

Modeling Wing Morphology Summary File

Data Cleaning And Exploration

Read Libraries

```
library(lme4) # fit regressions
library(dplyr) # data manipulation
library(ggformula) # ggplot plotting
library(cowplot) # ggplot helper functions to arrange multi-panel figures
library(binom) # binomial confidence intervals
```

Read Source Files

```
source_path = paste0(dir, "/Rsrc/")

script_names = c("compare_models.R", # 1 function: model_comparisonsAIC()
                 "clean_morph_data3.R", # 2 functions: read_morph_data(), remove_torn_wings()
                 "AICprobabilities.R") # 1 function: AICprobs()

for (script in script_names) {
  path = paste0(source_path, script)
  source(path)
}

source(paste0(dir, "/RTsrc/vartests.R"))
```

Read the Data

```
data_list <- read_morph_data(paste0(dir, "All_Morphology/stats/data/allmorphology05.18.21.csv"))

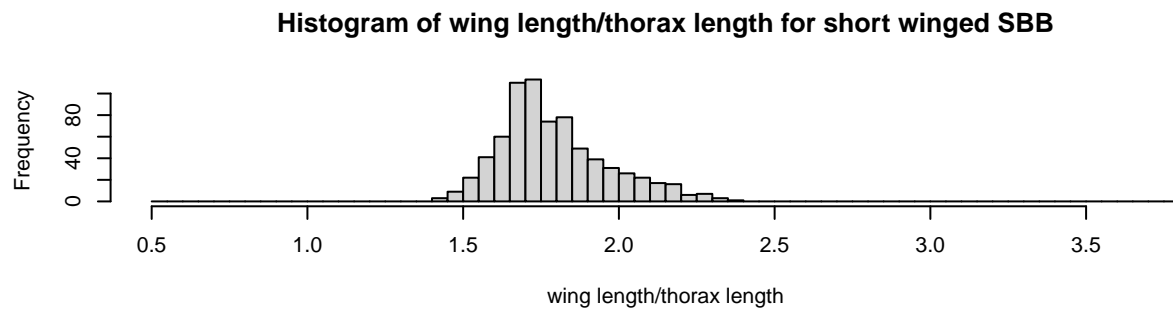
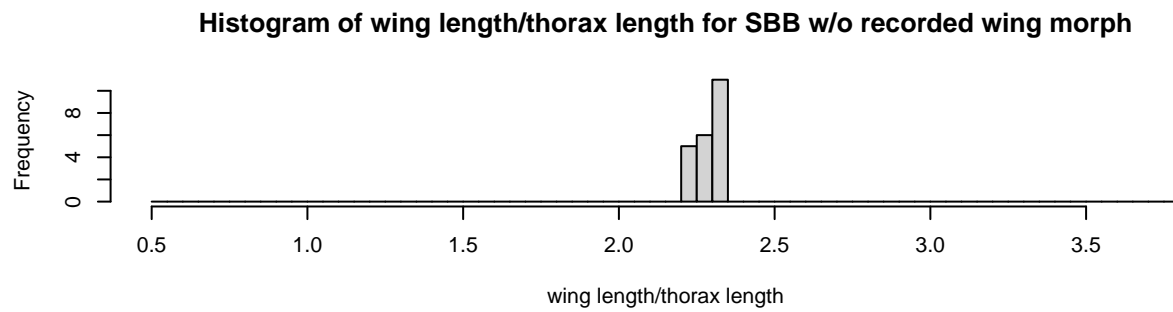
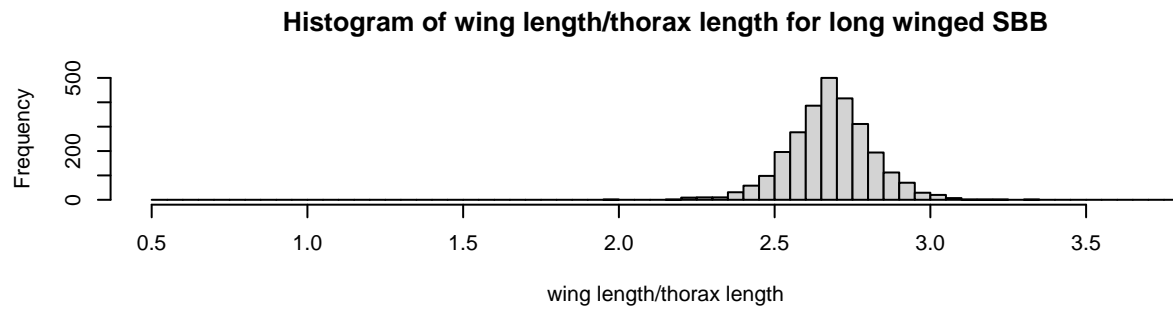
## number of missing dates: 0
##
## morph types: L S  NA LS SL
##   recoding missing morph types...
##   S if wing2thorax <=2.2, L if wing2thorax >=2.5
##
## ambiguous wing morph bug count:  48
##
## filtered out NA wing2body for data_long...

raw_data = data_list[[1]]
data_long = data_list[[2]] # long-wing bugs only

data_long = remove_torn_wings(data_long)

##
## number of bugs with torn wings: 193
```

