# Guppy Network Infection Experiment

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# 1 Introduction

## 1.1 Overall summary

This is an analysis to examine how host traits, particularly host sociality and sex, impacts the spread of disease within experimental epidemics of Trinidadian guppies and Monogenean parasites.

## 1.2 Quick experimental summary

We released 6 female guppies and 3 male guppies into experimental behavioral enclosures together and recorded their baseline sociality (Here defined as Contact Rate) for 2 days. We then introduced an infected female index fish on day 3 to see how quickly parasites spread within the group of fish and how likely specific individuals to pick up parasite infection. We repeated recording behavior for 7 days post infection for a total of 9 days of behavioral recordings, however the analysis within this document is limited to days 1-3.

## 1.3 Questions

### 1.3.1 Individual level

- Are females more likely to be infected than male hosts?
- Does host worm contact rate explain individual level probability of infection?
- Do infected index fish receive less contact rate from uninfected conspecifics relative to uninfected index fish?

-Do infected index fish with higher infection intensity receive less contact rate from uninfected conspecifics?

## 1.4 Data description, structure and type

This analysis uses a single master dataframe titled:DyadindividualContacts_20240726.csv that is subset into different portions based on what questions/analysis we are addressing. Variables within the data frame as follows:

**Ind**: The individual ID of each fish used in the trial.
**ContactRate**: The daily average contact rate for each individual ($contacts/dyad/min$)
**Day3ContactRatewoI**: The daily average contact rate for each non-index individual with other non-index individuals. Index fish is the fish introduced on Day 3 with infection (or not for uninfected conrols) ($contacts/dyad/min$)
**IndexContact**: The daily average contact rate with the index individual. Repeated for each individual since they only had one day with the index individual. ($contacts/dyad/min$)
**Day**: The day in which the behavior was taken. Days 1 and 2 are days without the infected index individual and day three is with the infected index individual. 3 levels. One level for each day.
**Popavg**: The average contact rate for each group ($Contacts/dyads/min/fish$)
**Pop**: The group ID for each replicate. One level per group.
**Treatment**: Whether the group received an infected or uninfected index fish at the beginning of day 3. 2 levels.
**TempTreatment**: The treatment (infected or uninfected) of each group for each day. For every group it will be Unf on days 1 and 2 due to not having an index, but Inf for Infected treatments for days 3. 2 levels.
**Sex**: The sex of each individual. 2 levels, F for female, M for male.
**Inf.**: This is renamed to Infection in some subset data sets. Whether or not an individual was infected at the end of day 3. 2 levels, 1 - infected, 0-uninfected
**worms**: The number of worms on each individual at the end of day 3.
**prev**: Prevalence (proportion of infected individuals) for the group at the end of day 3.
**IndexWorm**: Number of worms on the index fish at the end of day 3. This is used as a metric for the amount of worms an individual will have been exposed to during intitial epidemic spread.
**Index**: Whether the individual was an index fish or not. 2 levels, 0-not index, 1-index
**ChConWithIn**: Change in contact with including the contacts with the index between days 2 and 3.
**ChConWOIn**: Change in contact with with only non-index individuals between days 2 and 3.
**ChConPop**: Change in the group average contact rate between days 2 and 3
**PreSVL**: The snout to vent length of the guppy prior to introduction into behavioral arena. Measured in ($Millimeters$)
**PreWeight**: The weight of the individual prior to introduction into the behavior box. Measured in ($grams$)
**PostSVL**: The snout to vent length of the guppy after wrapping up entire experiment. Measured in ($Millimeters$)
**PostWeight**: The Weight of the guppy after wrapping up entire experiment. Measured in ($grams$)

```r
# Load in libraries for analysis and data wrangling Visualization
library(ggplot2)
library(visreg)
source("http://highstat.com/Books/BGS/GAMM/RCodeP2/HighstatLibV6.R")
# (generalized) Linear mixed modeling
library(lme4)
library(glmmTMB)
# Statistcal analysis reporting and model validation
library(performance)
library(car)
library(lmtest)
library(DHARMa)
# Data wrangling
library(dplyr)
library(plyr)
library(tidyverse)
library(emmeans)


# Importing the master data sheet check intro for description of
# factors Choose X datasheet (specify when finished)
IndContacts <- read.csv("DyadindividualContacts_20240726.csv")

# This is creating a variable to calcualte the contact rate with the
# infected individual for non-infected fish and combining them back
# together.  Subsetting to inidivudals who are not the index
# Addtitionally this code subsets down to only focusing on dyads with
# the index fish as the recipient

IndContactsNI <- IndContacts %>%
    filter(Index != "1" & day == "3" & str_detect(recipID2, "_10")) %>%
    dplyr::rename(IndexContactR = ContactInitR) %>%
    select(c(fishID2, recipID2, IndexContactR))

# Subseting to individuals who are the index fish
IndContactsI <- IndContacts %>%
    filter(Index == "1") %>%
    mutate(IndexContactR = NA) %>%
    select(c(fishID2, recipID2, IndexContactR))
# Rbinding our two variables together
IndContactsNI <- rbind(IndContactsNI, IndContactsI)

# Merging our dataframe back together by fishID to add in the
# indexcontactrate
IndContacts2 <- merge(IndContacts, IndContactsNI, by = c("fishID2"), .keep_all = TRUE) %>%
    # select(-c(recipID2.y, day.y, population.y))%>%
dplyr::rename(recipID2 = recipID2.x) %>%
    distinct(fishID2, recipID2, population, day, .keep_all = TRUE)

# Sum contact rate across all videos in a day for each dyad We want
# to combine all contacts across a day. We added 0.001 to each of
# these to help with further model fit without impacting the
# distribution of the data
```

```r
IndContactsSum <- IndContacts2 %>%
    select(-c(X, fishID, frame_num, recipID)) %>%
    mutate(ContactInitR = ContactInitR + 1e-04, TotalCR = TotalCR + 1e-04,
        RecipCR = RecipCR + 1e-04) %>%
    group_by(fishID2, recipID2, day) %>%
    dplyr::summarise(ContactInitRs = sum(ContactInitR), TotalCRs = sum(TotalCR),
        RecipCRs = sum(RecipCR), conttactinit = sum(contactinit), RecipfledCR = sum(RecipfledCR))

# Remove unneeded columns
IndContactssub <- IndContacts2 %>%
    select(-c(X, fishID, frame_num, recipID, ContactInitR, TotalCR, RecipCR,
        RecipfledCR)) %>%
    group_by(fishID2, day)

# Merge sheets together so that new data frame has all variables
IndContacts3 <- merge(IndContactsSum, IndContactssub, by = c("fishID2",
    "recipID2", "day"), .keep_all = TRUE)

# Going down to one row per indiviual
IndContacts3 <- IndContacts3 %>%
    group_by(fishID2, recipID2, population, day) %>%
    distinct(fishID2, recipID2, population, day, .keep_all = TRUE) %>%
    filter(fishID2 != "RCinf1_NA")

# Calculating important metrics that may apply across all subsetting
# of data

# Wormcontacts = Number of contacts a fish has had with infectious
# agents. So the multiplicative of contact rate with the infected
# index with the number of worms on the infected index
IndContacts3 <- IndContacts3 %>%
    mutate(WormContact = IndexContactR * IndexWorm)
# Assigning a fish label to the fish so that if we want to subset
# down to one metric for fish because not all metrics change across
# days. This currently doesnt work due to index only have day 3
# measure Fish<-c('1','0','0')

# Adding this factor to overall data frame
# PopulationContacts$Fish<-as.factor(Fish)

# Overall summary just checking that everything looks okay.
summary(IndContacts3)
```

```
##    fishID2            recipID2              day        ContactInitRs
##  Length:3213        Length:3213        Min.   :1.000   Min.   :0.000100
##  Class :character   Class :character   1st Qu.:1.000   1st Qu.:0.005731
##  Mode  :character   Mode  :character   Median :2.000   Median :0.015294
##                                        Mean   :2.098   Mean   :0.023234
##                                        3rd Qu.:3.000   3rd Qu.:0.031961
##                                        Max.   :3.000   Max.   :0.210114
##
##     TotalCRs          RecipCRs        conttactinit     RecipfledCR
##  Min.   :0.00010   Min.   :0.00010   Min.   :  0.0   Min.   :0.00000
```

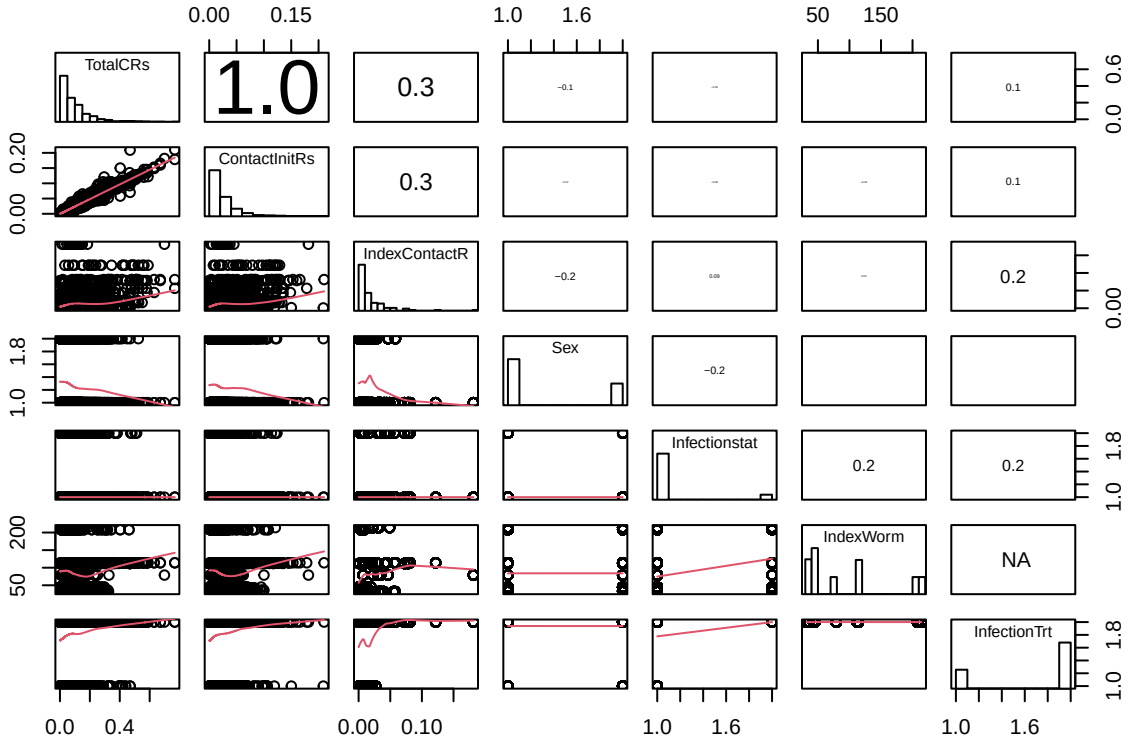
```
##  1st Qu.:0.02560   1st Qu.:0.00585   1st Qu.: 195.0   1st Qu.:0.00450
##  Median :0.06421   Median :0.01518   Median : 516.0   Median :0.01226
##  Mean   :0.09574   Mean   :0.02325   Mean   : 766.5   Mean   :0.01860
##  3rd Qu.:0.13188   3rd Qu.:0.03188   3rd Qu.:1060.0   3rd Qu.:0.02548
##  Max.   :0.76783   Max.   :0.21011   Max.   :7558.0   Max.   :0.19029
##
##   population        TotalContacts    contactinit       recipinit
##  Length:3213        Min.   :    0   Min.   :   0.0   Min.   :   0.0
##  Class :character   1st Qu.:  897   1st Qu.: 195.0   1st Qu.: 202.0
##  Mode  :character   Median : 2192   Median : 516.0   Median : 515.0
##                     Mean   : 3178   Mean   : 766.5   Mean   : 767.1
##                     3rd Qu.: 4405   3rd Qu.:1060.0   3rd Qu.:1061.0
##                     Max.   :27629   Max.   :7558.0   Max.   :7558.0
##
##    recipfled          Sex              recipsex            worms
##  Min.   :   0.0   Length:3213        Length:3213        Min.   :  0.00
##  1st Qu.: 154.0   Class :character   Class :character   1st Qu.:  0.00
##  Median : 416.0   Mode  :character   Mode  :character   Median :  0.00
##  Mean   : 615.7                                        Mean   : 10.16
##  3rd Qu.: 852.0                                        3rd Qu.:  1.00
##  Max.   :5987.0                                        Max.   :214.00
##                                                        NA's   :2313
##    Recipworm          Index         Infectionstat      InfectionTrt
##  Min.   :  0.00   Min.   :0.00000   Min.   :0.00000   Min.   :0.0000
##  1st Qu.:  0.00   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.0000
##  Median :  0.00   Median :0.00000   Median :0.00000   Median :1.0000
##  Mean   : 10.16   Mean   :0.03922   Mean   :0.09804   Mean   :0.7087
##  3rd Qu.:  1.00   3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:1.0000
##  Max.   :214.00   Max.   :1.00000   Max.   :1.00000   Max.   :1.0000
##  NA's   :2313
##    IndexWorm       recipID2.y        IndexContactR      WormContact
##  Min.   : 32.00   Length:3213        Min.   :0.00000   Min.   : 0.0000
##  1st Qu.: 43.00   Class :character   1st Qu.:0.00336   1st Qu.: 0.2600
##  Median : 79.00   Mode  :character   Median :0.00948   Median : 0.8368
##  Mean   : 94.05                      Mean   :0.01789   Mean   : 2.1099
##  3rd Qu.:114.00                      3rd Qu.:0.02156   3rd Qu.: 2.4295
##  Max.   :214.00                      Max.   :0.18141   Max.   :14.3317
##  NA's   :936                         NA's   :126       NA's   :1026
```

```
# Set data strcuture for some factors

# Setting Day as a factor instead of a numeric
IndContacts3$day <- as.factor(IndContacts3$day)
# Setting whether a fish was an index (intitial infection) or not as
# factor
IndContacts3$Index <- as.factor(IndContacts3$Index)
# Setting whether an fish was infected or not as factor
IndContacts3$Infectionstat <- as.factor(IndContacts3$Infectionstat)
# Setting whether fish were male or female as a factor
IndContacts3$Sex <- as.factor(IndContacts3$Sex)
IndContacts3$recipsex <- as.factor(IndContacts3$recipsex)
# Setting the treatment of fish group (infected index or not) as
# factor
IndContacts3$InfectionTrt <- as.factor(IndContacts3$InfectionTrt)
```

```
# Setting population the fish were from as a factor
IndContacts3$population <- as.factor(IndContacts3$population)
# Setting fish ID as a factor
IndContacts3$fishID2 <- as.factor(IndContacts3$fishID2)
# Setting recipient ID as a factor
IndContacts3$recipID2 <- as.factor(IndContacts3$recipID2)
```

