

warmXtrophic Project: Plant Composition Data Analyses

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Load in packages & data

```
# Clear all existing data
rm(list = ls())

# Load packages
library(tidyverse)
library(ggplot2)
library(lme4)
library(lmerTest)
library(olsrr)
library(predictmeans)
library(car)
library(fitdistrplus)
library(ggpubr)
library(rstatix)
library(vegan)
library(interactions)
library(sjPlot)
library(effects)
library(glmmTMB)
library(labdsrv) # used with Vegan package, the matrify() and matrify2() functions
library(agricolae) # HSD.test() function
library(emmeans)
library(scales)
library(fitdistrplus)
library(moments) # for calculating skewness of data
library(jtools) # summ() function
library(GGally) # ggpairs() function
library(bbmle) # AICtab() function

# Set working directory
Sys.getenv("L1DIR")

## [1] "/Volumes/GoogleDrive/Shared drives/SpaCE_Lab_warmXtrophic/data/L1"

L0_dir <- Sys.getenv("LODIR")
L1_dir <- Sys.getenv("L1DIR")
L2_dir <- Sys.getenv("L2DIR")
list.files(L1_dir)
```

```

## [1] "ANPP"           "climate_data"      "CN"
## [4] "Greenness"       "herbivory"        "HOB0_data"
## [7] "PAR"             "phenology"        "plant_composition"
## [10] "SLA"

# Set ggplot2 plotting This code for ggplot2 sets the theme to mostly black and
# white (Arial font, and large font, base size=24)
theme_set(theme_bw(14))
theme_update(axis.text.x = element_text(size = 12, angle = 90), axis.text.y = element_text(size = 12))

# read in plant comp data
comp_species <- read.csv(file.path(L2_dir, "plant_composition/final_plant_comp_species_L2.csv"))
comp_plot <- read.csv(file.path(L2_dir, "plant_composition/final_plant_comp_plot_L2.csv"))
comp_plot_origin <- read.csv(file.path(L2_dir, "plant_composition/final_plant_comp_plot_origin_L2.csv"))
comp_plot_growthhabit <- read.csv(file.path(L2_dir, "plant_composition/final_plant_comp_plot_growthhabit"))

comp_species <- comp_species %>% select(-X) # get rid of 'X' column that shows up
comp_plot <- comp_plot %>% select(-X) # get rid of 'X' column that shows up
comp_plot_origin <- comp_plot_origin %>% select(-X)
comp_plot_growthhabit <- comp_plot_growthhabit %>% select(-X)

# Order warmed and ambient so that warmed shows up first in plotting (and is
# default is red = warmed; blue = ambient). First make it a factor
comp_species$state <- as.factor(comp_species$state)
levels(comp_species$state)

## [1] "ambient" "warmed"

# [1] 'ambient' 'warmed'
comp_species$state <- factor(comp_species$state, levels(comp_species$state)[c(2,
  1)])
levels(comp_species$state)

## [1] "warmed"   "ambient"

# [1] 'warmed' 'ambient'

comp_plot$state <- as.factor(comp_plot$state)
levels(comp_plot$state)

## [1] "ambient" "warmed"

# [1] 'ambient' 'warmed'
comp_plot$state <- factor(comp_plot$state, levels(comp_plot$state)[c(2, 1)])
levels(comp_plot$state)

## [1] "warmed"   "ambient"

```

```

# [1] 'warmed' 'ambient'

# create dataframes for kbs and umbs - remember that these contain species within
# plots
comp_kbs_spp <- subset(comp_species, site == "kbs")
comp_umbs_spp <- subset(comp_species, site == "umbs")
comp_umbs_spp <- subset(comp_umbs_spp, year_factor != "7") # delete 2021 data from umbs dataframe (does

# create dataframes for kbs and umbs
comp_kbs_plot <- subset(comp_plot, site == "kbs")
comp_umbs_plot <- subset(comp_plot, site == "umbs")
comp_umbs_plot <- subset(comp_umbs_plot, year_factor != "7") # delete 2021 data from umbs dataframe (does

kbs_comp_plot_origin <- subset(comp_plot_origin, site == "kbs")
kbs_comp_plot_growthhabit <- subset(comp_plot_growthhabit, site == "kbs")
umbs_comp_plot_origin <- subset(comp_plot_origin, site == "umbs")
umbs_comp_plot_origin <- subset(umbs_comp_plot_origin, year_factor != "7") # delete 2021 data
umbs_comp_plot_growthhabit <- subset(comp_plot_growthhabit, site == "umbs")
umbs_comp_plot_growthhabit <- subset(umbs_comp_plot_growthhabit, year_factor != "7") # delete 2021 data

```

Data exploration - some different ways of visualizing these data

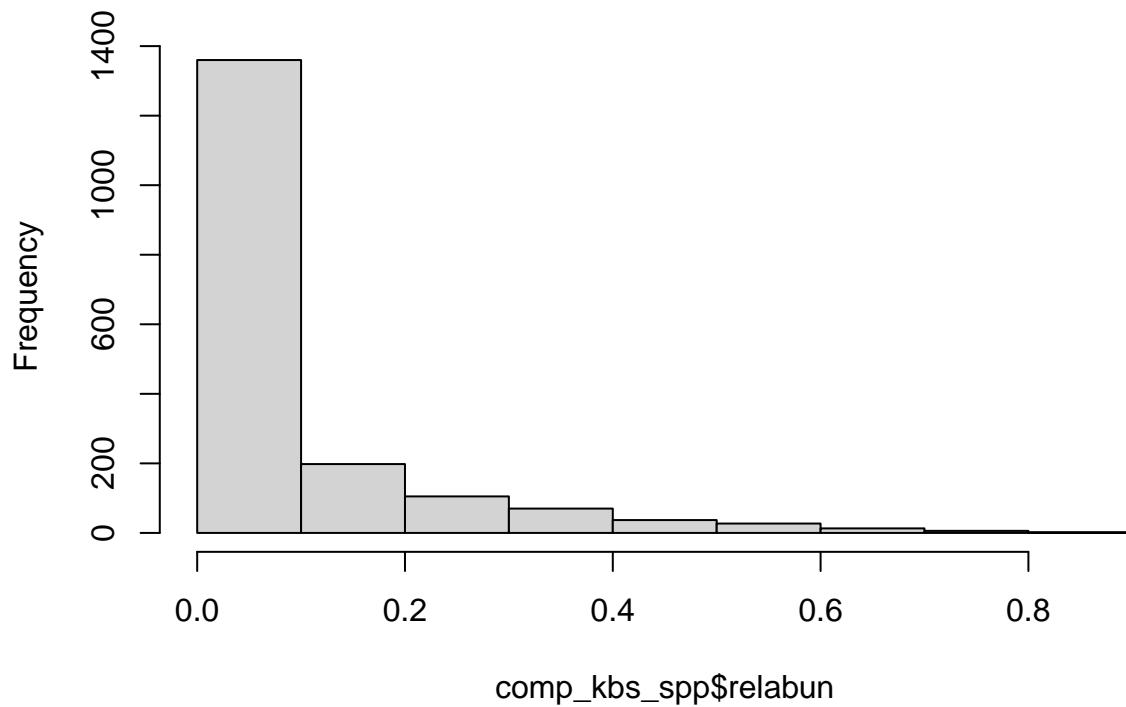
KBS SPECIES LEVEL - Looking at RELATIVE ABUNDANCE

```

### KBS ####
hist(comp_kbs_spp$relabun) # very skewed to the right

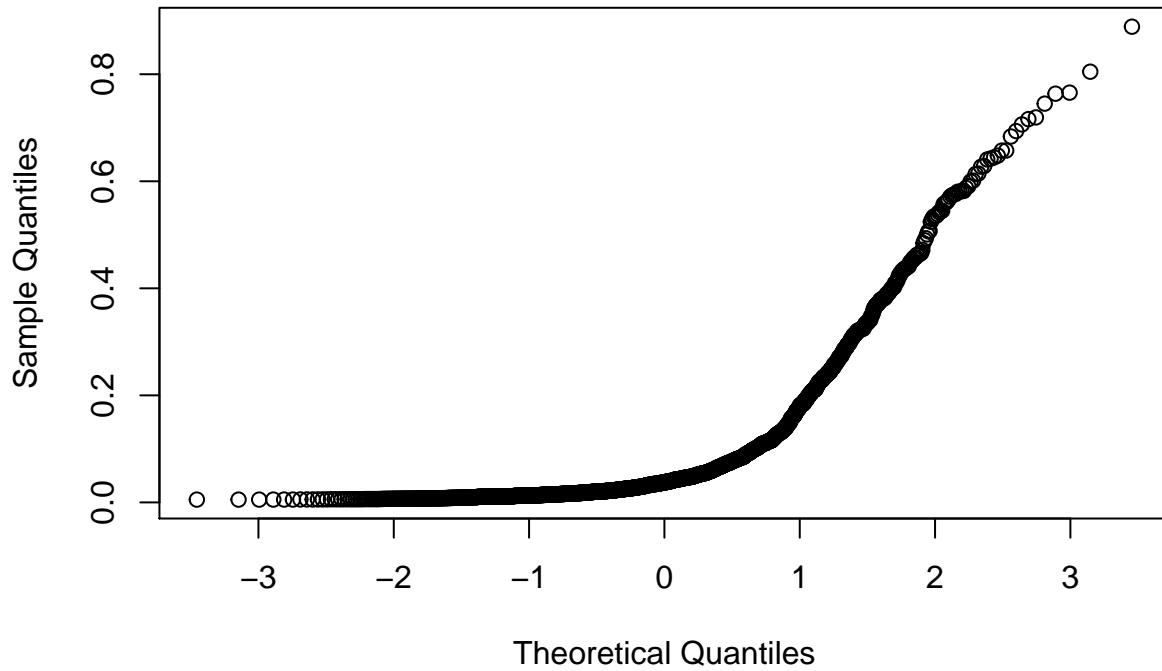
```

Histogram of comp_kbs_spp\$relabun



```
qqnorm(comp_kbs_spp$relabun)
```

Normal Q-Q Plot



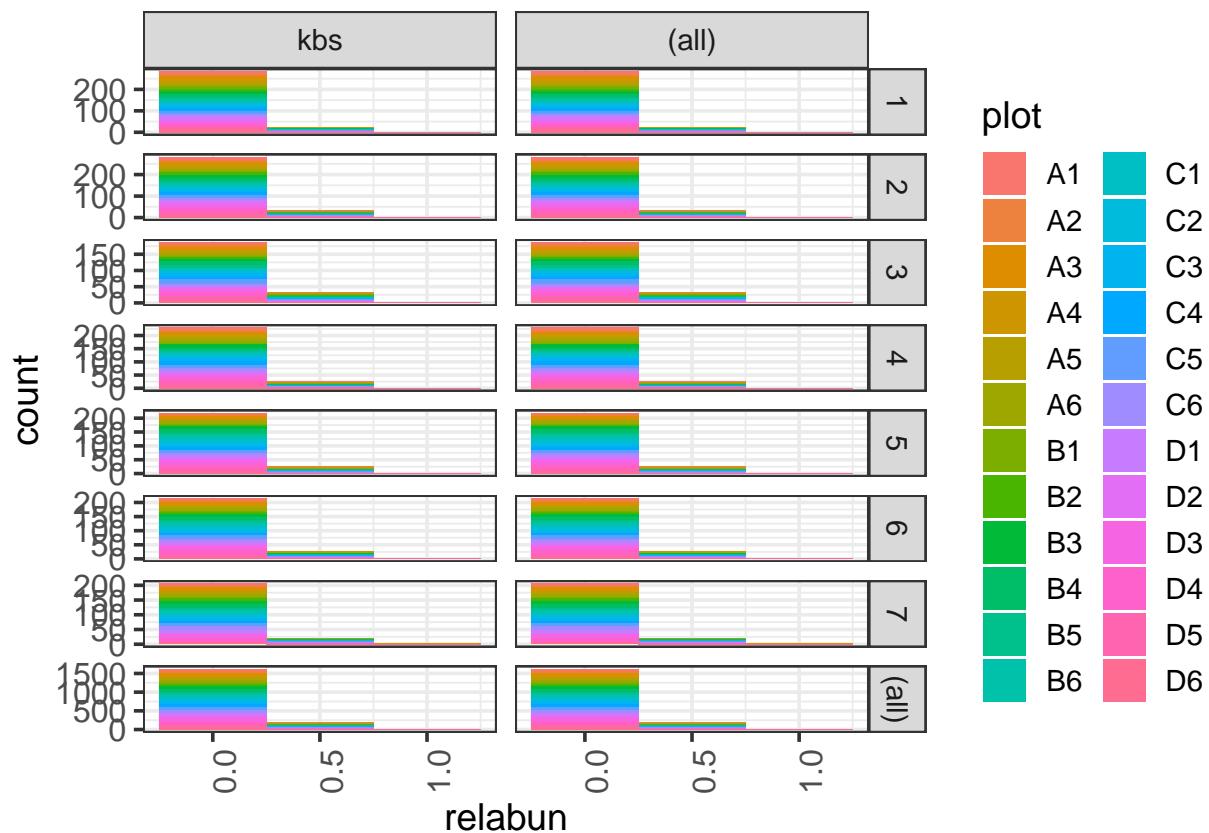
```

shapiro.test(comp_kbs_spp$relabun) # pvalue is < 0.05 so we reject the null hypothesis that the data is normal

## 
## Shapiro-Wilk normality test
## 
## data: comp_kbs_spp$relabun
## W = 0.65236, p-value < 2.2e-16

# Visualizing relative abundance for kbs at the PLOT LEVEL
ggplot(comp_kbs_spp, aes(relabun, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")

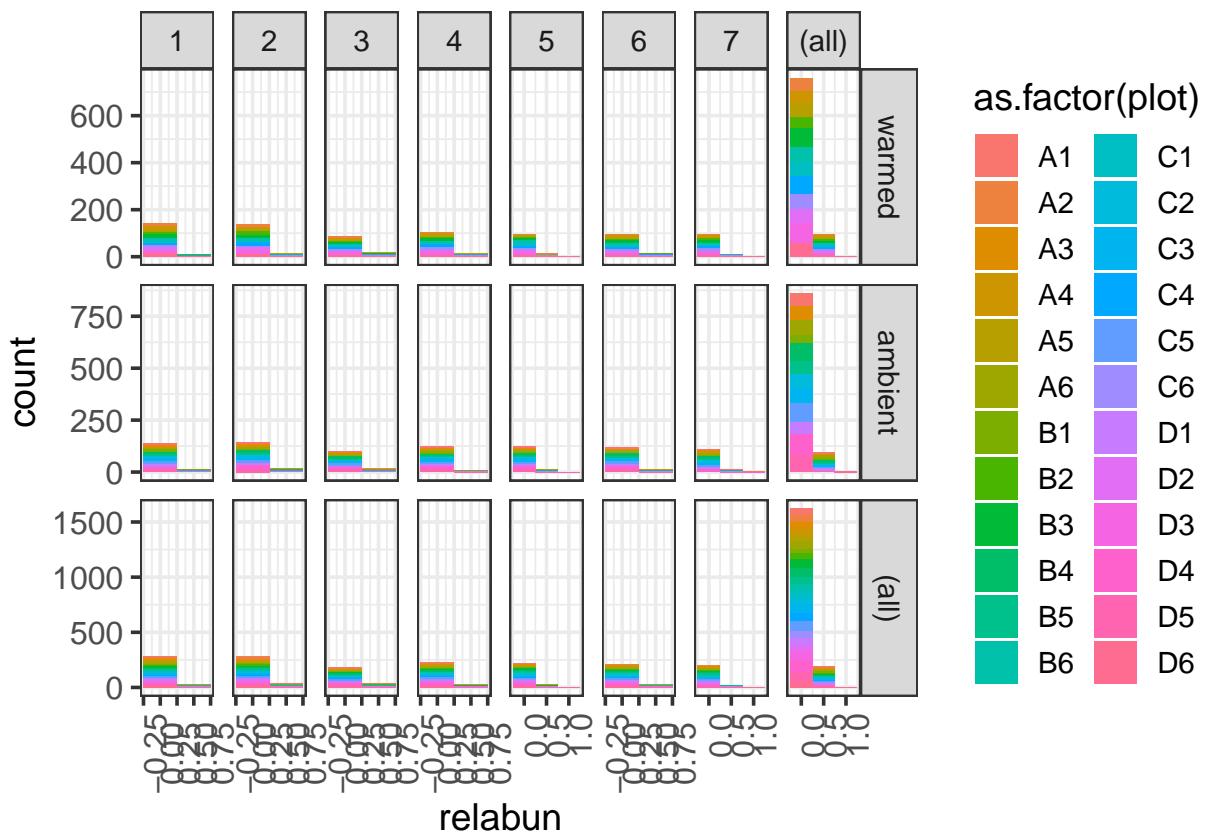
```



