Appendix B: Modeling Flight Response

for 'paper_title'; Bernat, AV, Cenzer, ML

Contents

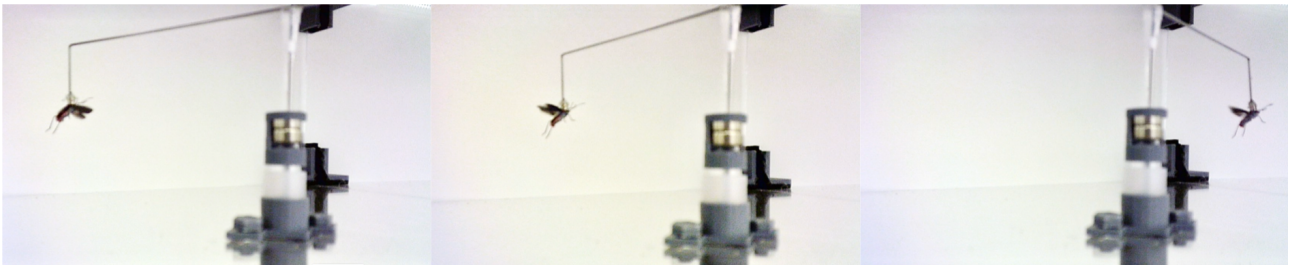
1 Details of the Analyses

This document was generated by R Markdown on 2021-12-09 using R version 4.0.5 (2021-03-31). The document provides the step-by-step analytical methods used in the manuscript by Anastasia Bernat (AVB) and Meredith Cenzer (MLC). Multiple draft scripts were written by AVB and MLC between 2020-03-01 and 2021-07-26 until being distilled and complied by AVB and code reviewed by MLC at the University of Chicago into this comprehensive script. All draft scripts can be viewed in the GitHub repository, SBB-dispersal (https://github.com/mlcenzer/SBB-dispersal), within the directory **avbernat > Dispersal > Winter_2020 > stats** .

All code and output from the statistical analyses are shown. Code for data cleaning and the generation of plots is not displayed, but can be viewed in the **appendix_B-flight_summary.Rmd** file and its accompanying sourced scripts. To repeat analyses and the generation of plots, all data files and sourced scripts should follow the directory structure presented in the SBB-dispersal repository.

1.1 Description of the Data

Soapberry bugs, *Jadera haematoloma*, were flight tested in the Fall 2019 (2019-10-15 to 2019-11-08) and Winter 2020 (2020-02-17 to 2020-03-10) seasons using a flight mill machine. Soapberry bugs were flight tested twice for either set time increments or multiple hours in the flight mill and observed from 8 AM to (5-8 PM) each day. For each trial, the mass, flight response, egg-laying response, distance, duration, average speed, and max speed of each soapberry bug was recorded and then processed.



All Python scripts used to process the flight records are located in the GitHub repository within the directory **avbernat > Dispersal > Winter_2020 > windaq_processing** . After trials, morphology measurements were taken for each bug. There are four morphology measurements: beak length, thorax width, wing length, and body length. The sex, wing morph (long-winged, shot-winged, or ambiguously-winged), host plant, and population of each bug were also recorded.

As a result of the experimental design, this document analyzes two main types of datasets: a full dataset and a unique dataset. A **full dataset** is a dataset where each row has a unique ID and trial type combination. A **unique dataset** is a dataset where each row has a unique ID because each trial has been grouped by ID. Examples are provided below. The advantage of generating a unique dataset is that changes between trials can be observed and analyzed.

1.2 Abbreviations Used in the Data and Code

- **SBB** - soapberry bug, *Jadera haematoloma*
- **S** - short-winged morph
- **L** - long-winged morph
- **LS** or **SL** - ambiguous wing morph
- **T1** - trial 1 of flight testing
- **T2** - trial 2 of flight testing
- **EWM** - eggs when massed, binary response (yes or no)
- **host_** - the host plant soapberry bugs were collected from, which was either *Koelreuteria elegans* or *Cardiospermum corindum*, occasionally called (and abbreviated) as goldenrain tree (GRT) or balloon vine (BV), respectively
- **sym_dist** - distance from the local sympatric zone, which is demarked as Homestead

- **wing2body** - a computed and unitless column that calculates the wing length divided by the body length of a soapberry bug
- **sd** - standard deviation
- **se** - standard error
- **w__** - a column name that starts with `w_` is abbreviated from "wing". Example column: w_morph is "wing morph"

1.3 Data Transformations

- `_b` - a column name that ends in `_b` is a column that has been recodified into binary data (0's and 1's). Example columns: flew_b, eggs_b
- `_c` - a column name that ends in `_c` is a column that has been centered. Example columns: sex_c, host_c, avg_days_c
- `_s` - a column name that ends in `_s` is a column that has been standardized. Example columns: wing2body_s, sym_dist_s, thorax_s
- `avg_` - a column name that starts in `avg_` is a column that has been averaged across trial 1 (T1) and trial 2 (T2). Example columns: avg_mass, avg_days, avg_time_start, avg_rec_dur (exception: average_speed)
- `_diff` - a column name that ends in `_diff` is a column that is the difference between T1 and T2 data values. Formula: data values
- `_per` - a column name that ends in `_per` is a column that is the percent change between T1 and T2 (T2-T1) data values. Formula: (T2-T1)/T1 * 100.
- `_logsqrt` - a column name that ends in `_logsqrt` is a column that has been normalized using a log-square-root transformation. Formula: `log(sqrt(<data_column>))-mean(log(sqrt(<data_column>))`. Example columns: avg_mass_logsqrt
- `_logsqrt_i` - a column name that ends in `_logsqrt_i` is a column that has been normalized using a log-square-root transformation but its sign is the inverse of the column. Formula: `log(sqrt(0.85-column))-mean(log(sqrt(0.85-column))`. Example columns: wing2body_logsqrt_i

2 Winter 2020 Data Cleaning

2.1 Read Libraries

The flight response of *J. haematoloma* was analyzed using multivariate, generalized linear modeling (GLM) as implemented in the R packages `lme4` and `binom`. All plots were generated using base R and supplemented with the `popbio` package to display logistic regressions and the `rethinking` package to display 95% confidence intervals of linear regressions. Additional R packages not show below but embedded in the sourced scripts are `lubridate`, `chron`, and `dplyr`. `lubridate` and `chron` both aid in datetime manipulation while `dplry` pipelines data grouping processes.

```
library(lme4)        # fit regressions
library(rethinking) # Bayesian data analysis and plotting
library(popbio)      # logistic regression plotting
library(binom)       # binomial confidence intervals
```

2.2 Read Source Files

Each sourced script below aides in either data cleaning (`read_flight_data()`, `center_data()`) or multivariate GLM (`model_comparisonsAIC()`, `get_model_probs()`, `catch_warnings()`). Additionally, the function `model_comparisonsAIC()` takes in the path of a generic multi-factor script specific to

the GLM family and link function needed to build the predictive models. All aforementioned, sourced scripts are located in the **Rscr** folder.

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

script_names = c("center_flight_data.R",  # 1 function: center_data()
                 "clean_flight_data.R",   # 1 function: clean_flight_data()
                 "unique_flight_data.R",  # 1 function: create_delta_data()
                 "compare_models.R",      # 1 function: model_comparisonsAIC()
                 "get_Akaike_weights.R",  # 1 function: get_model_probs()
                 "get_warnings.R")        # 1 function: catch_warnings()

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

2.3 Read the Data

The flight performance data read directly below are only from Winter 2020 flight trials. The `read_flight_data()` function standardizes data types and names of the ID, trial type, host plant, flight response, egg-laying response, sex, population, and wing morph inputs. The date, start time, and end time of trails are also converted into datetimes. Variables of interest like wing-to-body ratio are also calculated and centered. Using the `clean_flight_data()` function, all morphology, mass, and flight performance measurements are centered and/or standardized within the `read_flight_data()` function. Then, what is returned is a full dataset (n=758) that includes all bugs collected during Winter 2020 and a subset of the full dataset (n=614) that includes only bugs tested from the Winter 2020 collection.

The `create_delta_data()` function generates the unique dataset by grouping by ID. The function also computes trial differences, percent differences, and averages for variables of interest such as mass, flight response, egg-laying response, distance, and speed. Then, the unique data variables are centered and/or standardized.

```
data_path = paste0(dir,"/Dispersal/Winter_2020/stats/data/all_flight_data-Winter2020.csv")

data = read_flight_data(data_path) # centers each subset of data
data_all = data[[1]]               # full dataset
data_tested = data[[2]]            # subset of data_all, contains only bugs flight tested

# create the unique dataset
d <- create_delta_data(data_tested, remove_bugs_tested_once = FALSE)

# keep all bugs (even bugs only tested once), then re-center
dc <- center_data(d, is_not_unique_data = FALSE)
```

Example of a **full dataset** (each row has unique ID and trial type):

```
data_tested[c(1:2,400:401), c("ID", "trial_type")]
```

```
##      ID trial_type
## 1   114         T1
## 2   318         T1
## 400 316         T2
## 401 416         T2
```

Example of a **unique dataset** (each row has unique ID):

```
dc[c(1:2,295:296), c("ID", "trial_type")]
```

```
## # A tibble: 4 x 2
## # Groups:   ID [4]
##   ID    trial_type
##   <fct> <list>
## 1 1     <fct [2]>
## 2 2     <fct [2]>
## 3 400   <fct [2]>
## 4 401   <fct [2]>
```

The datatype of the `trial_type` column is a list because when expanded out, it would show `list(T1, T2)`.

3 Across-Trial Flight Response (T1 & T2)

Flight response (yes flew or did not fly) was recorded and modeled. Multivariate, GLM was performed using the `glm()` function in the `lme4` package. Models were compared using Akaike Information Criterion (AIC) and model selection was determined using Akaike weights. Model fit was further evaluated between two models using the `anova()` function.