## 1.5 Initial data exploration

```
# Pairs plot to look at autocorrelation and potential relationships
# before diving into analysis
pairs(~TotalCRs + ContactInitRs + IndexContactR + Sex + Infectionstat +
    IndexWorm + InfectionTrt, lower.panel = panel.smooth, diag.panel = panel.hist,
    upper.panel = panel.cor, data = IndContacts3)
```




```
# Checking to see if there are any day differences
daylm <- glmmTMB(TotalCRs ~ day + (1 | population), family = beta_family(),
    IndContacts3)
# summary of the model
summary(daylm)
```

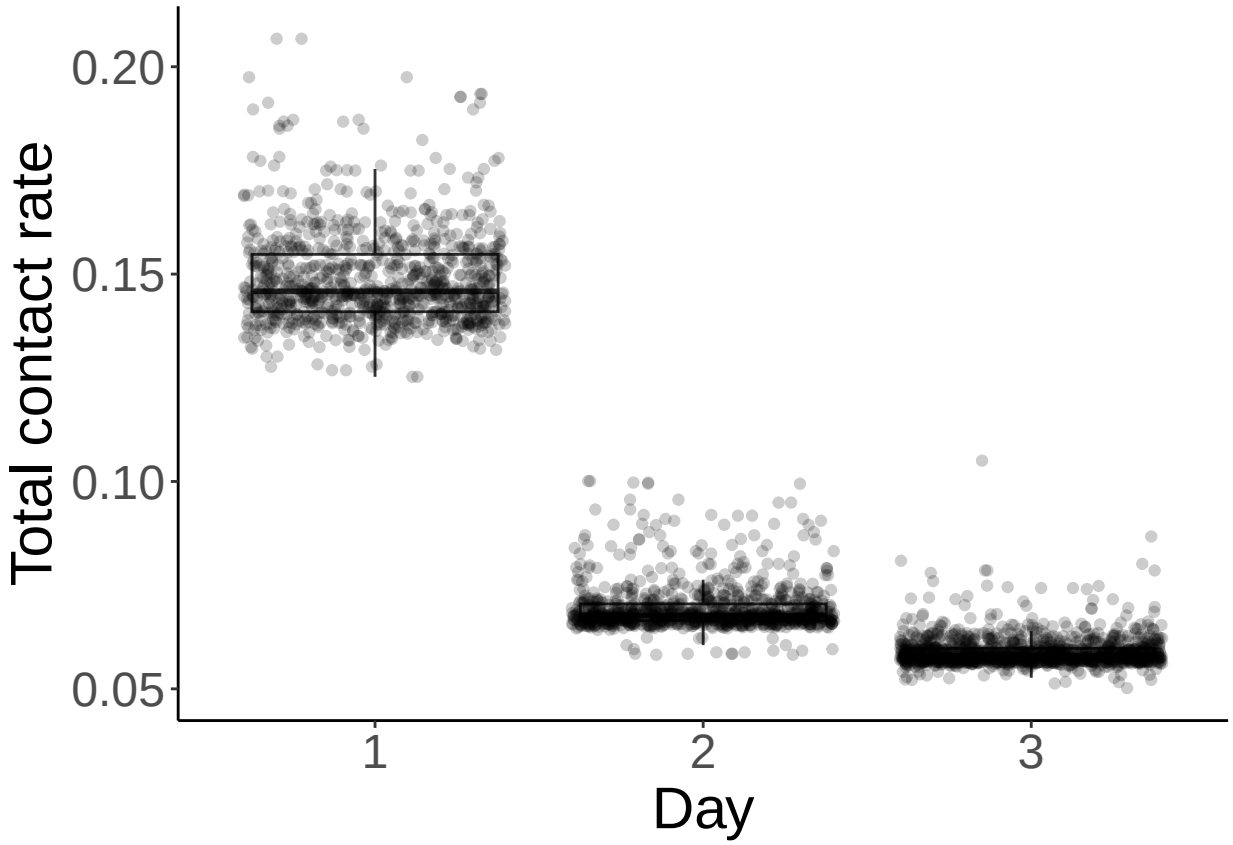
```
##  Family: beta  ( logit )
## Formula:          TotalCRs ~ day + (1 | population)
## Data: IndContacts3
##
##      AIC      BIC   logLik deviance df.resid
## -10194.6 -10164.3   5102.3 -10204.6     3208
```

```
##
## Random effects:
##
## Conditional model:
##  Groups     Name        Variance Std.Dev.
##  population (Intercept) 0.1611   0.4014
## Number of obs: 3213, groups:  population, 14
##
## Dispersion parameter for beta family ():   16
##
## Conditional model:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.71784    0.10950  -15.69   <2e-16 ***
## day2        -0.85657    0.03289  -26.04   <2e-16 ***
## day3        -1.02701    0.03251  -31.59   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing for significance
drop1(daylm, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## TotalCRs ~ day + (1 | population)
##        Df      AIC    LRT  Pr(>Chi)
## <none>    -10194.6
## day     2  -9273.4 925.29 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# It seems we have some high contact rate on day 1, we have to
# eliminate it due to acclimation


# Ploting behavior by individual across groups
daylmVR <- visreg(daylm, "day", scale = "response", partial = TRUE, plot = FALSE)
# Generate the fitted relationship
daylmVRfit <- daylmVR$fit
# Generate the residuals
daylmVRres <- daylmVR$res
# Plot this relationship
ggplot(daylmVRres, aes(x = day, y = visregRes)) + geom_boxplot(outliers = FALSE) +
    geom_jitter(alpha = 0.2) + theme_classic() + theme(legend.position = "none",
    text = element_text(size = 22)) + ylab("Total contact rate") + xlab("Day")
```




```
# There are significant differences in day so we have to subset out
# first day We need to remove first day measurements.
IndContactPW <- IndContacts3 %>%
    filter(day == "2" | day == "3" & Index == "0" & recipID2 != str_detect(recipID2,
        "_10")) %>%
    select(fishID2, day, ContactInitRs) %>%
    pivot_wider(names_from = day, values_from = ContactInitRs) %>%
    na.omit(2) %>%
    mutate(ChContactinit = `3` - `2`) %>%
    select(fishID2, recipID2, ChContactinit)
```

```
## Adding missing grouping variables: ‘recipID2‘, ‘population‘
## Adding missing grouping variables: ‘population‘
```

```
# Create a index only data frame and set its change in contact rate
# as NA given it only came in on day 3
IndContactI <- IndContacts3 %>%
    filter(Index == "1") %>%
    mutate(ChContactinit = NA)


IndContacts4 <- merge(IndContactPW, IndContacts3, by = c("fishID2", "recipID2",
    "population")) %>%
    filter(day != "1")

IndContacts4 <- rbind(IndContacts4, IndContactI)
```

```
# %>% filter(population == 'ADinf1' | population == 'ADunf1' |
# population == 'GZinf1' | population == 'GZunf1'| population ==
# 'SBinf1'| population =='SBunf1')
```

# 2 Individual Level Analysis

## 2.1 Are hosts with higher worm contact rate more likely to become infected?

For this first bit we need to select the data we need to answer this specific question

```
# Filtering down to only infected treatments, individuals who are not
# the index, one measure per fish and days 2 and 3. Note the days 2
# and 3 is because intitial viewing of behaviors across days looks
# like fish were not behaving normally on day 1 due to acclimation to
# the new environment.
IndContactsPI1 <- IndContacts3 %>%
    filter(Index != "1" & day == "3" & InfectionTrt == "1" & Sex == "F" &
        str_detect(recipID2, "_10"))
```

### 2.1.1 Fitting the contact rate versus probability of infection model

We're fitting a binomial generalized linear mixed model with whether an individual was infected or not at the end of day 3 as our response variable and worm contact rate as predictor variables. We have population as a random effect to control for non-independence of worm contact rate between individuals within the same group.

In addition to this, we fit a second GLMM examining the same relationship but with host contact rate instead of the product term of worm contact rate to see if it better fits our data.

```
# generalized linear mixed model to determine if individual sociality
# explained the probability of becoming infected
ProbinfLMF <- glmmTMB(Infectionstat ~ WormContact + I(WormContact^2) +
    (1 | population), family = binomial(), data = IndContactsPI1)


# We fit a second model with just contact rate to see if it does a
# better job than fitting the product term of contact rate and
# infection intensity of the index A model with just social contacts
# to test against using the social contacts
ProbinfLMFSC <- glmmTMB(Infectionstat ~ ContactInitRs + I(ContactInitRs^2) +
    (1 | population), family = binomial(), data = IndContactsPI1)

# Summary of our two models
summary(ProbinfLMF)
```

```
##  Family: binomial  ( logit )
## Formula:
## Infectionstat ~ WormContact + I(WormContact^2) + (1 | population)
## Data: IndContactsPI1
```

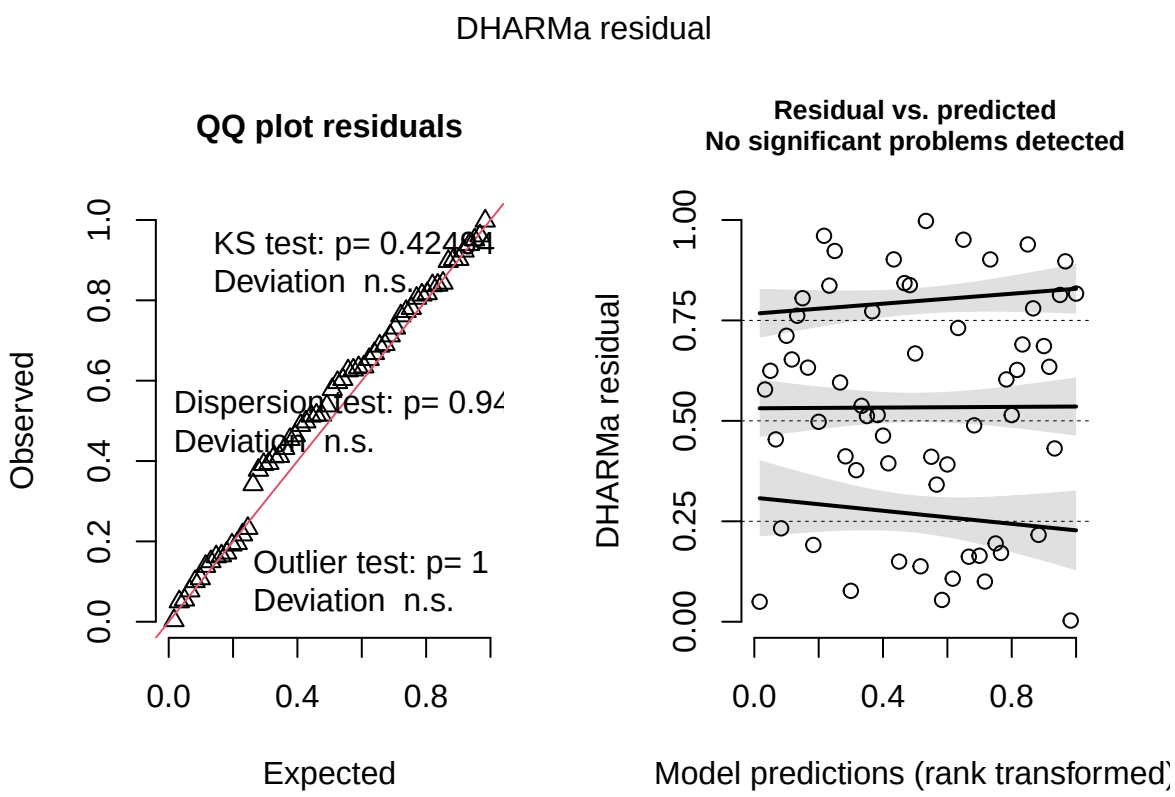
```
##
##      AIC      BIC   logLik deviance df.resid
##     72.9     81.3    -32.4     64.9       56
##
## Random effects:
##
## Conditional model:
##  Groups     Name        Variance Std.Dev.
##  population (Intercept) 0.4255   0.6523
## Number of obs: 60, groups:  population, 10
##
## Conditional model:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -1.75787    0.57614  -3.051  0.00228 **
## WormContact       1.03939    0.37157   2.797  0.00515 **
## I(WormContact^2) -0.07959    0.03400  -2.341  0.01925 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(ProbinfLMFSC)
```

