Ruffled Analyses

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```r
knitr::opts_chunk$set(tidy.opts = list(width.cutoff = 80),
    tidy = TRUE)
```

Loading in Packages and Data

Cleaning the Data

```r
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(prop_elongated = num_elongated/total_num + 0.001, prop_ruffled = num_ruffled/total_num +
        0.001, prop_buds = num_asexual_buds/total_num + 0.001, jar_code = as.factor(jar_code),
        treatment = as.factor(treatment), treatment = fct_relevel(treatment, "Control",
            "Caffeine", "Estradiol", "Combo"), log_elongated = log(num_elongated +
            1)) %>%
    dplyr::select(collection_day, jar_code, treatment, num_elongated, prop_elongated,
        num_ruffled, prop_ruffled, num_asexual_buds, prop_buds, total_num, log_elongated)
```

```
## Warning: Unknown levels in 'f': Combo
```

Fitting Distributions for Ruffled Data

```r
fitDist(num_ruffled, data = polyp_clean, type = "counts", try.gamlss = T)
```

```
##    |                                                            |
```

```
## Warning in MLE(ll2, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
##    |                                                            |==================
```

```
## Warning in MLE(ll3, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
##    |                                                                 |==================
```

```
## Warning in MLE(ll4, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
## Error in solve.default(oout$hessian) :
##   Lapack routine dgesv: system is exactly singular: U[4,4] = 0
##    |                                                                 |==================
```

```
##
## Family:  c("NBII", "Negative Binomial type II")
## Fitting method: "nlminb"
##
## Call:  gamlssML(formula = y, family = DIST[i])
##
## Mu Coefficients:
## [1]  2.832
## Sigma Coefficients:
## [1]  1.76
##
##  Degrees of Freedom for the fit: 2 Residual Deg. of Freedom    58
## Global Deviance:     440.109
##             AIC:     444.109
##             SBC:     448.298
```

```
# best fit: Negative Binomial type II (AIC = 444.109)

# model was having difficulty converging with NBII, so tried some other fits:

descdist(polyp_clean$num_ruffled)
```

Cullen and Frey graph
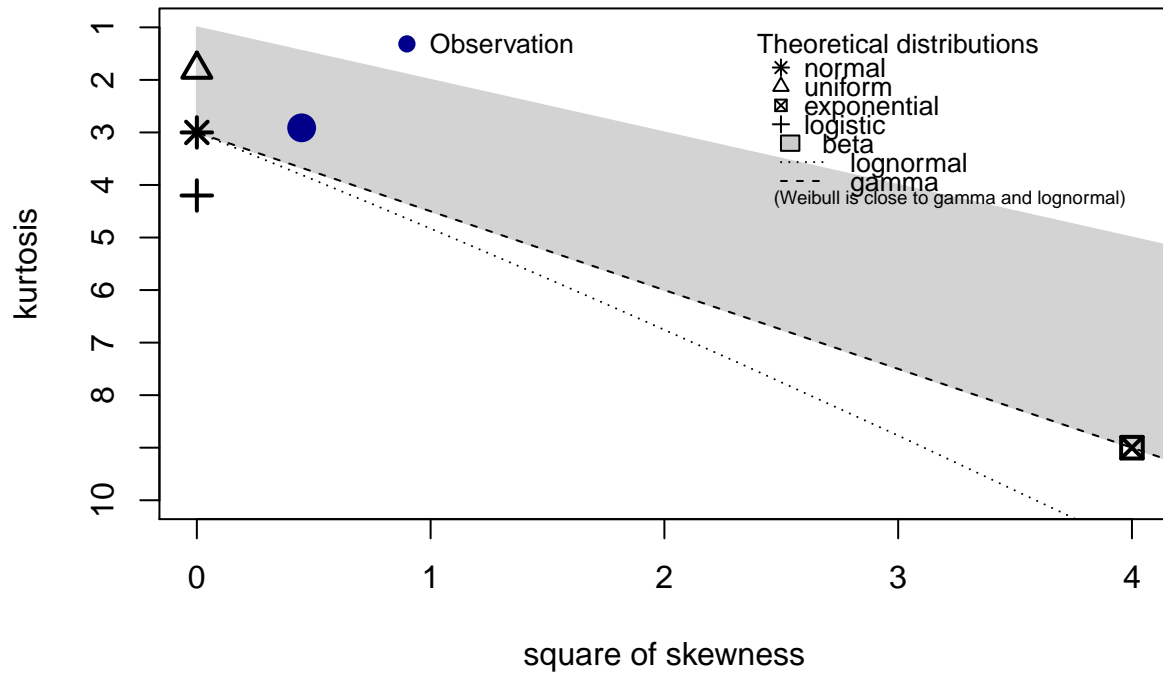

