# 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(dplyr) # data manipulation
#library(ggformula) # ggplot plotting
#library(cowplot) # ggplot helper functions to arrange multi-panel figures
```

#### Read Source Files

#### Read the Data

```
data <- read_flight_data("data/all_flight_data-Winter2020.csv")
data_all <- data[[1]]
data_tested <- data[[2]]
d <- create_delta_data(data_tested, tested_more_than_once=FALSE)</pre>
```

### Repeating Plot Parameters & Functions

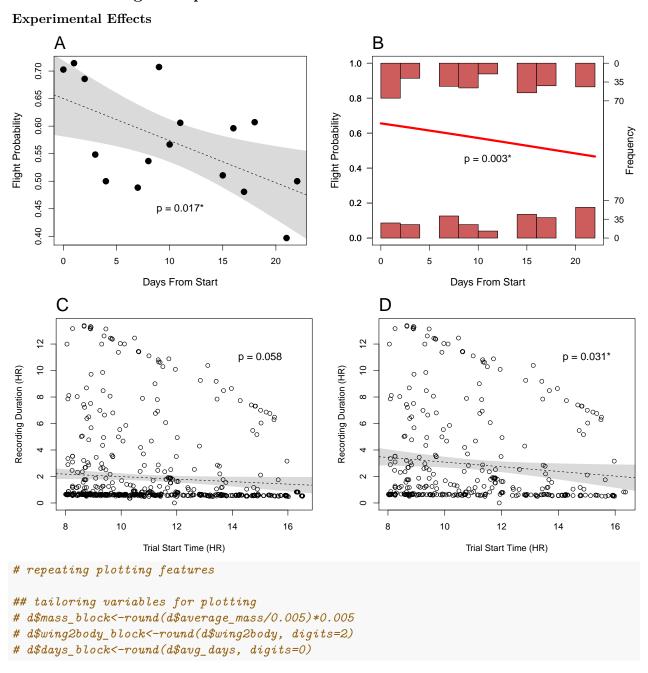
```
# scale/magnifications

c1 = 1.5 # size of points
c2 = 1.2 # size of text
c3 = 2 # size of title

# compute 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) # newdata
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))
}</pre>
```

### Across-Trial Flight Response



```
# group by sex and re-center
# data_fem <- d[d$sex=="F",]
# data_male <- d[d$sex=="M",]
# data_fem <- center_data(data_fem, is_not_binded = FALSE)
# data_male <- center_data(data_male, is_not_binded = FALSE)
#
# sex vs. flight prob
# 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$sex=="M"]
# #data_temp$CI <- aggregate(flew_prob~sex, data=d, FUN=function(x) qnorm(0.975)*sd(x)/length(x))$flew__#
# calculate binomial confidence interval
# data_temp$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")</pre>
```