

DS Project Stats

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```
library(FSA)
library(fGarch)
library(LambertW)
library(patchwork)
library(here)
library(tidyverse)

# 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))

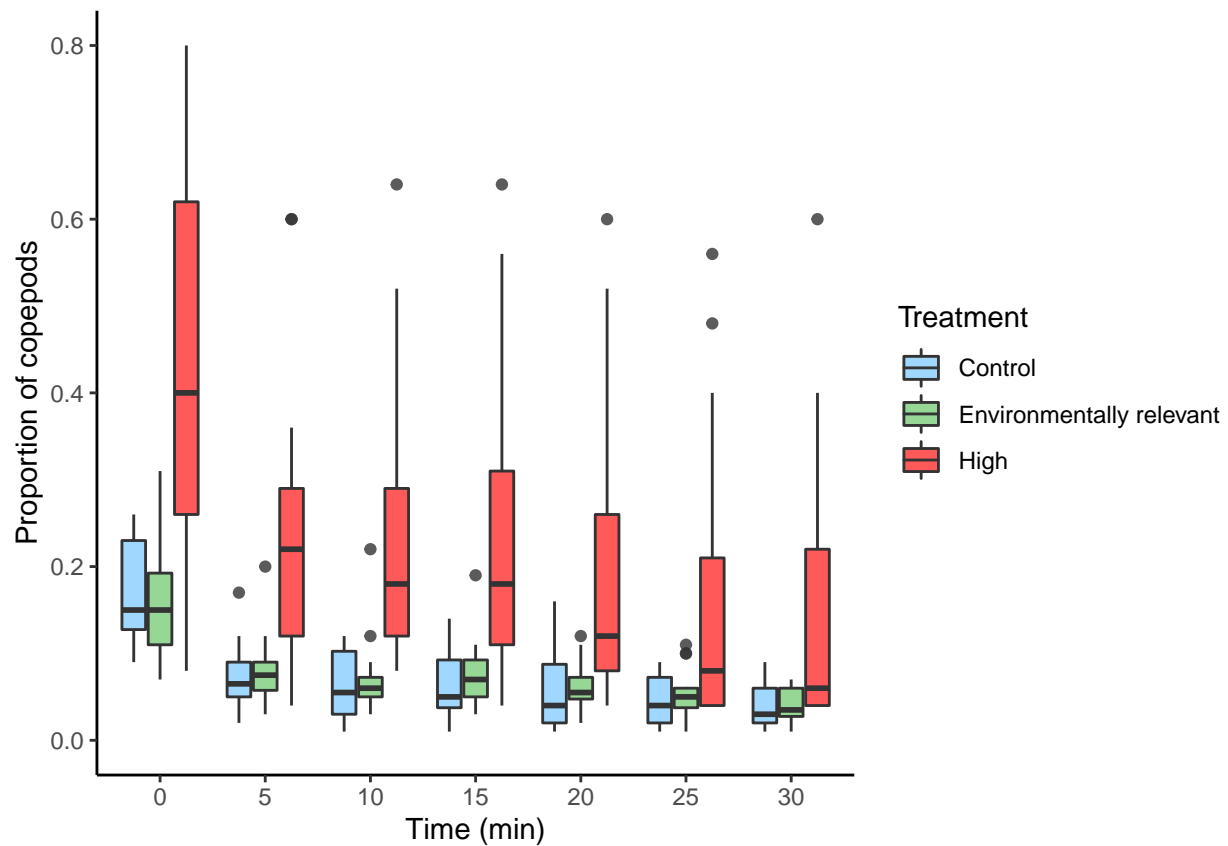
DPH_chronic_top = read_csv(here("./Data/DS copepod data - DPH chronic_top.csv")) %>%
  mutate(percentile = as.factor(percentile), time_min = as.factor(time_min))

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))

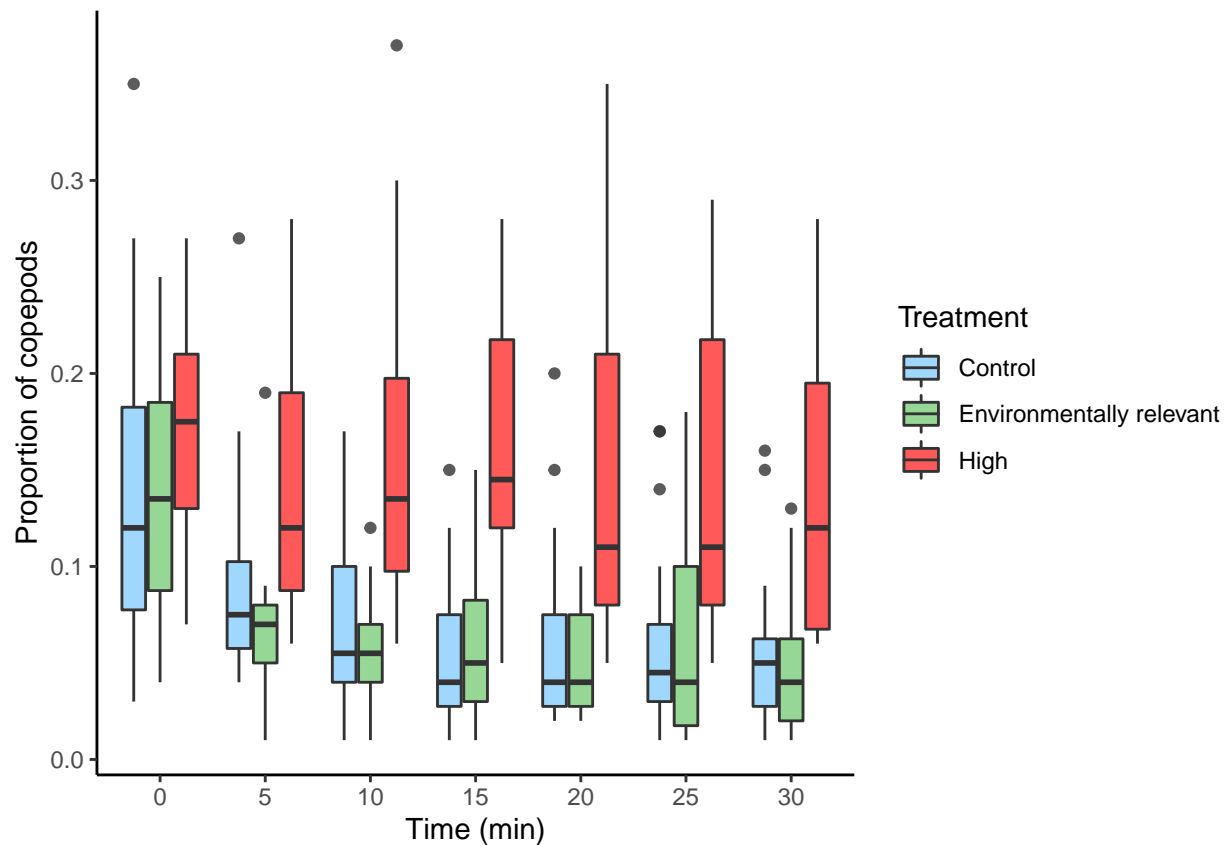
# Graphs combing the proportion of copepods in all light exposed sections.
# These graphs are not used in our report
ggplot(DPH_chronic, aes(x = time_min, y = proportion, fill = treatment), xlab = "Time (min)",
  ylab = "Proportion of copepods") + geom_boxplot(alpha = 0.8) + theme_classic() +
```

```
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("skyblue1", "palegreen3", "firebrick1"))
```

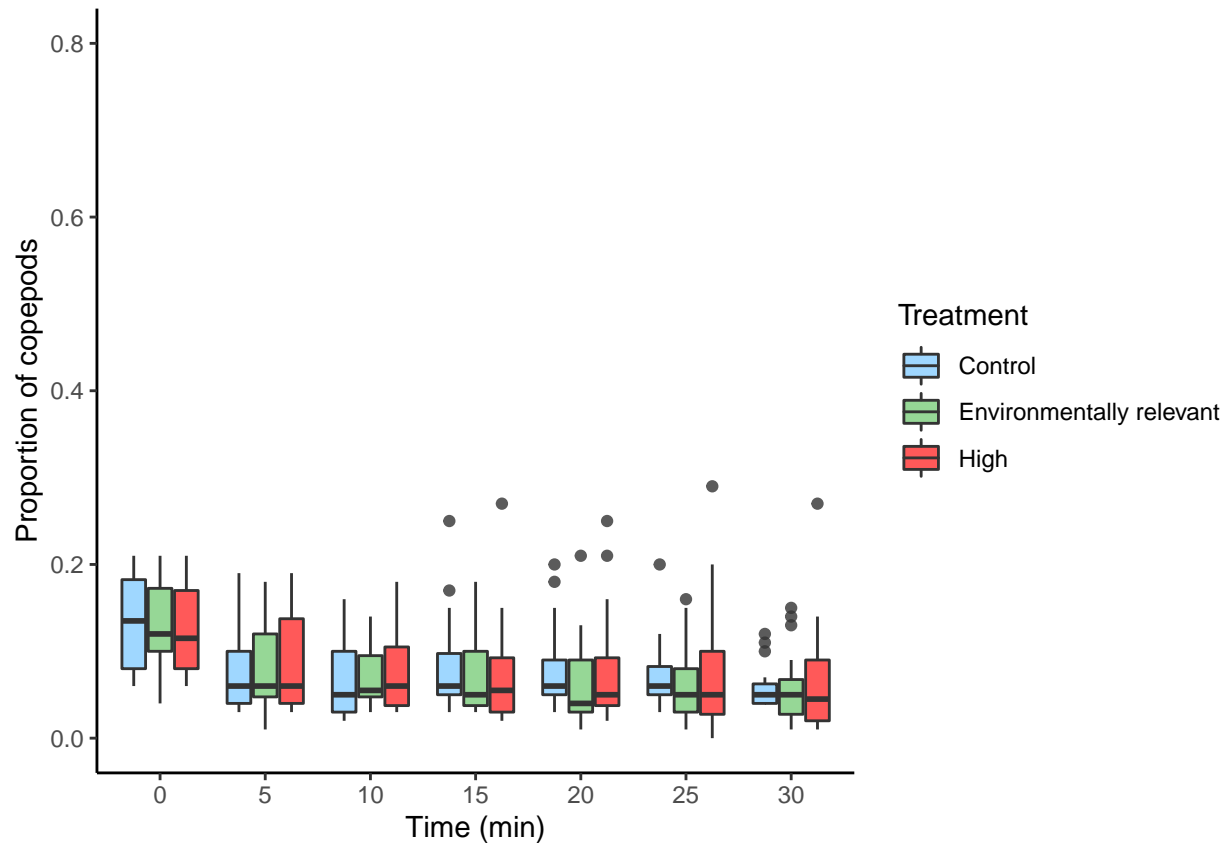
```
## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
```



```
ggplot(DPH_acute, 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") +
scale_fill_manual(labels = c("Control", "Environmentally relevant", "High"),
values = c("skyblue1", "palegreen3", "firebrick1"))
```



```
ggplot(lorazepam, 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("skyblue1", "palegreen3", "firebrick1"))
```



*# 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("skyblue1", "palegreen3", "firebrick1"))

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("skyblue1", "palegreen3", "firebrick1"))

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("skyblue1", "palegreen3", "firebrick1"))

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("skyblue1", "palegreen3", "firebrick1"))
```

```

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("skyblue1", "palegreen3", "firebrick1"))

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("skyblue1", "palegreen3", "firebrick1"))

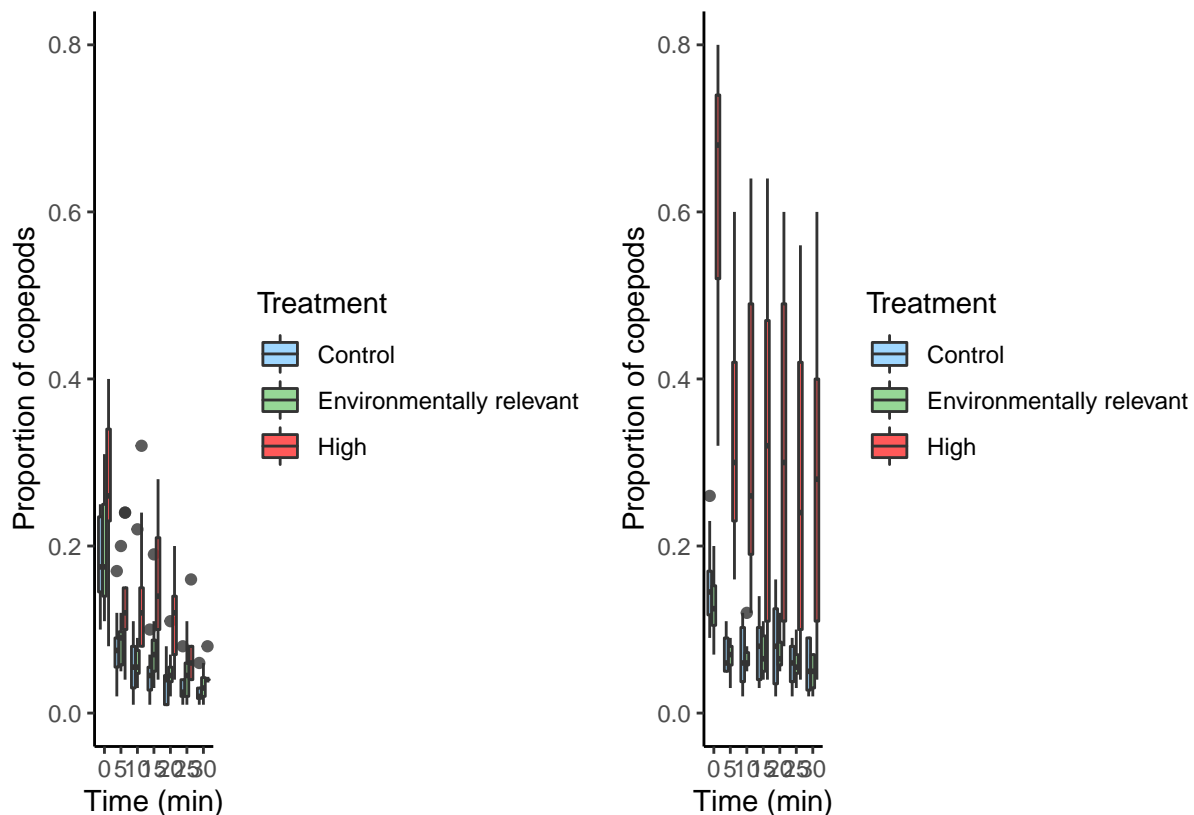
```

