Comparison of Avian Clutch Size, Physical Characterists, and Mating Tactics

https://github.com/jcf55/Fahrenholz_Costes_ENV872_EDA_FinalProject

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1 Rationale and Research Questions

According to the study from which this data was extracted, avian body size and the evolution of birds over time is a highly debated subject matter. Generally, there is agreement around the idea that body size of bird species impacts other characteristics. Because of this, this project intends to explore the correlation between body size and various measurements and observations in our data.

First, we ask the question if female tail size predicts clutch size. Tail length has a significant impact on control and agility (Evans 1999). Longer tails increase crash risk as well as reduces the ability to maneuver (Evans 1999). We believe that this may have an overall negative impact on clutch size, as birds with longer tail lengths may be less efficient at collecting food for their young. Second, we will explore interactions between male tail length and methods of display, mating system, and resource sharing systems. Tail length likely has a negative impact on navigation, and collecting food, while having a positive impact on sexual display. Physical characteristics of males are evaluated by females in search of a mate.

2 Dataset Information

Our dataset consists of data that was collected starting in 2005 and was last updated in January of 2007. Data for this collection come from regions that include:

- Western Palearctic
- Neararctic
- Africa
- Australia
- New Zealand
- Antarctica

The complete dataset (represented below by the variable `birds`) includes 41 variables, and represents 125 families. According to the metadata, the majority of this information was gathered from ornithological handbooks, with some data obtained from personal communications with authors who published information on species bird groups. More information on the sources used can be found at: https://esapubs.org/archive/ecol/E088/096/metadata.htm (also in /Data/Raw in the .tex file)

3 Exploratory Analysis

```r
#dimensions
dim(birds)
```

```
## [1] 3769   41
```

```r
#column names
colnames(birds)
```

```
##  [1] "ï..Family"         "Species_number"    "Species_name"      "English_name"
##  [5] "Subspecies"        "M_mass"            "M_mass_N"          "F_mass"
##  [9] "F_mass_N"          "unsexed_mass"      "unsexed_mass_N"    "M_wing"
## [13] "M_wing_N"          "F_wing"            "F_wing_N"          "Unsexed_wing"
## [17] "Unsexed_wing_N"    "M_tarsus"          "M_tarsus_N"        "F_tarsus"
## [21] "F_tarsus_N"        "Unsexed_tarsus"    "Unsexed_tarsus_N" "M_bill"
## [25] "M_bill_N"          "F_bill"            "F_bill_N"          "Unsexed_bill"
## [29] "Unsexed_bill_N"    "M_tail"            "M_tail_N"          "F_tail"
## [33] "F_tail_N"          "Unsexed_tail"      "Unsexed_tail_N"    "Clutch_size"
## [37] "Egg_mass"          "Mating_System"     "Display"           "Resource"
## [41] "References"
```

```r
#variable types?
str(birds)
```

```
## 'data.frame':    3769 obs. of  41 variables:
##  $ ï..Family        : int  115 101 116 116 116 116 116 116 116 116 ...
##  $ Species_number   : int  5351 3964 5402 5398 5400 5401 5396 5405 5404 5397 ...
##  $ Species_name     : chr  "Acanthagenys rufogularis" "Acanthisitta chloris" "Acanthiz
##  $ English_name     : chr  "Spiny-cheeked Honeyeater" "Rifleman" "Yellow-rumped Thornb
##  $ Subspecies       : chr  "-999" "-999" "leighi" "ewingii" ...
##  $ M_mass           : num  47.1 5.6 9.4 7.2 7.2 5.8 6.8 7.6 6.5 7.4 ...
##  $ M_mass_N         : int  4 33 25 16 43 16 10 25 27 37 ...
##  $ F_mass           : num  41.4 7 9.8 6.7 6.9 5.7 6.7 7.4 6.3 6.5 ...
##  $ F_mass_N         : int  5 20 16 19 76 12 7 27 23 20 ...
##  $ unsexed_mass     : num  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ unsexed_mass_N   : int  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ M_wing           : num  113.1 47.8 57.8 52.7 48.9 ...
##  $ M_wing_N         : int  25 10 25 21 28 29 11 36 25 52 ...
##  $ F_wing           : num  107.5 51.4 57.6 51 47 ...
##  $ F_wing_N         : num  21 10 26 22 26 25 7 26 29 30 ...
##  $ Unsexed_wing     : num  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ Unsexed_wing_N   : int  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ M_tarsus         : num  26.2 19.1 17.7 21.3 18 18.4 18.5 17.5 17.4 20.3 ...
##  $ M_tarsus_N       : int  10 10 23 21 28 29 11 36 25 51 ...
##  $ F_tarsus         : num  25.7 19.7 17.4 21.7 17.8 17.6 18.4 17.5 17.3 19.3 ...
##  $ F_tarsus_N       : int  5 7 24 23 25 25 7 25 27 29 ...
```

```
##  $ Unsexed_tarsus  : num  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ Unsexed_tarsus_N: int  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ M_bill          : num  26.8 13.2 11.9 11 11.3 9.7 11.6 10.2 10 11 ...
##  $ M_bill_N        : int  8 6 24 21 27 28 11 26 24 51 ...
##  $ F_bill          : num  25.5 14.4 11.7 10.9 11.4 9.6 11.2 9.9 10 10.5 ...
##  $ F_bill_N        : num  10 7 26 23 25 24 7 26 28 29 ...
##  $ Unsexed_bill    : num  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ Unsexed_bill_N  : int  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ M_tail          : num  113.4 23.3 40.8 47.8 36.3 ...
##  $ M_tail_N        : int  25 10 28 21 34 28 11 36 14 51 ...
##  $ F_tail          : num  106.4 22.1 39.3 46.8 35.4 ...
##  $ F_tail_N        : int  21 7 26 23 55 25 6 26 10 30 ...
##  $ Unsexed_tail    : num  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ Unsexed_tail_N  : int  -999 -999 -999 -999 -999 -999 -999 -999 -999 -999 ...
##  $ Clutch_size     : num  2.2 4 3.5 3.5 3 3 2.5 3 3 3 ...
##  $ Egg_mass        : num  5.45 1.34 1.44 1.46 1.35 0.93 -999 1.32 1.34 1.4 ...
##  $ Mating_System   : int  2 2 2 2 2 -999 -999 2 2 2 ...
##  $ Display         : int  3 1 1 1 -999 1 -999 2 -999 1 ...
##  $ Resource        : int  2 2 1 0 1 1 -999 0 -999 2 ...
##  $ References      : chr  "1, 21" "21" "1, 22, 31 " "22, 31" ...
```

```
#look at the first few lines
head(birds)
```

```
##   ï..Family Species_number             Species_name             English_name
## 1       115           5351 Acanthagenys rufogularis Spiny-cheeked Honeyeater
## 2       101           3964      Acanthisitta chloris                 Rifleman
## 3       116           5402    Acanthiza chrysorrhoa  Yellow-rumped Thornbill
## 4       116           5398        Acanthiza ewingii      Tasmanian Thornbill
## 5       116           5400       Acanthiza inornata        Western Thornbill
## 6       116           5401       Acanthiza iredalei Slender-billed Thornbill
##   Subspecies M_mass M_mass_N F_mass F_mass_N unsexed_mass unsexed_mass_N M_wing
## 1       -999   47.1        4   41.4        5         -999           -999  113.1
## 2       -999    5.6       33    7.0       20         -999           -999   47.8
## 3     leighi    9.4       25    9.8       16         -999           -999   57.8
## 4    ewingii    7.2       16    6.7       19         -999           -999   52.7
## 5       -999    7.2       43    6.9       76         -999           -999   48.9
## 6   iredalei    5.8       16    5.7       12         -999           -999   48.8
##   M_wing_N F_wing F_wing_N Unsexed_wing Unsexed_wing_N M_tarsus M_tarsus_N
## 1       25  107.5       21         -999           -999     26.2         10
## 2       10   51.4       10         -999           -999     19.1         10
## 3       25   57.6       26         -999           -999     17.7         23
## 4       21   51.0       22         -999           -999     21.3         21
## 5       28   47.0       26         -999           -999     18.0         28
## 6       29   47.5       25         -999           -999     18.4         29
```