Histograms of Wing Morph Data

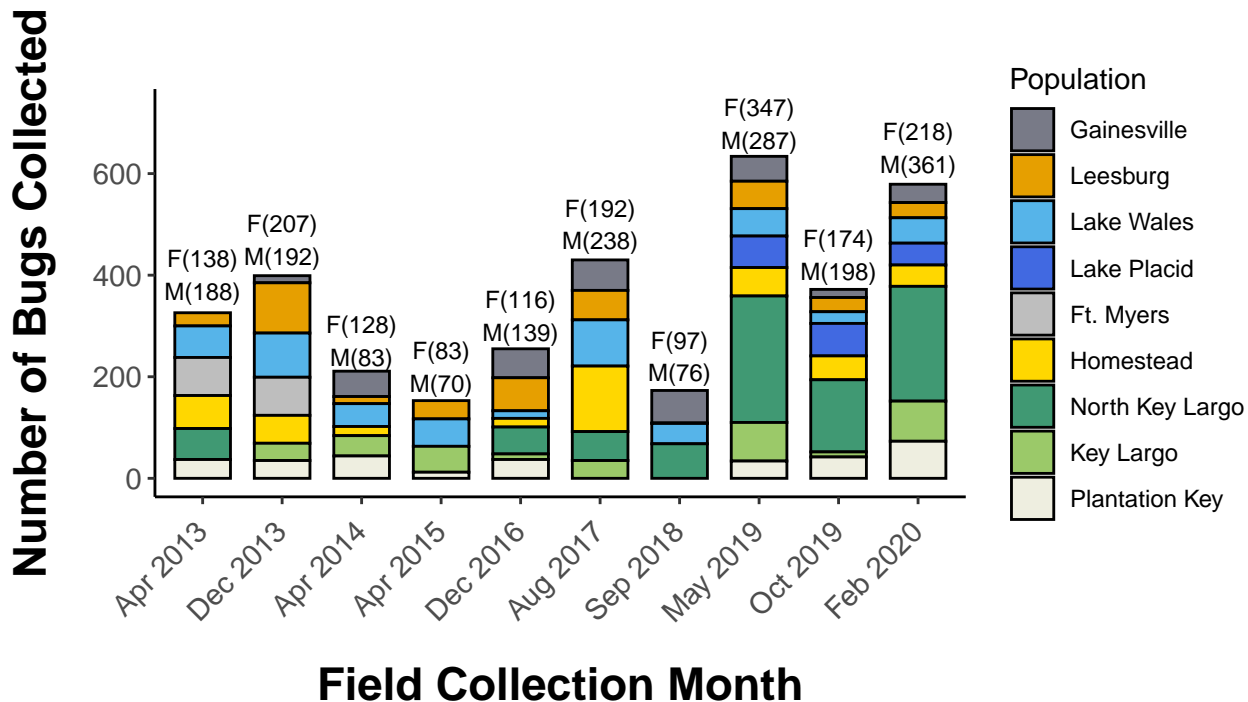


Notice that there are 30 bugs that are hard to identify as either S or L.