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

DPH Chronic

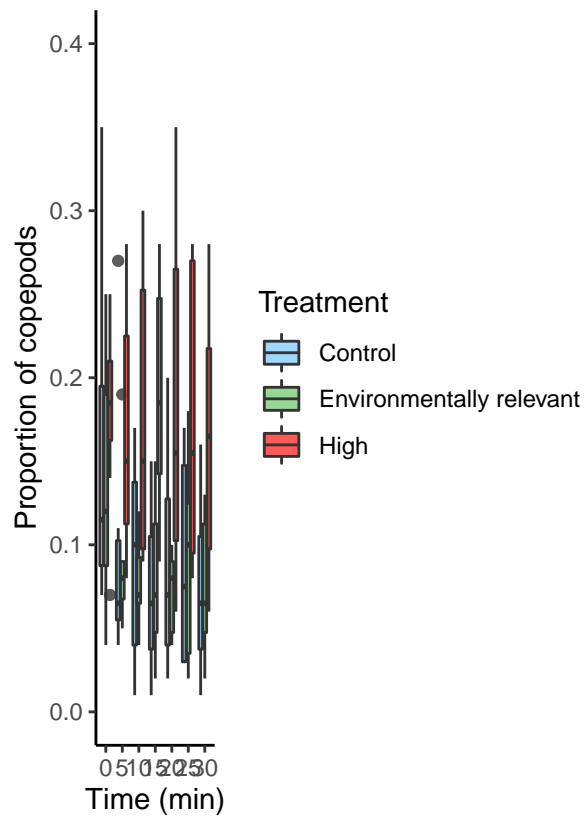
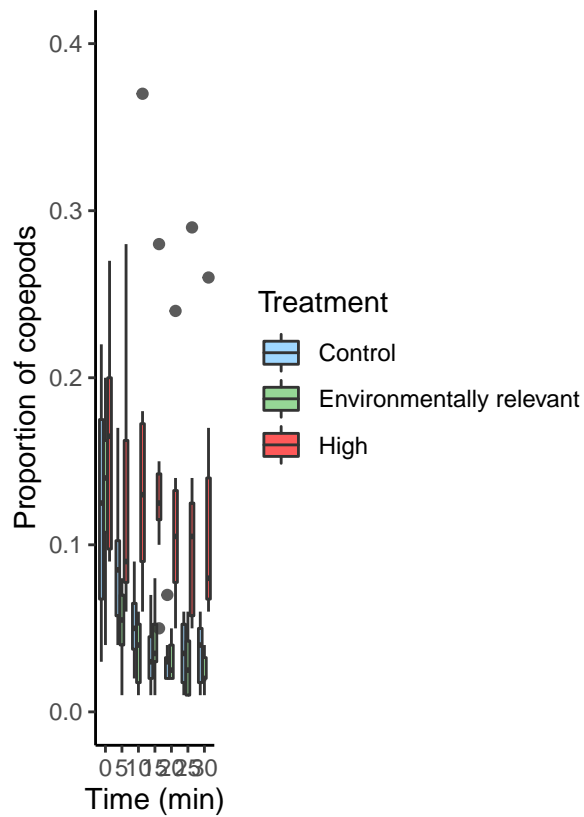
p1 | p2

Warning: Removed 1 rows containing non-finite values (stat_boxplot).

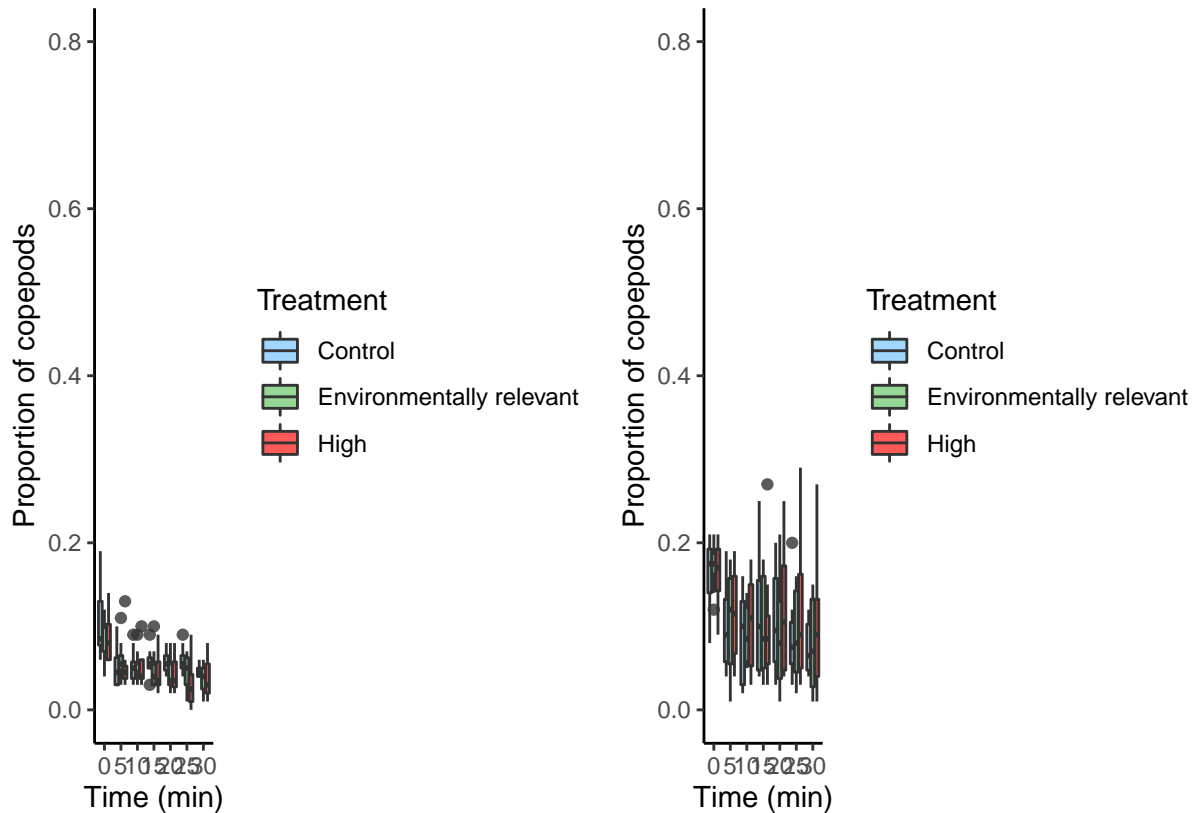


DPH acute

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)
```

```
## Warning: treatment was coerced to a factor.
```

```
## 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)
```

```
## Warning: treatment was coerced to a factor.
```

```
## 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
```



```
# Initial tests for the lorazepam exposure  
shapiro.test(lorazepam$proportion) # p-value = 4.922e-15, <0.05 therefore data is significantly different
```

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

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

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

```
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
```

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

```
## Warning: treatment was coerced to a factor.
```

```
## 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
```

```
library(fitdistrplus)
```

```
## Loading required package: survival
```

```
library(gamlss)
```

```
## Loading required package: splines
```

```
## Loading required package: gamlss.data
```

```
##
## Attaching package: 'gamlss.data'

## The following object is masked from 'package:datasets':
##
##     sleep

## Loading required package: gamlss.dist

## Loading required package: nlme

##
## Attaching package: 'nlme'

## The following object is masked from 'package:dplyr':
##
##     collapse

## Loading required package: parallel

## Registered S3 method overwritten by 'gamlss':
##   method      from
##   print.ri bit

## ***** GAMLSS Version 5.3-4 *****

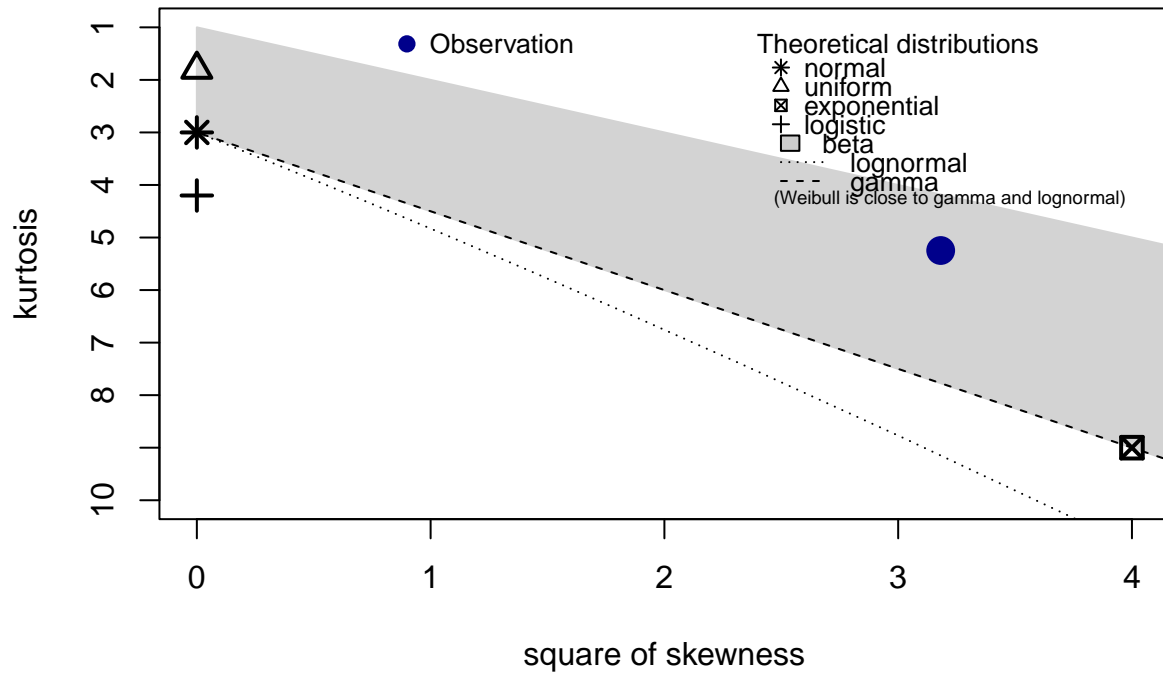
## For more on GAMLSS look at https://www.gamlss.com/

## Type gamlssNews() to see new features/changes/bug fixes.
```

```
library(tidyverse)
```

```
# 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)
```

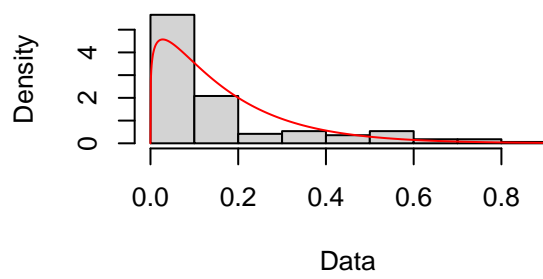
Cullen and Frey graph



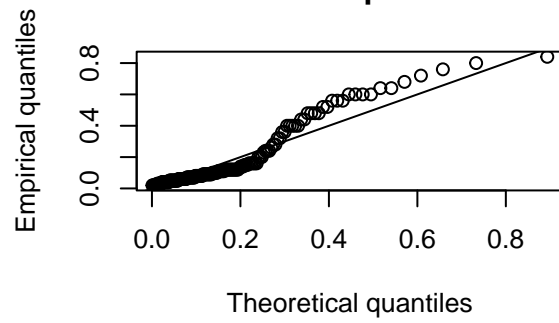
```
## summary statistics
## -----
## min: 0.02   max: 0.84
## median: 0.09
## mean: 0.17
## estimated sd: 0.1875432
## estimated skewness: 1.783793
## estimated kurtosis: 5.247405
```

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

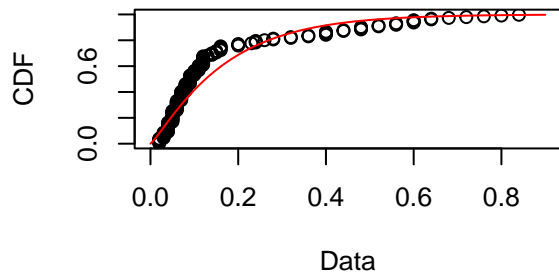
Empirical and theoretical dens.



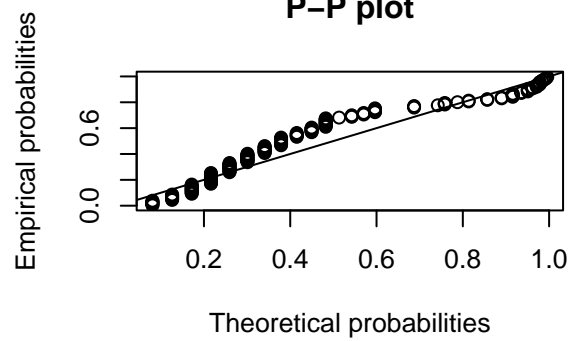
Q-Q plot



Empirical and theoretical CDFs

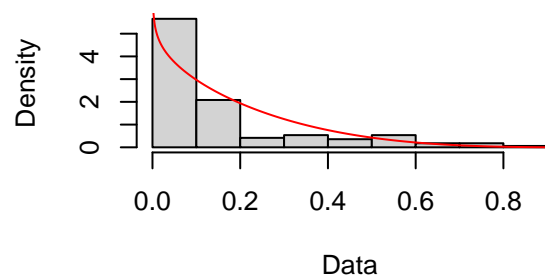


P-P plot

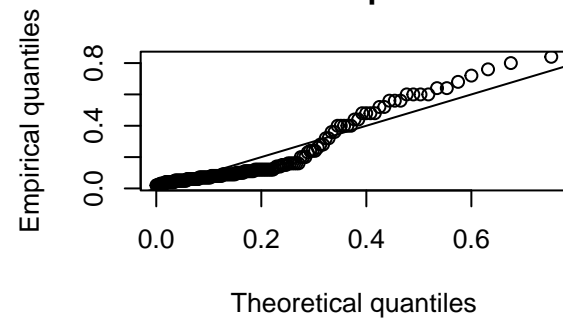


