Asexual Budding Analyses

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```
knitr::opts_chunk$set(tidy.opts=list(width.cutoff=70), tidy=TRUE)
# code above ensures no text is cut off when knit
```

Loading in Packages and Data

```
library(patchwork)
library(car)
library(performance)
library(DHARMa)
library(fitdistrplus)
library(gamlss)
library(tidyverse)

polyp_data <- read_csv("/Users/marabohm/Github/Jelly-Data/data/ds2021_polyp_data.csv")
```

Cleaning the Data

```
polyp_clean <- polyp_data %>%
    rename(collection_day = "Data collection day", jar_code = "Jar Code (ex. E1)",
        treatment = Chemical, num_elongated = "Elongation?", num_ruffled = "Ruffled?",
        num_asexual_buds = "Asexual Repro?", total_num = Total) %>%
    mutate(jar_code = as.factor(jar_code), treatment = as.factor(treatment),
        treatment = fct_relevel(treatment, "Control", "Caffeine", "Estradiol",
            "Combo")) %>%
    dplyr::select(collection_day, jar_code, treatment, num_elongated, num_ruffled,
        num_asexual_buds, total_num)
```

Fitting Distributions for Budding Data

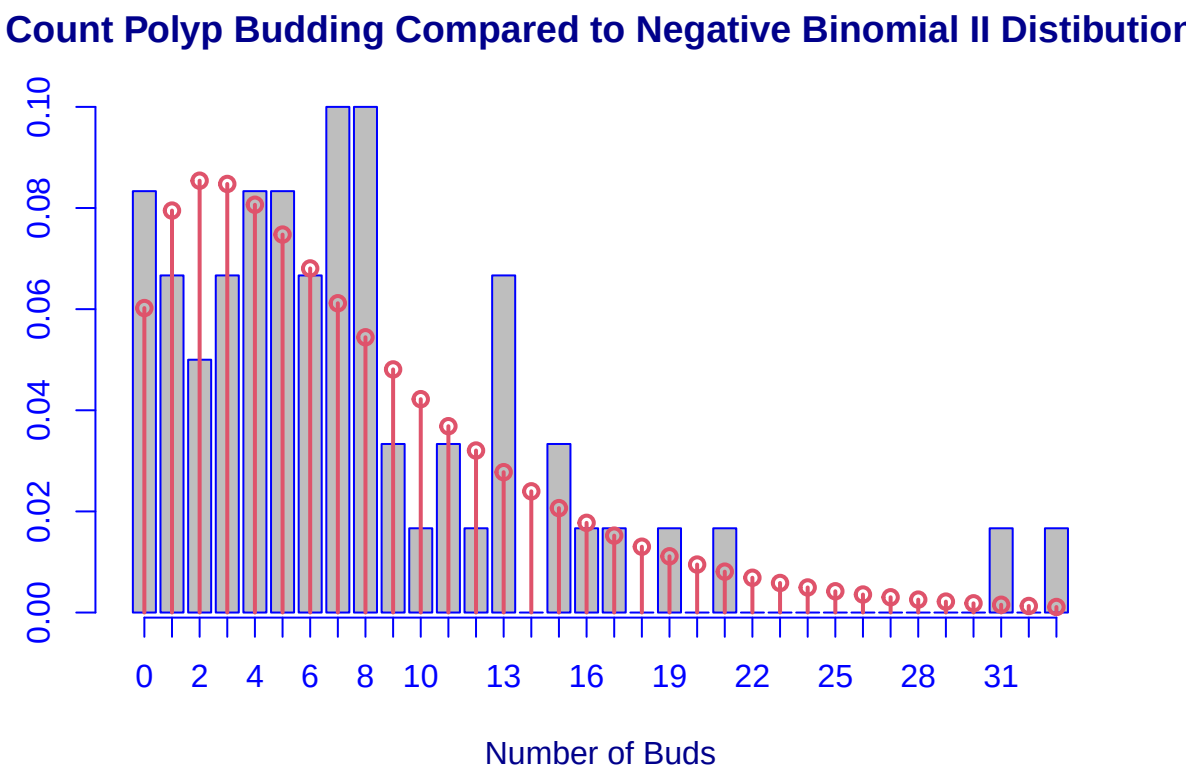
```
fitDist(num_asexual_buds, data = polyp_clean, type = "counts", try.gamlss = T)
# best fit: Negative Binomial type II (AIC = 372.321)
```

Creating The Budding Model