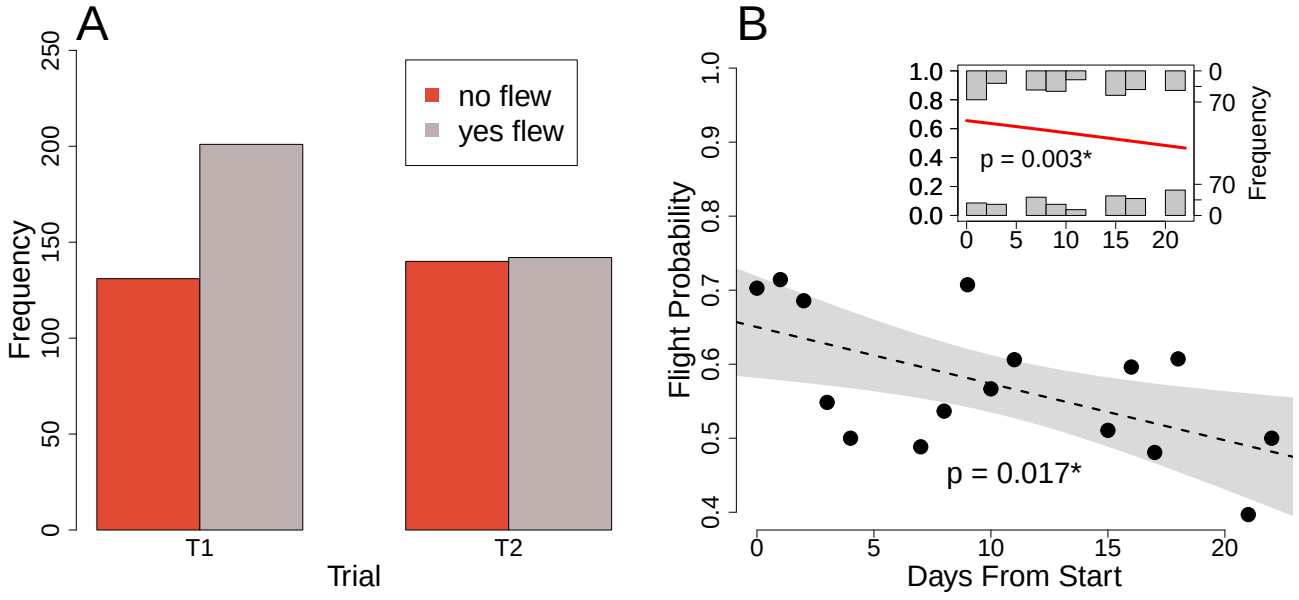
3.1 Experimental Effects

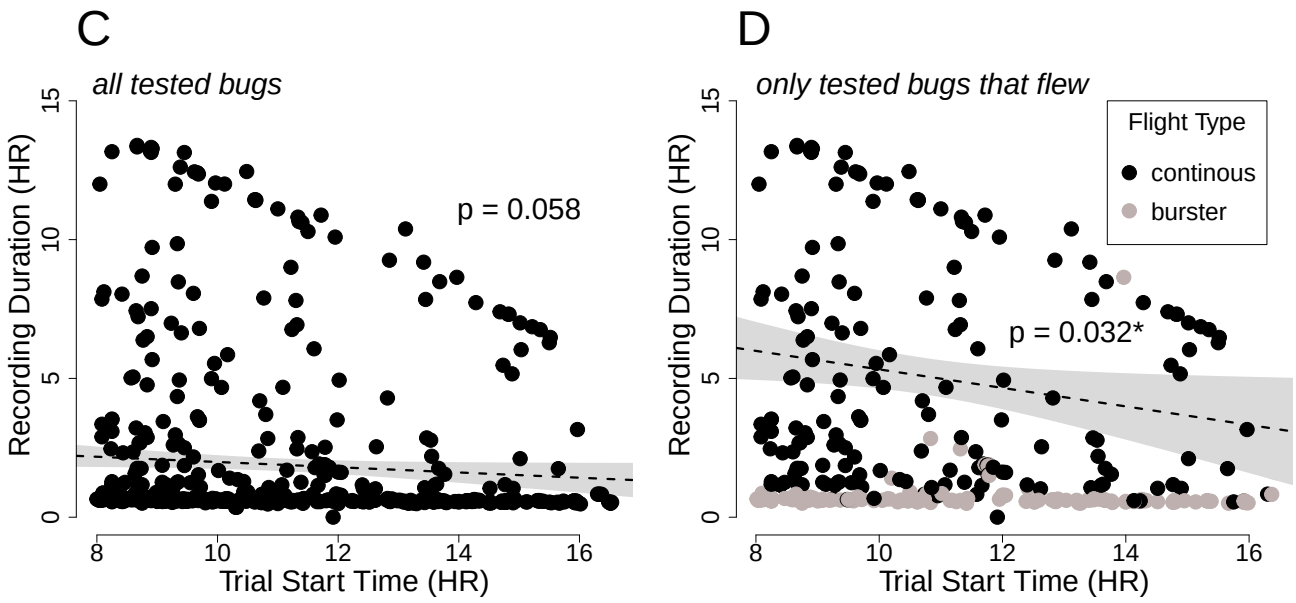
To determine how the design of the experiment affected flight response and/or performance, three design factors were modeled: trial type (T1 vs. T2), days from start, and trial start time.

3.1.1 Trial Type, Days from Start & Trial Start Time

```
# compute how many times flew yes or no per trial
binary_counts = table(data_tested$flew_b, data_tested$trial_type)[,2:3]

# aggregate by days since the trials began and flight response to determine flight prob
dd = aggregate(flew_b ~ days_from_start, data=data_tested, FUN=mean)
```





A & B. There was a negative effect of day a bug was tested (since the start of trials) on flight probability, but there was a significant effect only when the full dataset is considered. It is not significant for the unique dataset because days from start had to be averaged between trials. This is explored in the next section of the report. **C & D.** There was a negative effect of the trial start time on flight duration but only after removing bugs that did not fly ($p = 0.031$). Continuous flyers are driving this significant relationship (**D**).

3.2 Binomial Modeling

To understand SBB flight response, flight response across trials was modeled against sex, host plant, distance from the sympatric zone, wing-to-body ratio, and mass. This was done using the unique dataset.

Because the unique dataset was used, there exist multiple recorded counts of the number of times a SBB flew and did not fly between trials, T1 and T2. For that reason, we used `cbind(num_flew, num_notflew)` when modeling in order to account for all flight successes and failures for each individual.

Finally, we tested whether the data was over-dispersed, which could be resolved using a Quasibinomial:

```
# calculate the confidence interval for the mean of the data (Binomial vs. Quasibinomial)
fit <- glm(cbind(num_flew, num_notflew) ~ 1, family = binomial, data = dc)
plogis(confint(fit))
```

```
##     2.5 %    97.5 %
## 0.5191729 0.5976031
```

```
fit_q <- glm(cbind(num_flew, num_notflew) ~ 1, family = quasibinomial, data = dc)
plogis(confint(fit_q))
```

```
##     2.5 %    97.5 %
## 0.5108508 0.6056992
```

```
# estimate the dispersion parameter
summary(fit_q)$dispersion
```

```
## [1] 1.464596
```

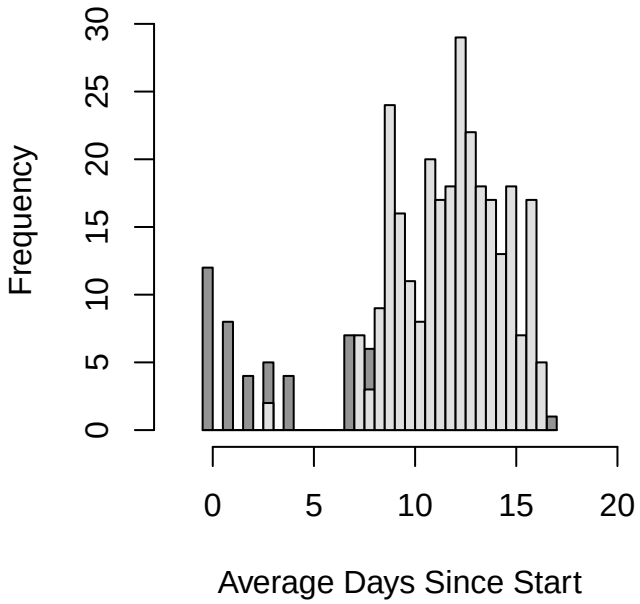
If the dispersion parameter is close to 1, the data is not over-dispersed, so there is not much of a necessity to apply a Quasibinomial model. Therefore, we selected the family as "binomial".

3.2.1 Average Days Since Start

For the unique dataset, average days since start (log-square-root transformed) was computed in order to determine how an experimental factor affected flight response. It proved to not be significant:

```
avg_days_model<-glm(cbind(num_flew,num_notflew)~avg_days_c, data=dc, family=binomial)
summary(avg_days_model)
```

```
##
## Call:
## glm(formula = cbind(num_flew, num_notflew) ~ avg_days_c, family = binomial,
##     data = dc)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8429  -1.7825  -0.1593   1.5162   1.5795
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.22942    0.08236   2.785  0.00535 **
## avg_days_c   0.01087    0.02354   0.462  0.64430
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 668.05  on 332  degrees of freedom
## Residual deviance: 667.84  on 331  degrees of freedom
## AIC: 759.17
##
## Number of Fisher Scoring iterations: 3
```



Average days since start accounts for bugs who died before they could be tested twice, which would most likely lead to an early average day value. The rest of the bugs that were tested twice would most likely have a later average day value. This testing regime shapes the bimodal distribution seen in the histogram. Additionally, the advantage of this computed variable is that it controls for the fact that some bugs were tested once late, and some had been tested twice early. In turn, because we randomized test day, when repeated measures for each individual are combined across days, they

balance each other out. Thus, average days since start allows the multi-variate models, which control for repeated tests per ID number, to converge, and we can be confident that non-random mortality is not impacting flight response.

3.2.2 Single-Variate Effects sex, mass, wing2body

We used aggregated datasets for single-variate modeling.

