Modeling Flight Response Summary File

Data Cleaning And Exploration

Read Libraries

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

Read Source Files

```
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()
                 "AICprobabilities.R") # 1 function: AICprobs()

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

Read the Data

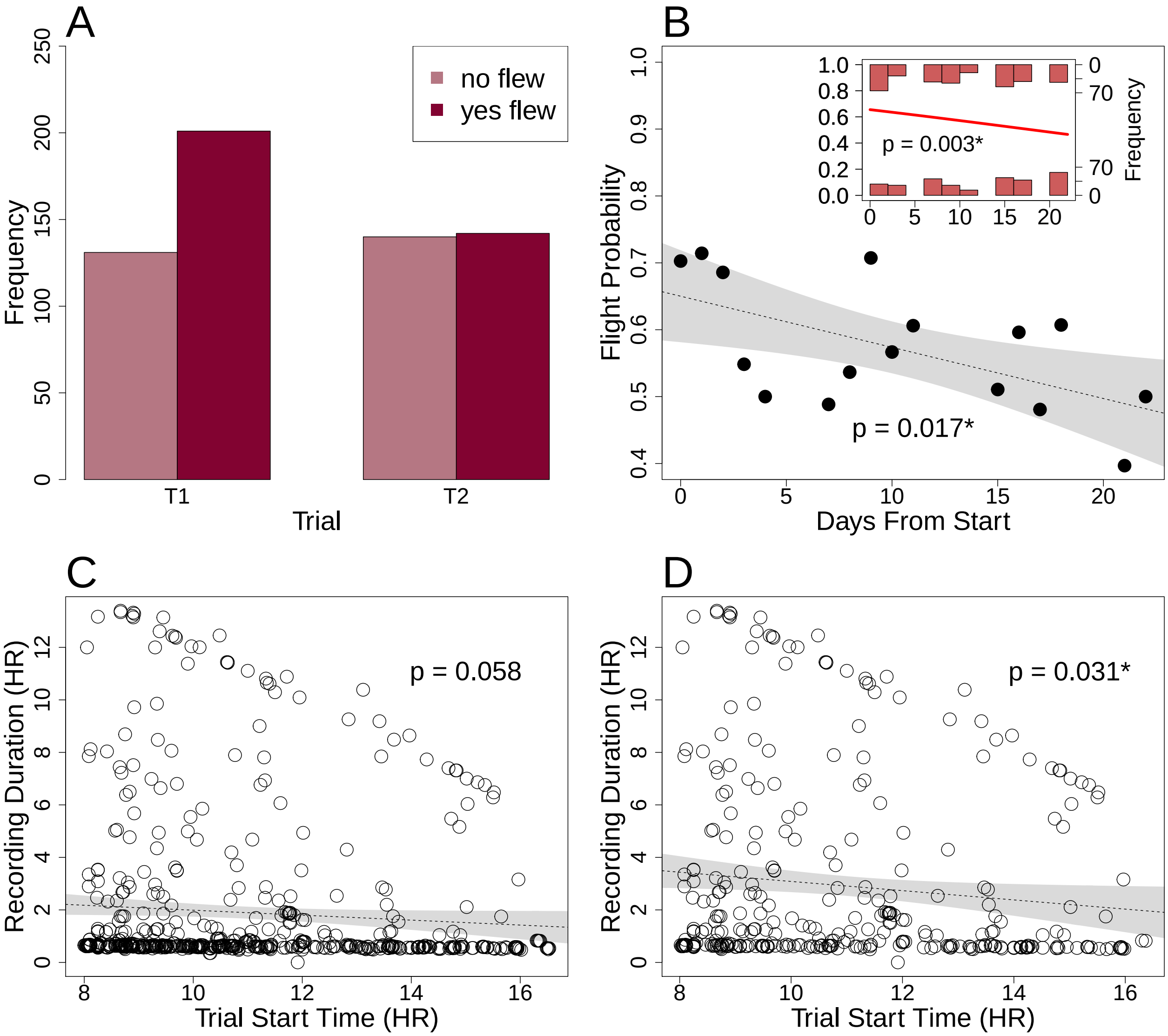
```
data_path = paste0(dir,"/Dispersal/Winter_2020/stats/data/all_flight_data-Winter2020.csv")

data = read_flight_data(data_path)
data_all = data[[1]]
data_tested = data[[2]]
d = create_delta_data(data_tested, remove_bugs_tested_once = FALSE) # keep bugs only tested once
```

Repeating Plot Parameters & Functions

```
# scale/magnifications
c1 = 1.3*2 # size of points
c2 = 1.2*2 # size of large text
c3 = 2 # size of smaller text
c4 = 2*2 # size of title

# compute 95% confidence interval
get_CI = function(x,y,m) {
  x.seq = seq(min(x) - sd(x), max(x) + sd(x), length.out=100)
  prd = data.frame(x=x.seq)
  err = predict(m, newdata = prd, se.fit = TRUE)
  prd$lci = err$fit - 1.96 * err$se.fit
  prd$fit = err$fit
  prd$uci = err$fit + 1.96 * err$se.fit
  mu_ci = t(matrix(c(prd$lci,prd$uci), ncol=2))
  return(list(mu_ci, prd))
}