```
plot(fit.beta)
```

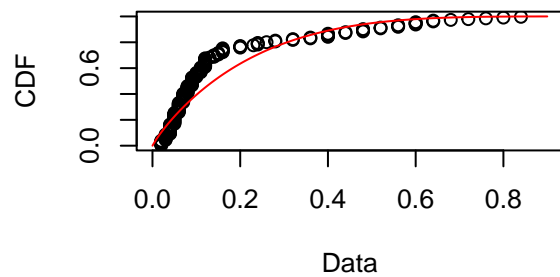
Empirical and theoretical dens.



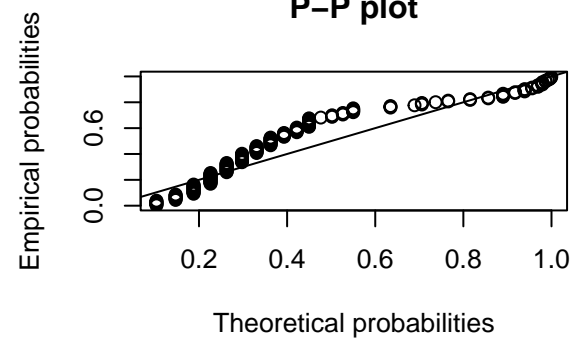
Q-Q plot



Empirical and theoretical CDFs

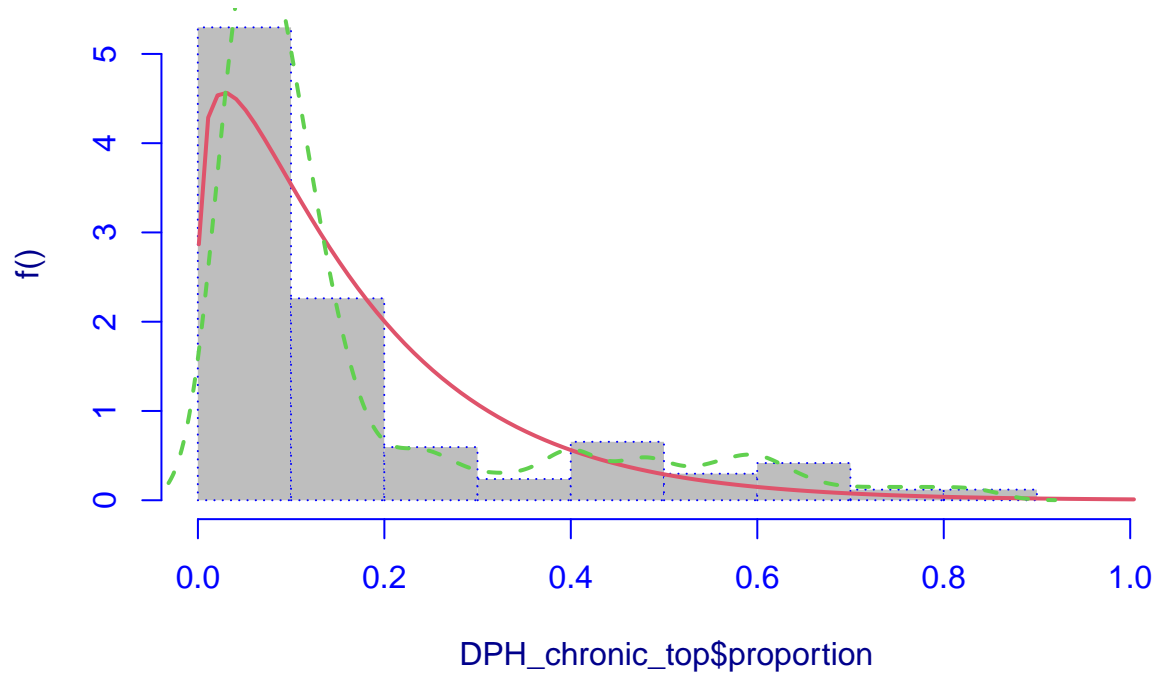


P-P plot



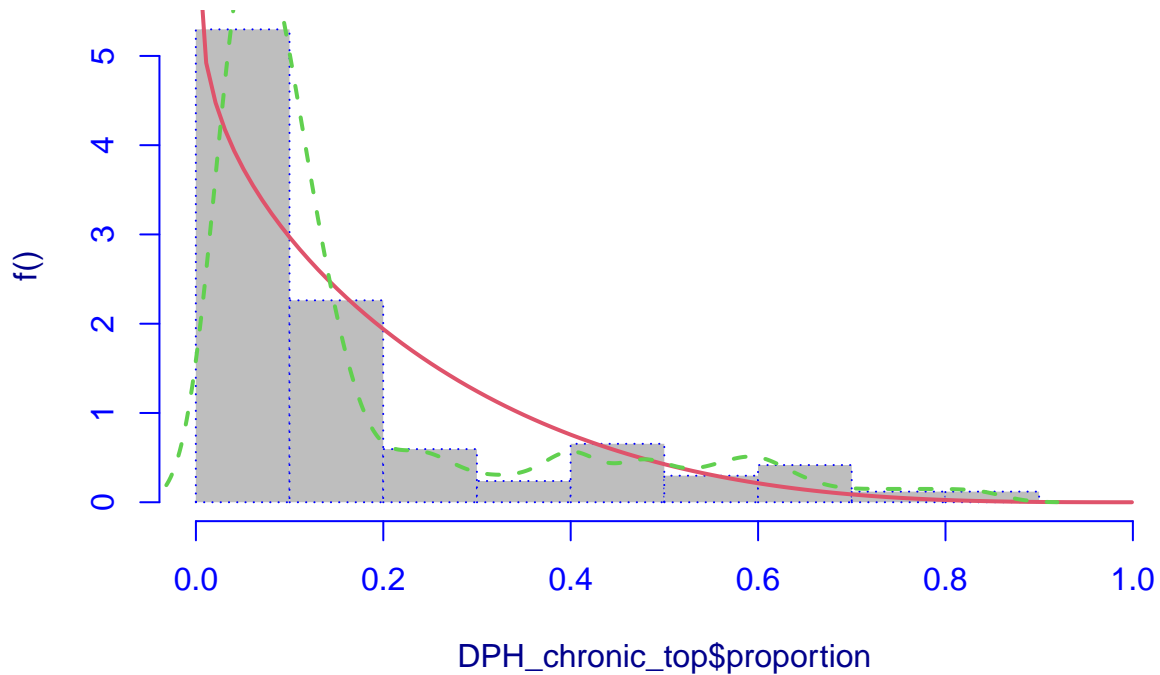
```
mGA <- histDist(DPH_chronic_top$proportion, "GA", density = T, main = "Gamma")
```

Gamma



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

Beta



```
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 = "inverse",
data = DPH_chronic_top)
```

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

```
formula(backward.chronic_top) # get the final formula , proportion ~ treatment +time_min
```

```
## 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)
```

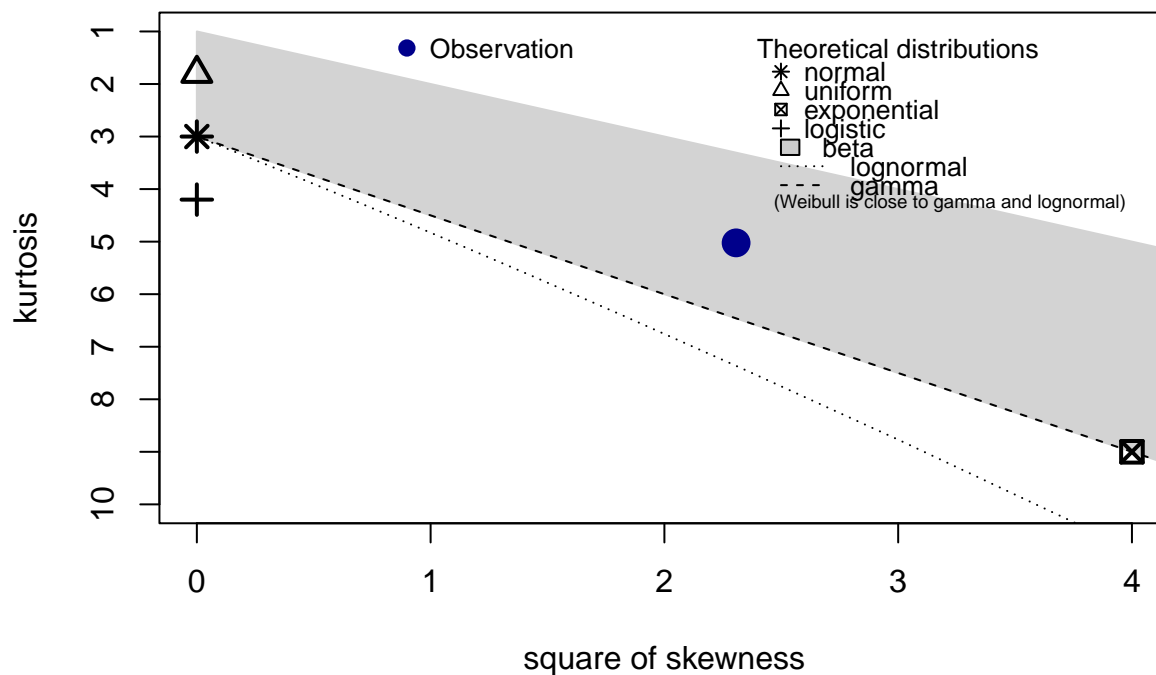
```
##
## Call:
## glm(formula = proportion ~ treatment + time_min + treatment:time_min,
##      family = Gamma(link = "inverse"), data = DPH_chronic_top)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.54316  -0.45247  -0.08589   0.36242   0.89628
##
## Coefficients:
##              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)
```

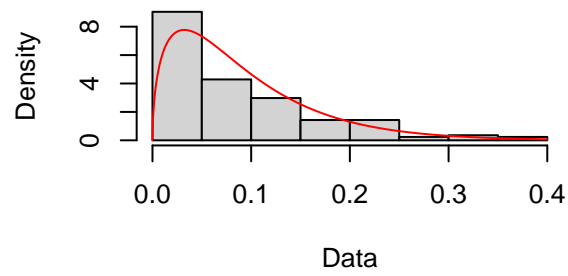
Cullen and Frey graph



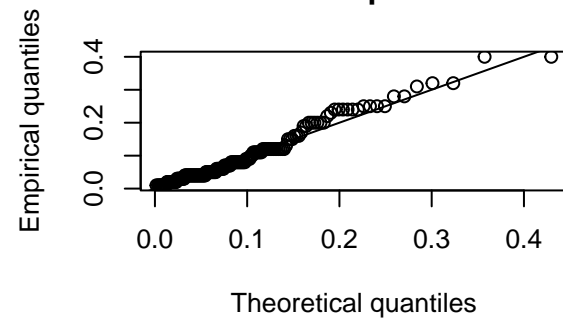
```
## summary statistics
## -----
## min: 0.01 max: 0.4
## median: 0.06
## mean: 0.09327381
## estimated sd: 0.08135453
## estimated skewness: 1.518791
## estimated kurtosis: 5.023683
```

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

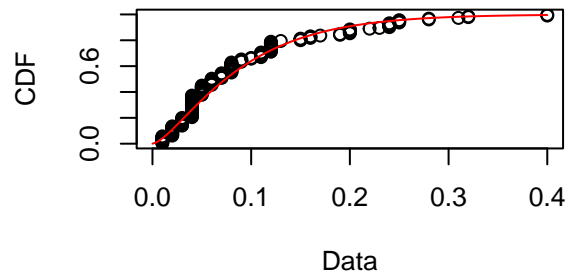
Empirical and theoretical dens.



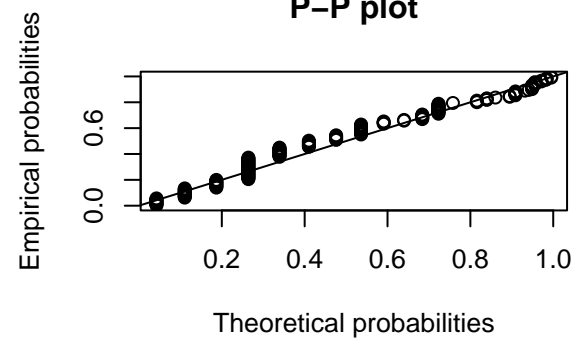
Q-Q plot



Empirical and theoretical CDFs

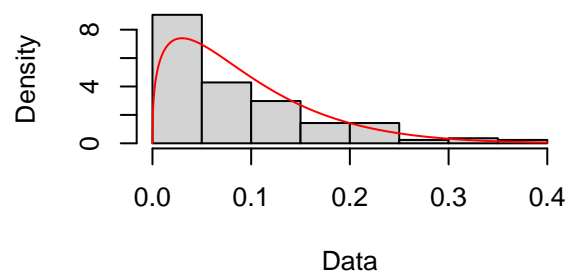


P-P plot

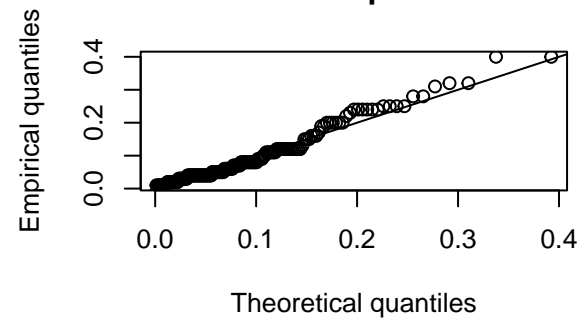


```
plot(fit.beta)
```

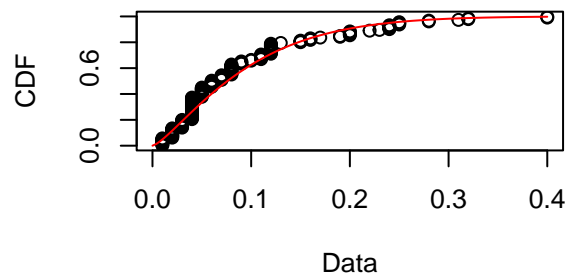
Empirical and theoretical dens.



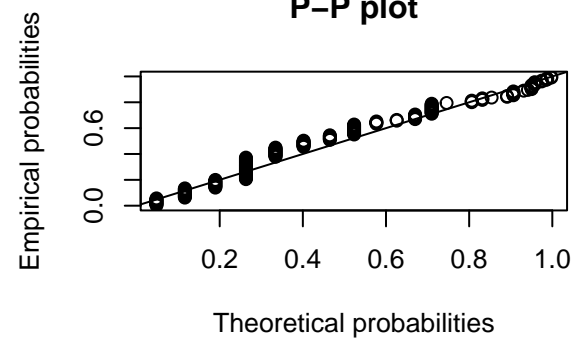
Q-Q plot



Empirical and theoretical CDFs

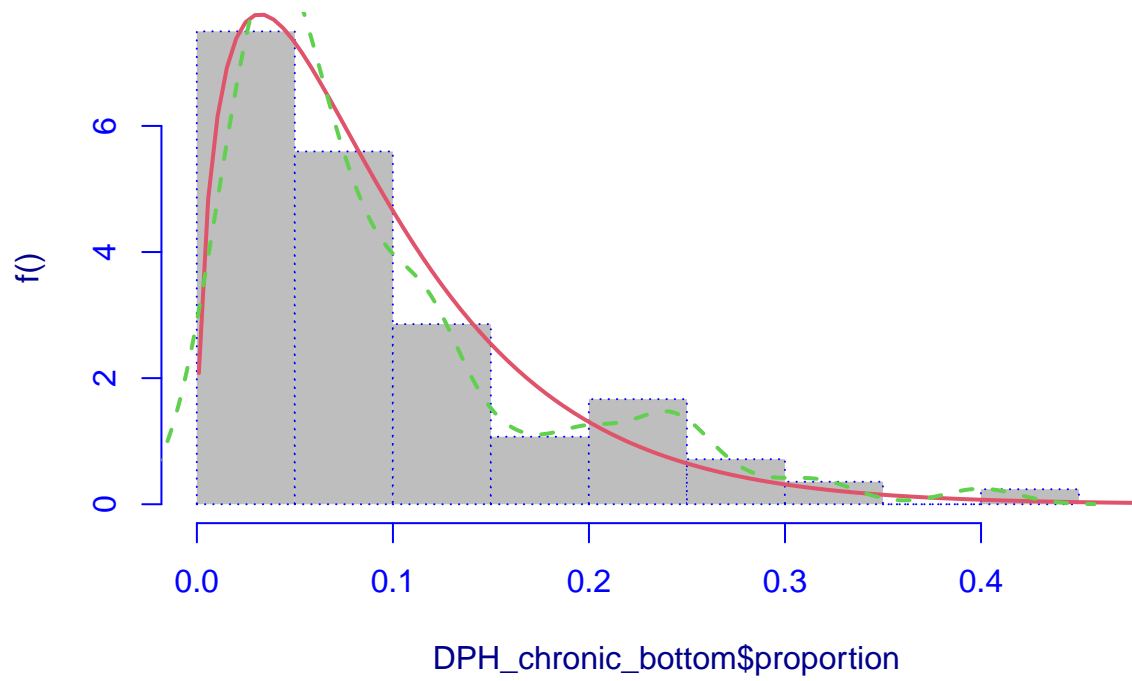


P-P plot



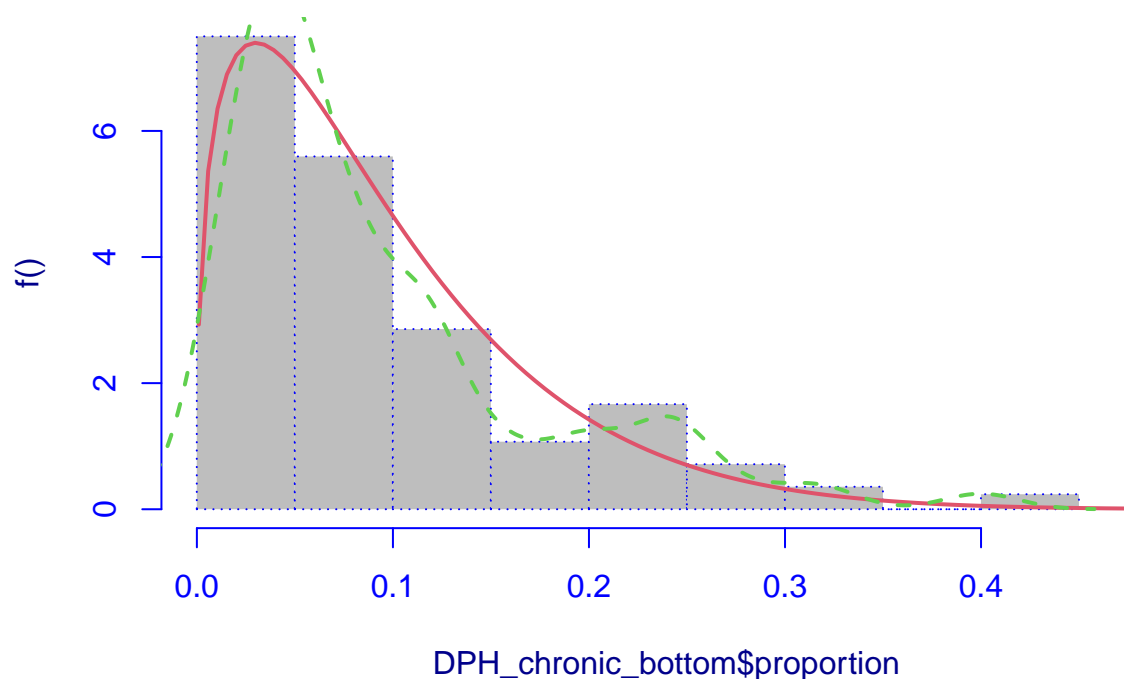
```
mGA <- histDist(DPH_chronic_bottom$proportion, "GA", density = T, main = "Gamma")
```

Gamma



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

Beta