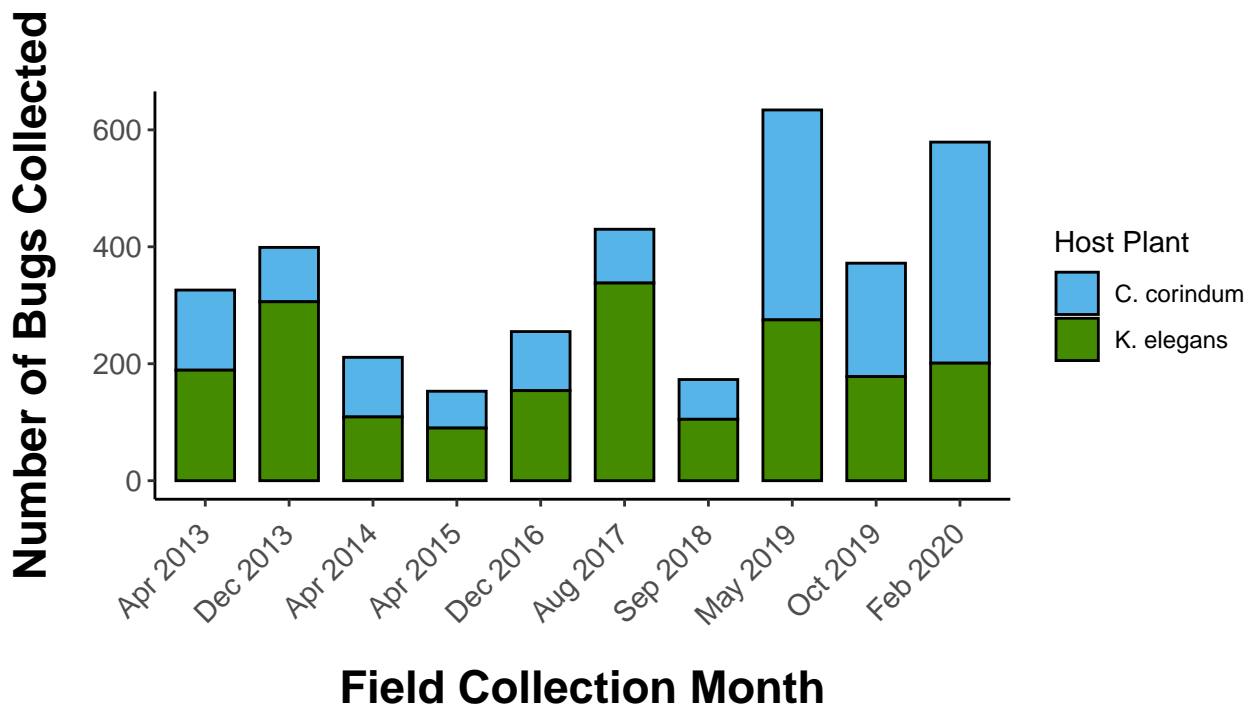
Barplots

Bugs were collected on different years and months. These barplots show the bugs collected per **population**, **host plant**, and **sex** across the years and months.

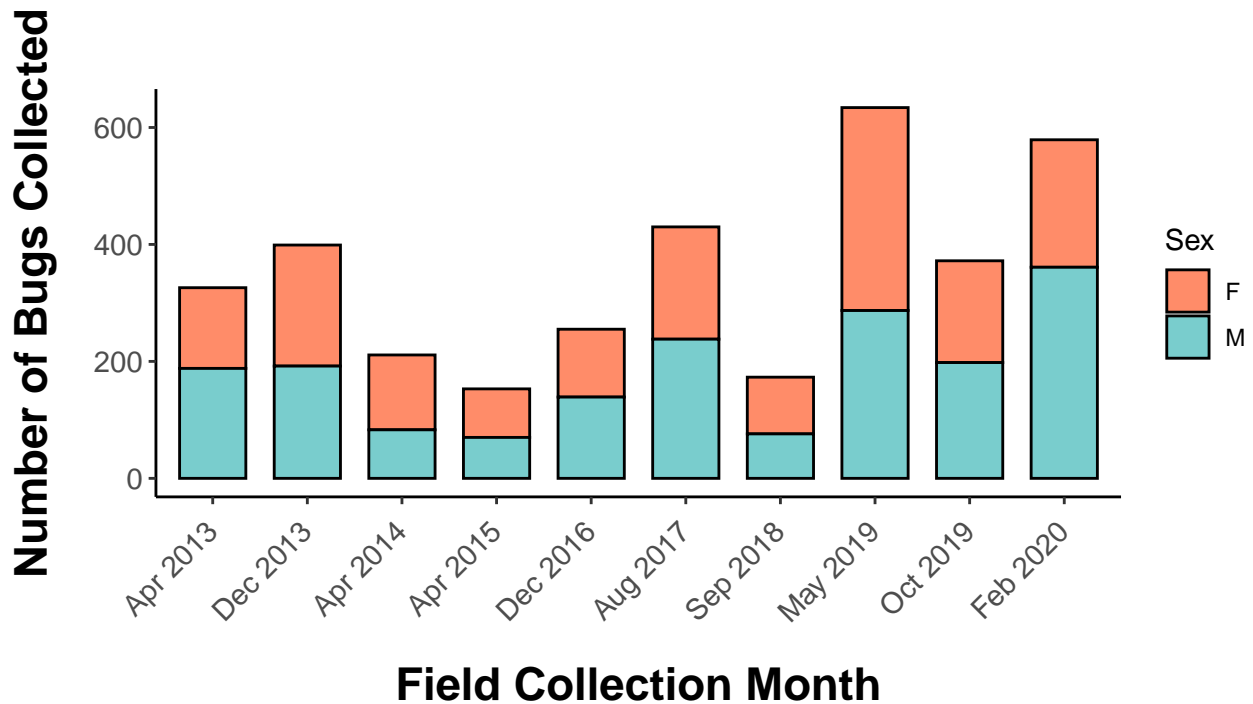
Plot 1: Collection numbers grouped by Population and Datetime



