

# binomial model for nudi reaction

Bri Over

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faster as got bigger but looking at interaction can see that bigger or smaller did not matter as temperature increased only difference was in 18 compared to 12 (nudis at 18 moved slower)

```
#this was a test run, tried modelling different variables to analyze the response  
#compared to the expected outcome but did not end up using
```

```
nudi_data <- read.csv("clean_data/Meyknecht_Over_Parker_MRNE475_2024_combinedraw.csv")%>%  
  mutate(temp_grp = as.factor(temp_grp))  
nudi_data$trial_type[nudi_data$trial_type=="conspecific "] <- "conspecific"  
# Read in the original dataset
```

```
# Create a new variable 'expected_direction' based on the trial_type  
#nudi_data$expected_direction <- ifelse(nudi_data$trial_type == "conspecific", 1, 0)
```

```
# Create a new variable 'move_as_expected' to indicate whether the observed direction matches the expected  
#nudi_data$move_as_expected <- ifelse(nudi_data$direction_binom == nudi_data$expected_direction, 1, 0)
```

```
# View the structure of the updated dataset to confirm that the new variables have been added  
str(nudi_data)
```

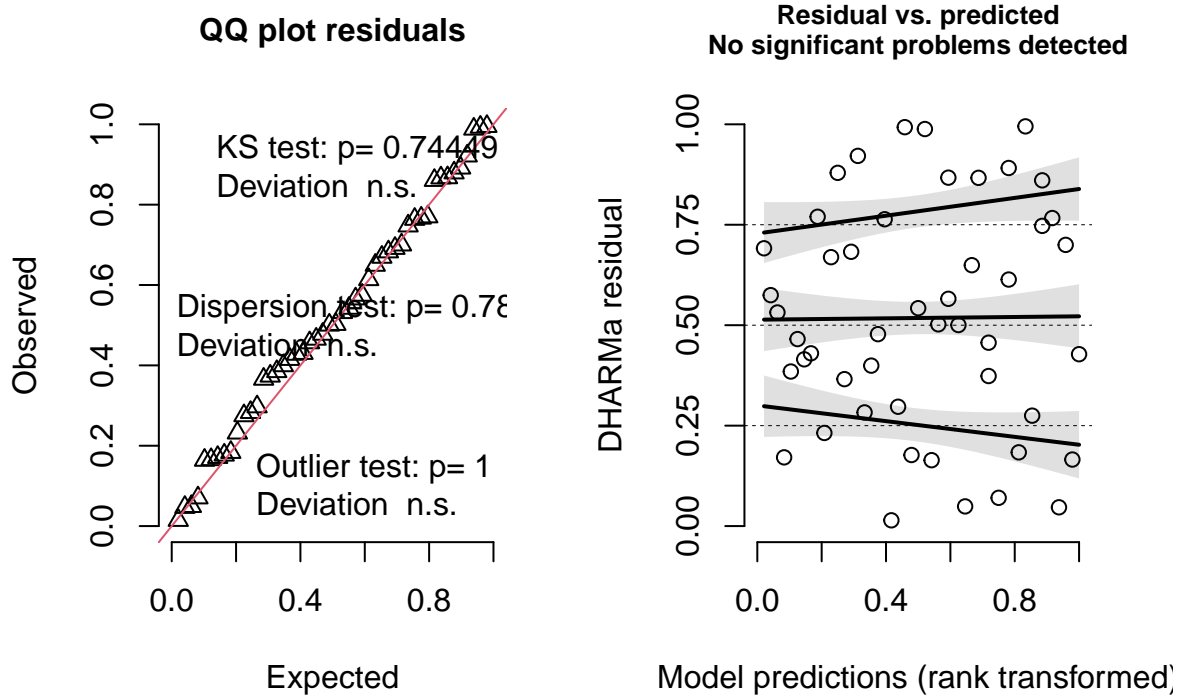
```
## 'data.frame':   48 obs. of  9 variables:  
## $ nudi_num      : int  2 2 3 3 4 4 5 5 6 6 ...  
## $ temp_grp      : Factor w/ 4 levels "12","14","16",...: 3 3 4 4 1 1 2 2 1 1 ...  
## $ trial_type    : chr  "conspecific" "predator" "conspecific" "predator" ...  
## $ mean_angle    : num  156 160 195 188 311 ...  
## $ sd_angle      : num  102 112 103 105 100 ...  
## $ mean_vel      : num  0.001379 0.001311 0.001302 0.000949 0.000613 ...  
## $ sd_vel        : num  0.00059 0.000769 0.00089 0.000788 0.000358 ...  
## $ avg_length_m  : num  0.033 0.033 0.037 0.037 0.0095 0.0095 0.04 0.04 0.034 0.034 ...  
## $ direction_binom: int  0 0 1 1 1 0 0 1 0 0 ...
```

```
#trial runs for the model (a model graveyard) to determine what the best fit was  
#including models for the altered data looking at expected outcomes
```

```
#glm_binom <- glmmTMB(move_as_expected ~ temp_grp * avg_length_m + trial_type, family = binomial(link =  
#simulateResiduals(glm_binom))%>%  
# plot()
```

```
glm_binom2 <- glmmTMB(direction_binom ~ temp_grp * avg_length_m + trial_type, family = binomial(link =  
simulateResiduals(glm_binom2))%>%  
plot()
```

