

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"))

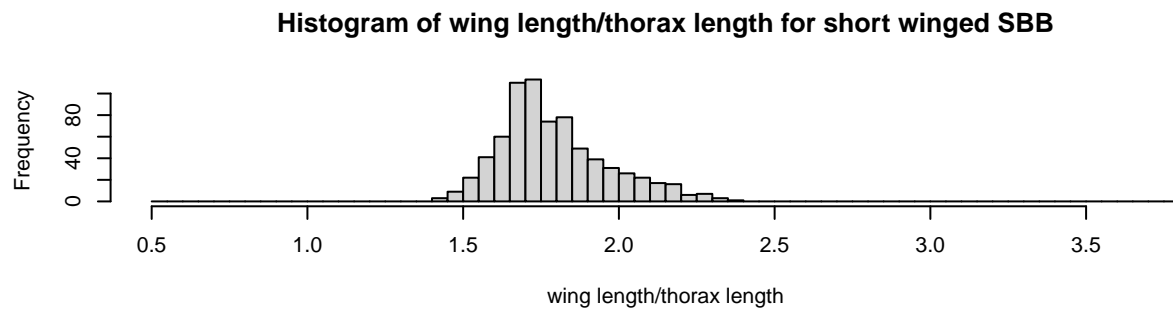
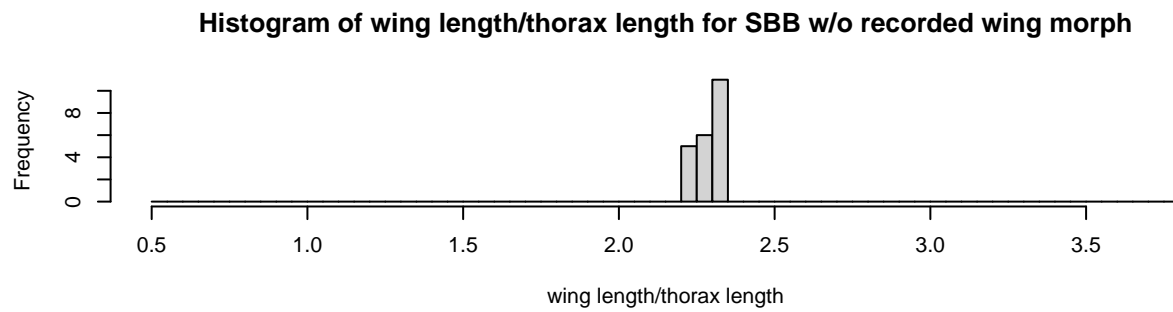
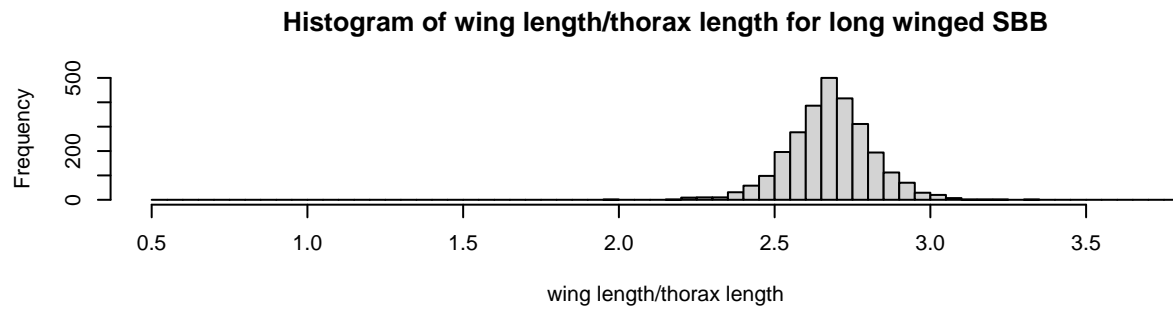
## number of missing dates: 0
##
## morph types: L S  NA LS SL
##   recoding missing morph types...
##   S if wing2thorax <=2.2, L if wing2thorax >=2.5
##
## ambiguous wing morph bug count:  48
##
## filtered out NA wing2body for data_long...

