

Behavioral Tolerance, Vigor, and resilience

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1 Introduction

1.1 Overall summary

1.2 Quick experimental summary

1.3 Load in packages needed for analysis

```
# Clear the working environment
rm(list = ls())
# Visualization
library(ggplot2)
library(visreg)
source("http://highstat.com/Books/BGS/GAMM/RCodeP2/HighstatLibV6.R")
# (generalized) Linear mixed modeling
library(lme4)
library(glmmTMB)
library(lmodel2)
# Statistical analysis reporting and model validation
library(performance)
library(car)
library(lmtest)
library(DHARMA)
# Data wrangling
library(dplyr)
```

```
library(plyr)
library(tidyverse)
library(tidylog)
```

1.4 Load in dataframe

```
# Loading in data set
IndBehav <- read_csv("VIEBehavior_20210913_V2.csv", col_types = cols(fishID = col_character(),
  Infection = col_character(), InfDate = col_character(), BehavGroup = col_character(),
  dayofinf = col_character(), CountDay = col_character(), Behavdate = col_character(),
  TOD = col_character(), Duration = col_double(), Velocity = col_double(), Distance = col_double()))
```

```
## New names:
## * 'fishID' -> 'fishID...2'
## * 'fishID' -> 'fishID...19'
## * 'AUC2' -> 'AUC2...21'
## * 'TrialTime' -> 'TrialTime...23'
## * 'Ratebf' -> 'Ratebf...24'
## * 'Recov' -> 'Recov...25'
## * 'TrialTime' -> 'TrialTime...31'
## * 'AUC2' -> 'AUC2...37'
## * 'Recov' -> 'Recov...40'
## * 'Ratebf' -> 'Ratebf...48'
```

```
# Filtering Data set so we can perform our analysis
IndBehav1 <- IndBehav %>%
  # Removing columns we dont need
  select(-c(Blind.ID, fishID...19, TrialTime...31, AUC2...37, InfLength, Recov...40,
    Ratebf...48, LateLength, dayofinf, Countintial, Notes, InfWeight)) %>%
  # Renaming some of the columns with funky names for ease of coding and
  # naming
  rename(fishID = fishID...2, AUC = AUC2...21, TrialTime = TrialTime...23, Ratebf = Ratebf...24,
    Recov = Recov...25)
```

```
## select: dropped 12 variables (Blind.ID, InfWeight, InfLength, LateLength, dayofinf, ...)
## rename: renamed 5 variables (fishID, AUC, TrialTime, Ratebf, Recov)
```

1.5 Calculate metrics needed for further analyses

1.5.1 Calculating all body condition metrics

```
IndBehav1 <- IndBehav %>%
  select(-c(Blind.ID, fishID...19, TrialTime...31, AUC2...37, InfLength, Recov...40,
    Ratebf...48, LateLength, dayofinf, Countintial, Notes, InfWeight)) %>%
  rename(fishID = fishID...2, AUC = AUC2...21, TrialTime = TrialTime...23, Ratebf = Ratebf...24,
    Recov = Recov...25)
```

```
## select: dropped 12 variables (Blind.ID, InfWeight, InfLength, LateLength, dayofinf, ...)
```

```

## rename: renamed 5 variables (fishID, AUC, TrialTime, Ratebf, Recov)

##### This code is just to examine how many fish cleared their infection
##### (13)##### IndBehavRec<- IndBehav1 %>% filter(Recov==1)%>% filter(Fish==1)

##### This code is just to examine how many fish died during their infection
##### (2)##### IndBehavDead<- IndBehav1 %>% filter(Died==1)%>% filter(Fish==1)

FemaleOnly <- IndBehav1 %>%
  filter(Sex == "F")

## filter: removed 541 rows (49%), 564 rows remaining

MaleOnly <- IndBehav1 %>%
  filter(Sex == "M")

## filter: removed 565 rows (51%), 540 rows remaining

# Calculating SMI metrics Preinfection SMI#####

# PreinfectionSMI for females To calculate the SMI we take the OLS slope
lmodel2(log(as.numeric(PreWeight) + 1) ~ log(as.numeric(PreLength) + 1), data = FemaleOnly)

## RMA was not requested: it will not be computed.

## No permutation test will be performed

##
## Model II regression
##
## Call: lmodel2(formula = log(as.numeric(PreWeight) + 1) ~
## log(as.numeric(PreLength) + 1), data = FemaleOnly)
##
## n = 564    r = 0.9103118    r-square = 0.8286675
## Parametric P-values:    2-tailed = 1.890218e-217    1-tailed = 9.451089e-218
## Angle between the two OLS regression lines = 4.099607 degrees
##
## Regression results
##   Method Intercept      Slope Angle (degrees) P-perm (1-tailed)
## 1    OLS -1.114762 0.4206982    22.81640      NA
## 2     MA -1.155627 0.4341311    23.46717      NA
## 3    SMA -1.240856 0.4621474    24.80390      NA
##
## Confidence intervals
##   Method 2.5%-Intercept 97.5%-Intercept 2.5%-Slope 97.5%-Slope
## 1    OLS      -1.163000    -1.066525  0.4048487  0.4365478
## 2     MA      -1.205686    -1.106162  0.4178711  0.4505866
## 3    SMA      -1.289899    -1.193466  0.4465696  0.4782687
##
## Eigenvalues: 0.009625885 0.0002518475
##
## H statistic used for computing C.I. of MA: 0.0001893902