## DHARMA residual



```
# Extract the coefficients directly from the model summary
binom_table <- as.data.frame(summary(glm_binom2)$coefficients$cond)

summary(glm_binom2)
```

```
## Family: binomial ( logit )
## Formula:          direction_binom ~ temp_grp * avg_length_m + trial_type
## Data: nudi_data
##
##      AIC      BIC   logLik deviance df.resid
##    64.2    81.0   -23.1    46.2      39
##
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.6804     1.6808   1.000  0.3174
## temp_grp14     -17.5703    10.5224  -1.670  0.0950 .
## temp_grp16     -13.5196    11.3046  -1.196  0.2317
## temp_grp18      -7.1760     3.5701  -2.010  0.0444 *
## avg_length_m    -40.9577    64.3139  -0.637  0.5242
## trial_typepredator -0.7745     0.7328  -1.057  0.2906
## temp_grp14:avg_length_m 453.1847   276.1705   1.641  0.1008
## temp_grp16:avg_length_m 349.7955   321.5785   1.088  0.2767
## temp_grp18:avg_length_m 205.3878   116.0277   1.770  0.0767 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Save the table as a CSV file
write.csv(binom_table, "bri_code/Meyknecht_Over_Parker_MRNE475_2024_binom_table.csv", row.names = TRUE)
```