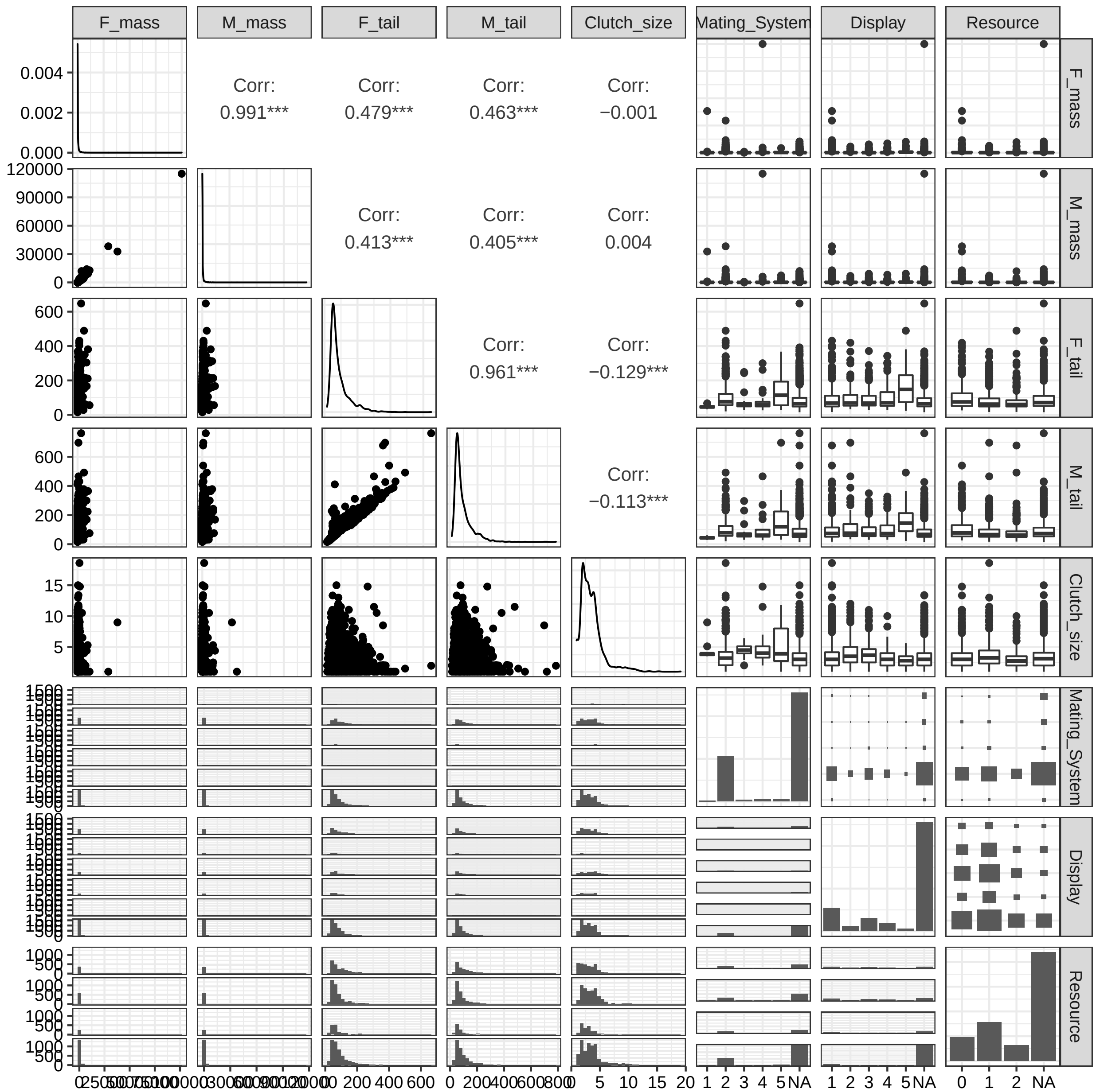
```
##   F_tarsus F_tarsus_N Unsexed_tarsus Unsexed_tarsus_N M_bill M_bill_N F_bill
## 1     25.7          5           -999             -999   26.8        8   25.5
## 2     19.7          7           -999             -999   13.2        6   14.4
## 3     17.4         24           -999             -999   11.9       24   11.7
## 4     21.7         23           -999             -999   11.0       21   10.9
## 5     17.8         25           -999             -999   11.3       27   11.4
## 6     17.6         25           -999             -999    9.7       28    9.6
##   F_bill_N Unsexed_bill Unsexed_bill_N M_tail M_tail_N F_tail F_tail_N
## 1       10         -999           -999  113.4       25  106.4       21
## 2        7         -999           -999   23.3       10   22.1        7
## 3       26         -999           -999   40.8       28   39.3       26
## 4       23         -999           -999   47.8       21   46.8       23
## 5       25         -999           -999   36.3       34   35.4       55
## 6       24         -999           -999   40.6       28   39.6       25
##   Unsexed_tail Unsexed_tail_N Clutch_size Egg_mass Mating_System Display
## 1         -999           -999         2.2     5.45             2       3
## 2         -999           -999         4.0     1.34             2       1
## 3         -999           -999         3.5     1.44             2       1
## 4         -999           -999         3.5     1.46             2       1
## 5         -999           -999         3.0     1.35             2    -999
## 6         -999           -999         3.0     0.93          -999       1
##   Resource References
## 1        2      1, 21
## 2        2         21
## 3        1 1, 22, 31
## 4        0     22, 31
## 5        1     22, 31
## 6        1     22, 31
```

```
# make sure family column is named correctly
colnames(birds)[1] <- "Family"
```

```
# Convert -999 to NAs and add genus column
birds <- birds %>%
  na_if(., -999) %>%
  separate(Species_name,
           sep = " ",
           into = c("Genus", "Sp"),
           remove = FALSE)

# Subset to columns we are interested in
birds.subset <- birds %>%
  select(Family, Species_name, Genus, F_mass, M_mass,
         F_tail, M_tail, Clutch_size, Mating_System,
         Display, Resource)
```

```r
# This function allows calculation of mode for categorical variables
Mode <- function(x) {
  ux <- unique(x)
  ux[which.max(tabulate(match(x, ux)))]
}

# Group male tail length by mating system to graph later
birds.mating.tail <- birds.subset %>%
  group_by(Mating_System) %>%
  summarise(M_tail = mean(M_tail, na.rm = TRUE))

# Group by family, average by mean or mode
birds.family <- birds.subset %>%
  group_by(Family) %>%
  summarise(F_mass = mean(F_mass, na.rm = TRUE),
            M_mass = mean(M_mass, na.rm = TRUE),
            F_tail = mean(F_tail, na.rm = TRUE),
            M_tail = mean(M_tail, na.rm = TRUE),
            Clutch_size = mean(Clutch_size, na.rm = TRUE),
            Common_Mating_System = Mode(Mating_System),
            Common_Display = Mode(Display),
            Common_Resource = Mode(Resource)) %>%
  filter(!is.na(Clutch_size), !is.na(F_tail),
         !is.na(F_mass), !is.na(M_tail))

# Set categorical variables as factors
birds.subset$Family <- as.factor(birds.subset$Family)
birds.subset$Mating_System <- as.factor(birds.subset$Mating_System)
birds.subset$Display <- as.factor(birds.subset$Display)
birds.subset$Resource <- as.factor(birds.subset$Resource)

# Write the csv file into our Processed data folder
write.csv(birds.subset, file = "../Data/Processed/birds_subset.csv")
write.csv(birds.family, file = "../Data/Processed/birds_family.csv")
```

```r
# View variable distributions and relationships
gg.birds.subset <- subset(birds.subset, select = -c(Family, Species_name, Genus))
ggpairs(gg.birds.subset)
```




```r
# View the counts of our factor variables
count(birds.subset, vars = Mating_System)
```

```
##   vars    n
## 1    1   23
## 2    2 1057
## 3    3   36
## 4    4   46
## 5    5   56
## 6 <NA> 2551
```

```r
# SUPER uneven! This could be an issue contributing to uneven variances?
count(birds.subset, vars = Display) # Also uneven but not quite as bad
```

```
##   vars    n
## 1    1  549
## 2    2  118
## 3    3  311
## 4    4  186
## 5    5   54
## 6 <NA> 2551
```

```r
count(birds.subset, vars = Resource) # Looks fine
```

```
##   vars    n
## 1    0  480
## 2    1  780
## 3    2  314
## 4 <NA> 2195
```

Table 1: Summary Statistics for Continuous Variables

	vars	n	mean	sd	min	max	range	se
F_mass	1	2706	411.472616	2320.49997	1.8	100000.0	99998.2	44.6085053
M_mass	2	2822	436.692275	2585.46747	2.0	115000.0	114998.0	48.6699134
F_tail	3	2352	88.340901	59.91081	15.4	647.5	632.1	1.2353402
M_tail	4	2390	92.410126	64.27592	15.8	762.0	746.2	1.3147688
Clutch_size	5	2392	3.448037	1.88880	1.0	18.6	17.6	0.0386194

```r
# Run regression to compare male and female tail length
lm.tail <- lm(data = birds.subset, M_tail ~ F_tail)
# Check summary
summary(lm.tail) # highly correlated
```

```
##
## Call:
## lm(formula = M_tail ~ F_tail, data = birds.subset)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -46.84  -3.21  -1.27   0.85 345.40
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.226565   0.652716   1.879   0.0603 .
## F_tail      1.033250   0.006115 168.974   <2e-16 ***
```