```

```
# Take the median length from summary
summary(FemaleOnly$PreLength)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    16.60   18.40   20.20   20.03   21.20   24.20
```

```
# Adding PreSMI to Dataframe
FemaleOnly <- FemaleOnly %>%
  group_by(fishID) %>%
  mutate(PreSMI = PreWeight * ((20.2/PreLength)^0.4206982))
```

```
## group_by: one grouping variable (fishID)
```

```
## mutate (grouped): new variable 'PreSMI' (double) with 47 unique values and 0% NA
```

```
# PreinfectionSMI for males
lmodel2(log(as.numeric(PreWeight) + 1) ~ log(as.numeric(PreLength) + 1), data = MaleOnly)
```

```
## RMA was not requested: it will not be computed.
```

```
## No permutation test will be performed
```

```
##
## Model II regression
##
## Call: lmodel2(formula = log(as.numeric(PreWeight) + 1) ~
## log(as.numeric(PreLength) + 1), data = MaleOnly)
##
## n = 540    r = 0.7784225    r-square = 0.6059415
## Parametric P-values:    2-tailed = 7.086423e-111    1-tailed = 3.543211e-111
## Angle between the two OLS regression lines = 6.76859 degrees
##
## Regression results
##      Method Intercept      Slope Angle (degrees) P-perm (1-tailed)
## 1      OLS -0.4620565 0.1938185      10.96898      NA
## 2       MA -0.4750867 0.1984879      11.22660      NA
## 3      SMA -0.6160126 0.2489888      13.98170      NA
##
## Confidence intervals
##      Method 2.5%-Intercept 97.5%-Intercept 2.5%-Slope 97.5%-Slope
## 1      OLS      -0.4990055      -0.4251076 0.1805813 0.2070557
## 2       MA      -0.5130172      -0.4373522 0.1849657 0.2120803
## 3      SMA      -0.6539329      -0.5800547 0.2361033 0.2625776
##
## Eigenvalues: 0.00431447 9.773707e-05
##
## H statistic used for computing C.I. of MA: 0.0001701002
```

```
# Take the median length from summary
summary(MaleOnly$PreLength)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      13.70   14.50   15.30   15.32   16.00   18.50
```

```
# Adding PreSMI to Dataframe
MaleOnly <- MaleOnly %>%
  group_by(fishID) %>%
  mutate(PreSMI = PreWeight * ((15.3/PreLength)^0.1938185))
```

```
## group_by: one grouping variable (fishID)
```

```
## mutate (grouped): new variable 'PreSMI' (double) with 44 unique values and 0% NA
```

```
##### Late Infection SMI#####
```

```
# Late infection SMI for females Take OLS slope from this model
lmodel2(log(as.numeric(LateWeight) + 1) ~ log(as.numeric(PreLength) + 1), data = FemaleOnly)
```

```
## RMA was not requested: it will not be computed.
```

```
## No permutation test will be performed
```

```
##
```

```
## Model II regression
```

```
##
```

```
## Call: lmodel2(formula = log(as.numeric(LateWeight) + 1) ~
```

```
## log(as.numeric(PreLength) + 1), data = FemaleOnly)
```

```
##
```

```
## n = 516    r = -0.127178    r-square = 0.01617424
```

```
## Parametric P-values:    2-tailed = 0.003807557    1-tailed = 0.001903778
```

```
## Angle between the two OLS regression lines = 57.58662 degrees
```

```
##
```

```
## Regression results
```