Plot 2: Collection numbers grouped by Host Plant and Datetime



Plot 3: Collection numbers grouped by Sex and Datetime



Regression Modeling

Long-Wing Morph Frequency

How does sex, host plant, month, and/or year effect whether a soapberry bug is long-winged (wing_morph_binom=1) or short-winged (wing_morph_binom=0)?

```
data<-data.frame(R=raw_data$wing_morph_binom,
                 A=raw_data$sex_binom,
                 B=raw_data$pophost_binom,
                 C=(raw_data$month_of_year),
                 D=raw_data$months_since_start)
```

```
model_script = paste0(source_path,"generic models-binomial glm 4-FF.R")
model_comparisonsAIC(model_script)
```

```
##      [,1]      [,2]      [,3]      [,4]      [,5]
## AICs 3145.306 3146.842 3147.157 3147.201 3148.521
## models 98      110      84      107      105
## probs 0.2529382 0.1173602 0.1002697 0.09808583 0.05068685
##
## m98 glm(formula = R ~ A * B + A * D + B * C + C * D, family = binomial,
##      data = data)
## m110 glm(formula = R ~ A * B + A * D + B * C + B * D + C * D, family = binomial,
##      data = data)
## m84 glm(formula = R ~ A * D + B * C + C * D, family = binomial, data = data)
## m107 glm(formula = R ~ A * B + A * C + A * D + B * C + C * D, family = binomial,
##      data = data)
```

```
## m105      glm(formula = R ~ A * D + B * C + B * D + C * D, family = binomial,
##          data = data)
```

```
anova(m98, m110, test="Chisq") # adding B*D does not improve fit
anova(m84, m98, test="Chisq") # adding A*B improves fit
anova(m63, m84, test="Chisq") # Adding C*D improves fit
anova(m51, m63, test="Chisq") # Adding B improves fit
```

```
## Analysis of Deviance Table
```

```
##
```

```
## Model 1: R ~ A * B + A * D + B * C + C * D
```

```
## Model 2: R ~ A * B + A * D + B * C + B * D + C * D
```

```
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
```

```
## 1         3461         3127.3
```

```
## 2         3460         3126.8  1  0.46421  0.4957
```

```
## Analysis of Deviance Table
```

```
##
```

```
## Model 1: R ~ A * D + B * C + C * D
```

```
## Model 2: R ~ A * B + A * D + B * C + C * D
```

```
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
```

```
## 1         3462         3131.2
```

```
## 2         3461         3127.3  1   3.8506  0.04973 *
```

```
## ---
```

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

```
## Analysis of Deviance Table
```

```
##
```

```
## Model 1: R ~ A * D + C * D + B
```

```
## Model 2: R ~ A * D + B * C + C * D
```

```
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
```

```
## 1         3463         3137.3
```

```
## 2         3462         3131.2  1   6.1886  0.01286 *
```

```
## ---
```

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

```
## Analysis of Deviance Table
```

```
##
```

```
## Model 1: R ~ A * D + C * D
```

```
## Model 2: R ~ A * D + C * D + B
```

```
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
```

```
## 1         3464         3497.3
```

```
## 2         3463         3137.3  1   359.93 < 2.2e-16 ***
```

```
## ---
```

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

Best Fit

```
M1 = glm(wing_morph_binom ~ sex_binom * pophost_binom + sex_binom * months_since_start +
        pophost_binom * month_of_year + month_of_year * months_since_start,
        data=raw_data, family="binomial")
summary(M1)
```

```
##
## Call:
## glm(formula = wing_morph_binom ~ sex_binom * pophost_binom +
##      sex_binom * months_since_start + pophost_binom * month_of_year +
##      month_of_year * months_since_start, family = "binomial",
##      data = raw_data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.3803   0.3597   0.4321   0.8450   1.2552
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.7516501   0.1841942   4.081 4.49e-05 ***
## sex_binom      -0.2597900   0.0902673  -2.878 0.004002 **
## pophost_binom   1.1256358   0.1142931   9.849 < 2e-16 ***
## months_since_start 0.0107239   0.0029582   3.625 0.000289 ***
## month_of_year   0.0995560   0.0255307   3.899 9.64e-05 ***
## sex_binom:pophost_binom 0.0973323   0.0495811   1.963 0.049635 *
## sex_binom:months_since_start 0.0037212   0.0015337   2.426 0.015254 *
## pophost_binom:month_of_year -0.0379395   0.0150617  -2.519 0.011771 *
## months_since_start:month_of_year -0.0014557   0.0004553  -3.198 0.001386 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 3562.3  on 3469  degrees of freedom
## Residual deviance: 3127.3  on 3461  degrees of freedom
##      (62 observations deleted due to missingness)
## AIC: 3145.3
##
## Number of Fisher Scoring iterations: 5
```