did not move based on cues, different cues but same directions look at difference between 12 and 18 movement proportion moved tws and proportion moved away

```
# Load necessary libraries
library(dplyr)
library(ggplot2)

# Summarize the data: Count nudibranchs that moved towards or away for each combination of trial_type,
nudi_data_summary <- nudi_data %>%
  group_by(trial_type, temp_grp, direction_binom) %>%
  summarise(count = n(), .groups = 'drop')

# Calculate total number of nudibranchs in each trial_type and temp_grp
nudi_data_totals <- nudi_data %>%
  group_by(trial_type, temp_grp) %>%
  summarise(total = n(), .groups = 'drop')

# Join the summarized data with the total counts to calculate proportions
nudi_data_prop <- nudi_data_summary %>%
  left_join(nudi_data_totals, by = c("trial_type", "temp_grp")) %>%
  mutate(proportion = count / total) # Calculate proportion for each direction

# Ensure 'direction_binom' is a factor with appropriate levels
nudi_data_prop$direction_binom <- factor(nudi_data_prop$direction_binom, levels = c(0, 1))

# Handle missing data for "towards" direction in case there are no nudibranchs for that direction
nudi_data_prop_complete <- nudi_data_prop %>%
  complete(trial_type, temp_grp, direction_binom, fill = list(count = 0)) # Ensures missing rows are a

# Set any NA values in proportion to 0 (this handles cases where count is 0 or missing)
nudi_data_prop_complete$proportion[is.na(nudi_data_prop_complete$proportion)] <- 0

# Get the maximum proportion to set the y-axis limit
y_max <- max(nudi_data_prop_complete$proportion, na.rm = TRUE)

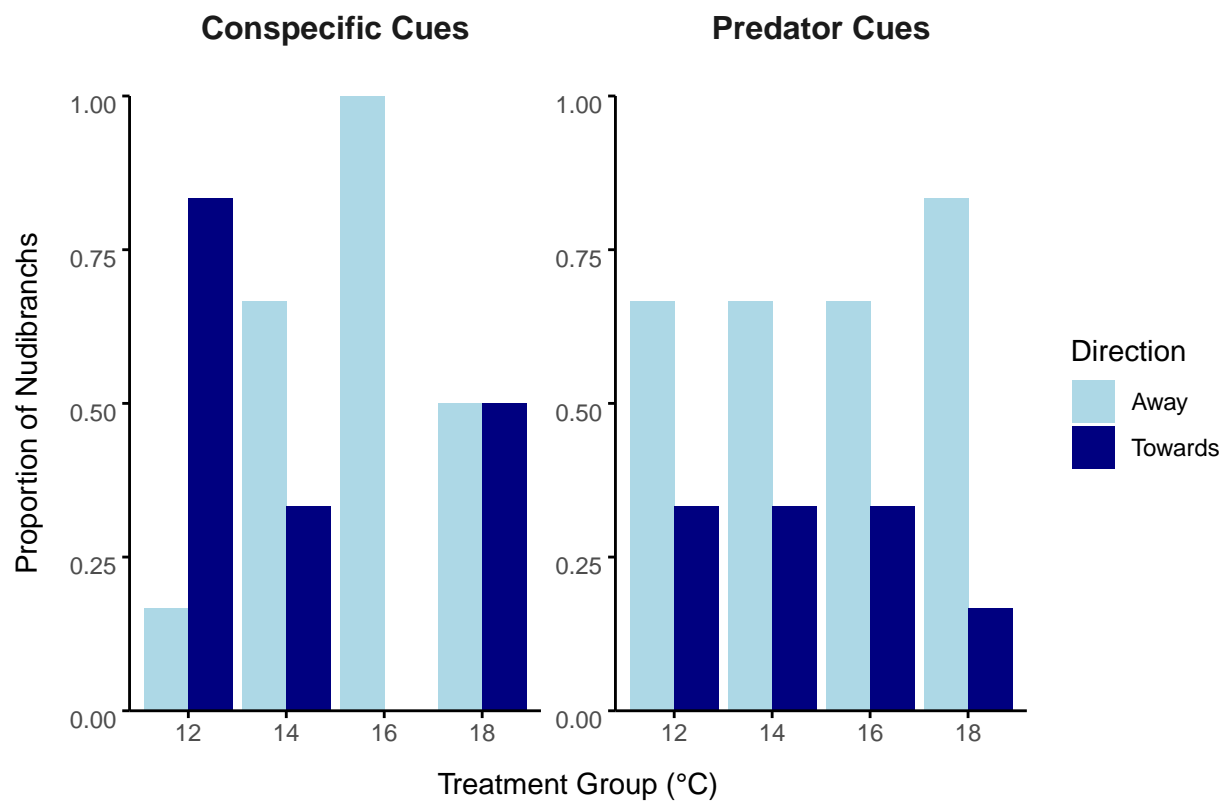
# Create the bar chart with the correct facet and fixed y-axis
plot_rxn_probs <- ggplot(nudi_data_prop_complete, aes(x = factor(temp_grp), y = proportion, fill = fact
  geom_bar(stat = "identity", position = "dodge") + # dodge bars so they do not overlap
  facet_wrap(~ trial_type, scales = "free_y",
    labeller = labeller(trial_type = c("conspecific" = "Conspecific Cues", "predator" = "Preda
  labs(
    title = "",
    x = "Treatment Group (°C)",
    y = "Proportion of Nudibranchs",
    fill = "Direction"
  ) +
  scale_fill_manual(values = c("0" = "lightblue", "1" = "navyblue"), labels = c("Away", "Towards")) +
  scale_y_continuous(limits = c(0, y_max), expand = c(0, 0)) + # Fixed y-axis scale across both graphs
  scale_x_discrete(expand = c(0.2, 0)) + # Increase space between the categories on the x-axis
  theme_minimal() +
```

```

theme(
  axis.text.y = element_text(vjust = 1), # Adjust vertical alignment of y-axis text
  panel.grid.major = element_blank(), # Remove major gridlines
  panel.grid.minor = element_blank(), # Remove minor gridlines
  axis.line = element_line(color = "black", linewidth = 0.5), # Add axis lines for both x and y axes
  axis.ticks = element_line(color = "black", linewidth = 0.5), # Add ticks to both x and y axes
  axis.title.x = element_text(margin = margin(t = 10)), # Add space between x-axis labels and numbers
  axis.title.y = element_text(margin = margin(r = 10)), # Add space between y-axis labels and numbers
  strip.text = element_text(size = 12, face = "bold", margin = margin(b = 20)) # Add space between fac
)

plot_rxn_probs

```



```

summary_table <- nudi_data_prop_complete %>%
  dplyr::select(trial_type, temp_grp, direction_binom, proportion) %>%
  arrange(trial_type, temp_grp, direction_binom)

print(summary_table)

```

```

## # A tibble: 16 x 4
##   trial_type temp_grp direction_binom proportion
##   <chr>      <fct>    <fct>          <dbl>
## 1 conspecific 12      0            0.167
## 2 conspecific 12      1            0.833
## 3 conspecific 14      0            0.667