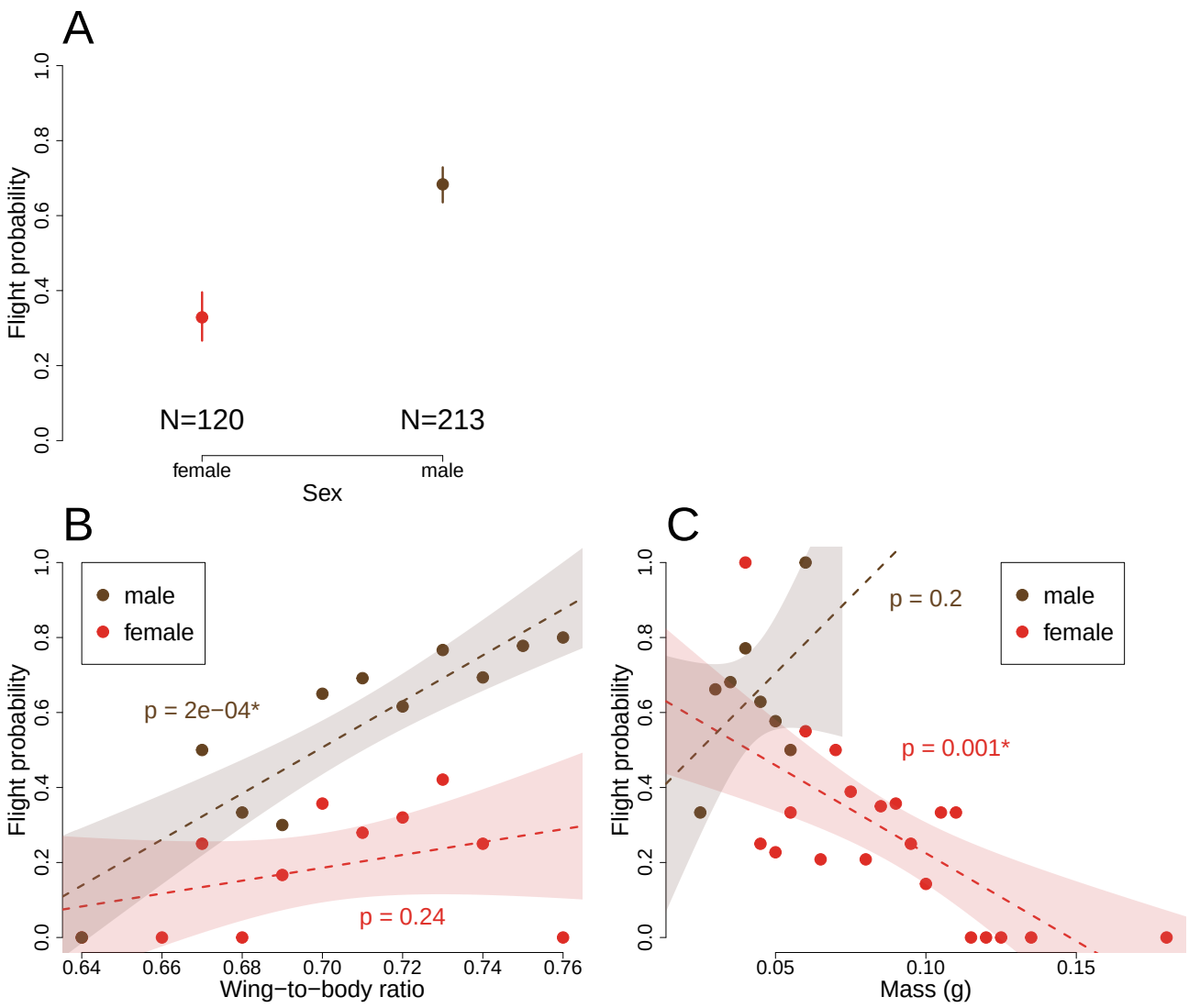
```
# tailoring variables for plotting
d$mass_block=round(d$avg_mass/0.005)*0.005      # 0.005 g blocks
d$wing2body_block=round(d$wing2body, digits=2)  # 0.01 blocks
d$days_block=round(d$avg_days, digits=0)        # integer blocks
```

```
# aggregate data for plotting
dt=aggregate(flew_prob~sex, data=d, FUN=mean)
dt$trials=c(sum(d$num_flew[d$sex=="F"]+d$num_notflew[d$sex=="F"]),
            sum(d$num_flew[d$sex=="M"]+d$num_notflew[d$sex=="M"]))

ds=aggregate(flew_prob~sex*wing2body_block, data=d, FUN=mean)
ds$n=aggregate(flew_prob~sex*wing2body_block, data=d, FUN=length)$flew_prob

dm=aggregate(flew_prob~sex*mass_block, data=d, FUN=mean)
dm$n=aggregate(flew_prob~sex*mass_block, data=d, FUN=length)$flew_prob

# calculate binomial confidence interval
dt$successes = c(sum(d$num_flew[d$sex=="F"]), sum(d$num_flew[d$sex=="M"]))
dt$CI = binom.confint(dt$successes, dt$trials, methods="exact")
```



3.2.3 Multi-Variate Models

sex, mass, wing2body, host plant, distance from sympatric zone

We used the unique dataset for multi-variate modeling.

```
data<-data.frame(R1 = dc$num_flew,
                 R2 = dc$num_notflew,
                 A = dc$host_c,
                 B = dc$sex_c,
                 C = dc$sym_dist,
                 D = dc$avg_mass_logsqrt,
                 E = dc$avg_days_c)

model_script = paste0(source_path,"generic models-binomial glm 2R ~ 4-FF + E.R")
errors = catch_warnings(model_comparisonsAIC(model_script))
cat("Number of models that failed to converge: ", length(errors$warnings))
```

```
##        [,1]       [,2]       [,3]
## AICs   683.3791   683.95     684.4483
## models 85         63         50
## probs  0.08873418 0.06669969 0.05198815
##
## m85  glm(formula = cbind(R1, R2) ~ A * D + B * D + C * D + E, family = binomial,
```

```
##     data = data)
## m63  glm(formula = cbind(R1, R2) ~ A * D + C * D + B + E, family = binomial,
##     data = data)
## m50  glm(formula = cbind(R1, R2) ~ A * D + B * D + E, family = binomial,
##     data = data)
## Number of models that failed to converge:  0
```

```
anova(m63, m85, test="Chisq") # Adding B*D does not improve fit
anova(m63, m36, test="Chisq") # Adding C*D does improve fit
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * D + C * D + B + E
## Model 2: cbind(R1, R2) ~ A * D + B * D + C * D + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       325     580.61
## 2       324     578.04  1   2.5709   0.1088
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * D + C * D + B + E
## Model 2: cbind(R1, R2) ~ A * D + B + C + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       325     580.61
## 2       326     585.11 -1  -4.4988  0.03392 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
M1 <- glm(cbind(num_flew, num_notflew) ~ host_c * avg_mass_logsqrt
          + sym_dist_s * avg_mass_logsqrt + sex_c + avg_days_c, data=d, family=binomial)
summary(M1)
```

3.2.3.1 Best Fit

```
##
## Call:
## glm(formula = cbind(num_flew, num_notflew) ~ host_c * avg_mass_logsqrt +
##     sym_dist_s * avg_mass_logsqrt + sex_c + avg_days_c, family = binomial,
##     data = d)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.54691  -1.08562  -0.03924   1.17713   2.41023
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 0.03733    0.11152   0.335  0.73785
## host_c                     -0.14197    0.13044  -1.088  0.27643
## avg_mass_logsqrt           -1.00302    0.88134  -1.138  0.25510
## sym_dist_s                 -0.03954    0.12352  -0.320  0.74890
## sex_c                      -0.46077    0.16797  -2.743  0.00609 **
## avg_days_c                  0.01138    0.02596   0.438  0.66111
## host_c:avg_mass_logsqrt     1.85594    0.59204   3.135  0.00172 **
```

```
## avg_mass_logsqrt:sym_dist_s -1.36386    0.66258  -2.058  0.03955 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 668.05  on 332  degrees of freedom
## Residual deviance: 580.61  on 325  degrees of freedom
## AIC: 683.95
##
## Number of Fisher Scoring iterations: 4
```

3.2.4 Multi-Variate Models Split By Sex

```
data_fem <- dc[dc$sex=="F",]
data_fem <- center_data(data_fem, is_not_unique_data = FALSE)
```

```
data<-data.frame(R1 = data_fem$num_flew,
                 R2 = data_fem$num_notflew,
                 A = data_fem$host_c,
                 B = data_fem$sym_dist,
                 C = data_fem$avg_mass_logsqrt,
                 D = data_fem$wing2body_logsqrt_i,
                 E = data_fem$avg_days_c)

model_script = paste0(source_path,"generic models-binomial glm 2R ~ 4-FF + E.R")
errors = catch_warnings(model_comparisonsAIC(model_script))
cat("Number of models that failed to converge: ", length(errors$warnings))
```

3.2.4.1 Females

```
##         [,1]       [,2]       [,3]
## AICs   238.8713   239.0635   239.8444
## models 45         25         10
## probs  0.08178418 0.07429069 0.0502761
##
## m45  glm(formula = cbind(R1, R2) ~ A * C + A * D + E, family = binomial,
##     data = data)
## m25  glm(formula = cbind(R1, R2) ~ A * C + D + E, family = binomial,
##     data = data)
## m10  glm(formula = cbind(R1, R2) ~ C + D + E, family = binomial, data = data)
## Number of models that failed to converge:  0
```

```
anova(m25, m45, test='Chisq') #adding A*D does not improve fit
anova(m25, m13, test='Chisq') #adding A*C improves fit
anova(m25, m17, test="Chisq") #adding D improves fit
anova(m25, m45, test="Chisq") #adding D improves fit
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * C + D + E
```

```
## Model 2: cbind(R1, R2) ~ A * C + A * D + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       114     202.11
## 2       113     199.92  1   2.1922   0.1387
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * C + D + E
## Model 2: cbind(R1, R2) ~ A + C + D + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       114     202.11
## 2       115     206.87 -1   -4.764  0.02906 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * C + D + E
## Model 2: cbind(R1, R2) ~ A * C + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       114     202.11
## 2       115     206.35 -1   -4.243  0.03941 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * C + D + E
## Model 2: cbind(R1, R2) ~ A * C + A * D + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       114     202.11
## 2       113     199.92  1   2.1922   0.1387
```

```
M2 <- glm(cbind(num_flew, num_notflew) ~ host_c * avg_mass_logsqrt +  wing2body_logsqrt_i +
            avg_days_c, data=data_fem, family=binomial)
summary(M2)
```

3.2.4.1.1 Best Fit

```
##
## Call:
## glm(formula = cbind(num_flew, num_notflew) ~ host_c * avg_mass_logsqrt +
##     wing2body_logsqrt_i + avg_days_c, family = binomial, data = data_fem)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.1849  -1.1189  -0.7523   1.1182   2.7357
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -0.15913    0.34121  -0.466   0.6409
## host_c                   -0.61037    0.33019  -1.849   0.0645 .
## avg_mass_logsqrt         -2.08700    1.45468  -1.435   0.1514
## wing2body_logsqrt_i      -5.37017    2.66359  -2.016   0.0438 *
## avg_days_c                0.11558    0.04757   2.430   0.0151 *
## host_c:avg_mass_logsqrt   3.02237    1.39976   2.159   0.0308 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 223.66  on 119  degrees of freedom
## Residual deviance: 202.11  on 114  degrees of freedom
## AIC: 239.06
##
## Number of Fisher Scoring iterations: 4
```

```
data_male <- dc[dc$sex=="M",]
data_male <- center_data(data_male, is_not_unique_data = FALSE)
```