Modeling Variance

In addition to modeling how sex, host plant, month, or year effects whether a soapberry bug is long-winged or short-winged, we modeled how those same factors affected the variance of wing morph.

```
SE = function(x){sd(x)/sqrt(length(x))}
```

```
wmorph_table<-aggregate(wing_morph_binom~sex_binom*pophost_binom*month_of_year*months_since_start,
                        data=raw_data, FUN=mean)
wmorph_table$sd<-aggregate(wing_morph_binom~sex_binom*pophost_binom*month_of_year*months_since_start,
                          data=raw_data,FUN=sd)$wing_morph_binom
wmorph_table$se<-aggregate(wing_morph_binom~sex_binom*pophost_binom*month_of_year*months_since_start,
                          data=raw_data,FUN=SE)$wing_morph_binom
wmorph_table$n<-aggregate(wing_morph_binom~sex_binom*pophost_binom*month_of_year*months_since_start,
```

```
data=raw_data,FUN=length)$wing_morph_binom
```

```
data = wmorph_table
data<-data.frame(R=data$sd,
                 A=data$sex_binom,
                 B=data$pophost_binom,
                 C=(data$month_of_year),
                 D=data$months_since_start)

model_script = paste0(source_path,"generic models-gaussian glm 4-FF.R")
model_comparisonsAIC(model_script)
```

```
##      [,1]      [,2]      [,3]      [,4]
## AICs -92.39855 -90.95292 -90.75898 -90.41465
## models 2      5      8      9
## probs 0.183788 0.0892081 0.08096352 0.06815837
##
## m2  glm(formula = R ~ B, family = gaussian, data = data)
## m5  glm(formula = R ~ A + B, family = gaussian, data = data)
## m8  glm(formula = R ~ B + C, family = gaussian, data = data)
## m9  glm(formula = R ~ B + D, family = gaussian, data = data)
```

```
anova(m2, m5, test="Chisq") # Adding A does not improve fit
anova(m2, m8, test="Chisq") # Adding C does not improve fit
anova(m2, m9, test="Chisq") # Adding D does not improve fit
anova(m0, m2, test="Chisq") # Adding B improves fit
```

```
## Analysis of Deviance Table
##
## Model 1: R ~ B
## Model 2: R ~ A + B
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1      38     0.20009
## 2      37     0.19734  1 0.0027541   0.4724
## Analysis of Deviance Table
##
## Model 1: R ~ B
## Model 2: R ~ B + C
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1      38     0.20009
## 2      37     0.19830  1 0.0017949   0.5628
## Analysis of Deviance Table
##
## Model 1: R ~ B
## Model 2: R ~ B + D
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1      38     0.20009
## 2      37     0.20001  1 8.0534e-05   0.9029
## Analysis of Deviance Table
##
## Model 1: R ~ 1
## Model 2: R ~ B
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
```

```
## 1      39      0.62439
## 2      38      0.20010  1  0.42429 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Best Fit

```
M2 = glm(sd ~ pophost_binom, data=wmorph_table, family="gaussian")
summary(M2)

##
## Call:
## glm(formula = sd ~ pophost_binom, family = "gaussian", data = wmorph_table)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.249168  -0.041487   0.005877   0.041147   0.171269
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.35216    0.01147  30.693 < 2e-16 ***
## pophost_binom -0.10299    0.01147  -8.976 6.28e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.005265667)
##
##      Null deviance: 0.62439  on 39  degrees of freedom
## Residual deviance: 0.20010  on 38  degrees of freedom
## AIC: -92.399
##
## Number of Fisher Scoring iterations: 2
```

Wing-to-body Ratio

How does sex, host plant, month, and/or year effect the wing-to-body ratio of long-winged soapberry bugs?

```
data<-data.frame(R=data_long$wing2body_c, # centered
                 A=data_long$sex_binom,
                 B=data_long$pophost_binom,
                 C=data_long$month_of_year_c, # centered
                 D=data_long$months_since_start_c) # centered

model_script = paste0(source_path,"generic models-gaussian glm 4-FF.R")
model_comparisonsAIC(model_script)

##      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## AICs -9722.301 -9721.371 -9720.852 -9720.339 -9720.331 -9719.674
## models 88      99      58      92      97      76
## probs 0.1948772 0.1224324 0.09441271 0.07306166 0.07277994 0.05239229
##
## m88  glm(formula = R ~ A * B + A * D + B * D + C, family = gaussian,
##      data = data)
```



```
## m99  glm(formula = R ~ A * B + A * D + B * D + C * D, family = gaussian,
##      data = data)
## m58  glm(formula = R ~ A * B + B * D + C, family = gaussian, data = data)
## m92  glm(formula = R ~ A * B + A * C + A * D + B * D, family = gaussian,
##      data = data)
## m97  glm(formula = R ~ A * B + A * D + B * C + B * D, family = gaussian,
##      data = data)
## m76  glm(formula = R ~ A * B + B * D + C * D, family = gaussian, data = data)
```

```
anova(m88, m58, test="Chisq") # Adding A*D marginally improves fit
anova(m76, m58, test="Chisq") # Adding C*D does not improve fit
anova(m88, m99, test="Chisq") # adding C*D does not improve fit
anova(m34, m58, test="Chisq") # Adding B*D improves fit
```