# tailoring variables for plotting
d$mass_block=round(d$average_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
```

Across-Trial Flight Response

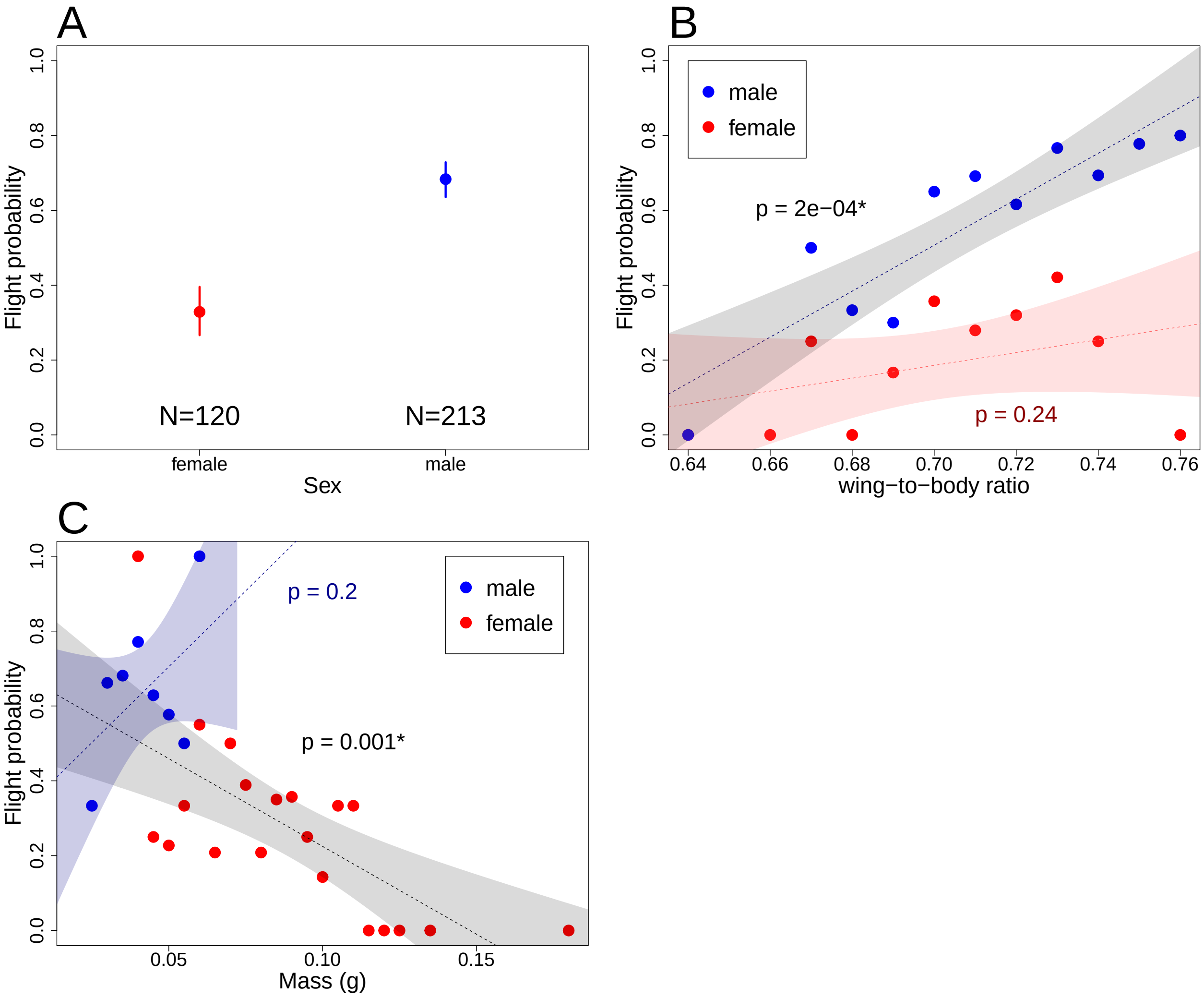
Experimental Effects



A & B. There was a negative effect of day a bug was tested (since the start of trials), but there was a significant effect only when the full dataset is considered (not the delta dataset, which is not shown here). **C & D.** There was a negative effect of the trial start time but only after removing bugs that didn't fly (D).

Single-Variate Effects

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

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



Between-Trial Flight Response (T1 vs. T2)

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
```

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)
}
```

Read the Data

```
d = create_delta_data(data_tested, remove_bugs_tested_once=TRUE) # remove bugs tested only once
```

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

Multinomial Modeling

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")
```

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
```

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)
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)
```

```
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
```

Best Fit

```
M1 = multinom(flight_case ~ mass_per + sex_c, data = df)
model_table = calculate_P2(M1, "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.

Compare Models - predictors: % mass, sex, wing2body (w2b)

