DS Project Stats

Lyubava Erko and Carys Hughes

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```r
library(FSA)
library(fGarch)
library(LambertW)
library(patchwork)
library(here)
library(tidyverse)
library(fitdistrplus)
library(gamlss)
library(tidyverse)
```

```r
# Reading in all the data files. We imported the complete data files and the
# top and bottom covered sections individually

lorazepam = read_csv(here("./Data/DS copepod data - Lorazepam acute.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

lorazepam_bottom = read_csv(here("./Data/DS copepod data - Lorazepam_bottom.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

lorazepam_top = read_csv(here("./Data/DS copepod data - Lorazepam_top.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

DPH_acute = read_csv(here("./Data/DS copepod data - DPH acute_right one.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

DPH_acute_bottom = read_csv(here("./Data/DS copepod data - DPH acute_bottom.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

DPH_acute_top = read_csv(here("./Data/DS copepod data - DPH acute_top.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

DPH_chronic = read_csv(here("./Data/DS copepod data - DPH chronic.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

DPH_chronic_top = read_csv(here("./Data/DS copepod data - DPH chronic_top.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

DPH_chronic_bottom = read_csv(here("./Data/DS copepod data - DPH chronic_bottom.csv")) %>%
    mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))
```

```r
# Graphs separating the proportion of copepods in the light when the top or
# bottom was covered for all treatments.

p1 = ggplot(DPH_chronic_bottom, aes(x = time_min, y = proportion, fill = treatment),
    xlab = "Time (min)", ylab = "Proportion of copepods") + geom_boxplot(alpha = 0.8) +
    theme_classic() + labs(x = "Time (min)", y = "Proportion of copepods") + labs(fill = "Treatment") +
    ylim(0, 0.8) + scale_fill_manual(labels = c("Control", "Environmentally relevant",
    "High"), values = c("lightcyan", "palegreen3", "red4")) + theme(axis.title = element_text(size = 19)

p2 = ggplot(DPH_chronic_top, aes(x = time_min, y = proportion, fill = treatment),
    xlab = "Time (min)", ylab = "Proportion of copepods") + geom_boxplot(alpha = 0.8) +
    theme_classic() + labs(x = "Time (min)", y = "Proportion of copepods") + labs(fill = "Treatment") +
    ylim(0, 0.8) + scale_fill_manual(labels = c("Control", "Environmentally relevant",
    "High"), values = c("lightcyan", "palegreen3", "red4")) + theme(axis.title = element_text(size = 19)

p3 = ggplot(DPH_acute_bottom, aes(x = time_min, y = proportion, fill = treatment),
    xlab = "Time (min)", ylab = "Proportion of copepods") + geom_boxplot(alpha = 0.8) +
    theme_classic() + labs(x = "Time (min)", y = "Proportion of copepods") + labs(fill = "Treatment") +
    ylim(0, 0.4) + scale_fill_manual(labels = c("Control", "Environmentally relevant",
    "High"), values = c("lightcyan", "palegreen3", "red4")) + theme(axis.title = element_text(size = 19)

p4 = ggplot(DPH_acute_top, aes(x = time_min, y = proportion, fill = treatment), xlab = "Time (min)",
    ylab = "Proportion of copepods") + geom_boxplot(alpha = 0.8) + theme_classic() +
    labs(x = "Time (min)", y = "Proportion of copepods") + labs(fill = "Treatment") +
    ylim(0, 0.4) + scale_fill_manual(labels = c("Control", "Environmentally relevant",
    "High"), values = c("lightcyan", "palegreen3", "red4")) + theme(axis.title = element_text(size = 19)

p5 = ggplot(lorazepam_bottom, aes(x = time_min, y = proportion, fill = treatment),
    xlab = "Time (min)", ylab = "Proportion of copepods") + geom_boxplot(alpha = 0.8) +
    theme_classic() + labs(x = "Time (min)", y = "Proportion of copepods") + labs(fill = "Treatment") +
    ylim(0, 0.8) + scale_fill_manual(labels = c("Control", "Environmentally relevant",
    "High"), values = c("lightcyan", "palegreen3", "red4")) + theme(axis.title = element_text(size = 19)

p6 = ggplot(lorazepam_top, aes(x = time_min, y = proportion, fill = treatment), xlab = "Time (min)",
    ylab = "Proportion of copepods") + geom_boxplot(alpha = 0.8) + theme_classic() +
    labs(x = "Time (min)", y = "Proportion of copepods") + labs(fill = "Treatment") +
    ylim(0, 0.8) + scale_fill_manual(labels = c("Control", "Environmentally relevant",
    "High"), values = c("lightcyan", "palegreen3", "red4")) + theme(axis.title = element_text(size = 19)

# Plotting the figures together. These are the figures used in our report

# DPH Chronic
p1 | p2
```
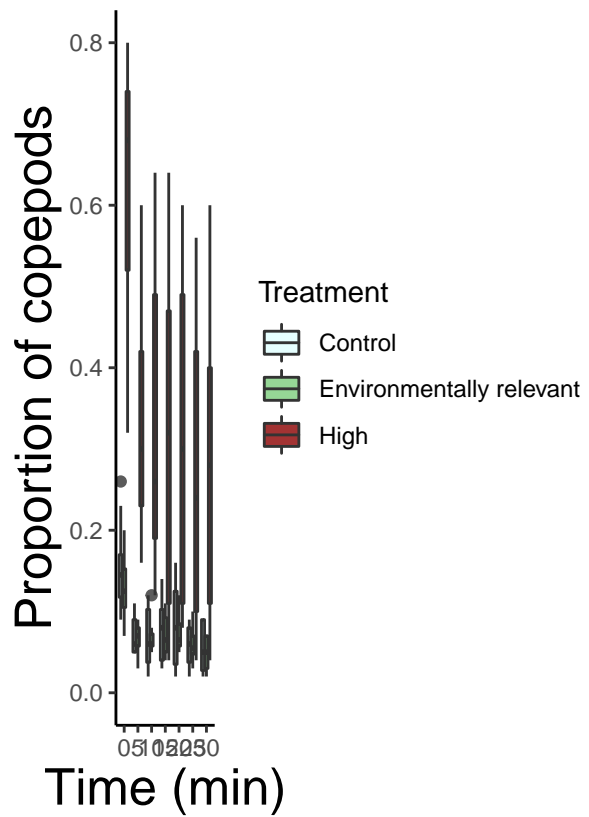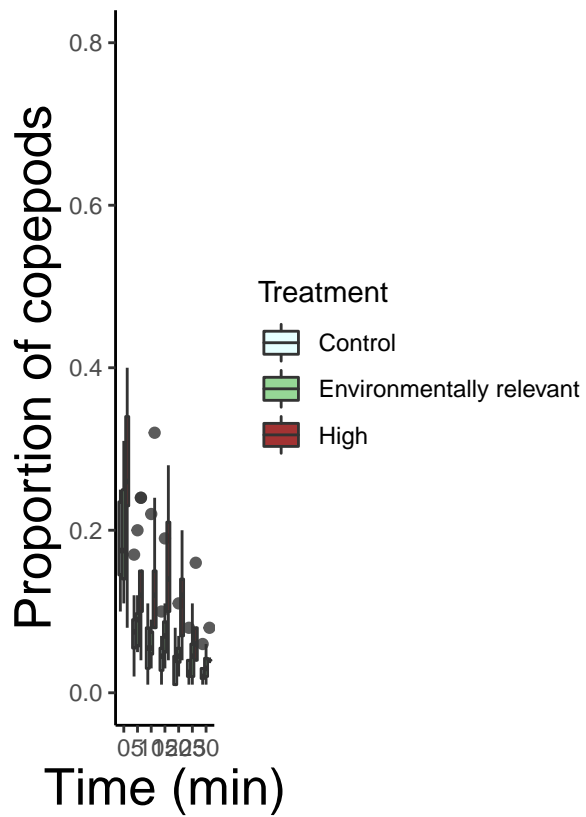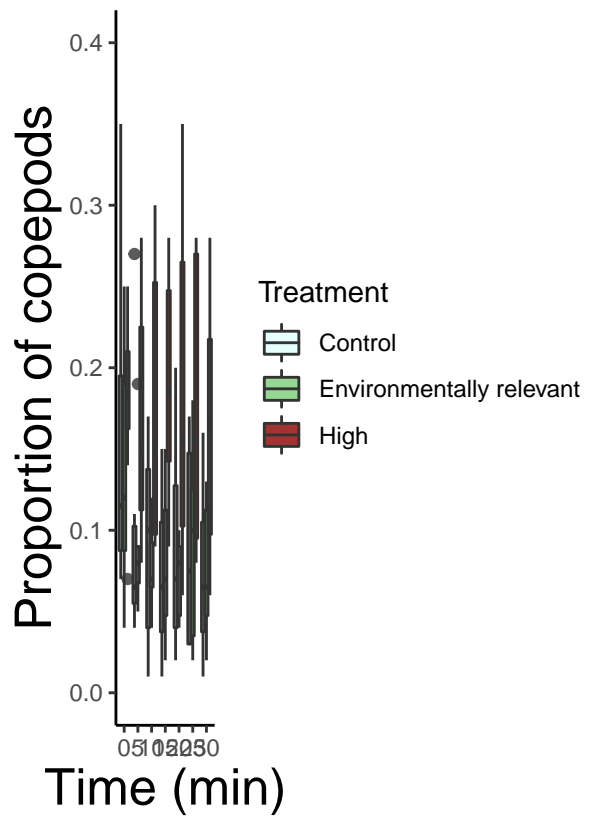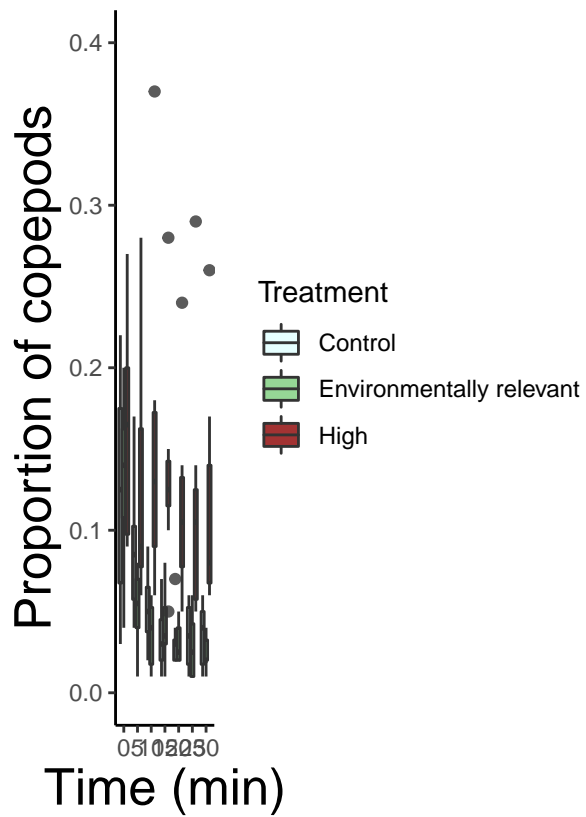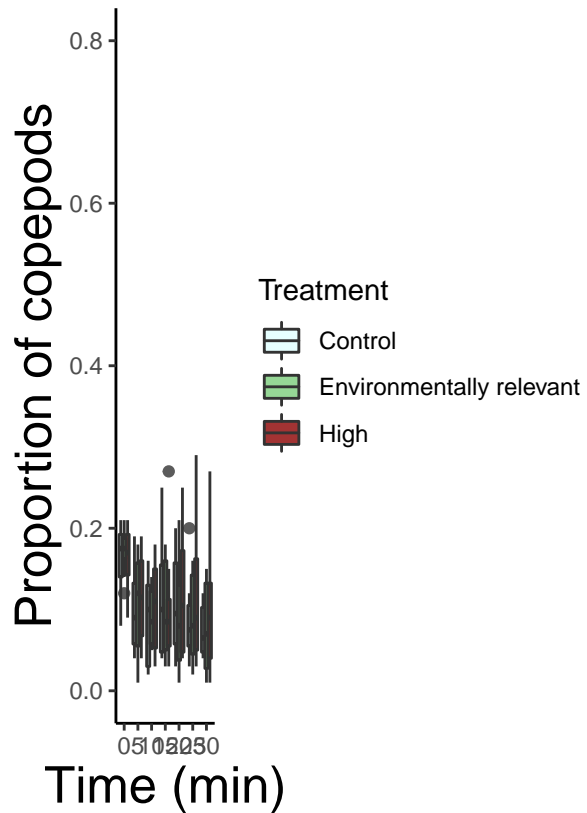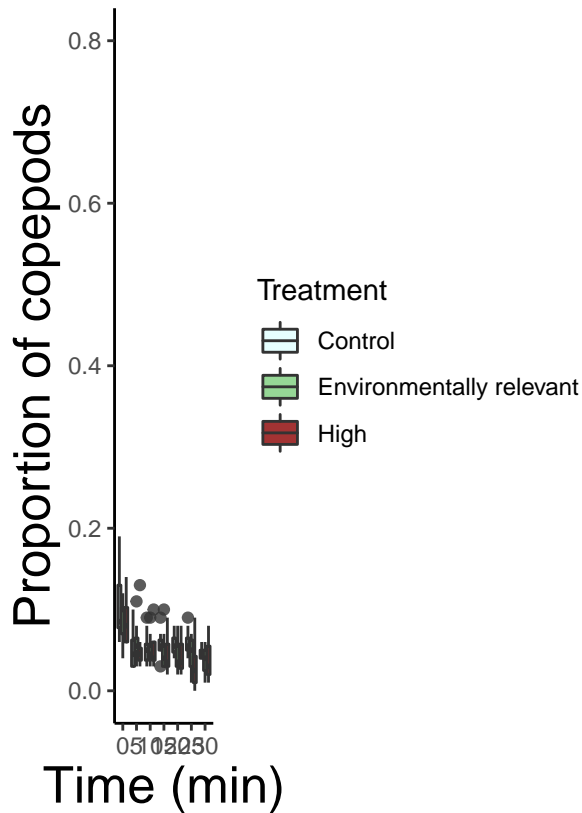
```
# DPH acute
p3 | p4
```