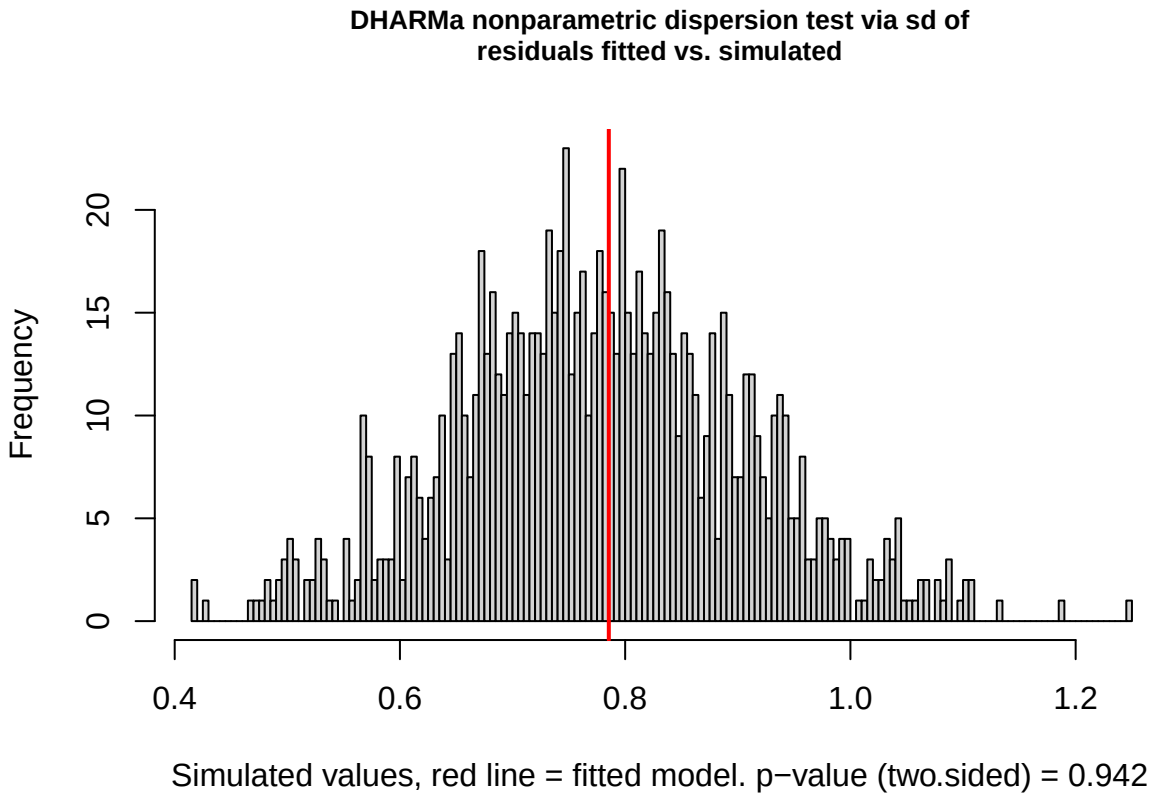
```
##  Family: binomial  ( logit )
## Formula:
## Infectionstat ~ ContactInitRs + I(ContactInitRs^2) + (1 | population)
## Data: IndContactsPI1
##
##      AIC      BIC   logLik deviance df.resid
##     78.3     86.7    -35.1     70.3       56
##
## Random effects:
##
## Conditional model:
##  Groups     Name        Variance Std.Dev.
##  population (Intercept) 1.702    1.305
## Number of obs: 60, groups:  population, 10
##
## Conditional model:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -1.4958     0.8086  -1.850   0.0643 .
## ContactInitRs        69.5154    44.7783   1.552   0.1206
## I(ContactInitRs^2) -615.9132   453.3311  -1.359   0.1743
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### 2.1.2 Next we see will validate the model to make sure everything is looking good.

```
# Using DHARMa package to look at quantile residuals to validate the
# worm contact rate model fit
sim_residuals_ProbinfLM <- simulateResiduals(ProbinfLMF, 1000)
# Quantile residuals Ploting the quantile residuals
plot(sim_residuals_ProbinfLM)
```

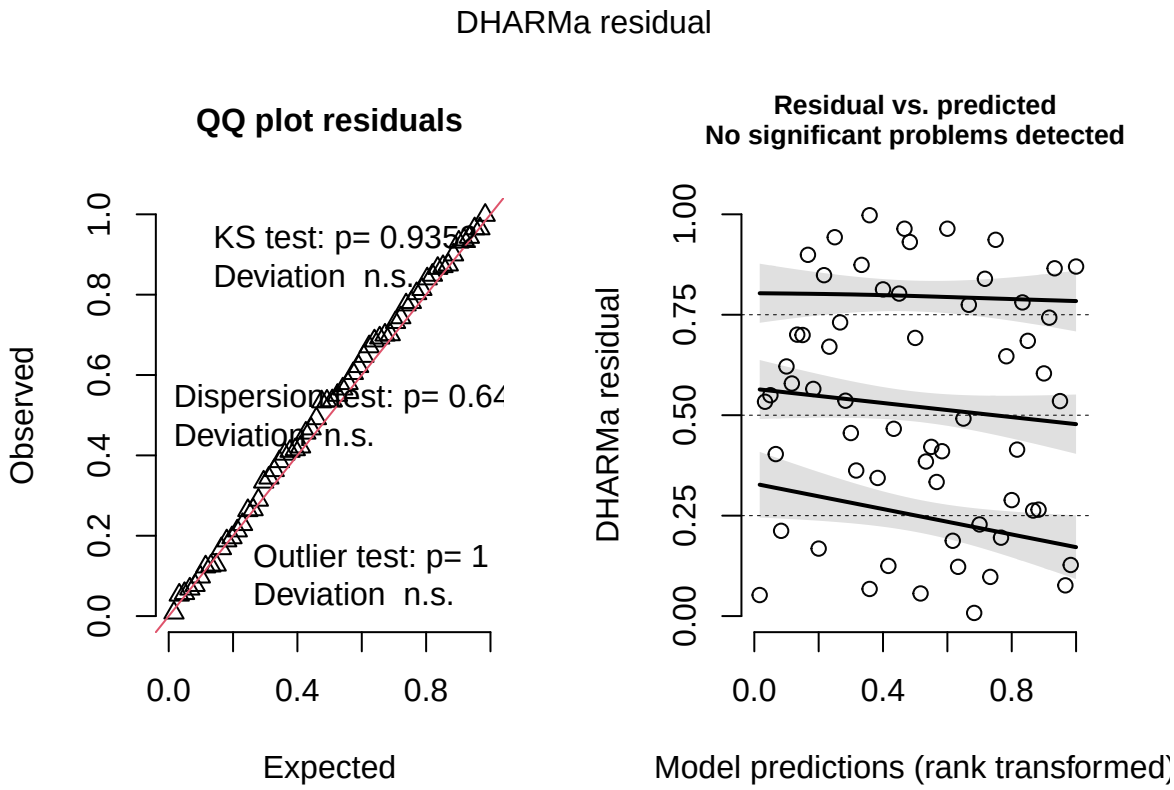



```
# Testing dispersion
testDispersion(sim_residuals_ProbinfLM)
```

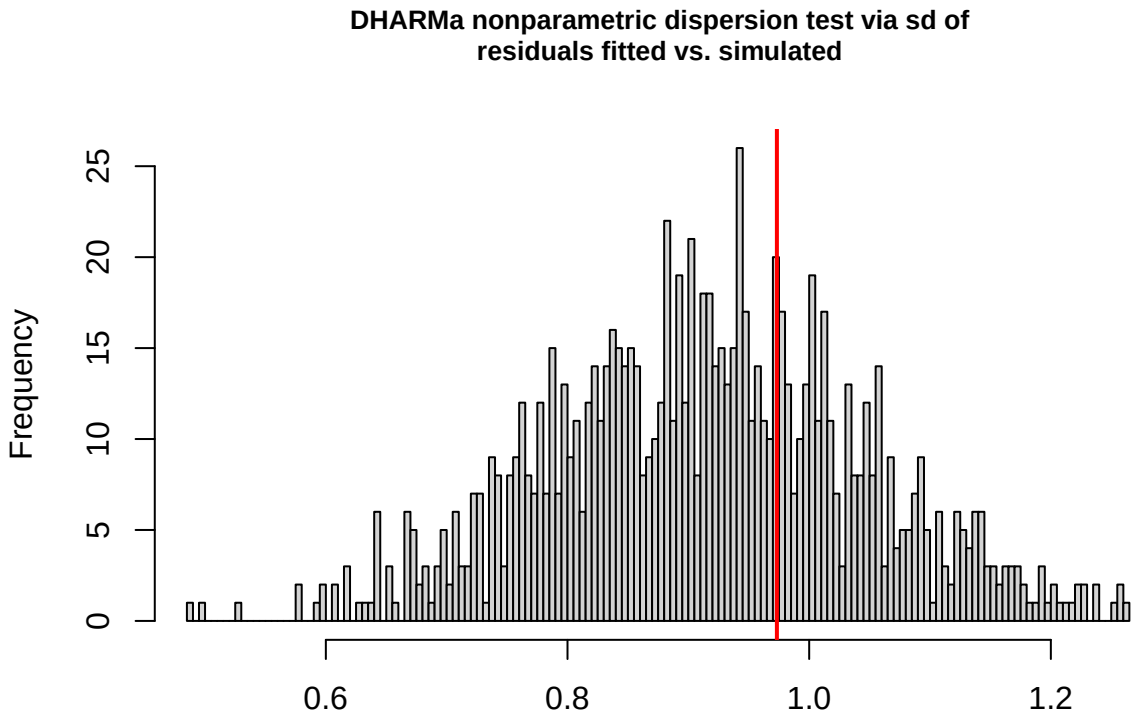


```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 1.0087, p-value = 0.942
## alternative hypothesis: two.sided
```

```r
# Using DHARMa package to look at quantile residuals to validate the
# contact rate model fit
sim_residuals_ProbinfLMSC <- simulateResiduals(ProbinfLMFSC, 1000)
# Quantile residuals Ploting the quantile residuals
plot(sim_residuals_ProbinfLMSC)
```



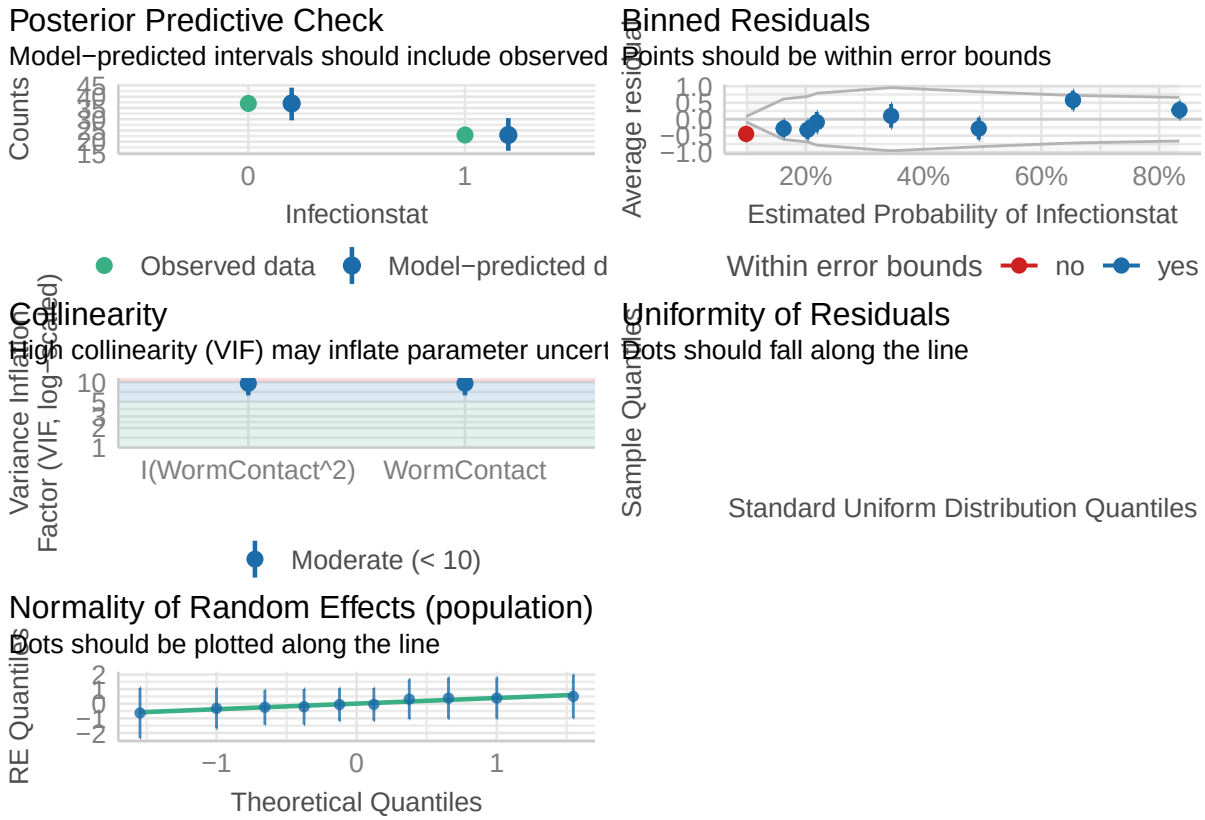

```r
# Testing dispersion
testDispersion(sim_residuals_ProbinfLMSC)
```




```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 1.065, p-value = 0.648
## alternative hypothesis: two.sided
```