```
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
```

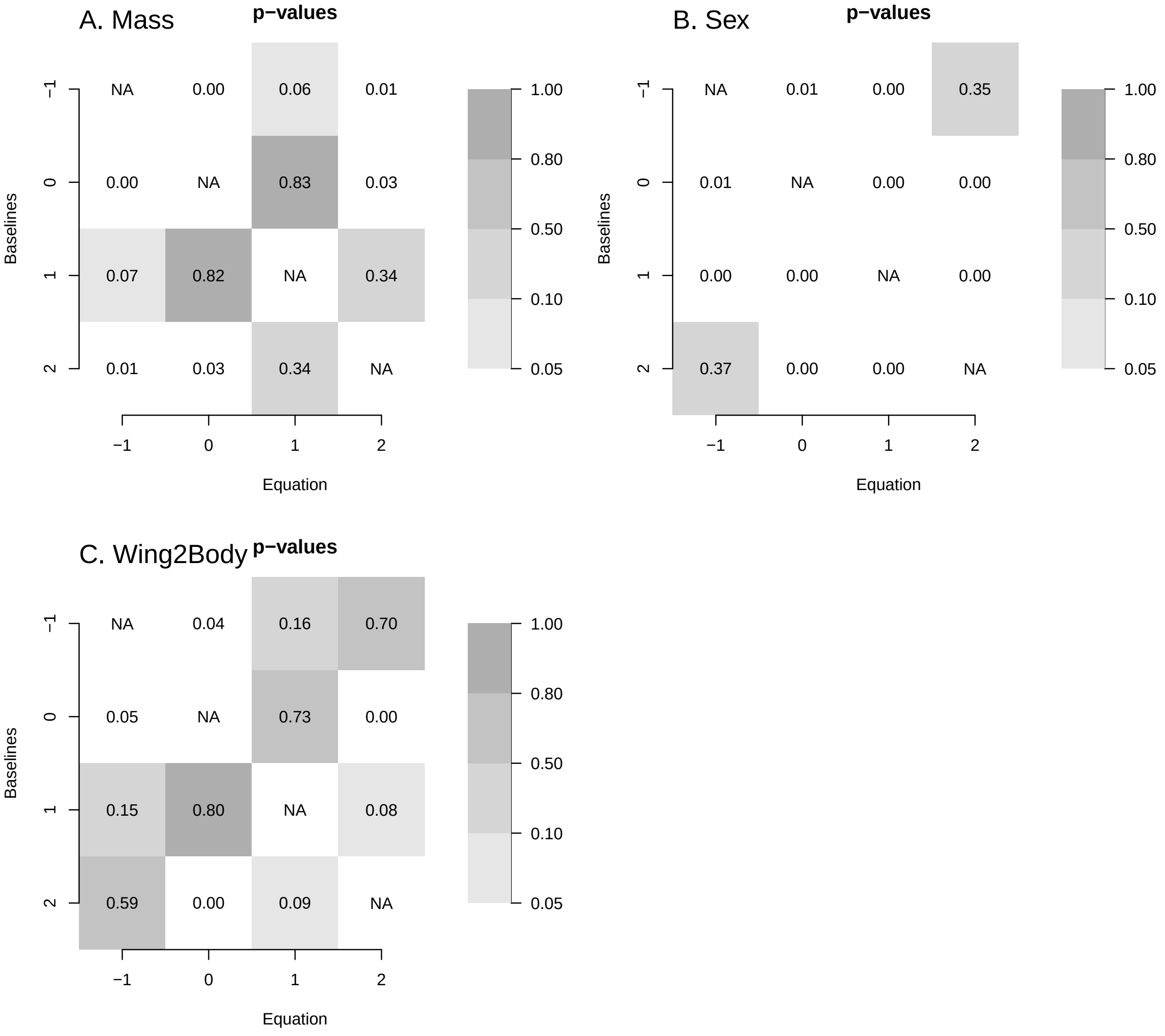
Best Fit

```
M2 = multinom(flight_case ~ mass_per + sex_c + wing2body_c, data = df)
model_table = calculate_P3(M2)
```