```
# Lorazepam acute
p5 | p6
```

```
# Initial tests for the chronic DPH exposure
shapiro.test(DPH_chronic$proportion)   #p-value < 2.2e-16 (violates assumption)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  DPH_chronic$proportion
## W = 0.69469, p-value < 2.2e-16
```

```
bartlett.test(proportion ~ treatment, data = DPH_chronic)   #p-value < 2.2e-16 (violates)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  proportion by treatment
## Bartlett's K-squared = 264.7, df = 2, p-value < 2.2e-16
```

```
kruskal.test(proportion ~ treatment, data = DPH_chronic)   #p-value = 0.0006316
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  proportion by treatment
## Kruskal-Wallis chi-squared = 75.801, df = 2, p-value < 2.2e-16
```

```
dunnTest(proportion ~ treatment, data = DPH_chronic)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison

##   p-values adjusted with the Holm method.

##          Comparison         Z      P.unadj        P.adj
## 1 control - env_rel -1.012700 3.112035e-01 3.112035e-01
## 2    control - high -7.995091 1.294782e-15 3.884347e-15
## 3    env_rel - high -6.982391 2.901983e-12 5.803965e-12
```

```
# Initial tests for the acute DPH exposure
shapiro.test(DPH_acute$proportion)  #p-value = 1.958e-07 (violates assumption)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  DPH_acute$proportion
## W = 0.88917, p-value = 6.828e-15
```

```
bartlett.test(proportion ~ treatment, data = DPH_acute)  #p-value = 6.849e-06 (violates)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  proportion by treatment
## Bartlett's K-squared = 21.55, df = 2, p-value = 2.091e-05
```

```
kruskal.test(proportion ~ treatment, data = DPH_acute)  #p-value = 0.0006316
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  proportion by treatment
## Kruskal-Wallis chi-squared = 92.181, df = 2, p-value < 2.2e-16
```

```
dunnTest(proportion ~ treatment, data = DPH_acute)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison

##   p-values adjusted with the Holm method.

##          Comparison         Z      P.unadj        P.adj
## 1 control - env_rel  0.6059564 5.445437e-01 5.445437e-01
## 2    control - high -7.9952488 1.293125e-15 2.586249e-15
## 3    env_rel - high -8.6012052 7.888327e-18 2.366498e-17
```

```r
# Initial tests for the lorazepam exposure
shapiro.test(lorazepam$proportion)  # p-value = 4.922e-15, (violates)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  lorazepam$proportion
## W = 0.8872, p-value = 4.922e-15
```

```r
bartlett.test(proportion ~ treatment, data = lorazepam)  #p-value = 0.03296
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  proportion by treatment
## Bartlett's K-squared = 6.8247, df = 2, p-value = 0.03296
```

```r
kruskal.test(proportion ~ treatment, data = lorazepam)  #p-value = 0.4573
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  proportion by treatment
## Kruskal-Wallis chi-squared = 1.5647, df = 2, p-value = 0.4573
```

```r
dunnTest(proportion ~ treatment, data = lorazepam)
```

```
## Dunn (1964) Kruskal-Wallis multiple comparison

##   p-values adjusted with the Holm method.

##          Comparison          Z   P.unadj      P.adj
## 1 control - env_rel  1.1651765 0.2439475 0.7318426
## 2    control - high  0.9766769 0.3287291 0.6574583
## 3    env_rel - high -0.1884997 0.8504850 0.8504850
```
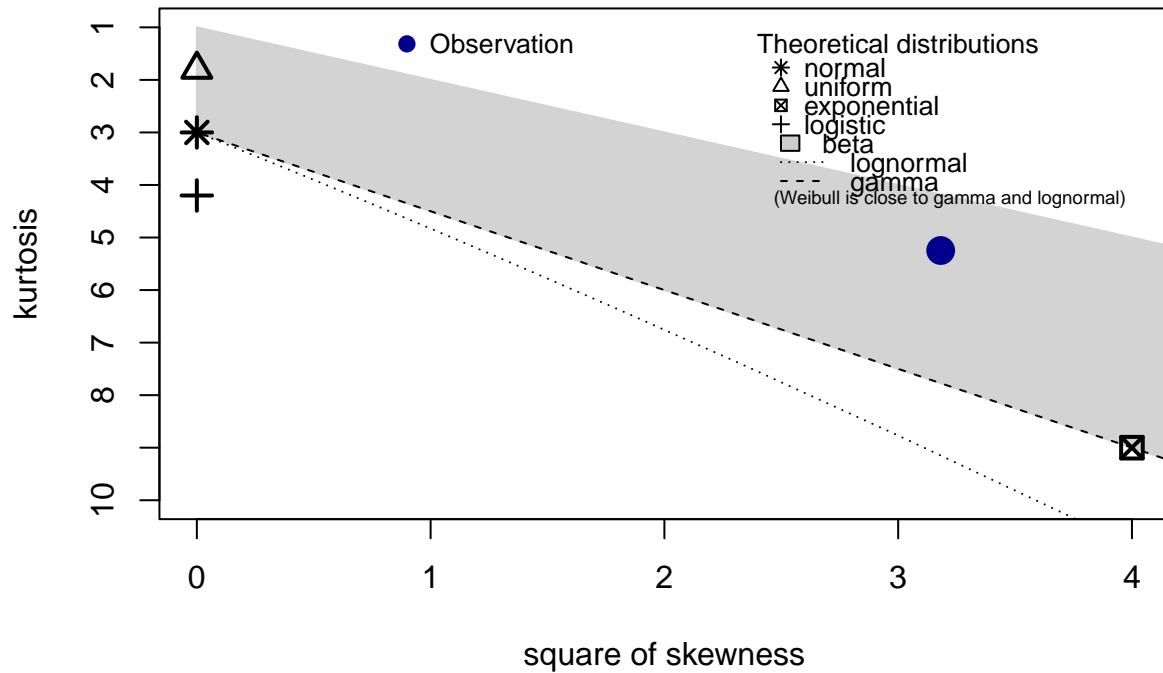
```r
# Testing for the best distribution fit for DPH chronic exposure when the top
# section was covered and running the model using the backwards selection
descdist(DPH_chronic_top$proportion)
```

Cullen and Frey graph


```
## summary statistics
## ------
## min:  0.02    max:  0.84
## median:  0.09
## mean:  0.17
## estimated sd:  0.1875432
## estimated skewness:  1.783793
## estimated kurtosis:  5.247405
```

```
fit.gamma <- fitdist(DPH_chronic_top$proportion, "gamma")
fit.beta <- fitdist(DPH_chronic_top$proportion, "beta")
plot(fit.gamma)
```
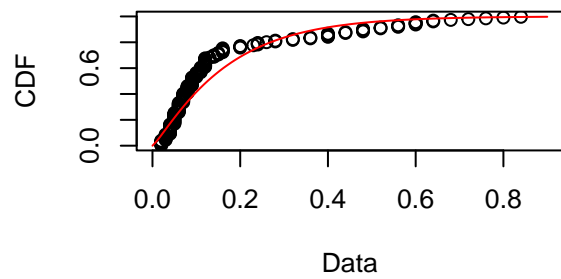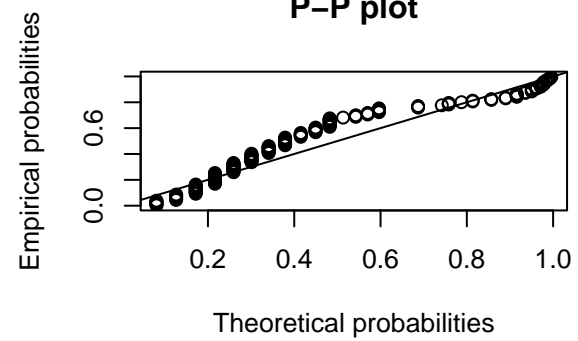
Empirical and theoretical dens.

Q−Q plot

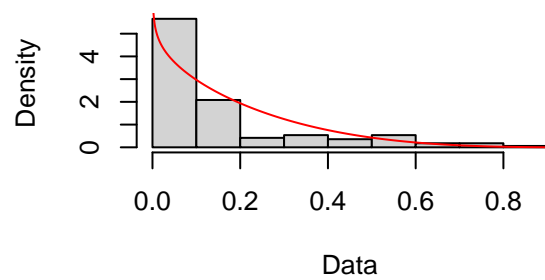## Empirical and theoretical CDFs
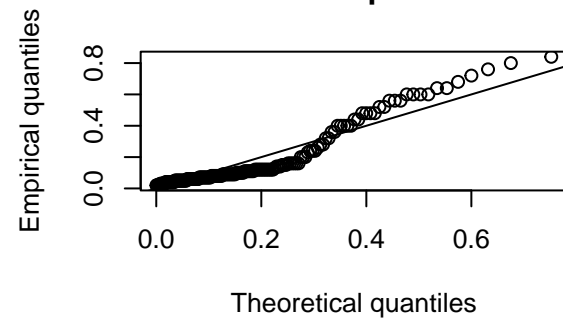

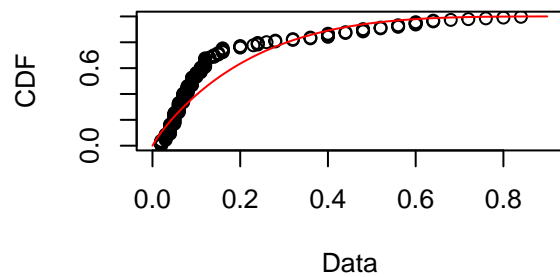## P−P plot