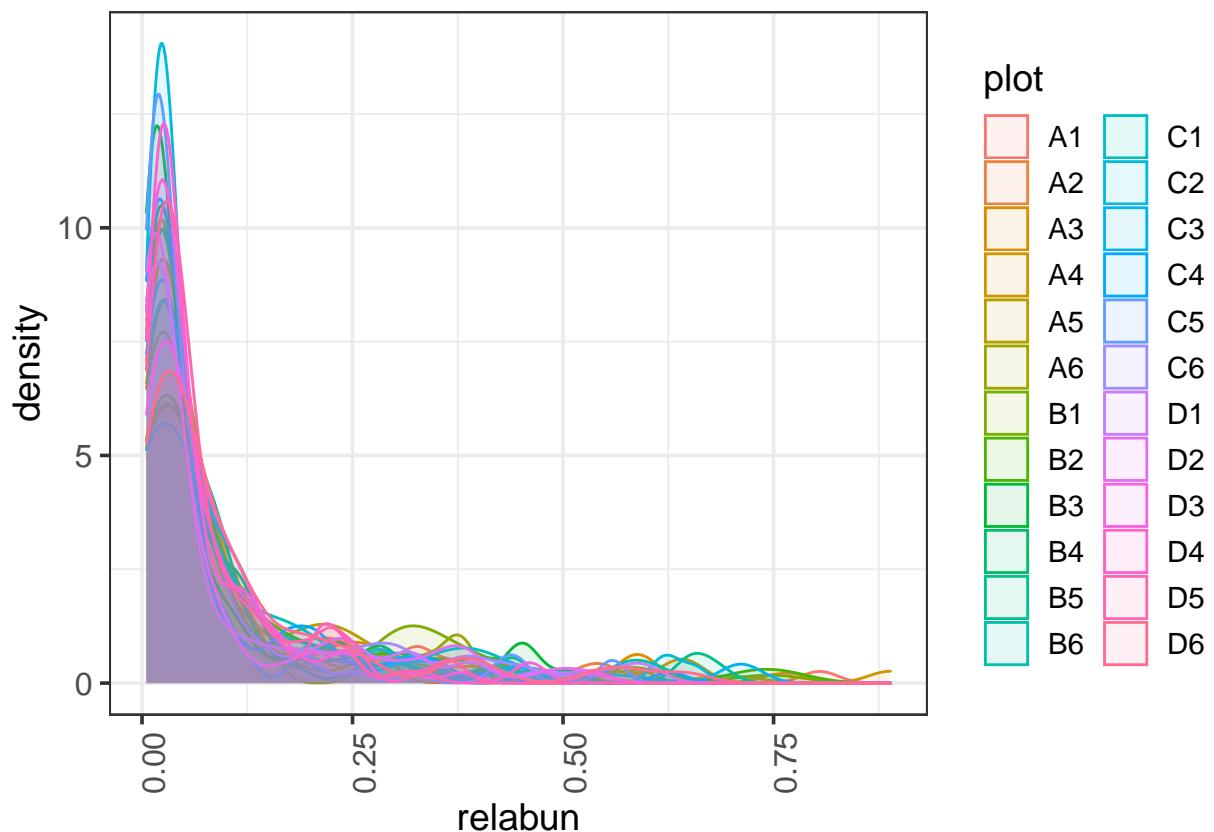
```

ggplot(comp_kbs_spp, aes(relabun, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year_factor, margins = TRUE, scales = "free")

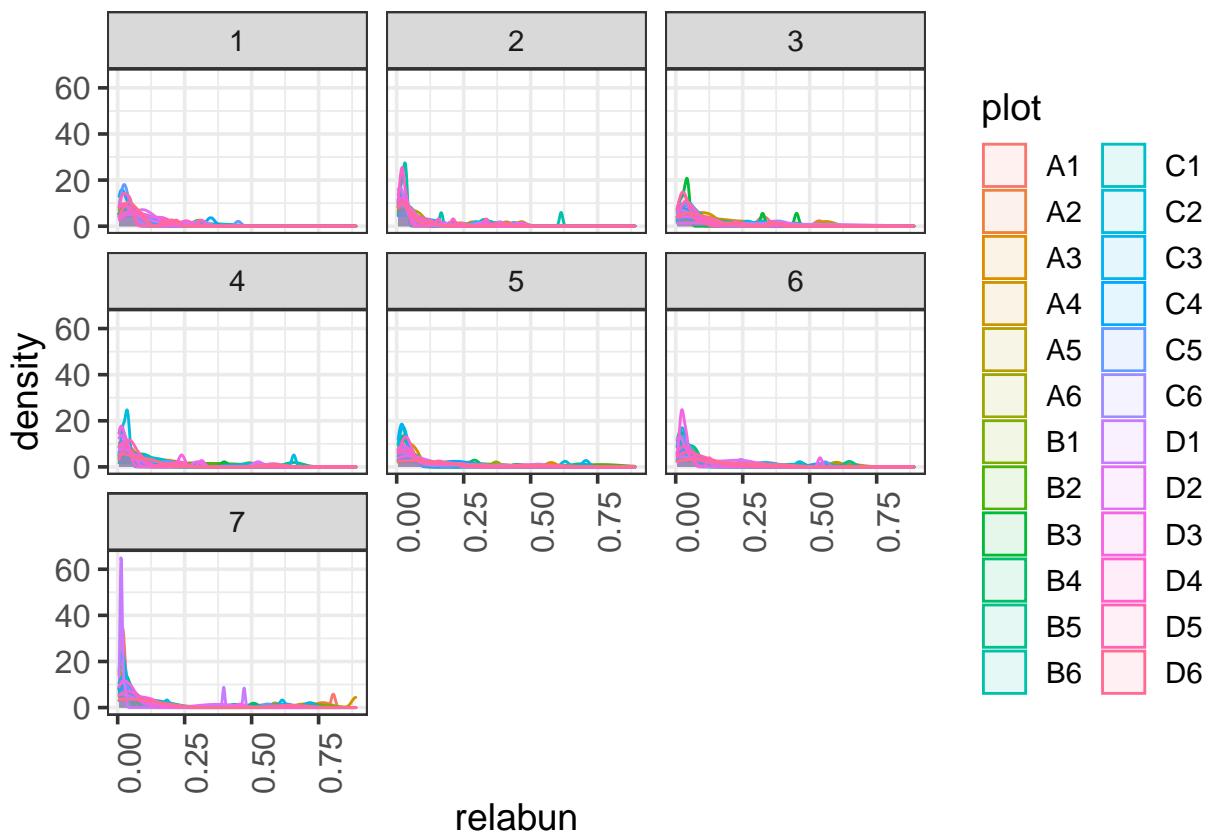
```



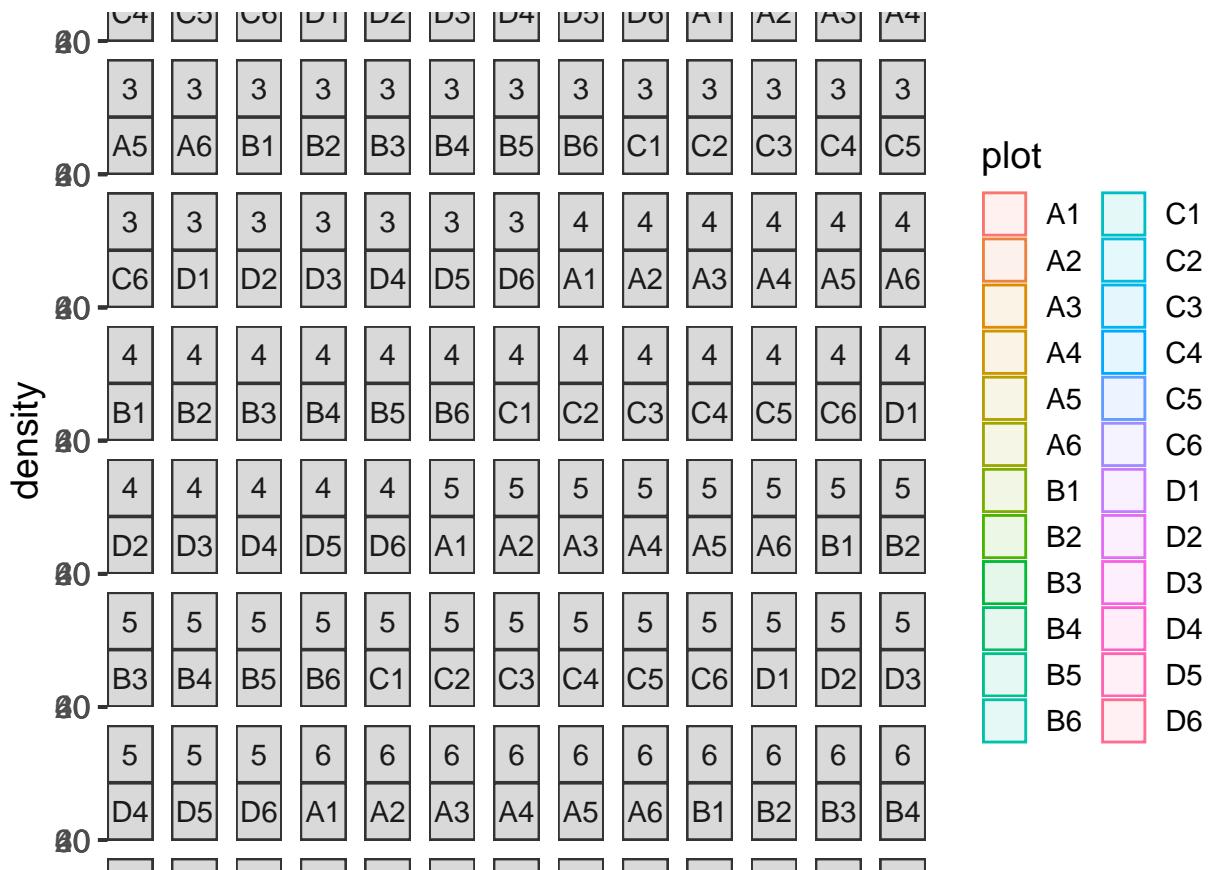
```
ggplot(comp_kbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(comp_kbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor)
```

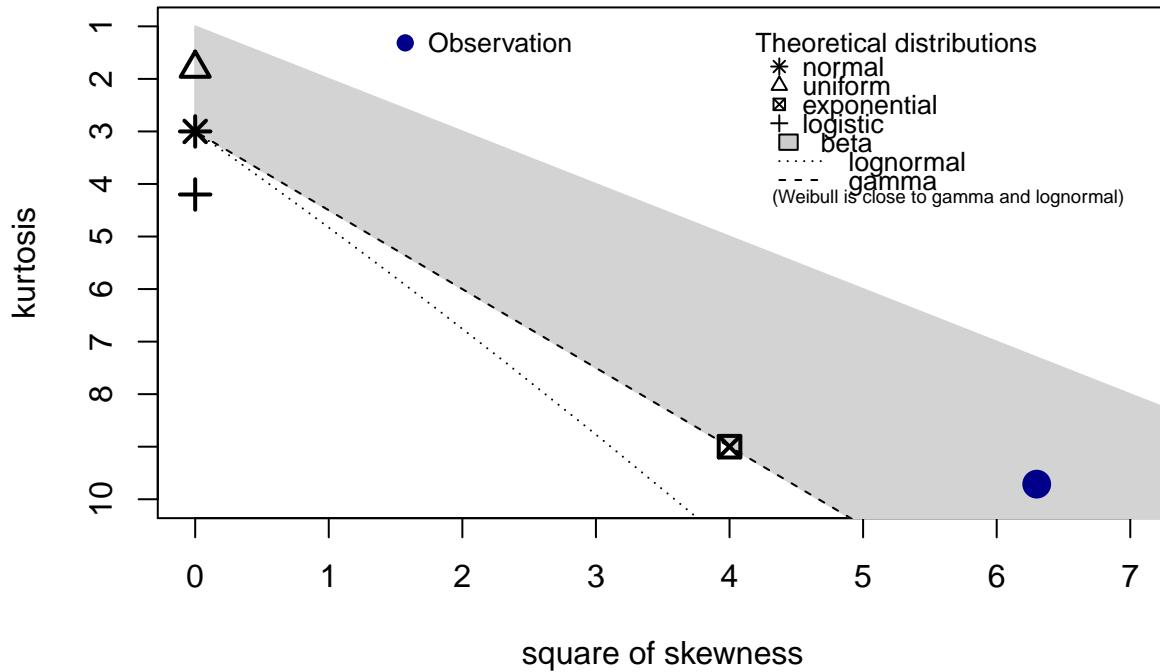


```
ggplot(comp_kbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor + plot)
```



```
# Exploring distributions for these right-skewed data:  
descdist(comp_kbs_spp$relabun, discrete = FALSE)
```

Cullen and Frey graph



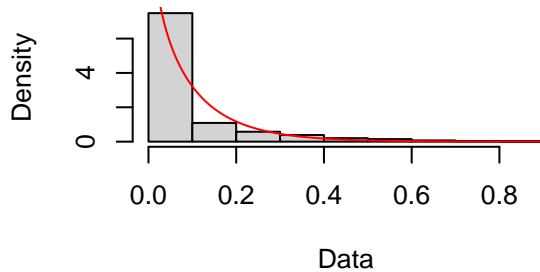
```

## summary statistics
## -----
## min:  0.005242388  max:  0.8888504
## median:  0.03707022
## mean:  0.09185919
## estimated sd:  0.1308706
## estimated skewness:  2.509919
## estimated kurtosis:  9.712586

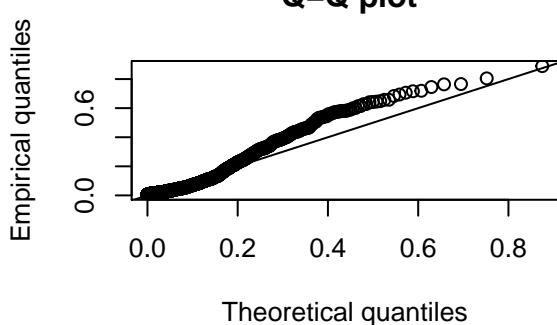
# Gamma distribution
fit.gamma <- fitdist(comp_kbs_spp$relabun, "gamma")
plot(fit.gamma)

```

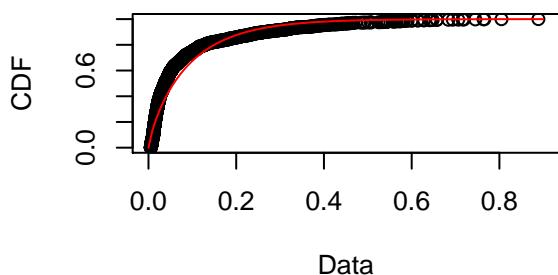
Empirical and theoretical dens.



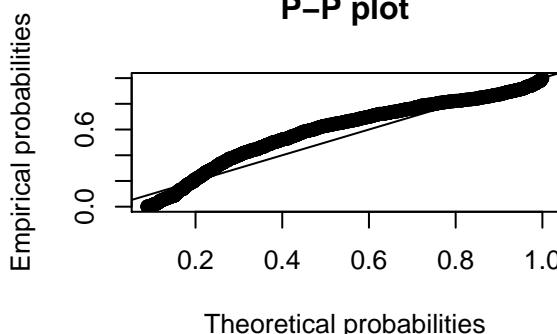
Q-Q plot



Empirical and theoretical CDFs

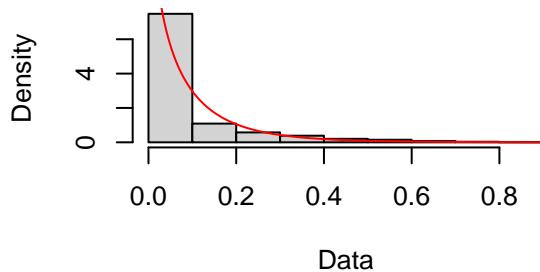


P-P plot

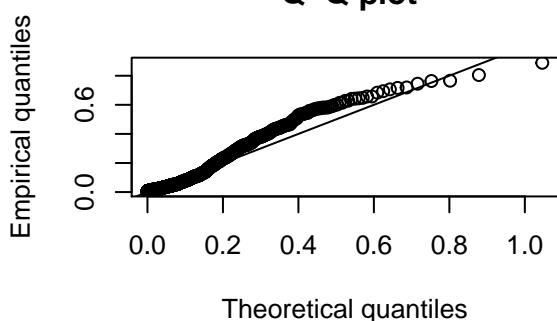


```
# Weibull distribution
fit.weibull <- fitdist(comp_kbs_spp$relabun, "weibull")
plot(fit.weibull)
```

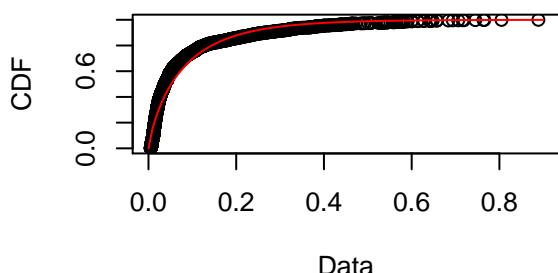
Empirical and theoretical dens.



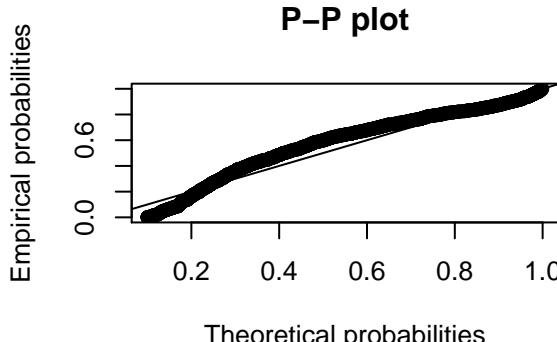
Q-Q plot



Empirical and theoretical CDFs

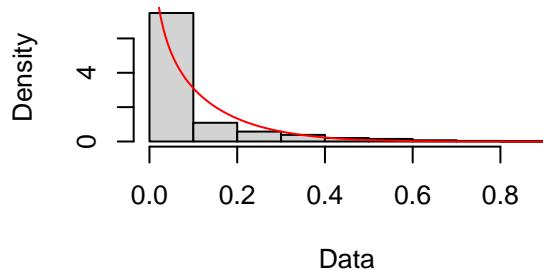


P-P plot

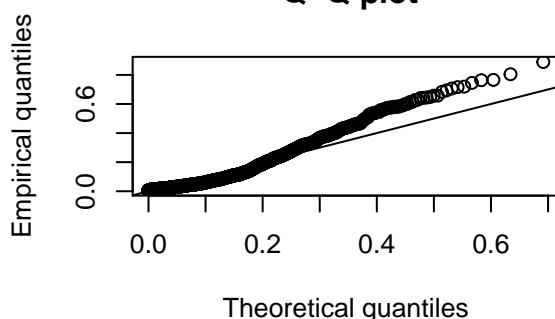


```
# Beta distribution
fit.beta <- fitdist(comp_kbs_spp$relabun, "beta")
plot(fit.beta)
```

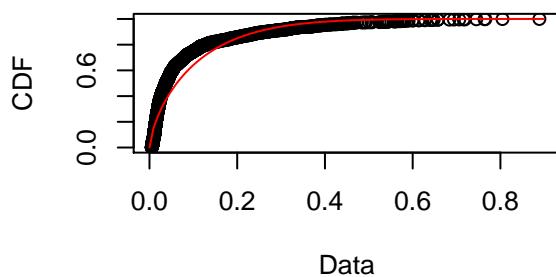
Empirical and theoretical dens.



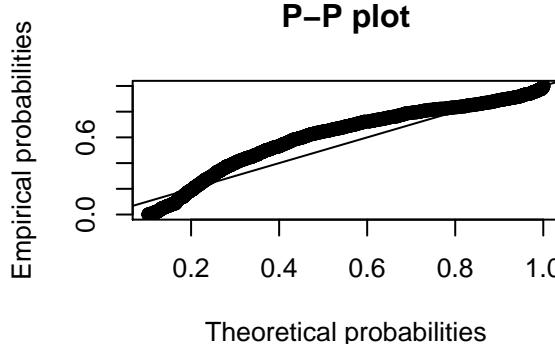
Q–Q plot



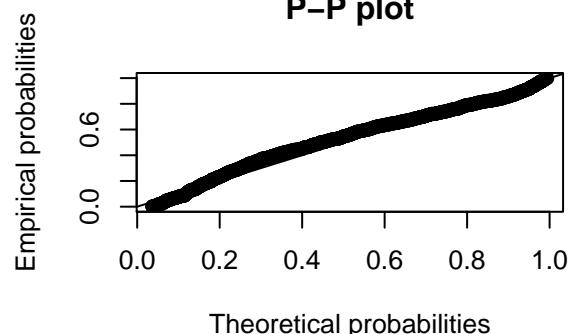
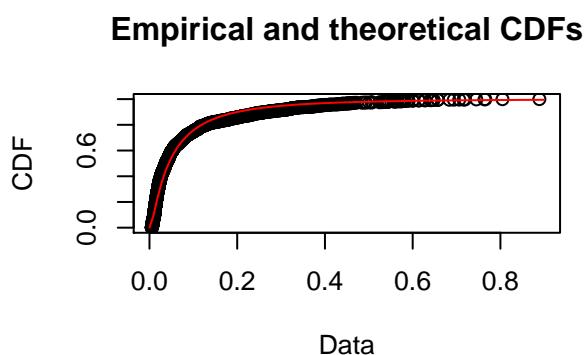
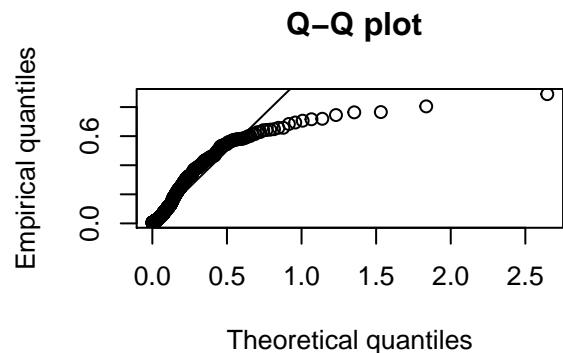
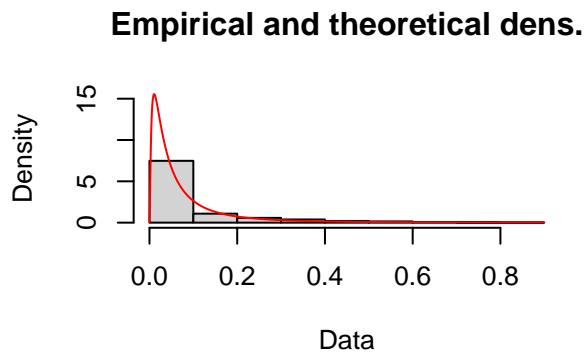
Empirical and theoretical CDFs