```
# Below we are exmaining the quantile residuals among the fixed
# variables to see if there are any funky patterns. Excluded from
# main run for space but remove # to see plots
# plotResiduals(sim_residuals_InfCRlm, IndividualInfDFD2$Sex)
# plotResiduals(sim_residuals_InfCRlm, IndividualInfDFD2$ContactRate)

check_model(ProbinfLMF)
```

```
## ‘check_outliers()‘ does not yet support models of class ‘glmmTMB‘.
```



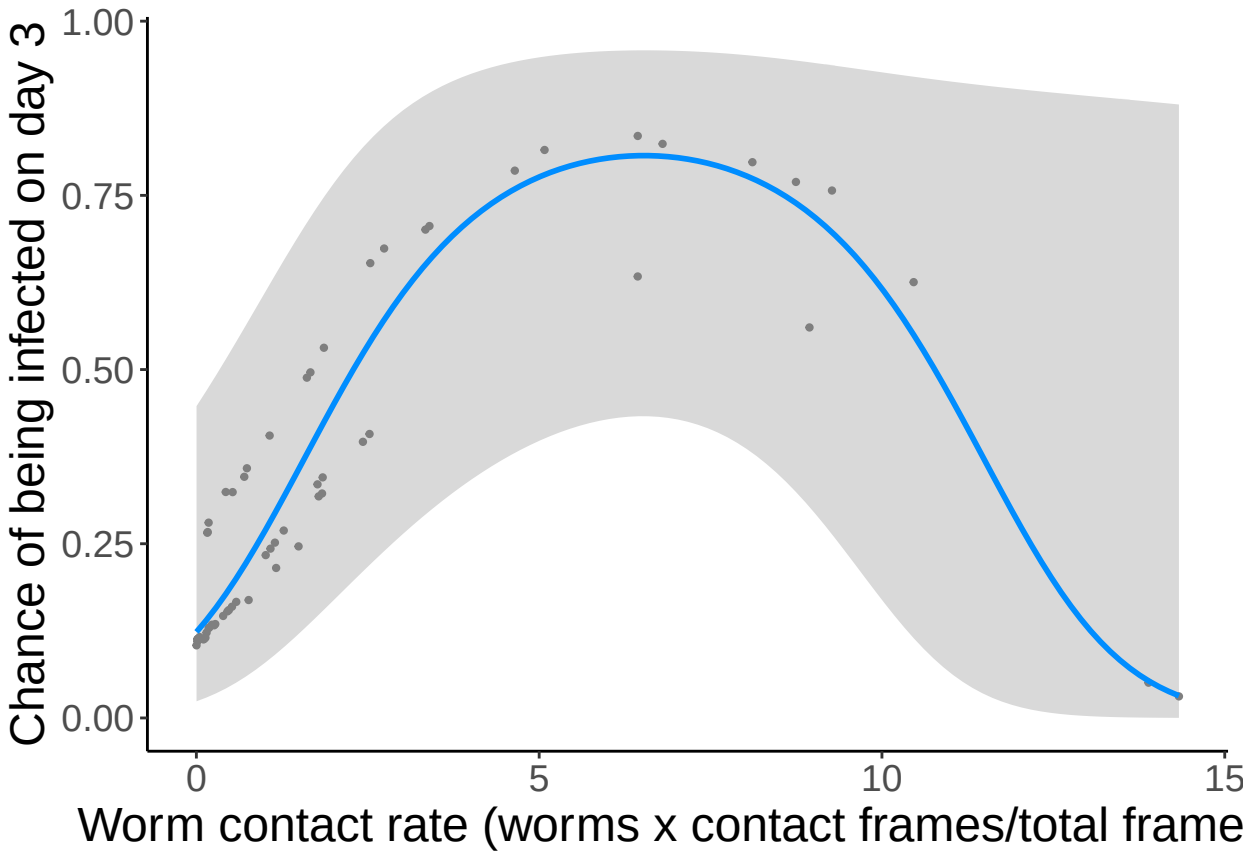

### 2.1.3 Likelihood ratio test to test for significance in our model

```
# Drop 1 with chisq test to do a likelihood ratio test for our model
drop1(ProbinfLMF, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Infectionstat ~ WormContact + I(WormContact^2) + (1 | population)
##                  Df    AIC    LRT Pr(>Chi)
## <none>              72.889
## WormContact       1 80.081 9.1926 0.002430 **
## I(WormContact^2)  1 79.620 8.7310 0.003128 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### 2.1.4 Visualization of the relationships between worm contact rate and probability of infection

```
# Visreg of contact rate effect
InfWCRvr <- visreg(ProbinfLMF, "WormContact", scale = "response", partial = T,
    overlay = TRUE, gg = TRUE) + xlab("Worm contact rate (worms x contact frames/total frames) ") +
    ylab("Chance of being infected on day 3") + theme_classic() + theme(text = element_text(size = 18))
print(InfWCRvr)
```




## 2.2 Do hosts contact uninfected index as much as infected index individuals?

```
# Filtering down to only Getting index contact rate
IndContactsIndexrecip <- IndContacts4 %>%
    filter(Index == "1")
```

### 2.2.1 Fitting a model to test for total contact rate for infected versus uninfected index individuals

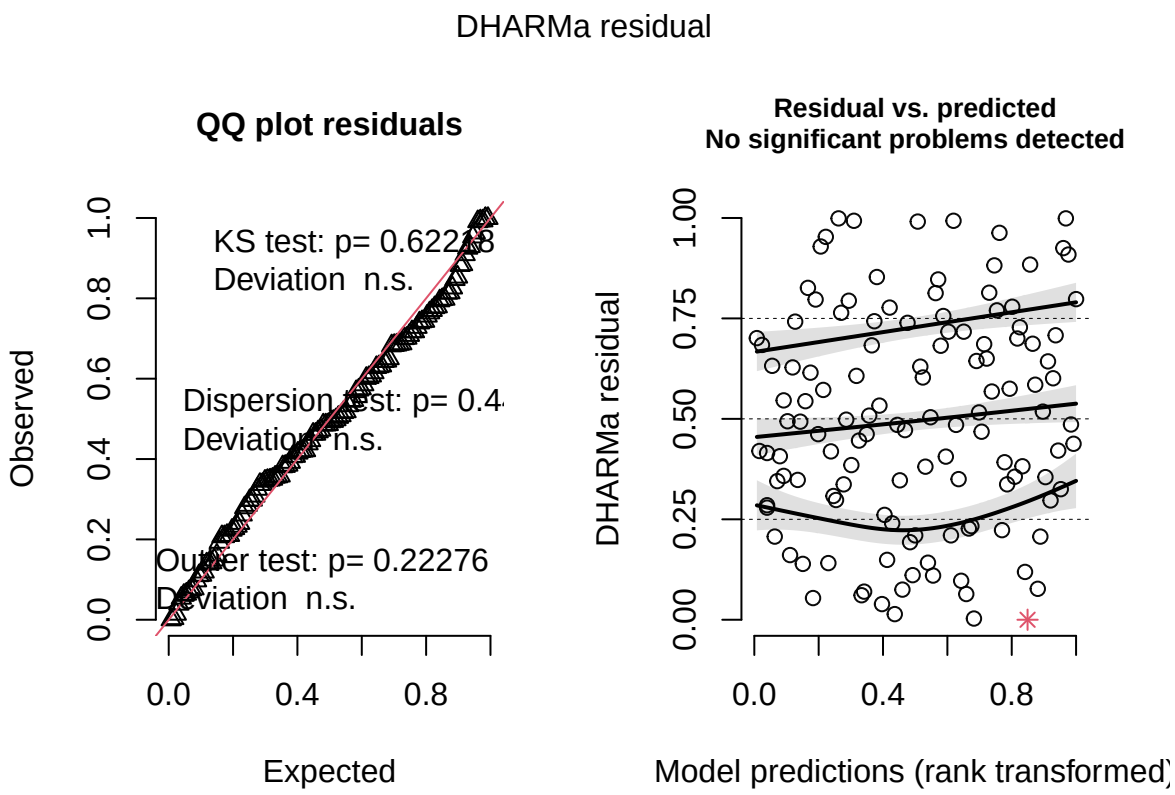
```
# Logging and scaling contact rate due to heavy skew and the desire
# to be comparable between explanatory variables
IndContactsIndexrecip$ScContactInitRs <- scale(log10(IndContactsIndexrecip$ContactInitRs))

# Fitting the glmmTMNB for received contacts by infection treatment
# of the group
IndexTClm <- glmmTMB(RecipCRs ~ InfectionTrt + recipsex + ScContactInitRs +
    I(ScContactInitRs^2) + (1 | fishID2), family = beta_family(link = "logit"),
    data = IndContactsIndexrecip)


# summary of the model
summary(IndexTClm)
```

```
##  Family: beta  ( logit )
```

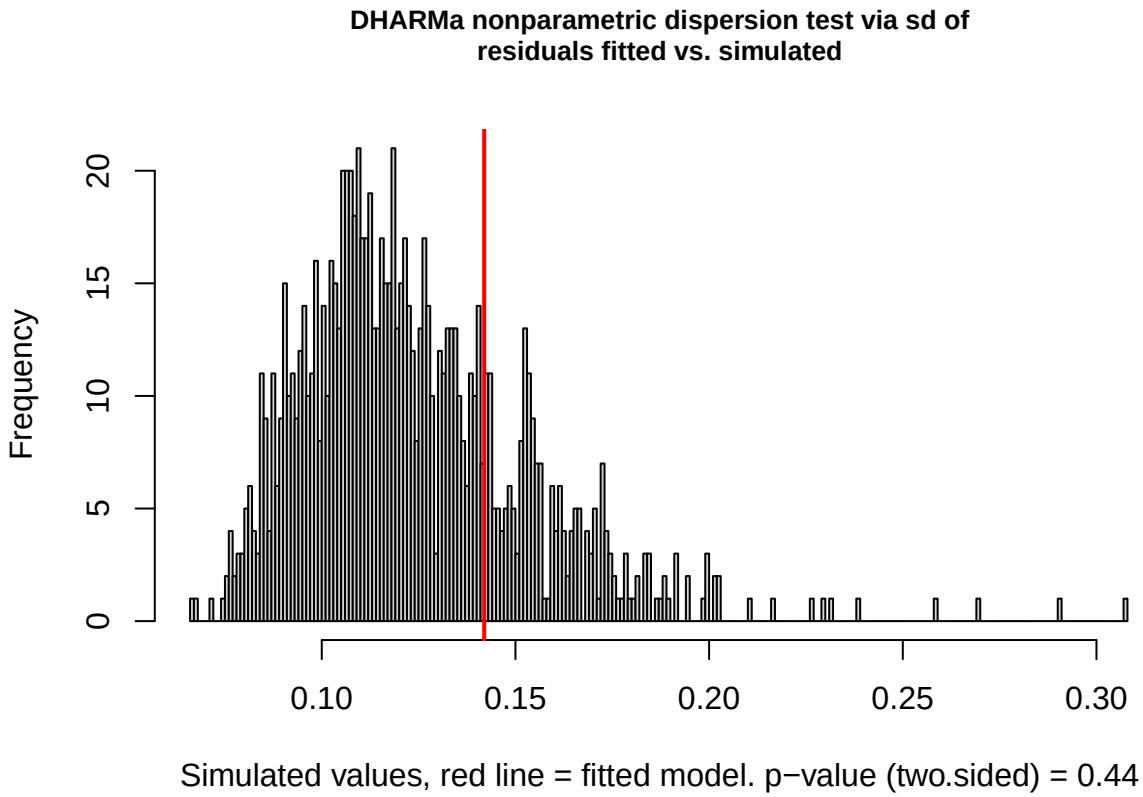
```
## Formula:
## RecipCRs ~ InfectionTrt + recipsex + ScContactInitRs + I(ScContactInitRs^2) +
##     (1 | fishID2)
## Data: IndContactsIndexrecip
##
##      AIC      BIC   logLik deviance df.resid
##  -1025.0  -1005.2    519.5  -1039.0      119
##
## Random effects:
##
## Conditional model:
##  Groups  Name        Variance Std.Dev.
##  fishID2 (Intercept) 0.01133  0.1064
## Number of obs: 126, groups:  fishID2, 14
##
## Dispersion parameter for beta family ():  478
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -4.82983    0.10340  -46.71  < 2e-16 ***
## InfectionTrt1        -0.06979    0.11463   -0.61 0.542613
## recipsexM             0.34583    0.08221    4.21 2.59e-05 ***
## ScContactInitRs       1.30765    0.06359   20.56  < 2e-16 ***
## I(ScContactInitRs^2)  0.14887    0.03936    3.78 0.000155 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### 2.2.2 Validating the recipient initiated contact with index model

```
sim_residuals_IndexTClm <- simulateResiduals(IndexTClm, 1000)  #Quantile residuals
# Ploting the quantile residuals
plot(sim_residuals_IndexTClm)
```



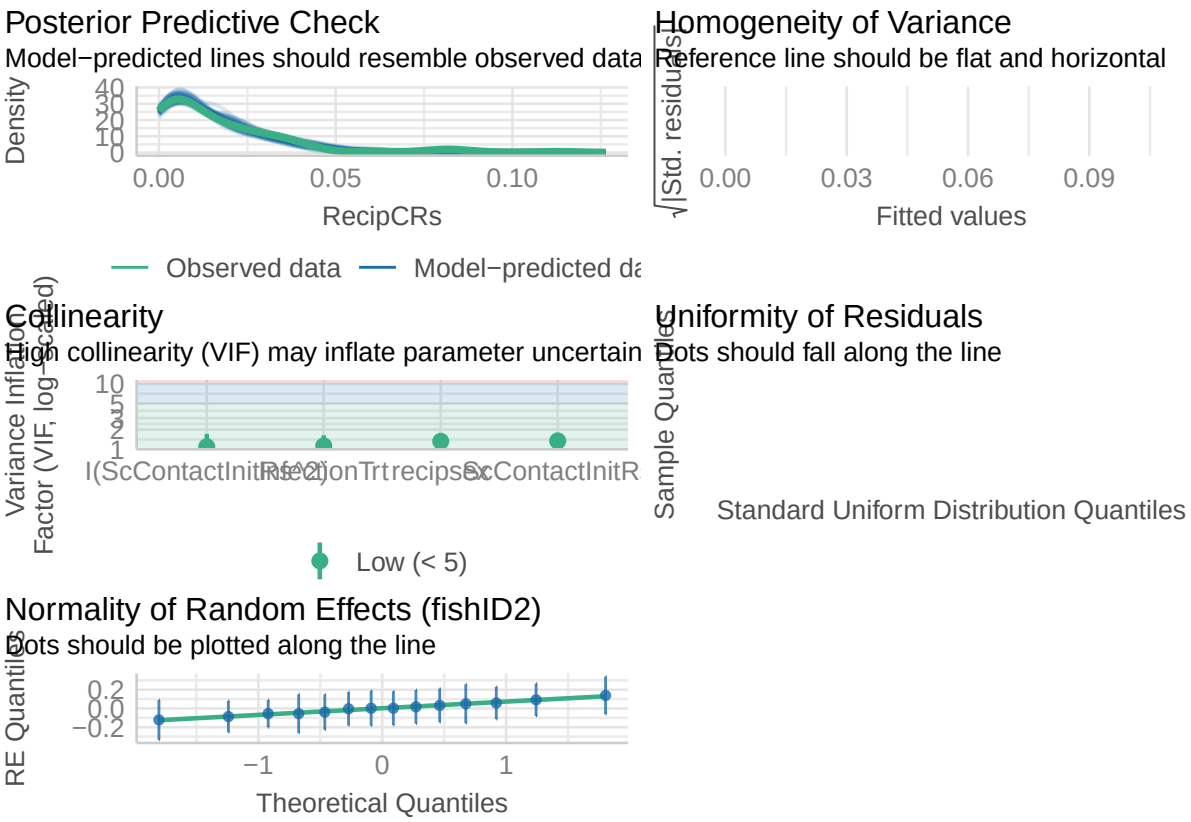