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

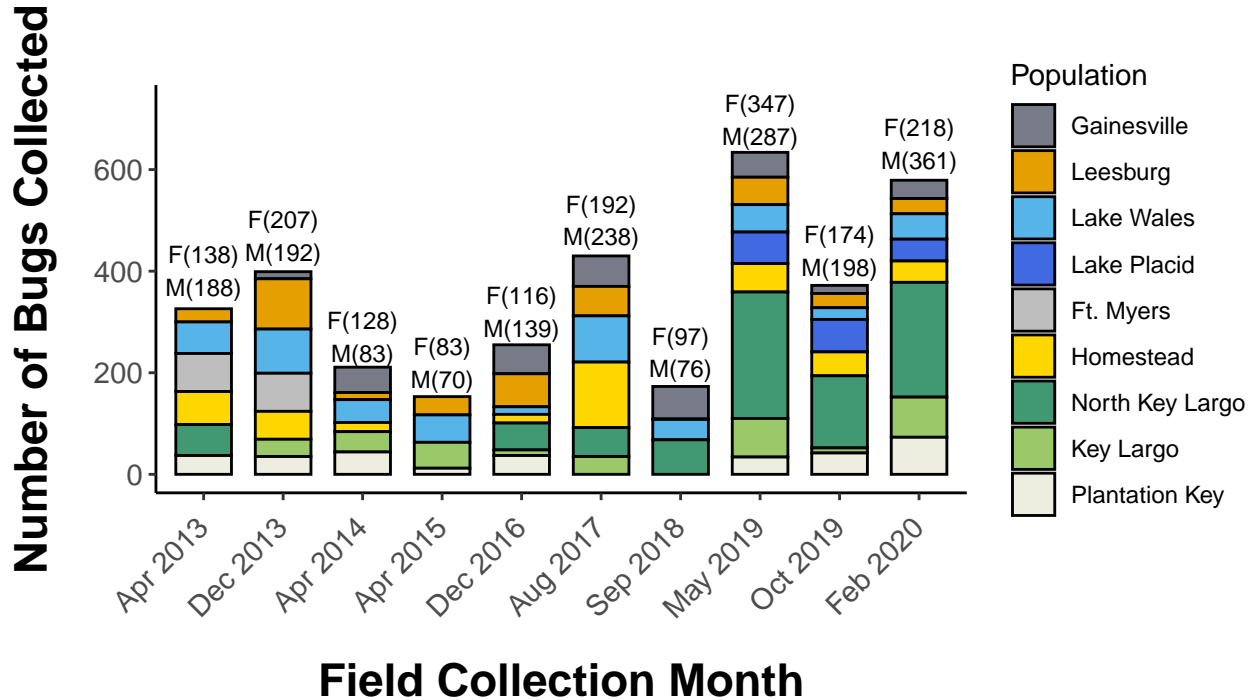


Notice that there are 30 bugs that are hard to identify as either S or L.

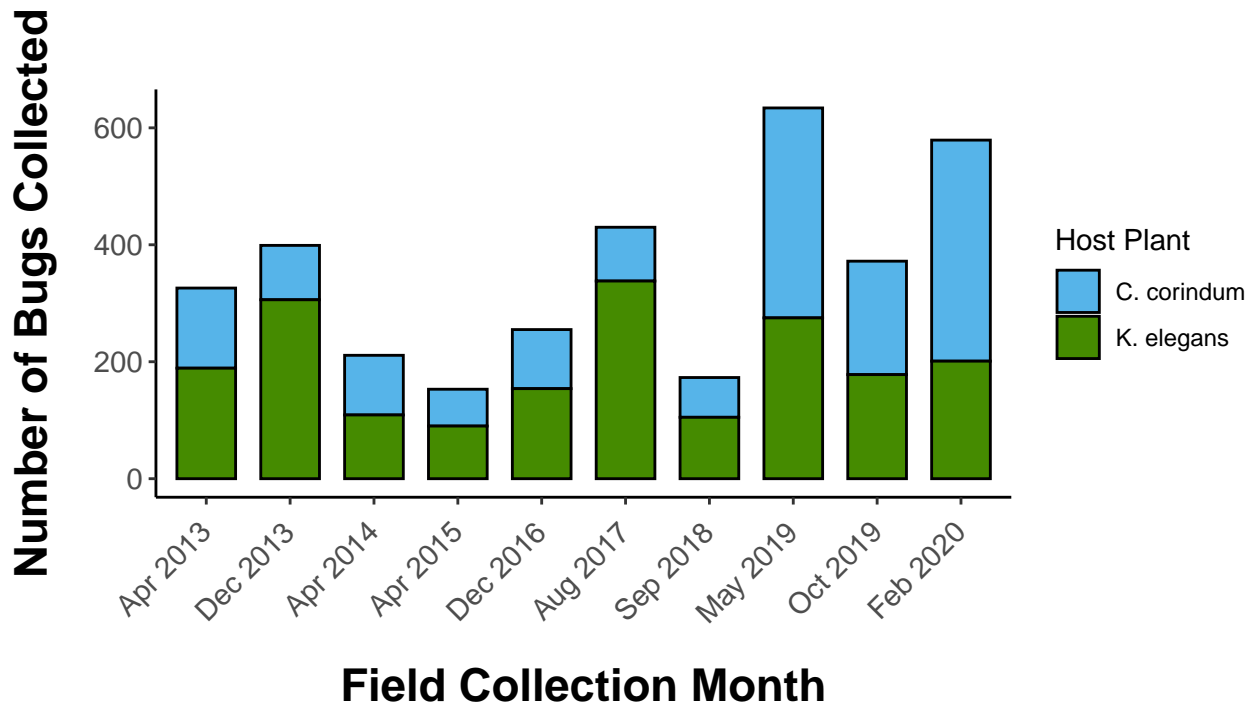
Barplots

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.