```
## # 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
```

Visualize Significant Multinomial Functions

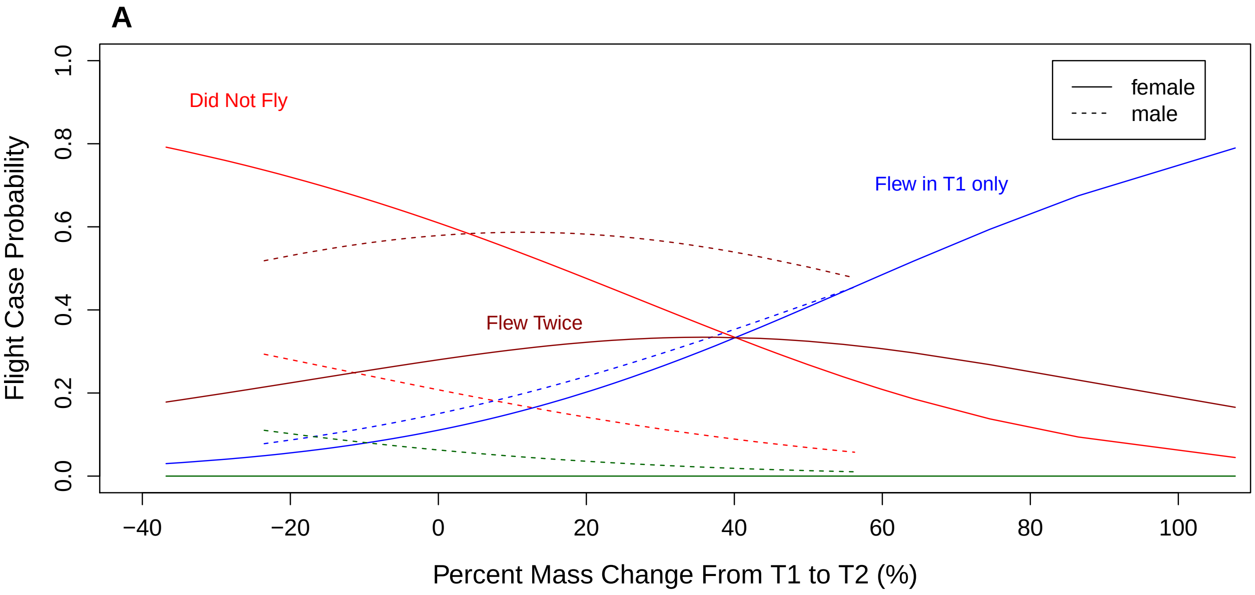
```r
# define a run_multinom_model function based on the best fit model
run_multinom_model = function(d) {
  m = multinom(flight_case ~ mass_per + sex_c + wing2body_c, trace=FALSE, data = d)
  model_table = calculate_P3(m, print_table=FALSE)
  return(model_table)
}

# 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)
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)
```



Plot Predicted Probabilities

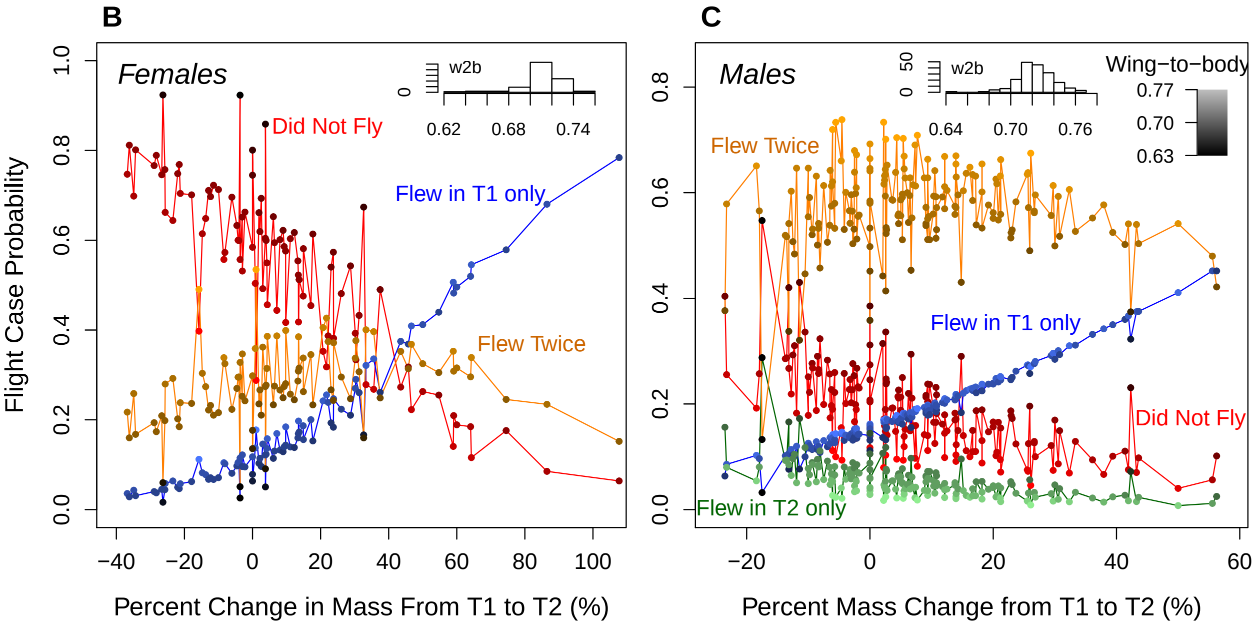
```
head(pp <- fitted(M1),3) # compute fitted values of the best fit model without wing-to-body ratio
```

```
##           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(M2), 3) # compute fitted values of the best fit model with wing-to-body ratio
```

```
##           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
```



Multinomial Modeling (Females Only)

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

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
```

Null model

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

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

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_diff*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.