```
plot(fit.beta)
```
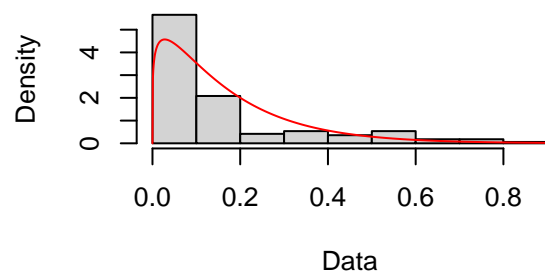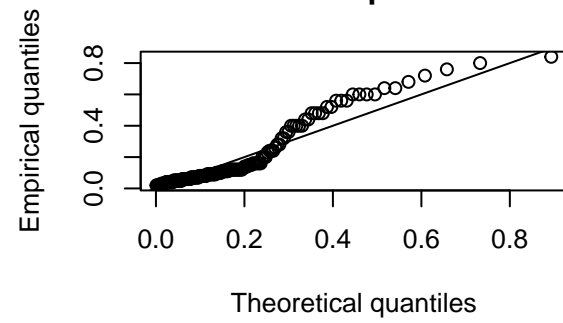
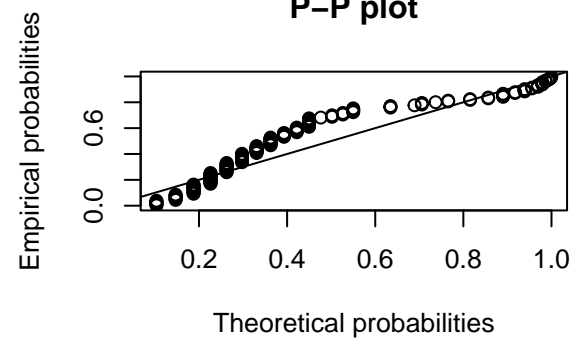## Empirical and theoretical dens.

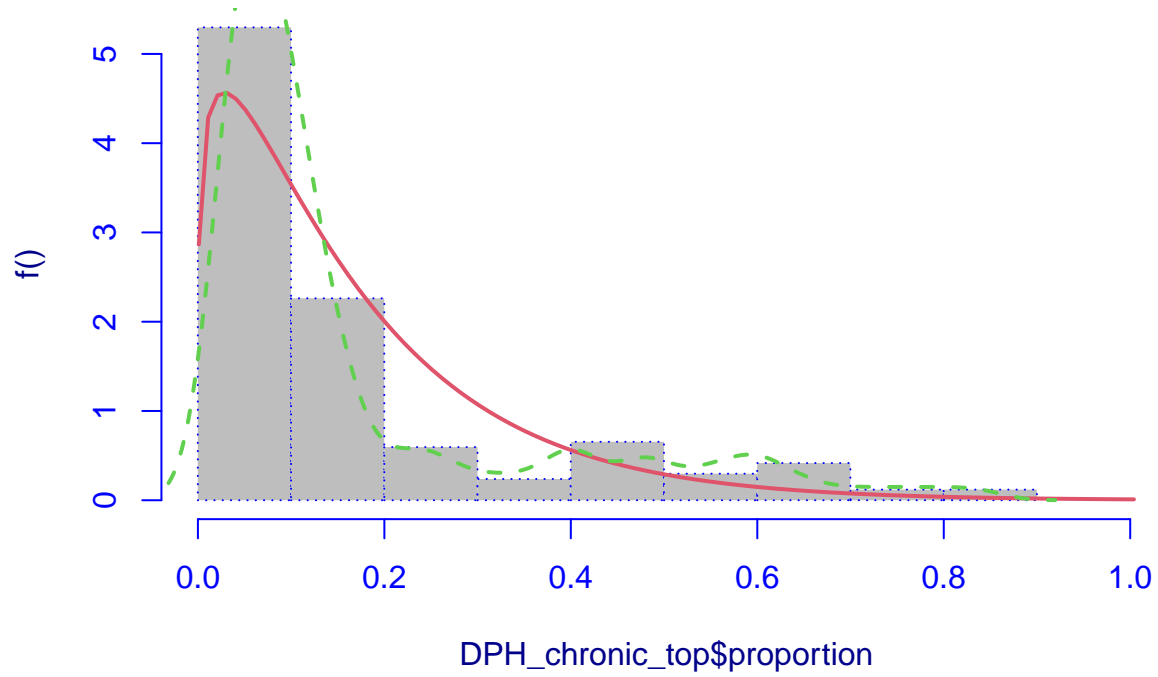## Q–Q plot

Empirical and theoretical CDFs

P–P plot


```r
mGA <- histDist(DPH_chronic_top$proportion, "GA", density = T, main = "Gamma")
```

Gamma

```
mBE <- histDist(DPH_chronic_top$proportion, "BE", density = T, main = "Beta")
```

Beta

DPH_chronic_top$proportion
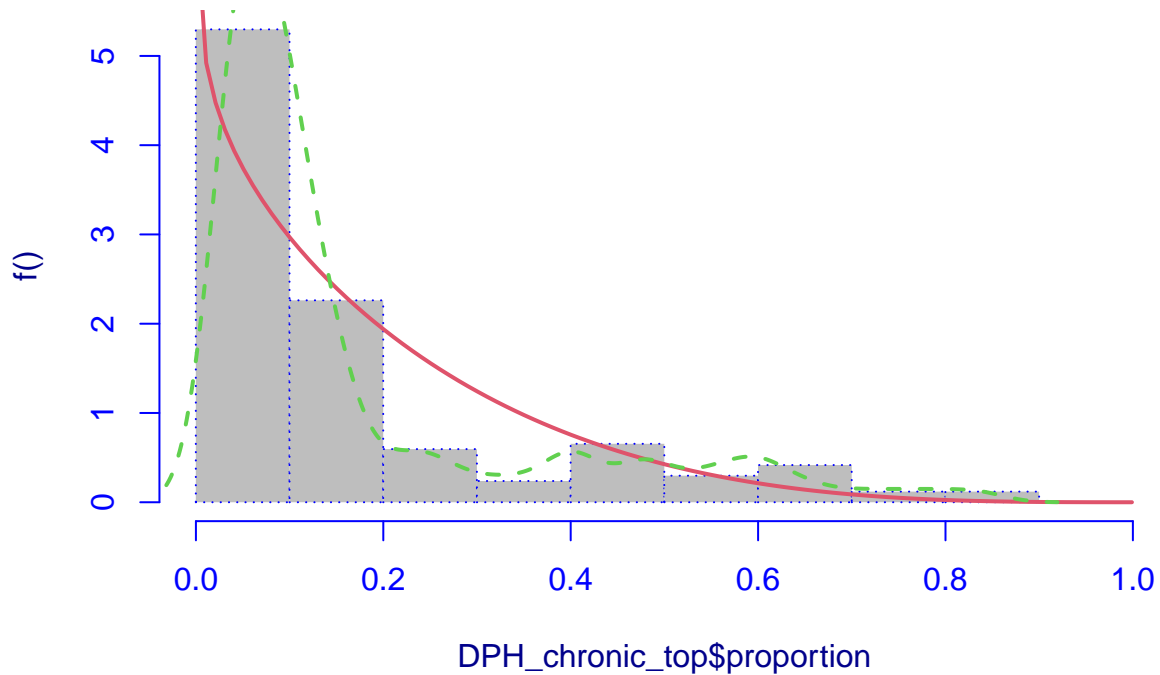
```
GAIC(mGA, mBE)
```

```
##      df        AIC
## mGA  2 -258.6090
## mBE  2 -236.8981
```

```
chronic_top.mod <- glm(proportion ~ treatment + time_min + treatment:time_min, family = Gamma(link = "i
    data = DPH_chronic_top)
```

```
backward.chronic_top <- stepAIC(chronic_top.mod, direction = "backward", trace = F)
```

```
formula(backward.chronic_top)
```

```
## proportion ~ treatment + time_min + treatment:time_min
```

```
backward.chronic_top$anova
```

```
## Stepwise Model Path
## Analysis of Deviance Table
##
## Initial Model:
## proportion ~ treatment + time_min + treatment:time_min
##
## Final Model:
```

```
## proportion ~ treatment + time_min + treatment:time_min
##
##
##   Step Df Deviance Resid. Df Resid. Dev       AIC
## 1                        147    48.9209 -432.5897
```

summary(backward.chronic_top)

```
##
## Call:
## glm(formula = proportion ~ treatment + time_min + treatment:time_min,
##     family = Gamma(link = "inverse"), data = DPH_chronic_top)
##
## Deviance Residuals:
##      Min       1Q    Median        3Q       Max
## -1.54316  -0.45247  -0.08589   0.36242   0.89628
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  6.40000    1.16585   5.490 1.72e-07 ***
## treatmentenv_rel             1.36699    1.83331   0.746  0.45708
## treatmenthigh               -4.84961    1.19957  -4.043 8.49e-05 ***
## time_min5                    7.88571    2.85156   2.765  0.00641 **
## time_min10                   8.41481    2.93978   2.862  0.00482 **
## time_min15                   6.50323    2.62375   2.479  0.01432 *
## time_min20                   5.72121    2.49693   2.291  0.02337 *
## time_min25                  10.99130    3.37577   3.256  0.00140 **
## time_min30                  11.78182    3.51127   3.355  0.00101 **
## treatmentenv_rel:time_min5  -0.55836    4.20639  -0.133  0.89458
## treatmenthigh:time_min5     -6.53755    2.91375  -2.244  0.02635 *
## treatmentenv_rel:time_min10 -1.63635    4.20295  -0.389  0.69759
## treatmenthigh:time_min10    -6.93490    3.00446  -2.308  0.02238 *
## treatmentenv_rel:time_min15 -0.23513    3.92715  -0.060  0.95234
## treatmenthigh:time_min15    -4.87901    2.70153  -1.806  0.07296 .
## treatmentenv_rel:time_min20  0.07112    3.78649   0.019  0.98504
## treatmenthigh:time_min20    -4.04579    2.58065  -1.568  0.11909
## treatmentenv_rel:time_min25 -2.43176    4.71624  -0.516  0.60690
## treatmenthigh:time_min25    -8.76811    3.45661  -2.537  0.01224 *
## treatmentenv_rel:time_min30  0.96401    5.31918   0.181  0.85643
## treatmenthigh:time_min30    -9.69584    3.58435  -2.705  0.00764 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.265469)
##
##     Null deviance: 158.835  on 167  degrees of freedom
## Residual deviance:  48.921  on 147  degrees of freedom
## AIC: -432.59
##
## Number of Fisher Scoring iterations: 6
```

Testing for the best distribution fit for DPH chronic exposure when the
bottom section was covered and running the model using the backwards

```
# selection
descdist(DPH_chronic_bottom$proportion)
```

Cullen and Frey graph


```
## summary statistics
## ------
## min:  0.01   max:  0.4
## median:  0.06
## mean:  0.09327381
## estimated sd:  0.08135453
## estimated skewness:  1.518791
## estimated kurtosis:  5.023683
```
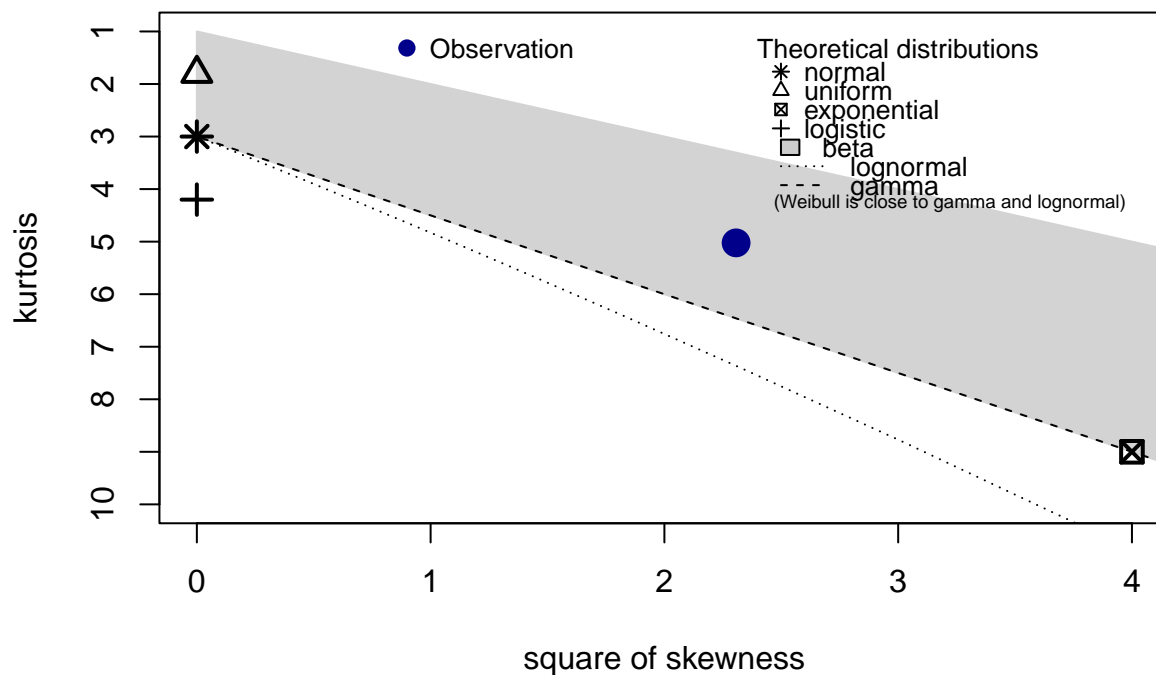
```
fit.gamma <- fitdist(DPH_chronic_bottom$proportion, "gamma")
fit.beta <- fitdist(DPH_chronic_bottom$proportion, "beta")
plot(fit.gamma)
```

Empirical and theoretical dens.

Q–Q plot

Empirical and theoretical CDFs

P–P plot