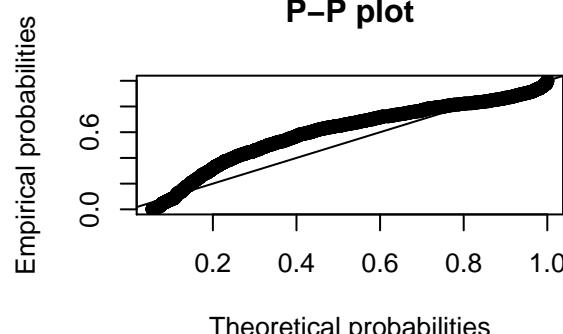
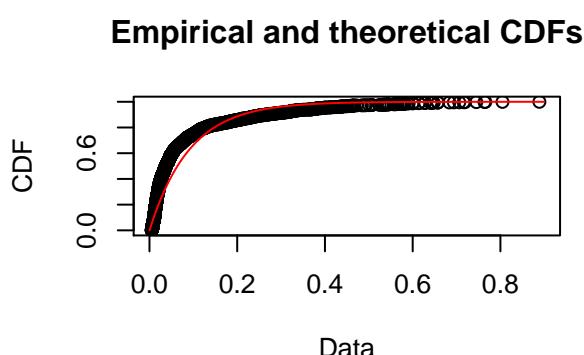
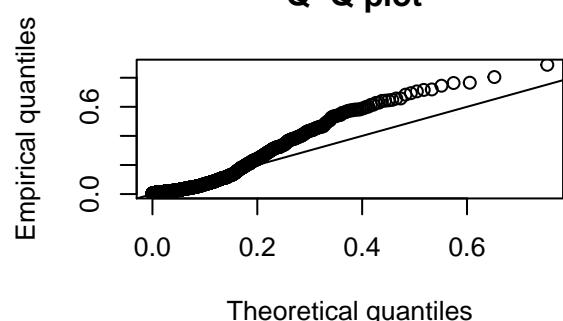
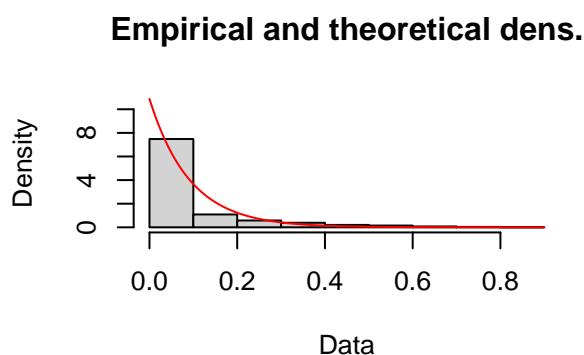
P–P plot



```
# Lognormal distribution
fit.ln <- fitdist(comp_kbs_spp$relabun, "lnorm")
plot(fit.ln)
```



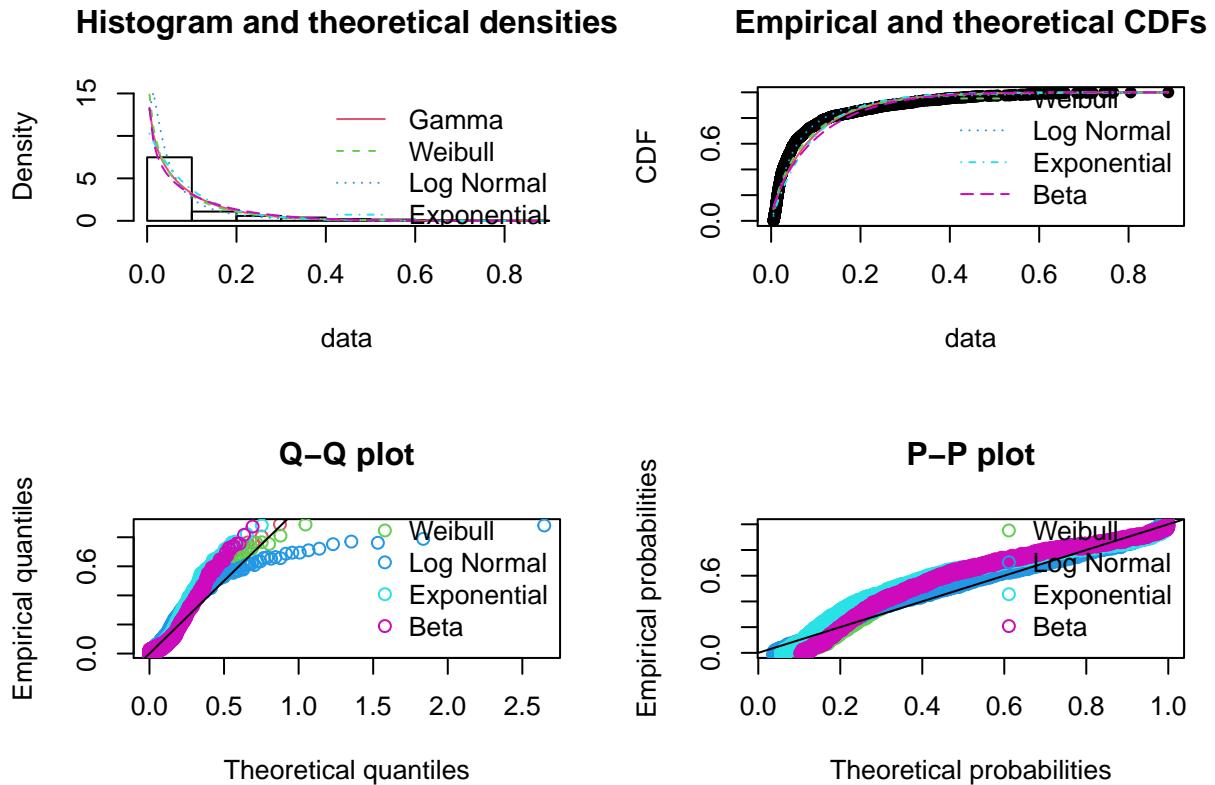
```
# Exponential distribution is another option
fit.exp <- fitdist(comp_kbs_spp$relabun, "exp")
plot(fit.exp)
```



```

par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal", "Exponential", "Beta")
denscomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)

```



```

# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), fitnames = c("Gamma",
    "Weibull", "Log Normal", "Exp", "Beta"))

```

```

## Goodness-of-fit statistics
##                                     Gamma   Weibull  Log Normal      Exp
## Kolmogorov-Smirnov statistic 0.1344308 0.1033437 0.07028364 0.1745875
## Cramer-von Mises statistic  11.5969326 7.4683494 2.61728997 20.4114453
## Anderson-Darling statistic  63.7686160 46.8700036 17.18469890 105.2325017
##                                     Beta
## Kolmogorov-Smirnov statistic 0.1528005
## Cramer-von Mises statistic 15.1430209
## Anderson-Darling statistic 80.6642522
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull  Log Normal      Exp
## Akaike's Information Criterion -5106.036 -5187.224 -5591.800 -5042.944
## Bayesian Information Criterion -5095.025 -5176.213 -5580.789 -5037.439
##                                     Beta

```

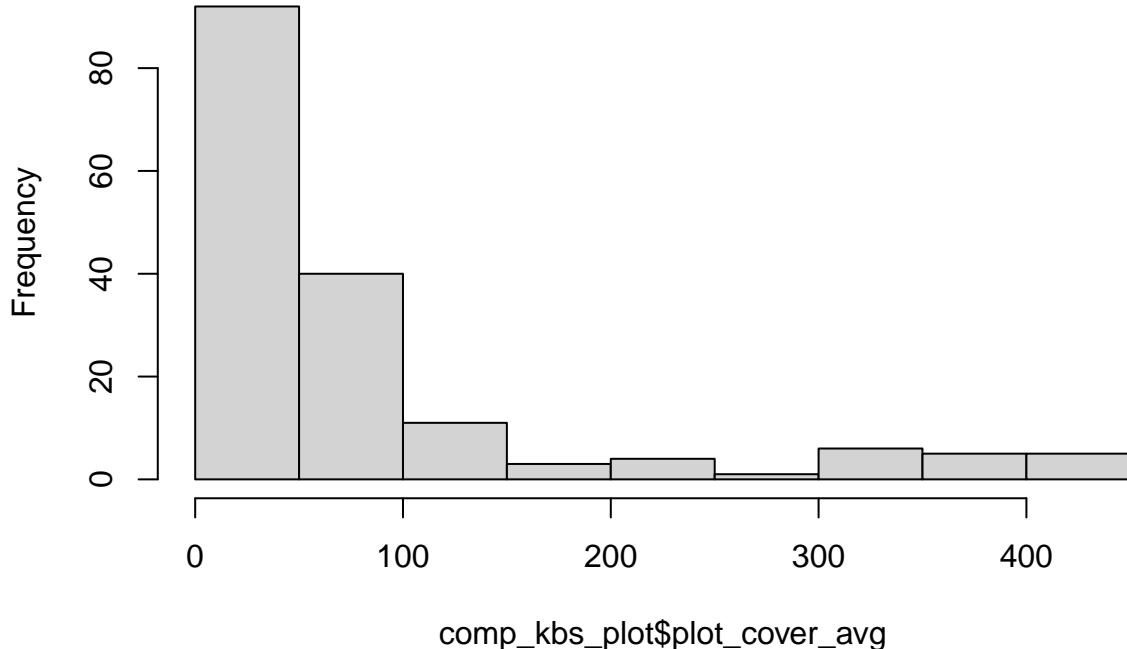
```
## Akaike's Information Criterion -4939.073
## Bayesian Information Criterion -4928.062

# Beta and exp distributions look to be the best based on AIC and BIC values
```

KBS PLOT LEVEL - Looking at PLOT AVG TOTALS

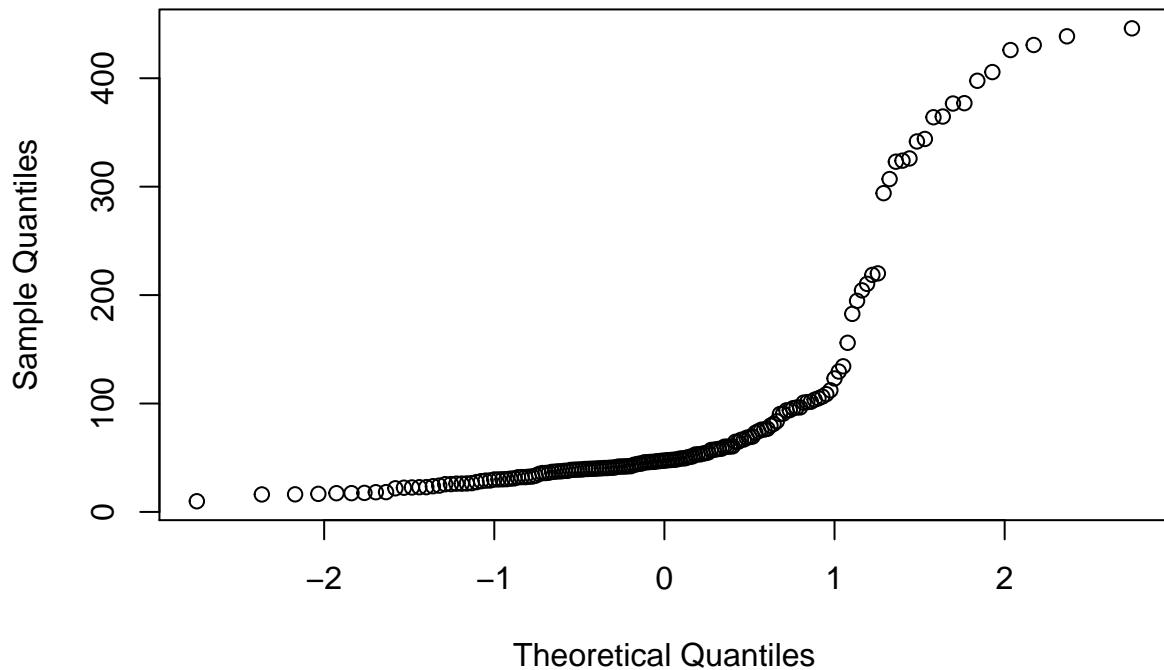
```
### KBS ####
hist(comp_kbs_plot$plot_cover_avg) # skewed to the right
```

Histogram of comp_kbs_plot\$plot_cover_avg



```
qqnorm(comp_kbs_plot$plot_cover_avg)
```

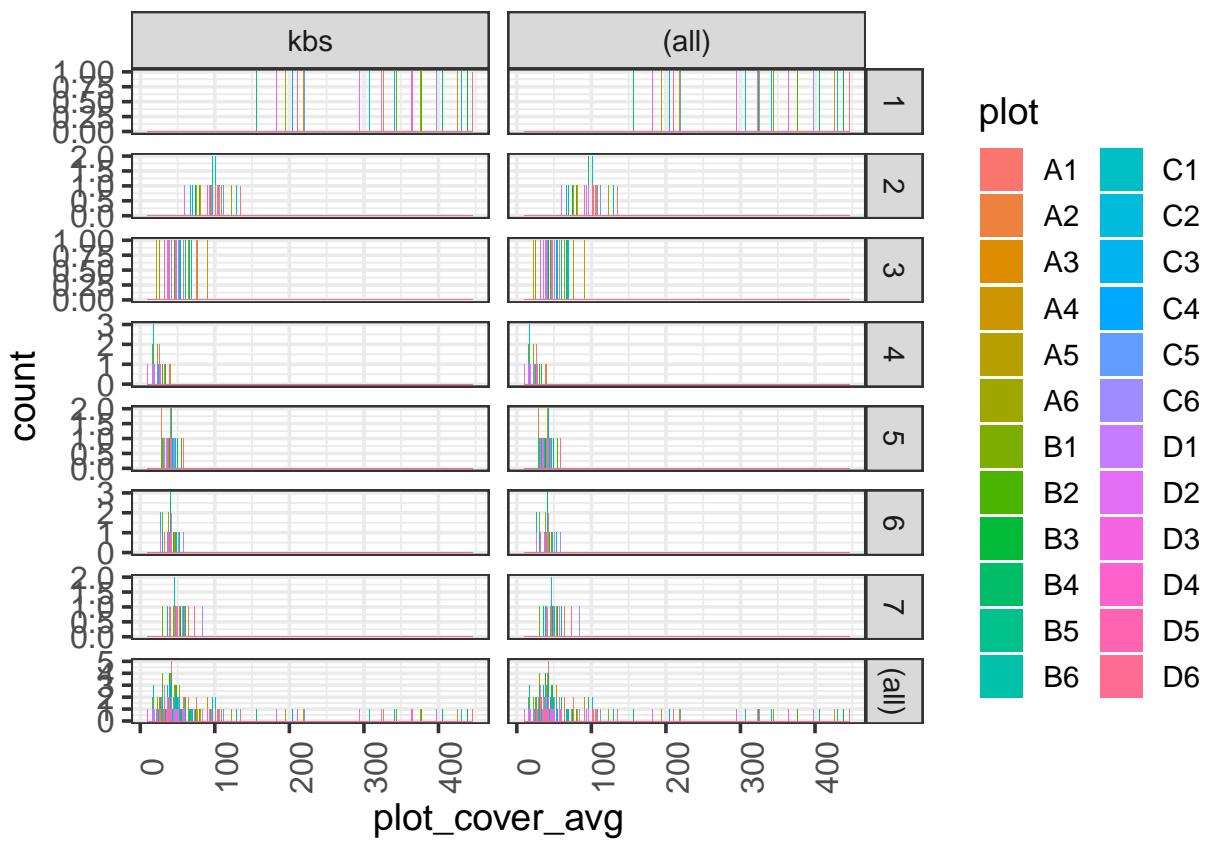
Normal Q-Q Plot



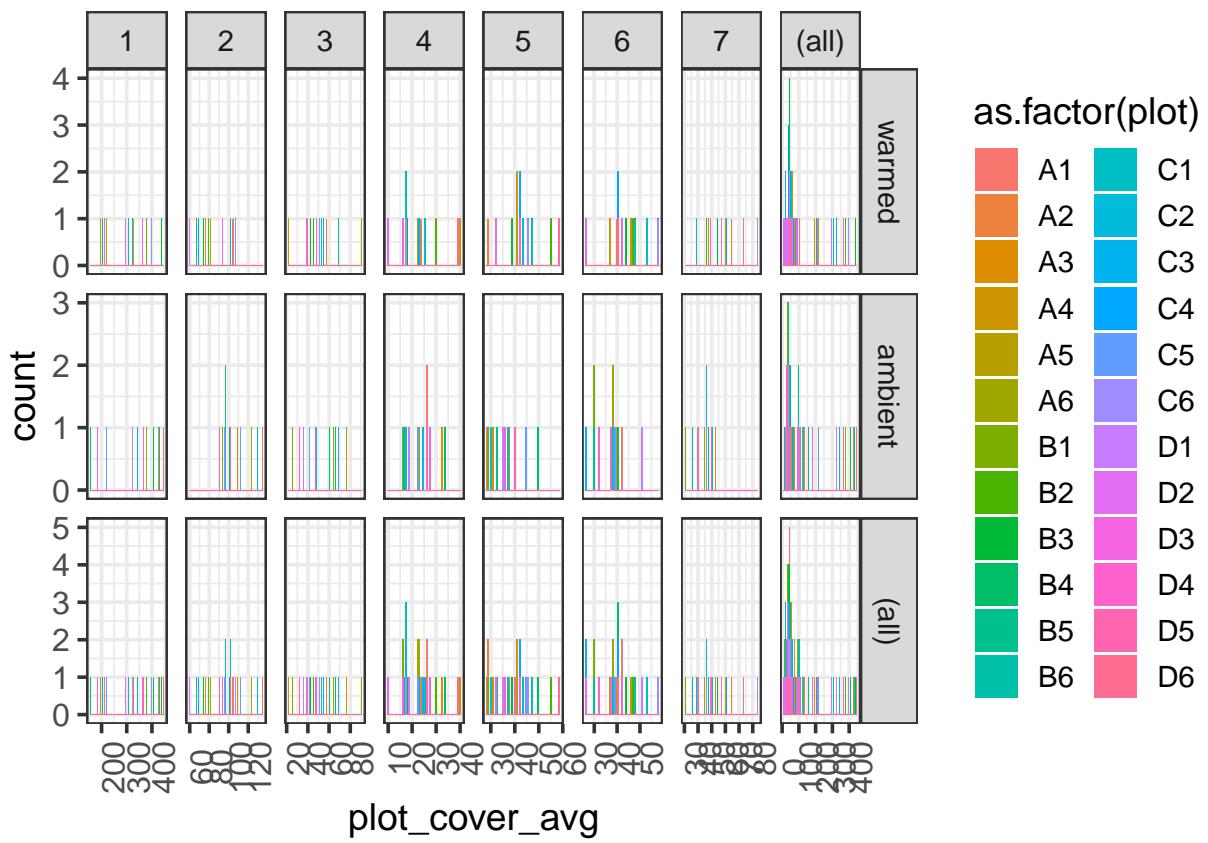
```
shapiro.test(comp_kbs_plot$plot_cover_avg) # pvalue is < 0.05 so we reject the null hypothesis that the data is normally distributed

## 
## Shapiro-Wilk normality test
##
## data: comp_kbs_plot$plot_cover_avg
## W = 0.62827, p-value < 2.2e-16

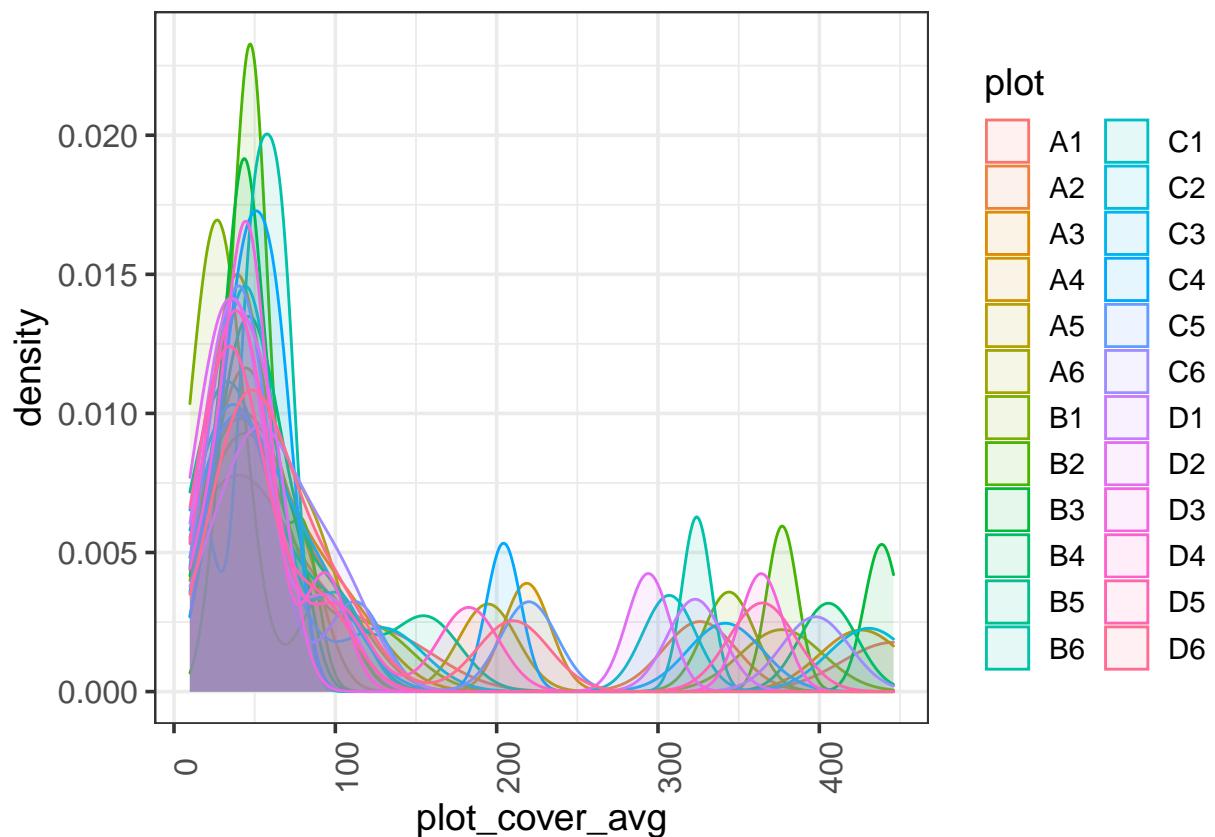
# Visualizing plot average totals for kbs at the PLOT LEVEL
ggplot(comp_kbs_plot, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")
```