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 include 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
```

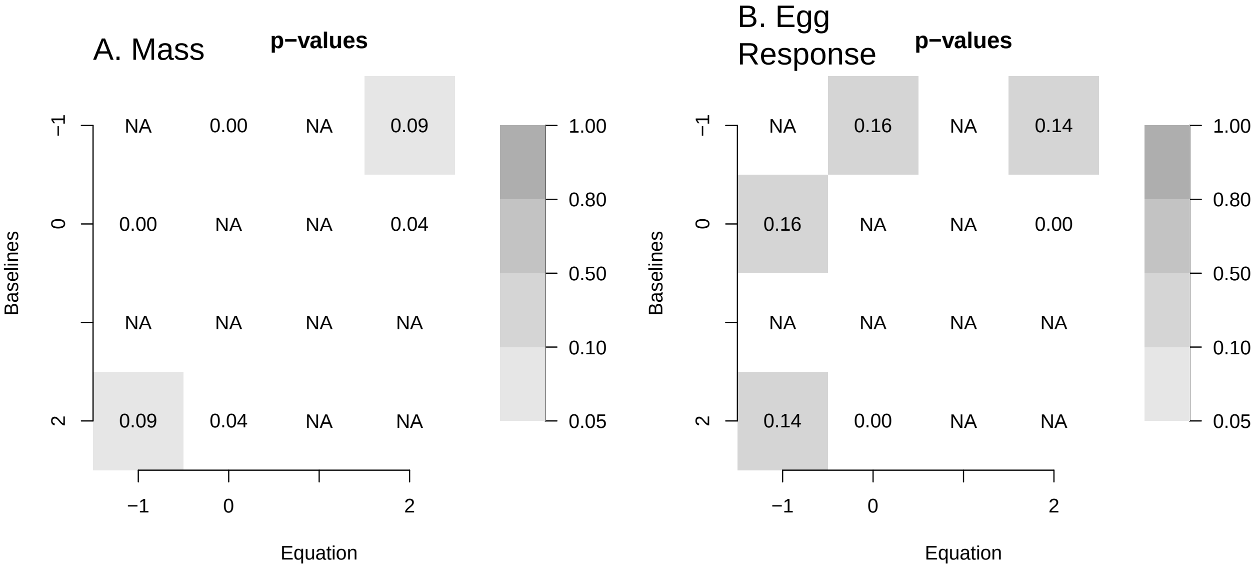
Best Fit

```
M3 <- multinom(flight_case ~ mass_per + egg_case, data = df) # same top model
model_table = calculate_P2(M3, "mass_per", "egg_case")
```

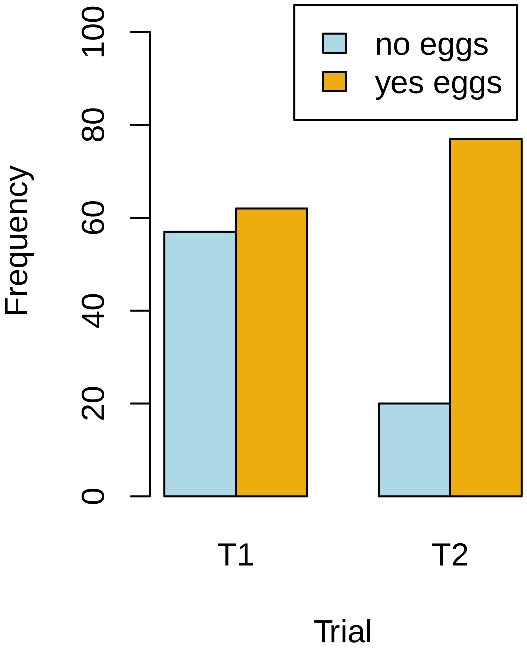
```
## Warning in cbind(s$coefficients, c(s$edf, s$edf, s$edf), s$standard.errors[, :
## number of rows of result is not a multiple of vector length (arg 2)
```

```
## # 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
```

```
# 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)
```



Barplot

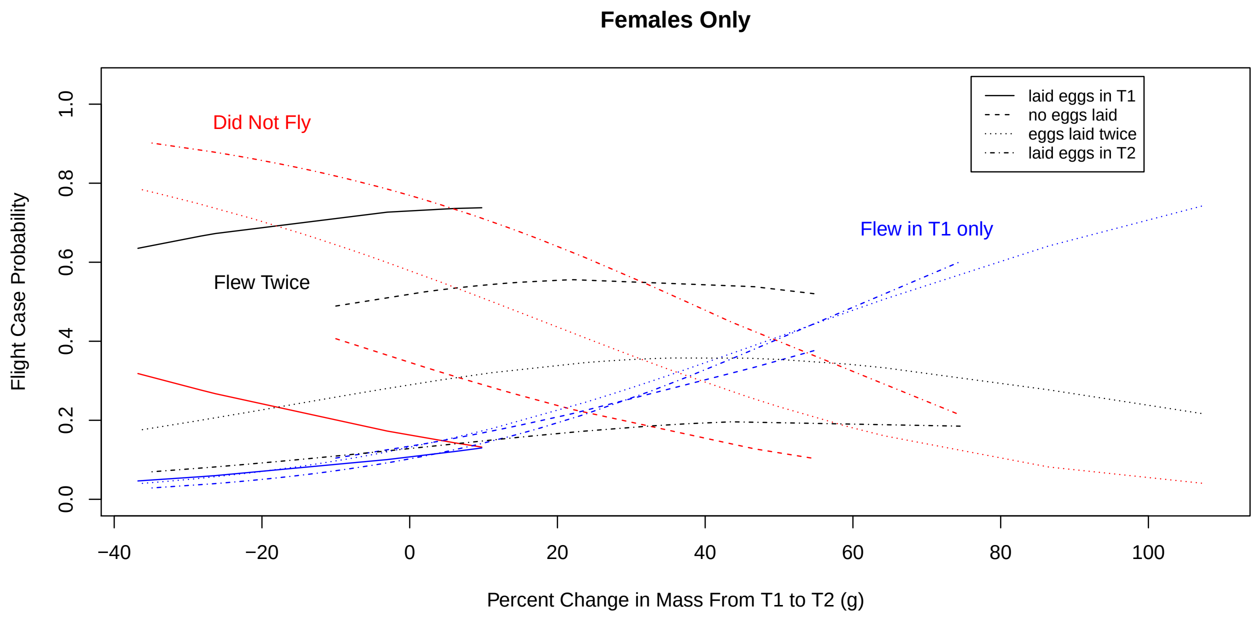


Notice that female bugs were laying more during the second trial (T2) than the first trial (T1).

Plot Predicted Probabilities