```
mod_countwtotal_buds <- gamlss(num_asexual_buds ~ treatment * collection_day +
    re(random = ~1 | jar_code) + re(random = ~1 | total_num), family = NBII(),
    data = polyp_clean, control = gamlss.control(n.cyc = 250))
```

```
## GAMLSS-RS iteration 1: Global Deviance = 291.0988
## GAMLSS-RS iteration 2: Global Deviance = 274.0581
## GAMLSS-RS iteration 3: Global Deviance = 272.0645
## GAMLSS-RS iteration 4: Global Deviance = 271.8039
## GAMLSS-RS iteration 5: Global Deviance = 271.7566
## GAMLSS-RS iteration 6: Global Deviance = 271.7423
## GAMLSS-RS iteration 7: Global Deviance = 271.7397
## GAMLSS-RS iteration 8: Global Deviance = 271.739
```

```
histDist(polyp_clean$num_asexual_buds, "NBII", density = T, main = "Count Polyp Budding Compared to Nega
    xlab = "Number of Buds")
```




```
##
## Family:  c("NBII", "Negative Binomial type II")
## Fitting method: "nlminb"
##
## Call:  gamlssML(formula = polyp_clean$num_asexual_buds, family = "NBII")
```

```
##
## Mu Coefficients:
## [1]  2.041
## Sigma Coefficients:
## [1]  1.575
##
##  Degrees of Freedom for the fit: 2 Residual Deg. of Freedom   58
## Global Deviance:     368.321
##             AIC:     372.321
##             SBC:     376.509
```

```
# summarizing the model to determine p-values:
summary(mod_countwtotal_buds)
```

```
## ******************************************************************
## Family:  c("NBII", "Negative Binomial type II")
##
## Call:  gamlss(formula = num_asexual_buds ~ treatment * collection_day +
##     re(random = ~1 | jar_code) + re(random = ~1 | total_num),
##     family = NBII(), data = polyp_clean, control = gamlss.control(n.cyc = 250))
##
##
## Fitting method: RS()
##
## ------------------------------------------------------------------
## Mu link function:  log
## Mu Coefficients:
##                                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)                          -0.54561    0.44010  -1.240  0.22097
## treatmentCaffeine                     0.79621    0.54887   1.451  0.15326
## treatmentEstradiol                    0.17758    0.57850   0.307  0.76017
## treatmentCombination                  1.66274    0.50878   3.268  0.00198 **
## collection_day                        0.60862    0.10430   5.835  4.2e-07 ***
## treatmentCaffeine:collection_day     -0.08091    0.13120  -0.617  0.54027
## treatmentEstradiol:collection_day     0.06207    0.13640   0.455  0.65108
## treatmentCombination:collection_day -0.26110    0.12315  -2.120  0.03908 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## ------------------------------------------------------------------
## Sigma link function:  log
## Sigma Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.526      2.645  -0.955    0.344
##
## ------------------------------------------------------------------
## NOTE: Additive smoothing terms exist in the formulas:
##  i) Std. Error for smoothers are for the linear effect only.
## ii) Std. Error for the linear terms maybe are not accurate.
## ------------------------------------------------------------------
## No. of observations in the fit:  60
## Degrees of Freedom for the fit:  11.04057
##       Residual Deg. of Freedom:  48.95943
##                       at cycle:  8
```

```
##
## Global Deviance:     271.739
##              AIC:    293.8201
##              SBC:    316.9429
## ****************************************************************
```