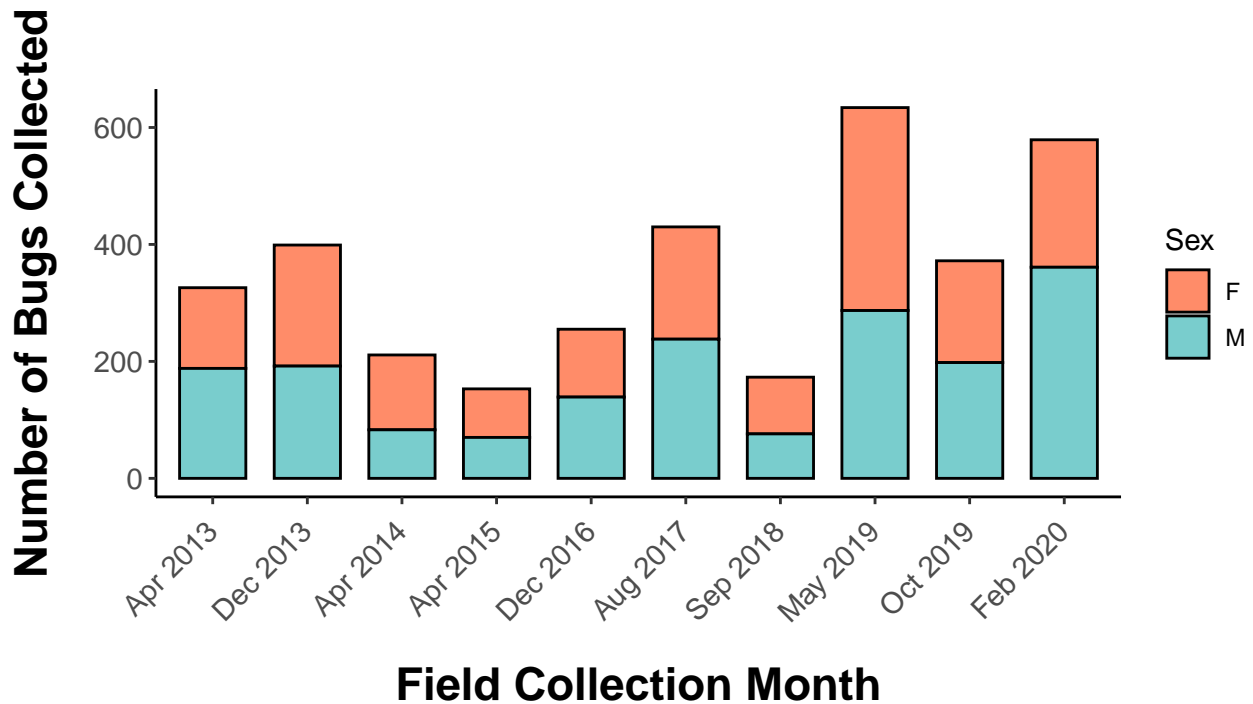
Plot 1: Collection numbers grouped by Population and Datetime