```
head(pp <- fitted(M3),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
```



Flight Response Predictions

Read Libraries

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

Read Source Files

```
script_names = c("clean_flight_data-Fall2.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)
}
```

Read the Data

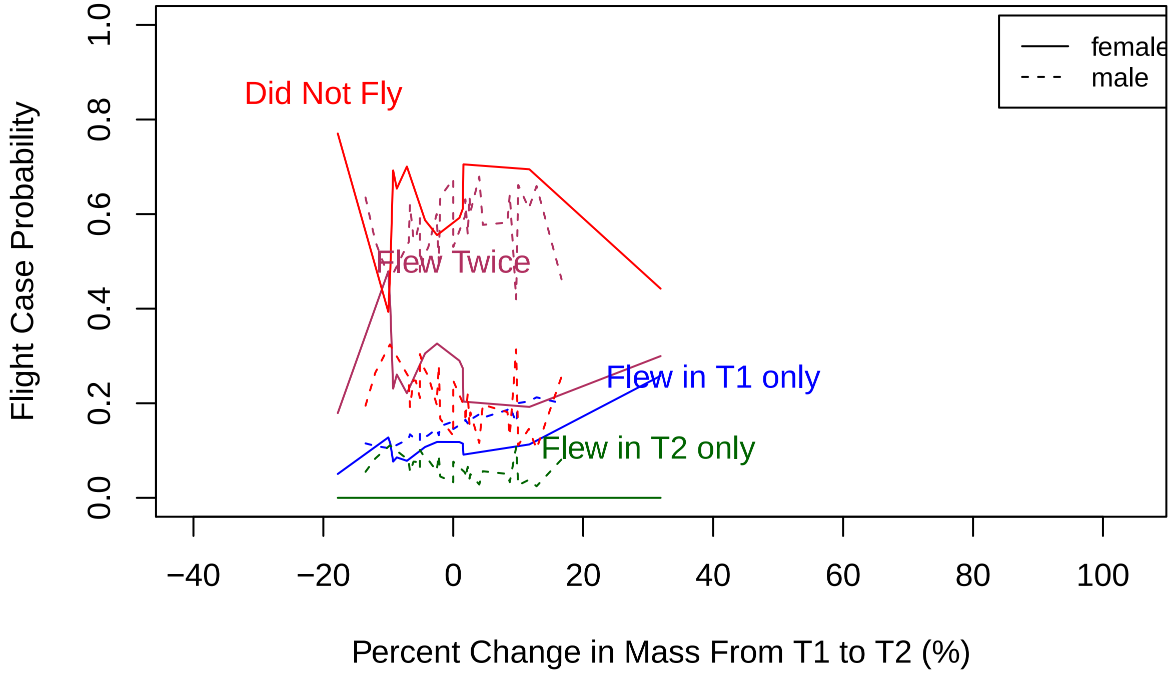
```
dataFall = clean_flight_data.Fall("data/full_data-Fall2019.csv")

# extract sets with an experimental design similar to the Winter tests
ongoing_data = dataFall %>%
  filter(!is.na(mass))  %>%
  filter(set_number > 71)

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

Compute predicted probabilities

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

```r
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$wing[[i]][1] / d$body[[i]][1]
  w = d$wing2body_c[i]
  top0 = exp(0) # just equals 1
  #top1 = exp(-17.862 + 0.041*m - 0.571*s + 23.558*w )
  #top2 = exp(-4.395 - 0.005*m - 9.580*s - 8.937*w)
  #top3 = exp(-19.931 + 0.018*m - 0.760*s + 28.019*w)
  top1 = exp(-0.935 + 0.041*m - 0.571*s + 23.739*w)
  top2 = exp(-8.177 - 0.005*m - 6.954*s - 6.595*w)
  top3 = exp(0.201 + 0.018*m - 0.760*s + 28.094*w)
  bottom = top0 + top1 + top2 + top3
  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)
}
```

Plot predicted probabilities



Overall and Grouped Accuracies

```
probs = round(cbind(neither, T1_rather_than_none, T2_rather_than_none, both_rather_than_none),2)
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))
```

```
## [1] "Overall prediction accuracy,  0.6"
```

```
# by sex
femdata = dataframe %>%
  filter(sex=="F")
maledata = dataframe %>%
  filter(sex=="M")

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

```
## [1] "Female prediction accuracy,  0.38"
```

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