```
plot(fit.beta)
```

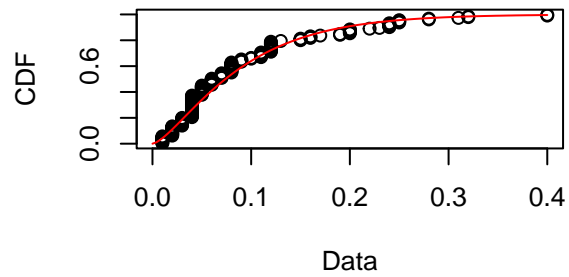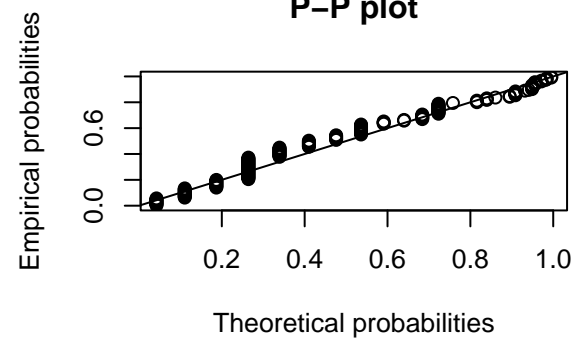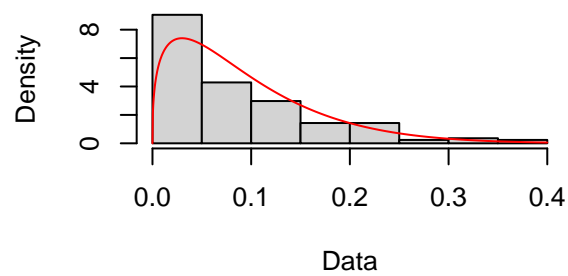## Empirical and theoretical dens.

Q–Q plot

Empirical and theoretical CDFs

P–P plot


```r
mGA <- histDist(DPH_chronic_bottom$proportion, "GA", density = T, main = "Gamma")
```

Gamma

DPH_chronic_bottom$proportion

```
mBE <- histDist(DPH_chronic_bottom$proportion, "BE", density = T, main = "Beta")
```
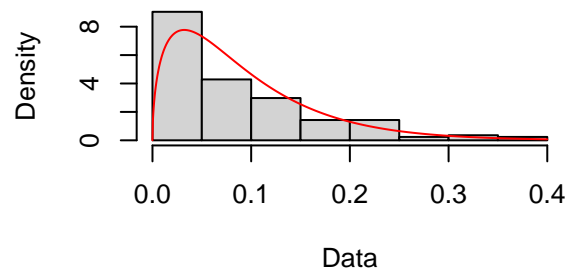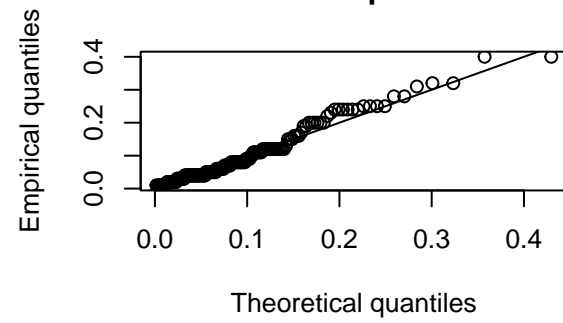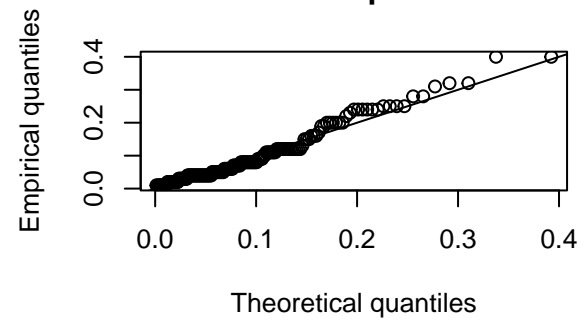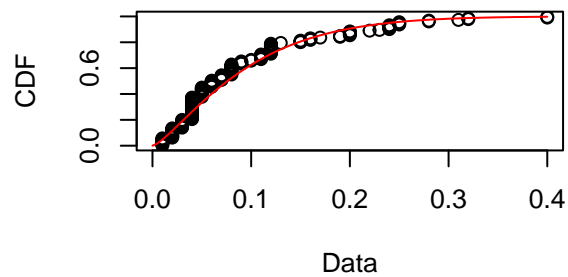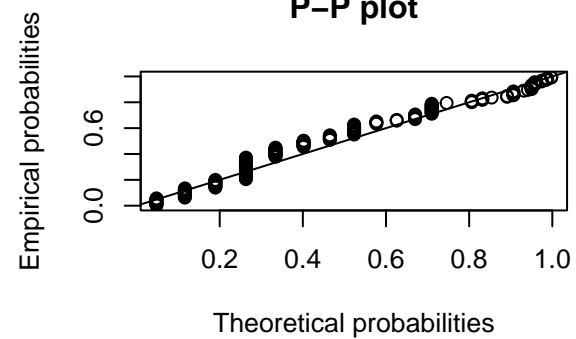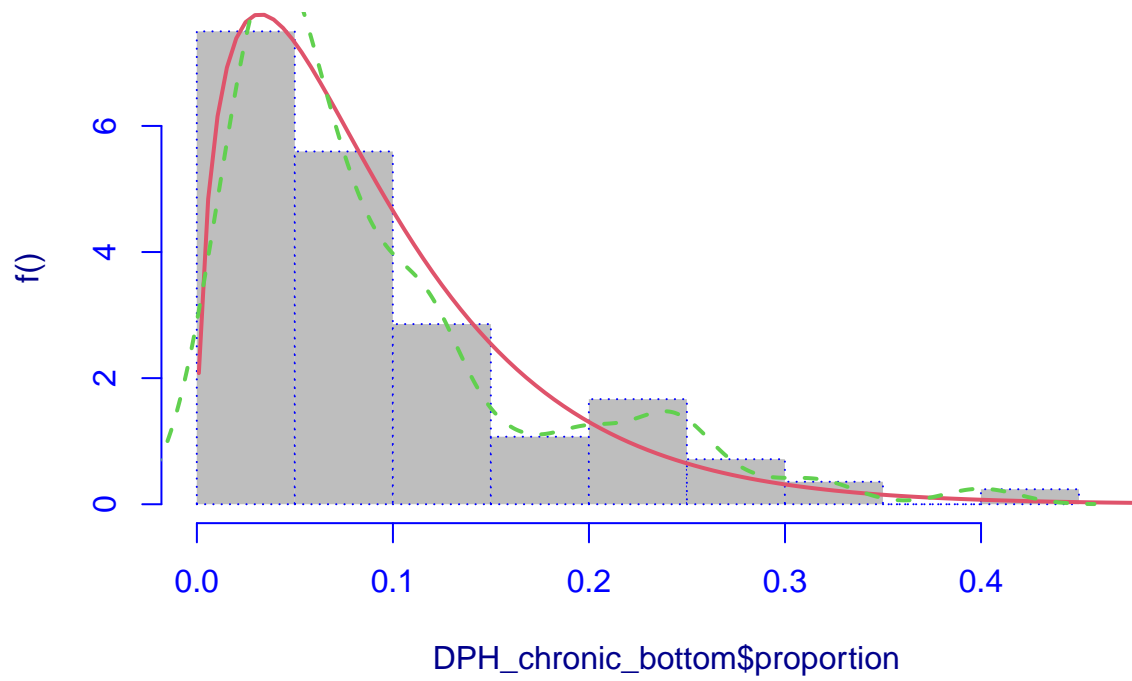
Beta

DPH_chronic_bottom$proportion
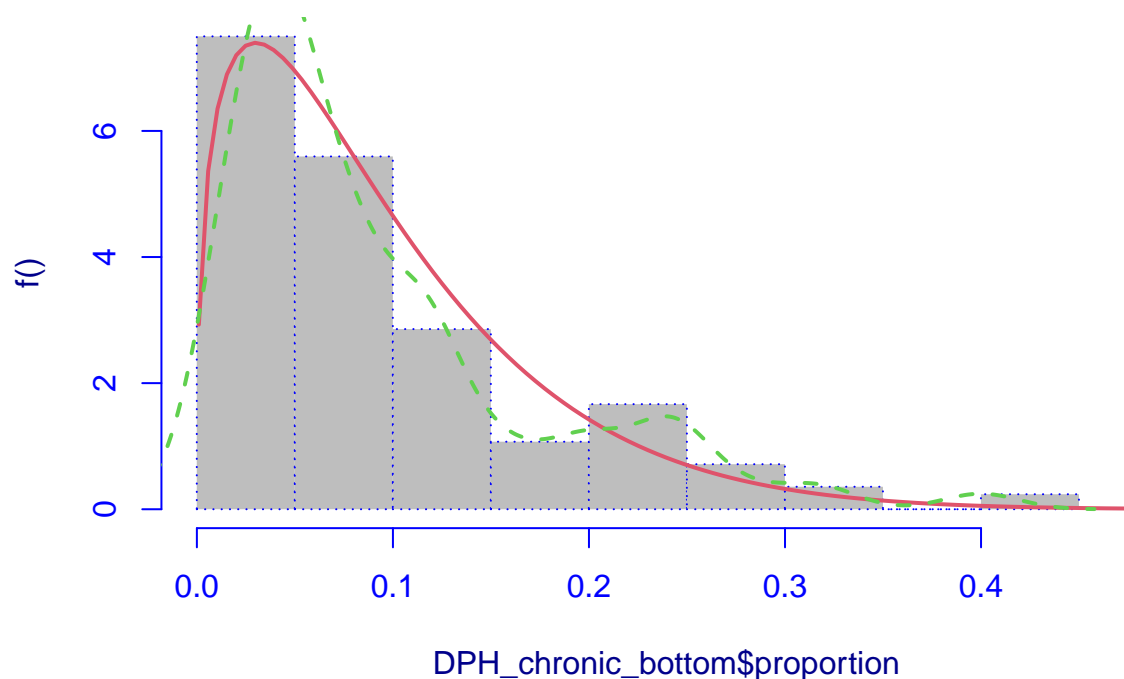
```
GAIC(mGA, mBE)
```

```
##     df        AIC
## mGA  2 -473.2265
## mBE  2 -469.8868
```

```
chronic_bottom.mod <- glm(proportion ~ treatment + time_min + treatment:time_min,
    family = Gamma(link = "inverse"), data = DPH_chronic_bottom)

backward.chronic_bottom <- stepAIC(chronic_bottom.mod, direction = "backward", trace = F)

formula(backward.chronic_bottom)
```

```
## proportion ~ treatment + time_min + treatment:time_min
```

```
backward.chronic_bottom$anova
```

```
## Stepwise Model Path
## Analysis of Deviance Table
##
## Initial Model:
## proportion ~ treatment + time_min + treatment:time_min
##
## Final Model:
```

```
## proportion ~ treatment + time_min + treatment:time_min
##
##
##   Step Df Deviance Resid. Df Resid. Dev       AIC
## 1                       147     50.7582 -590.5576
```