##	Method	Intercept	Slope	Angle (degrees)	P-perm (1-tailed)
## 1	OLS	2.033718	-0.5976124	-30.86306	NA
## 2	MA	107.560934	-35.3034151	-88.37748	NA
## 3	SMA	14.504560	-4.6990243	-77.98610	NA

```
##
```

```
## Confidence intervals
```

##	Method	2.5%-Intercept	97.5%-Intercept	2.5%-Slope	97.5%-Slope
## 1	OLS	0.8050897	3.262347	-1.001497	-0.1937279
## 2	MA	64.2522935	331.105245	-108.822693	-21.0600644
## 3	SMA	13.3291795	15.785299	-5.120234	-4.3124649

```
##
```

```
## Eigenvalues: 0.1896132 0.008435402
```

```
##
```

```
## H statistic used for computing C.I. of MA: 0.0003658854
```

```
# Take the median length from summary
summary(FemaleOnly$PreLength)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      16.60   18.40   20.20   20.03   21.20   24.20
```

```

# Adding PreSMI to Dataframe
FemaleOnly <- FemaleOnly %>%
  group_by(fishID) %>%
  mutate(LateSMI = PreWeight * ((20.1/PreLength)^-0.5976124))

## group_by: one grouping variable (fishID)

## mutate (grouped): new variable 'LateSMI' (double) with 47 unique values and 0% NA

# Late Infection SMI for males Take OLS slope from this model
lmodel2(log(as.numeric(LateWeight) + 1) ~ log(as.numeric(PreLength) + 1), data = MaleOnly)

## RMA was not requested: it will not be computed.

## No permutation test will be performed

##
## Model II regression
##
## Call: lmodel2(formula = log(as.numeric(LateWeight) + 1) ~
## log(as.numeric(PreLength) + 1), data = MaleOnly)
##
## n = 456    r = -0.06095677    r-square = 0.003715728
## Parametric P-values:    2-tailed = 0.1938354    1-tailed = 0.09691771
## Angle between the two OLS regression lines = 64.27059 degrees
##
## Regression results
##   Method  Intercept      Slope Angle (degrees) P-perm (1-tailed)
## 1    OLS    1.492739   -0.472241    -25.27860             NA
## 2     MA  348.385697 -124.982883    -89.54158             NA
## 3    SMA   21.760991   -7.747145    -82.64494             NA
##
## Confidence intervals
##   Method 2.5%-Intercept 97.5%-Intercept 2.5%-Slope 97.5%-Slope
## 1    OLS    -0.4947141    3.480193   -1.185443    0.2409615
## 2     MA   138.8775568   -682.296809  244.961036  -49.7839131
## 3    SMA    19.8652425    23.839279   -8.493107   -7.0667022
##
## Eigenvalues: 0.204658 0.003396832
##
## H statistic used for computing C.I. of MA: 0.0001459962

# Take the median length from summary
summary(MaleOnly$PreLength)

##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  13.70  14.50   15.30   15.32  16.00   18.50

# Adding PreSMI to Dataframe
MaleOnly <- MaleOnly %>%
  group_by(fishID) %>%
  mutate(LateSMI = PreWeight * ((15.3/PreLength)^-0.472241))

```

```
## group_by: one grouping variable (fishID)

## mutate (grouped): new variable 'LateSMI' (double) with 44 unique values and 0% NA
```

```
#####

# Bringing the male and female dataframes together to create our overall
# dataframe
IndBehav2 <- rbind(FemaleOnly, MaleOnly)

# View(IndBehav2)
```