3.2.4.2 Males

```
## Warning in d$latitude - sym_zone: longer object length is not a multiple of
## shorter object length
```

```
data<-data.frame(R1 = data_male$num_flew,
                 R2 = data_male$num_notflew,
                 A = data_male$host_c,
                 B = data_male$sym_dist,
                 C = data_male$avg_mass_logsqrt,
                 D = data_male$wing2body_logsqrt_i,
                 E = data_male$avg_days_c)

model_script = paste0(source_path,"generic models-binomial glm 2R ~ 4-FF + E.R")
errors = catch_warnings(model_comparisonsAIC(model_script))
cat("Number of models that failed to converge: ", length(errors$warnings))
```

```
##         [,1]       [,2]       [,3]
## AICs   427.3929   427.649    428.1156
## models 105        50         83
## probs  0.08393807 0.07384843 0.05848274
##
## m105     glm(formula = cbind(R1, R2) ~ A * D + B * C + B * D + C * D +
##     E, family = binomial, data = data)
## m50  glm(formula = cbind(R1, R2) ~ A * D + B * D + E, family = binomial,
##     data = data)
## m83  glm(formula = cbind(R1, R2) ~ A * D + B * C + B * D + E, family = binomial,
##     data = data)
## Number of models that failed to converge:  0
```

```
anova(m83, m105, test="Chisq") # adding C*D marginally improves fit
anova(m83, m62, test="Chisq") # adding B*C marginally improves fit
anova(m50, m62, test="Chisq") # adding C does not improve fit
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * D + B * C + B * D + E
## Model 2: cbind(R1, R2) ~ A * D + B * C + B * D + C * D + E
```

```
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       204     347.73
## 2       203     345.01  1   2.7227  0.09893 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * D + B * C + B * D + E
## Model 2: cbind(R1, R2) ~ A * D + B * D + C + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       204     347.73
## 2       205     351.01 -1  -3.2786  0.07019 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Deviance Table
##
## Model 1: cbind(R1, R2) ~ A * D + B * D + E
## Model 2: cbind(R1, R2) ~ A * D + B * D + C + E
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       206     351.27
## 2       205     351.01  1  0.25488   0.6137
```

```
M3<-glm(cbind(num_flew, num_notflew)~host_c*wing2body_logsqrt_i + sym_dist*wing2body_logsqrt_i
        + avg_days_c, family=binomial, data=data_male)
summary(M3)
```

3.2.4.2.1 Best Fit

```
##
## Call:
## glm(formula = cbind(num_flew, num_notflew) ~ host_c * wing2body_logsqrt_i +
##     sym_dist * wing2body_logsqrt_i + avg_days_c, family = binomial,
##     data = data_male)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.6331  -0.7526   0.8309   1.1667   2.0726
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                    0.46487    0.22478   2.068   0.0386 *
## host_c                        -0.38219    0.18897  -2.023   0.0431 *
## wing2body_logsqrt_i          -15.20652    5.22315  -2.911   0.0036 **
## sym_dist                       0.11229    0.13852   0.811   0.4176
## avg_days_c                    -0.03316    0.03421  -0.969   0.3323
## host_c:wing2body_logsqrt_i    -9.46041    4.27524  -2.213   0.0269 *
## wing2body_logsqrt_i:sym_dist   6.31131    3.02643   2.085   0.0370 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 372.15  on 212  degrees of freedom
```

```
## Residual deviance: 351.27  on 206  degrees of freedom
## AIC: 427.65
##
## Number of Fisher Scoring iterations: 4
```

4 Between-Trial Flight Response (T1 vs. T2)

4.1 Read Libraries

```
library(dplyr) # data manipulation
library(zoo) # data manipulation
library(nnet) # multinomial modeling
library(kableExtra) # table formatting
library(plot.matrix) # enables matrix/heatmap plotting
```

4.2 Read Source Files

```
script_names = c("multinom_functions.R") # 4 relevant functions:
                                         # calculate_P2(), calculate_P3(),
                                         # get_significant_models(),
                                         # get_significant_modelsf(),

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

4.3 Read the Data

```
# only keep bugs tested twice
d = create_delta_data(data_tested, remove_bugs_tested_once=TRUE)
```

4.4 Encodings & Signs

We aimed to model the probability of different delta flight response cases with sex, host plant, percent changes in mass, and percent changes in egg-laying response as predictors. Since the outcomes (or response variables) were no longer binomial, we used multi-categorical logit models. Below are the categorical encodings and/or signs used. See the Appendix for additional explanations and examples of computing multi-categorical logit models.

Delta Flight Response Key	
Event	Encoding
flew in both trials	2
flew in T2 only	1
flew in neither trials	0
flew in T1 only	-1

Delta Percent Mass Key (%)	
Event	Sign
gained % mass from T1 to T2	+
no % mass change between trails	0
lost % mass from T1 to T2	-

Host Plant Key	
Host	Encoding
Golden Rain Tree (GRT)	1
Balloon Vine (BV)	-1

Sex Key	
Sex	Encoding
Female	1
Male	-1

4.5 Multinomial Modeling

4.5.1 Baseline

```
# remove any missing values for flight case or mass percent change between trials
df = d[with(d,!is.na(flight_case) & !is.na(mass_per)),]

# order the dataset by ascending mass percent change values
df = df[with(df, order(mass_per)),]

# relevel the flight case factors so as to set 0 as the first level.
df$flight_case = relevel(as.factor(df$flight_case), ref = "0")
```

4.5.2 Null Model

```
null = multinom(flight_case ~ 1, data = df)
```

```
## # weights:  8 (3 variable)
## initial  value 385.389832
## iter  10 value 319.269929
## final  value 319.269680
## converged
```

4.5.3 Compare Models - predictors: % mass, sex, host

```
data = data.frame(R = df$flight_case,
         A = df$mass_per,
         B = df$sex_c,
         C = df$host_c)
```

```r
model_script = paste0(source_path,"generic multinomial models- multinom 1RF + 3 FF.R")
model_comparisonsAIC(model_script)
```

```
##        [,1]      [,2]      [,3]       [,4]
## AICs   587.5607  591.9016  592.3168   592.4231
## models 4         7         13         12
## probs  0.7141852 0.0815063 0.06622882 0.06280119
##
## m4   multinom(formula = R ~ A + B, data = data, trace = FALSE)
## m7   multinom(formula = R ~ A + B + C, data = data, trace = FALSE)
## m13  multinom(formula = R ~ B * C + A, data = data, trace = FALSE)
## m12  multinom(formula = R ~ A * C + B, data = data, trace = FALSE)
```

```r
anova(m4, m7, test="Chisq") # Adding C (host plant) does not improve fit
anova(m4, m8, test="Chisq") # Adding A*B does not improve fit
```

```
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##       Model Resid. df Resid. Dev   Test    Df LR stat.   Pr(Chi)
## 1     A + B       825   569.5607
## 2 A + B + C       822   567.9016 1 vs 2     3 1.659076 0.6460701
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##   Model Resid. df Resid. Dev   Test    Df  LR stat.   Pr(Chi)
## 1 A + B       825   569.5607
## 2 A * B       822   569.4209 1 vs 2     3 0.1398496 0.9866598
```

4.5.4 Best Fit

```r
M4 = multinom(flight_case ~ mass_per + sex_c, data = df)
model_table4 = calculate_P2(M4, "mass_per", "sex_c")
```

```
## # weights:  16 (9 variable)
## initial  value 385.389832
## iter  10 value 286.869825
## iter  20 value 284.809036
## iter  30 value 284.797822
## final  value 284.780360
## converged
##
##  AIC:  587.5607
##    (Intercept) mass_per  sex_c DF   SEi   SE1   SE2      zi     z1      z2
## -1      -1.015    0.043 -0.692  9 0.239 0.010 0.203  -4.248  4.390  -3.408
## 1       -6.820   -0.009 -5.626  9 0.183 0.026 0.183 -37.245 -0.348 -30.721
## 2        0.124    0.019 -0.902  9 0.167 0.008 0.159   0.742  2.334  -5.684
##       waldi  wald1   wald2 Pi > |z| P1 > |z| P2 > |z|
## -1   18.049 19.272  11.617    0.000    0.000    0.001
## 1  1387.197  0.121 943.764    0.000    0.728    0.000
## 2     0.551  5.447  32.310    0.458    0.020    0.000
```

Host plant was not a significant predictor, so we tested the wing-to-body ratio as a predictor next.

4.5.5 Compare Models - predictors: % mass, sex, wing2body

```
df$wing2body_c = df$wing2body - mean(df$wing2body) # re-center the w2b predictor
```

```
data = data.frame(R = df$flight_case,
                  A = df$mass_per,
                  B = df$sex_c,
                  C = df$wing2body_c)
model_script = paste0(source_path,"generic multinomial models- multinom 1RF + 3 FF.R")
model_comparisonsAIC(model_script)
```

```
##        [,1]      [,2]      [,3]
## AICs   582.2678  585.1197  587.133
## models 7         12        13
## probs  0.6671688 0.1603139 0.05858546
##
## m7   multinom(formula = R ~ A + B + C, data = data, trace = FALSE)
## m12  multinom(formula = R ~ A * C + B, data = data, trace = FALSE)
## m13  multinom(formula = R ~ B * C + A, data = data, trace = FALSE)
```

```
anova(m7, m12, test="Chisq") # adding A*C does not improve fit
anova(m7, m13, test="Chisq") # Adding B*C does not improve fit
```

```
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##       Model Resid. df Resid. Dev   Test    Df LR stat.   Pr(Chi)
## 1 A + B + C       822   558.2678
## 2 A * C + B       819   555.1197 1 vs 2     3 3.148182 0.3693379
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##       Model Resid. df Resid. Dev   Test    Df LR stat.   Pr(Chi)
## 1 A + B + C       822   558.2678
## 2 B * C + A       819   557.1330 1 vs 2     3 1.134887 0.7686596
```

4.5.6 Best Fit

```
M5 = multinom(flight_case ~ mass_per + sex_c + wing2body_c, data = df)
model_table5 = calculate_P3(M5)
```

```
## # weights:  20 (12 variable)
## initial  value 385.389832
## iter  10 value 286.740091
## iter  20 value 280.436850
## iter  30 value 279.437125
## iter  40 value 279.174660
## iter  50 value 279.134087
## final  value 279.133921
## converged
```