```
# Testing dispersion
testDispersion(sim_residuals_IndexTClm)
```



```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 1.1523, p-value = 0.44
## alternative hypothesis: two.sided
```

```
# using the checkmodel function to validate model
check_model(IndexTClm)
```

```
## `check_outliers()` does not yet support models of class `glmmTMB`.
```




```
# sim_residuals_IndexInitTClm <-simulateResiduals(IndexInitTClm,
# 1000) #Quantile residuals #Ploting the quantile residuals
# plot(sim_residuals_IndexInitTClm) #Testing dispersion
# testDispersion(sim_residuals_IndexInitTClm)
```

### 2.2.3 Using a likelihood ratio test to test for significance in the recipient initiated contact with index model

```
drop1(IndexTClm, test = "Chisq")
```

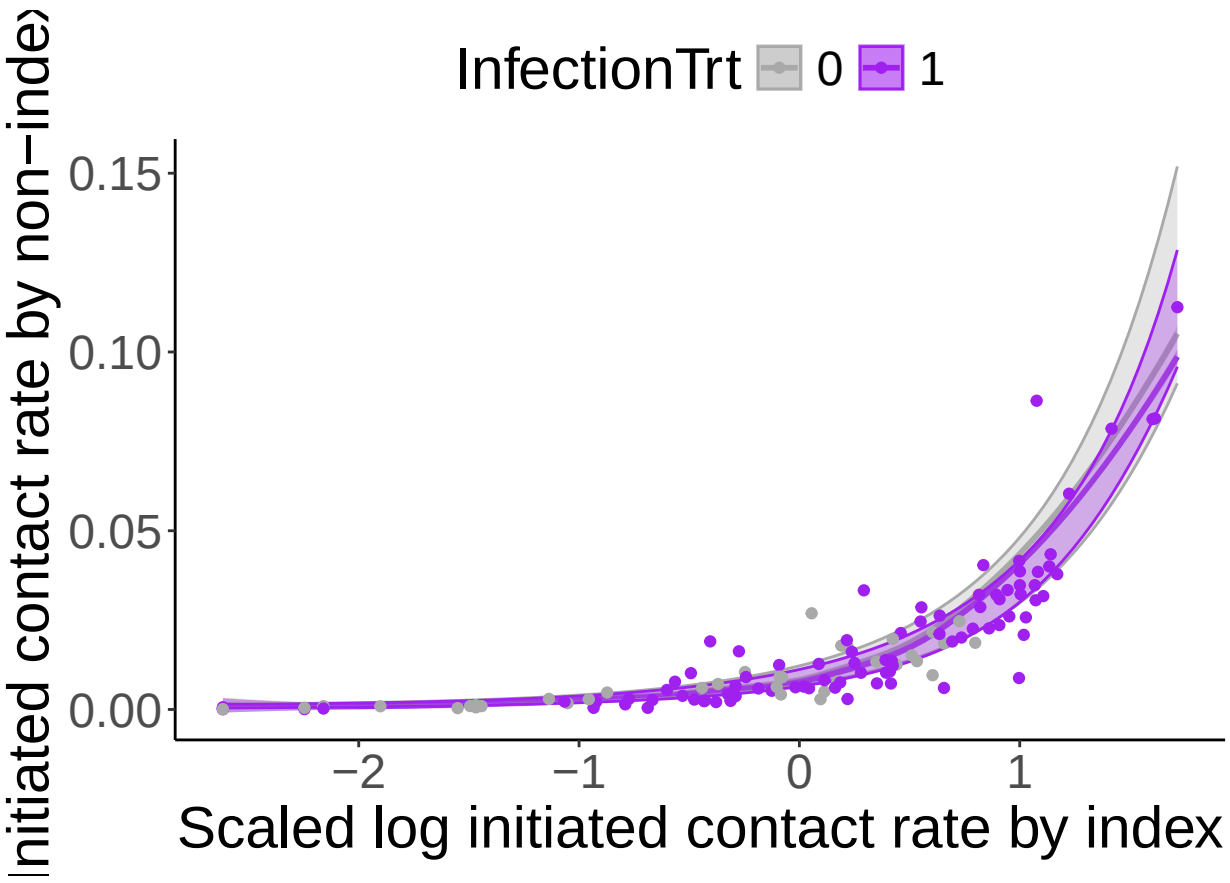
```
## Single term deletions
```

```
##
## Model:
## RecipCRs ~ InfectionTrt + recipsex + ScContactInitRs + I(ScContactInitRs^2) +
##     (1 | fishID2)
##                       Df      AIC     LRT  Pr(>Chi)
## <none>                   -1025.04
## InfectionTrt           1 -1026.68   0.359 0.5491749
## recipsex               1 -1011.25  15.794 7.063e-05 ***
## ScContactInitRs        1  -844.04 183.003 < 2.2e-16 ***
## I(ScContactInitRs^2)   1 -1013.99  13.054 0.0003027 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### 2.2.4 Visualizing the relationship between recipient sex and total contacts with index

```
# Generating fitted relationship and residuals for contact rate and
# infection treatment
RCind <- visreg(IndexTClm, "ScContactInitRs", "InfectionTrt", scale = "response",
    partial = T, plot = FALSE)

# Grabbing the fitted relationship
RCindfit <- RCind$fit
# Grabbing the partial residuals
RCinfres <- RCind$res
# Setting the color scheme for infected and uninfected groups
cpinf = c("darkgray", "purple")

# Plotting the relationship for received contact rate and infection
# treatment

ggplot(RCindfit, aes(x = ScContactInitRs, y = visregFit, group = InfectionTrt,
    colour = InfectionTrt, fill = InfectionTrt)) + geom_smooth(data = RCindfit,
    method = "loess", aes(x = ScContactInitRs, y = visregFit)) + geom_ribbon(aes(ymin = visregLwr,
    ymax = visregUpr), alpha = 0.3) + geom_point(data = IndContactsIndexrecip,
    aes(x = ScContactInitRs, y = RecipCRs)) + theme_classic() + xlab("Scaled log initiated contact rate
    ylab("Initiated contact rate by non-index") + theme(text = element_text(size = 22)) +
    theme(legend.position = "top") + scale_color_manual(values = cpinf) +
    scale_fill_manual(values = cpinf)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




### 2.3 Do index fish with higher infection intensity have less recipient contacts?

Subsetting the data frame down for this analysis

```
# subsetting down
IndContactsIndexinfrecip <- IndContactsIndexrecip %>%
    filter(InfectionTrt == "1")

# Sclaing some of our variables for the analysis Index infection
# intensity
IndContactsIndexinfrecip$ScIndexWorm <- scale(IndContactsIndexinfrecip$IndexWorm)
```

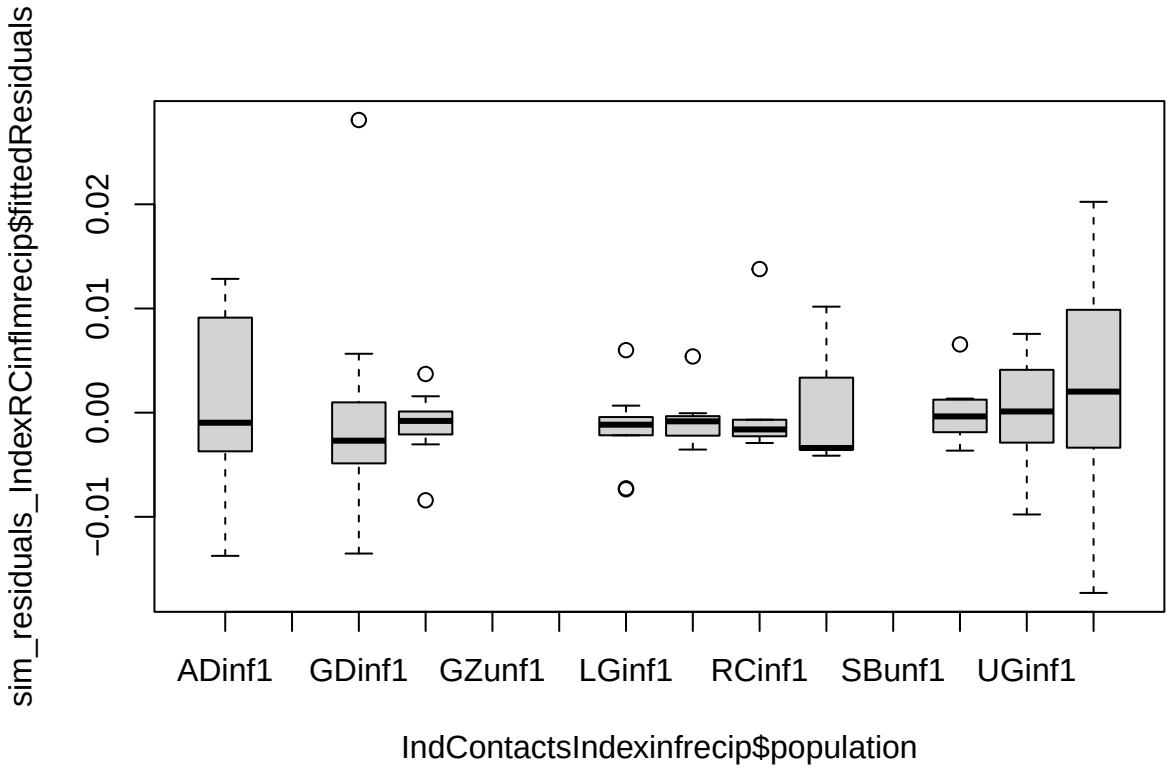
#### 2.3.1 Fitting our GLM for the receipient contacts by infection intensity

```
# Fitting the glmmtmb for index received contacts by infection
# intensity
IndexRCinflmrecip <- glmmTMB(RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) +
    recipsex + ScContactInitRs + I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs +
    ScIndexWorm:recipsex + I(ScIndexWorm^2):recipsex, family = beta_family(link = "logit"),
    data = IndContactsIndexinfrecip)

# summary of model
summary(IndexRCinflmrecip)
```

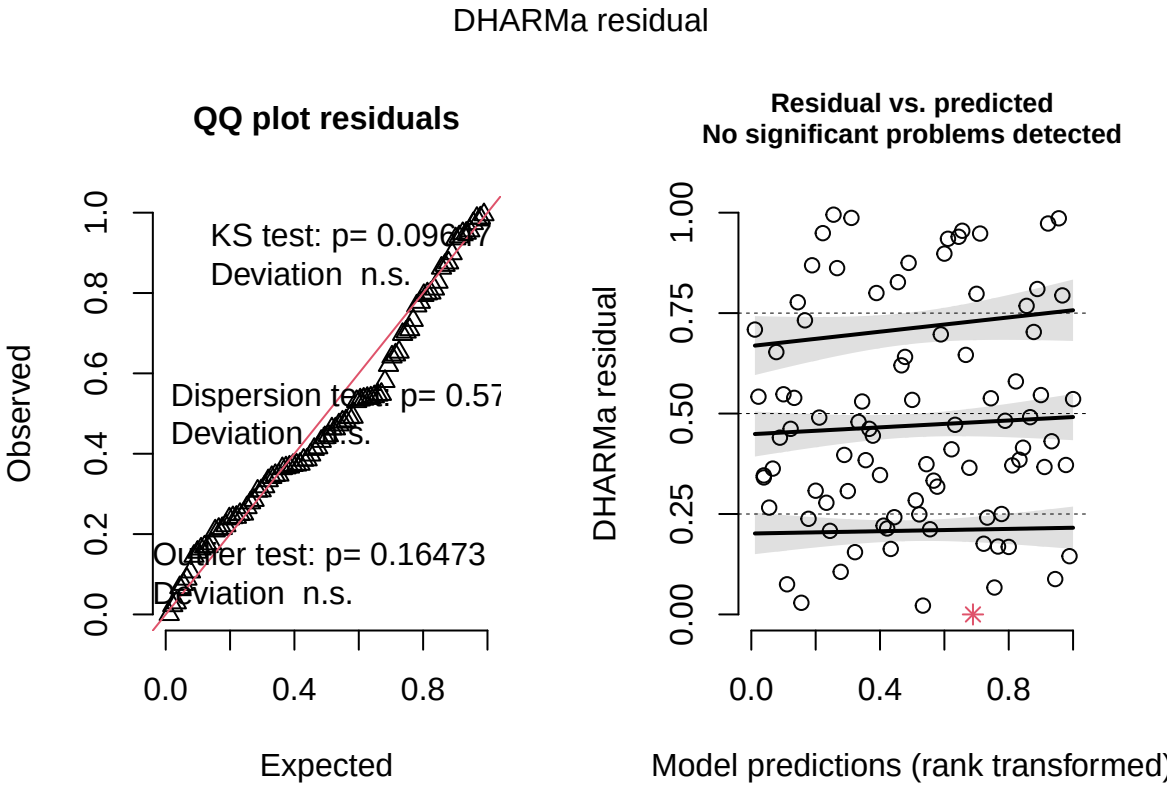
```
##  Family: beta  ( logit )
## Formula:
## RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) + recipsex + ScContactInitRs +
##     I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs + ScIndexWorm:recipsex +
##     I(ScIndexWorm^2):recipsex
## Data: IndContactsIndexinfrecip
##
##      AIC      BIC   logLik deviance df.resid
##   -714.2   -689.2    367.1   -734.2       80
##
##
## Dispersion parameter for beta family ():  506
##
## Conditional model:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -4.78131    0.10348  -46.20  < 2e-16 ***
## ScIndexWorm                -0.12330    0.10519   -1.17  0.24112
## I(ScIndexWorm^2)           -0.12916    0.05267   -2.45  0.01419 *
## recipsexM                   0.50868    0.11469    4.44  9.2e-06 ***
## ScContactInitRs             1.37431    0.07492   18.34  < 2e-16 ***
## I(ScContactInitRs^2)        0.10111    0.04347    2.33  0.02004 *
## ScIndexWorm:ScContactInitRs 0.19357    0.09342    2.07  0.03825 *
## ScIndexWorm:recipsexM       0.36632    0.13452    2.72  0.00646 **
## I(ScIndexWorm^2):recipsexM -0.18727    0.09899   -1.89  0.05852 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### 2.3.2 Validating the recipient contact rate by worm load model