1.5.2 Calculating the behavioral tolerance metrics needed for analyses

We are calculating behavioral tolerance through two metrics. First is a measure of behavioral tolerance using linear mixed models using slope random effects for fishID. This allows us to extract each individuals change in activity with parasite burden and therefore allow us to calculate the tolerance (fishID slope) for each individual. This also allows us to use the random effect intercept for fishID as a measure of behavioral vigor. The second way we could calculate these metrics are a measure of change in behavior between two points of behavior (often referred to as point tolerance, CITATION FOR THIS). This is calculated in the second half of the code as the change in behavior between pre-infection and early, late, and later points of infection.

```
# Calculating the behavioral tolerance metrics were interested in for our
# analysis

# Random slope from random effects model Random effects model with random slope
# for each fish by worm burden prior to measuring its activity. This slope is
# the tolerance an individual has to changing its behavior as infection
# increases. The slope of the behavior is the individuals behavioral vigor, or
# its pre-infection behavior
BehavTollLM <- lmer(Velocity ~ (Wormbf | fishID), IndBehav2)
summary(BehavTollLM)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Velocity ~ (Wormbf | fishID)
## Data: IndBehav2
##
## REML criterion at convergence: 1369.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.8571 -0.6195 -0.0263  0.5647  4.1663
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## fishID (Intercept) 6.101e-01 0.781095
## Wormbf 1.231e-05 0.003509 -0.42
## Residual 5.539e-01 0.744248
## Number of obs: 541, groups: fishID, 48
##
## Fixed effects:
```

```
##           Estimate Std. Error t value
## (Intercept)    1.906      0.111   17.17
## optimizer (nloptwrap) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 4.0577 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
## - Rescale variables?
```

```
# Extracting the intercept and slope from the linear mixed model
betaTol <- data.frame(coef(BehavTolLM)$fishID)
# Renaming the slope and intercept to align with our metrics
betaTol <- betaTol %>%
  rename(BehavTol = Wormbf, BehavVig = X.Intercept.)
```

```
## rename: renamed 2 variables (BehavTol, BehavVig)
```

```
View(betaTol)
# Creating a fishID column for combination with future dataframe
betaTol <- cbind(fishID = rownames(betaTol), betaTol)
# Narrowing our overall data set to one row per individual
IndBehav3 <- IndBehav2 %>%
  group_by(fishID, TrialTime) %>%
  filter(TOD == 2) %>%
  select(-c(InfDiff, Fish, Behavdate, Duration, Distance, comp3, Totworm, rate05,
    rate012, rate512, rate1216, rate18end)) %>%
  pivot_wider(names_from = TrialTime, values_from = c(Velocity, Wormbf, Ratebf))
```

```
## group_by: 2 grouping variables (fishID, TrialTime)
```

```
## filter (grouped): removed 736 rows (67%), 368 rows remaining
```

```
## select: dropped 12 variables (Fish, Totworm, comp3, Behavdate, Duration, ...)
```

```
## pivot_wider: reorganized (Wormbf, TrialTime, Ratebf, Velocity) into (Velocity_Before, Velocity_Early
```

```
# subset down to infected individuals only and calculate point tolerance
# metrics for each timeframe.
IndBehav3Inf <- IndBehav3 %>%
  group_by(fishID) %>%
  filter(Infection == 1) %>%
  mutate(EChBe = Velocity_Early - Velocity_Before, LChBe = Velocity_Late - Velocity_Before,
    LtrChBe = Velocity_Later - Velocity_Before, ERatebf = Wormbf_Early - Wormbf_Before/5,
    LRatebf = Wormbf_Late - Wormbf_Early/5, LtrRatebf = Wormbf_Later - Wormbf_Later/5) %>%
  pivot_longer(cols = starts_with("Wormbf"), names_to = "TrialTime", names_prefix = "Wormbf_",
    values_to = "Wormbf") %>%
  select(-c(Velocity_Before, Velocity_Early, Velocity_Late, Velocity_Later, Ratebf_Before,
    Ratebf_Early, Ratebf_Late, Ratebf_Later)) %>%
  filter(fishID != 44)
```

```
## group_by: one grouping variable (fishID)
```

```
## filter (grouped): removed 38 rows (41%), 54 rows remaining
```



```

## mutate (grouped): new variable 'EChBe' (double) with 49 unique values and 11% NA

##
## new variable 'LChBe' (double) with 48 unique values and 13% NA

##
## new variable 'LtrChBe' (double) with 42 unique values and 24% NA

##
## new variable 'ERatebf' (double) with 23 unique values and 13% NA

##
## new variable 'LRatebf' (double) with 45 unique values and 13% NA

##
## new variable 'LtrRatebf' (double) with 33 unique values and 26% NA

## pivot_longer: reorganized (Wormbf_Before, Wormbf_Early, Wormbf_Late, Wormbf_Later) into (TrialTime, V

## select: dropped 8 variables (Velocity_Before, Velocity_Early, Velocity_Late, Velocity_Later, Ratebf_L

## filter (grouped): removed 4 rows (2%), 212 rows remaining

# Make two dataframes with pivot longer for wormbf and velocity then merge them
# together on fishID and TrialTime
IndBehav3InfV <- IndBehav3 %>%
  filter(Infection == 1) %>%
  pivot_longer(cols = starts_with("Velocity"), names_to = "TrialTime", names_prefix = "Velocity_",
    values_to = "Velocity") %>%
  select(fishID, Velocity, TrialTime) %>%
  filter(fishID != 44)

## filter (grouped): removed 38 rows (41%), 54 rows remaining

## pivot_longer: reorganized (Velocity_Before, Velocity_Early, Velocity_Late, Velocity_Later) into (Tri

## select: dropped 29 variables (Sex, PreWeight, PreLength, Treatment, Infection, ...)

## filter (grouped): removed 4 rows (2%), 212 rows remaining

# Making the growth rate columns into one column for infected individuals
IndBehavGRInf <- IndBehav3 %>%
  filter(Infection == 1) %>%
  pivot_longer(cols = starts_with("Ratebf"), names_to = "TrialTime", names_prefix = "Ratebf_",
    values_to = "Ratebf") %>%
  select(fishID, TrialTime, Ratebf)

## filter (grouped): removed 38 rows (41%), 54 rows remaining

## pivot_longer: reorganized (Ratebf_Before, Ratebf_Early, Ratebf_Late, Ratebf_Later) into (TrialTime, L

## select: dropped 29 variables (Sex, PreWeight, PreLength, Treatment, Infection, ...)