```
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) # get the final formula , proportion ~ treatment +time_min
```

```
## 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:
```

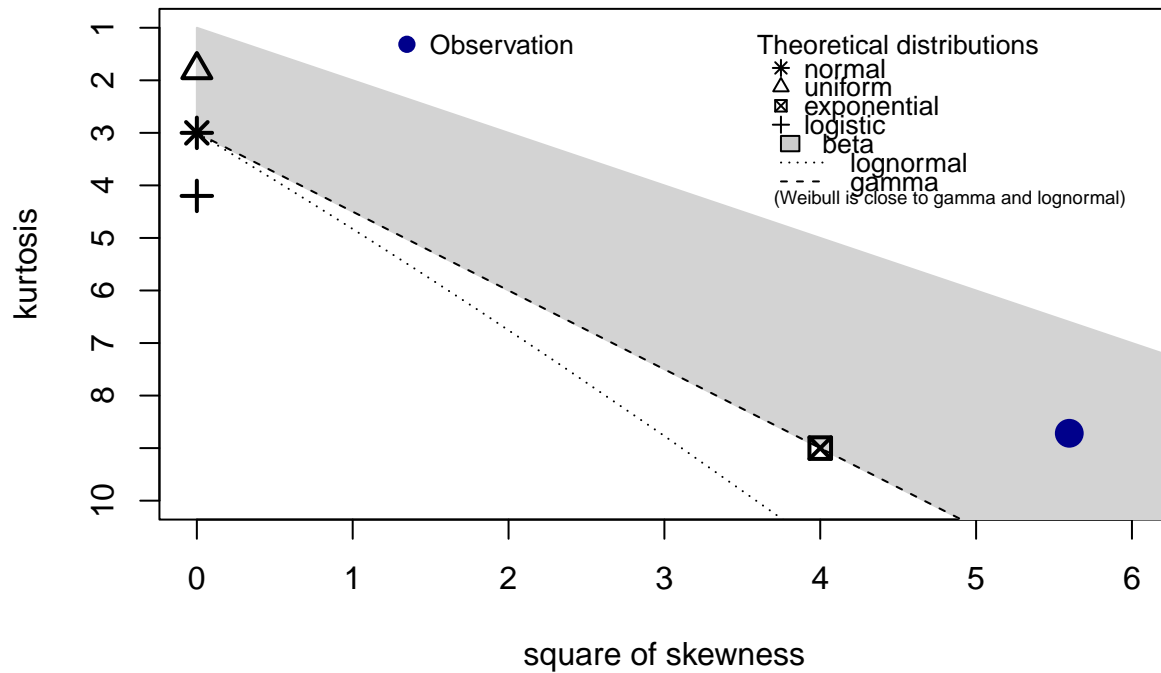
```
## proportion ~ treatment + time_min + treatment:time_min
##
##
## Step Df Deviance Resid. Df Resid. Dev      AIC
## 1              147      50.7582 -590.5576

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 overall chronic DPH exposure and
# running the model using the backwards selection
descdist(DPH_chronic$proportion)
```

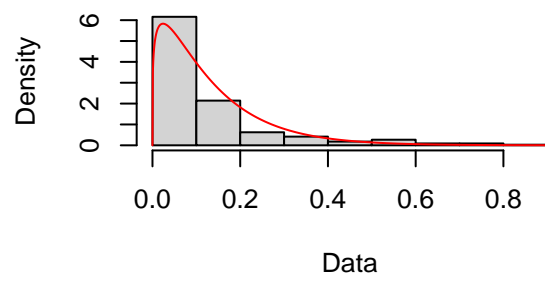
Cullen and Frey graph



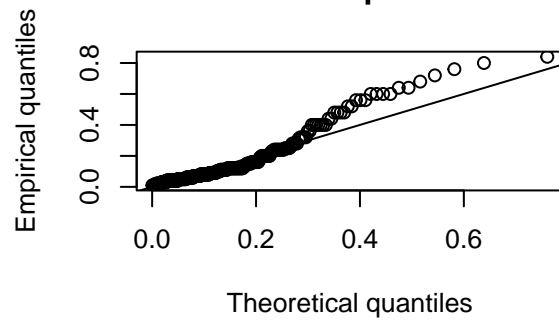
```
## summary statistics
## -----
## min: 0.01 max: 0.84
## median: 0.08
## mean: 0.1316369
## estimated sd: 0.1493628
## estimated skewness: 2.365977
## estimated kurtosis: 8.71785
```

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

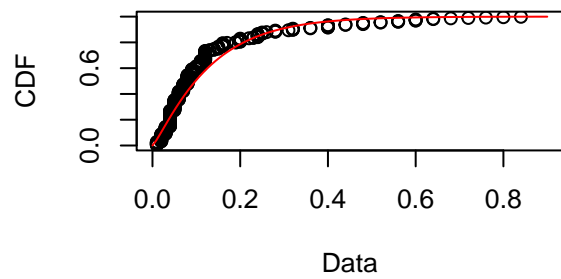
Empirical and theoretical dens.



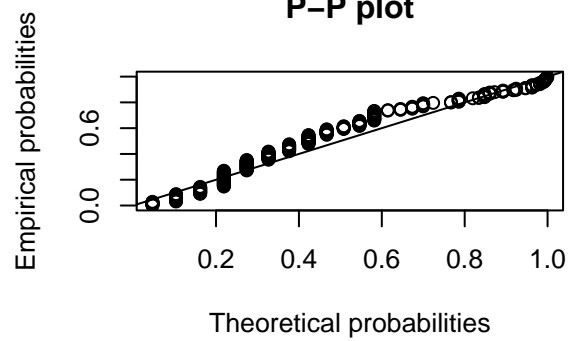
Q-Q plot



Empirical and theoretical CDFs

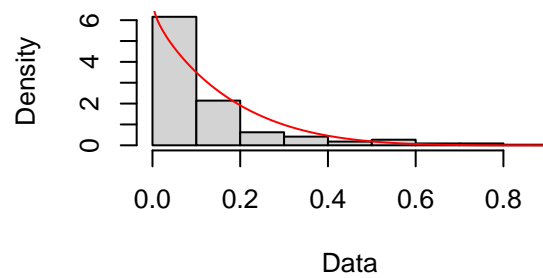


P-P plot

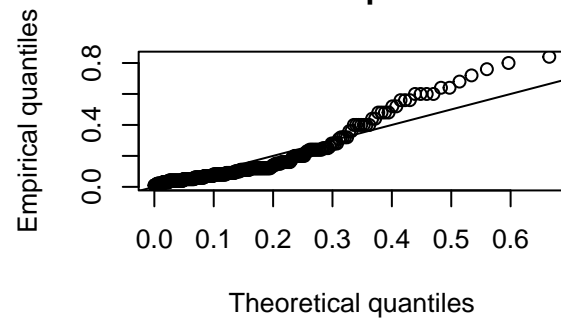


```
plot(fit.beta)
```

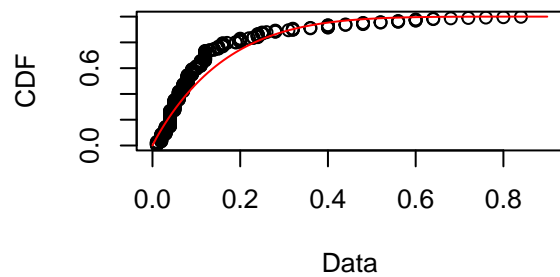

Empirical and theoretical dens.



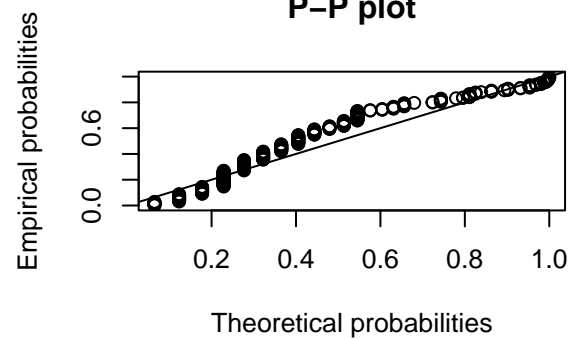
Q-Q plot



Empirical and theoretical CDFs

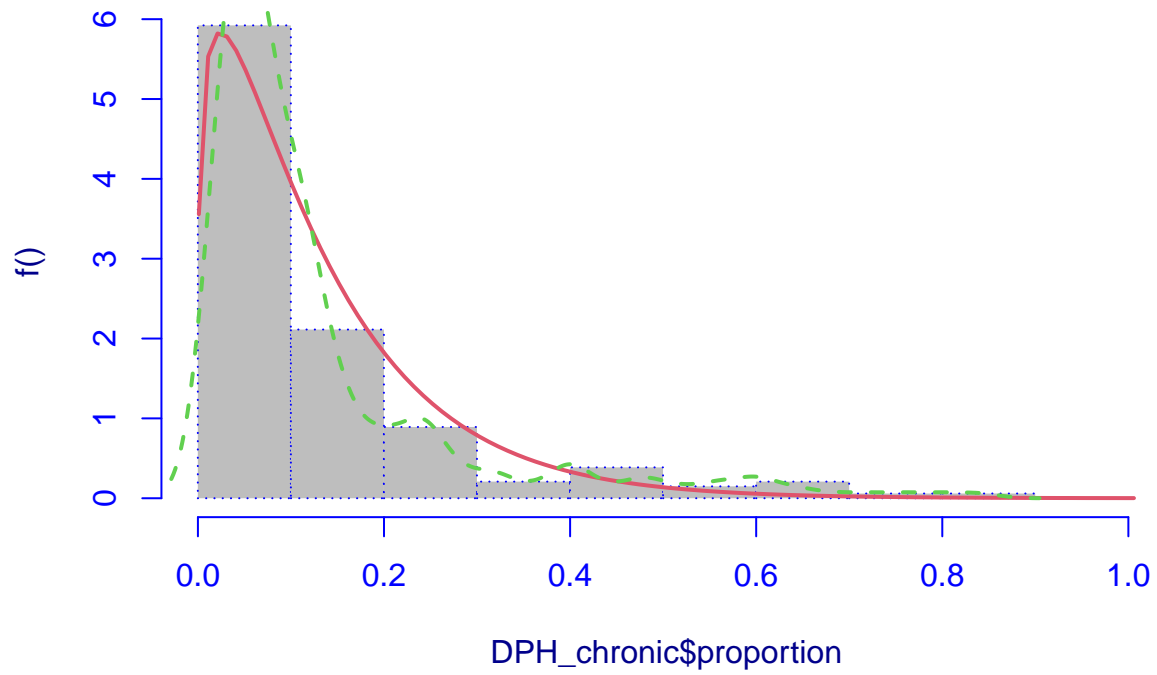


P-P plot



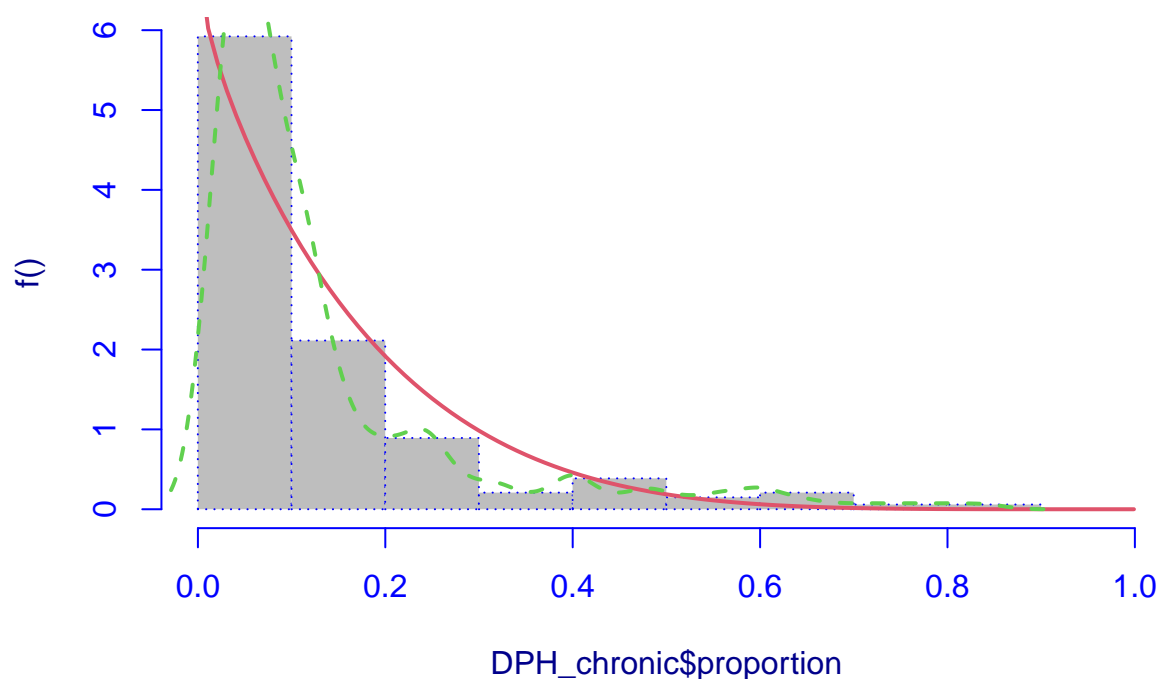
```
mGA <- histDist(DPH_chronic$proportion, "GA", density = T, main = "Gamma")
```

Gamma



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

Beta



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

