

Total Number Analyses

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10/12/2021

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

initial setup

```
knitr::opts_chunk$set(echo = TRUE)
library(patchwork)
library(car)
library(performance)
library(DHARMA)
library(fitdistrplus)
library(gamlss)
library(tidyverse)

polyp_data <- read.csv("Jelly data - Polyps.csv")
```

fixing polyp 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_aseexual_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_aseexual_buds, total_num)
```

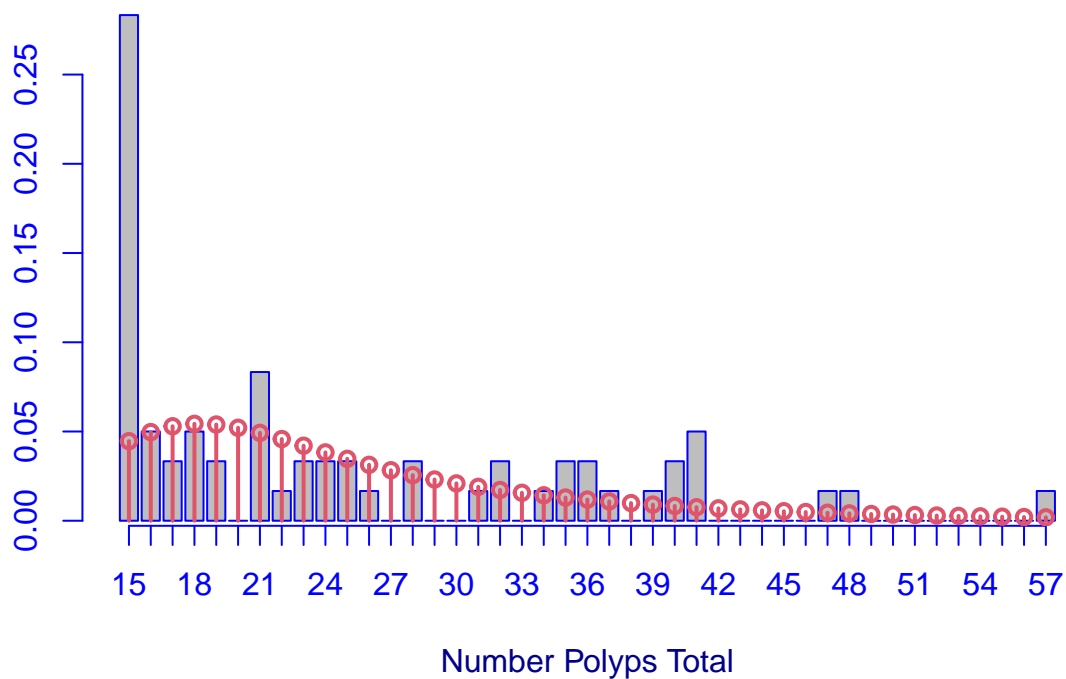
fitting distributions for data

```
fitDist(total_num, data = polyp_clean, type = "counts", try.gamlss = T)
# best fit: delaporte (AIC = 436.754)
```

creating the models with total

```
mod_total <- gamlss(total_num ~ treatment * collection_day + re(random = ~1 |  
  jar_code), family = DEL(), data = polyp_clean, control = gamlss.control(n.cyc = 60))  
histDist(polyp_clean$total_num, "DEL", density = T, main = "Count Polyp Total Compared to Delaporte Dis  
  xlab = "Number Polyps Total")
```

Count Polyp Total Compared to Delaporte Distribution



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