```

```

# Merging the tolerance and vigor metrics
IndBehav3Inf1 <- merge(IndBehav3Inf, betaTol, by.x = "fishID", by.y = "fishID")

# Merge the two dataframes together based on the fishID and TrialTime to get
# all variables we want into one dataframe
IndBehav4Inf <- merge(IndBehav3InfV, IndBehav3Inf1, by.x = c("fishID", "TrialTime"),
  by.y = c("fishID", "TrialTime"), all = TRUE)
IndBehav4Inf2 <- merge(IndBehav4Inf, IndBehavGRInf, by.x = c("fishID", "TrialTime"),
  by.y = c("fishID", "TrialTime"), all = TRUE)
# Subset down to uninfected individuals and calculate their point tolerance
# metrics Creating a dataframe for calculating the tolerance metrics and then
# pivot longer by Wormbf
IndBehav3Unf <- IndBehav3 %>%
  filter(Infection == 0) %>%
  mutate(EChBe = Velocity_Early - Velocity_Before, LChBe = Velocity_Late - Velocity_Before,
    LtrChBe = Velocity_Later - Velocity_Before, ERatebf = Wormbf_Early - Wormbf_Before/5,
    LRatebf = Wormbf_Late - Wormbf_Early/5, LtrRatebf = Wormbf_Later - Wormbf_Later/5,
    ) %>%
  group_by(fishID) %>%
  pivot_longer(cols = starts_with(c("Wormbf")), names_to = "TrialTime", names_prefix = c("Wormbf_"),
    values_to = "Wormbf") %>%
  select(-c(Velocity_Before, Velocity_Early, Velocity_Late, Velocity_Later, Ratebf_Before,
    Ratebf_Early, Ratebf_Late, Ratebf_Later))

```

```
## filter (grouped): removed 54 rows (59%), 38 rows remaining
```

```
## mutate (grouped): new variable 'EChBe' (double) with 38 unique values and 0% NA
```

```
## new variable 'LChBe' (double) with 38 unique values and 0% NA
```

```
## new variable 'LtrChBe' (double) with 38 unique values and 3% NA
```

```
## new variable 'ERatebf' (double) with one unique value and 100% NA
```

```
## new variable 'LRatebf' (double) with one unique value and 100% NA
```

```
## new variable 'LtrRatebf' (double) with one unique value and 100% NA
```

```
## group_by: one grouping variable (fishID)
```

```
## pivot_longer: reorganized (Wormbf_Before, Wormbf_Early, Wormbf_Late, Wormbf_Later) into (TrialTime, Wormbf)
```

```
## select: dropped 8 variables (Velocity_Before, Velocity_Early, Velocity_Late, Velocity_Later, Ratebf_Before, Ratebf_Early, Ratebf_Late, Ratebf_Later)
```

```

# Creating a second dataframe where we pivot longer for velocity
IndBehav3UnfV <- IndBehav3 %>%
  filter(Infection == 0) %>%
  pivot_longer(cols = starts_with("Velocity"), names_to = "TrialTime", names_prefix = "Velocity_",
    values_to = "Velocity") %>%
  select(fishID, TrialTime, Velocity)