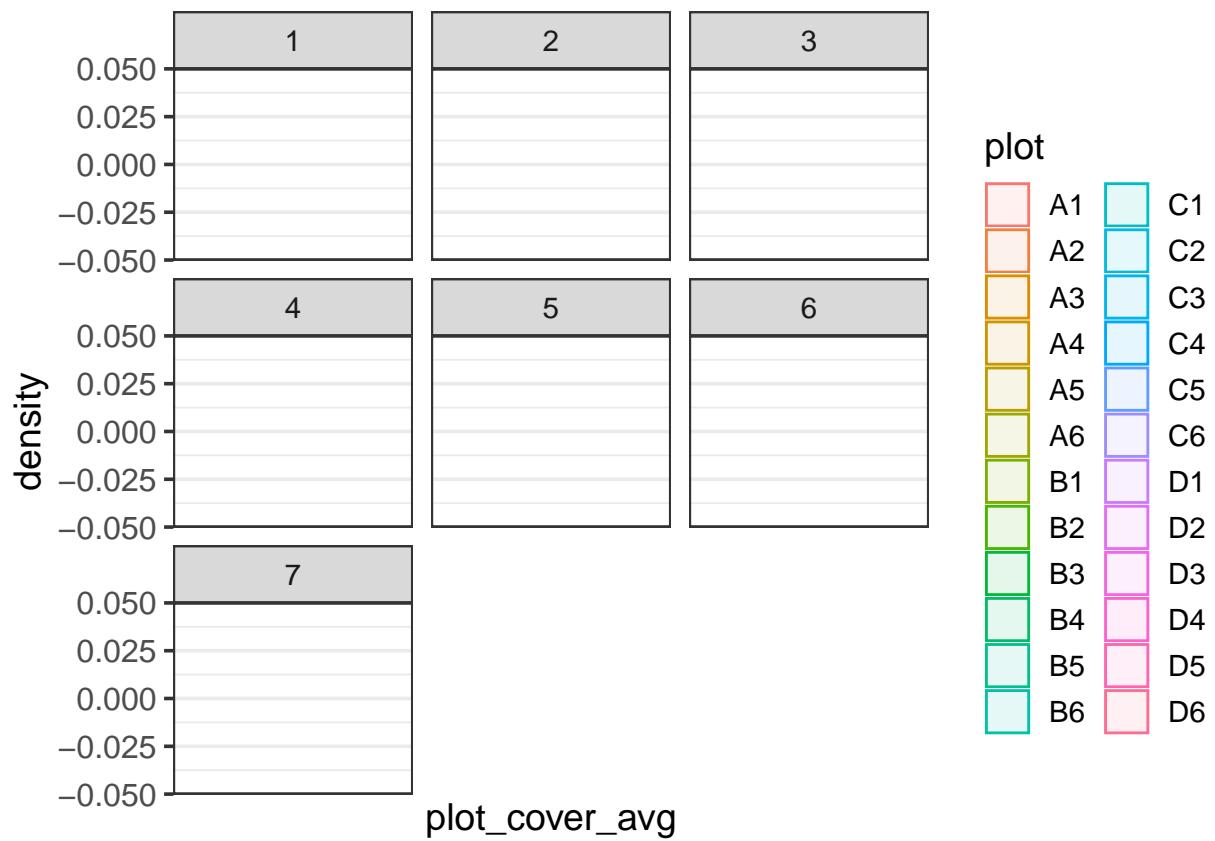
```
ggplot(comp_kbs_plot, aes(plot_cover_avg, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year_factor, margins = TRUE, scales = "free")
```



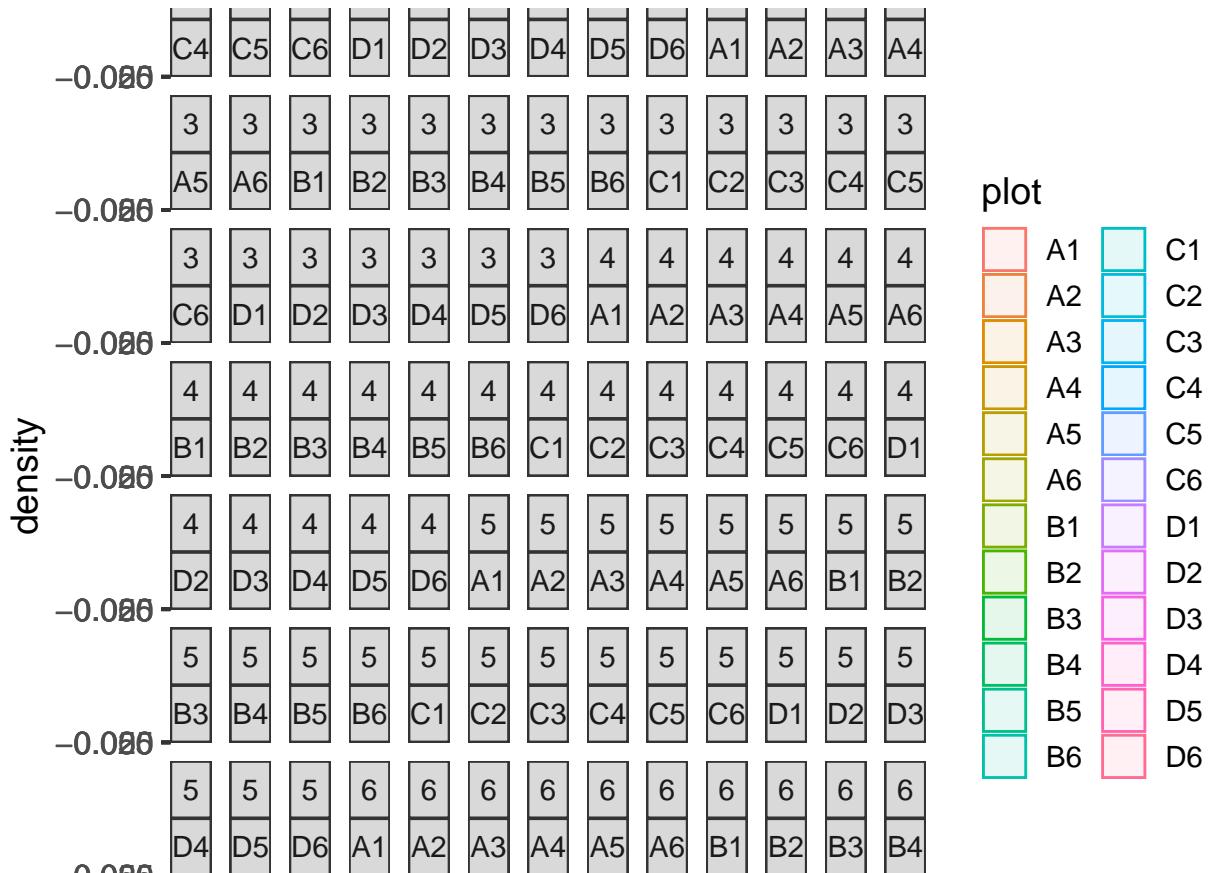
```
ggplot(comp_kbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(comp_kbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor)
```

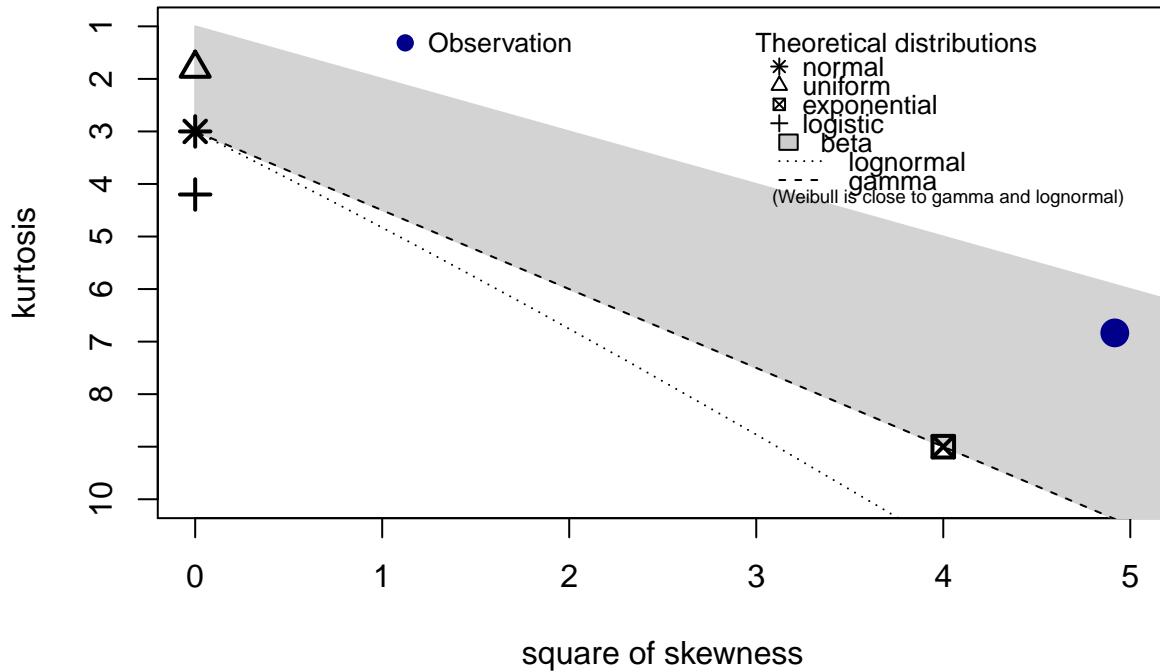


```
ggplot(comp_kbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor + plot)
```



```
# Exploring distributions for these right-skewed data:  
descdist(comp_kbs_plot$plot_cover_avg, discrete = FALSE)
```

Cullen and Frey graph

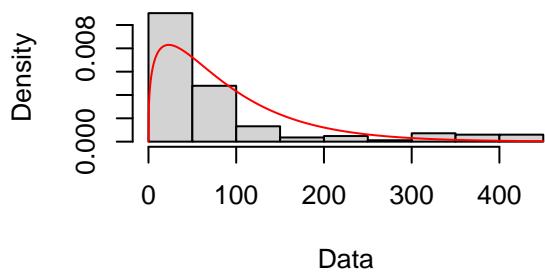
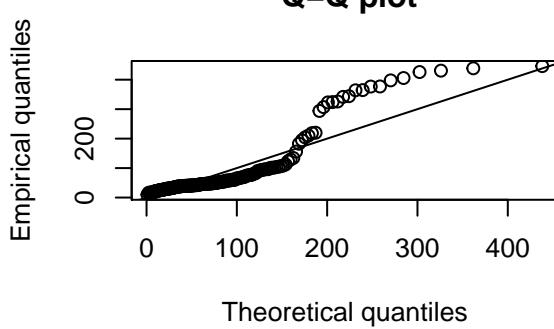
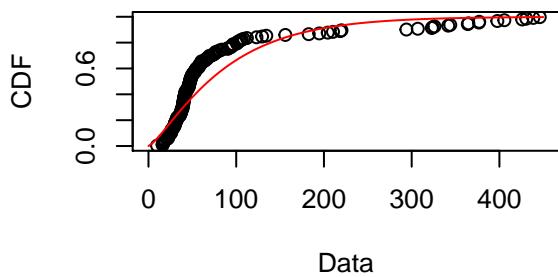
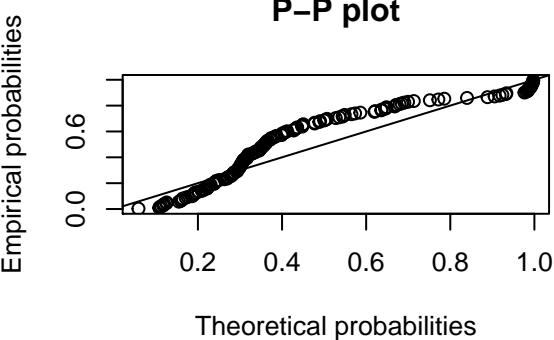


```

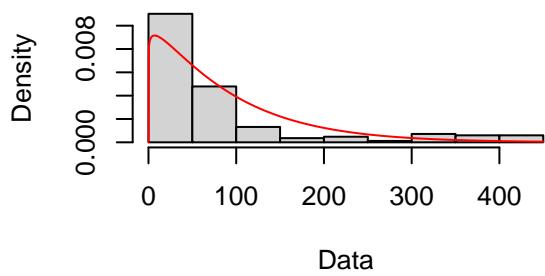
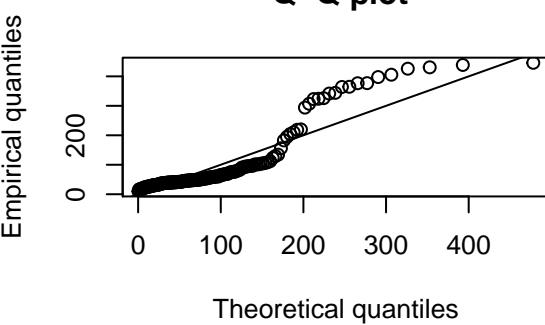
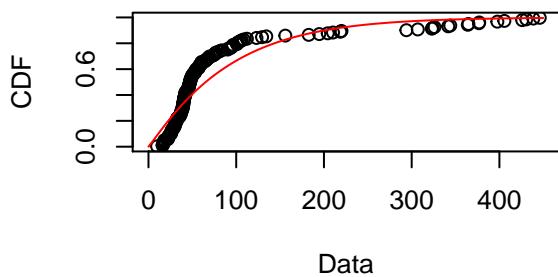
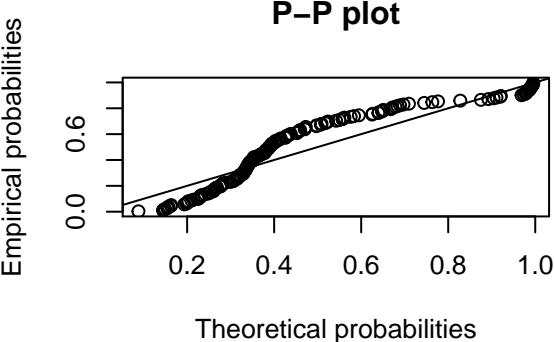
## summary statistics
## -----
## min:  9.857143  max:  446
## median: 47.23077
## mean:  89.1331
## estimated sd: 103.2916
## estimated skewness: 2.217462
## estimated kurtosis: 6.834041

# Gamma distribution
fit.gamma <- fitdist(comp_kbs_plot$plot_cover_avg, "gamma")
plot(fit.gamma)

```

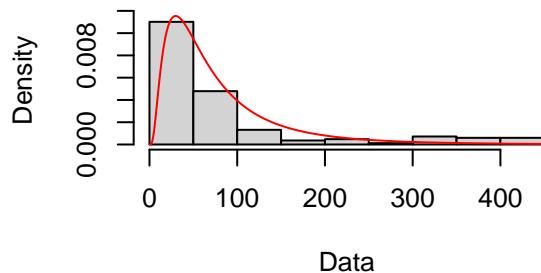
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Weibull distribution
fit.weibull <- fitdist(comp_kbs_plot$plot_cover_avg, "weibull")
plot(fit.weibull)
```

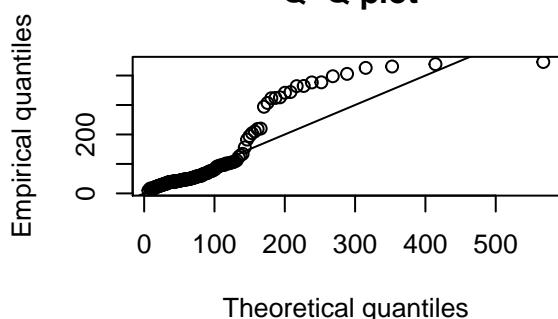
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Lognormal distribution
fit.ln <- fitdist(comp_kbs_plot$plot_cover_avg, "lnorm")
plot(fit.ln)
```

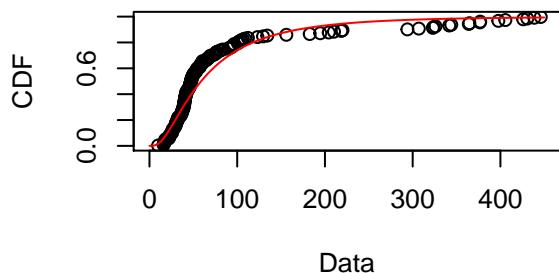
Empirical and theoretical dens.