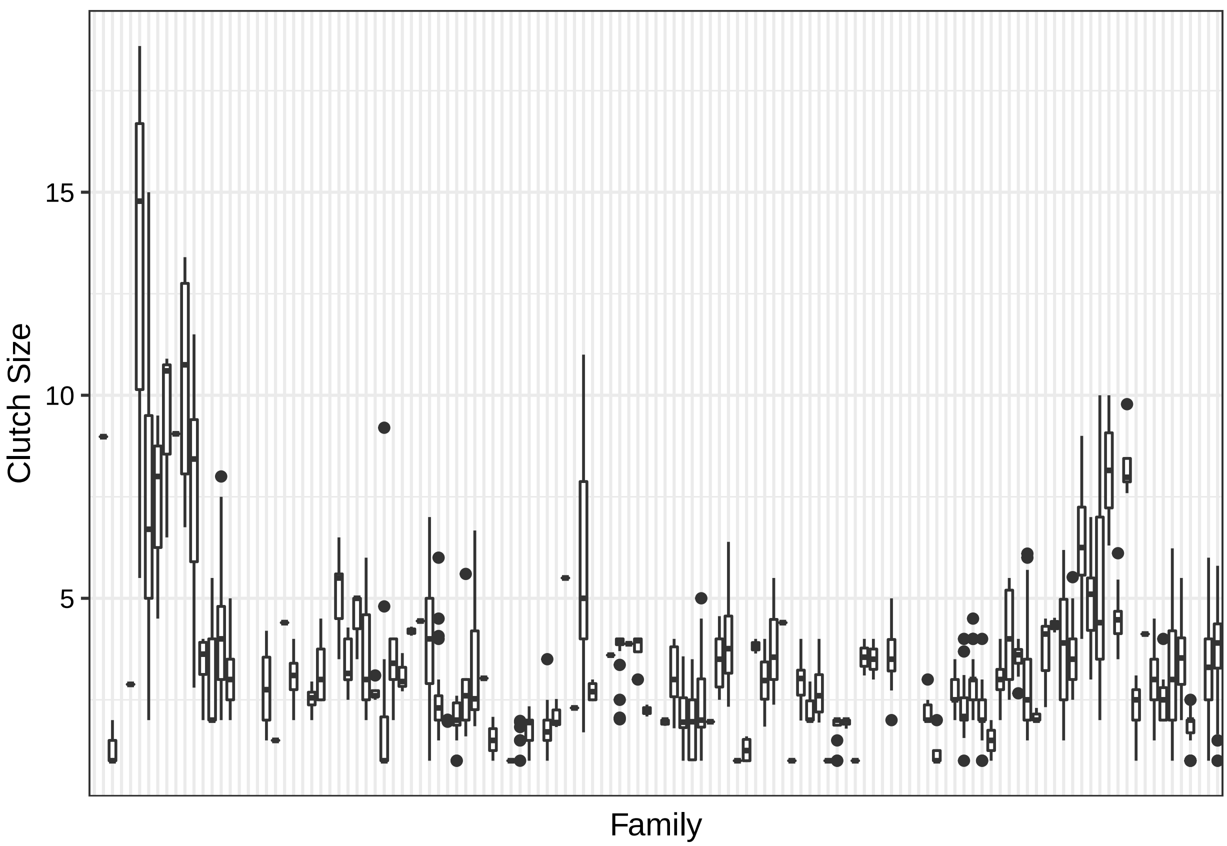


Figure 1: Exploratory Plot of Wrangled Data

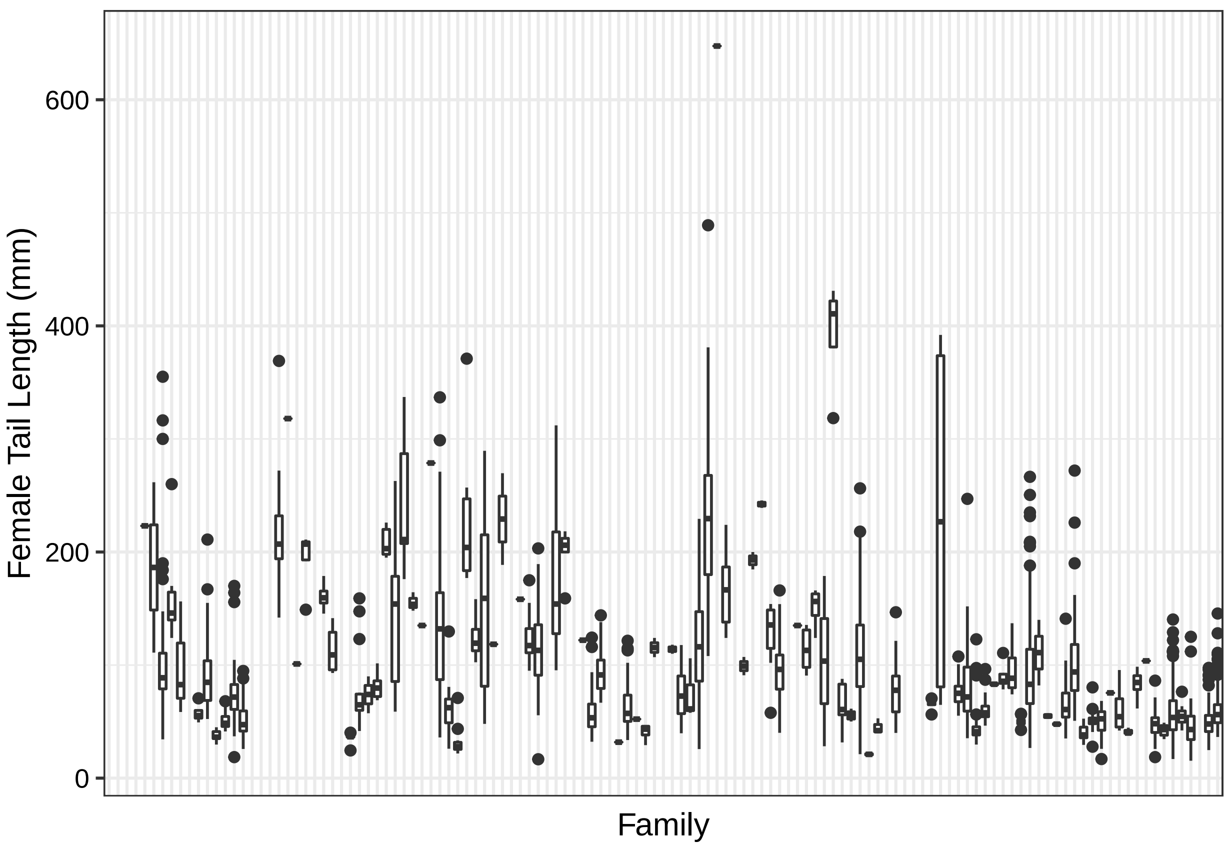


Figure 2: Exploratory Plot of Wrangled Data

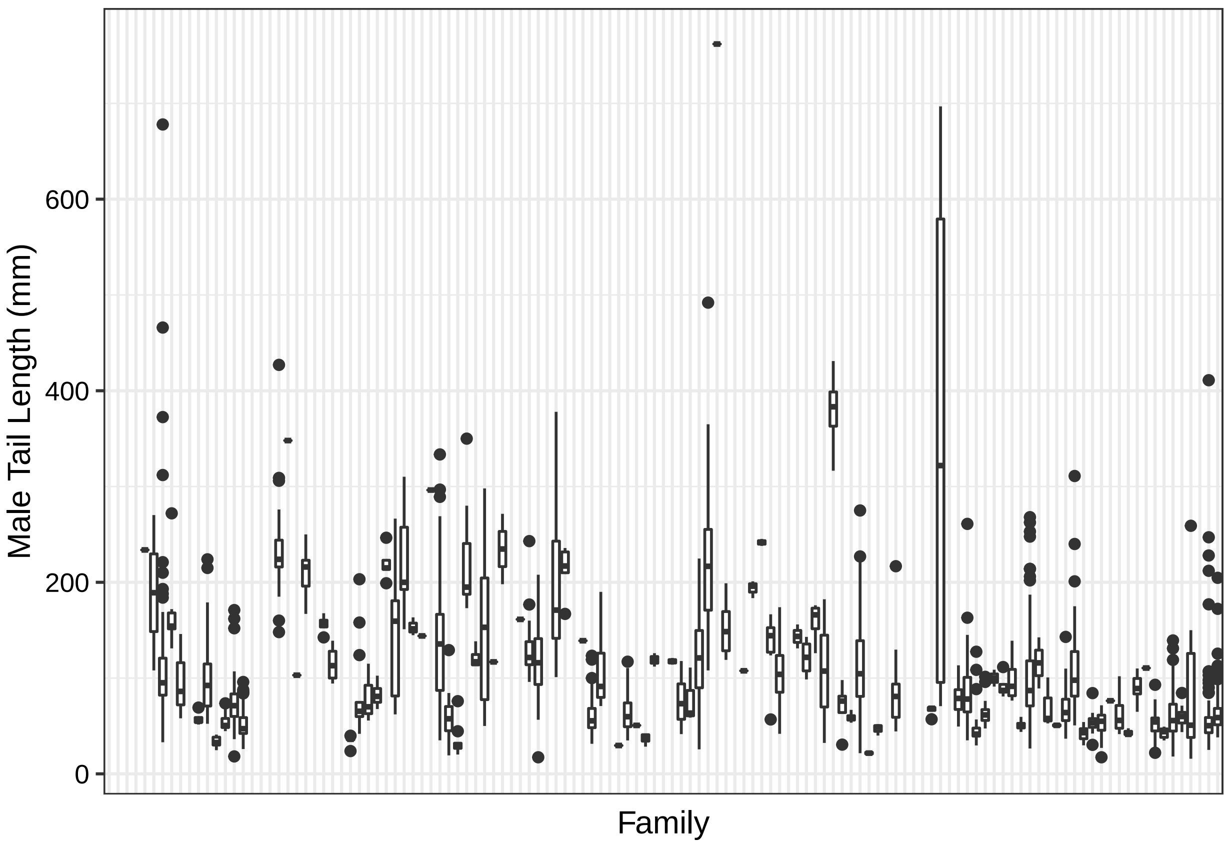


Figure 3: Exploratory Plot of Wrangled Data

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.76 on 2348 degrees of freedom
##   (1419 observations deleted due to missingness)
## Multiple R-squared:  0.924,  Adjusted R-squared:  0.924
## F-statistic: 2.855e+04 on 1 and 2348 DF,  p-value: < 2.2e-16

## `geom_smooth()` using formula 'y ~ x'
```

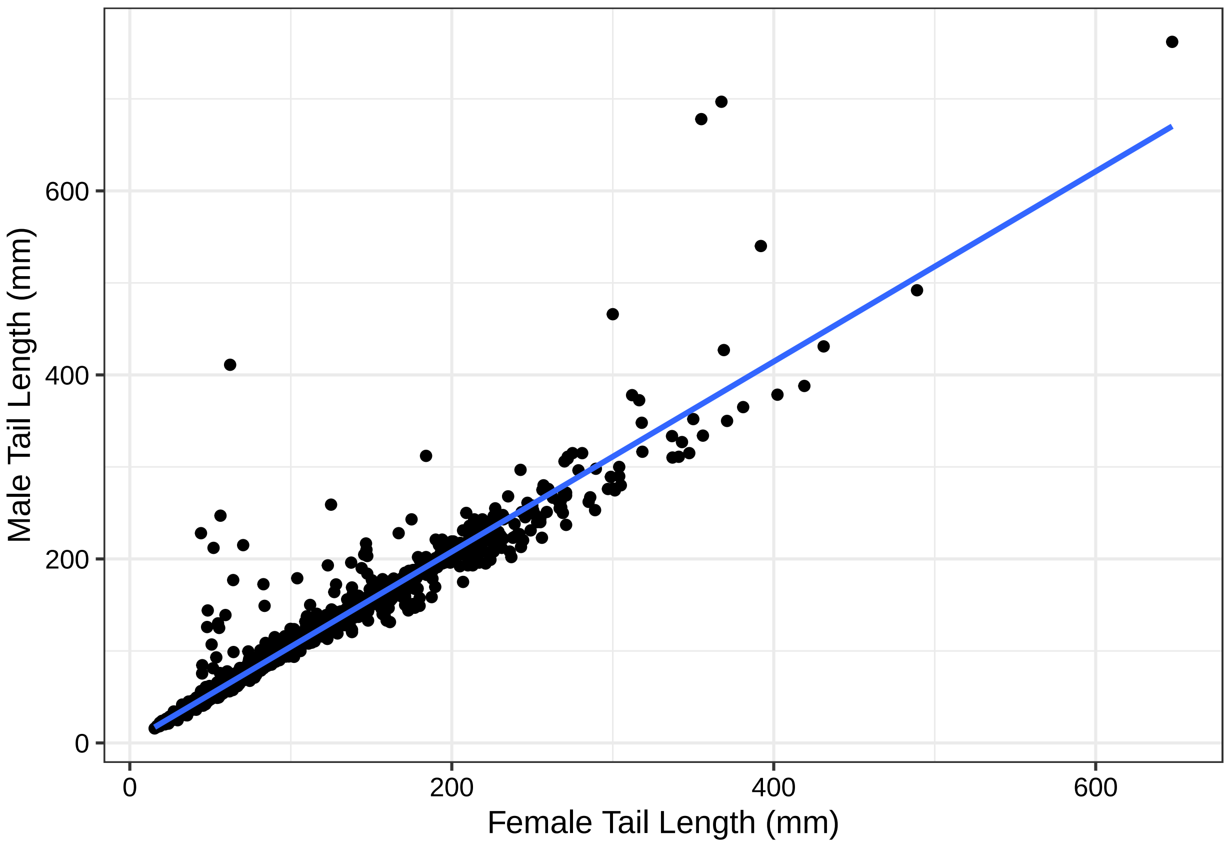


Figure 4: Exploratory Plot of Wrangled Data