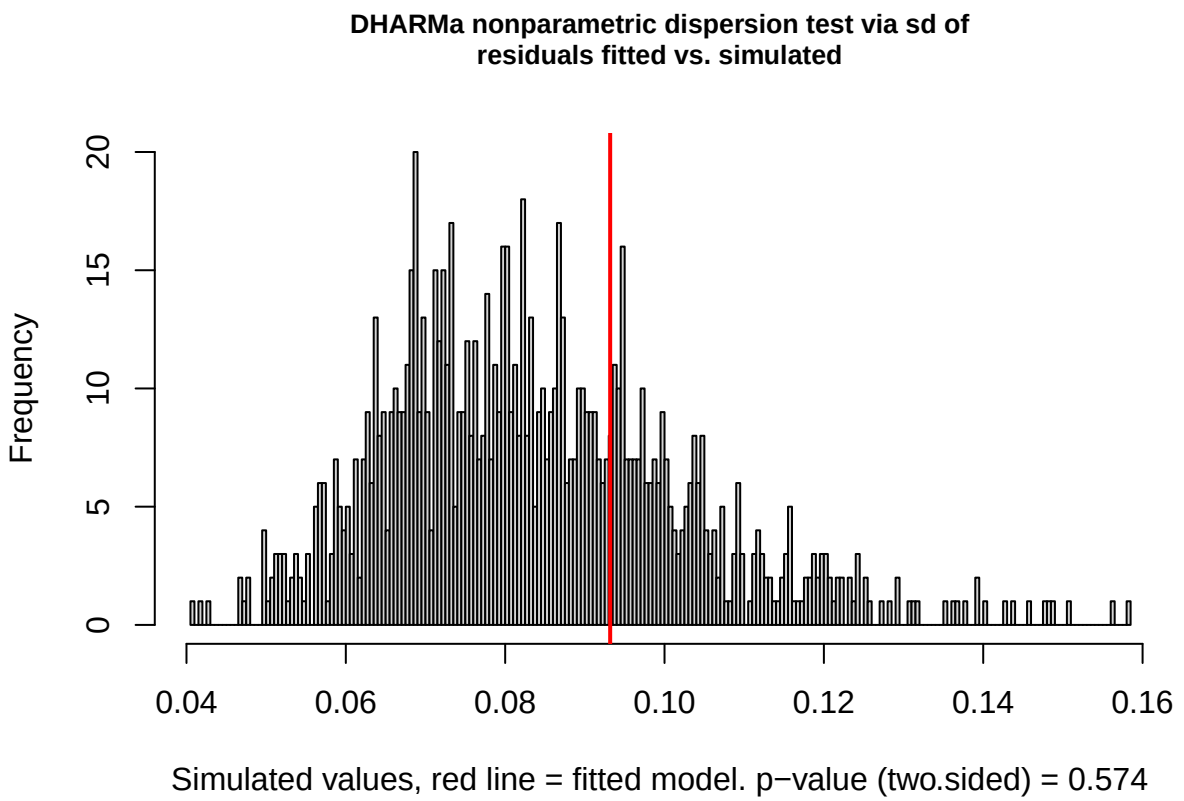
```
sim_residuals_IndexRCinflmrecip <- simulateResiduals(IndexRCinflmrecip,
    1000)  #Quantile residuals

# Confirming there is no differences in median between groups
plot(sim_residuals_IndexRCinflmrecip$fittedResiduals ~ IndContactsIndexinfrecip$population)
```




```
# Ploting the quantile residuals
plot(sim_residuals_IndexRCinflmrecip)
```



```
# Testing dispersion
testDispersion(sim_residuals_IndexRCinflmrecip)
```




```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 1.1119, p-value = 0.574
## alternative hypothesis: two.sided
```

```
# sim_residuals_IndexRCinflminit
# <-simulateResiduals(IndexRCinflminit, 1000) #Quantile residuals
# #Ploting the quantile residuals
# plot(sim_residuals_IndexRCinflminit) #Testing dispersion
# testDispersion(sim_residuals_IndexRCinflminit)
```

### 2.3.3 Using a likelihood ratio test to test for significance in recipient contact by index worm load model

```
drop1(IndexRCinflmrecip, test = "Chisq")
```

```
## Single term deletions
##
## Model:
```

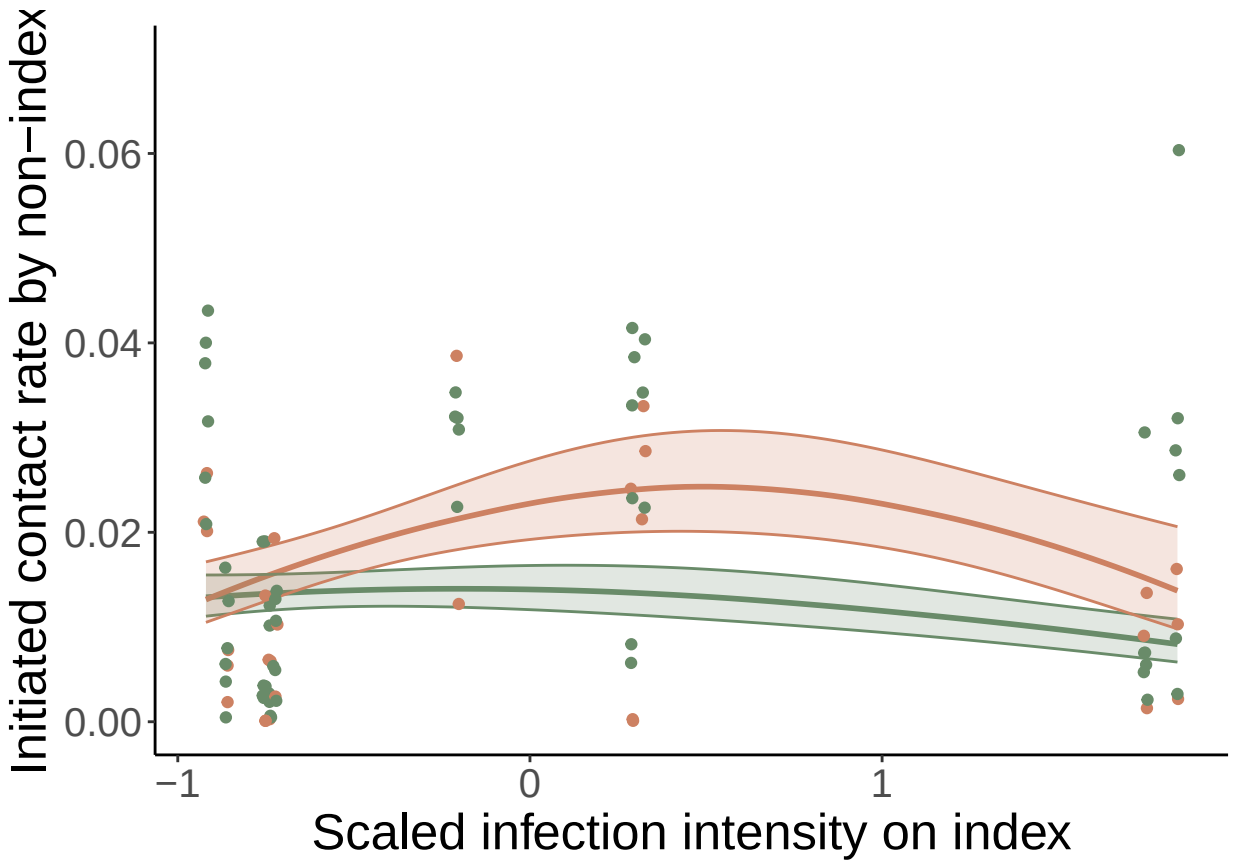
```
## RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) + recipsex + ScContactInitRs +
##     I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs + ScIndexWorm:recipsex +
##     I(ScIndexWorm^2):recipsex
##                             Df     AIC    LRT Pr(>Chi)
## <none>                         -714.22
## I(ScContactInitRs^2)         1 -711.54 4.6840 0.030446 *
## ScIndexWorm:ScContactInitRs  1 -711.70 4.5242 0.033419 *
## ScIndexWorm:recipsex         1 -708.94 7.2791 0.006976 **
## I(ScIndexWorm^2):recipsex    1 -712.71 3.5147 0.060827 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#### 2.3.4 Visualizing the relationship between recipient sex and recipient contact and worm load model

```
# Extracting fit and residuals from our model
IndexRCinflmVR <- visreg(IndexRCinflmrecip, "ScIndexWorm", "recipsex",
    scale = "response", partial = T, plot = FALSE)
# Extracting fit
IndexRCinflmVRfit <- IndexRCinflmVR$fit
# Extracting residuals
IndexRCinflmVRres <- IndexRCinflmVR$res
# Setting sex colorscheme
cpsex = c("darkseagreen4", "lightsalmon3")
# Plotting our relationship
ggplot(IndexRCinflmVRfit, aes(x = ScIndexWorm, y = visregFit, group = recipsex,
    fill = recipsex, color = recipsex)) + geom_smooth(method = "loess") +
    geom_ribbon(aes(ymin = visregLwr, ymax = visregUpr), alpha = 0.2) +
    geom_jitter(data = IndContactsIndexinfrecip, aes(x = ScIndexWorm, y = RecipCRs)) +
    theme_classic() + xlab("Scaled infection intensity on index") + ylab("Initiated contact rate by non
    theme(text = element_text(size = 19)) + theme(legend.position = "none") +
    scale_fill_manual(values = cpsex) + scale_color_manual(values = cpsex) +
    ylim(0, 0.07)
```

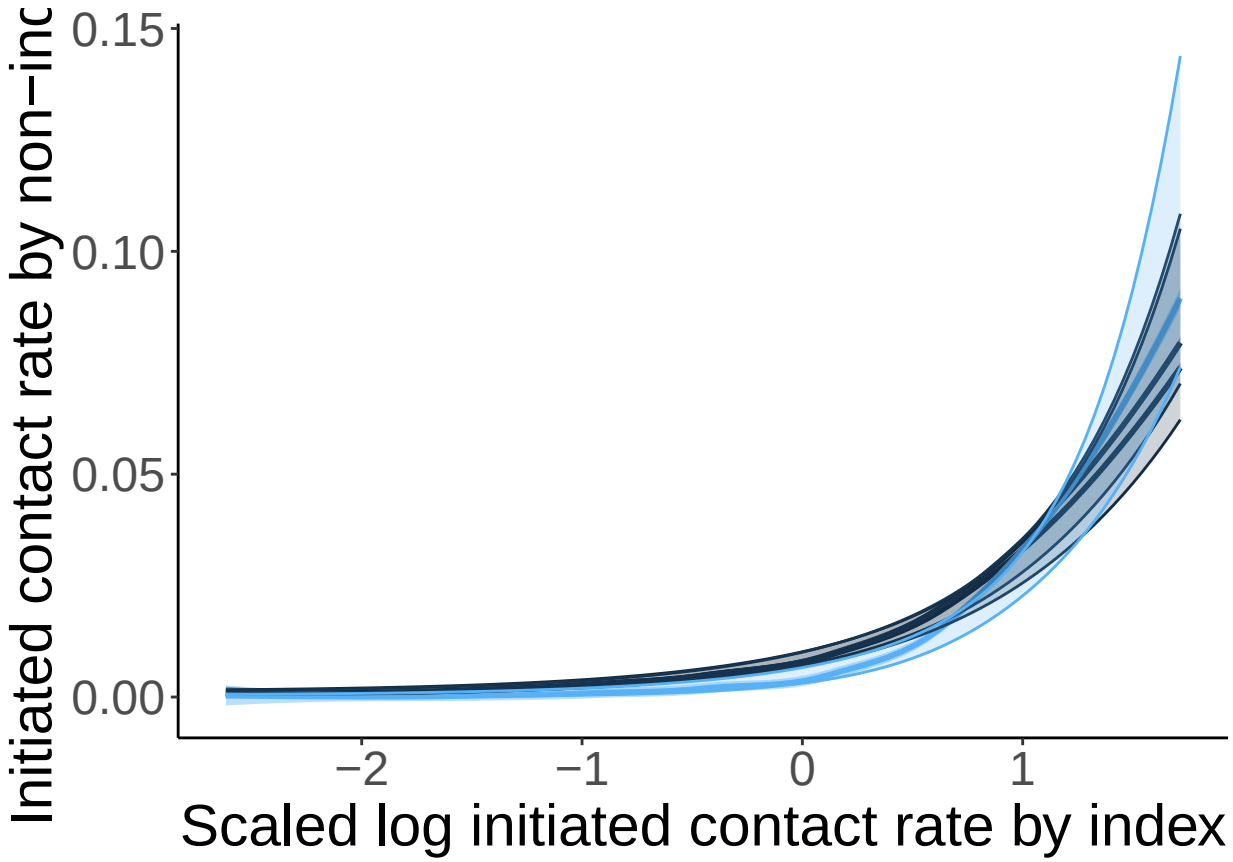
```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 5 rows containing missing values or values outside the scale range
## (`geom_point()`).
```