```
##      df      AIC
## mGA  2 -694.6341
## mBE  2 -648.8242
```

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

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

```
formula(backward.chronic) # get the final formula , proportion ~ treatment +time_min
```

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

```
backward.chronic$anova
```

```
## Stepwise Model Path
```

```
## Analysis of Deviance Table
```

```
##
```

```
## Initial Model:
```

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

```
##
```

```
## Final Model:
```

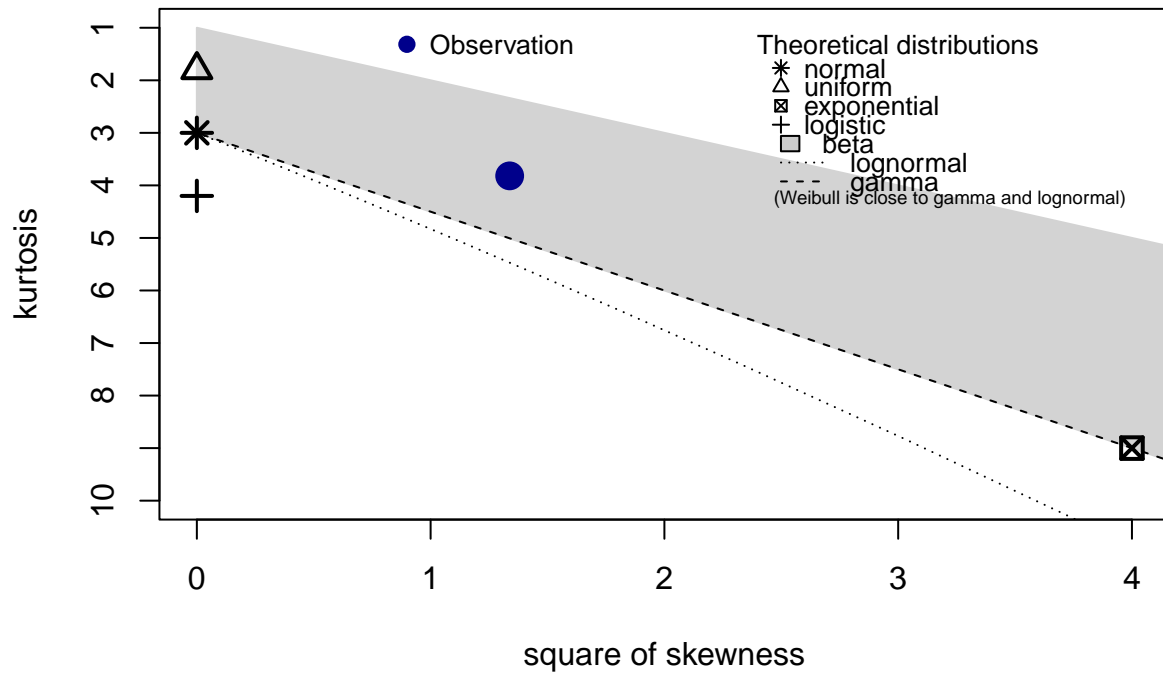
```
## proportion ~ treatment + time_min + treatment:time_min
##
##
## Step Df Deviance Resid. Df Resid. Dev      AIC
## 1              315    143.4565 -937.5555
```

```
summary(backward.chronic)
```

```
##
## Call:
## glm(formula = proportion ~ treatment + time_min + treatment:time_min,
##      family = Gamma(link = "inverse"), data = DPH_chronic)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4149  -0.5959  -0.1835   0.2641   1.6901
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.9041     0.9919   5.952 7.05e-09 ***
## treatmentenv_rel    0.3459     1.4445    0.239 0.810881
## treatmenthigh     -3.7183     1.0577  -3.515 0.000504 ***
## time_min5         7.4293     2.4499    3.032 0.002627 **
## time_min10        9.9375     2.8404    3.499 0.000535 ***
## time_min15       10.2576     2.8908    3.548 0.000447 ***
## time_min20       10.9380     2.9984    3.648 0.000309 ***
## time_min25       16.3182     3.8630    4.224 3.14e-05 ***
## time_min30       19.0959     4.3157    4.425 1.33e-05 ***
## treatmentenv_rel:time_min5 -1.1793     3.3934  -0.348 0.728432
## treatmenthigh:time_min5    -5.4045     2.5763  -2.098 0.036720 *
## treatmentenv_rel:time_min10 -2.3944     3.8132  -0.628 0.530503
## treatmenthigh:time_min10   -7.9128     2.9501  -2.682 0.007699 **
## treatmentenv_rel:time_min15 -3.3928     3.7834  -0.897 0.370533
## treatmenthigh:time_min15   -8.1423     3.0023  -2.712 0.007055 **
## treatmentenv_rel:time_min20 -1.1880     4.1616  -0.285 0.775468
## treatmenthigh:time_min20   -8.4180     3.1226  -2.696 0.007399 **
## treatmentenv_rel:time_min25 -3.9635     5.0790  -0.780 0.435754
## treatmenthigh:time_min25  -12.5338     4.0080  -3.127 0.001929 **
## treatmentenv_rel:time_min30 -0.7306     6.0689  -0.120 0.904261
## treatmenthigh:time_min30  -15.0317     4.4568  -3.373 0.000837 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.4516279)
##
## Null deviance: 310.27  on 335  degrees of freedom
## Residual deviance: 143.46  on 315  degrees of freedom
## AIC: -937.56
##
## Number of Fisher Scoring iterations: 6
```

```
# Testing for the best distribution fit for the overall DPH acute exposure and
# running the model using the backwards selection
descdist(DPH_acute$proportion)
```

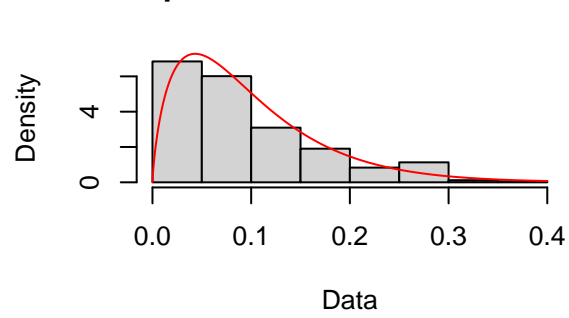
Cullen and Frey graph



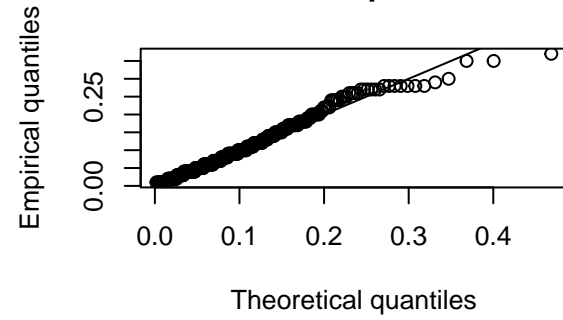
```
## summary statistics
## -----
## min: 0.01 max: 0.37
## median: 0.08
## mean: 0.09967262
## estimated sd: 0.07517272
## estimated skewness: 1.156784
## estimated kurtosis: 3.818839
```

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

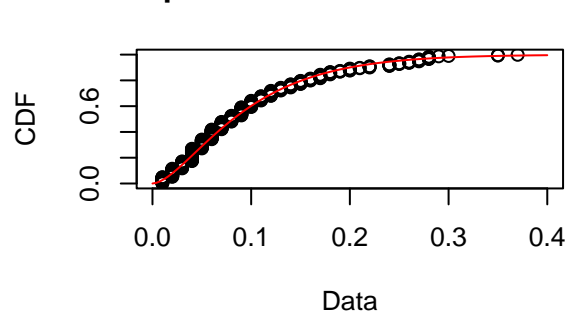
Empirical and theoretical dens.



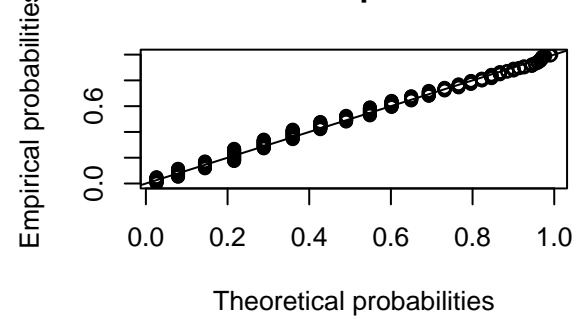
Q-Q plot



Empirical and theoretical CDFs

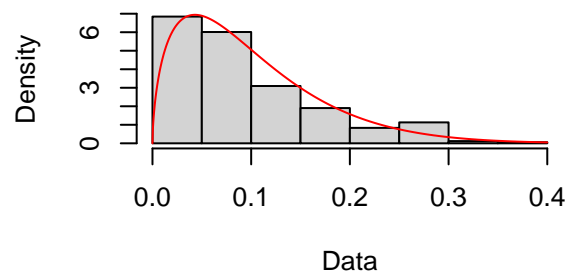


P-P plot

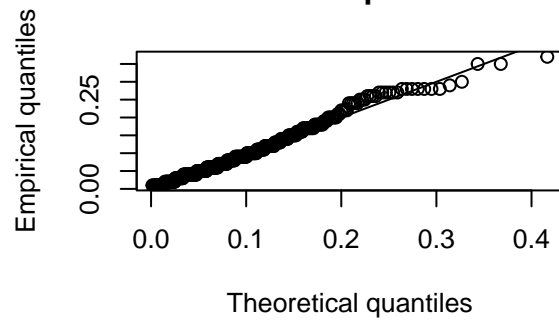


```
plot(fit.beta)
```

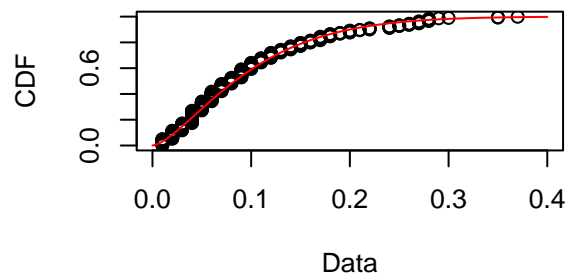
Empirical and theoretical dens.



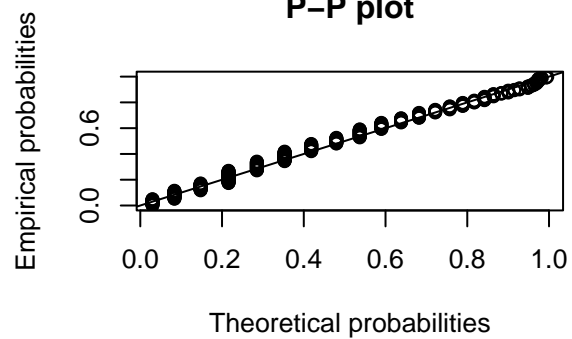
Q-Q plot



Empirical and theoretical CDFs

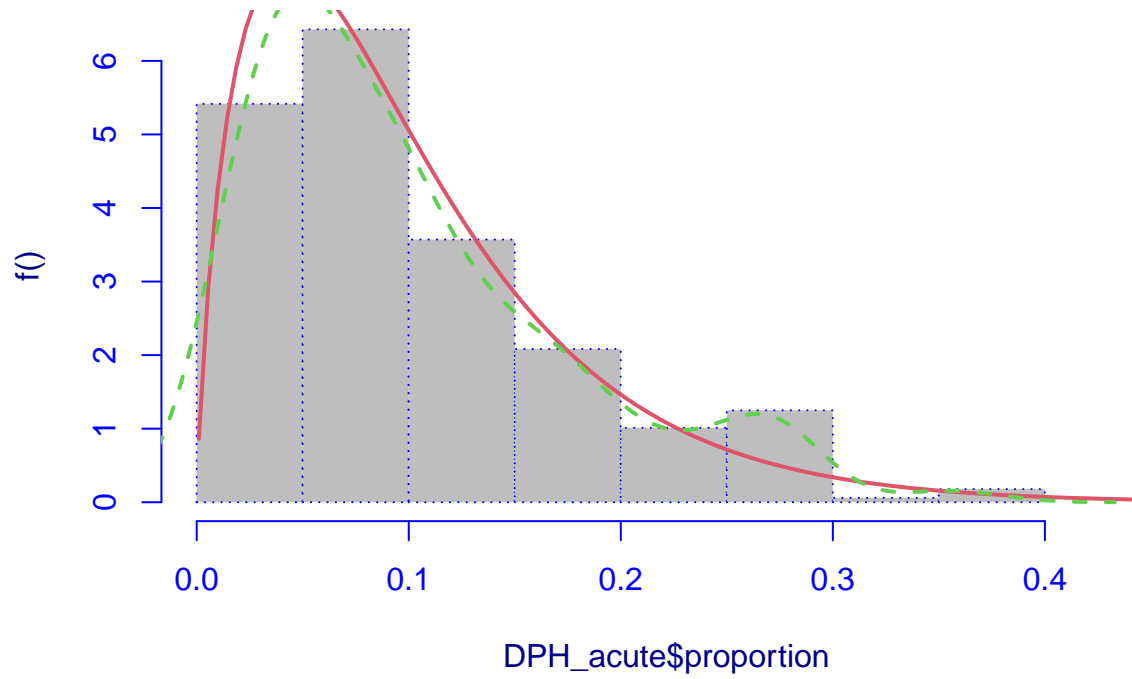


P-P plot

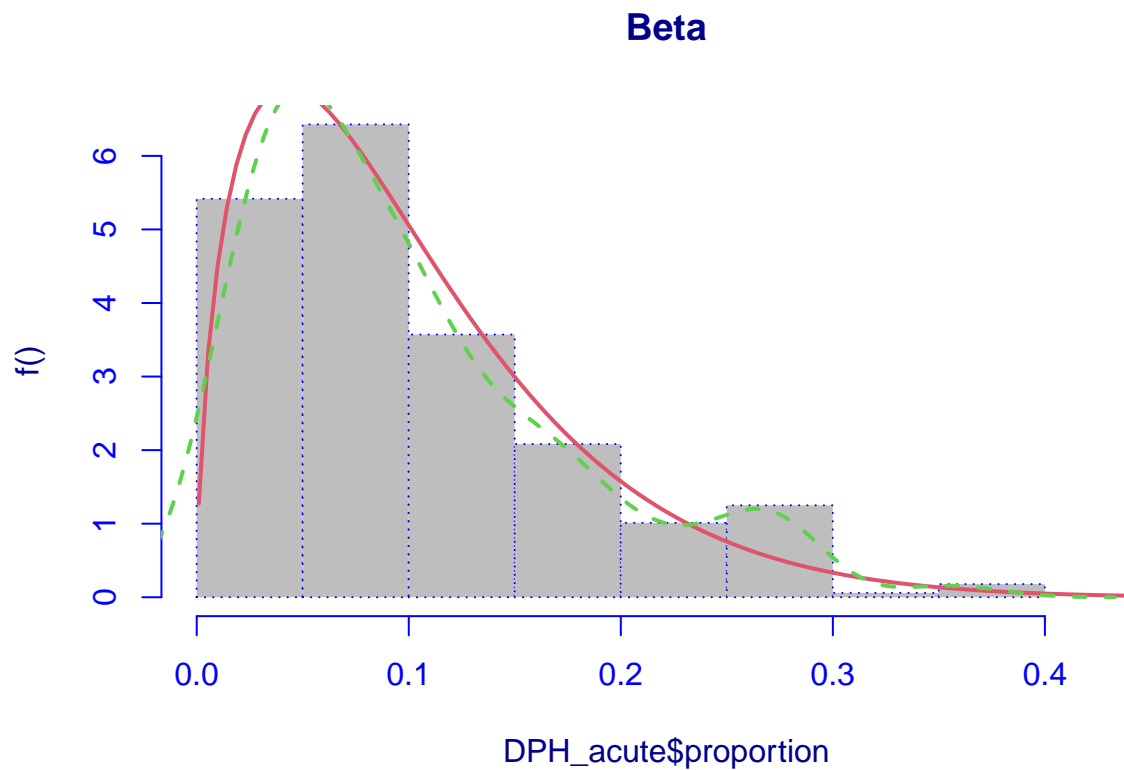