```
## Warning: Removed 1379 rows containing non-finite values (stat_boxplot).
```

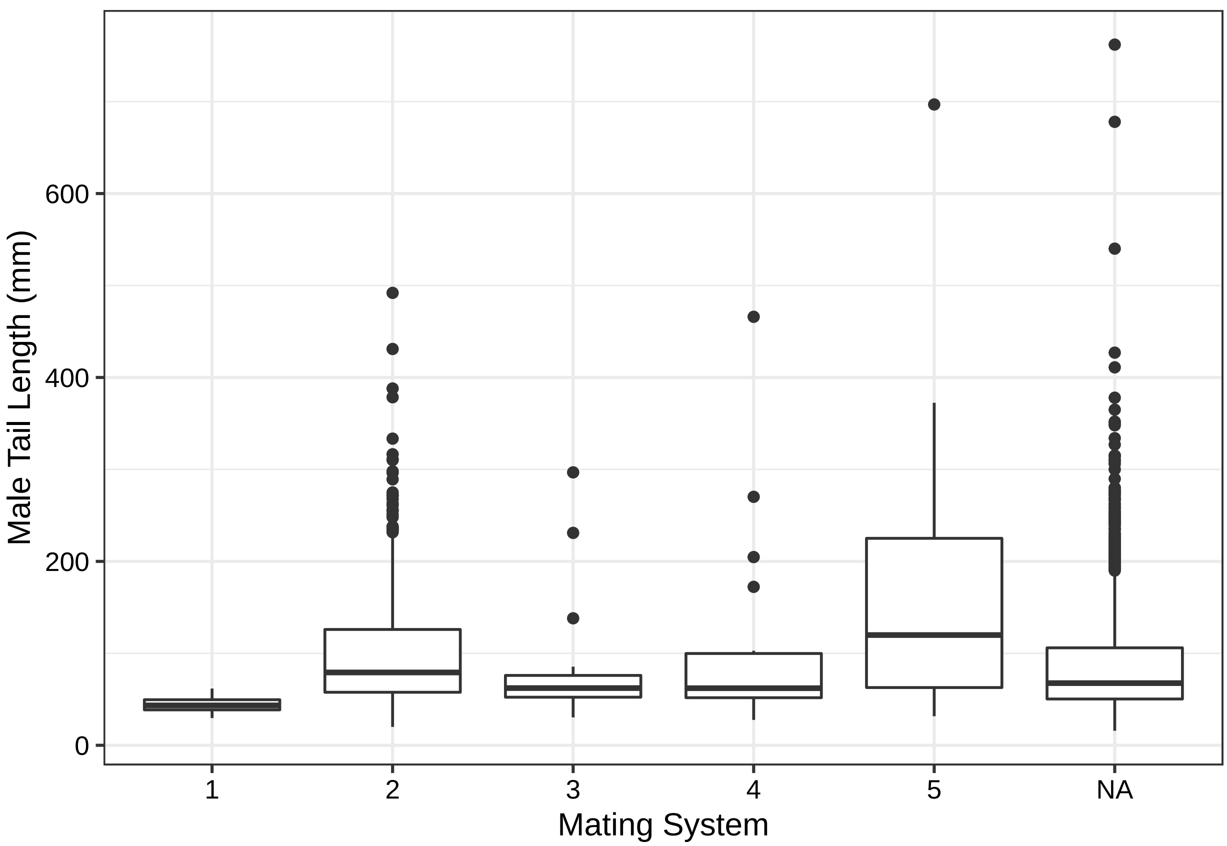


Figure 5: Exploratory Plot of Wrangled Data

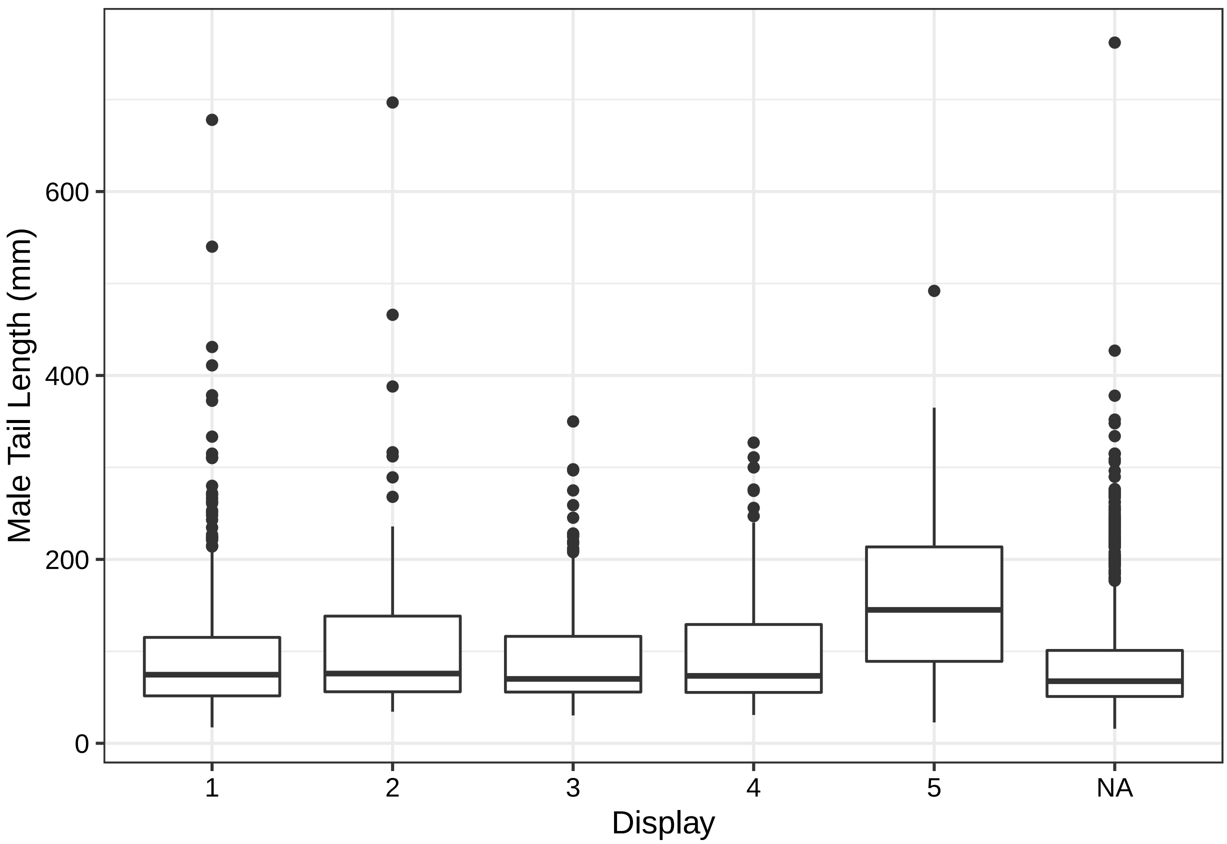
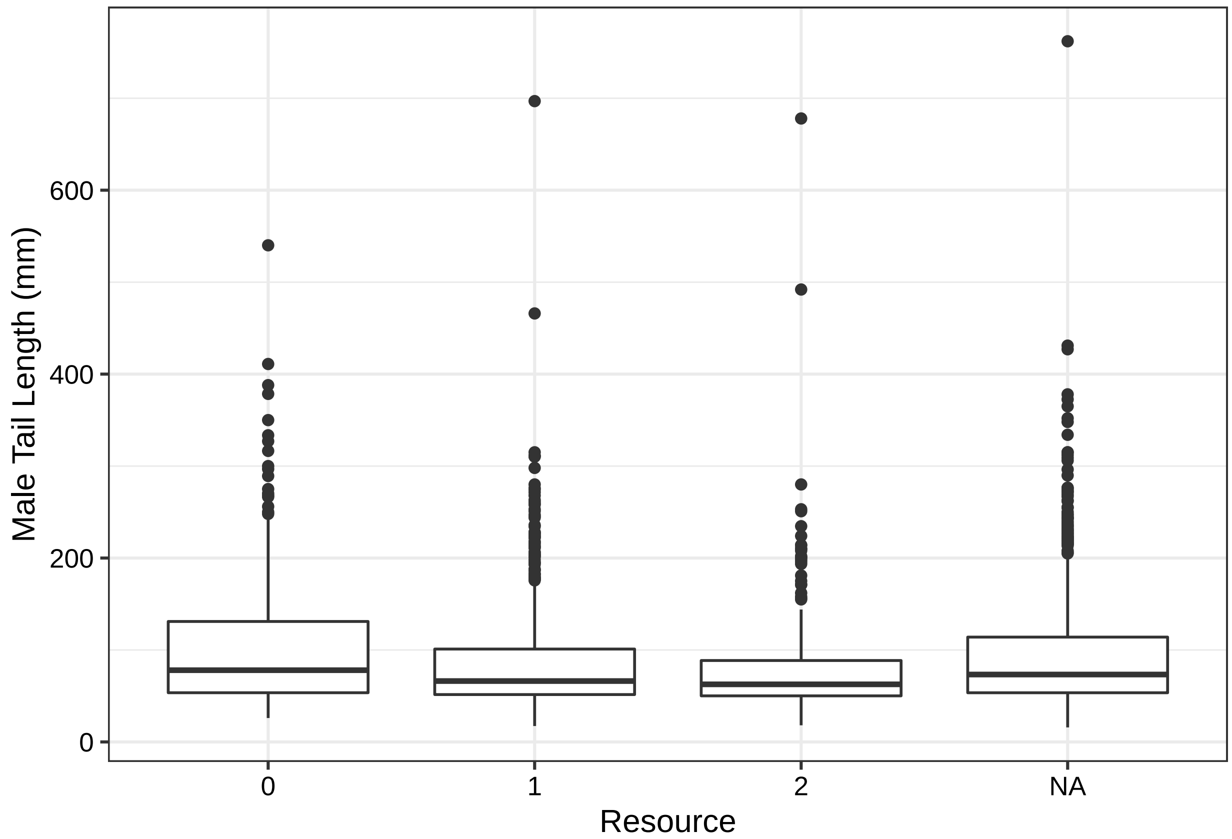


Figure 6: Exploratory Plot of Wrangled Data



Male Tail Length (mm)
600
400
200
0
0
1
2
NA
Resource

4 Analysis

To test our hypotheses using our subset data `birds.subset`, we will conduct a linear regression and an analysis of variance (ANOVA). Our first research question will be answered using a linear regression, while our second will be addressed with an ANOVA. Results will be clearly stated in words, and supplemented using graphing visualizations.

4.1 Question 1: Does female tail length predict clutch size?

H_0 : There is no significant difference between female tail length and clutch size.

H_A : There is a significant difference between female tail length and clutch size.

Prior to conducting this anlaysis, it was identified that there is a strong correlation between mass and tail length. We therefore included this variable in our model, to see the further implications of this.