```
summary(backward.chronic_bottom)
```

```
##
## Call:
## glm(formula = proportion ~ treatment + time_min + treatment:time_min,
##     family = Gamma(link = "inverse"), data = DPH_chronic_bottom)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3718  -0.4492  -0.1155   0.2151   1.2850
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   5.4795     1.1197   4.894 2.57e-06 ***
## treatmentenv_rel             -0.2507     1.5476  -0.162 0.871540
## treatmenthigh                -1.7757     1.3514  -1.314 0.190904
## time_min5                     7.0205     2.7888   2.517 0.012896 *
## time_min10                   11.5418     3.6539   3.159 0.001923 **
## time_min15                   16.1422     4.5578   3.542 0.000533 ***
## time_min20                   22.1068     5.7470   3.847 0.000178 ***
## time_min25                   25.2898     6.3862   3.960 0.000116 ***
## time_min30                   34.5205     8.2498   4.184 4.90e-05 ***
## treatmentenv_rel:time_min5   -1.5826     3.6973  -0.428 0.669238
## treatmenthigh:time_min5      -3.0319     3.2895  -0.922 0.358200
## treatmentenv_rel:time_min10  -3.6558     4.6555  -0.785 0.433560
## treatmenthigh:time_min10     -8.3490     3.9887  -2.093 0.038051 *
## treatmentenv_rel:time_min15  -9.0632     5.3141  -1.706 0.090213 .
## treatmenthigh:time_min15    -13.1792     4.8168  -2.736 0.006984 **
## treatmentenv_rel:time_min20  -7.8233     7.0758  -1.106 0.270685
## treatmenthigh:time_min20    -17.1148     6.0629  -2.823 0.005419 **
## treatmentenv_rel:time_min25  -8.8969     7.8387  -1.135 0.258223
## treatmenthigh:time_min25    -14.7078     7.0624  -2.083 0.039026 *
## treatmentenv_rel:time_min30  -8.9801    10.4275  -0.861 0.390533
## treatmenthigh:time_min30    -16.0020     9.4473  -1.694 0.092418 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.3340313)
##
##     Null deviance: 121.613  on 167  degrees of freedom
## Residual deviance:  50.758  on 147  degrees of freedom
## AIC: -590.56
##
## Number of Fisher Scoring iterations: 6
```

```
# Testing for the best distribution fit for DPH acute exposure when the top
# section was covered and running the model using the backwards selection
descdist(DPH_acute_top$proportion)
```

Cullen and Frey graph


```
## summary statistics
## ------
## min:  0.01    max:  0.35
## median:  0.1
## mean:  0.1198214
## estimated sd:  0.07745559
## estimated skewness:  0.8860857
## estimated kurtosis:  3.041897
```

```
fit.gamma <- fitdist(DPH_acute_top$proportion, "gamma")
fit.beta <- fitdist(DPH_acute_top$proportion, "beta")
plot(fit.gamma)
```

Empirical and theoretical dens.
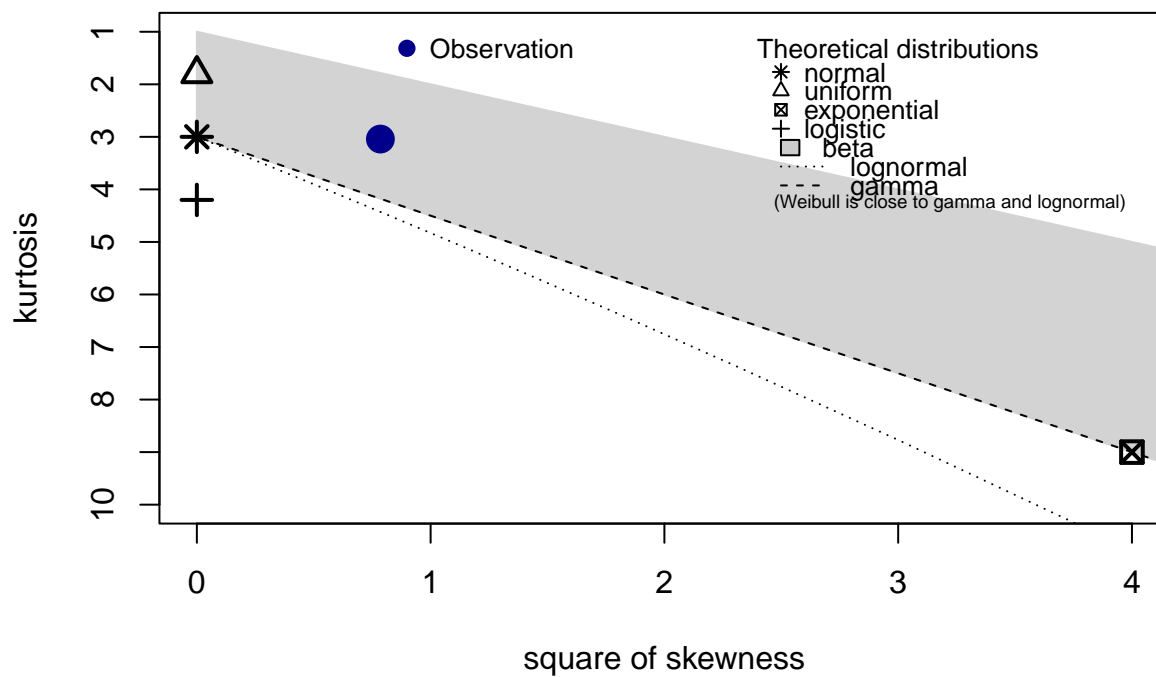
Q–Q plot

Empirical and theoretical CDFs

P–P plot

```
plot(fit.beta)
```

Empirical and theoretical dens.

Q–Q plot

Empirical and theoretical CDFs

P–P plot


```r
mGA <- histDist(DPH_acute_top$proportion, "GA", density = T, main = "Gamma")
```

Gamma

f()

DPH_acute_top$proportion

```
mBE <- histDist(DPH_acute_top$proportion, "BE", density = T, main = "Beta")
```
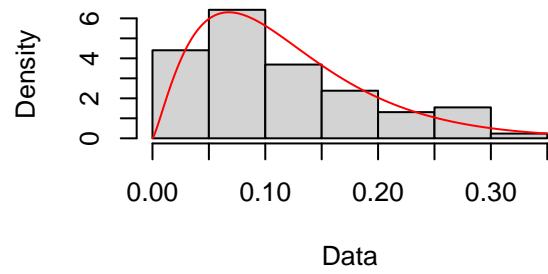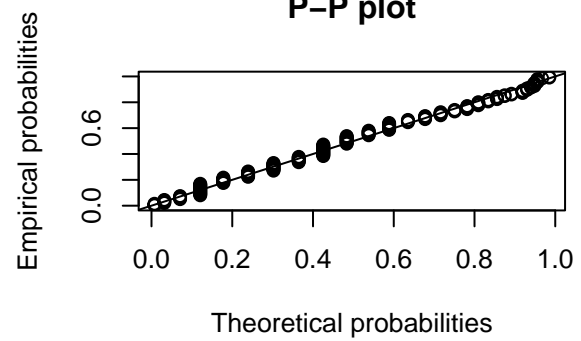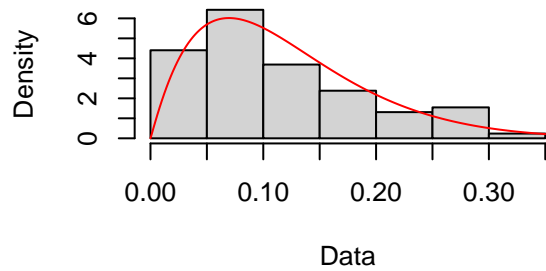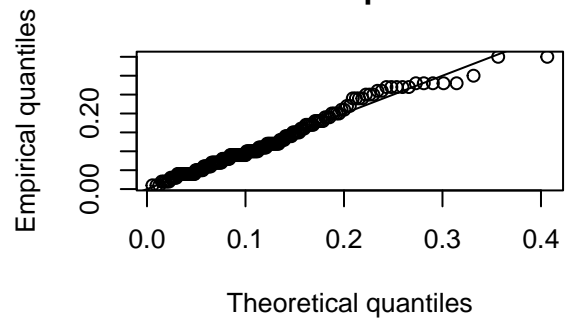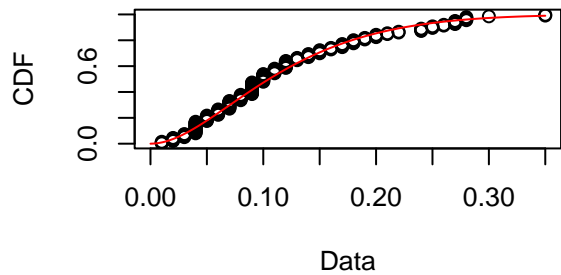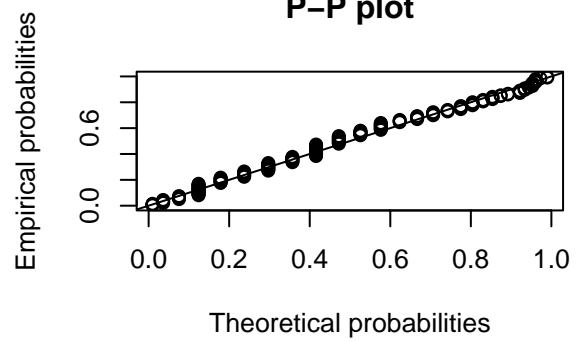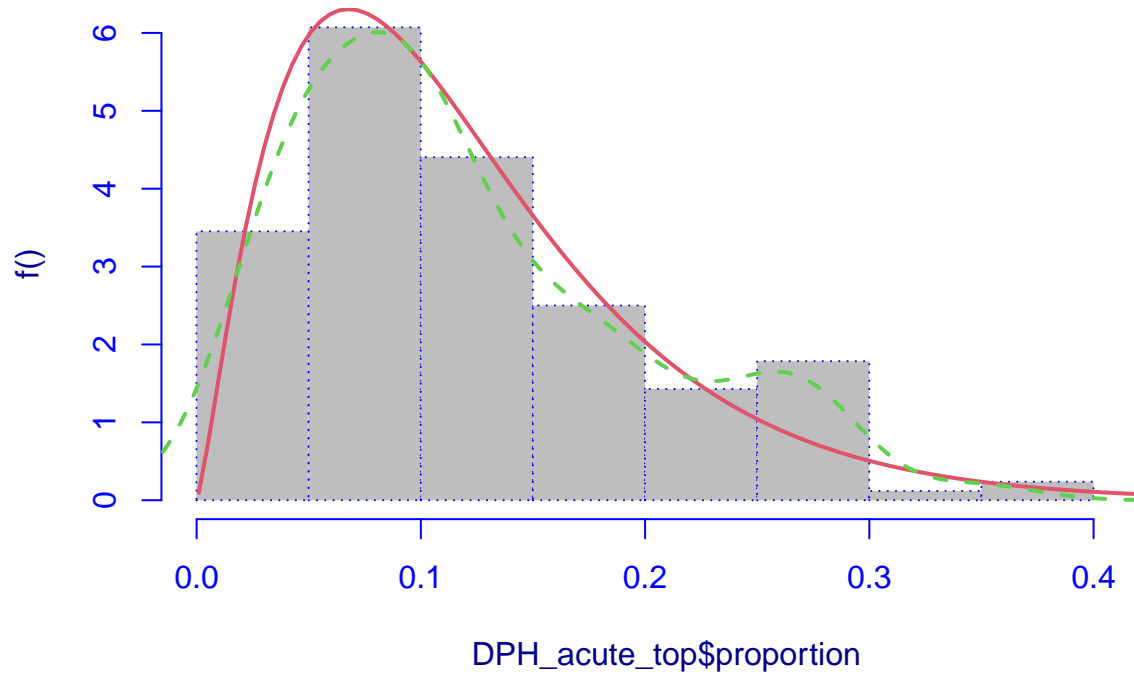
Beta
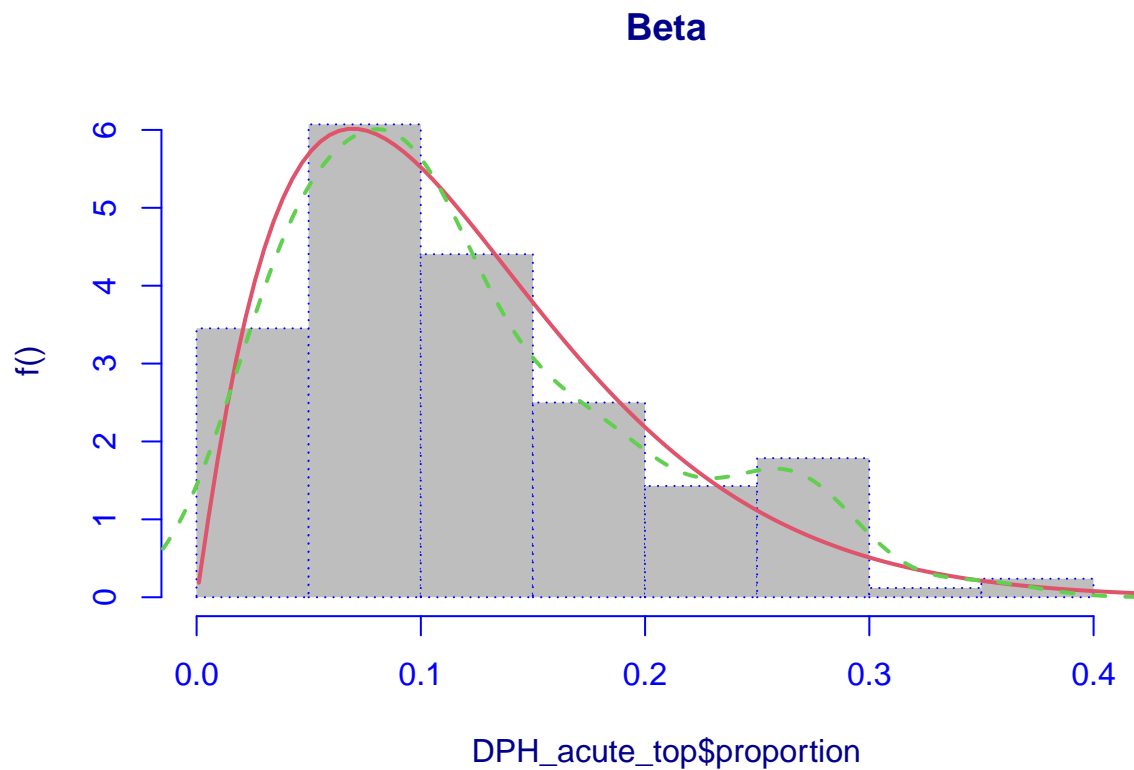