```
##
##  AIC:  582.2678
##    (Intercept) mass %    sex wing2body DF   SEi   SE1   SE2    SE3      zi
## -1      -0.935  0.041 -0.571    23.739 12 0.243 0.010 0.212 12.059  -3.854
## 1       -8.177 -0.005 -6.954    -6.595 12 0.187 0.025 0.187 18.786 -43.767
## 2        0.201  0.018 -0.760    28.094 12 0.172 0.008 0.166  9.718   1.173
##        z1      z2     z3    waldi  wald1    wald2 wald3 Pi>|z| P1>|z| P2>|z|
## -1  4.254  -2.698  1.969   14.850 18.096    7.278 3.875  0.000  0.000  0.007
## 1  -0.215 -37.102 -0.351 1915.510  0.046 1376.550 0.123  0.000  0.830  0.000
## 2   2.141  -4.590  2.891    1.375  4.585   21.071 8.357  0.241  0.032  0.000
##    P3>|z|
## -1  0.049
## 1   0.726
## 2   0.004
```

4.5.7 Prediction Equations

```
get_prediction_eq = function(tb, table_rowA, table_rowB, var_lab1, var_lab2, var_lab3,
                             log_lab, title_lab) {
  I = (tb[table_rowA,1] - tb[table_rowB,1])
  M = (tb[table_rowA,2] - tb[table_rowB,2])
  S = (tb[table_rowA,3] - tb[table_rowB,3])
  W = (tb[table_rowA,4] - tb[table_rowB,4])
  EQ = paste0(log_lab, round(I, 2), " + ", round(M,2), var_lab1, " + ", round(S, 2),
              var_lab2, " + ", round(W, 2), var_lab3, title_lab)
  print(EQ)

  return(EQ)
}
```

```
EQ1 = get_prediction_eq(model_table5, 1, 2, " Mass %", " Sex", " Wing-to-Body",
                        "log(pi_-1 / pi_1) = ","   Flew in T1, not T2")
EQ2 = get_prediction_eq(model_table5, 3, 1, " Mass %", " Sex", " Wing-to-Body",
                        "log(pi_2 / pi_-1) = ", "   Flew in both, not T1" )
EQ3 = get_prediction_eq(model_table5, 3, 2, " Mass %", " Sex", " Wing-to-Body",
                        "log(pi_2 / pi_1) = ", "   Flew in both, not T2" )
```

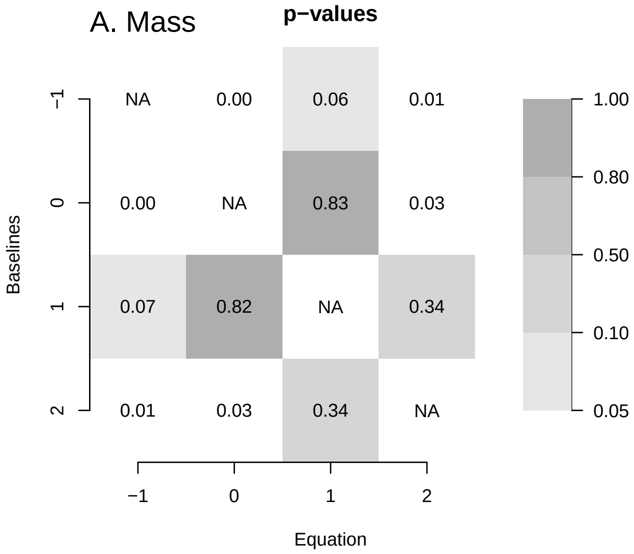
```
## [1] "log(pi_-1 / pi_1) = 7.24 + 0.05 Mass % + 6.38 Sex + 30.33 Wing-to-Body   Flew in T1, n
## [1] "log(pi_2 / pi_-1) = 1.14 + -0.02 Mass % + -0.19 Sex + 4.36 Wing-to-Body   Flew in both
## [1] "log(pi_2 / pi_1) = 8.38 + 0.02 Mass % + 6.19 Sex + 34.69 Wing-to-Body   Flew in both,
```

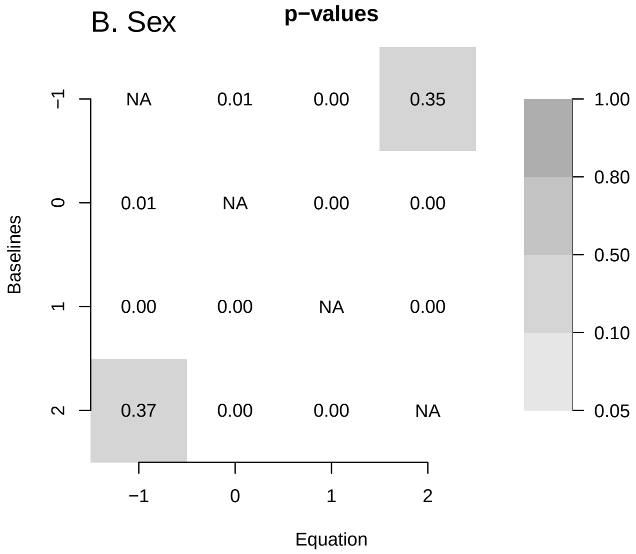
4.5.8 Visualize Significant Multinomial Functions

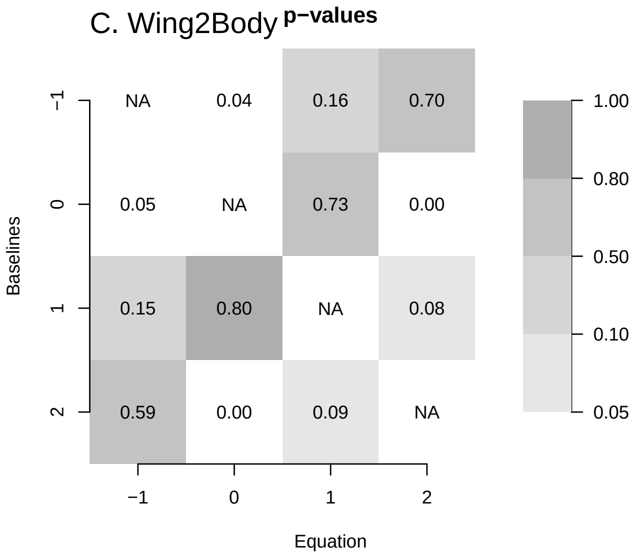
```
# define a run_multinom_model function based on the best fit model
run_multinom_model = function(d) {
  m = multinom(flight_case ~ mass_per + sex_c + wing2body_c, trace=FALSE, data = d)
  model_table = calculate_P3(m, print_table=FALSE)
  return(model_table)
}

# determine which multinomial model equations are significant with a plot
par(mfrow=c(2,2))
mass_per_ML = get_significant_models(19) # % mass
  mtext("A. Mass", side=3, adj=0, line=0.5, cex=1.3, font=1)
```

```r
sex_ML = get_significant_models(20) # sex
  mtext("B. Sex", side=3, adj=0, line=0.5, cex=1.3, font=1)
w2b_ML = get_significant_models(21) # wing2body
  mtext("C. Wing2Body", side=3, adj=0, line=0.5, cex=1.3, font=1)
```





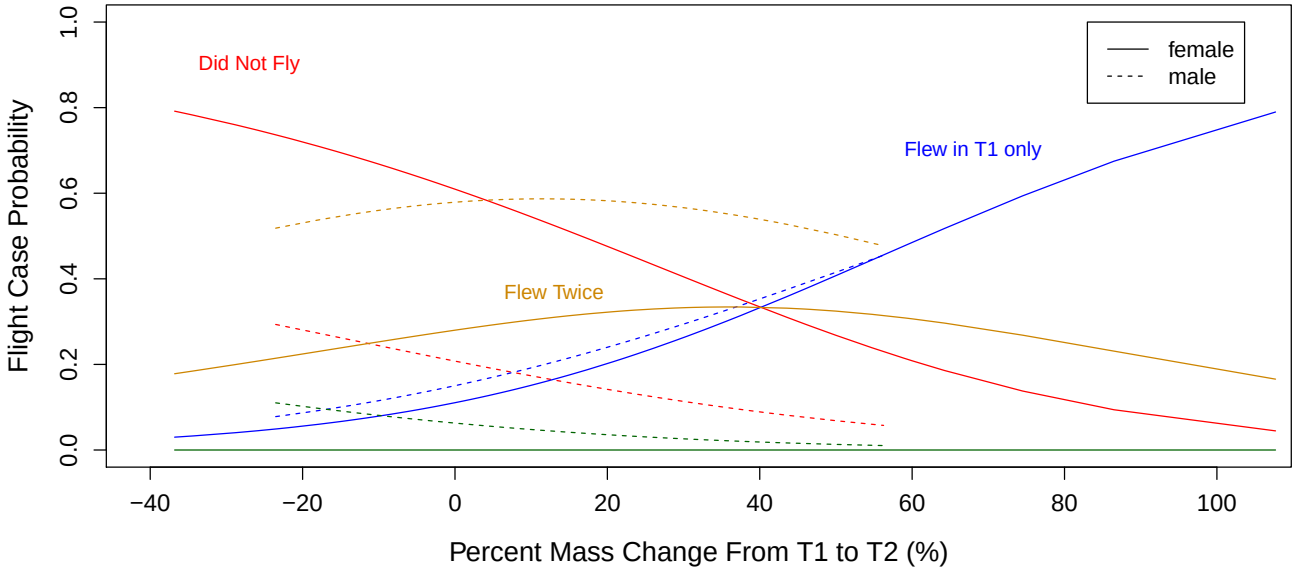