```
##
## Call:
## lm(formula = F_mass ~ F_tail)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2100.1  -229.3   -65.0    36.4 11412.3
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -322.771     34.310  -9.407   <2e-16 ***
## F_tail         7.330      0.314  23.342   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 826.3 on 1827 degrees of freedom
##   (1940 observations deleted due to missingness)
## Multiple R-squared:  0.2297, Adjusted R-squared:  0.2293
## F-statistic: 544.9 on 1 and 1827 DF,  p-value: < 2.2e-16
```

```
##
## Call:
## lm(formula = Clutch_size ~ F_tail * F_mass)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.9660 -1.2529 -0.2852  0.7347 11.9351
##
## Coefficients:
##                     Estimate    Std. Error t value  Pr(>|t|)
```

```
## (Intercept)    3.8970630035  0.0920673618  42.328   < 2e-16 ***
## F_tail        -0.0038295564  0.0009331300  -4.104 0.0000426 ***
## F_mass         0.0002587737  0.0000979394   2.642   0.00832 **
## F_tail:F_mass -0.0000010753  0.0000004436  -2.424   0.01546 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.891 on 1642 degrees of freedom
##   (2123 observations deleted due to missingness)
## Multiple R-squared:  0.02398,    Adjusted R-squared:  0.02219
## F-statistic: 13.45 on 3 and 1642 DF,  p-value: 0.00000001141
```

```
##        F_tail        F_mass F_tail:F_mass
##      1.564475      4.086442      4.876822
```

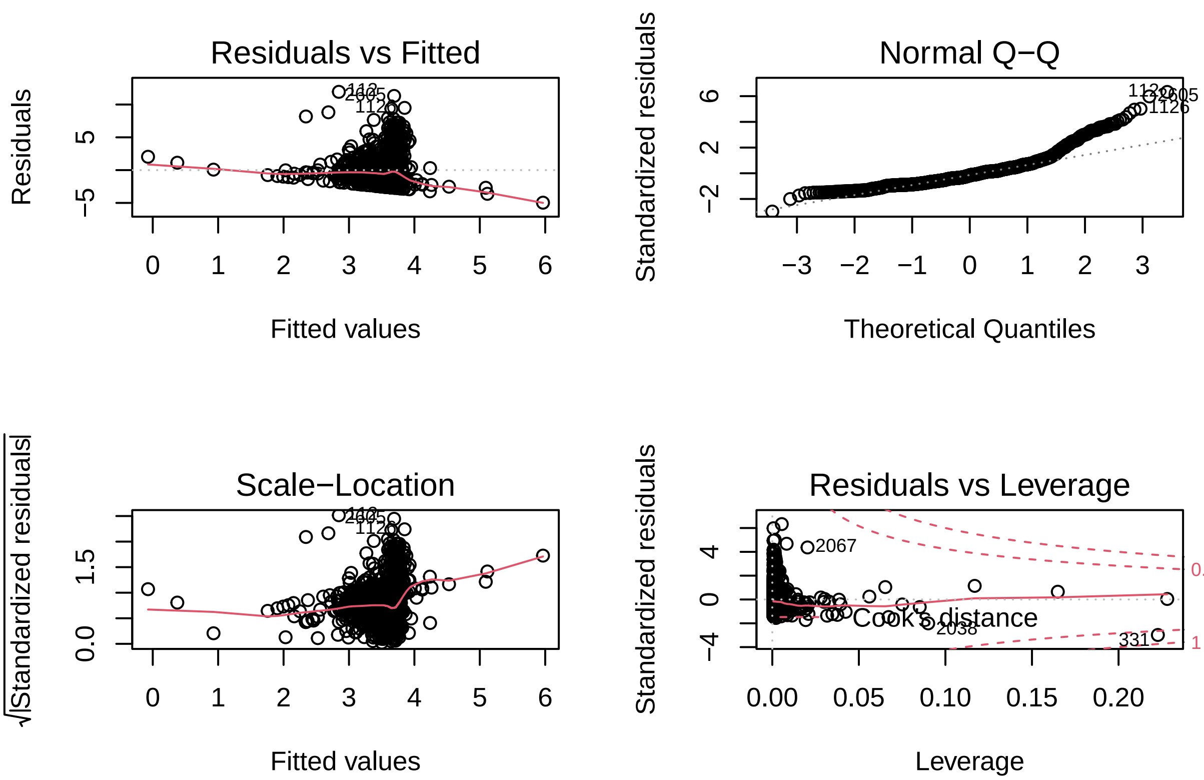


Figure 7: Residual Plots for Question 1

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```

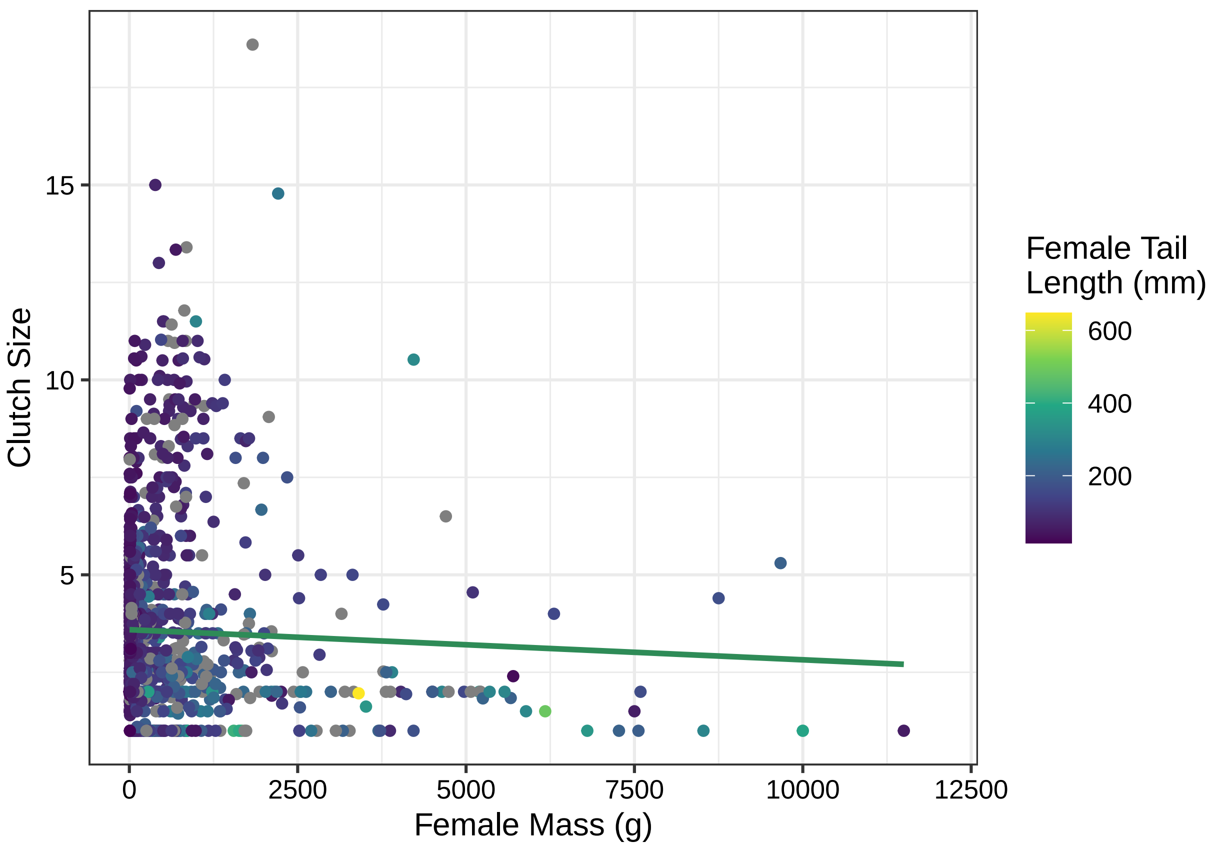


Figure 8: Female Mass vs Clutch Size

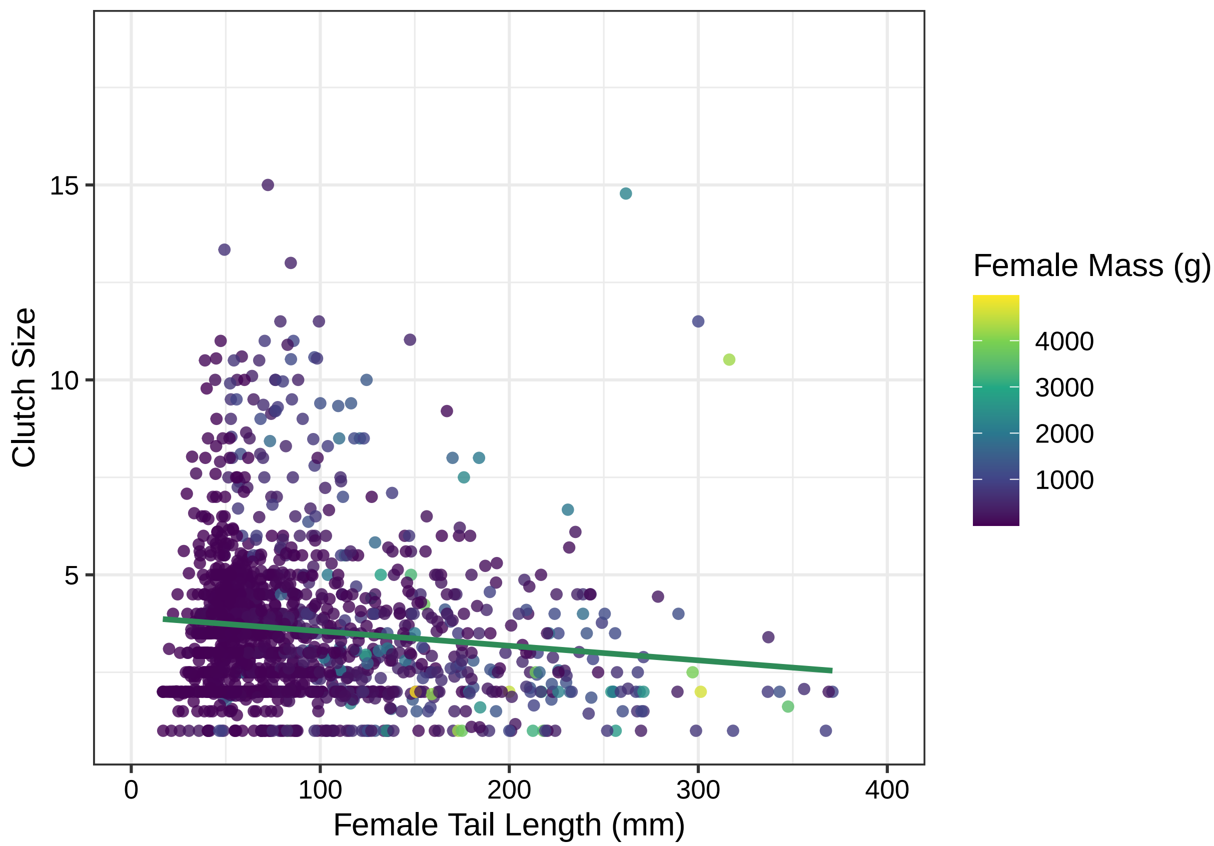


Figure 9: A Closer Look: Female Mass vs Clutch Size

4.2 Question 2: Does male tail length relate to mating approaches?

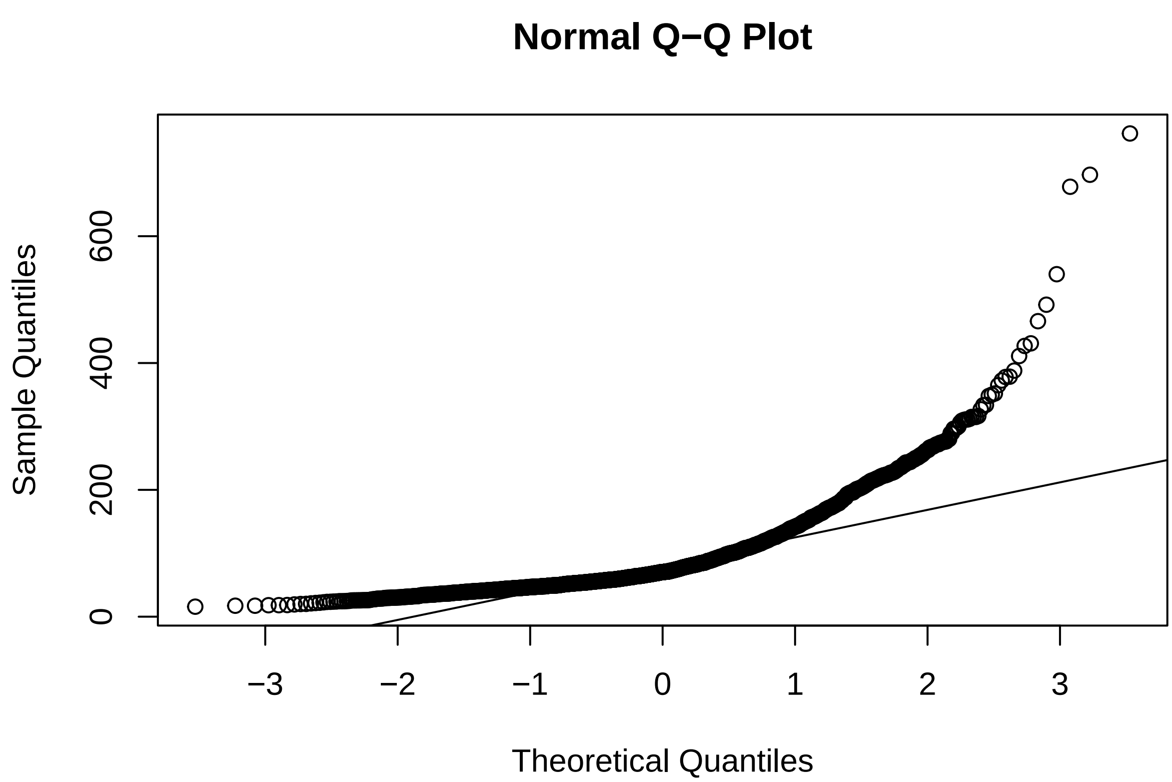
H_0 : Mating system and display behavior do not predict tail size.

H_A : Mating system and/or display behavior do predict tail size.