```
GAIC(mGA, mBE)
```

```
##      df       AIC
## mBE  2 -426.8298
## mGA  2 -426.1819
```

```
acute_top.mod <- glm(proportion ~ treatment + time_min + treatment:time_min, family = Gamma(link = "inve
    data = DPH_acute_top)
```

```
backward.acute_top <- stepAIC(acute_top.mod, direction = "backward", trace = F)
```

```
formula(backward.acute_top)
```

```
## proportion ~ treatment
```

```
backward.acute_top$anova
```

```
## Stepwise Model Path
## Analysis of Deviance Table
##
## Initial Model:
## proportion ~ treatment + time_min + treatment:time_min
##
## Final Model:
```

```
## proportion ~ treatment
##
##
##                     Step Df Deviance Resid. Df Resid. Dev       AIC
## 1                                          147    55.62360 -446.9089
## 2 - treatment:time_min 12 3.763413       159    59.38701 -459.2901
## 3           - time_min  6 2.412009       165    61.79902 -464.2046
```

```
summary(backward.acute_top)
```

```
##
## Call:
## glm(formula = proportion ~ treatment, family = Gamma(link = "inverse"),
##     data = DPH_acute_top)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.65324  -0.58909  -0.06458   0.32435   1.64334
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      10.4089     0.8222  12.660  < 2e-16 ***
## treatmentenv_rel  0.9271     1.2156   0.763    0.447
## treatmenthigh    -4.7005     0.9377  -5.013 1.37e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.3493726)
##
##     Null deviance: 78.301  on 167  degrees of freedom
## Residual deviance: 61.799  on 165  degrees of freedom
## AIC: -464.2
##
## Number of Fisher Scoring iterations: 6
```

```
# Testing for the best distribution fit for DPH acute exposure when the bottom
# section was covered and running the model using the backwards selection
descdist(DPH_acute_bottom$proportion)
```
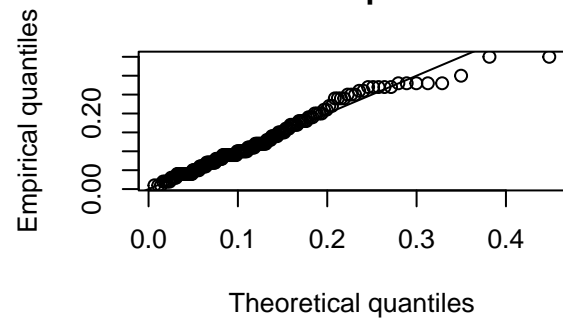
Cullen and Frey graph
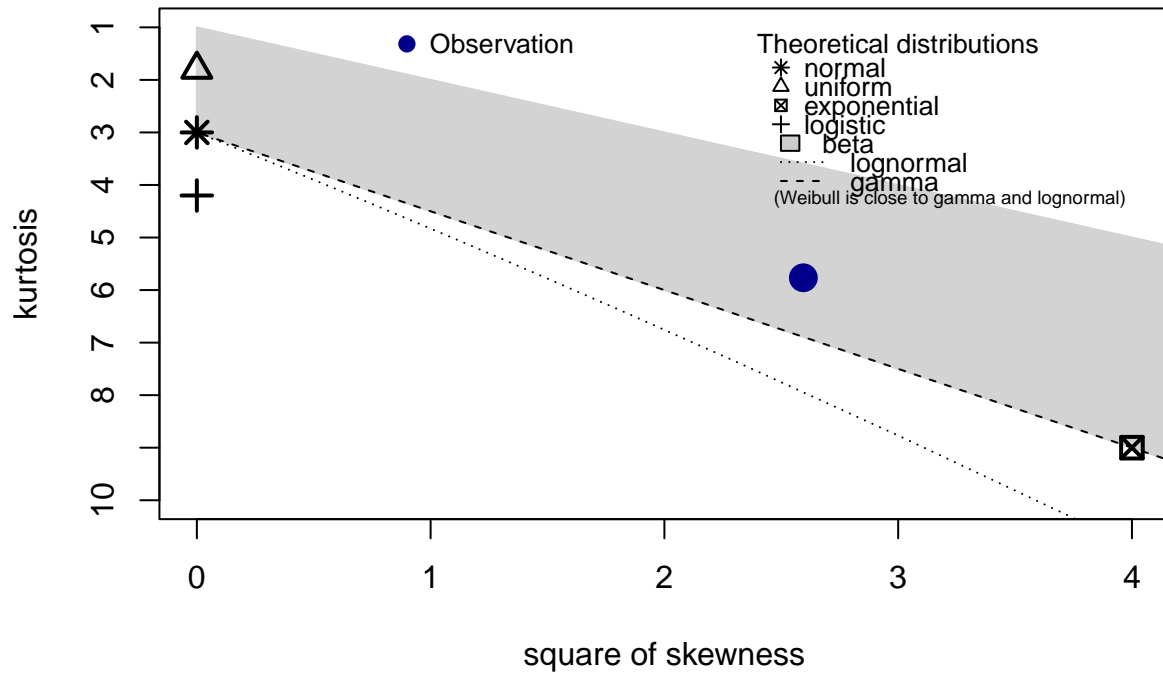

```
## summary statistics
## ------
## min:  0.01    max:  0.37
## median:  0.06
## mean:  0.07952381
## estimated sd:  0.06722747
## estimated skewness:  1.610722
## estimated kurtosis:  5.765863
```

```r
fit.gamma <- fitdist(DPH_acute_bottom$proportion, "gamma")
fit.beta <- fitdist(DPH_acute_bottom$proportion, "beta")
plot(fit.gamma)
```

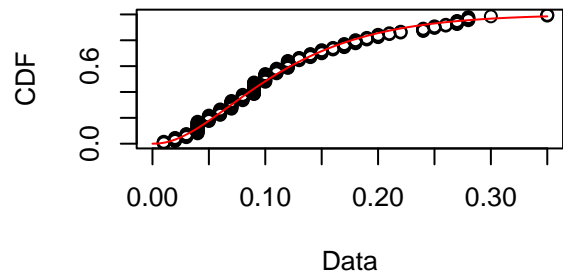**Empirical and theoretical dens.**

Q–Q plot

Empirical and theoretical CDFs

P–P plot

```
plot(fit.beta)
```

Empirical and theoretical dens.

Q–Q plot

Empirical and theoretical CDFs

## P–P plot


```r
mGA <- histDist(DPH_acute_bottom$proportion, "GA", density = T, main = "Gamma")
```

Gamma

DPH_acute_bottom$proportion