```
##             [,1]         [,2]         [,3]        [,4]
## [1,]          NA -0.041168533 -0.047132139 -0.02329390
## [2,] 0.04121460           NA -0.005450321  0.01790830
## [3,] 0.04699220  0.005882702           NA  0.02378072
## [4,] 0.02331345 -0.017835748 -0.023938109          NA
##             [,1]         [,2]         [,3]        [,4]
## [1,]          NA -0.041168533 -0.047132139 -0.02329390
## [2,] 0.04121460           NA -0.005450321  0.01790830
## [3,] 0.04699220  0.005882702           NA  0.02378072
## [4,] 0.02331345 -0.017835748 -0.023938109          NA
##             [,1]         [,2]         [,3]        [,4]
## [1,]          NA -0.041168533 -0.047132139 -0.02329390
## [2,] 0.04121460           NA -0.005450321  0.01790830
## [3,] 0.04699220  0.005882702           NA  0.02378072
## [4,] 0.02331345 -0.017835748 -0.023938109          NA
```

4.5.9 Plot Predicted Probabilities

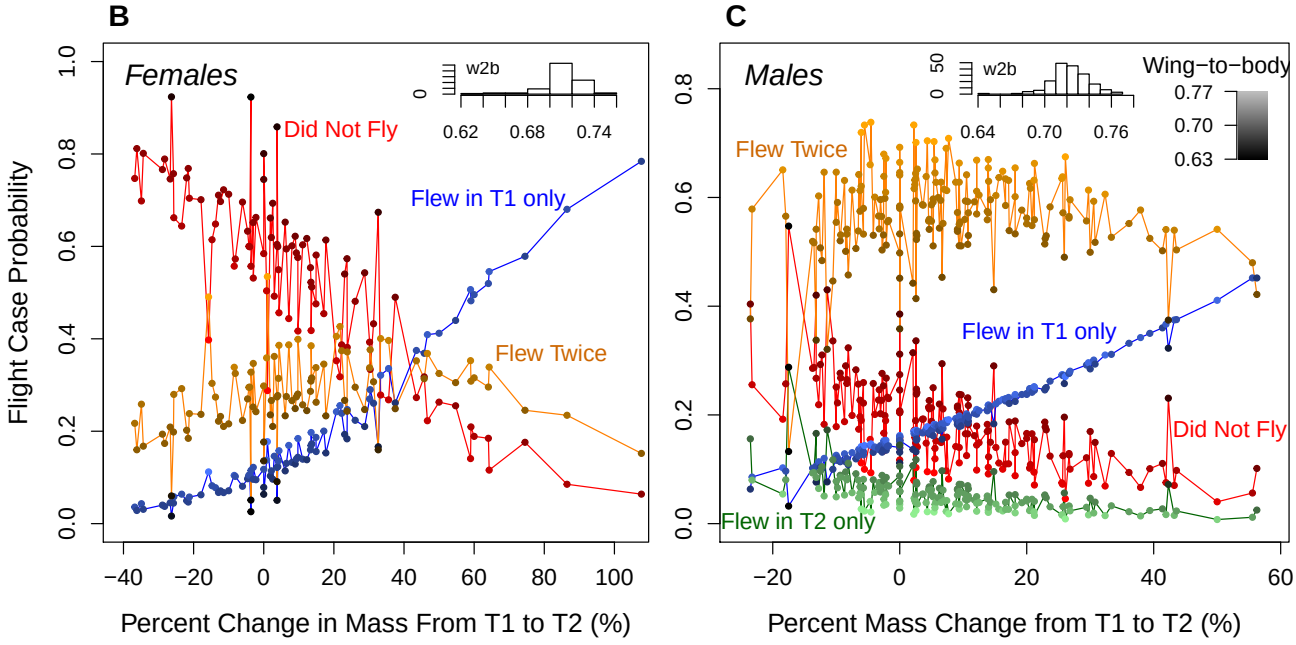
```
head(pp <- fitted(M4),3) # compute fitted values of the best fit model without wing-to-body ra
```

```
##           0         -1           1         2
## 1 0.7917303 0.03003973 4.362037e-06 0.1782256
## 2 0.7894639 0.03073036 4.325625e-06 0.1798015
## 3 0.7844677 0.03228066 4.247094e-06 0.1832474
```




```
head(pp <- fitted(M5), 3) # compute fitted values of the best fit model with wing-to-body rati
```

```
##           0         -1           1         2
## 1 0.7470322 0.03581826 2.459149e-07 0.2171493
## 2 0.8116776 0.02845344 2.925412e-07 0.1598686
## 3 0.6983200 0.04316854 2.166785e-07 0.2585113
```



4.6 Multinomial Modeling (Females Only)

4.6.1 Egg Case

Delta Egg Response Key	
Event	Encoding
laid eggs in both trials	2
laid eggs in T2 only	1
laid eggs in neither trials	0
laid eggs in T1 only	-1

4.6.2 Baseline

```
# filter for females &
# remove any missing values for flight case, mass percent change, and egg case between trials
df = d[with(d,!is.na(flight_case) & !is.na(mass_per) & !is.na(egg_case) & sex=="F"),]

# order the dataset by ascending mass percent change values
df = df[with(df, order(mass_per)),]

# relevel the flight case factors so as to set 0 as the first level.
df$flight_case = relevel(as.factor(df$flight_case), ref = "0")

unique(df$flight_case) # no female bug only flew in T2, so can drop factor "1"
df$flight_case = droplevels(df$flight_case)
```

```
## [1] 2  0  -1
## Levels: 0 -1 1 2
```

4.6.3 Null model

```
null <- multinom(flight_case ~ 1, data = df)
```

```
## # weights:  6 (2 variable)
## initial  value 102.170943
## final  value 93.055466
## converged
```

4.6.4 Comparing Models - predictors: % mass, egg diff, host

```
data <- data.frame(R = df$flight_case,
         A = df$egg_case,
         B = df$mass_per,
         C = df$host_c)
model_script = paste0(source_path,"generic multinomial models- multinom 1RF + 3 FF.R")
model_comparisonsAIC(model_script)
```

```
##         [,1]      [,2]      [,3]      [,4]       [,5]       [,6]
## AICs   164.3817  165.6054  166.336   167.5638   167.9891   168.3593
## models 7         4         13        11         16         12
## probs  0.3761191 0.2039899 0.1415644 0.07661927 0.06194208 0.0514745
##
```

```
## m7   multinom(formula = R ~ A + B + C, data = data, trace = FALSE)
## m4   multinom(formula = R ~ A + B, data = data, trace = FALSE)
## m13  multinom(formula = R ~ B * C + A, data = data, trace = FALSE)
## m11  multinom(formula = R ~ A * B + C, data = data, trace = FALSE)
## m16  multinom(formula = R ~ B * C + A * B, data = data, trace = FALSE)
## m12  multinom(formula = R ~ A * C + B, data = data, trace = FALSE)
```

```
anova(m4, m7, test="Chisq") # Adding C does not improve fit
anova(m7, m13, test="Chisq") # Adding mass_per*host does not improve fit
```

```
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##       Model Resid. df Resid. Dev   Test    Df LR stat.   Pr(Chi)
## 1     A + B       180   153.6054
## 2 A + B + C       178   148.3817 1 vs 2     2 5.223671 0.0733997
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##       Model Resid. df Resid. Dev   Test    Df LR stat.   Pr(Chi)
## 1 A + B + C       178   148.3817
## 2 B * C + A       176   146.3360 1 vs 2     2 2.045698 0.3595691
```

Host plant was not a significant predictor for females as well, so we tested the wing-to-body ratio as a predictor next.

4.6.5 Comparing Models - predictors: % mass, egg diff, wing2body

```
##        [,1]      [,2]      [,3]      [,4]
## AICs   164.5293  164.9831  165.6054  167.7955
## models 7         13        4         12
## probs  0.3174096 0.2529723 0.1853291 0.06199495
##
## m7   multinom(formula = R ~ A + B + C, data = data, trace = FALSE)
## m13  multinom(formula = R ~ B * C + A, data = data, trace = FALSE)
## m4   multinom(formula = R ~ A + B, data = data, trace = FALSE)
## m12  multinom(formula = R ~ A * C + B, data = data, trace = FALSE)
```

```
anova(m4, m7, test="Chisq") # adding wing2body does not improve fit
anova(m7, m13, test="Chisq") # Adding A*C does not improve fit
anova(m7, m12, test="Chisq") # Adding B*C does not improve fit
```

```
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##       Model Resid. df Resid. Dev   Test    Df LR stat.    Pr(Chi)
## 1     A + B       180   153.6054
## 2 A + B + C       178   148.5293 1 vs 2     2  5.07612 0.07901956
## Likelihood ratio tests of Multinomial Models
##
```

```
## Response: R
##       Model Resid. df Resid. Dev   Test    Df LR stat.  Pr(Chi)
## 1 A + B + C       178   148.5293
## 2 B * C + A       176   144.9831 1 vs 2     2 3.546174 0.169808
## Likelihood ratio tests of Multinomial Models
##
## Response: R
##       Model Resid. df Resid. Dev   Test    Df  LR stat.   Pr(Chi)
## 1 A + B + C       178   148.5293
## 2 A * C + B       176   147.7955 1 vs 2     2 0.7337197 0.6929067
```

4.6.6 Best Fit

```
M6 = multinom(flight_case ~ mass_per + egg_case, data = df) # same top model
model_table6 = calculate_P2(M6, "mass_per", "egg_case")
```

```
## # weights:  12 (6 variable)
## initial  value 102.170943
## iter  10 value 76.802714
## final  value 76.802689
## converged
##
##  AIC:  165.6054
##    (Intercept) mass_per egg_case DF   SEi   SE1   SE2    zi    z1     z2 waldi
## -1      -0.950    0.041   -0.533  6 0.617 0.012 0.380 -1.539 3.389 -1.402 2.370
## 2        0.406    0.022   -1.098  6 0.424 0.011 0.297  0.957 2.038 -3.700 0.917
##     wald1  wald2 Pi > |z| P1 > |z| P2 > |z|
## -1 11.488  1.966    0.124    0.001    0.161
## 2   4.154 13.693    0.338    0.042    0.000
```

4.6.7 Prediction Equations

```
get_prediction_eq = function(tb, table_rowA, table_rowB, var_lab1, var_lab2,
                             log_lab, title_lab) {
  I = (tb[table_rowA,1] - tb[table_rowB,1])
  M = (tb[table_rowA,2] - tb[table_rowB,2])
  E = (tb[table_rowA,3] - tb[table_rowB,3])
  EQ = paste0(log_lab, round(I, 2), " + ", round(M,2), var_lab1, " + ", round(E, 2),
              var_lab2, title_lab)
  print(EQ)

  return(EQ)
}
```

```
EQ = get_prediction_eq(model_table6, 1, 2, " Mass %", " Egg Case",
                       "log(pi_-1 / pi_1) = ","   Flew in T1, not T2")
```

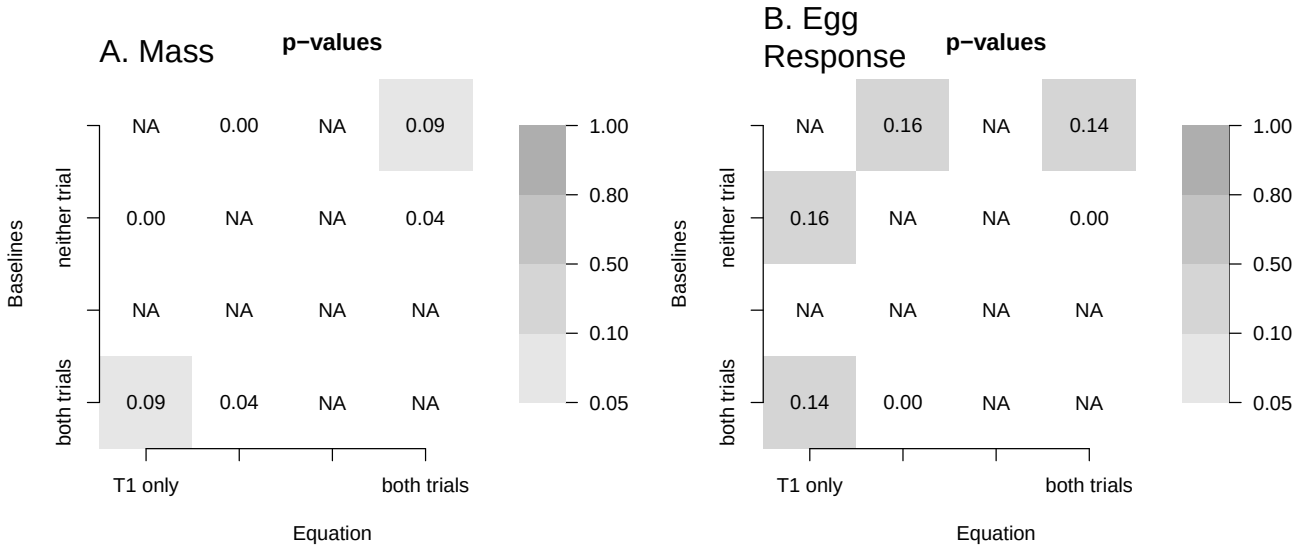
```
## [1] "log(pi_-1 / pi_1) = -1.36 + 0.02 Mass % + 0.56 Egg Case   Flew in T1, not T2"
```

4.6.8 Visualize Significant Multinomial Functions