```
## summary statistics
## ------
## min:  1    max:  46
## median:  15.5
## mean:  16.98333
## estimated sd:  10.37679
## estimated skewness:  0.6695946
## estimated kurtosis:  2.912065
```

```r
# Cullen and Frey plot indicates Lognormal, Gamma and Weibull distributions may
# be a good fit, so we compare to each other using Generalized AIC:

b_NB2 <- histDist(polyp_clean$num_ruffled, "NBII", density = T)
```
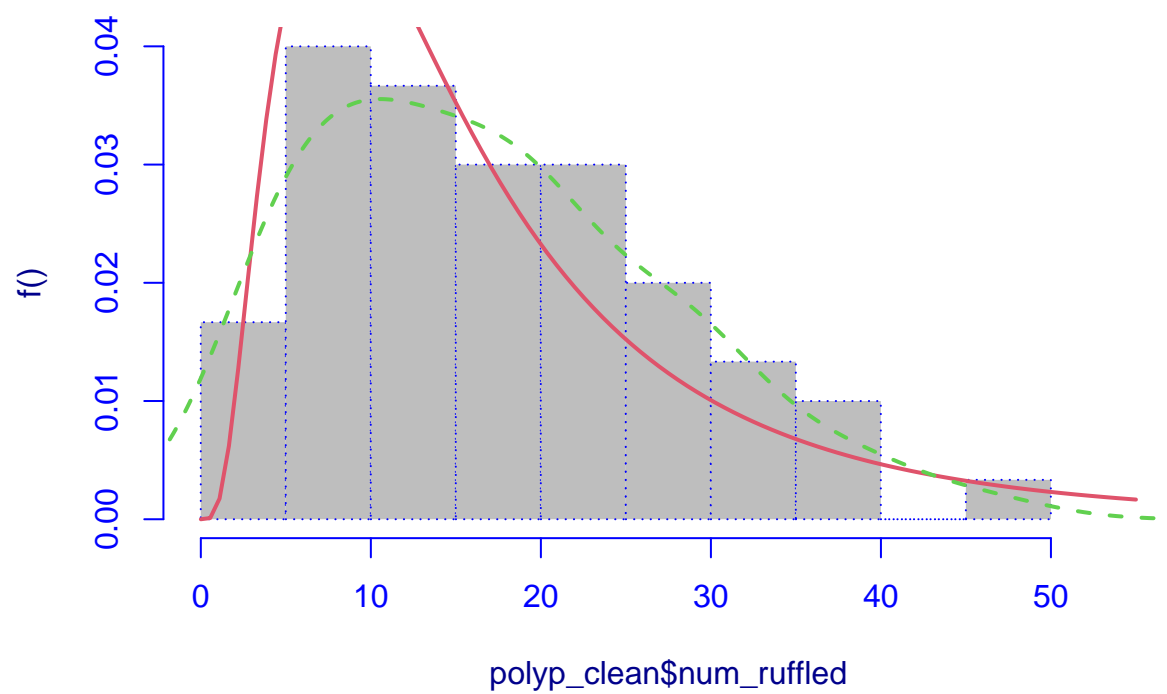
of the polyp_clean$num_ruffled and the fitted Negative Binomial type I
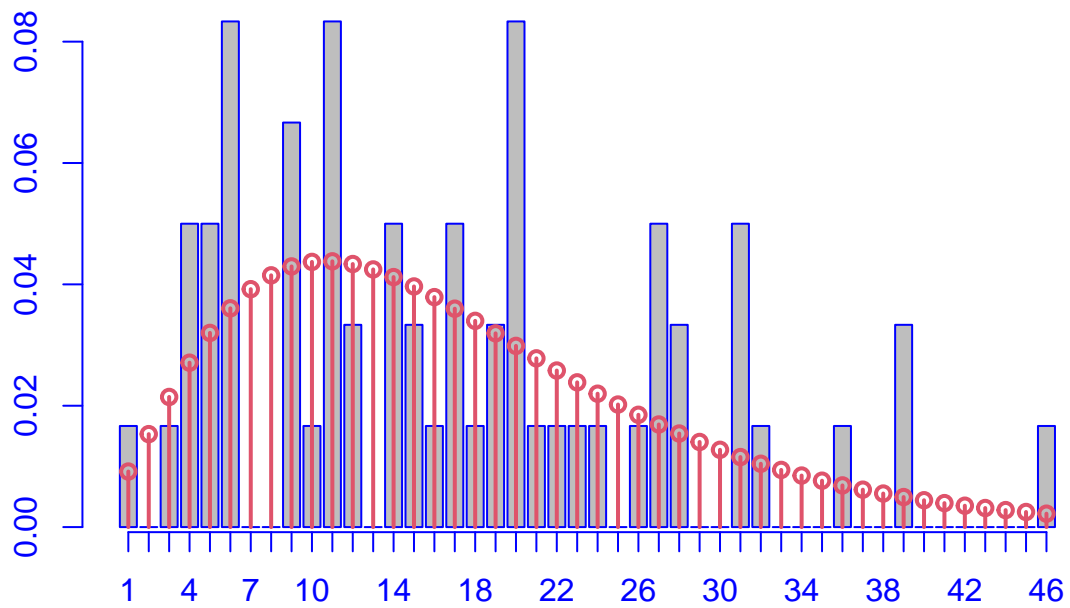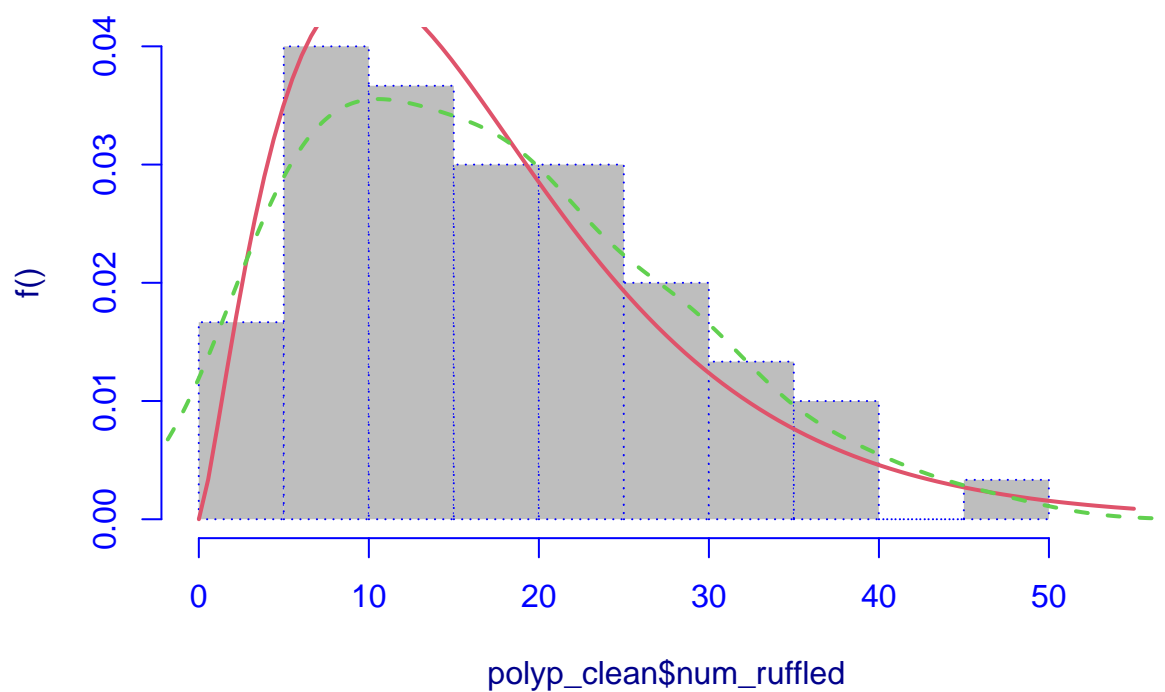


```
b_lNO <- histDist(polyp_clean$num_ruffled, "LOGNO", density = T)
```

The polyp_clean$num_ruffled and the fitted LOGNO distribution