```
mBE <- histDist(DPH_acute_bottom$proportion, "BE", density = T, main = "Beta")
```
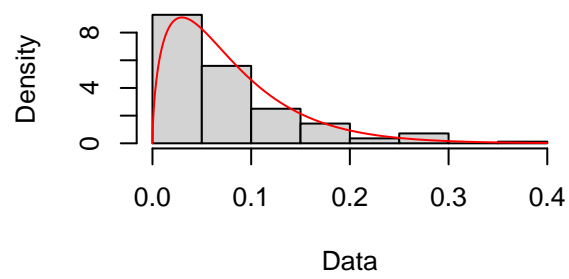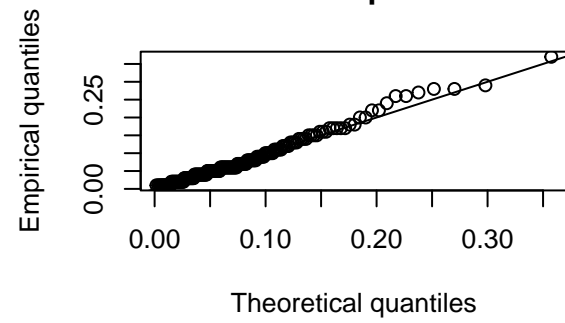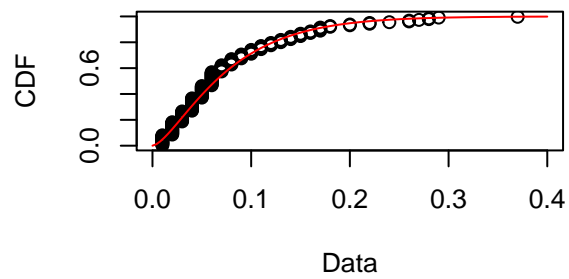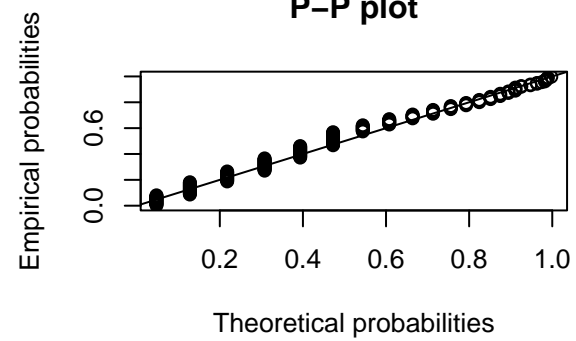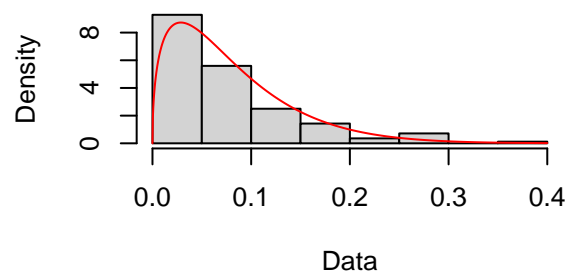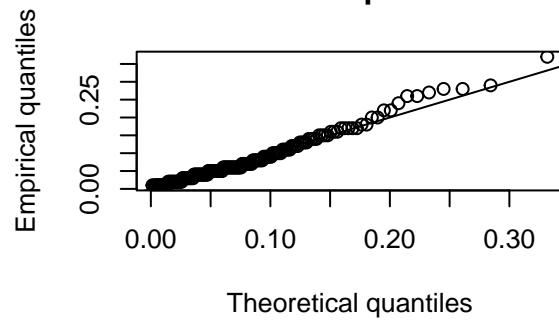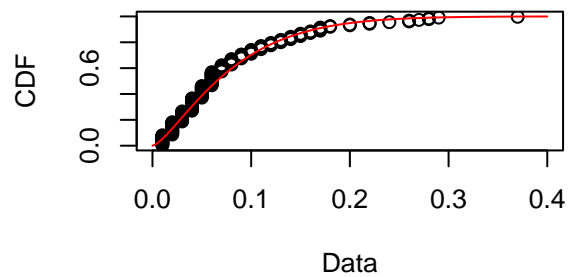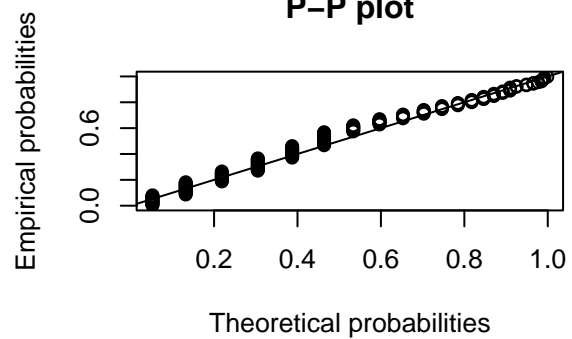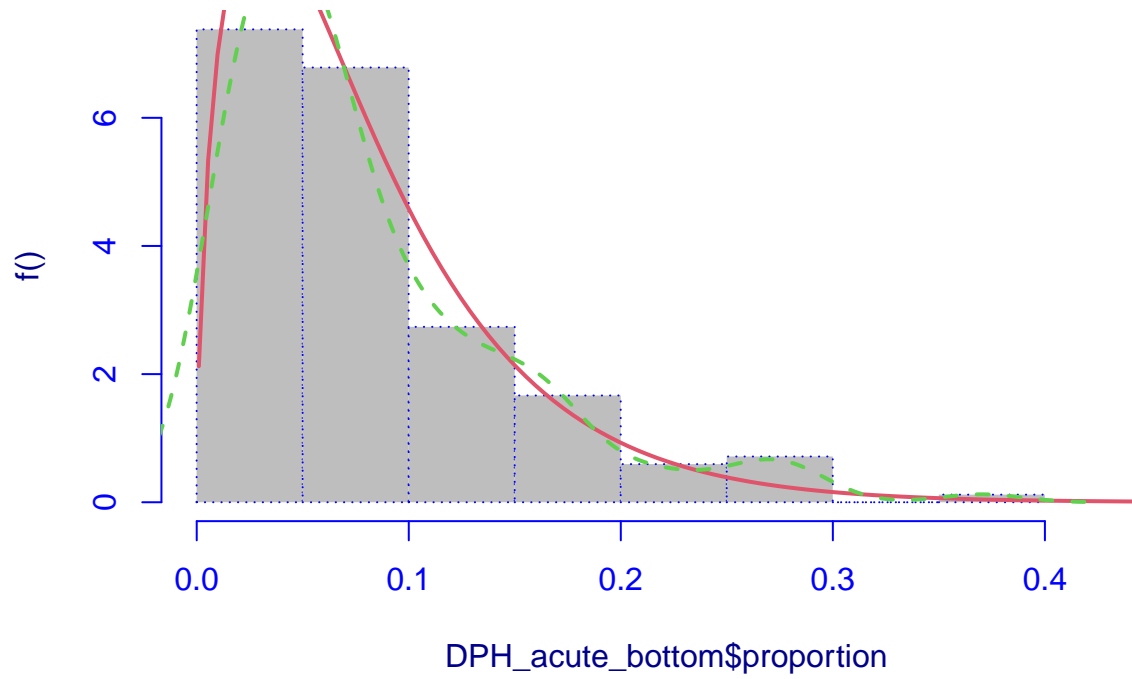
Beta

DPH_acute_bottom$proportion
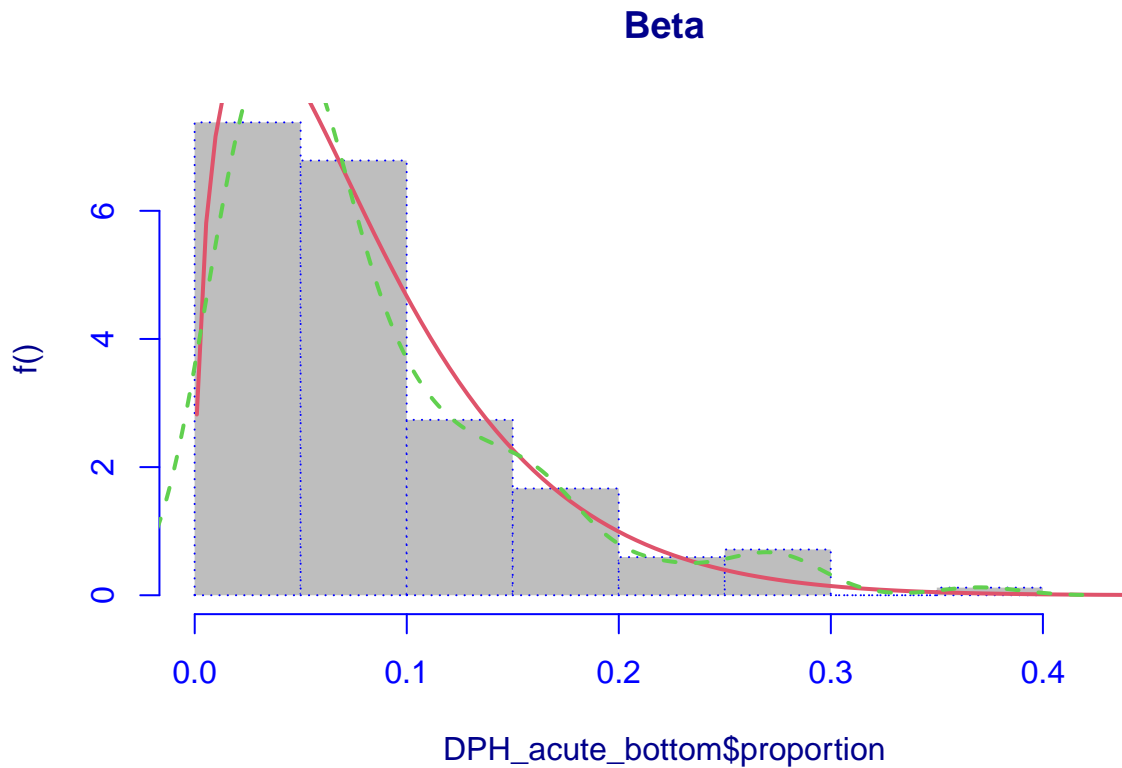
```
GAIC(mGA, mBE)
```

```
##      df       AIC
## mGA   2 -530.1792
## mBE   2 -527.6462
```

```
acute_bottom.mod <- glm(proportion ~ treatment + time_min + treatment:time_min, family = Gamma(link = "
    data = DPH_acute_bottom)

backward.acute_bottom <- stepAIC(acute_bottom.mod, direction = "backward", trace = F)

formula(backward.acute_bottom)
```

```
## proportion ~ treatment + time_min + treatment:time_min
```

```
backward.acute_bottom$anova
```

```
## Stepwise Model Path
## Analysis of Deviance Table
##
## Initial Model:
## proportion ~ treatment + time_min + treatment:time_min
##
## Final Model:
```

```
## proportion ~ treatment + time_min + treatment:time_min
##
##
##   Step Df Deviance Resid. Df Resid. Dev      AIC
## 1                      147    47.47162 -649.9473
```

```
summary(backward.acute_bottom)
```

```
##
## Call:
## glm(formula = proportion ~ treatment + time_min + treatment:time_min,
##     family = Gamma(link = "inverse"), data = DPH_acute_bottom)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.30285  -0.45947  -0.07899   0.30216   1.09251
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                    7.9208     1.5233   5.200 6.57e-07 ***
## treatmentenv_rel              -0.3736     2.1041  -0.178 0.859303
## treatmenthigh                 -1.8602     1.9180  -0.970 0.333720
## time_min5                      3.5078     2.6741   1.312 0.191653
## time_min10                    11.1268     3.9672   2.805 0.005718 **
## time_min15                    20.6506     5.7019   3.622 0.000402 ***
## time_min20                    22.8484     6.1103   3.739 0.000264 ***
## time_min25                    20.6506     5.7019   3.622 0.000402 ***
## time_min30                    20.6506     5.7019   3.622 0.000402 ***
## treatmentenv_rel:time_min5     7.9927     4.7620   1.678 0.095386 .
## treatmenthigh:time_min5       -1.5684     3.2980  -0.476 0.635092
## treatmentenv_rel:time_min10    8.9122     6.7817   1.314 0.190838
## treatmenthigh:time_min10     -10.5208     4.3291  -2.430 0.016293 *
## treatmentenv_rel:time_min15   -3.9554     7.5069  -0.527 0.599059
## treatmenthigh:time_min15     -19.3718     5.9885  -3.235 0.001504 **
## treatmentenv_rel:time_min20    2.9377     8.9742   0.327 0.743868
## treatmenthigh:time_min20     -20.2134     6.4413  -3.138 0.002055 **
## treatmentenv_rel:time_min25    6.5848     8.9081   0.739 0.460969
## treatmenthigh:time_min25     -18.0156     6.0553  -2.975 0.003424 **
## treatmentenv_rel:time_min30   11.8022     9.6848   1.219 0.224934
## treatmenthigh:time_min30     -17.9200     6.0604  -2.957 0.003622 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.2958797)
##
##     Null deviance: 115.627  on 167   degrees of freedom
## Residual deviance:  47.472  on 147   degrees of freedom
## AIC: -649.95
##
## Number of Fisher Scoring iterations: 5
```

```
# automatic distribution fitting with fitDist for lorazepam when the top
# section was covered and running the model
fitDist(proportion, data = lorazepam_top, type = "realAll", try.gamlss = T)
```

```
##    |                                                                    |
##    Lapack routine dgesv: system is exactly singular: U[3,3] = 0
##    |                                                       |==========
##    Lapack routine dgesv: system is exactly singular: U[4,4] = 0
##    |                                                       |================
##    Lapack routine dgesv: system is exactly singular: U[4,4] = 0
##    |                                                       |================
##    Lapack routine dgesv: system is exactly singular: U[4,4] = 0
##    |                                                       |================
##    Lapack routine dgesv: system is exactly singular: U[4,4] = 0
##    |                                                       |================
##    Lapack routine dgesv: system is exactly singular: U[4,4] = 0
##    |                                                       |================


##
## Family:  c("BCPE", "Box-Cox Power Exponential")
## Fitting method: "nlminb"
##
## Call:  gamlssML(formula = y, family = DIST[i])
##
## Mu Coefficients:
## [1]   0.09708
## Sigma Coefficients:
## [1]   -0.4512
## Nu Coefficients:
## [1]   0.5163
## Tau Coefficients:
## [1]   1.406
##
##  Degrees of Freedom for the fit: 4 Residual Deg. of Freedom    164
## Global Deviance:      -487.541
##            AIC:       -479.541
##            SBC:       -467.045
```