```

```

## filter (grouped): removed 54 rows (59%), 38 rows remaining

## pivot_longer: reorganized (Velocity_Before, Velocity_Early, Velocity_Late, Velocity_Later) into (Tri

## select: dropped 29 variables (Sex, PreWeight, PreLength, Treatment, Infection, ...)

# Making the growth rate columns into one column for uninfected individuals
IndBehavGRUnf <- IndBehav3 %>%
  filter(Infection == 0) %>%
  pivot_longer(cols = starts_with("Ratebf"), names_to = "TrialTime", names_prefix = "Ratebf_",
    values_to = "Ratebf") %>%
  select(fishID, TrialTime, Ratebf)

## filter (grouped): removed 54 rows (59%), 38 rows remaining

## pivot_longer: reorganized (Ratebf_Before, Ratebf_Early, Ratebf_Late, Ratebf_Later) into (TrialTime,

## select: dropped 29 variables (Sex, PreWeight, PreLength, Treatment, Infection, ...)

# Merge the two different datasets together
IndBehav4Unf <- merge(IndBehav3UnfV, IndBehav3Unf, by.x = c("fishID", "TrialTime"),
  by.y = c("fishID", "TrialTime"), all = TRUE)
IndBehav4Unf2 <- merge(IndBehav4Unf, IndBehavGRUnf, by.x = c("fishID", "TrialTime"),
  by.y = c("fishID", "TrialTime"), all = TRUE)

# Creating the BehavTol and BehavVig columns for the uninfected and calculating
# the metric for uninfected individual so we can combine these dataframes
# together
IndBehav4Unf2 <- IndBehav4Unf2 %>%
  group_by(fishID) %>%
  add_column(BehavTol = 0, BehavVig = 0)

## group_by: one grouping variable (fishID)

# Rbinding our infected and uninfected dataframes together into one overall
# dataframe
IndBehav4 <- rbind(IndBehav4Unf2, IndBehav4Inf2)

# Remove some unwanted columns to clean up dataset in preparation for analysis
IndBehav4 <- IndBehav4 %>%
  select(-c(day, TOD, linf, maxlinf, maxworm, peakday, Ddate, Rdate, CountDay))

## select: dropped 9 variables (CountDay, day, TOD, linf, maxlinf, ...)

View(IndBehav4)

```

Now we have to decide how best to calculate whether an individual has recovered. In the experiment only had 13 fish recover from infection totally, therefore we are thinking of another metric that indicates a fish is in recovery during infection.

1.6 Description of data, structure, and type

fishID: The individual ID of each fish used in the trial.

TrialTime: The point of infection where each behavior trial happened. Early - early infection (6 days), Late - late in infection (12 days), Later - later in infection (18 days)

Velocity: The average velocity of each fish during their behavior trial (*cm/s*)

Sex: The sex of the individual. F - female, M - male

PreWeight: The weight of the individual prior to their first behavior trial and pre-infection. (*grams*)

PreLength: The length of the individual prior to their first behavior trial and pre-infection (*mm*)

Treatment: What treatment the fish received prior to their first behavior and pre-infection. VIE - visible implant elastomer implant, UNTOUCHED - control individual, received no injection nor implant (*mm*)

Infection: Whether or not the individual was infected with *Gyrodactylus turnbulli*. 1 - infected, 0 - uninfected

LateWeight: The weight of the individual after their final behavior trial and after infection. (*grams*)

wormJump: The number of worms that jumped from the donor fish to the trial fish during manual infections.

AUC: The area under the curve of infection over the total infection trajectory for each individual.

Recov: Whether or not the individual recovered from infection during the experimental trial. 1 - recovered, 0 - did not recover

Died: Whether or not the individual Died from infection during the experimental trial. 1 - Died, 0 - did not died

PreSMI: The body condition of the individual prior to their first behavioral trial and pre infection. (*mm/g*)

LateSMI: The body condition of the individual after to their last behavioral trial and after infection. (*mm/g*)

EChBe: The change in velocity between the early infection behavioral trial and the before trial. (*cm/s*)

LChBe: The change in velocity between the Late infection behavioral trial and the before trial. (*cm/s*)

LtrChBe: The change in velocity between the Later infection behavioral trial and the before trial. (*cm/s*)

Wormbf: The number of worms on the fish prior to each trial.

Ratebf: The rate of growth of worms on the fish prior to each trial.

BehavTol: The behavioral tolerance of each individual calculated as the slope of a random effect model where fishID is the random effect term.

BehavVig: The behavioral Vigor of each individual calculated as the intercept of a random effect model where fishID is the random effect term