```
# Extracting the fit and residuals from our model
InfIndexCR <- visreg(IndexRCinflmrecip, "ScContactInitRs", "ScIndexWorm",
    scale = "response", partial = T, overlay = TRUE, gg = TRUE, plot = FALSE)
# Extracting the fit of our model
InfIndexCRfit <- InfIndexCR$fit
# Extracting the residuals from the model
InfIndexCRres <- InfIndexCR$res

# Plotting the relationship between received contact rate, initiated
# contact rate, and infection intensity
ggplot(InfIndexCRfit, aes(x = ScContactInitRs, y = visregFit, group = ScIndexWorm,
    colour = ScIndexWorm, fill = ScIndexWorm)) + geom_smooth(data = InfIndexCRfit,
    aes(x = ScContactInitRs, y = visregFit)) + geom_ribbon(aes(ymin = visregLwr,
    ymax = visregUpr), alpha = 0.2) + theme_classic() + xlab("Scaled log initiated contact rate by inde
    ylab("Initiated contact rate by non-index") + theme(text = element_text(size = 22)) +
    theme(legend.position = "none")
```

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```




### 2.3.5 Post hoc analysis for the popularity of index based on sex and index worms

```
# Subsetting down to females
IndContactsIndexinfrecipF <- IndContactsIndexinfrecip %>%
    filter(recipsex == "F")

# Subsetting down to males
IndContactsIndexinfrecipM <- IndContactsIndexinfrecip %>%
    filter(recipsex == "M")

# Fitting a GLMM for females only for post hoc analysis
IndexRCinflmrecipF <- glmmTMB(RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) +
    ScContactInitRs + I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs,
    family = beta_family(), data = IndContactsIndexinfrecipF)
# Summary for the female model model
summary(IndexRCinflmrecipF)
```

```
##  Family: beta  ( logit )
## Formula:
## RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) + ScContactInitRs +
##     I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs
## Data: IndContactsIndexinfrecipF
##
##      AIC      BIC   logLik deviance df.resid
##   -453.4   -438.8    233.7   -467.4       53
```

```
##
##
## Dispersion parameter for beta family ():  476
##
## Conditional model:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -4.76123    0.11525  -41.31   <2e-16 ***
## ScIndexWorm                 -0.16894    0.13282   -1.27   0.2034
## I(ScIndexWorm^2)            -0.13398    0.05521   -2.43   0.0152 *
## ScContactInitRs              1.34848    0.13756    9.80   <2e-16 ***
## I(ScContactInitRs^2)         0.10363    0.08248    1.26   0.2089
## ScIndexWorm:ScContactInitRs  0.25914    0.12749    2.03   0.0421 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Likelihood ratio test for significance in the female model
drop1(IndexRCinflmrecipF, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) + ScContactInitRs +
##     I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs
##                             Df     AIC    LRT Pr(>Chi)
## <none>                         -453.41
## I(ScIndexWorm^2)             1 -449.79 5.6269  0.01769 *
## I(ScContactInitRs^2)         1 -453.99 1.4190  0.23356
## ScIndexWorm:ScContactInitRs  1 -450.91 4.5031  0.03383 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Fitting a GLMM for male post hoc analysis
IndexRCinflmrecipM <- glmmTMB(RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) +
    ScContactInitRs + I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs,
    , family = beta_family(), data = IndContactsIndexinfrecipM)
# Summary for the male model
summary(IndexRCinflmrecipM)
```

```
##  Family: beta  ( logit )
## Formula:
## RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) + ScContactInitRs +
##     I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs
## Data: IndContactsIndexinfrecipM
##
##      AIC      BIC   logLik deviance df.resid
##   -256.9   -247.1    135.5   -270.9       23
##
##
## Dispersion parameter for beta family ():  668
##
## Conditional model:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -4.390565   0.139093 -31.566  < 2e-16 ***
```

```
## ScIndexWorm                   0.280794   0.105600   2.659 0.007837 **
## I(ScIndexWorm^2)             -0.295458   0.086609  -3.411 0.000646 ***
## ScContactInitRs               1.494855   0.124637  11.994  < 2e-16 ***
## I(ScContactInitRs^2)          0.150132   0.079416   1.890 0.058698 .
## ScIndexWorm:ScContactInitRs -0.009143   0.156285  -0.059 0.953349
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Likelihood ratio test for significance in the male
drop1(IndexRCinflmrecipM, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## RecipCRs ~ ScIndexWorm + I(ScIndexWorm^2) + ScContactInitRs +
##     I(ScContactInitRs^2) + ScIndexWorm:ScContactInitRs
##                              Df     AIC    LRT Pr(>Chi)
## <none>                          -256.95
## I(ScIndexWorm^2)              1 -249.41 9.5334 0.002018 **
## I(ScContactInitRs^2)          1 -255.60 3.3430 0.067491 .
## ScIndexWorm:ScContactInitRs   1 -258.94 0.0034 0.953382
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## 2.4 Do groups with infected versus uninfected index fish change their contact rate different across days 2 and 3 and does this vary by sex?

Subsetting down to the data we need for this analysis

```
IndContacts4ch <- IndContacts4 %>%
    distinct(fishID2, recipID2, .keep_all = TRUE)
# Subsetting down to females
IndContacts4chF <- IndContacts4ch %>%
    filter(Sex == "F")
# Subsetting down to males
IndContacts4chM <- IndContacts4ch %>%
    filter(Sex == "M")
```

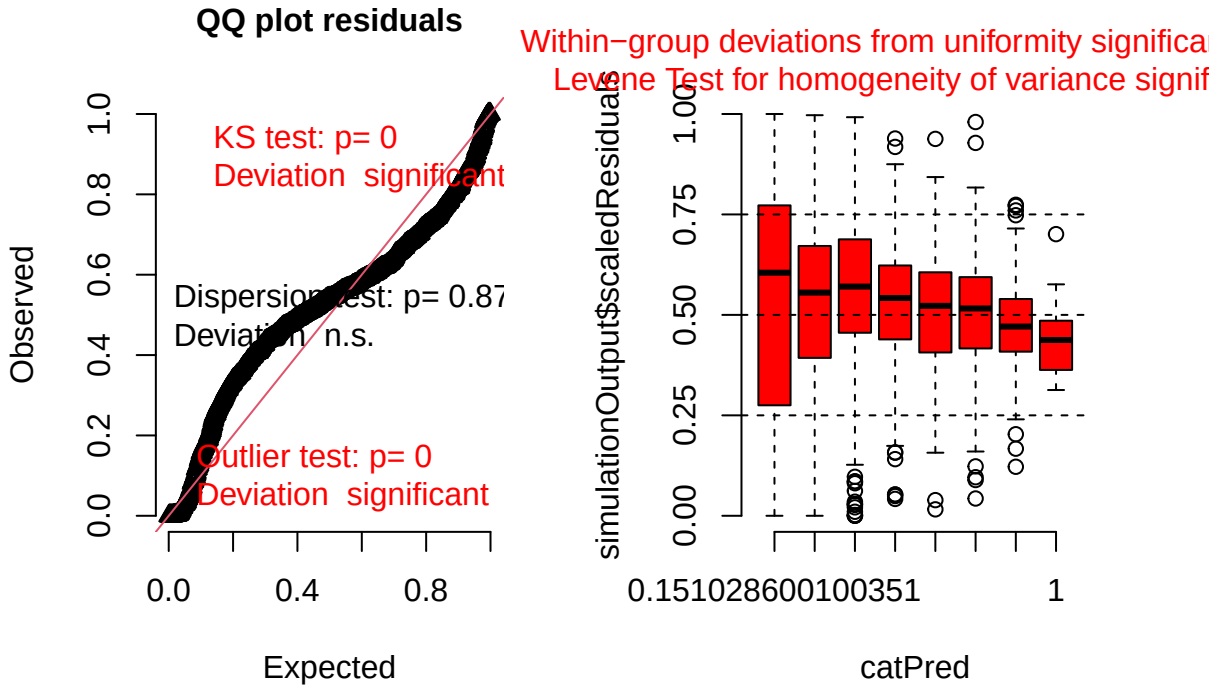
We are fitting a linear mixed model with change in contact rate between dyas 2 and 3 for all uninfected fish in the experiment.

### 2.4.1 Fitting our linear model for the change in behavior across days 2 and 3

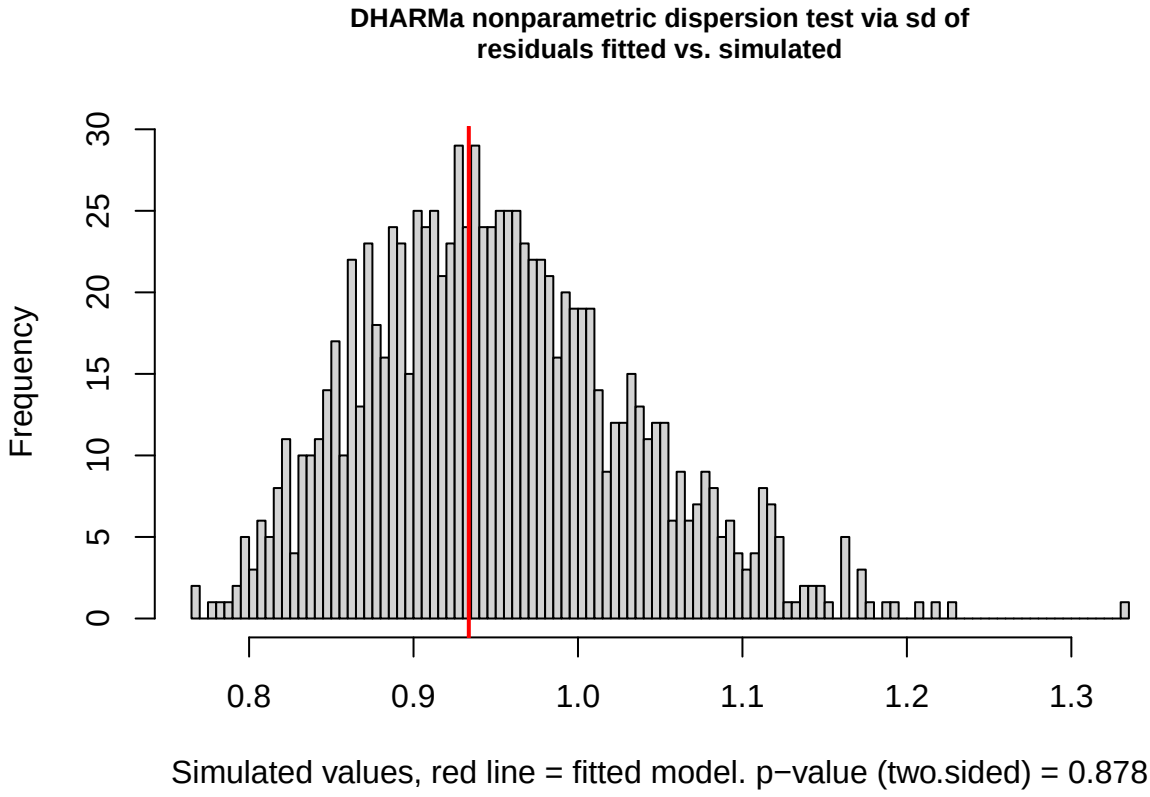
```
# fitting glmmtmb for total contacts over sex and infection treatment
Contactsmodel <- lmer(ChContactinit ~ InfectionTrt + Sex + recipsex + (1 |
    population) + (1 | fishID2), data = IndContacts4ch)


# Summary for our model
summary(Contactsmodel)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ChContactinit ~ InfectionTrt + Sex + recipsex + (1 | population) +
##     (1 | fishID2)
##    Data: IndContacts4ch
##
## REML criterion at convergence: -5040.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.8411 -0.3423  0.0428  0.4171  6.0639
##
## Random effects:
##  Groups     Name        Variance  Std.Dev.
##  fishID2    (Intercept) 5.565e-05 0.007460
##  population (Intercept) 9.093e-05 0.009536
##  Residual               3.314e-04 0.018204
## Number of obs: 1008, groups:  fishID2, 126; population, 14
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)   -0.002680   0.005101  -0.525
## InfectionTrt1 -0.006581   0.005967  -1.103
## SexM           0.003802   0.001868   2.035
## recipsexM      0.005012   0.001226   4.088
##
## Correlation of Fixed Effects:
##             (Intr) InfcT1 SexM
## InfectnTrt1 -0.835
## SexM        -0.129  0.000
## recipsexM   -0.090  0.000  0.082
```

```
sim_residuals_Contactsmodel <- simulateResiduals(Contactsmodel, 1000)  #Quantile residuals
# Ploting the quantile residuals
plot(sim_residuals_Contactsmodel)
```