```
b_GA <- histDist(polyp_clean$num_ruffled, "GA", density = T)
```
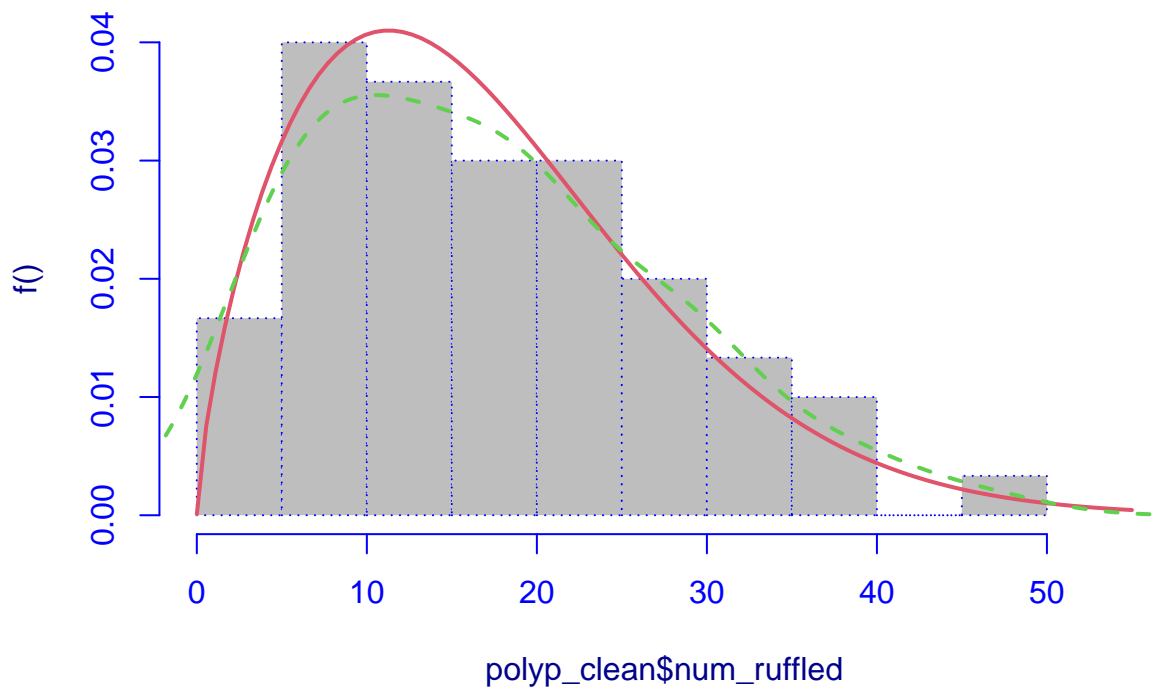
The polyp_clean$num_ruffled and the fitted GA distribution

x-axis: polyp_clean$num_ruffled
y-axis: f()

```
b_WEI <- histDist(polyp_clean$num_ruffled, "WEI", density = T)
```

The polyp_clean$num_ruffled and the fitted WEI distribution

```r
GAIC(b_lNO, b_GA, b_WEI, b_NB2)
```

```
##        df      AIC
## b_WEI   2 442.8371
## b_NB2   2 444.1095
## b_GA    2 444.1204
## b_lNO   2 451.8062
```

```r
# best fit: Weibull Distribution (AIC = 442.8371)
```

Creating The Ruffled Model

```r
mod_countwtotal_ruffled <- gamlss(num_ruffled ~ treatment * collection_day + re(random = ~1 |
    jar_code) + re(random = ~1 | total_num), family = WEI(), data = polyp_clean,
    control = gamlss.control(n.cyc = 60))
```

```
## GAMLSS-RS iteration 1: Global Deviance = 325.9507
## GAMLSS-RS iteration 2: Global Deviance = 319.6725
## GAMLSS-RS iteration 3: Global Deviance = 319.673
```