```
histDist(lorazepam_top$proportion, "SHASH", density = T)
```

The lorazepam_top$proportion and the fitted SHASH distribution

lorazepam_top$proportion
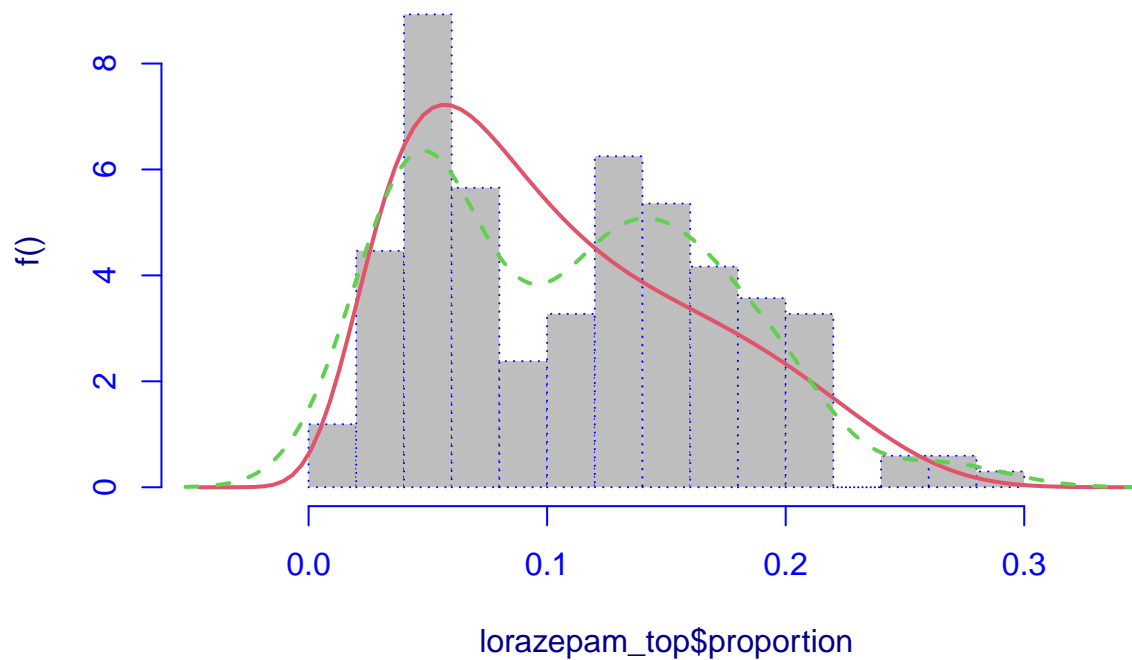
```
##
## Family:  c("SHASH", "Sinh-Arcsinh")
## Fitting method: "nlminb"
##
## Call:  gamlssML(formula = lorazepam_top$proportion, family = "SHASH")
##
## Mu Coefficients:
## [1]  0.0929
## Sigma Coefficients:
## [1]  -1.179
## Nu Coefficients:
## [1]  1.77
## Tau Coefficients:
## [1]  1.105
##
##  Degrees of Freedom for the fit: 4 Residual Deg. of Freedom   164
## Global Deviance:     -478.835
##          AIC:        -470.835
##          SBC:        -458.339
```

```r
lo_top.mod <- gamlss(proportion ~ treatment + time_min + treatment:time_min, family = SHASH(),
    data = lorazepam_top, method = CG())
```

```
## GAMLSS-CG iteration 1: Global Deviance = 1.940289e+66
## GAMLSS-CG iteration 2: Global Deviance = 1.940289e+66
```

```
summary(lo_top.mod)
```

```
## *********************************************************************
## Family:  c("SHASH", "Sinh-Arcsinh")
##
## Call:
## gamlss(formula = proportion ~ treatment + time_min + treatment:time_min,
##     family = SHASH(), data = lorazepam_top, method = CG())
##
## Fitting method: CG()
##
## ---------------------------------------------------------------------
## Mu link function:  identity
## Mu Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  0.1704403  0.0106609  15.987   <2e-16 ***
## treatmentenv_rel            -0.0001677  0.0148417  -0.011    0.991
## treatmenthigh               -0.0037943  0.0147841  -0.257    0.798
## time_min5                   -0.0067633  0.0143576  -0.471    0.638
## time_min10                  -0.0152300  0.0142359  -1.070    0.286
## time_min15                  -0.0029937  0.0145965  -0.205    0.838
## time_min20                  -0.0007704  0.0145263  -0.053    0.958
## time_min25                  -0.0060707  0.0147336  -0.412    0.681
## time_min30                  -0.0025669  0.0152541  -0.168    0.867
## treatmentenv_rel:time_min5  -0.0063255  0.0201606  -0.314    0.754
## treatmenthigh:time_min5      0.0106985  0.0199608   0.536    0.593
## treatmentenv_rel:time_min10  0.0155878  0.0202257   0.771    0.442
## treatmenthigh:time_min10     0.0077202  0.0203070   0.380    0.704
## treatmentenv_rel:time_min15 -0.0025374  0.0204779  -0.124    0.902
## treatmenthigh:time_min15    -0.0034206  0.0207514  -0.165    0.869
## treatmentenv_rel:time_min20 -0.0156574  0.0205573  -0.762    0.447
## treatmenthigh:time_min20     0.0014994  0.0203372   0.074    0.941
## treatmentenv_rel:time_min25 -0.0051656  0.0206823  -0.250    0.803
## treatmenthigh:time_min25     0.0072570  0.0205450   0.353    0.724
## treatmentenv_rel:time_min30 -0.0206006  0.0207693  -0.992    0.323
## treatmenthigh:time_min30    -0.0053279  0.0209589  -0.254    0.800
## ---
## 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)  -1.0366     0.1668  -6.215 3.96e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## ---------------------------------------------------------------------
## Nu link function:  log
## Nu Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.2391     0.1545   33.92   <2e-16 ***
## ---
```

```
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## -------------------------------------------------------------------
## Tau link function:  log
## Tau Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.1867     0.1361  -1.371    0.172
##
## -------------------------------------------------------------------
## No. of observations in the fit:  168
## Degrees of Freedom for the fit:  24
##         Residual Deg. of Freedom:  144
##                       at cycle:  2
##
## Global Deviance:     1.940289e+66
##            AIC:     1.940289e+66
##            SBC:     1.940289e+66
## *************************************************************
```

```r
# automatic distribution fitting with fitDist for lorazepam when the bottom
# section was covered and running the model
fitDist(proportion, data = lorazepam_bottom, type = "realAll", try.gamlss = T)
```

```
##   |                                                              |
```

```r
histDist(lorazepam_bottom$proportion, "SHASH", density = T)
```

The lorazepam_bottom$proportion and the fitted SHASH distributio
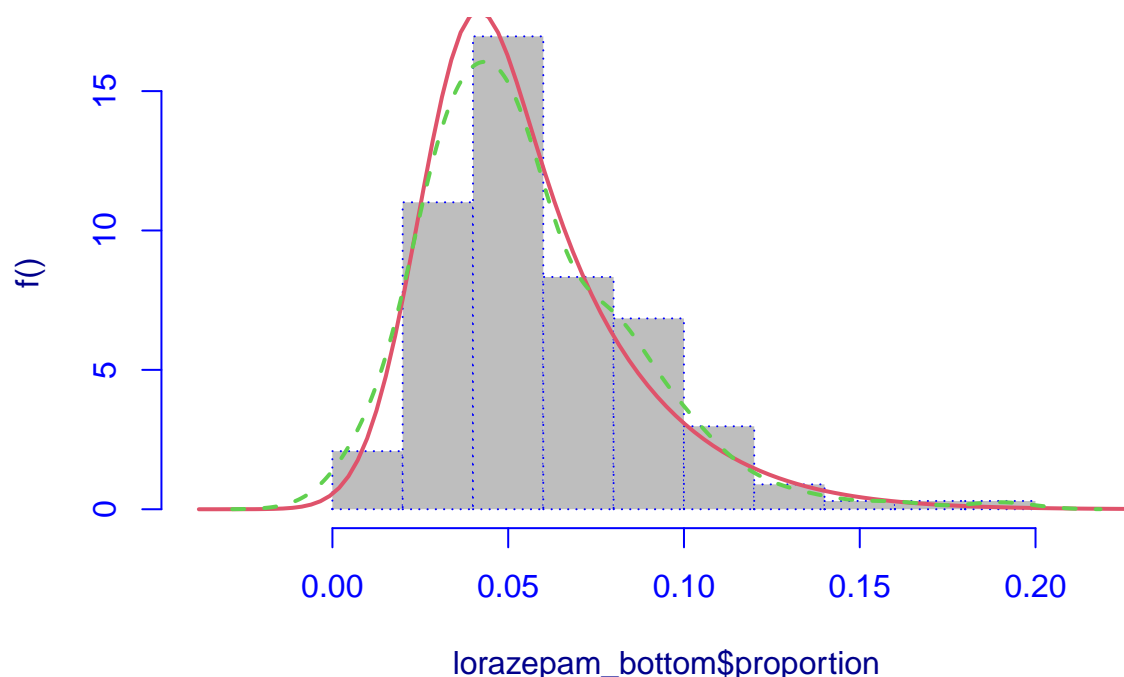

```
## 
## Family:  c("SHASH", "Sinh-Arcsinh")
## Fitting method: "nlminb"
## 
## Call:  gamlssML(formula = lorazepam_bottom$proportion, family = "SHASH")
## 
## Mu Coefficients:
## [1]  0.04935
## Sigma Coefficients:
## [1]  -3.774
## Nu Coefficients:
## [1]  0.1636
## Tau Coefficients:
## [1]  -0.3358
## 
##  Degrees of Freedom for the fit: 4 Residual Deg. of Freedom   164
## Global Deviance:     -745.082
##            AIC:     -737.082
##            SBC:     -724.586
```

```r
lo_bottom.mod <- gamlss(proportion ~ treatment + time_min + treatment:time_min, family = SHASH(),
    data = lorazepam_bottom, method = CG())
```

```
## GAMLSS-CG iteration 1: Global Deviance = 7.73885e+79
## GAMLSS-CG iteration 2: Global Deviance = 7.73885e+79
```

```
summary(lo_bottom.mod)
```

```
## *********************************************************************
## Family:  c("SHASH", "Sinh-Arcsinh")
##
## Call:
## gamlss(formula = proportion ~ treatment + time_min + treatment:time_min,
##     family = SHASH(), data = lorazepam_bottom, method = CG())
##
## Fitting method: CG()
##
## ---------------------------------------------------------------------
## Mu link function:  identity
## Mu Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 0.0856545  0.0050608  16.925   <2e-16 ***
## treatmentenv_rel            0.0016492  0.0069774   0.236    0.813
## treatmenthigh               0.0001180  0.0073259   0.016    0.987
## time_min5                  -0.0046604  0.0068148  -0.684    0.495
## time_min10                 -0.0069966  0.0069269  -1.010    0.314
## time_min15                 -0.0090506  0.0071536  -1.265    0.208
## time_min20                 -0.0068545  0.0069245  -0.990    0.324
## time_min25                 -0.0082930  0.0071531  -1.159    0.248
## time_min30                 -0.0085313  0.0068114  -1.253    0.212
## treatmentenv_rel:time_min5 -0.0029330  0.0097087  -0.302    0.763
## treatmenthigh:time_min5    -0.0012064  0.0098554  -0.122    0.903
## treatmentenv_rel:time_min10 -0.0010468  0.0094974  -0.110    0.912
## treatmenthigh:time_min10    0.0037007  0.0098104   0.377    0.707
## treatmentenv_rel:time_min15  0.0028851  0.0096603   0.299    0.766
## treatmenthigh:time_min15    0.0037354  0.0099890   0.374    0.709
## treatmentenv_rel:time_min20 -0.0011822  0.0095072  -0.124    0.901
## treatmenthigh:time_min20   -0.0004865  0.0098261  -0.050    0.961
## treatmentenv_rel:time_min25 -0.0053037  0.0098127  -0.540    0.590
## treatmenthigh:time_min25    -0.0117015  0.0101334  -1.155    0.250
## treatmentenv_rel:time_min30 -0.0118720  0.0098142  -1.210    0.228
## treatmenthigh:time_min30    -0.0055277  0.0097896  -0.565    0.573
## ---
## 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)  -2.5456     0.1303  -19.54   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## ---------------------------------------------------------------------
## Nu link function:  log
## Nu Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   4.8000     0.1306   36.76   <2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## -------------------------------------------------------------------
## Tau link function:  log
## Tau Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.4198     0.1030  -4.077 7.05e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## -------------------------------------------------------------------
## No. of observations in the fit:  168
## Degrees of Freedom for the fit:  24
##        Residual Deg. of Freedom:  144
##                      at cycle:  2
##
## Global Deviance:     7.73885e+79
##             AIC:     7.73885e+79
##             SBC:     7.73885e+79
## ******************************************************************
```