitrogen, log tannins (marginally), log SLA, slope, site Maharira, site Valohoaka, log fruit length, and log fruit width are significantly related to the density of this species (p < 0.001). The model explained 97.13% of the variability in density. The model for* Propithecus edwardsi* indicated that latitude, log seed width, log tannins, longitude, site Maharira, site Miaranony, siteValohoaka, siteVohiparara, log fruit length, and log fruit width are relevant to the densities of the species (p < 0.001). This model explained about 75% of the variability in the density of the species (Adjusted R-squared: 0.7452).

7   Summary and Conclusions

There is a significant difference in Lemur population density between different species and between different sites. Although Miaranony and Valohoaka have greater lemur densities than the other sites, this is likely driven by outliers. Ampatsoana, Maharira, and Vohiparara all have similar lemur densities. *Eulemur rubriventer, Propithecus edwardsi*, and *Microcebus rufus* all tend to have higher densities than the other lemur species, while *Varecia variegata, Lepilemur microdon, Avahi laniger*, and *Cheirogaleus crossleyi* tend to have lower densities. Our analyses demonstrate that these differences are related to fruit length, nitrogen content, and fruit width. Latitude, roughness, slope, and site also may be relevant, as indicated by the best linear model created using species and transect site as the only random effects. These results highlight the potential importance of plant functional traits in driving patterns of lemur density across a landscape. This is consistent with the literature; for example, lemur population sizes are known to be related to the presence of fruiting trees (Herrera et al. 2018). Latitude, roughness, and slope could also be expected to influence which plant species occur in different sites. However, differences in densities could also be reflective of life history characteristics or other variables that were not included in this study, such as human disturbance. These results could have management implications. For example, it could be beneficial to focus tree restoration efforts on species that contain the traits that are positively related to lemur densities, such as nitrogen content. In fact, restoration schemes based on lemur feeding trees have already been proposed in Madagascar (Steffens et al. 2020). Fruit length and fruit width are also related to lemur densities, although further studies would be needed to determine which fruit sizes and lengths best support various lemur species. Strategic decisions on which species to plant based could be made based off of the length and width of fruit provided by tree to best support the populations of specific lemur species.

Our analyses further demonstrated that the variables related to lemur density differ between the various lemur species, although fruit width and fruit length are related to the densities of each of the four species we analyzed in depth. Fruit characteristics such as tannin concentration, seed length, and seed width were relevant to the densities of certain lemur species, while they weren't found to be relevant to the densities of other lemur species. Similarly, landscape characteristics such as slope and latitude were found to be relevant to the densities of certain lemur species. The differences between the models of the individual lemur species suggests that traits of the lemurs might also be important in determining what habitat variables relate to their densities. Lemurs vary greatly in their diets, habitat preferences, and foraging ecology, and lemur social structure is related to ecological variables (Overdorff 1996).

Future studies ought to integrate other variables into the analysis of this question. For example, other studies could investigate how functional traits and climatic variables interact with anthropogenic disturbance to drive patterns in lemur densities. Human disturbance is known to impact mammal population densities in the neotropics (Tucker et al. 2021), so there might be similar dynamics in Madagascar. It would also be interesting to incorporate lemur functional traits to analyze if lemur diets, body sizes, and behavioral traits are significantly related to their densities in a given area. Furthermore, a similar study at a larger scale could be interesting because mouse lemur densities are related to biogeographical variables (Setash

et al. 2017), so it would be interesting to identify the biogeogrphical variables that are related to other species.

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