```
#test for normality
shapiro.test(birds.subset$M_tail)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  birds.subset$M_tail
## W = 0.75655, p-value < 2.2e-16
```

```
# Not normally distributed

qqnorm(birds.subset$M_tail); qqline(birds.subset$M_tail)
```




```
# test for equal variance
with(birds.subset, bartlett.test(M_tail ~ Display))
```

```
##
##  Bartlett test of homogeneity of variances
```

```
##
## data:  M_tail by Display
## Bartlett's K-squared = 71.043, df = 4, p-value = 0.00000000000001367
```

```
with(birds.subset, bartlett.test(M_tail ~ Mating_System))
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  M_tail by Mating_System
## Bartlett's K-squared = 102.13, df = 4, p-value < 2.2e-16
```

```
# All significant; the variances are not equal

mating.anova <- aov(data = birds.subset, M_tail ~ Mating_System * Display * Resource)
summary(mating.anova)
```

```
##                                 Df  Sum Sq Mean Sq F value            Pr(>F)
## Mating_System                    4   59317   14829   3.548           0.00737
## Display                          4  164931   41233   9.865 0.000000129331941
## Resource                         2   18622    9311   2.228           0.10914
## Mating_System:Display           11  377637   34331   8.214 0.000000000000544
## Mating_System:Resource           3   13812    4604   1.102           0.34832
## Display:Resource                 8   35663    4458   1.067           0.38570
## Mating_System:Display:Resource   4   12473    3118   0.746           0.56109
## Residuals                      393 1642577    4180
##
## Mating_System                  **
## Display                        ***
## Resource
## Mating_System:Display          ***
## Mating_System:Resource
## Display:Resource
## Mating_System:Display:Resource
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3339 observations deleted due to missingness
```

```
# Reduce the model to achieve significance
# Remove 3-way interaction
mating.anova.1 <- update(mating.anova, .~.-Mating_System:Display:Resource)
summary(mating.anova.1)
```

```
##                         Df  Sum Sq Mean Sq F value            Pr(>F)
## Mating_System            4   59317   14829   3.557           0.00725 **
## Display                  4  164931   41233   9.891 0.000000122810784 ***
```

```
## Resource                  2   18622    9311   2.233            0.10851
## Mating_System:Display    11  377637   34331   8.235 0.000000000000484 ***
## Mating_System:Resource    3   13812    4604   1.104            0.34714
## Display:Resource          8   35663    4458   1.069            0.38371
## Residuals               397 1655050    4169
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3339 observations deleted due to missingness
```

```
# Remove Display:Resource
mating.anova.2 <- update(mating.anova.1, .~.-Display:Resource)
summary(mating.anova.2)
```

```
##                          Df  Sum Sq Mean Sq F value            Pr(>F)
## Mating_System             4   59317   14829   3.552            0.0073 **
## Display                   4  164931   41233   9.877 0.000000123796776 ***
## Resource                  2   18622    9311   2.230            0.1088
## Mating_System:Display    11  377637   34331   8.224 0.000000000000476 ***
## Mating_System:Resource    3   13812    4604   1.103            0.3477
## Residuals               405 1690713    4175
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3339 observations deleted due to missingness
```

```
# Remove Mating_System:Resource
mating.anova.3 <- update(mating.anova.2, .~.-Mating_System:Resource)
summary(mating.anova.3)
```

```
##                         Df  Sum Sq Mean Sq F value            Pr(>F)
## Mating_System            4   59317   14829   3.550           0.00732 **
## Display                  4  164931   41233   9.870 0.000000124706921 ***
## Resource                 2   18622    9311   2.229           0.10898
## Mating_System:Display   11  377637   34331   8.217 0.000000000000477 ***
## Residuals              408 1704525    4178
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3339 observations deleted due to missingness
```