```
histDist(polyp_clean$num_ruffled, "WEI", density = T, main = "Count Polyp Ruffling Compared to Weibull I
      xlab = "Number Ruffled")
```

Count Polyp Ruffling Compared to Weibull Distribution
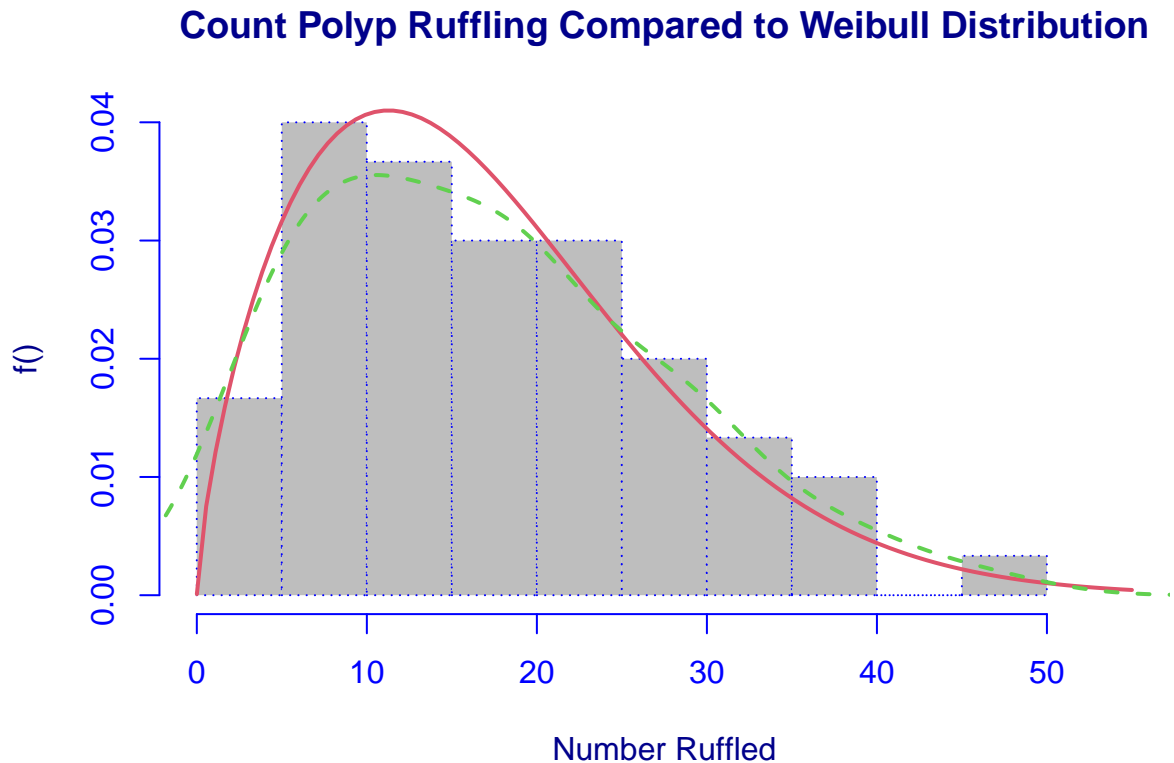

```
##
## Family:  c("WEI", "Weibull")
## Fitting method: "nlminb"
##
## Call:  gamlssML(formula = polyp_clean$num_ruffled, family = "WEI")
##
## Mu Coefficients:
## [1]  2.947
## Sigma Coefficients:
## [1]  0.529
##
##  Degrees of Freedom for the fit: 2 Residual Deg. of Freedom    58
## Global Deviance:     438.837
##             AIC:     442.837
##             SBC:     447.026
```

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

```
## ************************************************************
## Family:  c("WEI", "Weibull")
```

```
## 
## Call:  gamlss(formula = num_ruffled ~ treatment * collection_day +
##     re(random = ~1 | jar_code) + re(random = ~1 | total_num),
##     family = WEI(), data = polyp_clean, control = gamlss.control(n.cyc = 60))
## 
## Fitting method: RS() 
## 
## ---------------------------------------------------------------------
## Mu link function:  log
## Mu Coefficients:
##                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)                       1.231058   0.161918   7.603 1.25e-09 ***
## treatmentCaffeine                 0.471997   0.207627   2.273   0.0278 *
## treatmentEstradiol                0.103466   0.224071   0.462   0.6465
## treatmentCombination              0.503957   0.224694   2.243   0.0298 *
## collection_day                    0.442230   0.050638   8.733 2.84e-11 ***
## treatmentCaffeine:collection_day  -0.063279   0.064249  -0.985   0.3299
## treatmentEstradiol:collection_day -0.008946   0.070142  -0.128   0.8991
## treatmentCombination:collection_day -0.055425   0.070382  -0.787   0.4351
## ---
## 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)   1.5480     0.1053    14.7   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## ---------------------------------------------------------------------
## 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:  14.64746
##       Residual Deg. of Freedom:  45.35254
##                      at cycle:  3
## 
## Global Deviance:     319.673
##            AIC:      348.9679
##            SBC:      379.6448
## *******************************************************************
```