Elongation 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

```
knitr::opts_chunk$set(echo = TRUE)
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")</pre>
```

Cleaning the Data

Fitting Distributions for Elongation Data

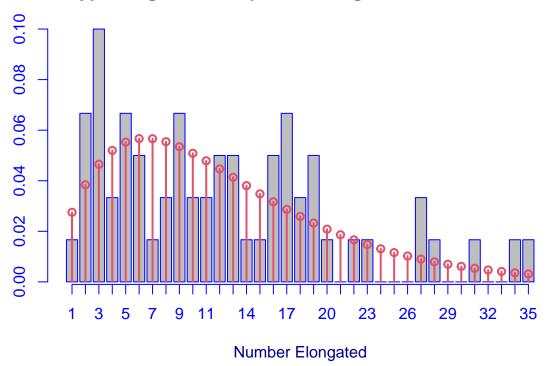
```
fitDist(num_elongated, data = polyp_clean, type = "counts", try.gamlss = T)
# best fit: Negative Binomial type II (AIC = 414.587)
```

Creating The Elongation Model

```
mod_countwtotal_elongation <- gamlss(num_elongated ~ treatment * collection_day +
    re(random = ~1 | jar_code) + re(random = ~1 | total_num), family = NBII(),
    method = RS(), data = polyp_clean, control = gamlss.control(n.cyc = 200))</pre>
```

```
## GAMLSS-RS iteration 1: Global Deviance = 326.5503
## GAMLSS-RS iteration 2: Global Deviance = 315.3428
## GAMLSS-RS iteration 3: Global Deviance = 316.6887
## GAMLSS-RS iteration 4: Global Deviance = 316.5585
## GAMLSS-RS iteration 5: Global Deviance = 316.5898
## GAMLSS-RS iteration 6: Global Deviance = 316.6333
## GAMLSS-RS iteration 7: Global Deviance = 316.5941
## GAMLSS-RS iteration 8: Global Deviance = 316.6303
## GAMLSS-RS iteration 9: Global Deviance = 316.5979
## GAMLSS-RS iteration 10: Global Deviance = 316.6278
## GAMLSS-RS iteration 11: Global Deviance = 316.6011
## GAMLSS-RS iteration 12: Global Deviance = 316.6257
## GAMLSS-RS iteration 13: Global Deviance = 316.6037
## GAMLSS-RS iteration 14: Global Deviance = 316.624
## GAMLSS-RS iteration 15: Global Deviance = 316.6058
## GAMLSS-RS iteration 16: Global Deviance = 316.6225
## GAMLSS-RS iteration 17: Global Deviance = 316.6076
## GAMLSS-RS iteration 18: Global Deviance = 316.6214
## GAMLSS-RS iteration 19: Global Deviance = 316.6091
## GAMLSS-RS iteration 20: Global Deviance = 316.6204
## GAMLSS-RS iteration 21: Global Deviance = 316.6103
## GAMLSS-RS iteration 22: Global Deviance = 316.6196
## GAMLSS-RS iteration 23: Global Deviance = 316.6113
## GAMLSS-RS iteration 24: Global Deviance = 316.619
## GAMLSS-RS iteration 25: Global Deviance = 316.6121
## GAMLSS-RS iteration 26: Global Deviance = 316.6184
## GAMLSS-RS iteration 27: Global Deviance = 316.6128
## GAMLSS-RS iteration 28: Global Deviance = 316.618
## GAMLSS-RS iteration 29: Global Deviance = 316.6133
## GAMLSS-RS iteration 30: Global Deviance = 316.6176
## GAMLSS-RS iteration 31: Global Deviance = 316.6138
## GAMLSS-RS iteration 32: Global Deviance = 316.6173
## GAMLSS-RS iteration 33: Global Deviance = 316.6142
## GAMLSS-RS iteration 34: Global Deviance = 316.6171
## GAMLSS-RS iteration 35: Global Deviance = 316.6145
## GAMLSS-RS iteration 36: Global Deviance = 316.6169
## GAMLSS-RS iteration 37: Global Deviance = 316.6147
## GAMLSS-RS iteration 38: Global Deviance = 316.6167
## GAMLSS-RS iteration 39: Global Deviance = 316.6149
## GAMLSS-RS iteration 40: Global Deviance = 316.6166
## GAMLSS-RS iteration 41: Global Deviance = 316.6151
## GAMLSS-RS iteration 42: Global Deviance = 316.6165
## GAMLSS-RS iteration 43: Global Deviance = 316.6155
```

Count Polyp Elongation Compared to Negative Binomial II Distibutic



```
## Family: c("NBII", "Negative Binomial type II")
## Fitting method: "nlminb"
##
## Call: gamlssML(formula = polyp_clean$num_elongated, family = "NBII")
##
## Mu Coefficients:
## [1] 2.504
## Sigma Coefficients:
## [1]
      1.662
##
  Degrees of Freedom for the fit: 2 Residual Deg. of Freedom
##
                                                              58
## Global Deviance:
                      410.587
##
              AIC:
                      414.587
              SBC:
                      418.776
##
# summarizing model to determine p-values:
summary(mod_countwtotal_elongation)
## *************
## Family: c("NBII", "Negative Binomial type II")
```

```
##
## Call: gamlss(formula = num_elongated ~ treatment * collection_day +
     re(random = ~1 | jar code) + re(random = ~1 | total num),
     family = NBII(), data = polyp_clean, method = RS(),
##
##
     control = gamlss.control(n.cyc = 200))
##
## Fitting method: RS()
## -----
## Mu link function: log
## Mu Coefficients:
                              Estimate Std. Error t value Pr(>|t|)
                              ## (Intercept)
                             -0.17935 0.38941 -0.461 0.647033
## treatmentCaffeine
## treatmentEstradiol
                              0.03055 0.37398 0.082 0.935219
                              0.11280 0.36307 0.311 0.757292
## treatmentCombination
                              ## collection_day
## treatmentCaffeine:collection day 0.11929 0.09911 1.204 0.234253
## treatmentEstradiol:collection_day    0.10750    0.09556
                                               1.125 0.265833
## treatmentCombination:collection day 0.14295 0.09252 1.545 0.128455
## 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) -1.4610 0.9872 -1.48 0.145
## -----
## 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: 8.35727
##
     Residual Deg. of Freedom: 51.64273
##
                   at cycle: 43
## Global Deviance:
                  316.6155
                  333.33
          AIC:
           SBC:
                  350.833
```