```
## Analysis of Deviance Table
##
## Model 1: R ~ A * B + A * D + B * D + C
## Model 2: R ~ A * B + B * D + C
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      1895      0.66692
## 2      1896      0.66813 -1 -0.00121  0.06371 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Deviance Table
##
## Model 1: R ~ A * B + B * D + C * D
## Model 2: R ~ A * B + B * D + C
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1      1895      0.66784
## 2      1896      0.66813 -1 -0.0002886   0.3655
## Analysis of Deviance Table
##
## Model 1: R ~ A * B + A * D + B * D + C
## Model 2: R ~ A * B + A * D + B * D + C * D
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1      1895      0.66692
## 2      1894      0.66655  1 0.00037502   0.3019
## Analysis of Deviance Table
##
## Model 1: R ~ A * B + C + D
## Model 2: R ~ A * B + B * D + C
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1      1897      0.67063
## 2      1896      0.66813  1 0.0024994  0.00774 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Best Fit

```
M3 = glm(wing2body_c ~ sex_binom*pophost_binom + pophost_binom*months_since_start_c
+ month_of_year_c, data=data_long, family=gaussian)
```

```
summary(M3)
```

```
##
## Call:
## glm(formula = wing2body_c ~ sex_binom * pophost_binom + pophost_binom *
##     months_since_start_c + month_of_year_c, family = gaussian,
##     data = data_long)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.070837  -0.010794  -0.000093   0.010596   0.113993
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -4.542e-04  4.601e-04  -0.987  0.32368
## sex_binom      -1.787e-03  4.467e-04  -4.001  6.55e-05 ***
## pophost_binom   4.289e-03  4.613e-04   9.297  < 2e-16 ***
## months_since_start_c -1.727e-05  2.225e-05  -0.776  0.43763
## month_of_year_c    7.155e-04  1.379e-04   5.188  2.35e-07 ***
## sex_binom:pophost_binom  1.804e-03  4.466e-04   4.038  5.60e-05 ***
## pophost_binom:months_since_start_c  5.904e-05  2.217e-05   2.663  0.00781 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.0003523901)
##
##      Null deviance: 0.72538  on 1902  degrees of freedom
## Residual deviance: 0.66813  on 1896  degrees of freedom
## AIC: -9720.9
##
## Number of Fisher Scoring iterations: 2
```

Modeling Variance

In addition to modeling how sex, host plant, month, or year effects the wing-to-body ratio of a soapberry bug, we modeled how those same factors affected the variance of wing-to-body ratio.

```
w2b_table<-aggregate(wing2body~sex_binom*pophost_binom*month_of_year*months_since_start,
                      data=data_long, FUN=mean)
w2b_table$sd<-aggregate(wing2body~sex_binom*pophost_binom*month_of_year*months_since_start,
                        data=data_long, FUN=sd)$wing2body
w2b_table$se<-aggregate(wing2body~sex_binom*pophost_binom*month_of_year*months_since_start,
                        data=data_long, FUN=SE)$wing2body
```

```
data = w2b_table
data<-data.frame(R=data$sd,
                 A=data$sex_binom,
                 B=data$pophost_binom,
                 C=(data$month_of_year),
                 D=data$months_since_start)

model_script = paste0(source_path,"generic models-gaussian glm 4-FF.R")
model_comparisonsAIC(model_script)
```

```
##           [,1]      [,2]      [,3]
## AICs      -280.1872 -279.8713 -279.4758
## models    8         19         2
## probs    0.1198675 0.1023577 0.08398967
##
## m8      glm(formula = R ~ B + C, family = gaussian, data = data)
## m19     glm(formula = R ~ B * C, family = gaussian, data = data)
## m2      glm(formula = R ~ B, family = gaussian, data = data)
```

```
anova(m8, m19, test="Chisq") # Adding B*C does not improve fit
anova(m2, m8, test="Chisq") # Adding C does not improve fit
anova(m0, m2, test="Chisq") # Adding B improves fit
```

```
## Analysis of Deviance Table
##
## Model 1: R ~ B + C
## Model 2: R ~ B * C
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1          33 0.00070342
## 2          32 0.00067127  1 3.215e-05   0.2157
## Analysis of Deviance Table
##
## Model 1: R ~ B
## Model 2: R ~ B + C
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1          34 0.00075844
## 2          33 0.00070342  1 5.5025e-05   0.1081
## Analysis of Deviance Table
##
## Model 1: R ~ 1
## Model 2: R ~ B
##   Resid. Df Resid. Dev Df   Deviance Pr(>Chi)
## 1          35 0.00087733
## 2          34 0.00075844  1 0.00011888 0.02097 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Best Fit

```
M4 = glm(sd ~ pophost_binom, data=w2b_table, family=gaussian)
summary(M4)
```

```
##
## Call:
## glm(formula = sd ~ pophost_binom, family = gaussian, data = w2b_table)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0059374 -0.0033018 -0.0006274  0.0022332  0.0147212
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0165999  0.0007872  21.088  <2e-16 ***
```

```
## pophost_binom 0.0018172 0.0007872 2.309 0.0272 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 2.230719e-05)
##
## Null deviance: 0.00087733 on 35 degrees of freedom
## Residual deviance: 0.00075844 on 34 degrees of freedom
## AIC: -279.48
##
## Number of Fisher Scoring iterations: 2
```

LOESS & Linear Regression Plots

Wing Morph Frequency

Group significant elements

```
# function to calculate 95% confidence interval (CI).
CI_95 <- function(x){qnorm(0.975)*sd(x)/sqrt(length(x))}
CI_95_binom_upper <- function(y) {binom.confint(x=sum(y, na.rm=TRUE), n=length(y[!is.na(y)]),
                                                conf.level=0.95, methods='exact')$upper}
CI_95_binom_lower <- function(y) {binom.confint(x=sum(y, na.rm=TRUE), n=length(y[!is.na(y)]),
                                                conf.level=0.95, methods='exact')$lower}