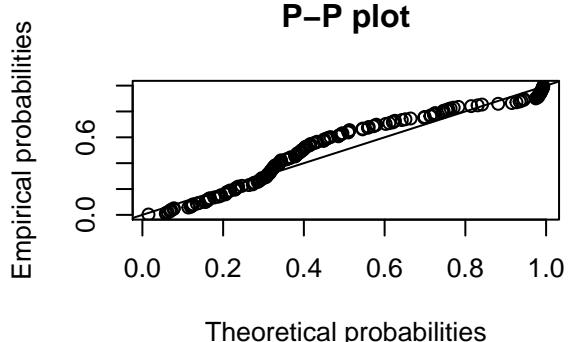
Q-Q plot



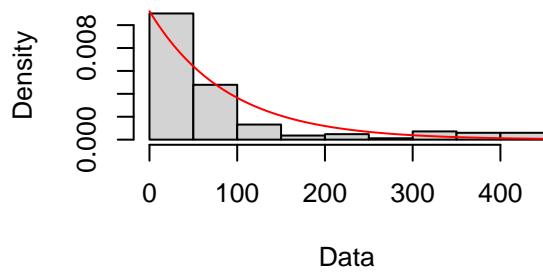
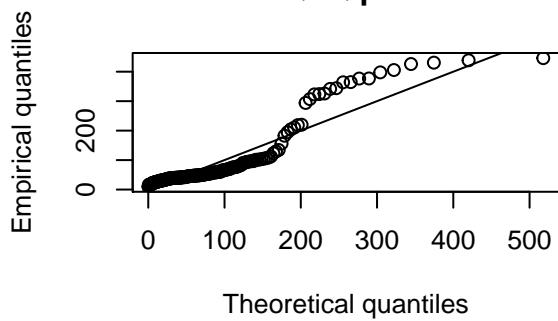
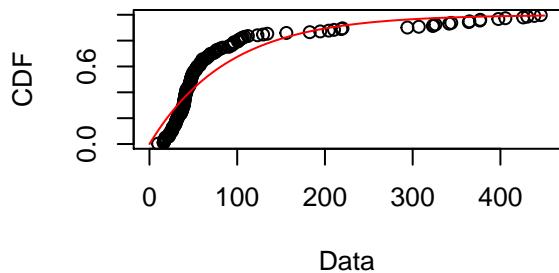
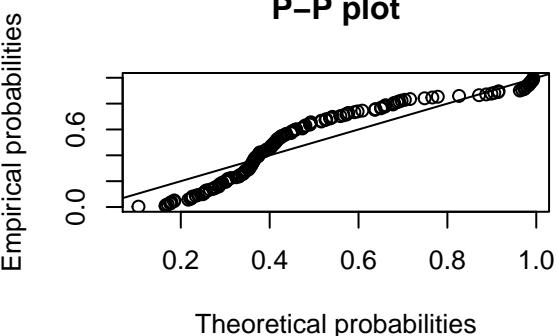
Empirical and theoretical CDFs



P-P plot

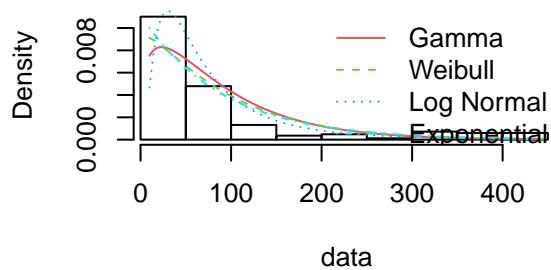


```
# Exponential distribution is another option
fit.exp <- fitdist(comp_kbs_plot$plot_cover_avg, "exp")
plot(fit.exp)
```

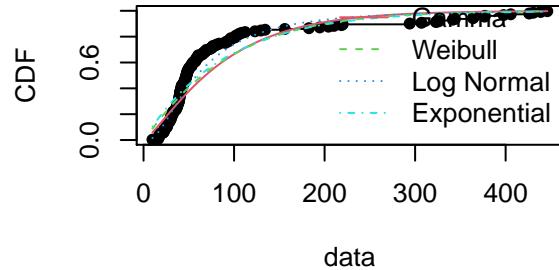
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal", "Exponential")
denscomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
```

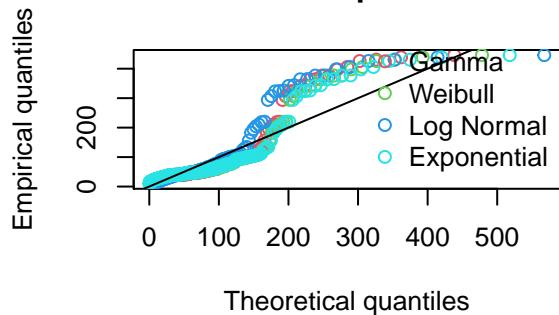
Histogram and theoretical densities



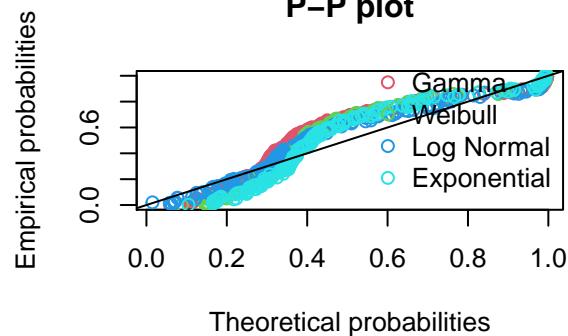
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
# Goodness of fit comparisons across fits
gofstat(list(fit.gamma, fit.weibull, fit.ln, fit.exp), fitnames = c("Gamma", "Weibull",
  "Log Normal", "Exp"))
```

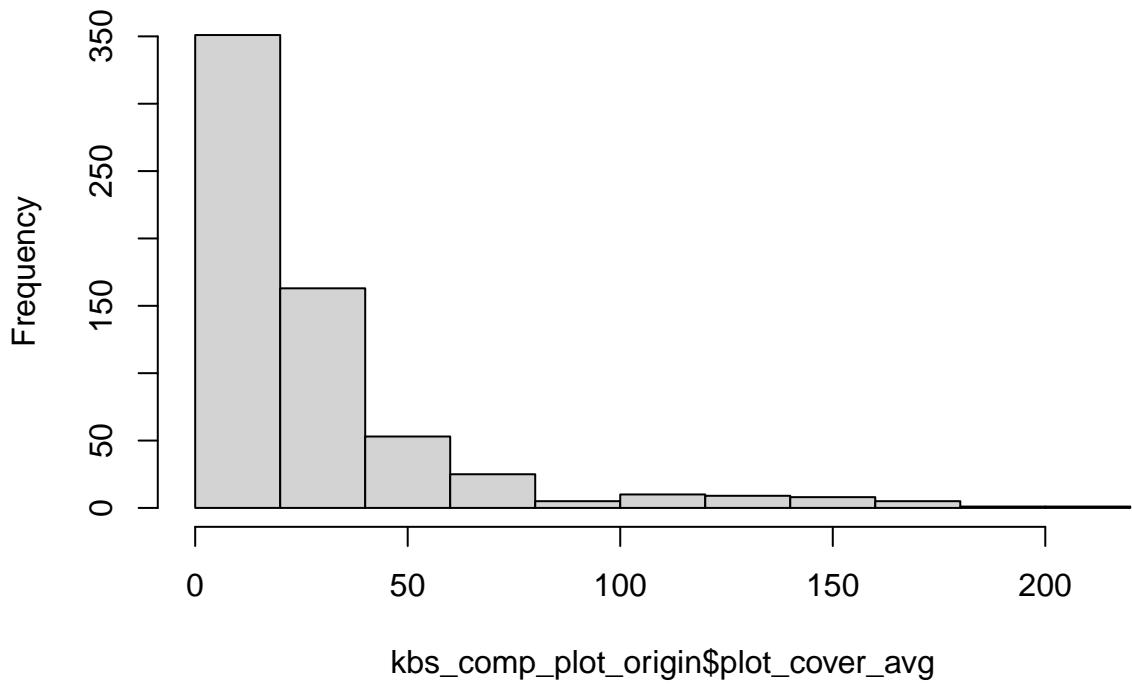
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal      Exp
## Kolmogorov-Smirnov statistic 0.2084312 0.1860727 0.1457357 0.1659281
## Cramer-von Mises statistic  2.1039134 1.9334703 0.9063833 1.8481234
## Anderson-Darling statistic 11.5222610 10.9721217 5.3825803 10.7379076
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal      Exp
## Akaike's Information Criterion 1829.221 1836.325 1774.742 1835.704
## Bayesian Information Criterion 1835.457 1842.561 1780.978 1838.822
```

```
# log normal distribution looks to be the best based on AIC and BIC values
```

KBS PLOT LEVEL ORIGIN - Looking at PLOT AVG TOTALS

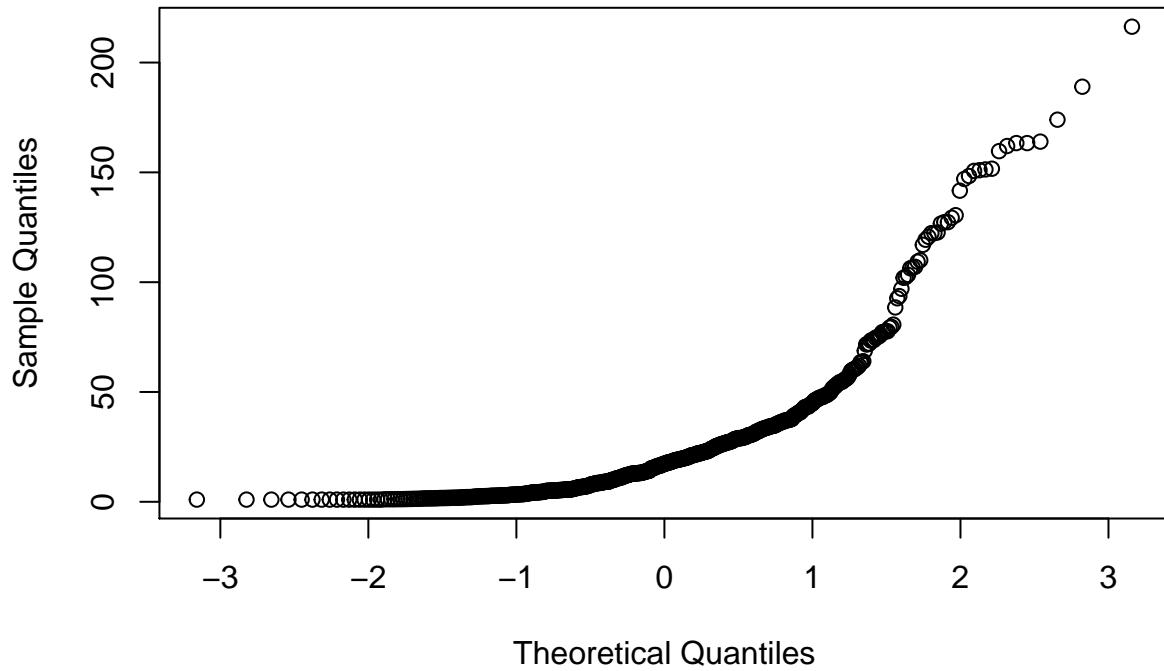
```
### KBS ####
hist(kbs_comp_plot_origin$plot_cover_avg) # skewed to the right
```

Histogram of kbs_comp_plot_origin\$plot_cover_avg



```
qqnorm(kbs_comp_plot_origin$plot_cover_avg)
```

Normal Q–Q Plot



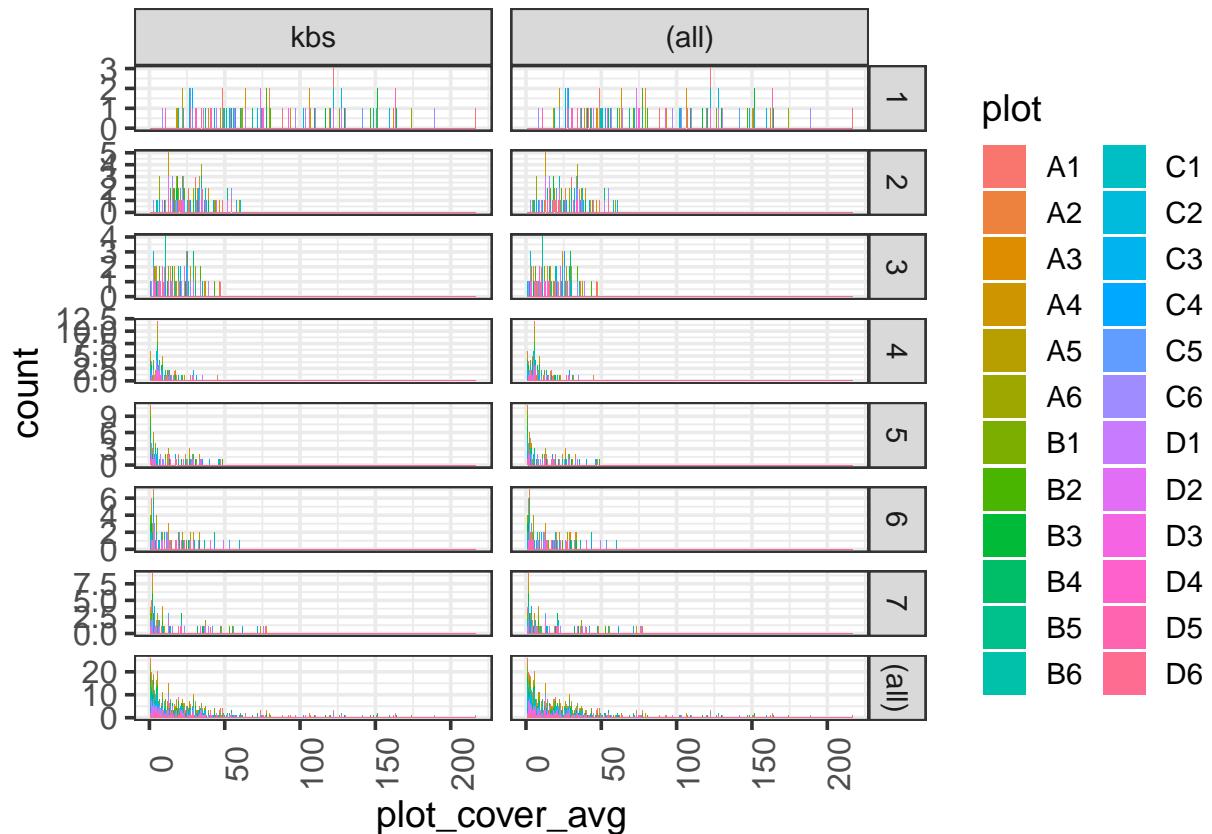
```

shapiro.test(kbs_comp_plot_origin$plot_cover_avg) # pvalue is < 0.05 so we reject the null hypothesis

## 
## Shapiro-Wilk normality test
## 
## data: kbs_comp_plot_origin$plot_cover_avg
## W = 0.71214, p-value < 2.2e-16

# Visualizing plot average totals for kbs at the PLOT LEVEL
ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")

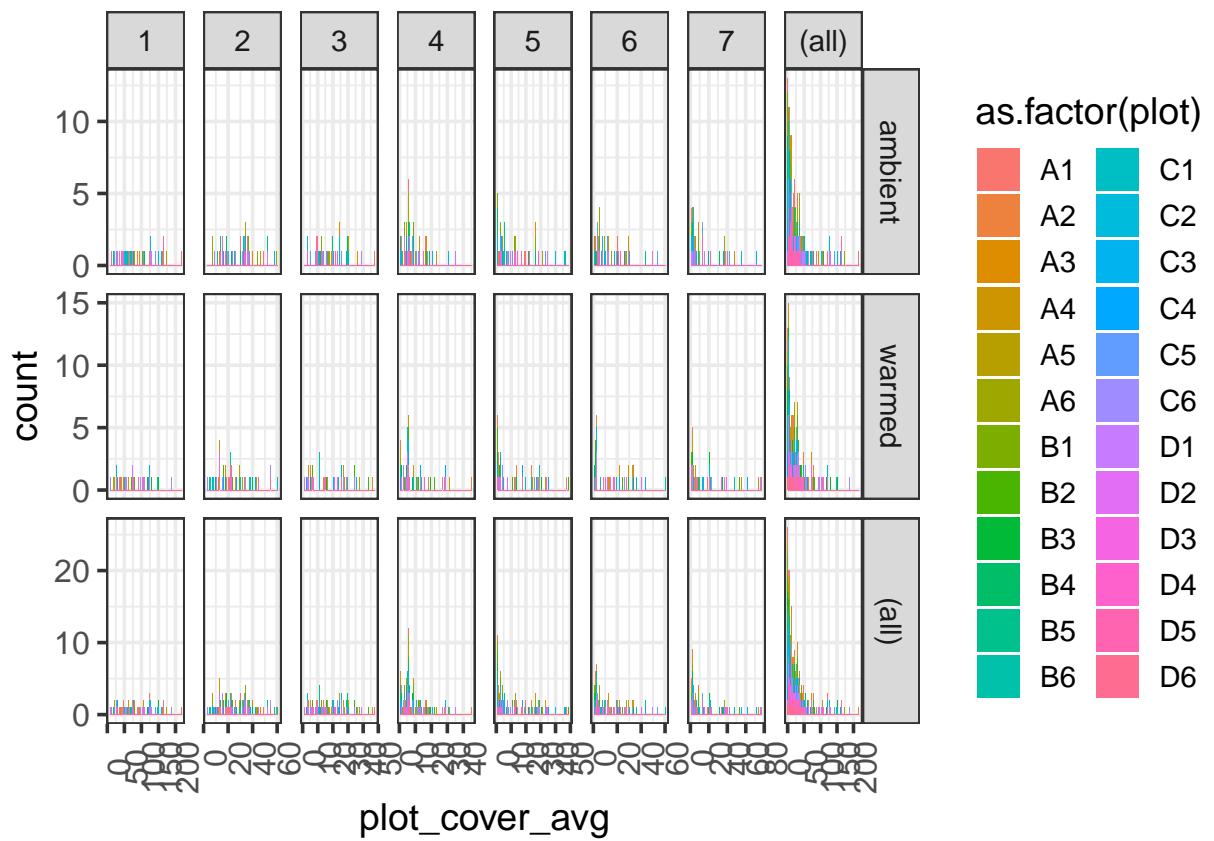
```



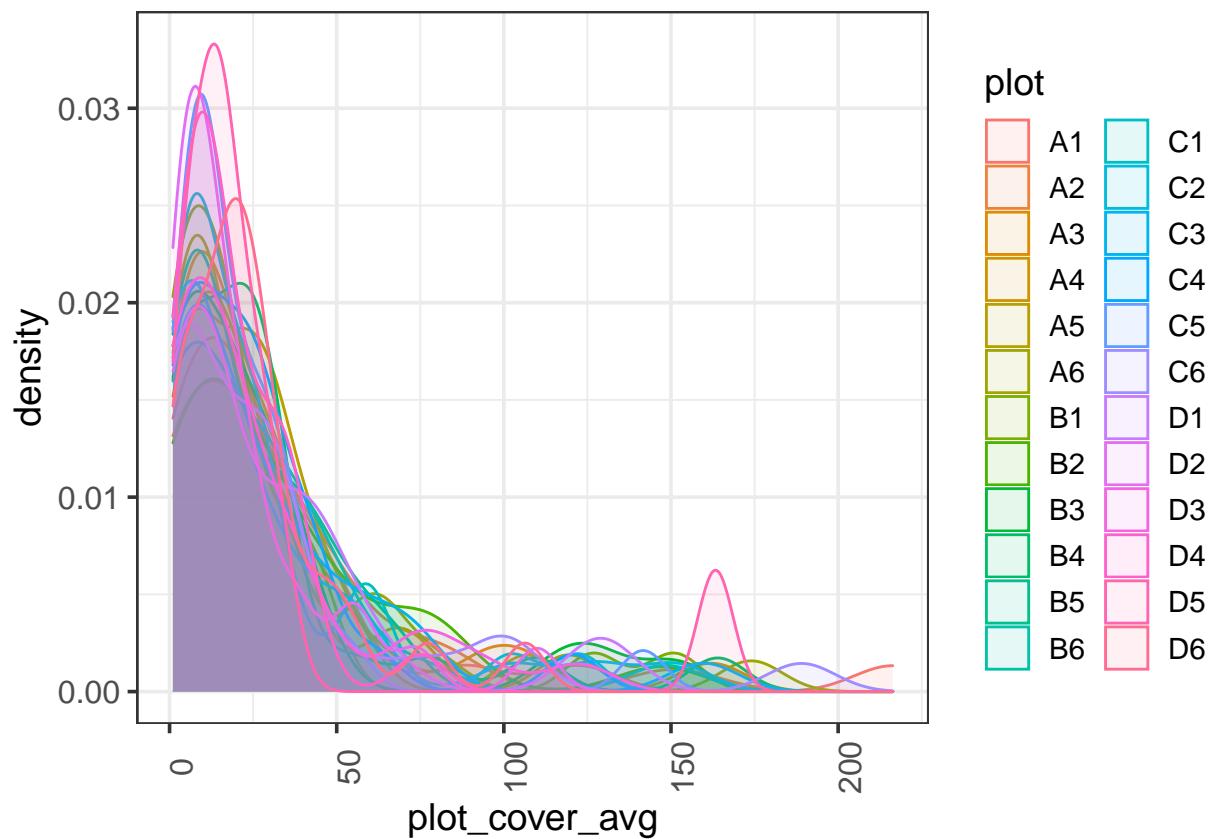
```

ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year_factor, margins = TRUE, scales = "free")

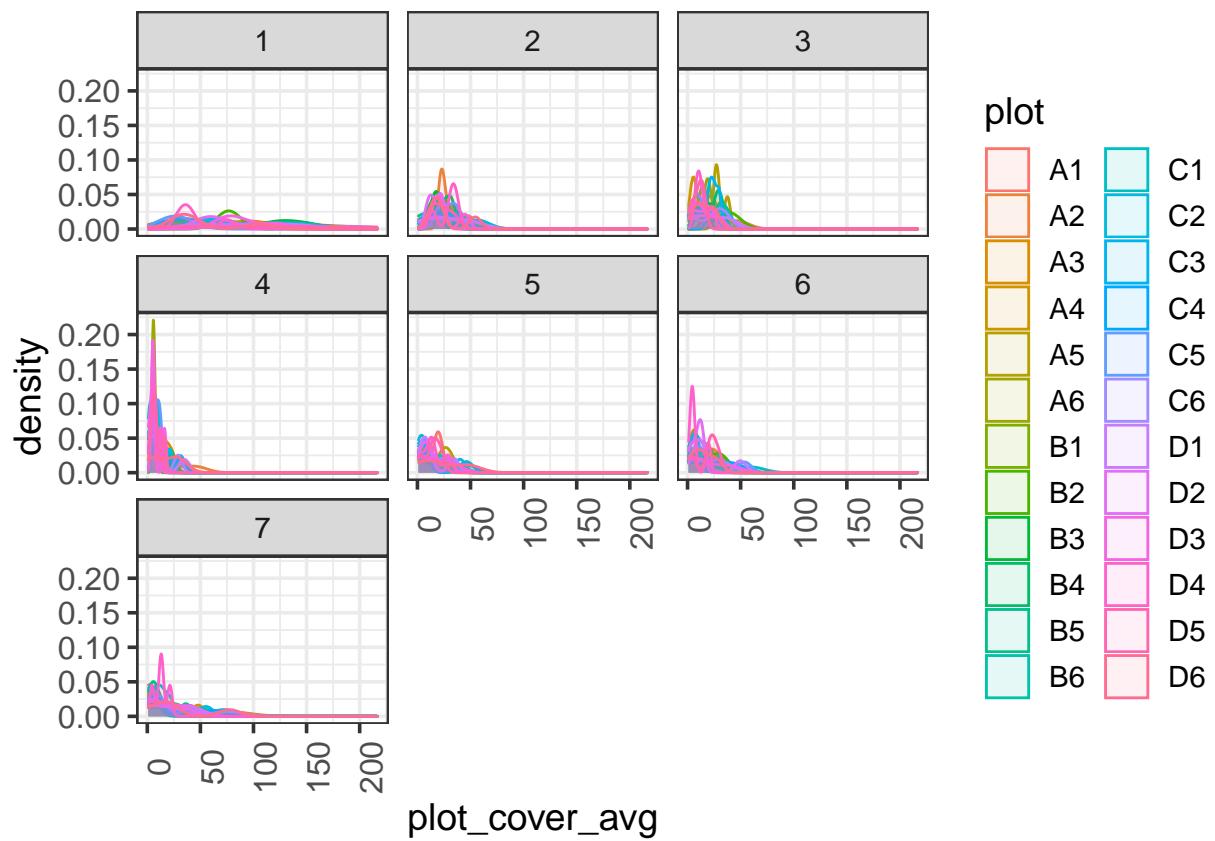
```



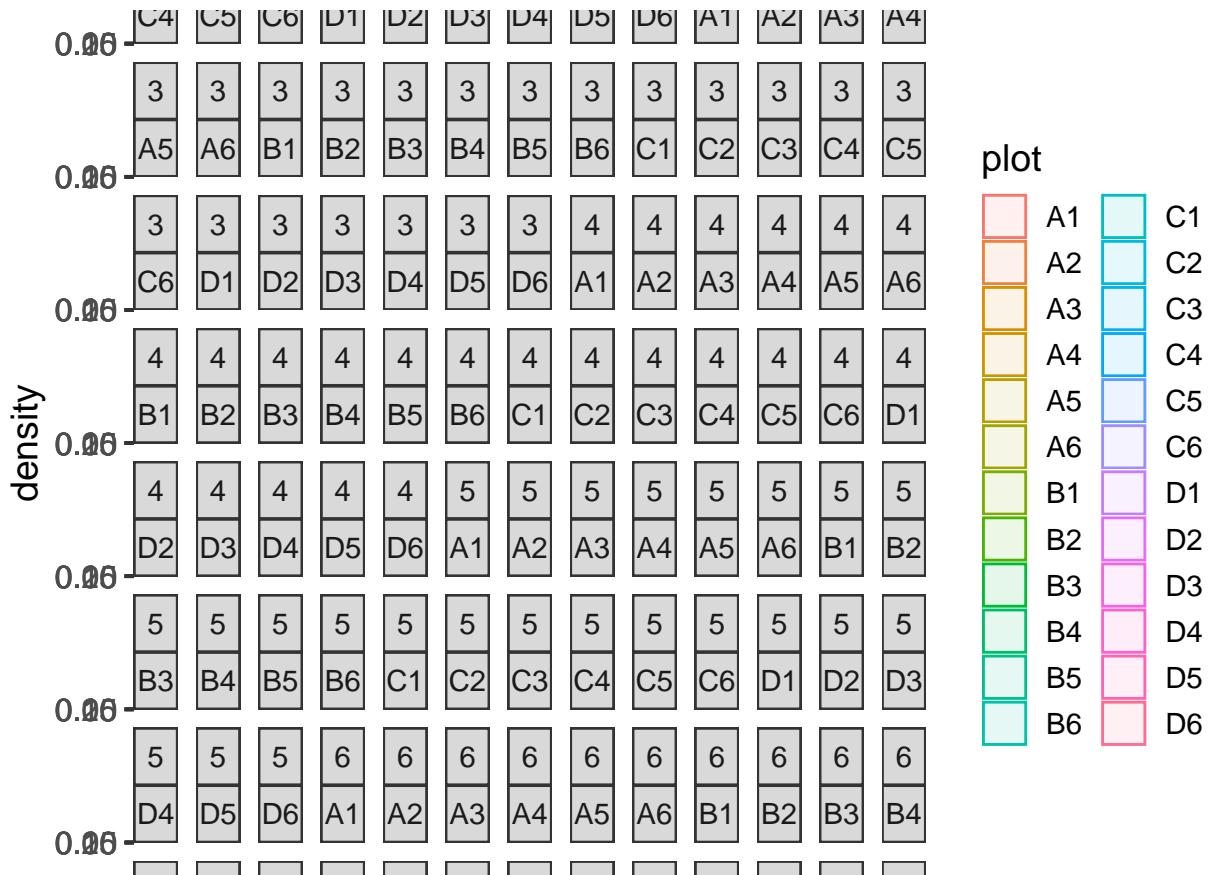
```
ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)  
  facet_wrap(~year_factor)
```

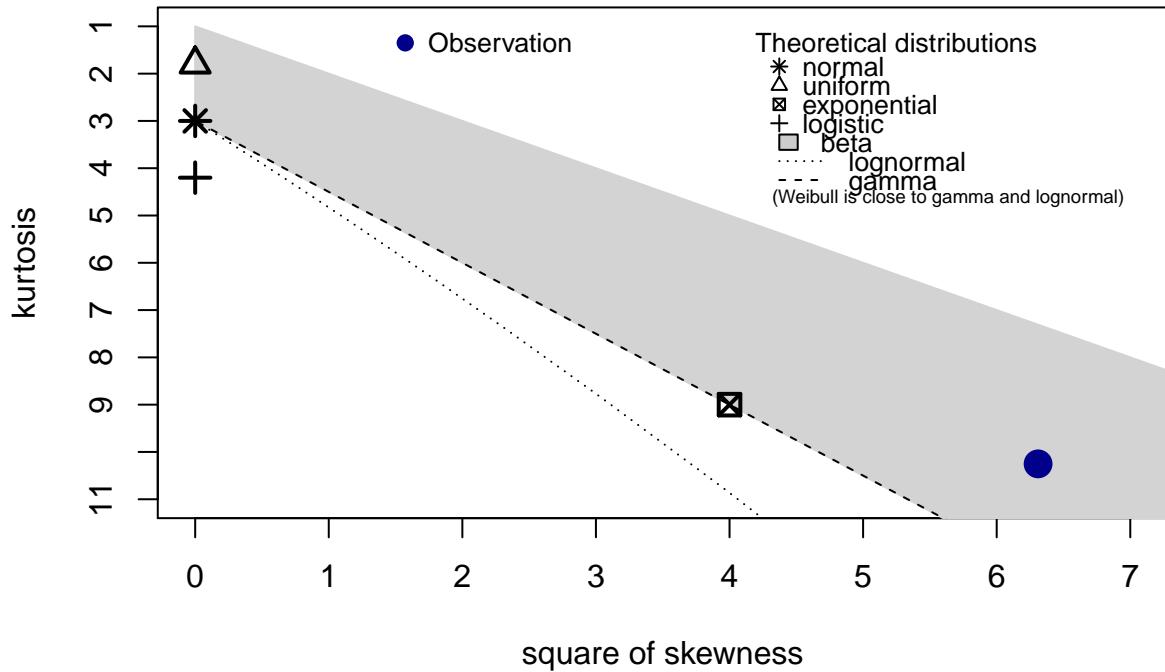


```
ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
  facet_wrap(~year_factor + plot)
```



```
# Exploring distributions for these data:  
descdist(kbs_comp_plot_origin$plot_cover_avg, discrete = FALSE)
```

Cullen and Frey graph

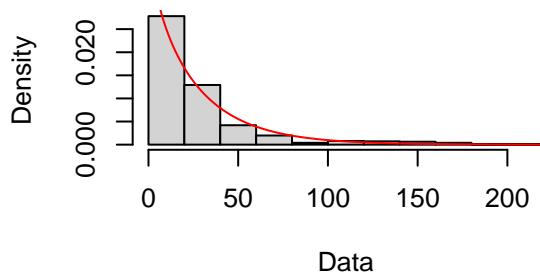
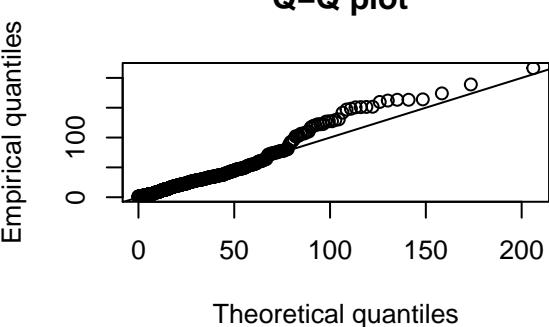
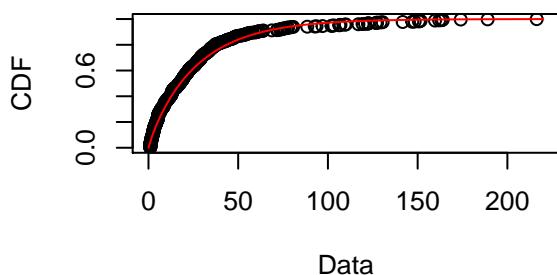
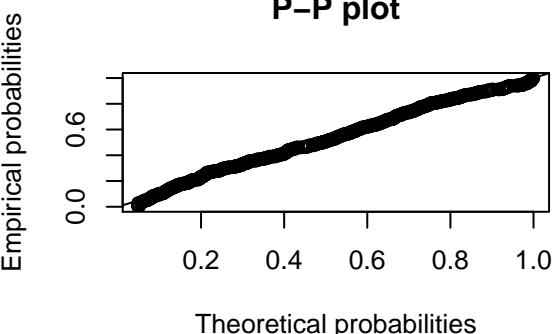


```

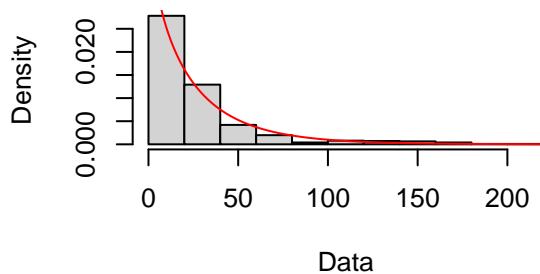
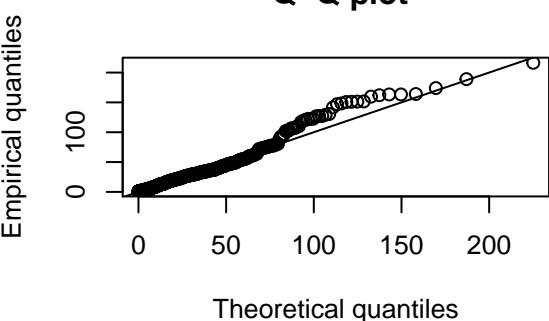
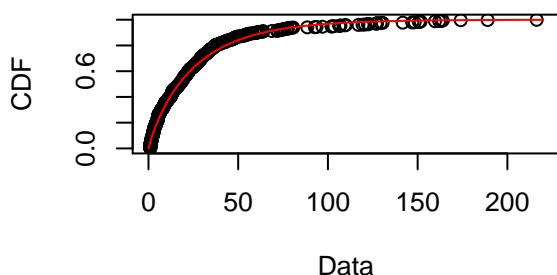
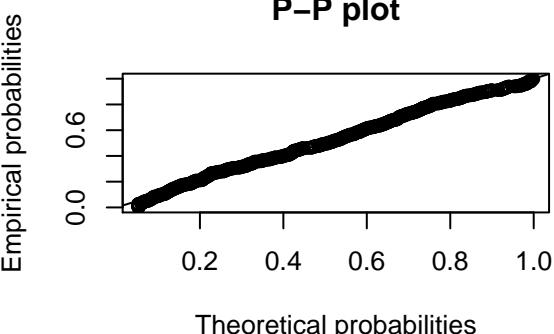
## summary statistics
## -----
## min: 1   max: 216.3333
## median: 17.28571
## mean: 26.83611
## estimated sd: 32.6559
## estimated skewness: 2.511938
## estimated kurtosis: 10.25197

# Gamma distribution
fit.gamma <- fitdist(kbs_comp_plot_origin$plot_cover_avg, "gamma")
plot(fit.gamma)

```

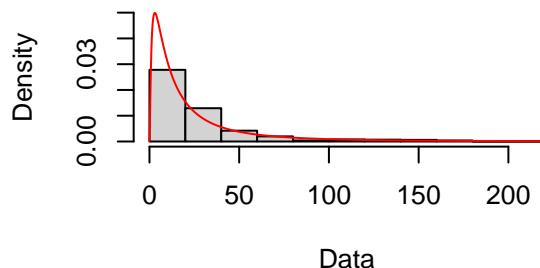
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Weibull distribution
fit.weibull <- fitdist(kbs_comp_plot_origin$plot_cover_avg, "weibull")
plot(fit.weibull)
```