```

##	4	conspecific	14	1	0.333
##	5	conspecific	16	0	1
##	6	conspecific	16	1	0
##	7	conspecific	18	0	0.5
##	8	conspecific	18	1	0.5
##	9	predator	12	0	0.667
##	10	predator	12	1	0.333
##	11	predator	14	0	0.667
##	12	predator	14	1	0.333
##	13	predator	16	0	0.667
##	14	predator	16	1	0.333
##	15	predator	18	0	0.833
##	16	predator	18	1	0.167

```
ggsave(plot = plot_rxn_probs, filename = here("bri_code", "Meyknecht_Over_Parker_MRNE475_2024_plot_rxn_"))
```

```
# Summarize the data to calculate the overall proportions of "towards" and "away" for each temp_grp
nudi_data_summary_overall <- nudi_data %>%
  group_by(temp_grp, direction_binom) %>%
  summarise(count = n(), .groups = 'drop')

# Calculate total number of nudibranchs in each temp_grp
nudi_data_totals_overall <- nudi_data %>%
  group_by(temp_grp) %>%
  summarise(total = n(), .groups = 'drop')

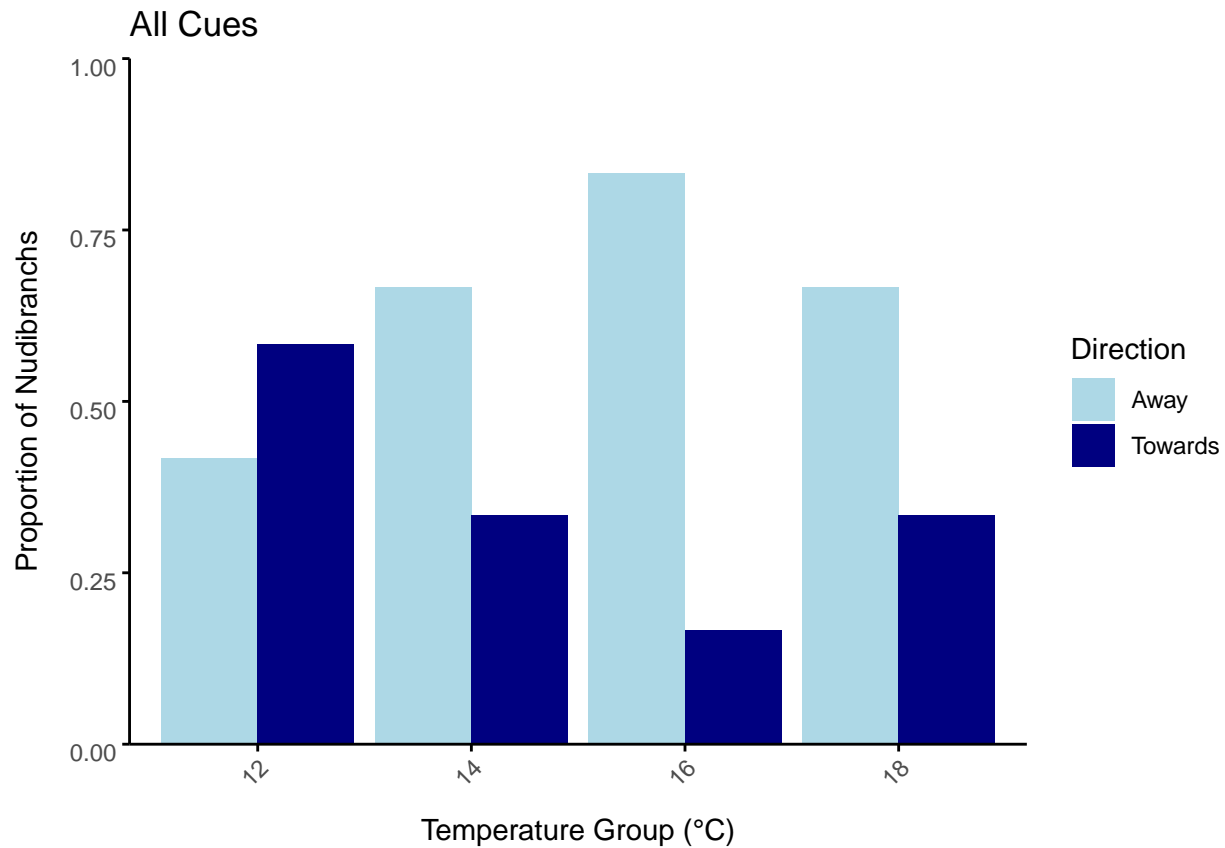
# Join the summarized data with the total counts to calculate proportions
nudi_data_prop_overall <- nudi_data_summary_overall %>%
  left_join(nudi_data_totals_overall, by = "temp_grp") %>%
  mutate(proportion = count / total) # Calculate proportion for each direction

# Ensure 'direction_binom' is a factor with appropriate levels
nudi_data_prop_overall$direction_binom <- factor(nudi_data_prop_overall$direction_binom, levels = c(0, 1))

# Create the plot showing overall movement for each temp_grp
ggplot(nudi_data_prop_overall, aes(x = factor(temp_grp), y = proportion, fill = factor(direction_binom))) +
  geom_bar(stat = "identity", position = "dodge") + # Bar chart with dodged bars for direction
  labs(
    title = "All Cues",
    x = "Temperature Group (°C)",
    y = "Proportion of Nudibranchs",
    fill = "Direction"
  ) +
  scale_fill_manual(values = c("0" = "lightblue", "1" = "navyblue"), labels = c("Away", "Towards")) +
  scale_y_continuous(limits = c(0, y_max), expand = c(0, 0)) + # Fixed y-axis scale across both graphs
  scale_x_discrete(expand = c(0.2, 0)) + # Increase space between the categories on the x-axis
  theme_minimal() +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1, vjust = 1), # Rotate x-axis labels for readability
    axis.text.y = element_text(vjust = 1), # Adjust vertical alignment of y-axis text
    panel.grid.major = element_blank(), # Remove major gridlines
    panel.grid.minor = element_blank(), # Remove minor gridlines
    axis.line = element_line(color = "black", size = 0.5), # Add axis lines for both x and y axes
    axis.ticks = element_line(color = "black", size = 0.5), # Add ticks to both x and y axes
  )
```

```
axis.title.x = element_text(margin = margin(t = 10)), # Add space between x-axis labels and numbers
axis.title.y = element_text(margin = margin(r = 10)), # Add space between y-axis labels and numbers
strip.text = element_text(size = 12, face = "bold", margin = margin(b = 20)) # Add space between facets
)
```

```
## Warning: The 'size' argument of 'element_line()' is deprecated as of ggplot2 3.4.0.
## i Please use the 'linewidth' argument instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```