```
# define a run_multinom_model function based on the best fit model
run_multinom_model = function(d) {
  m <- multinom(flight_case ~ mass_per + egg_case, trace=FALSE, data = d)
```

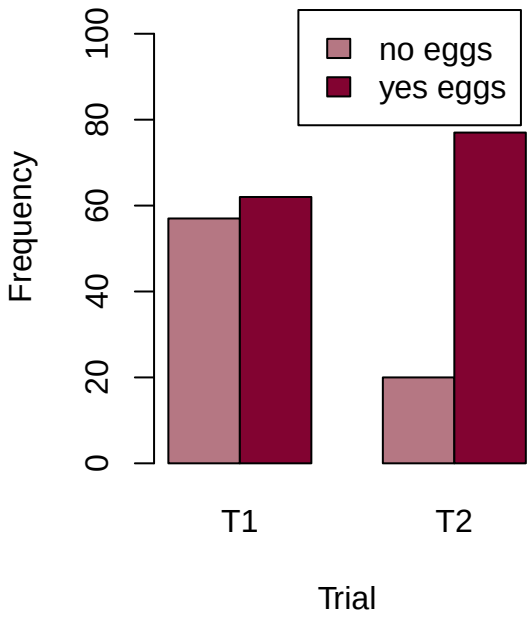
```
  model_table = calculate_P2(m, "mass_per", "egg_case", print_table=FALSE)
  return(model_table)
}

# determine which multinomial model equations are significant with a plot
par(mfrow=c(1,2))
mass_per_ML = get_significant_modelsf(15) # mass_per
  mtext("A. Mass", side=3, adj=0, line=0.5, cex=1.6, font=1)
egg_case_ML = get_significant_modelsf(16) # egg_case
  mtext("B. Egg \nResponse", side=3, adj=0, line=0.3, cex=1.6, font=1)
```



4.6.9 Barplot

```
data_fem = data_tested[data_tested$sex=="F",]
binary_counts <- table(data_fem$eggs_b, data_fem$trial_type)[,2:3]
```

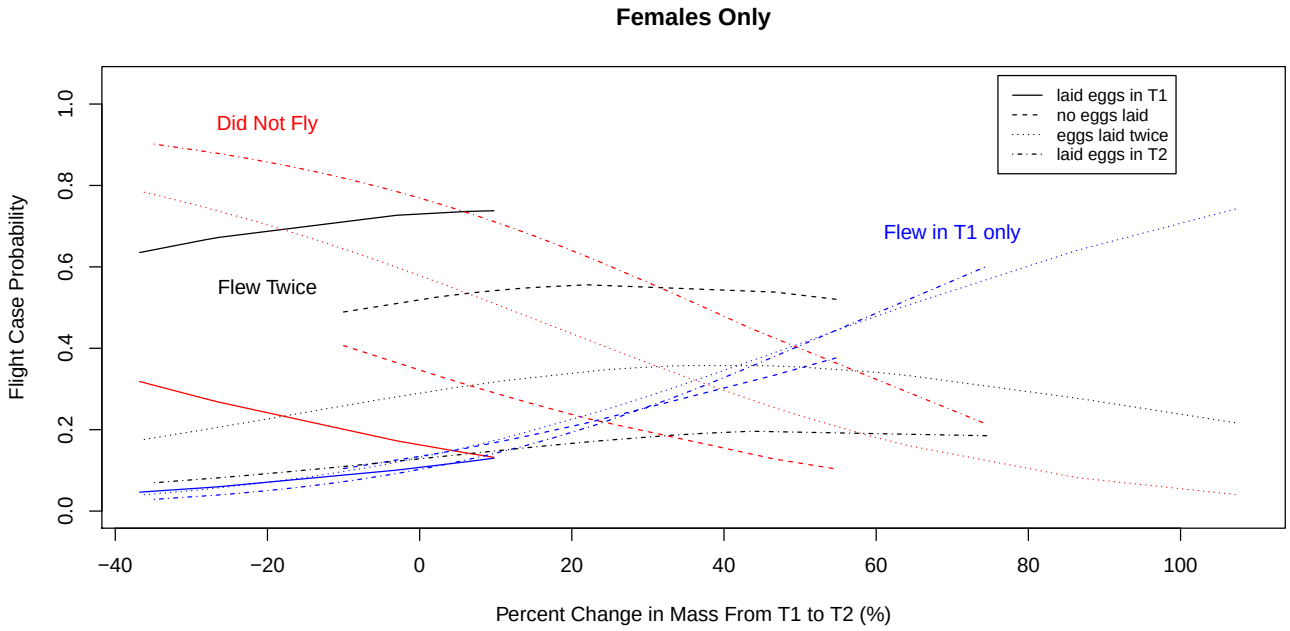


Notice that female bugs were laying more during the second trial (T2) than the first trial (T1).

4.6.10 Plot Predicted Probabilities

```
head(pp <- fitted(M6),3)
```

```
##           0         -1          2
## 1 0.3182776 0.04652361 0.63519881
## 2 0.7833277 0.04039434 0.17627792
## 3 0.9015654 0.02877502 0.06965959
```



5 Fall 2019 Data Cleaning

5.1 Read Libraries

```
library(cvms) # cross-validating regressions
```

5.2 Read Source Files

```
script_names = c("clean_flight_data-Fall.R", # 1 function: clean_flight_data.Fall()
                 "unique_flight_data-Fall.R", # 1 function: create_delta_data.Fall()
                 "prediction_accuracy.R",     # 1 function: calculate_accuracy()
                 "confusion_matrix.R")        # 1 function: get_confusion_matrix()

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

5.3 Read the Data

```
data_path = paste0(dir,"/Dispersal/Winter_2020/stats/data/full_data-Fall2019.csv")
dataFall = clean_flight_data.Fall(data_path)

# extract sets with an experimental design similar to the Winter tests
```

```
ongoing_data = dataFall[with(dataFall,!is.na(mass) & set_number > 71),]

# create delta data
d = create_delta_data.Fall(ongoing_data)
```

6 Flight Response Predictions

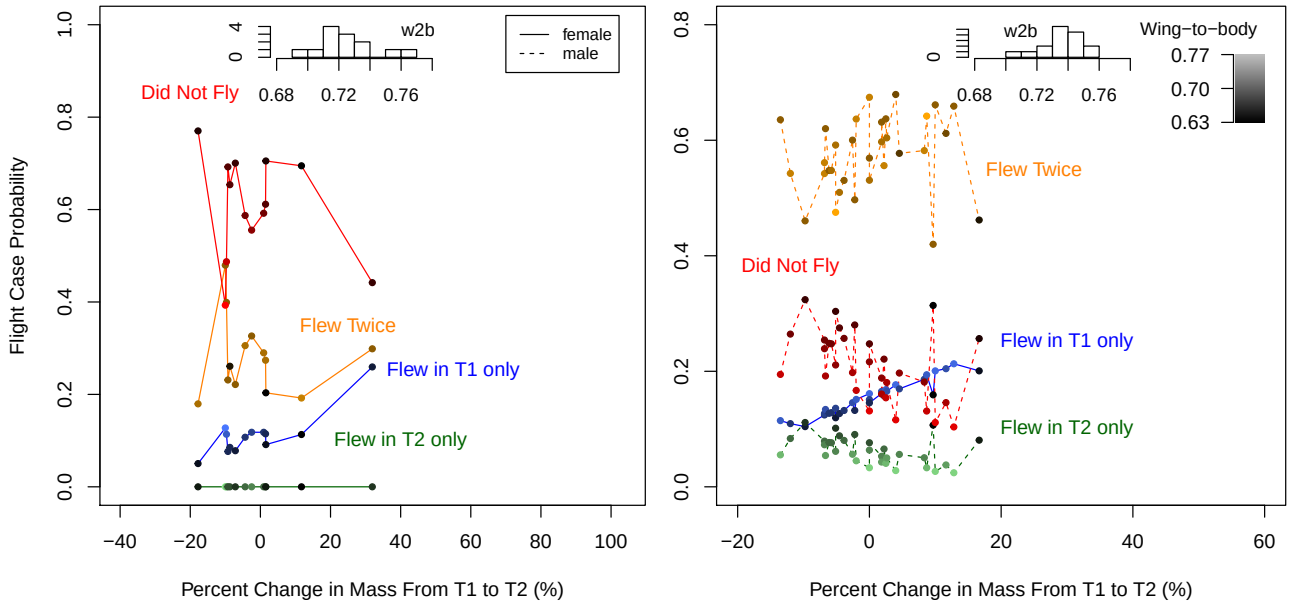
6.1 Compute predicted probabilities

```
d <- d[with(d, order(mass_per)),]
```

```
neither = c()
T1_rather_than_none = c()
T2_rather_than_none = c()
both_rather_than_none = c()

for (i in 1:nrow(d)) {
  m = d$mass_per[[i]]
  s = d$sex_c[[i]]
  w = d$wing2body_c[i]
  # extract effects from the best fit model
  top0 = exp(0) # equals 1
  top1 = exp(model_table5[1,1] + model_table5[1,2]*m + model_table5[1,3]*s + model_table5[1,4]
  top2 = exp(model_table5[2,1] + model_table5[2,2]*m + model_table5[2,3]*s + model_table5[2,4]
  top3 = exp(model_table5[3,1] + model_table5[3,2]*m + model_table5[3,3]*s + model_table5[3,4]
  bottom = top0 + top1 + top2 + top3
  # calculate predicted probabilities
  neither = c(neither, top0/bottom)
  T1_rather_than_none = c(T1_rather_than_none, top1/bottom)
  T2_rather_than_none = c(T2_rather_than_none, top2/bottom)
  both_rather_than_none = c(both_rather_than_none, top3/bottom)
}
```