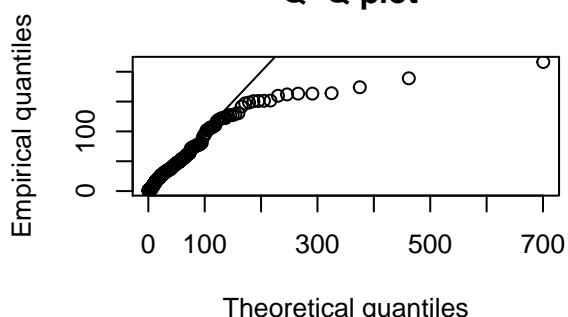
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Lognormal distribution
fit.ln <- fitdist(kbs_comp_plot_origin$plot_cover_avg, "lnorm")
plot(fit.ln)
```

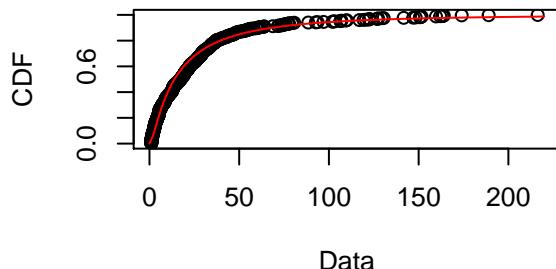
Empirical and theoretical dens.



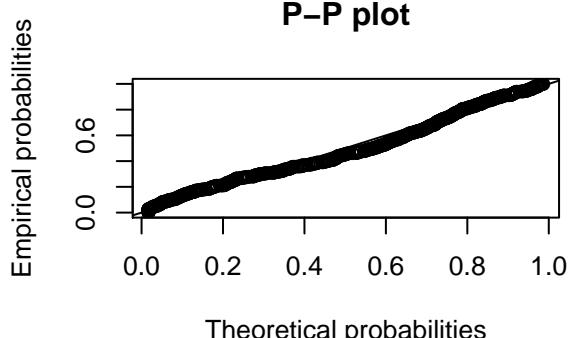
Q-Q plot



Empirical and theoretical CDFs

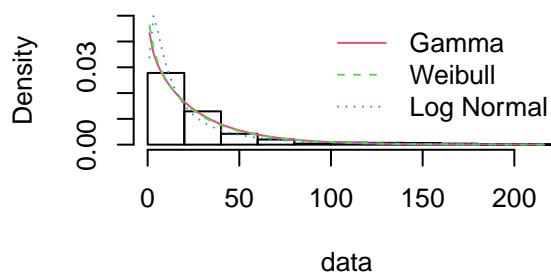


P-P plot

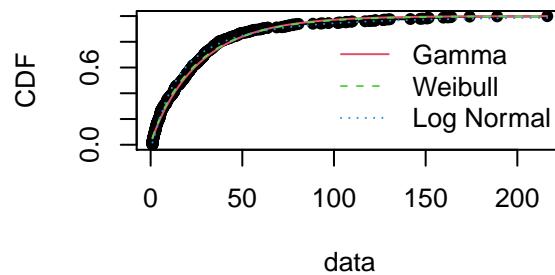


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```

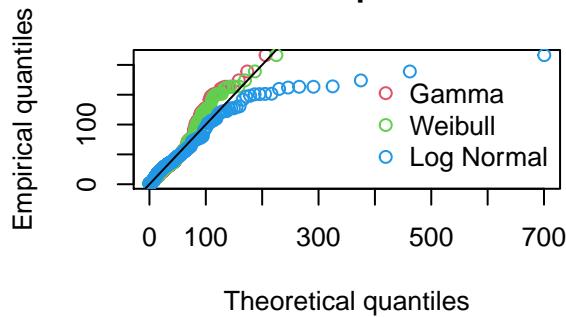
Histogram and theoretical densities



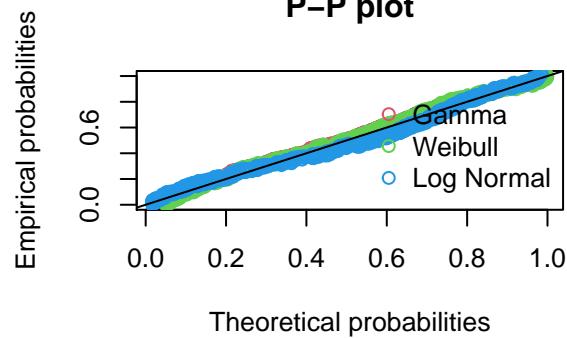
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
# Goodness of fit comparisons across fits
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

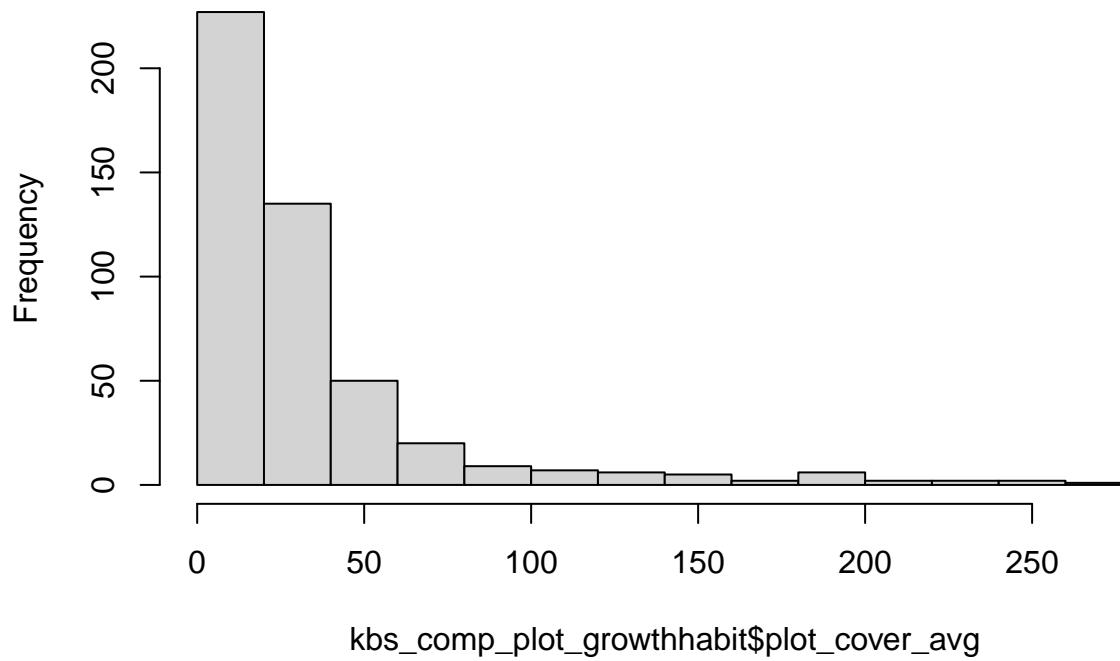
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.05150168 0.05273026 0.07179812
## Cramer-von Mises statistic   0.43058339 0.24636972 0.75485282
## Anderson-Darling statistic   3.60928359 2.60647008 4.19051306
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 5411.983 5404.915 5389.716
## Bayesian Information Criterion 5420.878 5413.809 5398.611
```

```
# log normal looks like it's the best fit
```

KBS PLOT LEVEL GROWTH HABIT - Looking at PLOT AVG TOTALS

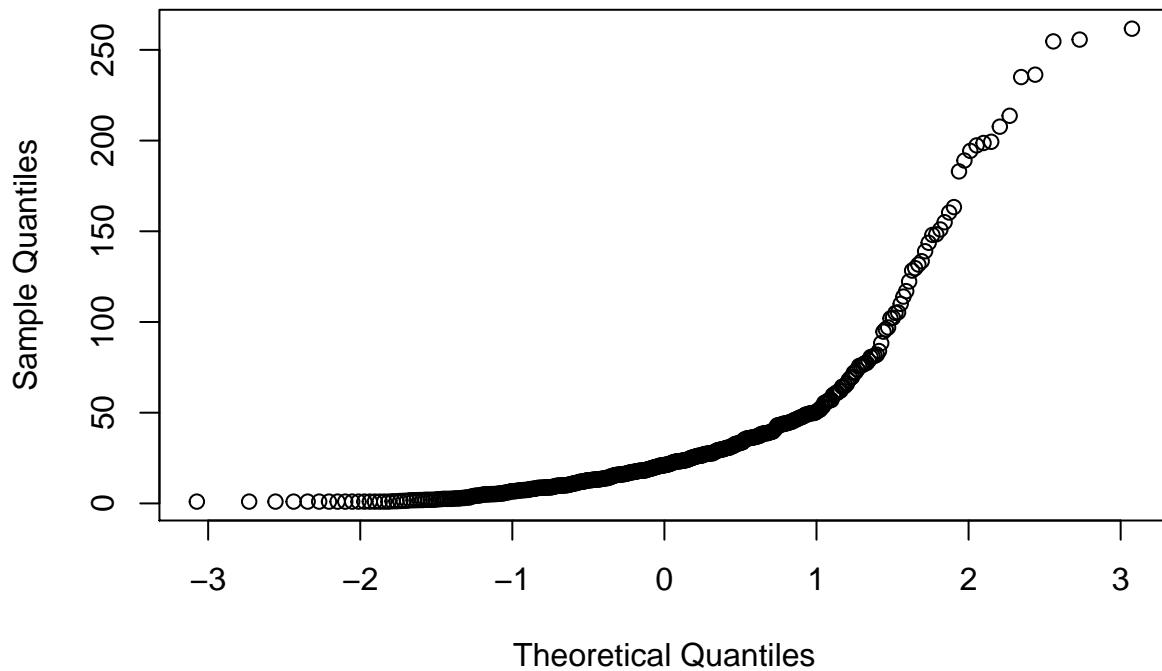
```
### KBS ####
hist(kbs_comp_plot_growthhabit$plot_cover_avg) # skewed to the right
```

Histogram of kbs_comp_plot_growthhabit\$plot_cover_avg



```
qqnorm(kbs_comp_plot_growthhabit$plot_cover_avg)
```

Normal Q-Q Plot



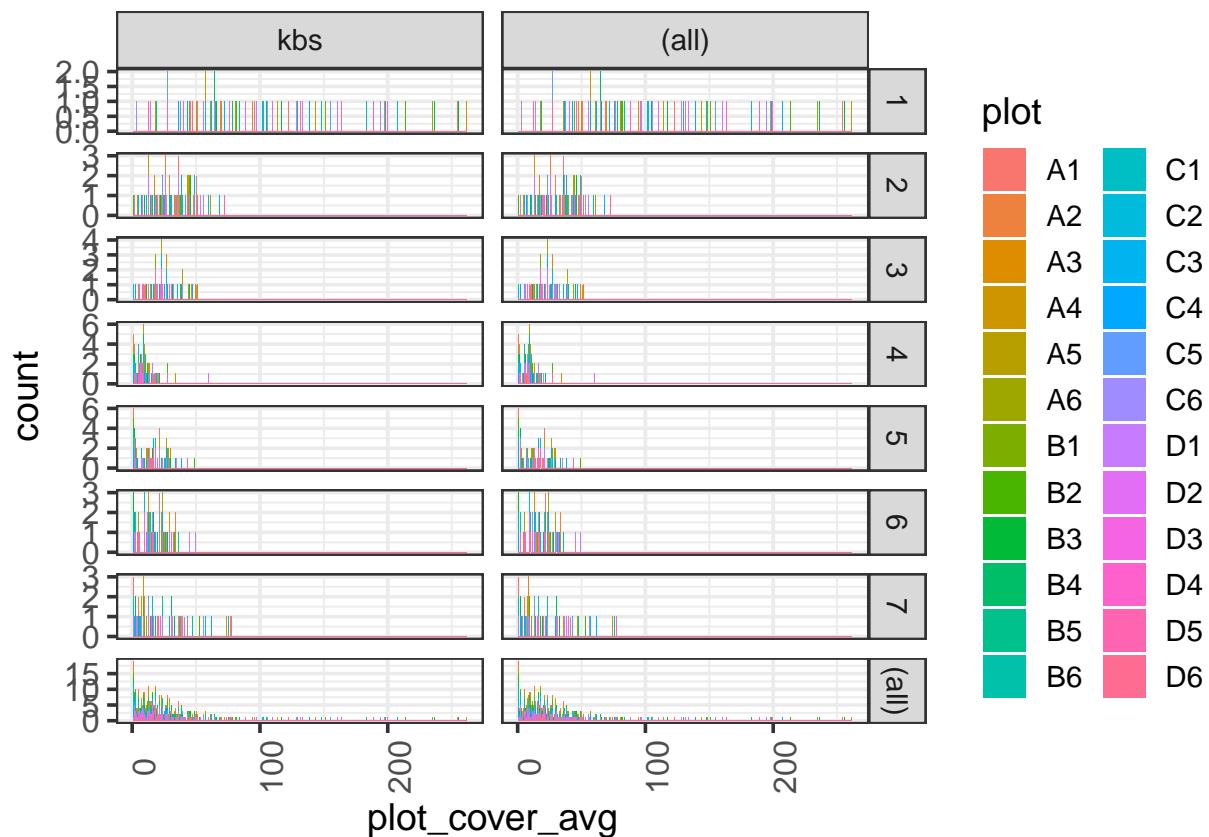
```

shapiro.test(kbs_comp_plot_growthhabit$plot_cover_avg) # pvalue is < 0.05 so we reject the null hypothesis

## 
## Shapiro-Wilk normality test
## 
## data: kbs_comp_plot_growthhabit$plot_cover_avg
## W = 0.6636, p-value < 2.2e-16

# Visualizing plot average totals for kbs at the PLOT LEVEL
ggplot(kbs_comp_plot_growthhabit, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")

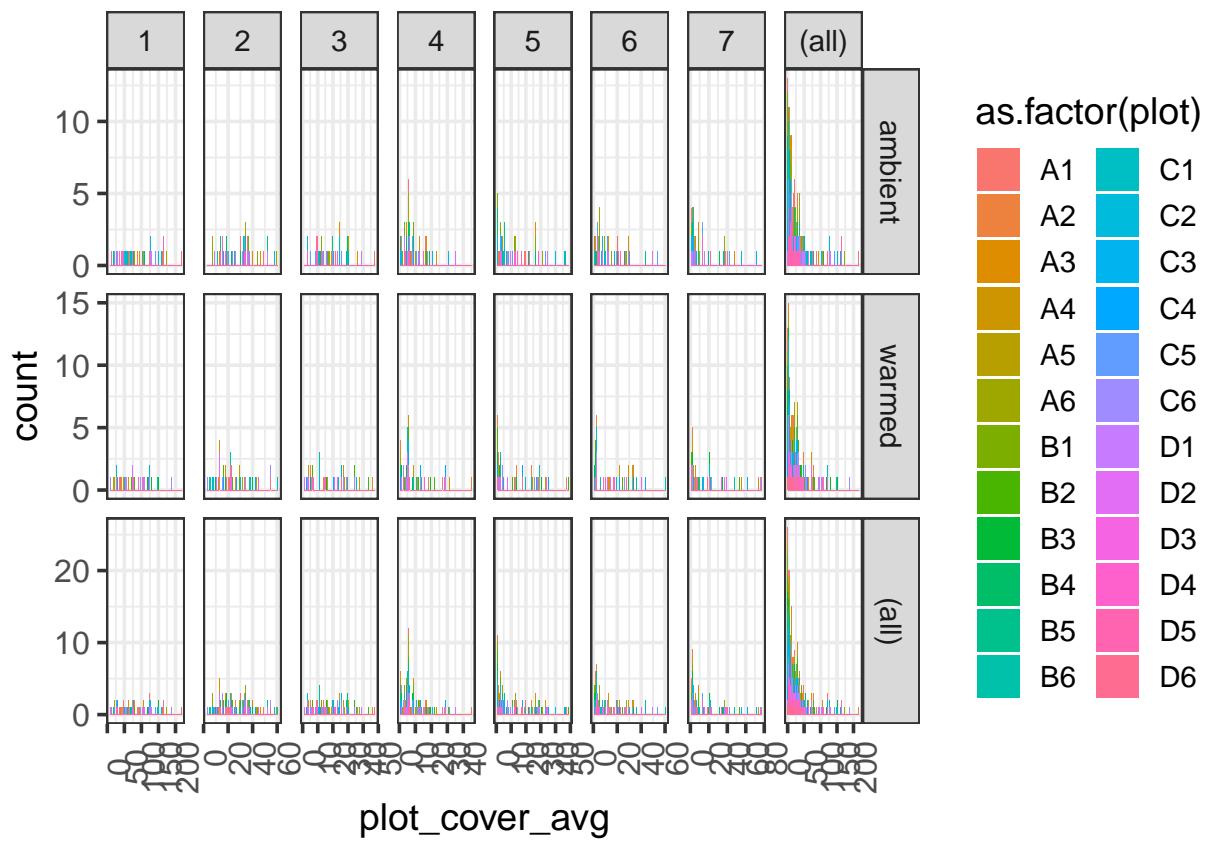
```



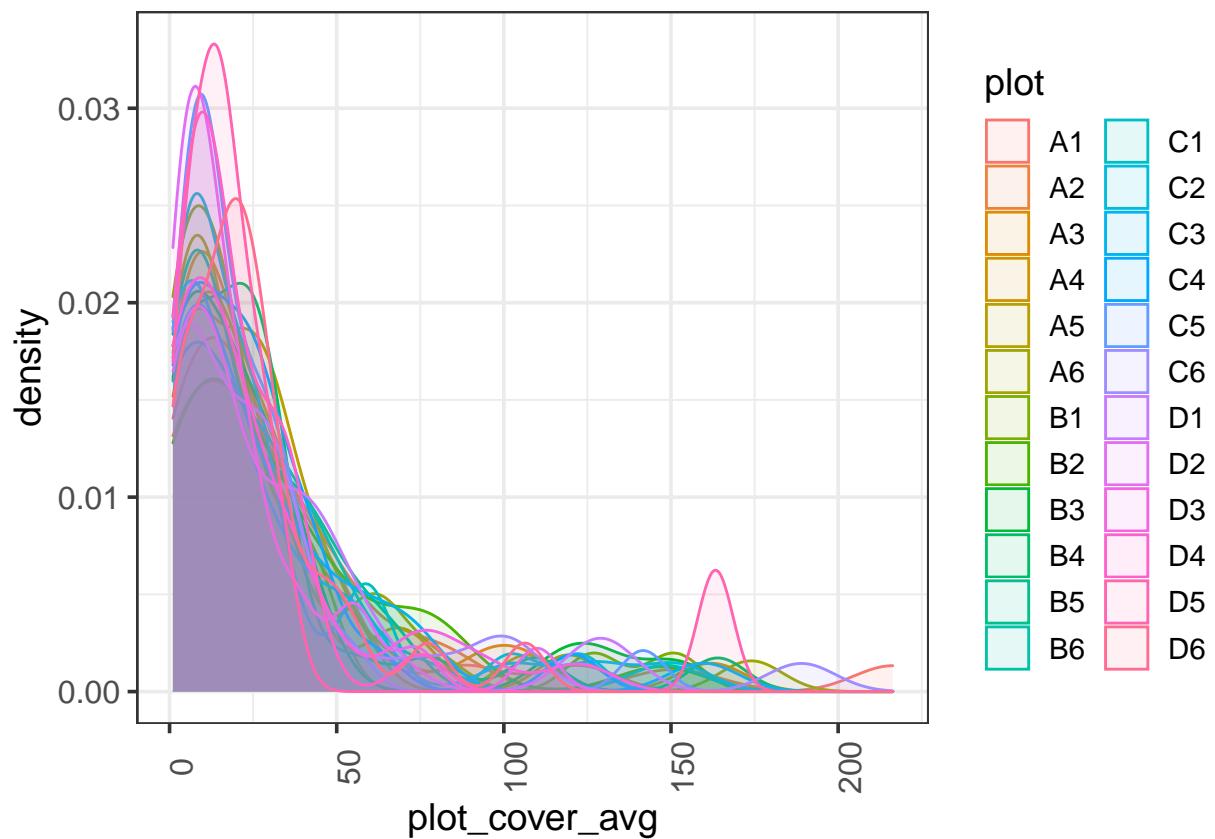
```

ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year_factor, margins = TRUE, scales = "free")

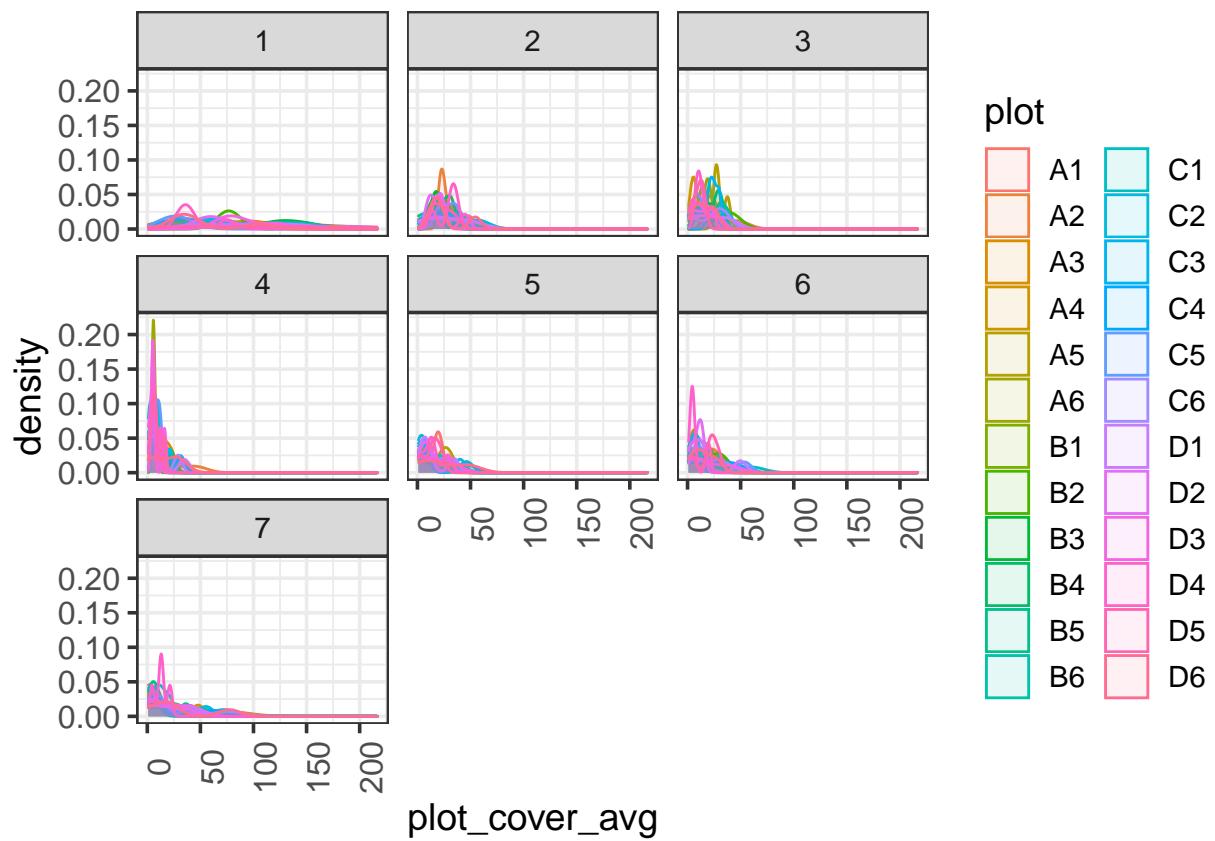
```