```
mGA <- histDist(DPH_acute$proportion, "GA", density = T, main = "Gamma")
```

Gamma



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

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

```
##      df      AIC
## mGA  2 -928.4186
## mBE  2 -927.5552
```

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

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

```
formula(backward.acute) # get the final formula , proportion ~ treatment + time_min
```

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

```
backward.acute$anova
```

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

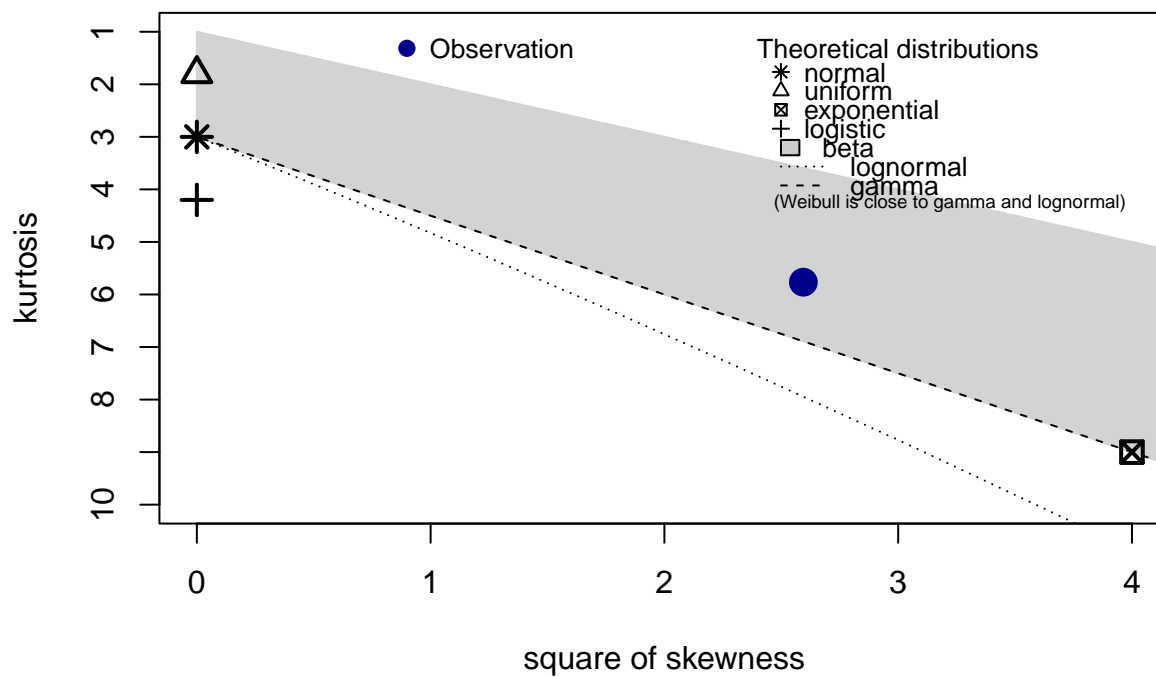
```
## proportion ~ treatment + time_min + treatment:time_min
##
##
## Step Df Deviance Resid. Df Resid. Dev      AIC
## 1              315    136.6197 -1039.682

summary(backward.acute)

##
## Call:
## glm(formula = proportion ~ treatment + time_min + treatment:time_min,
##      family = Gamma(link = "inverse"), data = DPH_acute)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5009  -0.5483  -0.1875   0.2828   1.4869
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         7.0485     1.1485   6.137 2.52e-09 ***
## treatmentenv_rel      0.3589     1.6661   0.215 0.829560
## treatmenthigh     -1.2514     1.4870  -0.842 0.400703
## time_min5           3.9860     2.1335   1.868 0.062648 .
## time_min10          6.6268     2.5068   2.643 0.008617 **
## time_min15         11.5562     3.2418   3.565 0.000421 ***
## time_min20          9.4464     2.9228   3.232 0.001360 **
## time_min25          8.9515     2.8488   3.142 0.001836 **
## time_min30         10.9291     3.1464   3.474 0.000586 ***
## treatmentenv_rel:time_min5  2.7659     3.3662   0.822 0.411900
## treatmenthigh:time_min5    -2.9162     2.5877  -1.127 0.260622
## treatmentenv_rel:time_min10  3.7436     4.0165   0.932 0.352020
## treatmenthigh:time_min10   -6.2463     2.8618  -2.183 0.029800 *
## treatmentenv_rel:time_min15 -2.2969     4.3978  -0.522 0.601837
## treatmenthigh:time_min15  -11.2230     3.5212  -3.187 0.001580 **
## treatmentenv_rel:time_min20  2.8993     4.5121   0.643 0.520979
## treatmenthigh:time_min20   -8.4924     3.2627  -2.603 0.009681 **
## treatmentenv_rel:time_min25  0.4832     4.1357   0.117 0.907072
## treatmenthigh:time_min25   -7.8222     3.2065  -2.439 0.015261 *
## treatmentenv_rel:time_min30  1.6635     4.6879   0.355 0.722939
## treatmenthigh:time_min30   -9.4534     3.4923  -2.707 0.007162 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.4248057)
##
## Null deviance: 207.95  on 335  degrees of freedom
## Residual deviance: 136.62  on 315  degrees of freedom
## AIC: -1039.7
##
## 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)
```

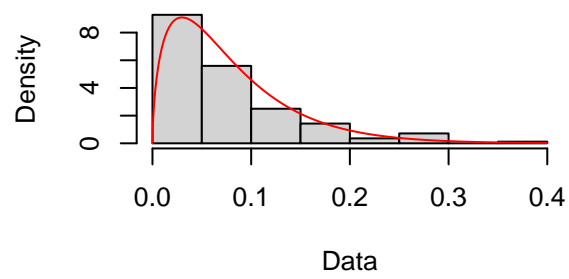
Cullen and Frey graph



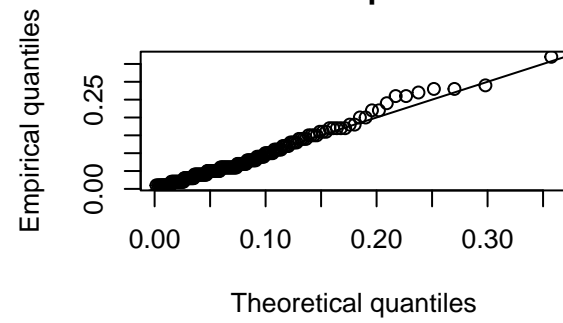
```
## summary statistics
## -----
## min: 0.01 max: 0.37
## median: 0.06
## mean: 0.07952381
## estimated sd: 0.06722747
## estimated skewness: 1.610722
## estimated kurtosis: 5.765863
```

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

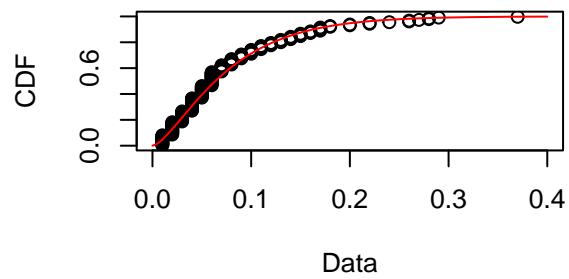
Empirical and theoretical dens.



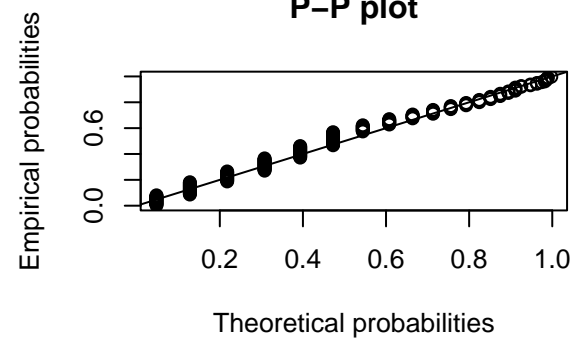
Q-Q plot



Empirical and theoretical CDFs

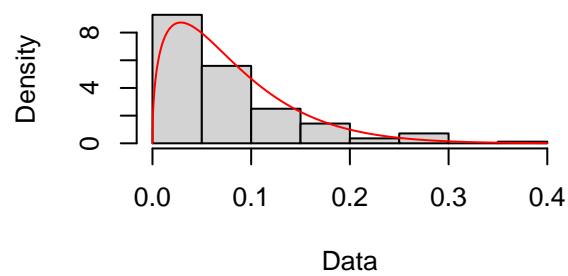


P-P plot

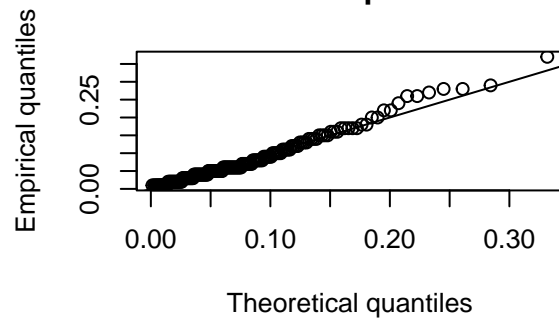


```
plot(fit.beta)
```

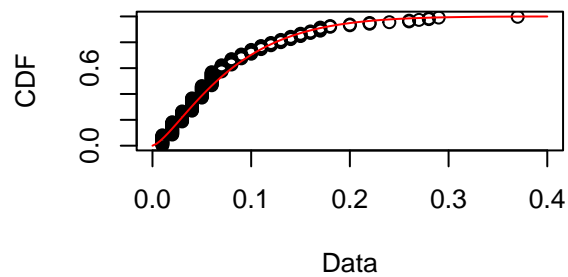
Empirical and theoretical dens.



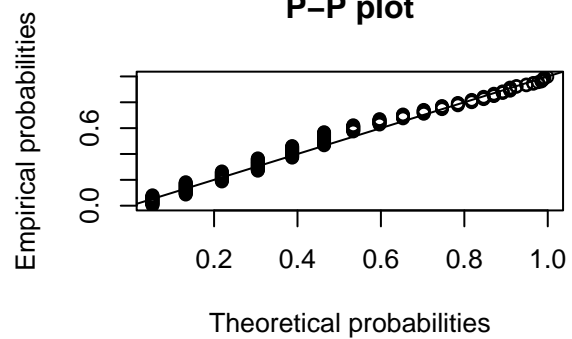
Q-Q plot



Empirical and theoretical CDFs

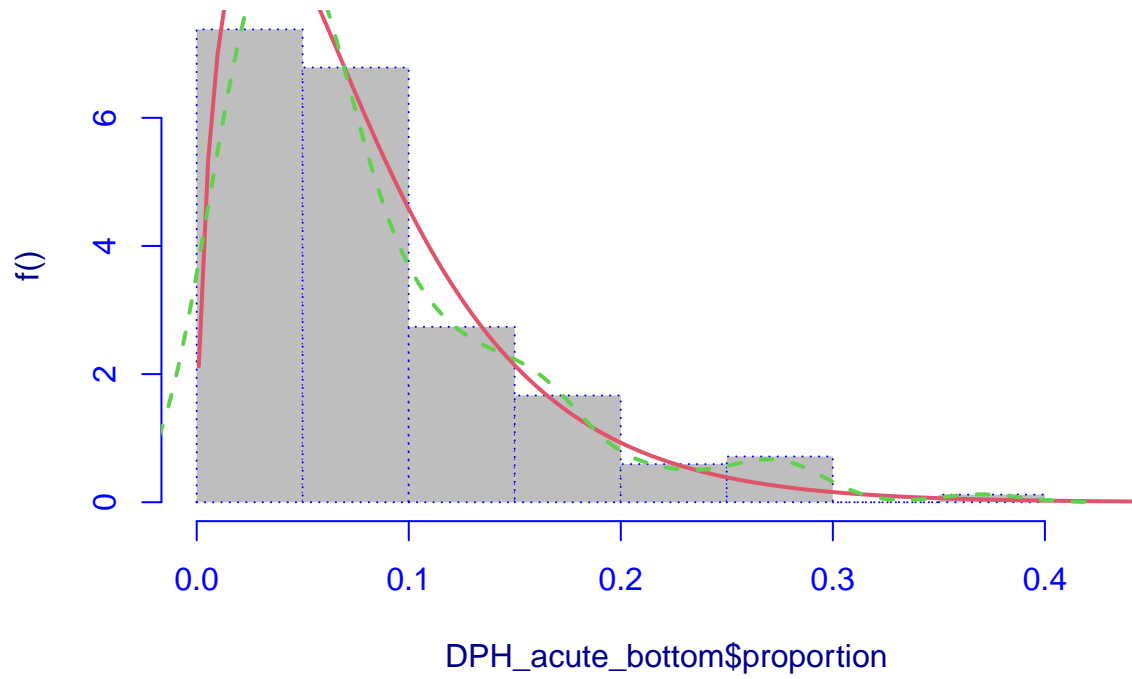


P-P plot



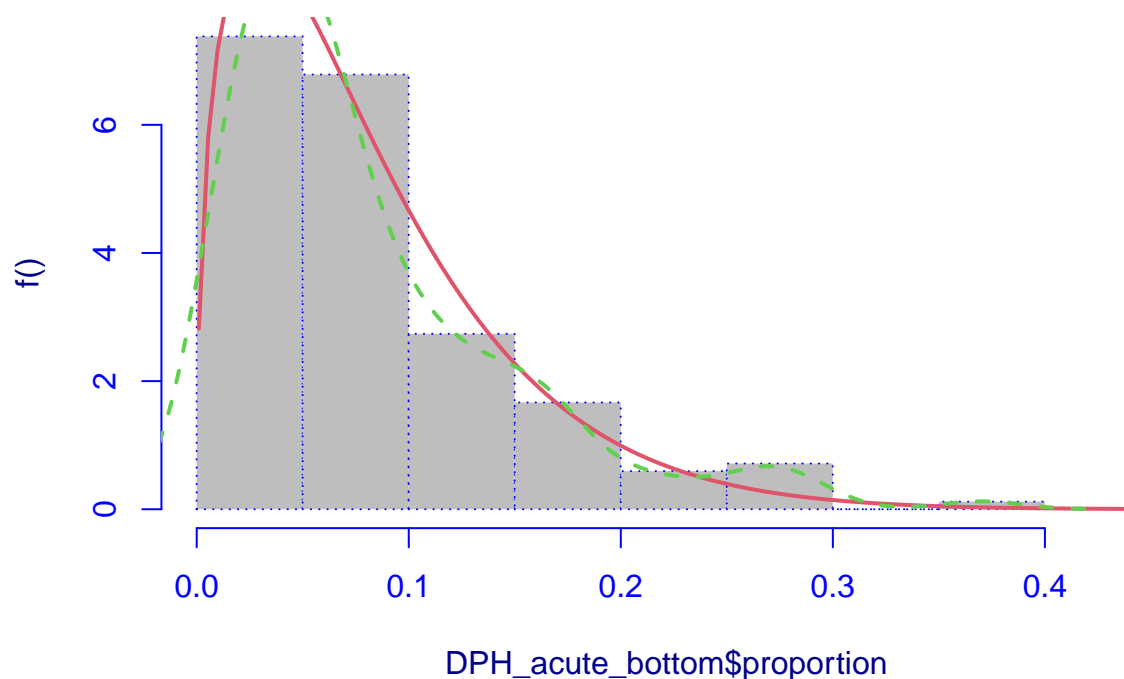
```
mGA <- histDist(DPH_acute_bottom$proportion, "GA", density = T, main = "Gamma")
```

Gamma



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

Beta