6.2 Plot predicted probabilities



6.3 Overall and Grouped Accuracies

```
probs = round(cbind(neither, T1_rather_than_none, T2_rather_than_none, both_rather_than_none),
summary_probs = cbind(as.character(d$flight_case), as.character(d$sex), probs)
colnames(summary_probs) = c("event", "sex", "none", "T1", "T2", "both")
dataframe = as.data.frame(summary_probs)
nrow(dataframe)
```

```
## [1] 45
```

```
# overall
acc = calculate_accuracy(dataframe,3,6)
paste("Overall prediction accuracy, ", round(acc,2))

# by sex
femdata = dataframe[dataframe$sex=="F",]
maledata = dataframe[dataframe$sex=="M",]

accF = calculate_accuracy(femdata,3,6)
paste("Female prediction accuracy, ", round(accF,2))
accM = calculate_accuracy(maledata,3,6)
paste("Male prediction accuracy, ", round(accM,2))
```

```
## [1] "Overall prediction accuracy,  0.6"
## [1] "Female prediction accuracy,  0.38"
## [1] "Male prediction accuracy,  0.69"
```

6.4 Confusion Matrix

```
acc_table = get_confusion_matrix(dataframe,3,6)
acc_table[,1:5]
```

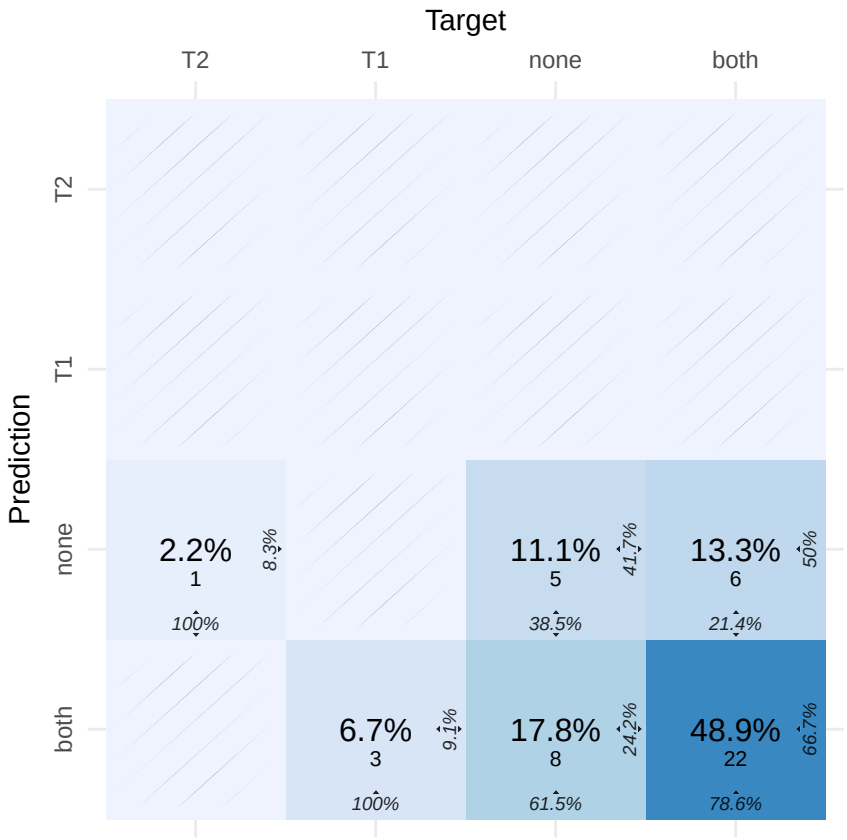
```
## # A tibble: 1 x 5
##   `Overall Accuracy` `Balanced Accuracy`    F1 Sensitivity Specificity
##                <dbl>               <dbl> <dbl>       <dbl>       <dbl>
## 1                0.6               0.538   NaN       0.293       0.784
```

```
confusion_matrix <- acc_table$'Confusion Matrix'[[1]]
confusion_matrix
```

```
## # A tibble: 16 x 3
##    Prediction Target     N
##    <chr>      <chr>  <int>
##  1 both       both      22
##  2 none       both       6
##  3 T1         both       0
##  4 T2         both       0
##  5 both       none       8
##  6 none       none       5
##  7 T1         none       0
##  8 T2         none       0
##  9 both       T1         3
## 10 none       T1         0
## 11 T1         T1         0
## 12 T2         T1         0
## 13 both       T2         0
```

```
## 14 none       T2          1
## 15 T1         T2          0
## 16 T2         T2          0
```

```
plot_confusion_matrix(confusion_matrix, add_sums=FALSE)
```



6.5 Females

```
dfem = d[d$sex=="F",]
```

```
dfem <- dfem[with(dfem, order(mass_per)),]
```

```
neither = c()
T1_rather_than_none = c()
both_rather_than_none = c()
for (i in 1:nrow(dfem)) {
  M = dfem$mass_per[[i]]
  EC = dfem$egg_diff[[i]]
  top0 = exp(0) #  equals 1
  top1 = exp(model_table6[1,1] + model_table6[1,2]*M + model_table6[1,3]*EC)
  top2 = exp(model_table6[2,1] + model_table6[2,2]*M + model_table6[2,3]*EC)
  bottom = top0 + top1 + top2
  neither = c(neither, top0/bottom)
  T1_rather_than_none = c(T1_rather_than_none, top1/bottom)
  both_rather_than_none = c(both_rather_than_none, top2/bottom)
}
```

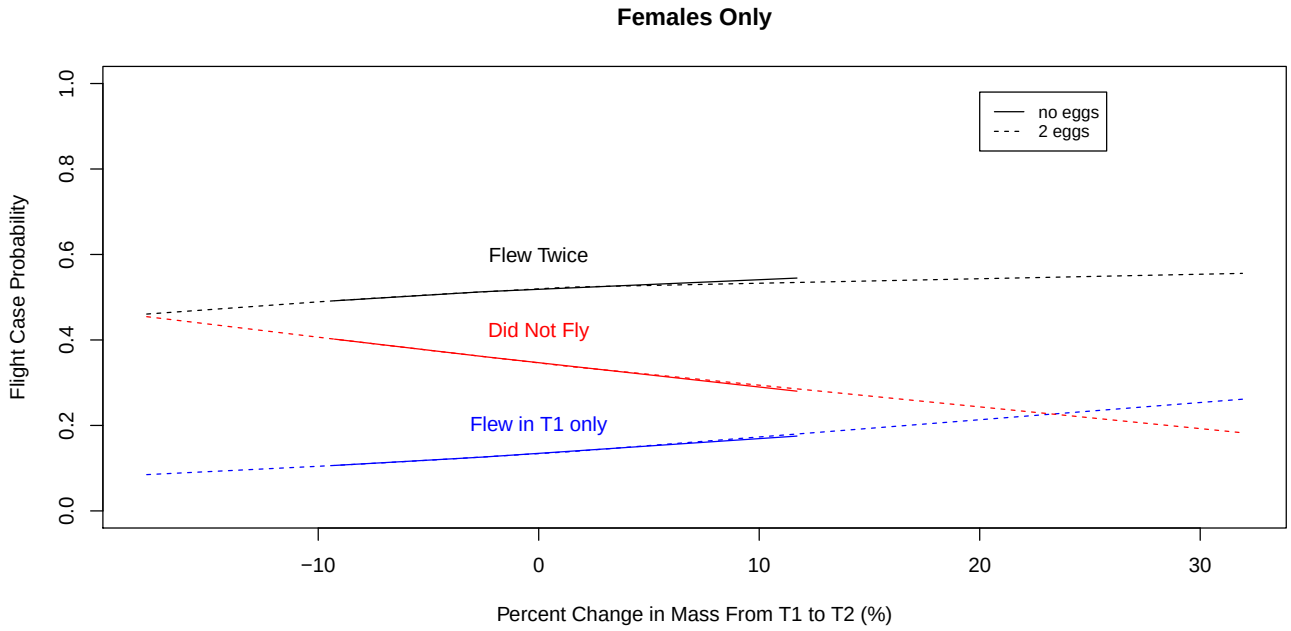
6.5.1 Compute predicted probabilities

```
probs = round(cbind(neither, T1_rather_than_none, both_rather_than_none),2)
summary_probs = cbind(as.character(dfem$flight_case), as.character(dfem$egg_diff), probs)
colnames(summary_probs) = c("event", "egg_diff", "none", "T1", "both")

egg2 = c(1,2,3,5,6,7,9,10,11,13)
noegg = c(4,8,12)

dataframe = as.data.frame(summary_probs)
dataframe$egg_cat = c(2,2,2,0,2,2,2,0,2,2,2,0,2)
```

6.5.2 Plot predicted probabilities



6.5.3 Overall and Grouped Accuracies

```
accF_eggs = calculate_accuracy(dataframe,3,5)
paste("Female prediction accuracy for mass diff and egg model, ", round(accF_eggs,2))
```

```
## [1] "Female prediction accuracy for mass diff and egg model,  0.46"
```

6.5.4 Confusion Matrix

```
acc_table = get_confusion_matrix(dataframe,3,5)
acc_table[,1:5]
```

```
## # A tibble: 1 x 5
##   `Overall Accuracy` `Balanced Accuracy`    F1 Sensitivity Specificity
##                <dbl>                <dbl> <dbl>       <dbl>       <dbl>
## 1              0.462                  0.5   NaN       0.333       0.667
```

```
confusion_matrix <- acc_table$'Confusion Matrix'[[1]]
confusion_matrix
```

```
## # A tibble: 9 x 3
##   Prediction Target     N
##   <chr>      <chr>  <int>
## 1 both       both       6
```

```
## 2 none       both       0
## 3 T2         both       0
## 4 both       none       6
## 5 none       none       0
## 6 T2         none       0
## 7 both       T2         1
## 8 none       T2         0
## 9 T2         T2         0
```

```
plot_confusion_matrix(confusion_matrix, add_sums=FALSE)
```