### Initial Milestone EDA

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#### EDA of the data

```
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
      filter, lag
## The following objects are masked from 'package:base':
##
      intersect, setdiff, setequal, union
library(ggplot2)
library(rstanarm)
## Loading required package: Rcpp
## This is rstanarm version 2.21.3
## - See https://mc-stan.org/rstanarm/articles/priors for changes to default priors!
## - Default priors may change, so it's safest to specify priors, even if equivalent to the defaults.
## - For execution on a local, multicore CPU with excess RAM we recommend calling
    options(mc.cores = parallel::detectCores())
library(tidyverse)
## -- Attaching packages ----- tidyverse 1.3.2 --
## v tibble 3.1.8
                     v purrr
                              0.3.4
## v tidyr
           1.2.1
                     v stringr 1.4.1
## v readr
           2.1.2
                     v forcats 0.5.2
## -- Conflicts -----
                                          ## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                   masks stats::lag()
library(devtools)
## Loading required package: usethis
library(ggpubr)
quabbin_data_all <- read.csv("/Users/billg/Desktop/MA 675/Initial-Milestone/binomial_quabbin_data_all.c
```

#Data Cleaning, data has values where time.delay = "one " instead of "one", get rid of the blank

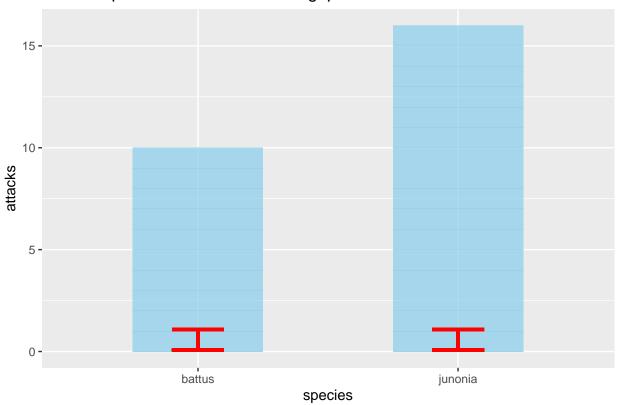
```
one_to_one <- function(string){</pre>
  if (string == "one "){
    return(string ="one")
  }
  else {return(string)}
quabbin_data_all$time.delay <- sapply(quabbin_data_all$time.delay, one_to_one)</pre>
#Separate the data all file based on time.delay
# Model
quabbin_model <- subset(quabbin_data_all, trial %in% "model")</pre>
quabbin model four <- subset(quabbin model, time.delay %in% "four")
quabbin_model_two <- subset(quabbin_model, time.delay %in% "two")</pre>
quabbin_model_one <- subset(quabbin_model, time.delay %in% "one")</pre>
quabbin_mimic <- subset(quabbin_data_all, trial %in% "mimic")</pre>
quabbin_mimic_four <- subset(quabbin_mimic, time.delay %in% "four")</pre>
quabbin_mimic_two <- subset(quabbin_mimic, time.delay %in% "two")</pre>
quabbin_mimic_one <- subset(quabbin_mimic, time.delay %in% "one")</pre>
# Simultaneous
quabbin_simul <- subset(quabbin_data_all, trial %in% "simultaneously")</pre>
```

#### Bar Plots with error bars

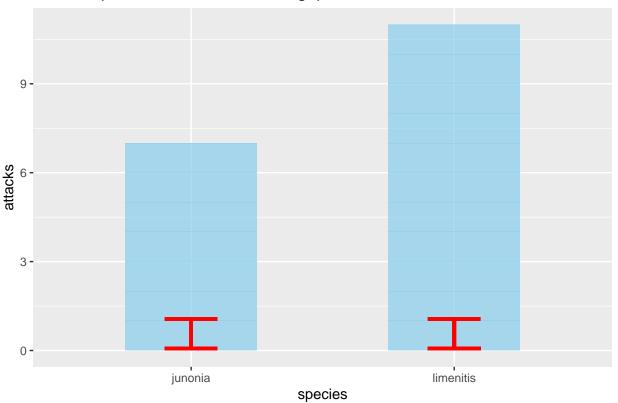
#The length of an Error Bar helps reveal the uncertainty of a data point: a short Error Bar shows that values are concentrated, signalling that the plotted average value is more likely, while a long Error Bar would indicate that the values are more spread out and less reliable.