```
## [1] "Male prediction accuracy,  0.69"
```

Confusion Matrix

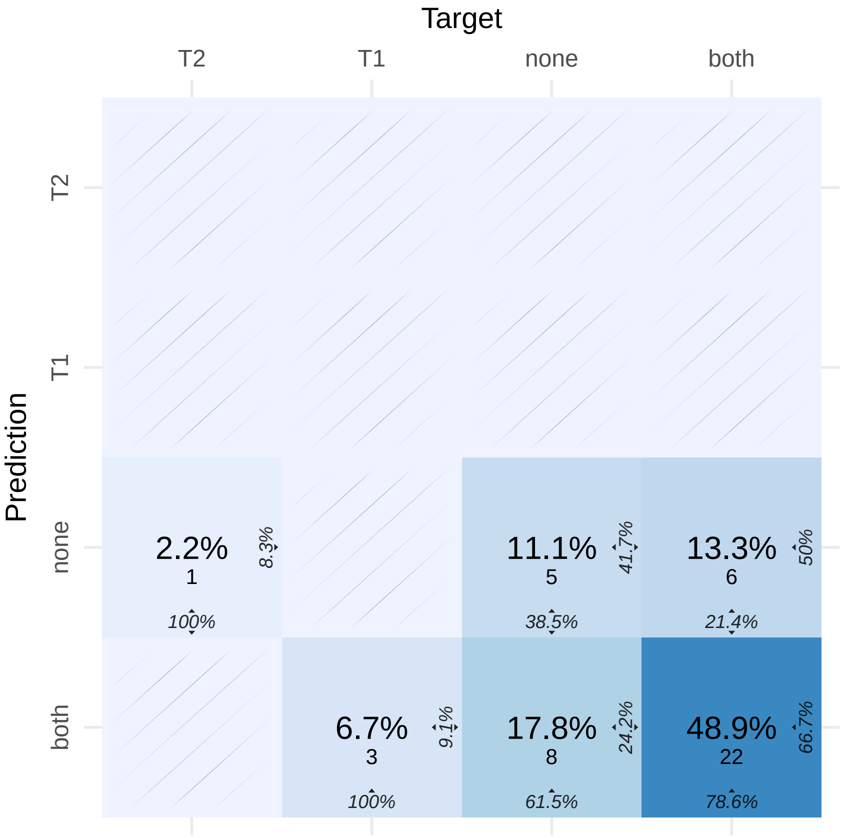
```
acc_table = get_confusion_matrix(dataframe,3,6)
acc_table
```

```
## # A tibble: 1 x 16
##   `Overall Accuracy` `Balanced Accuracy`    F1 Sensitivity Specificity
##                <dbl>               <dbl> <dbl>       <dbl>       <dbl>
## 1                0.6               0.538   NaN       0.293       0.784
## # ... with 11 more variables: Pos Pred Value <dbl>, Neg Pred Value <dbl>,
## #   Kappa <dbl>, MCC <dbl>, Detection Rate <dbl>, Detection Prevalence <dbl>,
## #   Prevalence <dbl>, Predictions <list>, Confusion Matrix <list>,
## #   Class Level Results <list>, Process <list>
```

```
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)
```



Females Only

```
dfem = d %>%
  filter(sex=="F")
```

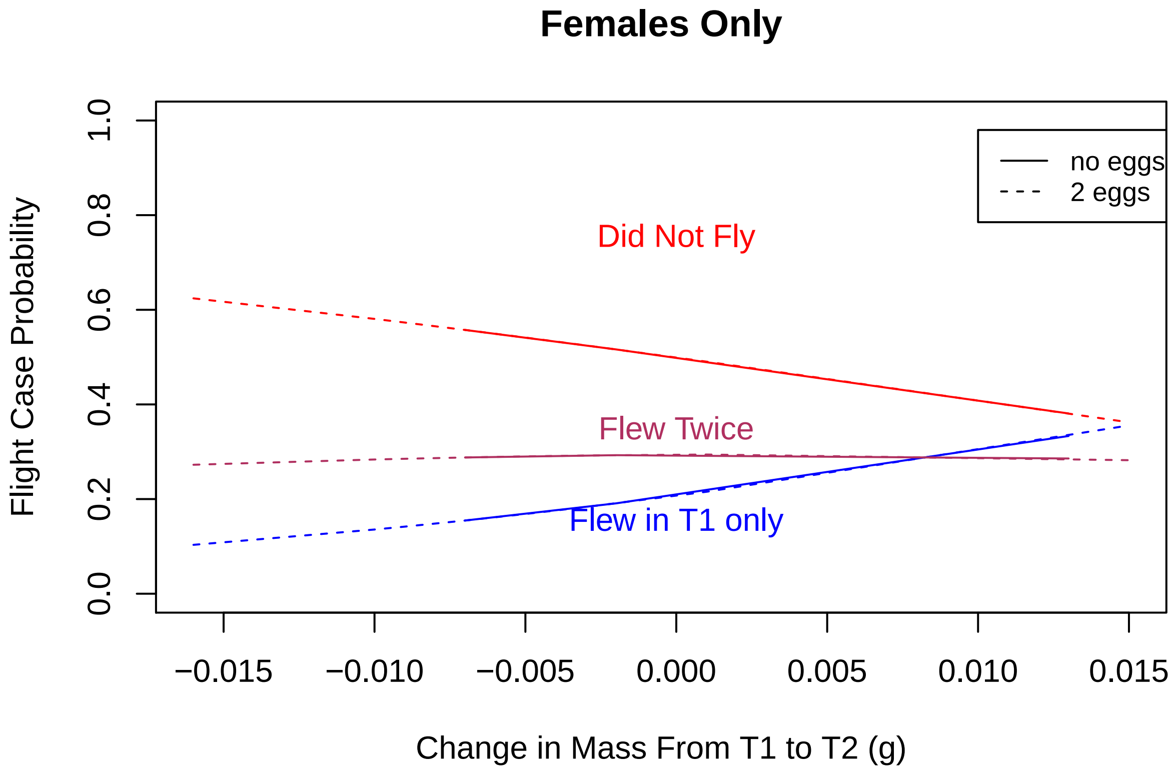
```
dfem <- dfem[with(dfem, order(mass_diff)),]
```