# aggregate the full data and calculate standard error (SE), upper and lower CI, and sample size (n)
w_morph_summary<-aggregate(wing_morph_binom~sex*pophost*month_of_year*months_since_start
                           , data=raw_data, FUN=mean)
w_morph_summary$se<-aggregate(wing_morph_binom~sex*pophost*month_of_year*months_since_start
                              , data=raw_data, FUN=SE)$wing_morph_binom
w_morph_summary$upper<-aggregate(wing_morph_binom~sex*pophost*month_of_year*months_since_start
                                 , data=raw_data, FUN=CI_95_binom_upper)$wing_morph_binom
w_morph_summary$lower<-aggregate(wing_morph_binom~sex*pophost*month_of_year*months_since_start
                                 , data=raw_data, FUN=CI_95_binom_lower)$wing_morph_binom
w_morph_summary$n<-aggregate(wing_morph_binom~sex*pophost*month_of_year*months_since_start
                             , data=raw_data, FUN=length)$wing_morph_binom

jitter = runif(n=nrow(w_morph_summary), min=-0.1, max=0.1) # jitter points slightly
w_morph_summary$dates <- w_morph_summary$month_of_year + jitter

dd = w_morph_summary
```

Check for LOESS Residuals

```
plot_lowess_residuals = function(lfit, x, y) {
  lfun <- approxfun(lfit)
  fitted <- lfun(x)
  resid <- y-fitted
  plot(fitted,resid)
  abline(h=0,col=8)
}
```

```
l1 = lowess(dd$dates, dd$wing_morph_binom, f=0.4) # f = alpha, the smoother span

par(mfrow=c(1,2))
plot(dd$dates, dd$wing_morph_binom)
lines(l1, type = "l")
plot_lowess_residuais(l1, dd$dates, dd$wing_morph_binom)
```

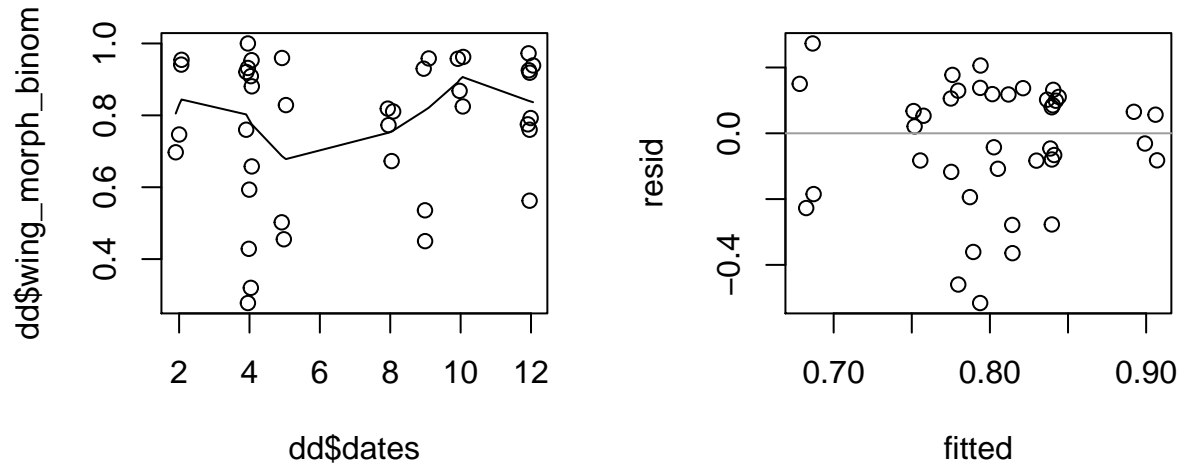


Figure: Panels A, B, C, D (long-wing morph freq with month) & E (long-wing morph freq with year)

Note: Single-variate models or simpler models substituted best fit slope calculations below in order to avoid multiple interaction terms found in the best fit model. This led to cleaner glm line plotting.

```
# single-variate model of month predicting wing morph
fit = glm(wing_morph_binom ~ month_of_year, family="binomial", data=raw_data)
xmonth <- seq(2,12, 0.01)
wing_probs <- predict(fit, list(month_of_year=xmonth), type="response")