#### Species

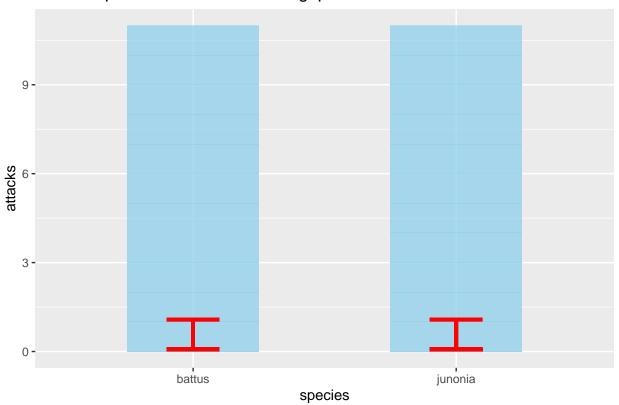
## Model experiment with four weeks gap



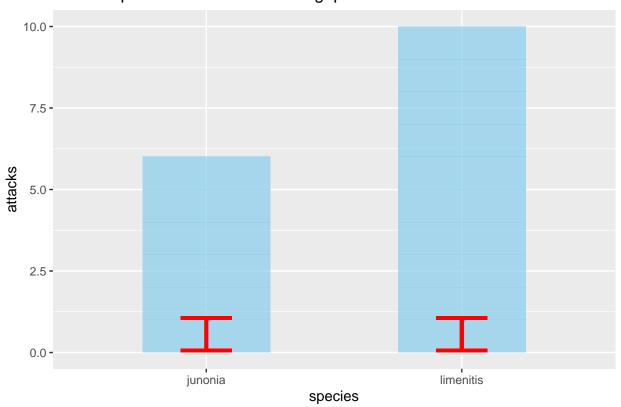
## Mimic experiment with four weeks gap



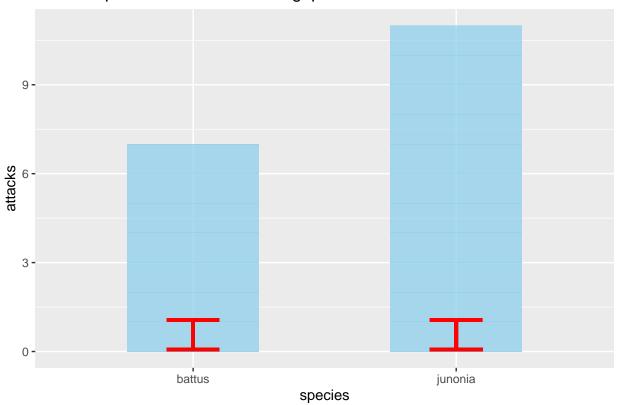
## Model experiment with two weeks gap



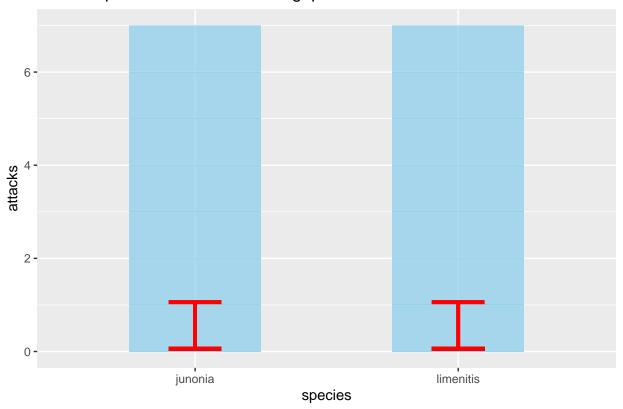
### Mimic experiment with two weeks gap

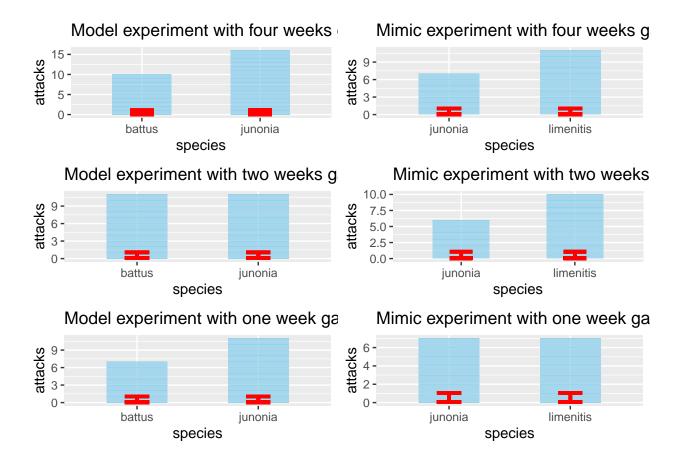