```
# Remove Resource
mating.anova.4 <- update(mating.anova.3, .~.-Resource)
summary(mating.anova.4)
```

```
##                         Df  Sum Sq Mean Sq F value     Pr(>F)
## Mating_System            4  135625   33906   7.198 0.00001259 ***
## Display                  4  148286   37071   7.870 0.00000386 ***
## Mating_System:Display   12  229022   19085   4.052 0.00000526 ***
## Residuals              455 2143223    4710
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3293 observations deleted due to missingness
```

```
# Everything is significant.
# Not possible to run an AIC comparison because
#the models do not contain the same number of observations.
# Go with mating.anova.4, which is M_tail ~ Mating_System * Display
```

```
#Grouping with Tukey HSD
anova.group <- HSD.test(mating.anova.4, "M_tail", group = TRUE)
anova.group
```

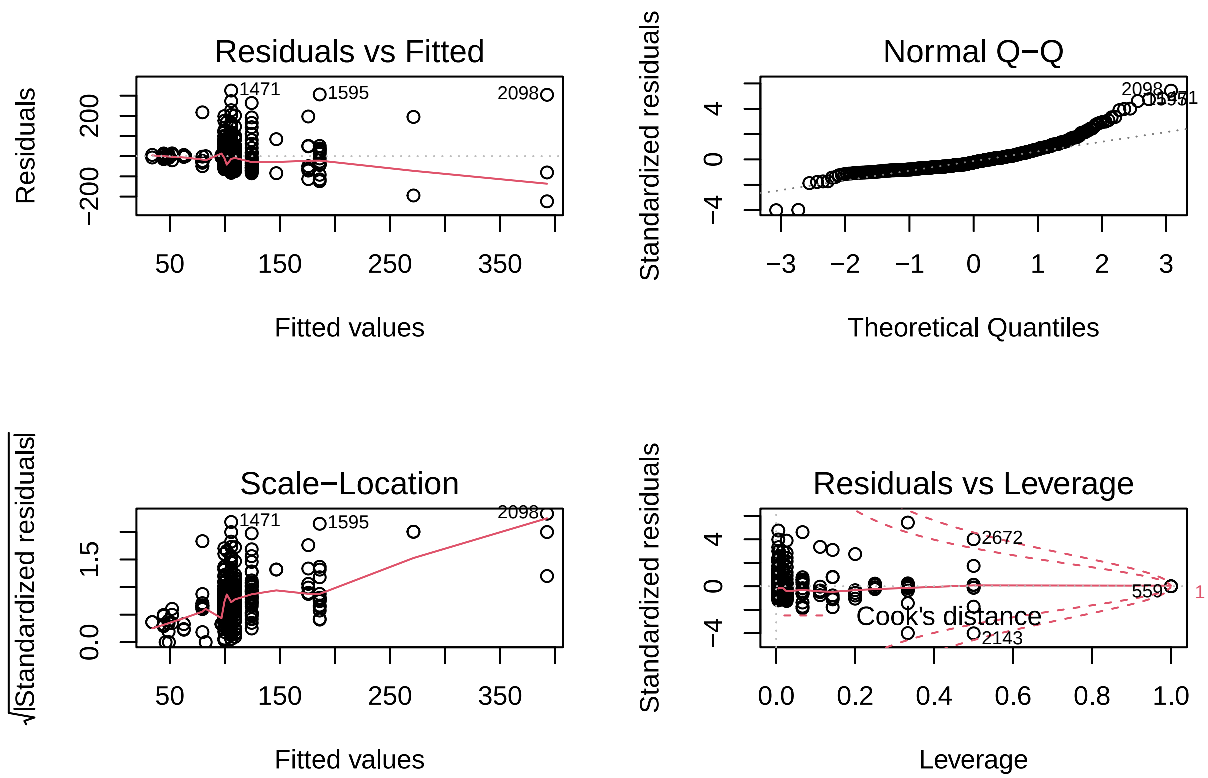


Figure 10: Residual Plots for Question 2

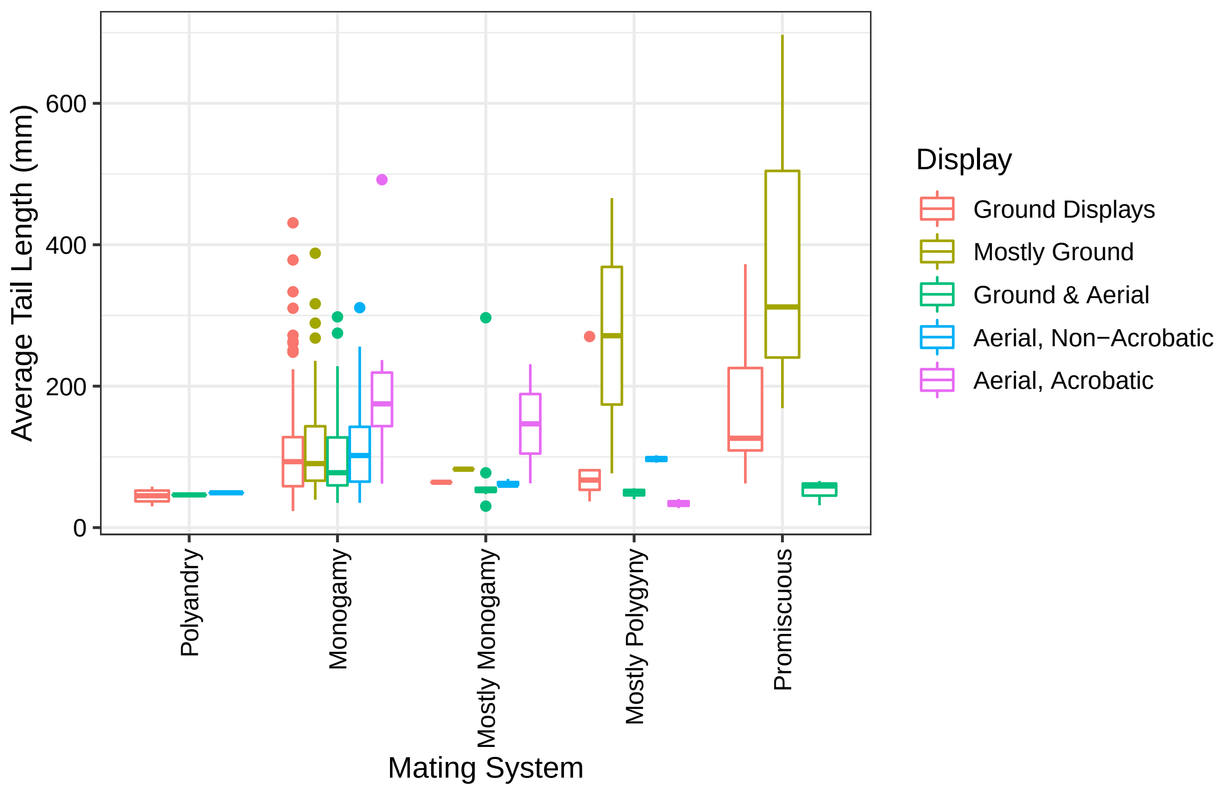


Figure 11: Male Tail Length vs Mating Tactics

5 Summary and Conclusions

Summarize your major findings from your analyses in a few paragraphs. What conclusions do you draw from your findings? Relate your findings back to the original research questions and rationale.

5.1 Part 1

The interaction between female mass and tail size predicts clutch size ($p < 0.001$, $n = 1642$, $R^2 = 0.022$). The effect of female tail size varies depending on the mass of the species. * tail is negative; mass is positive; interaction is negative. I can't remember how to interpret all this with the interaction

Limitations, Part 1 (do we need to run more assumption tests for this one?) * R2 is low - model doesn't explain very much of the variance * residuals plots - ?

5.2 Part 2

Mating system and display system together predict tail length ($n = 476$, is the p-value just the interaction p-value for this one?)

Limitations, Part 2 * tail is not normally distributed (consider transforming) * groups do not have equal variance (especially not surprising with Mating System because the vast majority of the bird species are Type 2 - Monogamous). * Need to check R2 for this one * residual plots - ?

6 References

Evans, M.R. 1999. The consequences of flight for the evolution of tail ornaments in birds. In: Adams, N.J. & Slotow, R.H. (eds) Proc. 22 Int. Ornithol. Congr., Durban: 1823-1843. Johannesburg: BirdLife South Africa.

Lislevand, T., Figuerola, J., and Székely, T. 2007. Avian body sizes in relation to fecundity, mating system, display behavior, and resource sharing. Ecology 88:1605.