```
neither = c()
T1_rather_than_none = c()
both_rather_than_none = c()
for (i in 1:nrow(dfem)) {
  md = dfem$mass_diff[[i]]
  ed = dfem$egg_diff[[i]]
  top0 = exp(0) # just equals 1
  top1 = exp(-0.88 - 0.53*ed + 57.43*md )
  top2 = exp(-0.53 - 1.09*ed + 18.67*md)
  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)
}
```

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)
```

Plot predicted probabilities



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"
```

Confusion Matrix

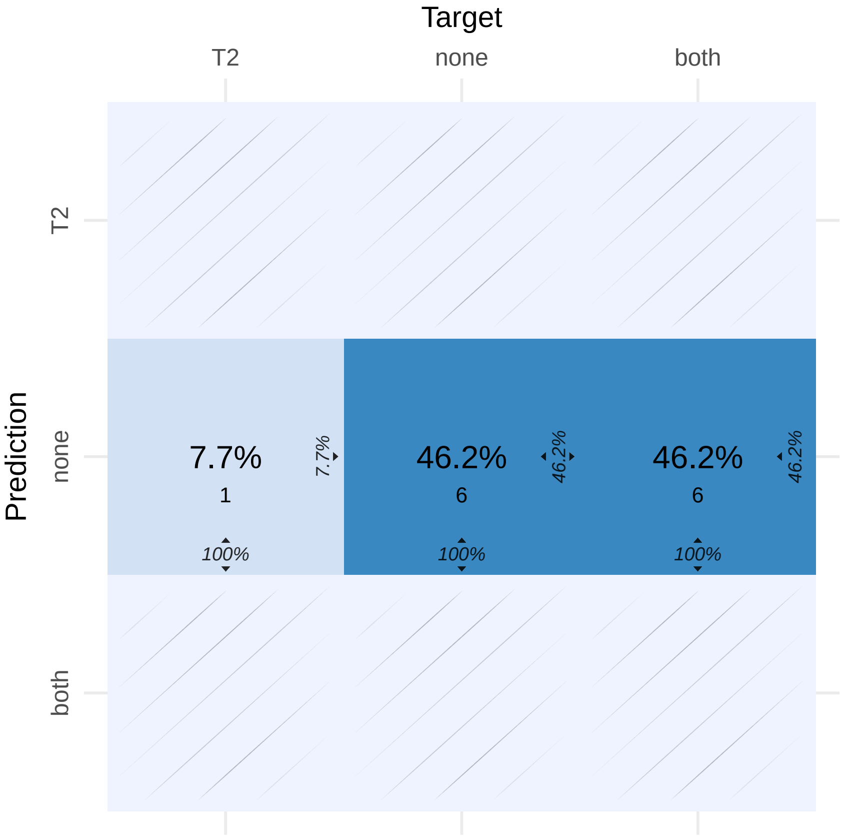
```
acc_table = get_confusion_matrix(dataframe,3,5)
acc_table
```

```
## # A tibble: 1 x 16
##   `Overall Accuracy` `Balanced Accuracy`    F1 Sensitivity Specificity
##                <dbl>               <dbl> <dbl>       <dbl>       <dbl>
## 1              0.462                 0.5   NaN       0.333       0.667
## # ... with 11 more variables: Pos Pred Value <dbl>, Neg Pred Value <dbl>,
## #   Kappa <dbl>, MCC <dbl>, Detection Rate <dbl>, Detection Prevalence <dbl>,
## #   Prevalence <dbl>, Predictions <list>, Confusion Matrix <list>,
## #   Class Level Results <list>, Process <list>
```

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

```
## # A tibble: 9 x 3
##   Prediction Target     N
##   <chr>      <chr>  <int>
## 1 both       both       0
## 2 none       both       6
## 3 T2         both       0
## 4 both       none       0
## 5 none       none       6
## 6 T2         none       0
## 7 both       T2         0
## 8 none       T2         1
## 9 T2         T2         0
```

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


Target
T2
none
both
Prediction
T2
none
both
7.7%
1
7.7%
100%
46.2%
6
46.2%
100%
46.2%
6
46.2%
100%