## Model experiment with one week gap



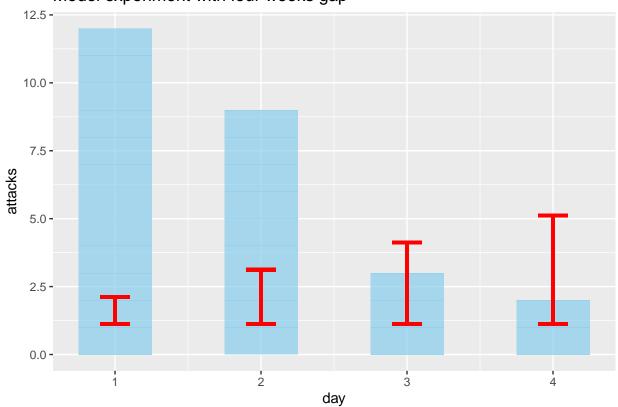
# Mimic experiment with one week gap



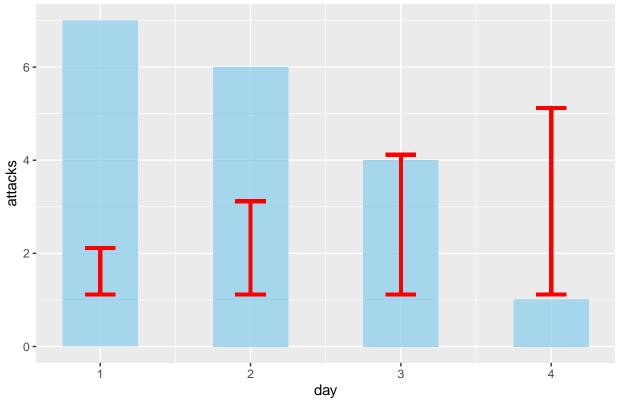


### Days

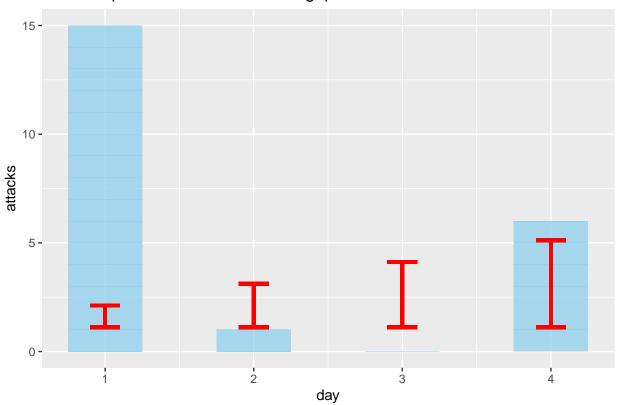
## Model experiment with four weeks gap



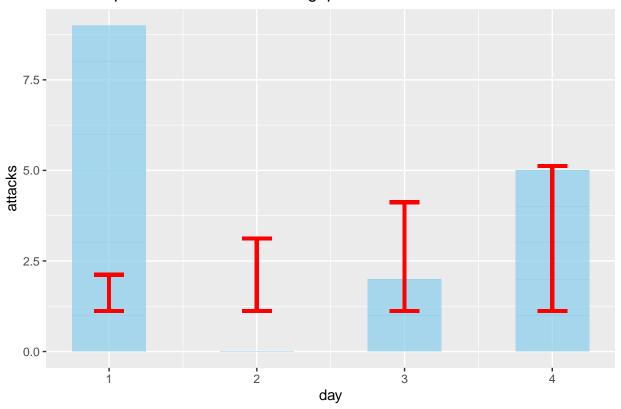
## Mimic experiment with four weeks gap



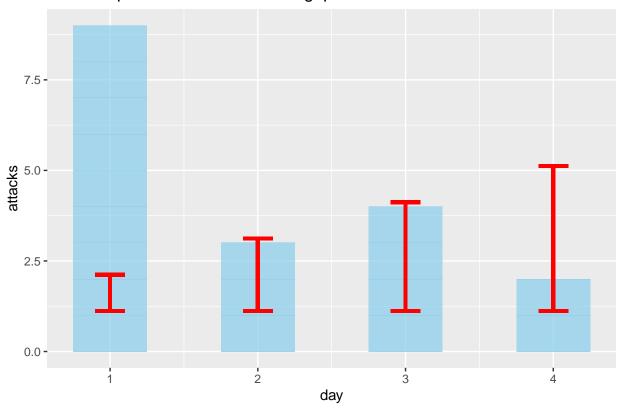
## Model experiment with two weeks gap



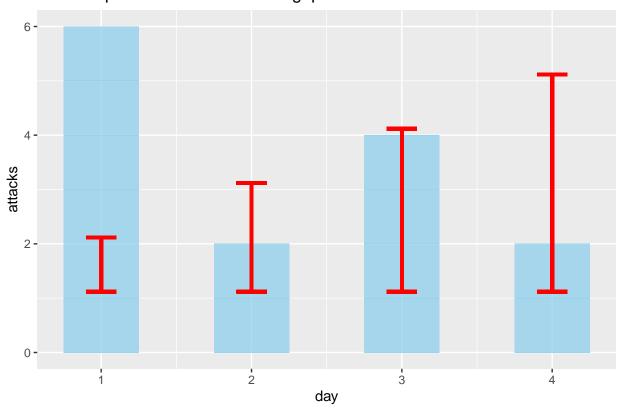