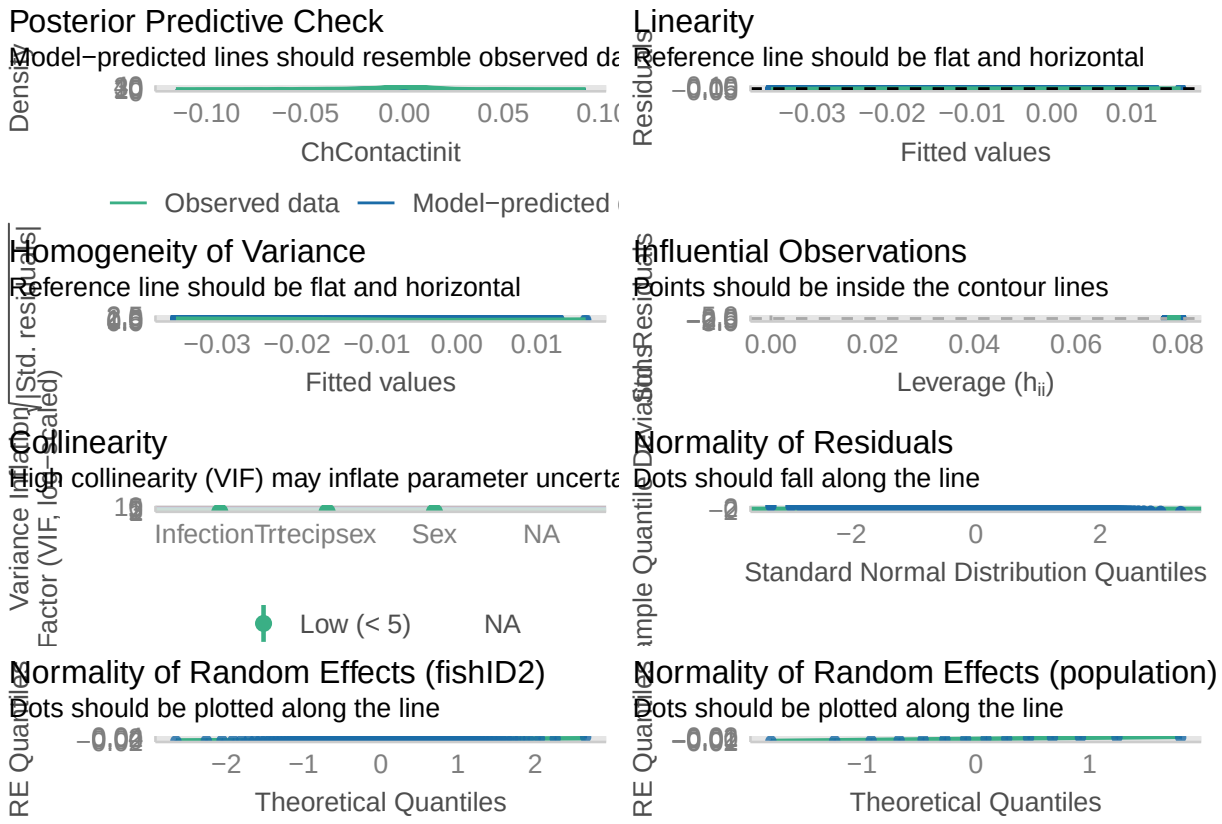



```
# Testing dispersion
testDispersion(sim_residuals_Contactsmodel)
```



```
##
##  DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##  simulated
##
## data:  simulationOutput
## dispersion = 0.98044, p-value = 0.878
## alternative hypothesis: two.sided
```

```
check_model(Contactsmodel)
```

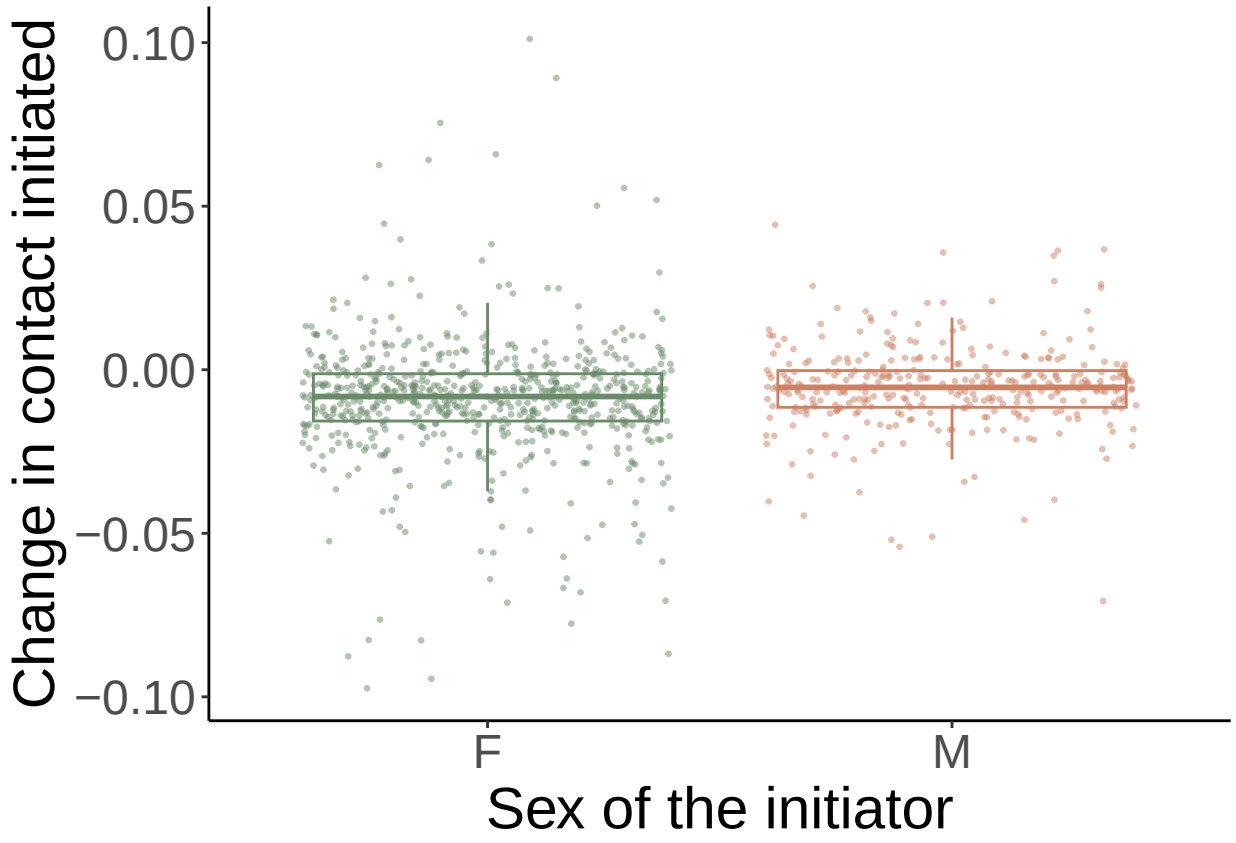



```
Anova(Contactsmodel, type = "2", test = "F")
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: ChContactinit
##                    F Df Df.res    Pr(>F)
## InfectionTrt  1.2165  1  12.00    0.2917
## Sex           4.1414  1 112.51    0.0442 *
## recipsex     16.7139  1 881.00 4.743e-05 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

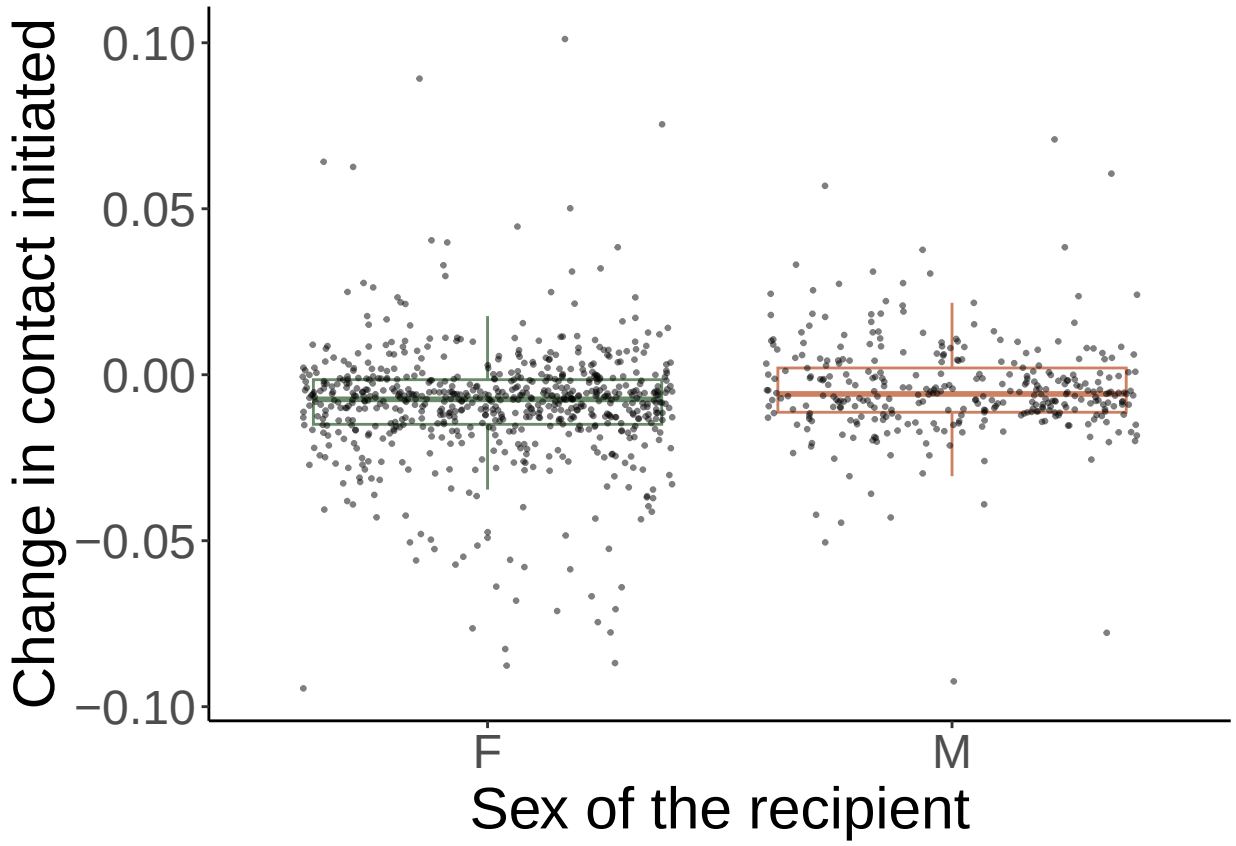
```
# Anova(ContactsmodelF, type='2', test='F') Anova(ContactsmodelM,
# type='2', test='F')
```

```r
# Setting a labeller to change axis names in the plot
labellerI <- labeller(InfectionTrt = c(`1` = "Infected Treatment", `0` = "Uninfected Treatment"))
# Setting colorscheme for infection and sex categorical variables
cpinf = c("darkgray", "purple")
cpsex = c("darkseagreen4", "lightsalmon3")
# Exporting the fit and residual for sex in our model
ContactsmodelVR <- visreg(Contactsmodel, "Sex", scale = "response", partial = T,
    plot = FALSE)
# Extracting fit
ContactsmodelVRfit <- ContactsmodelVR$fit
# Extracting residuals
ContactsmodelVRres <- ContactsmodelVR$res
# Plotting out the relationship
ggplot(ContactsmodelVRres, aes(x = Sex, y = visregRes, color = Sex)) +
    geom_boxplot(aes(color = Sex), outliers = FALSE) + geom_jitter(alpha = 0.5,
    size = 0.5) + theme_classic() + theme(text = element_text(size = 22)) +
    ylab("Change in contact initiated") + xlab("Sex of the initiator") +
    scale_color_manual(values = cpsex) + theme(legend.position = "none")
```




```r
# Extracting residuals and fit for the recipient sex in the model
ContactsmodelrecipVR <- visreg(Contactsmodel, "recipsex", scale = "response",
    partial = T, plot = FALSE)
# Extracting fit
ContactsmodelrecipVRfit <- ContactsmodelrecipVR$fit
# Extracting residuals
ContactsmodelrecipVRres <- ContactsmodelrecipVR$res
```

```
# Plotting the residuals
ggplot(ContactsmodelrecipVRres, aes(x = recipsex, y = visregRes)) + geom_boxplot(aes(color = recipsex),
    outliers = FALSE) + geom_jitter(alpha = 0.5, size = 0.5) + theme_classic() +
    theme(text = element_text(size = 22)) + ylab("Change in contact initiated") +
    xlab("Sex of the recipient") + scale_color_manual(values = cpsex) +
    theme(legend.position = "none")
```




### 2.4.2 Post-hoc analyses for exploring sex differences in the change in contact rate between days 2 and 3

```
# Fitting our post-hoc analysis for female change in contact model
ContactsmodelF <- lmer(ChContactinit ~ (1 | population) + (1 | fishID2),
    data = IndContacts4chF)
```

```
## boundary (singular) fit: see help('isSingular')
```

```
# Summary for the female model
summary(ContactsmodelF)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ChContactinit ~ (1 | population) + (1 | fishID2)
##    Data: IndContacts4chF
##
## REML criterion at convergence: -3278.5
```

```
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.5939 -0.3498  0.0270  0.4104  5.5912
##
## Random effects:
##  Groups     Name        Variance  Std.Dev.
##  fishID2    (Intercept) 0.0000000 0.00000
##  population (Intercept) 0.0001584 0.01259
##  Residual               0.0004134 0.02033
## Number of obs: 672, groups:  fishID2, 84; population, 14
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) -0.005501   0.003454  -1.593
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
# One sample t-test to test if the change in contact rate is
# different than zero
t.test(IndContacts4chF$ChContactinit)
```

```
##
##  One Sample t-test
##
## data:  IndContacts4chF$ChContactinit
## t = -6.0216, df = 671, p-value = 2.845e-09
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.007294344 -0.003707031
## sample estimates:
##    mean of x
## -0.005500688
```

```
# FItting our post-hoc analysis for male change in contact model
ContactsmodelM <- lmer(ChContactinit ~ (1 | population) + (1 | fishID2),
    data = IndContacts4chM)
```

```
## boundary (singular) fit: see help('isSingular')
```

```
# Summary for the male model
summary(ContactsmodelM)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ChContactinit ~ (1 | population) + (1 | fishID2)
##    Data: IndContacts4chM
##
## REML criterion at convergence: -1859.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.4324 -0.3528 -0.0027  0.3729  4.0355
```

```
##
## Random effects:
##  Groups     Name        Variance  Std.Dev.
##  fishID2    (Intercept) 0.0001385 0.01177
##  population (Intercept) 0.0000000 0.00000
##  Residual               0.0001754 0.01325
## Number of obs: 336, groups:  fishID2, 42; population, 14
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) -0.002325   0.001954   -1.19
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
# One sample t-test to test if the change in contact rate is
# different than zero
t.test(IndContacts4chM$ChContactinit)
```

```
##
##  One Sample t-test
##
## data:  IndContacts4chM$ChContactinit
## t = -2.4168, df = 335, p-value = 0.01619
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.0042177269 -0.0004326831
## sample estimates:
##    mean of x
## -0.002325205
```