```
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 = "log",
  data = DPH_acute_bottom)
```

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

```
formula(backward.acute_bottom) # get the final formula , proportion ~ treatment + time_min
```

```
## 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:
```

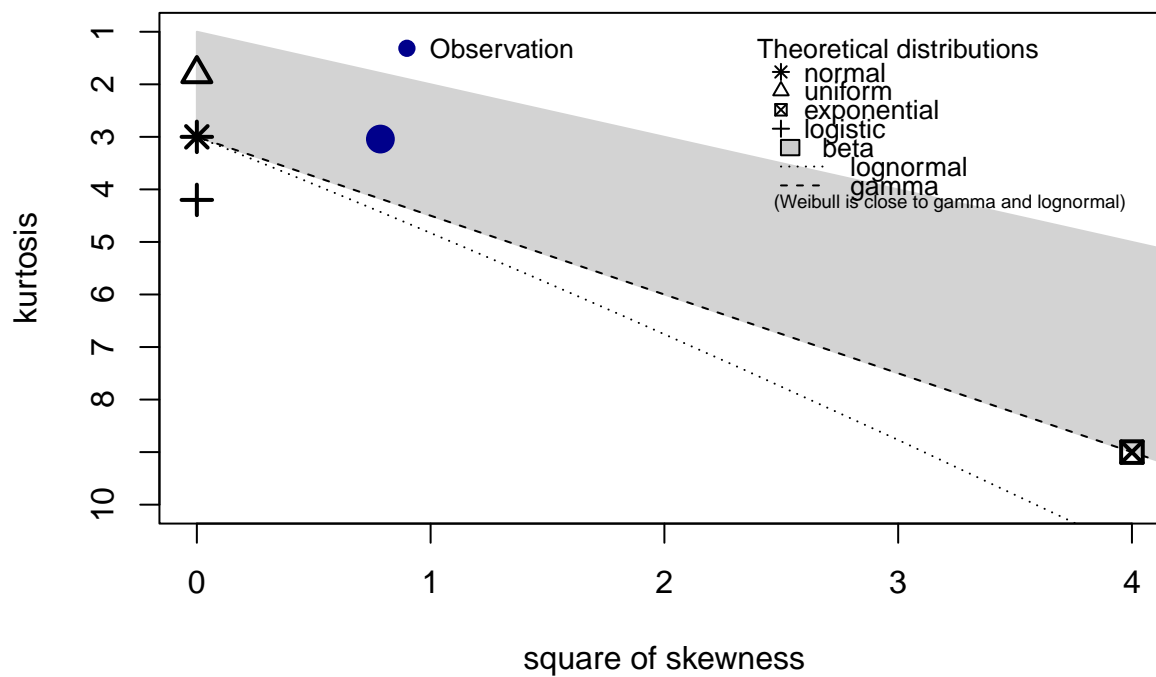
```
## proportion ~ treatment + time_min + treatment:time_min
##
##
## Step Df Deviance Resid. Df Resid. Dev      AIC
## 1              147    47.47162 -649.9473

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

# 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)
```

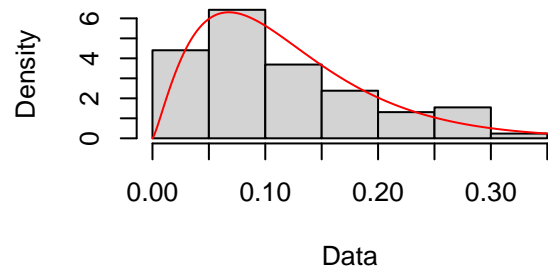

Cullen and Frey graph



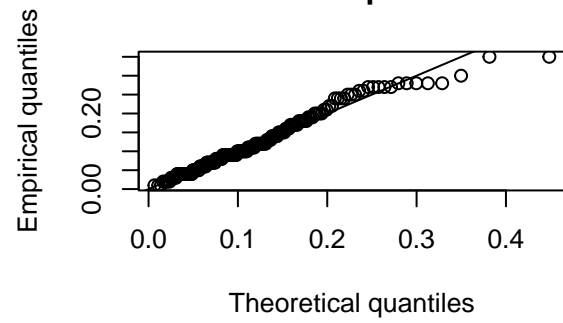
```
## summary statistics
## -----
## min: 0.01 max: 0.35
## median: 0.1
## mean: 0.1198214
## estimated sd: 0.07745559
## estimated skewness: 0.8860857
## estimated kurtosis: 3.041897
```

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

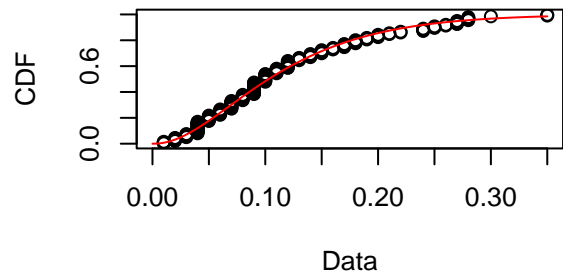
Empirical and theoretical dens.



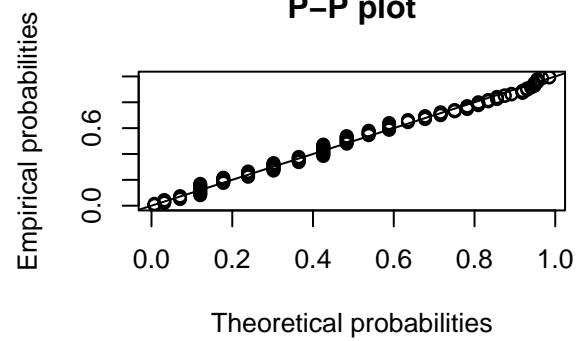
Q-Q plot



Empirical and theoretical CDFs

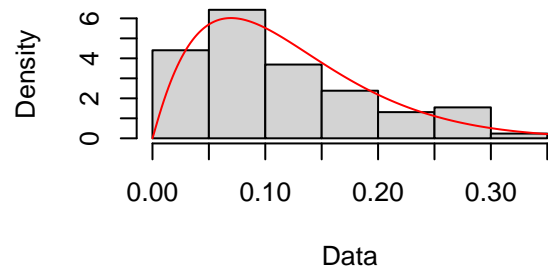


P-P plot

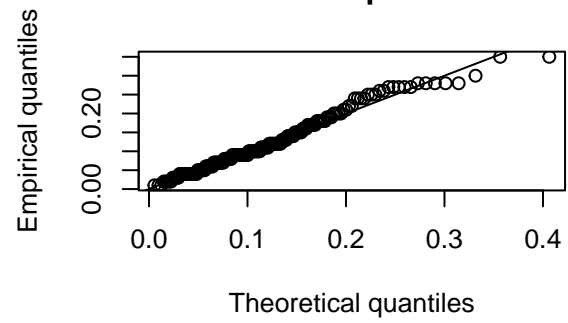


```
plot(fit.beta)
```

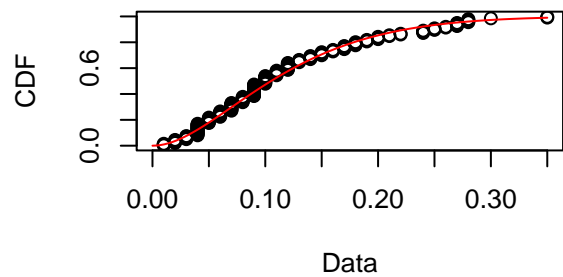
Empirical and theoretical dens.



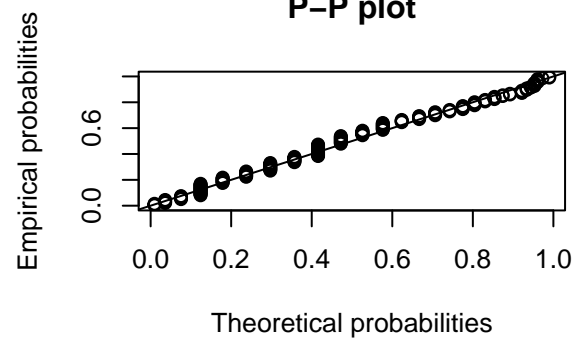
Q-Q plot



Empirical and theoretical CDFs

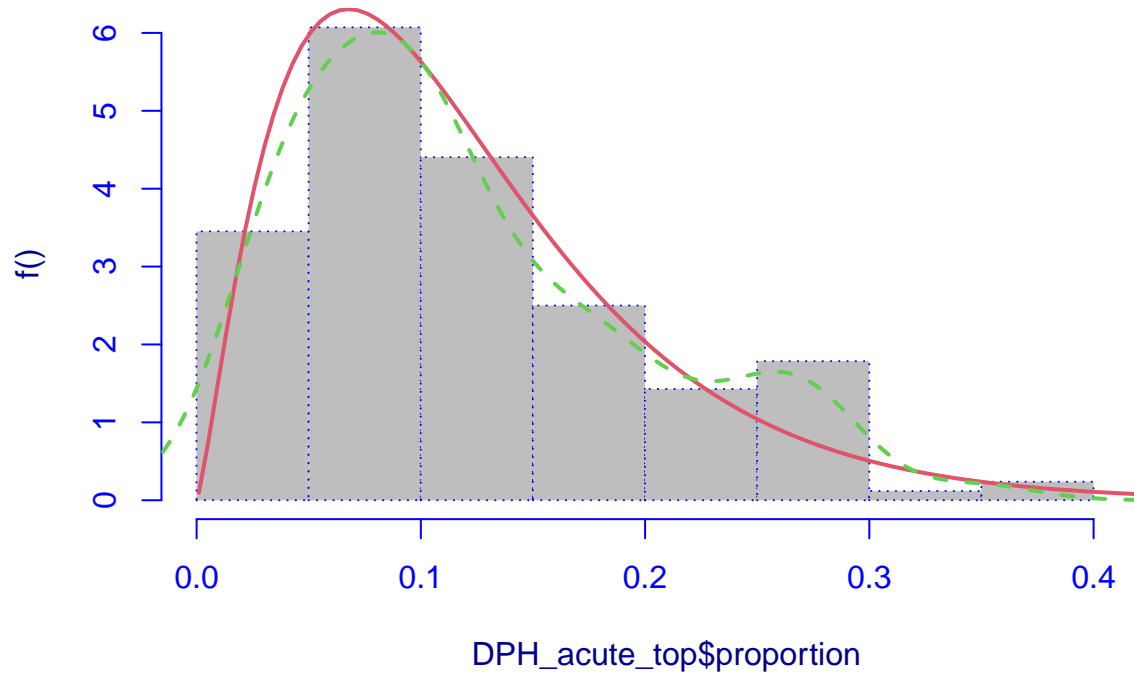


P-P plot

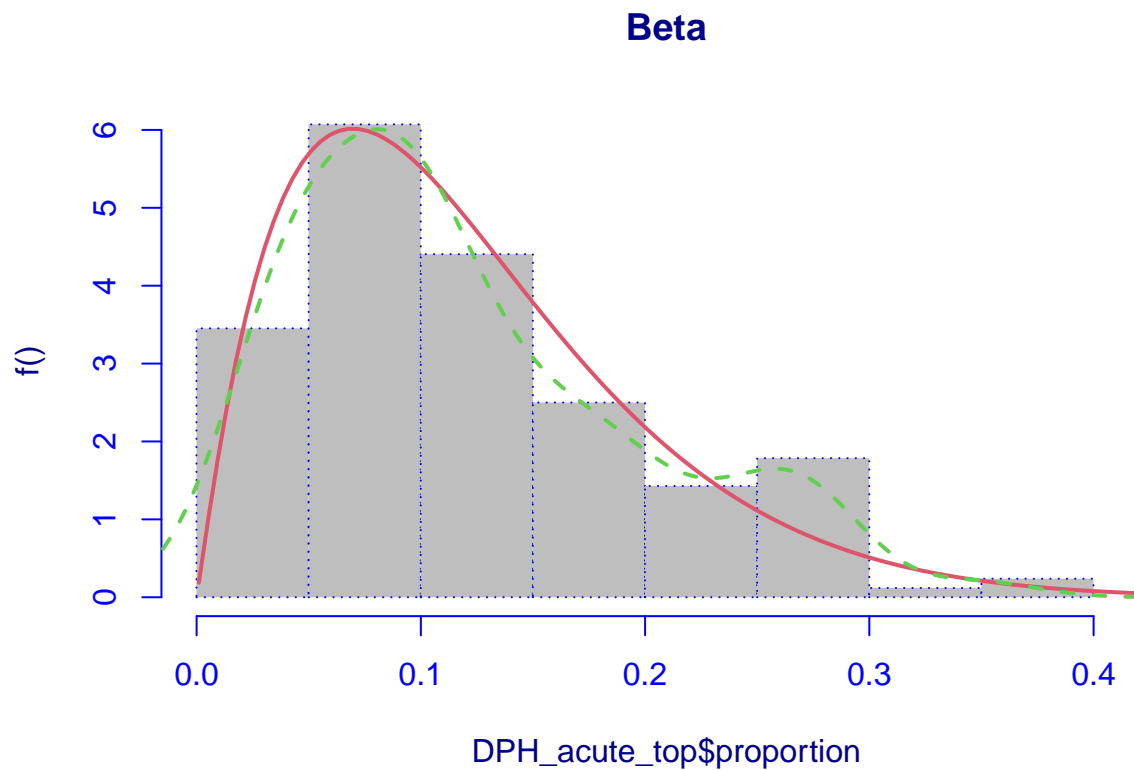