## Mimic experiment with two weeks gap

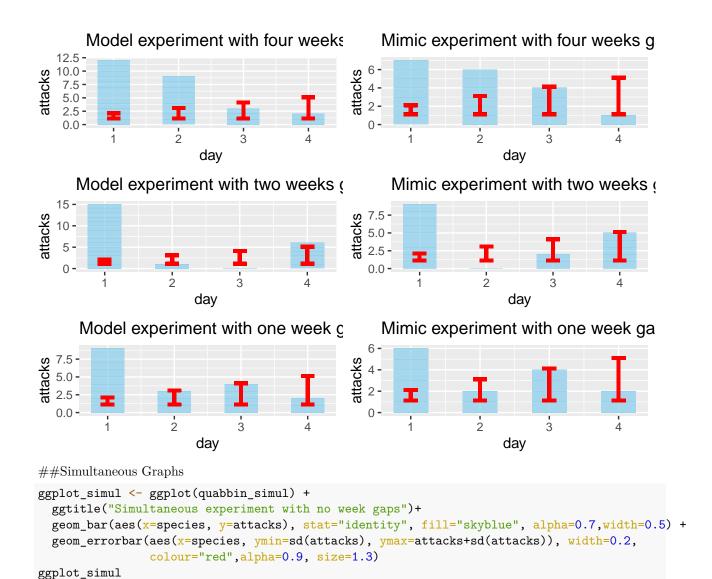


## Model experiment with one week gap

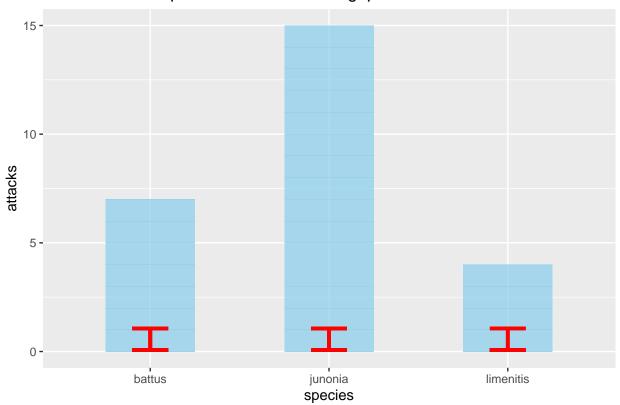


## Mimic experiment with one week gap





## Simultaneous experiment with no week gaps



Note that the  $\mbox{echo} = \mbox{FALSE}$  parameter was added to the code chunk to prevent printing of the R code that generated the plot.