```
#more model graveyard below, tried calculating AIC but did not have to as the binomial
#was clearly the correct fit
```

```
glm_bbinom <- glmmTMB(move_as_expected ~ temp_grp + avg_length_m, family = betabinomial(link = "logit"),
data = nudi_data) simulateResiduals(glm_bbinom)%>% plot() #treats temperature and length
separately
```

## Fit Zero-Inflated Binomial Model

```
glm_zib <- glmmTMB(direction_binom ~ temp_grp + avg_length_m, family = binomial(link = "logit"),
zi ~ temp_grp + avg_length_m, data = nudi_data)
```

## Check the model summary

```
summary(glm_zib)
simulateResiduals(glm_zib) %>% plot()
AIC(glm_bbinom, glm_binom, glm_zib)
#only AIC for binom
summary(glm_binom)
```

#Temperature effect: The p-value for temp\_grp is not significant at the standard 0.05 significance level: means that, based on this model, there is no strong evidence that temperature affects the nudibranchs' response to conspecific or predatory cues.

#Size effect: Similarly, the p-value for avg\_length\_m is greater than 0.05 suggesting that the size of the nudibranchs does not significantly impact their direction of movement.

#modeling both the main effects of each variable and their interaction: modeling the effect of temperature, the effect of size, and how the effect of temperature changes depending on the size of the nudibranch

## Fit the model with interaction between temperature and body size

```
glm_binom_int <- glmmTMB(move_as_expected ~ temp_grp * avg_length_m, family = binomial(link = "logit"), data = nudi_data)
simulateResiduals(glm_binom_int) %>% plot()
summary(glm_binom_int)
glm_bbinom_int <- glmmTMB(move_as_expected ~ temp_grp * avg_length_m, family = betabinomial(link = "logit"), data = nudi_data)
simulateResiduals(glm_bbinom_int) %>% plot()
summary(glm_binom_int)
```

## Fit Zero-Inflated Binomial Model

```
glm_zib_int <- glmmTMB(direction_binom ~ temp_grp * avg_length_m, family = binomial(link = "logit"), zi = ~ temp_grp + avg_length_m, data = nudi_data)
summary(glm_zib_int)
simulateResiduals(glm_zib_int) %>% plot()
AIC(glm_bbinom_int, glm_binom_int, glm_zib_int)
#interaction made this worse somehow
```