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}

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

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_residuais = 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)
```

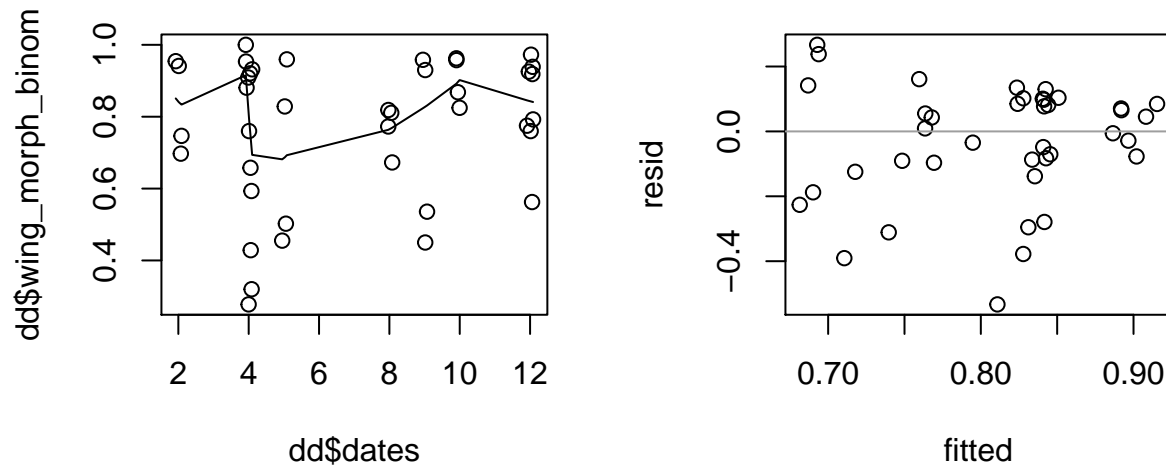


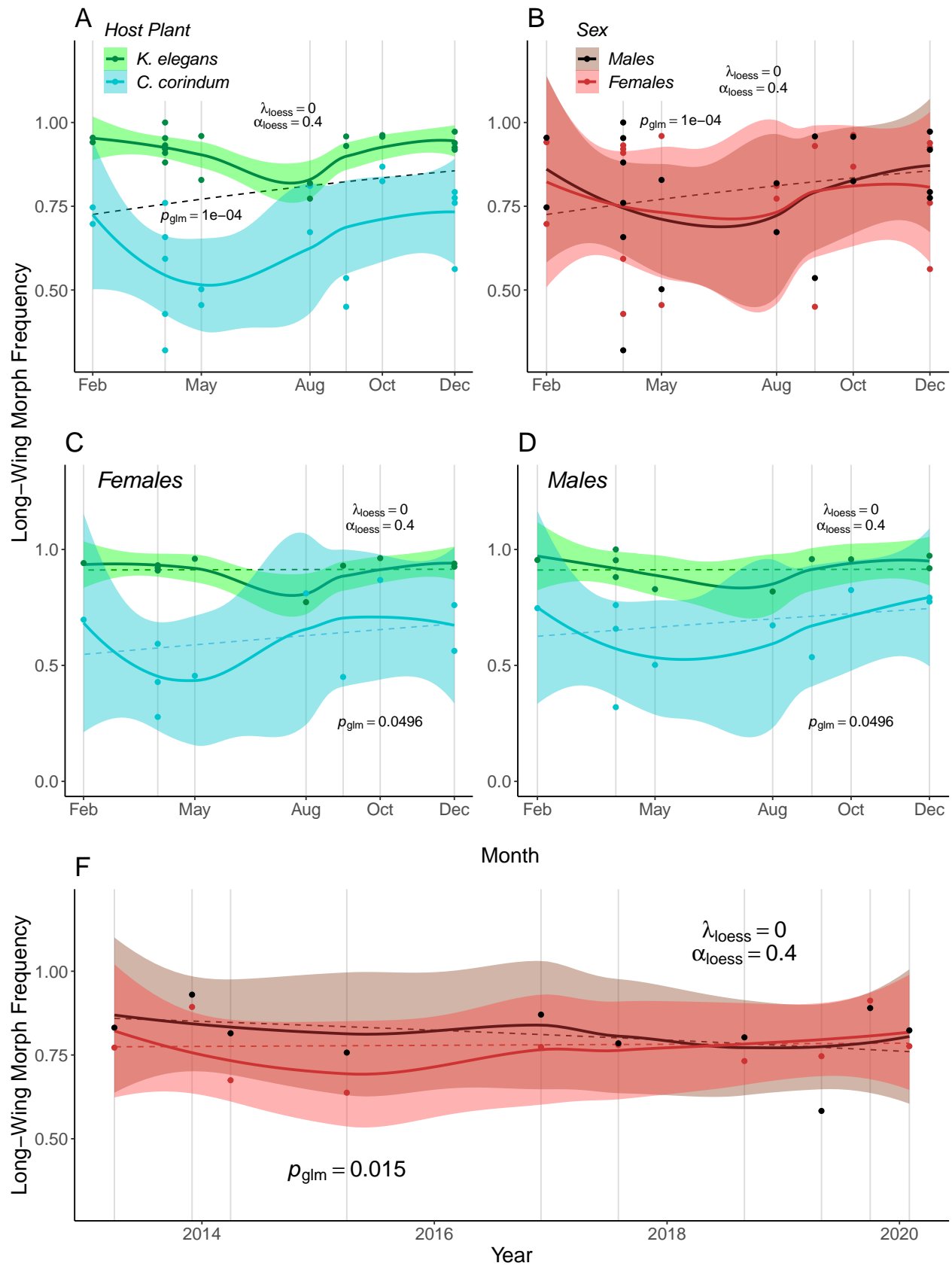
Figure: Panels A, B, C, D (long-wing morph freq with month) & E (long-wing morph freq with year)

```
# 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

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)
```