```
mGA <- histDist(DPH_acute_top$proportion, "GA", density = T, main = "Gamma")
```

Gamma



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

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

```
formula(backward.acute_top) # get the final formula , proportion ~ treatment + time_min
```

```
## 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
```

```
# automatic distribution fitting with fitDist for lorazepam and running the
# model
```

```
fitDist(proportion, data = lorazepam, type = "realAll", try.gamlss = T) # SHASH distribution
```

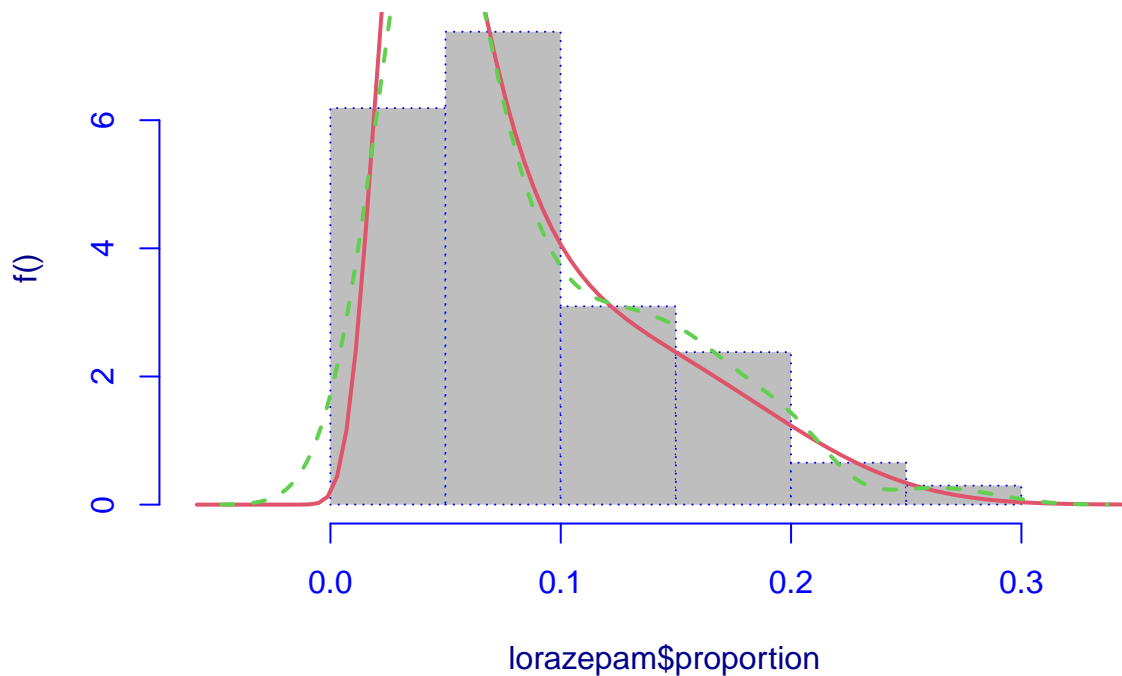
```
## |
```

```
|
```

```
## [1] 1.594
## Tau Coefficients:
## [1] 0.4369
##
## Degrees of Freedom for the fit: 4 Residual Deg. of Freedom 332
## Global Deviance: -1135.84
## AIC: -1127.84
## SBC: -1112.58
```

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

The lorazepam\$proportion and the fitted SHASH distribution



```
##
## Family: c("SHASH", "Sinh-Arcsinh")
## Fitting method: "nlminb"
##
## Call: gamlssML(formula = lorazepam$proportion, family = "SHASH")
##
## Mu Coefficients:
## [1] 0.06362
## Sigma Coefficients:
## [1] -1.863
## Nu Coefficients:
## [1] 1.594
## Tau Coefficients:
## [1] 0.4369
```

```
##
## Degrees of Freedom for the fit: 4 Residual Deg. of Freedom    332
## Global Deviance:      -1135.84
##           AIC:        -1127.84
##           SBC:        -1112.58

lo.mod <- gamlss(proportion ~ treatment + time_min + treatment:time_min, family = SHASH(),
  data = lorazepam, method = CG())

## GAMLSS-CG iteration 1: Global Deviance = 1.207772e+157
## GAMLSS-CG iteration 2: Global Deviance = 1.207772e+157

summary(lo.mod)

## *****
## Family:  c("SHASH", "Sinh-Arcsinh")
##
## Call:
## gamlss(formula = proportion ~ treatment + time_min + treatment:time_min,
##       family = SHASH(), data = lorazepam, method = CG())
##
## Fitting method: CG()
##
## -----
## Mu link function:  identity
## Mu Coefficients:
##
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.431e-01  7.498e-03  19.091  <2e-16 ***
## treatmentenv_rel -1.291e-03  9.857e-03  -0.131    0.896
## treatmenthigh    -2.452e-03  1.006e-02  -0.244    0.808
## time_min5        -3.377e-03  9.606e-03  -0.352    0.725
## time_min10       -1.011e-03  9.749e-03  -0.104    0.917
## time_min15       -1.300e-03  9.693e-03  -0.134    0.893
## time_min20       -1.569e-03  9.747e-03  -0.161    0.872
## time_min25       -4.442e-03  9.716e-03  -0.457    0.648
## time_min30       -2.027e-03  9.322e-03  -0.217    0.828
## treatmentenv_rel:time_min5  2.265e-03  1.310e-02   0.173    0.863
## treatmenthigh:time_min5    5.564e-03  1.318e-02   0.422    0.673
## treatmentenv_rel:time_min10 2.697e-04  1.299e-02   0.021    0.983
## treatmenthigh:time_min10   1.361e-03  1.320e-02   0.103    0.918
## treatmentenv_rel:time_min15 5.197e-04  1.307e-02   0.040    0.968
## treatmenthigh:time_min15  -1.502e-03  1.337e-02  -0.112    0.911
## treatmentenv_rel:time_min20 -6.125e-05  1.322e-02  -0.005    0.996
## treatmenthigh:time_min20   4.526e-03  1.365e-02   0.332    0.740
## treatmentenv_rel:time_min25 8.310e-04  1.307e-02   0.064    0.949
## treatmenthigh:time_min25  -1.986e-03  1.353e-02  -0.147    0.883
## treatmentenv_rel:time_min30 -2.770e-03  1.282e-02  -0.216    0.829
## treatmenthigh:time_min30  -3.754e-03  1.311e-02  -0.286    0.775
## ---
## 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) -1.9593      0.1061  -18.47  <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)  5.36699      0.08622   62.24  <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) -0.77935      0.09354   -8.332 2.07e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## -----
## No. of observations in the fit:  336
## Degrees of Freedom for the fit:  24
##      Residual Deg. of Freedom:  312
##                      at cycle:  2
##
## Global Deviance:      1.207772e+157
##           AIC:      1.207772e+157
##           SBC:      1.207772e+157
## *****
```

```
# 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) # SHASH distribution
```

```
## | |

## Warning in MLE(l13, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)

## | |=====

## Warning in MLE(l13, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)

## | |=====

## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```

##      |=====

## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)

##      |=====

## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in MLE(l12, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 false convergence (8)

##      |=====

```

```

## 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 nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

```

```

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##      |=====

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

```

```

## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

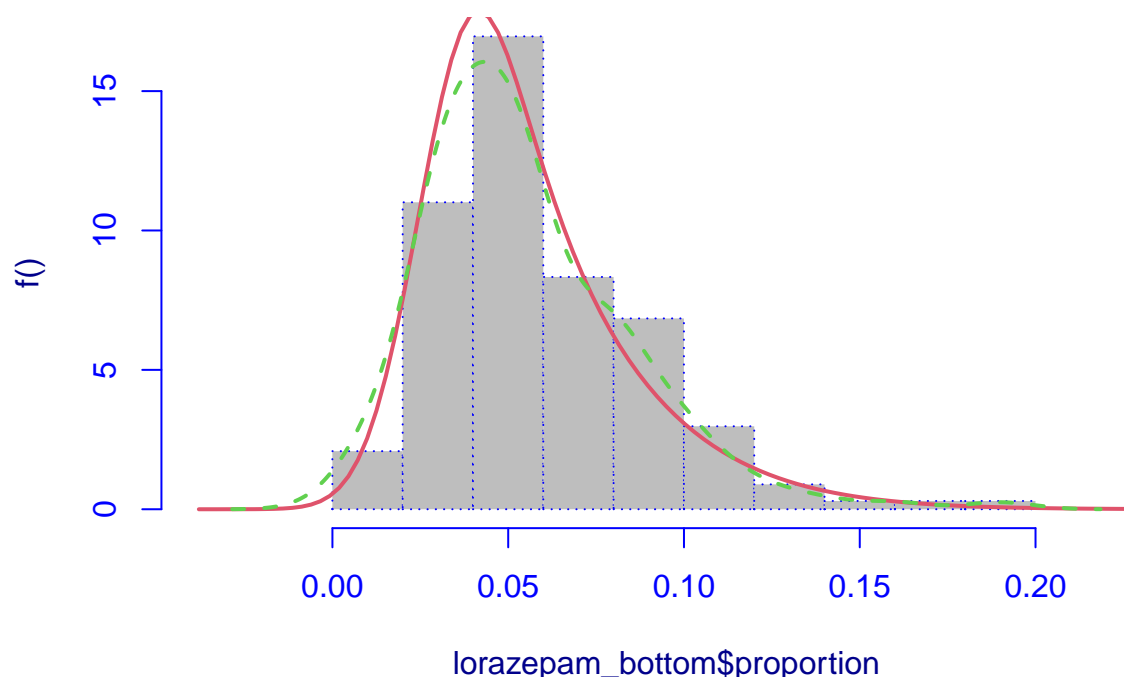
## Warning in nlminb(start = start, objective = f, control = optim.control): NA/NaN
## function evaluation

##
## Family: c("RG", "Reverse Gumbel")
## Fitting method: "nlminb"
##
## Call: gamlssML(formula = y, family = DIST[i])
##
## Mu Coefficients:
## [1] 0.04201
## Sigma Coefficients:
## [1] -3.794
##
## Degrees of Freedom for the fit: 2 Residual Deg. of Freedom 166
## Global Deviance: -744.078
## AIC: -740.078
## SBC: -733.83

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
```

```
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)
```

```
## Warning in summary.gamlss(lo_bottom.mod): summary: vcov has failed, option qr is used instead
```

```
## *****
## 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
## *****

# 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) # SHASH distribution

## Warning in MLE(l12, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 false convergence (8)

## | |

## Warning in MLE(l12, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 false convergence (8)

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

## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 function evaluation limit
## reached without convergence (9)

## | |=====

## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 function evaluation limit
## reached without convergence (9)

## | |=====

```



```
## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
## |
```

```
|=====
```

```
## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 function evaluation limit
## reached without convergence (9)
```

```
## |
```

```
|=====
```

```
## 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
```

```
## |
```

```
|=====
```

```
## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
## |
```

```
|=====
```

```
## Warning in MLE(l12, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
## |
```

```
|=====
```

```
## Warning in MLE(l12, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
## |
```

```
|=====
```

```
## Warning in MLE(l12, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma), :
## possible convergence problem: optim gave code=1 false convergence (8)
```

```
## |
```

```
|=====
```

```
## Warning in 'formals<-'('*tmp*', envir = new.env(), value = alist(nu = fv)):
## 'fun' is not a function
```

```
## Warning in body(fun): argument is not a function
```

```
## Warning in 'formals<-'('*tmp*', envir = new.env(), value = alist(nu = fv)):
## 'fun' is not a function
```

```
## Warning in body(fun): argument is not a function
```

```
## Warning in 'formals<-'('*tmp*', envir = new.env(), value = alist(nu = nu)):
## 'fun' is not a function
```

```

## Warning in body(fun): argument is not a function

## Warning in 'formals<-'('*tmp*', envir = new.env(), value = alist(nu = nu)):
## 'fun' is not a function

## Warning in body(fun): argument is not a function

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

## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 function evaluation limit
## reached without convergence (9)

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

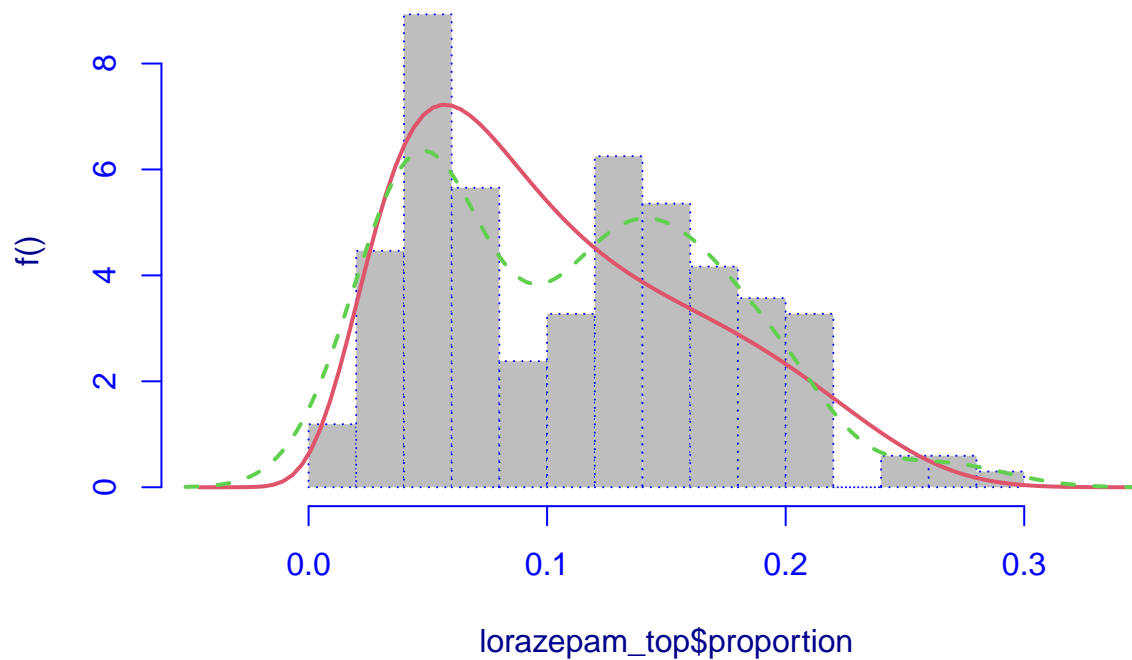
## Warning in MLE(l14, start = list(eta.mu = eta.mu, eta.sigma = eta.sigma, :
## possible convergence problem: optim gave code=1 function evaluation limit
## reached without convergence (9)

##
## 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



```
##
## 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

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)
```

```
## Warning in summary.gamlss(lo_top.mod): summary: vcov has failed, option qr is used instead
```

```
## *****
## 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
## *****

```