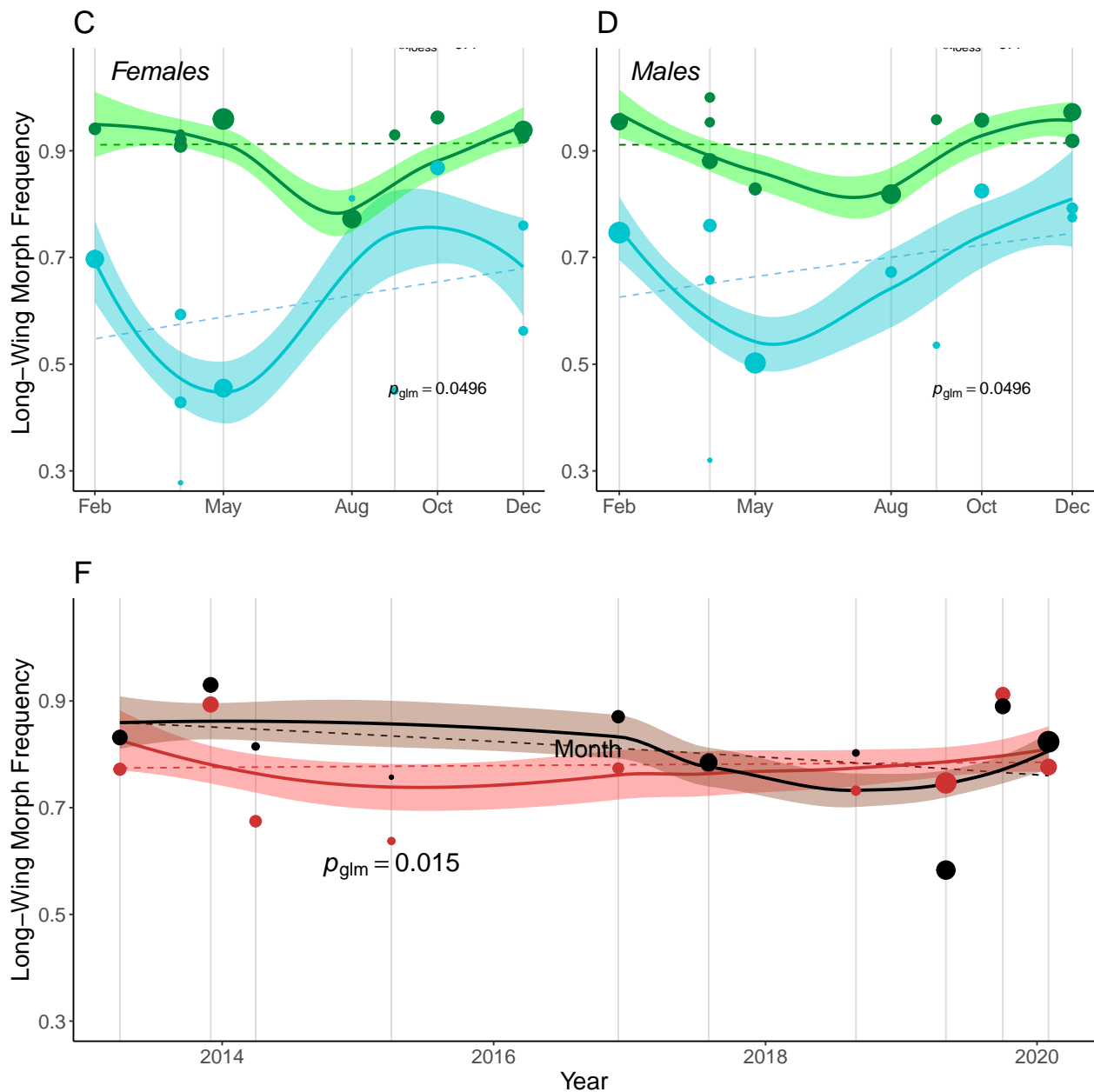
# extract pvalue from best fit regression model
fit_pvalue = round(summary(M1)$coeff[, "Pr(>|z|)"][5],5)
pvalue = paste0("italic(p)[glm]==", fit_pvalue)

# multi-variate model with year, sex, and host plant predicting wing morph
fit3 = glm(wing_morph_binom ~ sex_binom * dates, family = "binomial", data = raw_data)
xyr <- seq(sort(unique(dd$dates))[1], sort(unique(dd$dates))[10], 1)
set.seed(194842)
bsex = sample(c(-1,1), replace=TRUE, size=length(xyr))
bhost = sample(c(-1,1), replace=TRUE, size=length(xyr))
wprobs <- predict(fit3, list(sex_binom = bsex,
                           pophost_binom = bhost,
                           dates = xyr), type="response")

pred = cbind(xyr, bsex, bhost, wprobs)
pred = as.data.frame(pred)
pred$xyr = as.Date.numeric(pred$xyr)

predF = pred[pred$bsex==1,]
predM = pred[pred$bsex==-1,]
```

```
# extract pvalue from best fit regression model
fit_pvalue = round(summary(M1)$coeff[, "Pr(>|z|)"][7], 3)
pvalue = paste0("italic(p)[glm]==", fit_pvalue)
```



Wing-to-body Ratio

```
w2b_summary<-aggregate(wing2body~sex*pophost*dates*month_of_year, data=data_long, FUN=mean)
w2b_summary$se<-aggregate(wing2body~sex*pophost*dates, data=data_long,
                           FUN=SE)$wing2body
w2b_summary$n<-aggregate(wing2body~sex*pophost*dates, data=data_long,
                          FUN=length)$wing2body
```

```
jitter = runif(n=nrow(w2b_summary), min=-0.1, max=0.1) # jitter slightly
w2b_summary$dates <- w2b_summary$dates + jitter
d = w2b_summary
```

Check for LOESS Residuals

```
l1 = lowess(d$dates, d$wing2body, f=0.4)

par(mfrow=c(1,2))
plot(d$dates, d$wing2body)
lines(l1, type = "l")
plot_lowess_residuais(l1, d$dates, d$wing2body)
```