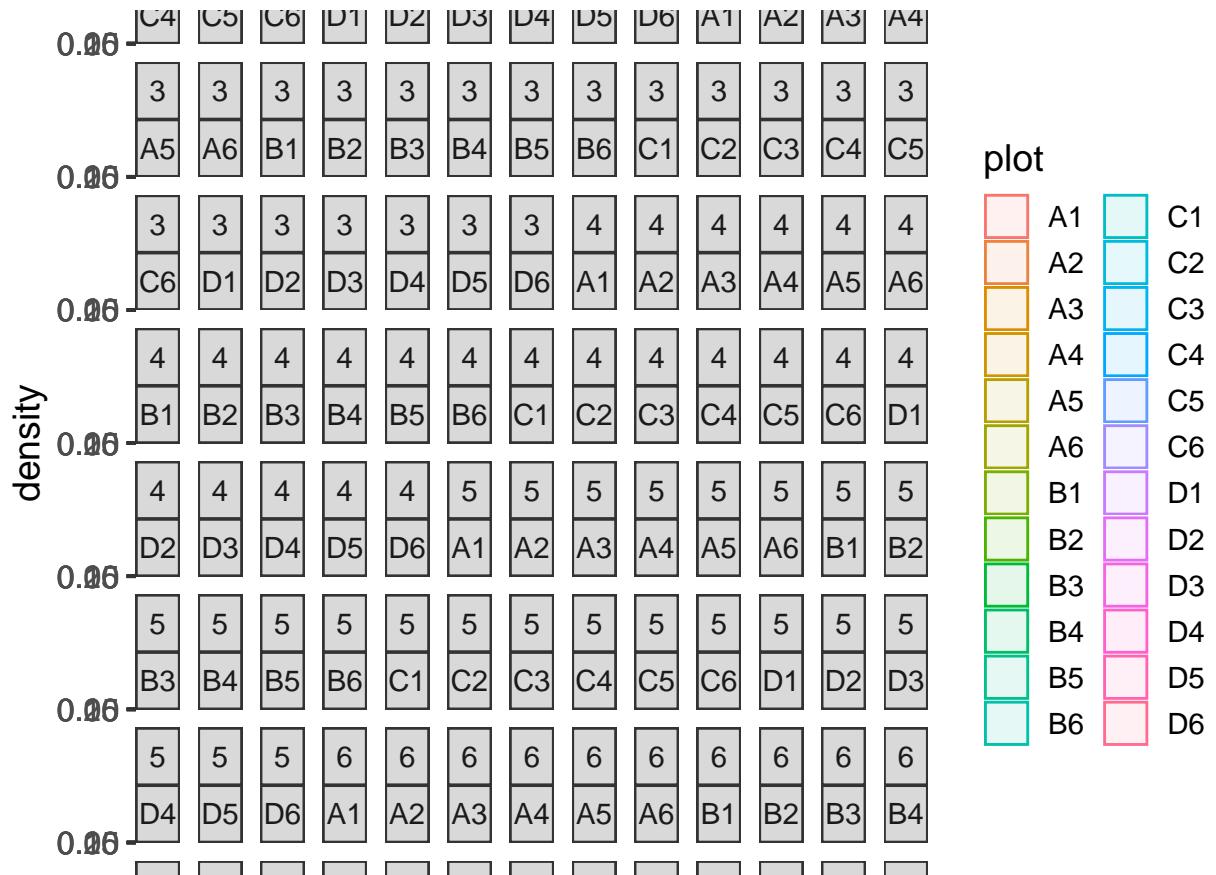
```
ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)  
  facet_wrap(~year_factor)
```

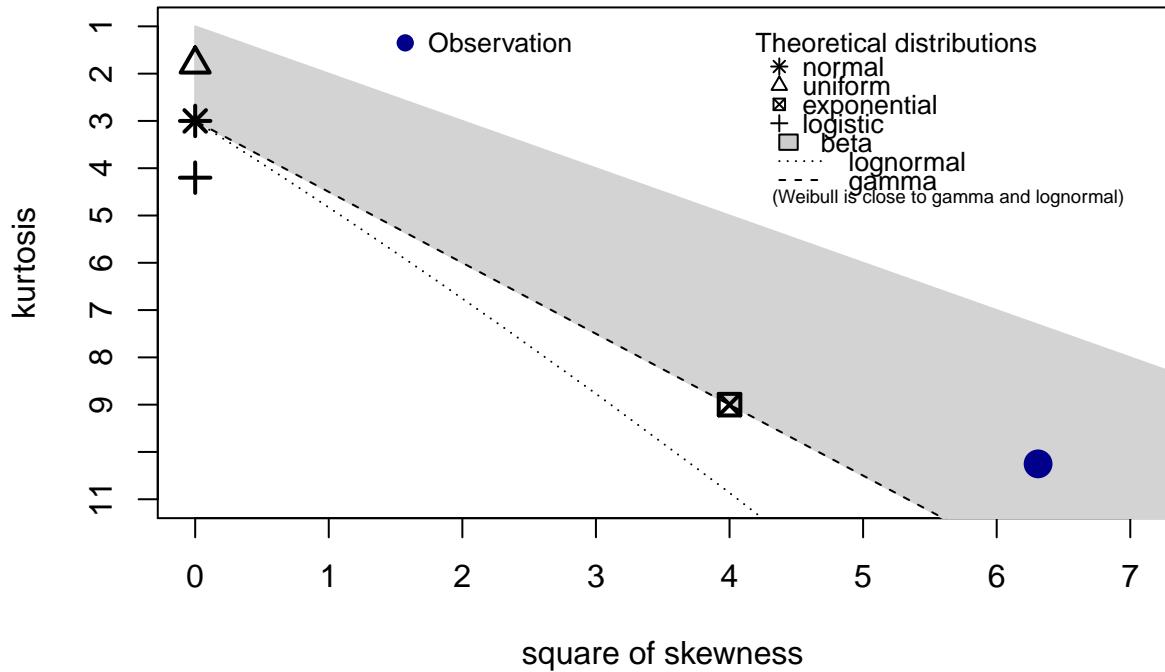


```
ggplot(kbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
  facet_wrap(~year_factor + plot)
```



```
# Exploring distributions for these data:  
descdist(kbs_comp_plot_origin$plot_cover_avg, discrete = FALSE)
```

Cullen and Frey graph

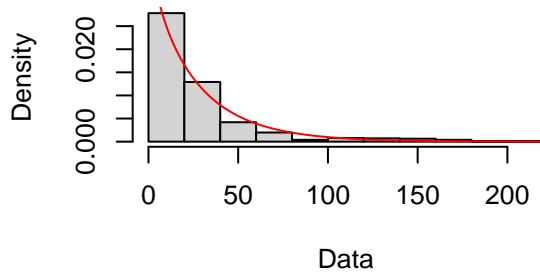
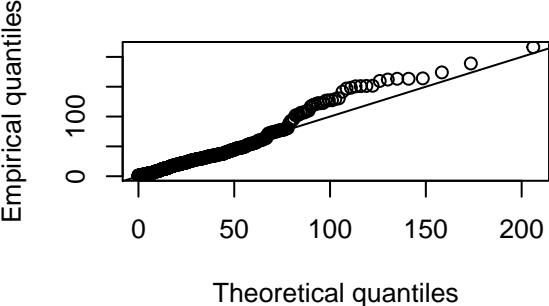
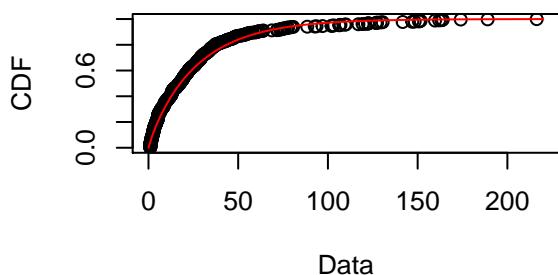
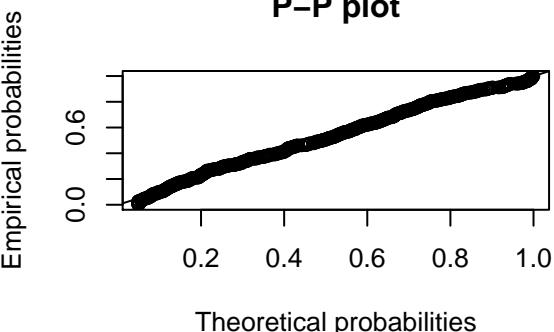


```

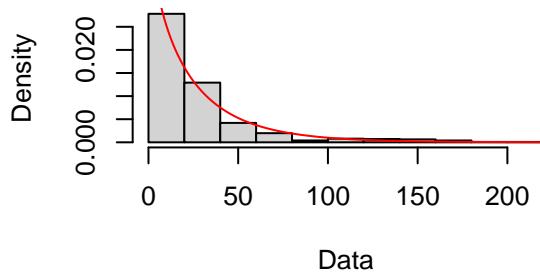
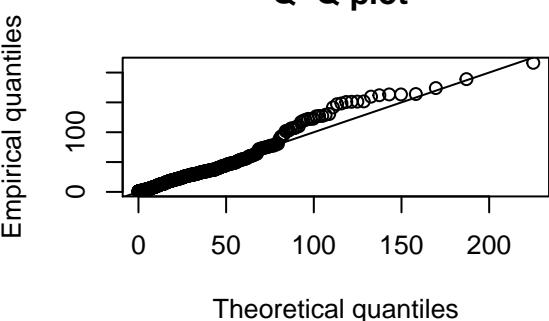
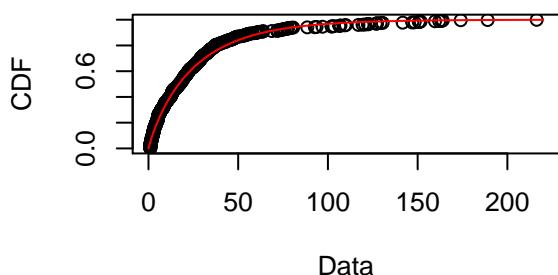
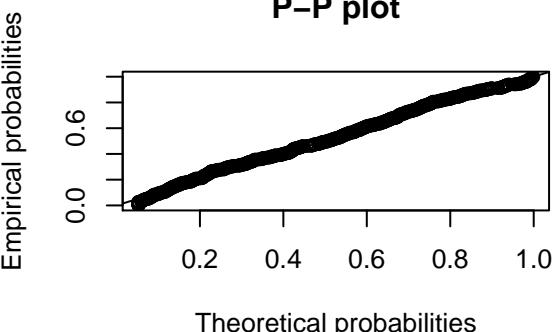
## summary statistics
## -----
## min: 1   max: 216.3333
## median: 17.28571
## mean: 26.83611
## estimated sd: 32.6559
## estimated skewness: 2.511938
## estimated kurtosis: 10.25197

# Gamma distribution
fit.gamma <- fitdist(kbs_comp_plot_origin$plot_cover_avg, "gamma")
plot(fit.gamma)

```

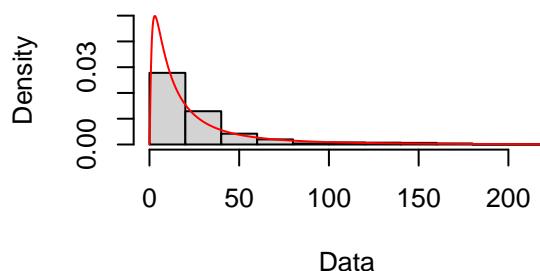
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Weibull distribution
fit.weibull <- fitdist(kbs_comp_plot_origin$plot_cover_avg, "weibull")
plot(fit.weibull)
```

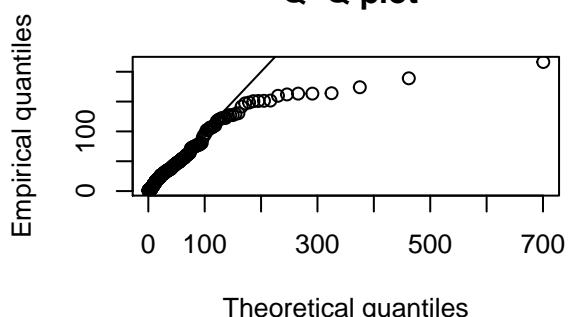
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Lognormal distribution
fit.ln <- fitdist(kbs_comp_plot_origin$plot_cover_avg, "lnorm")
plot(fit.ln)
```

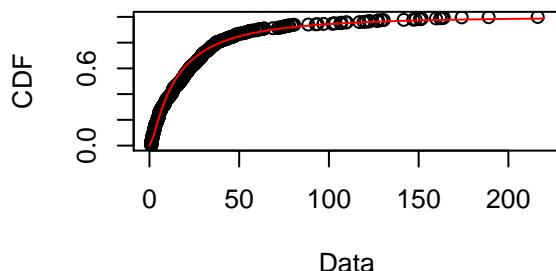
Empirical and theoretical dens.



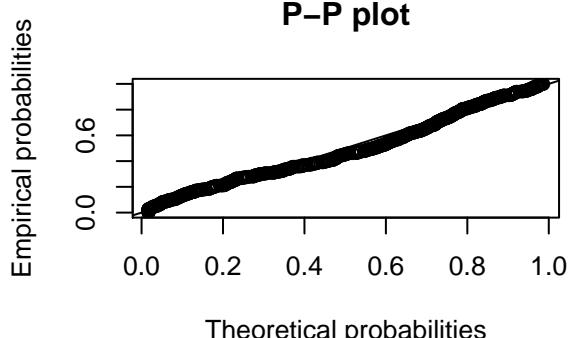
Q-Q plot



Empirical and theoretical CDFs

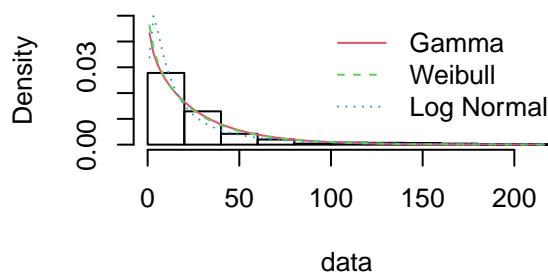


P-P plot

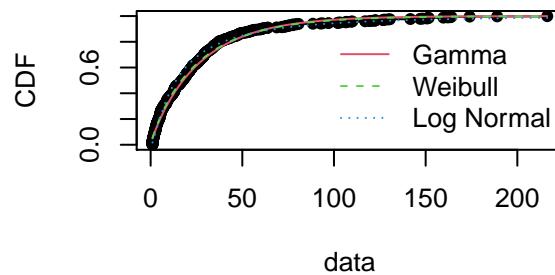


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```

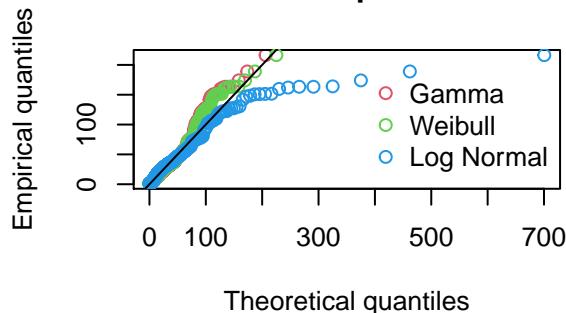
Histogram and theoretical densities



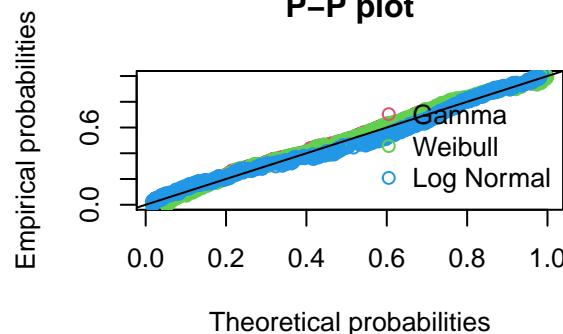
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

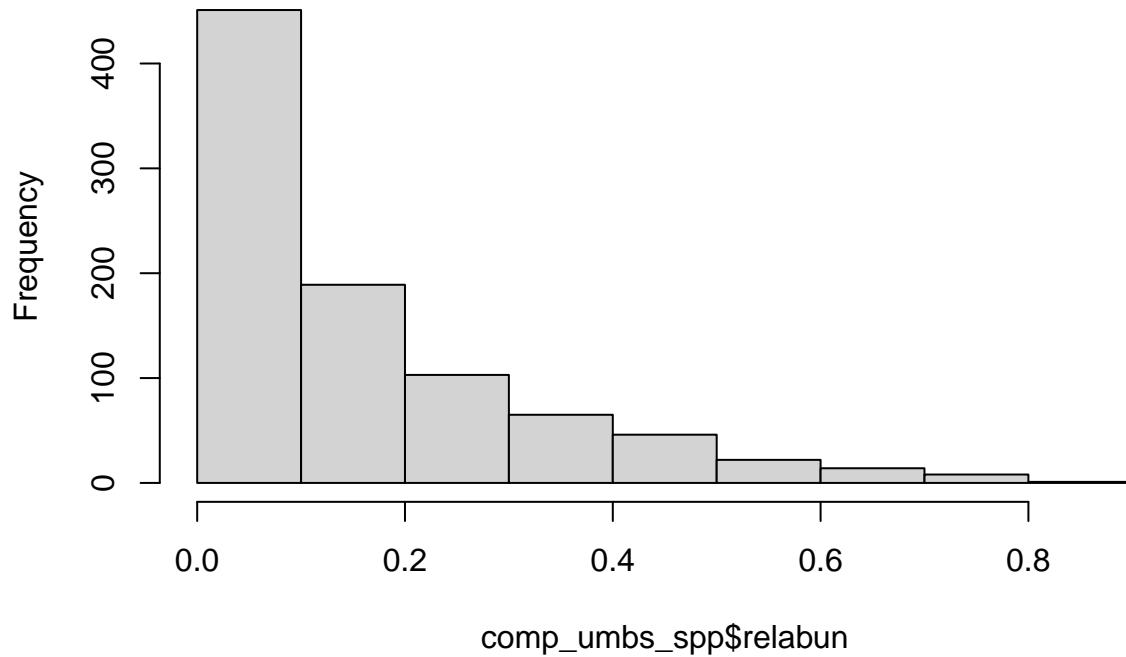
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.05150168 0.05273026 0.07179812
## Cramer-von Mises statistic   0.43058339 0.24636972 0.75485282
## Anderson-Darling statistic   3.60928359 2.60647008 4.19051306
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 5411.983 5404.915 5389.716
## Bayesian Information Criterion 5420.878 5413.809 5398.611
```

log normal looks like it's the best fit

UMBS SPECIES LEVEL - Looking at RELATIVE ABUNDANCE

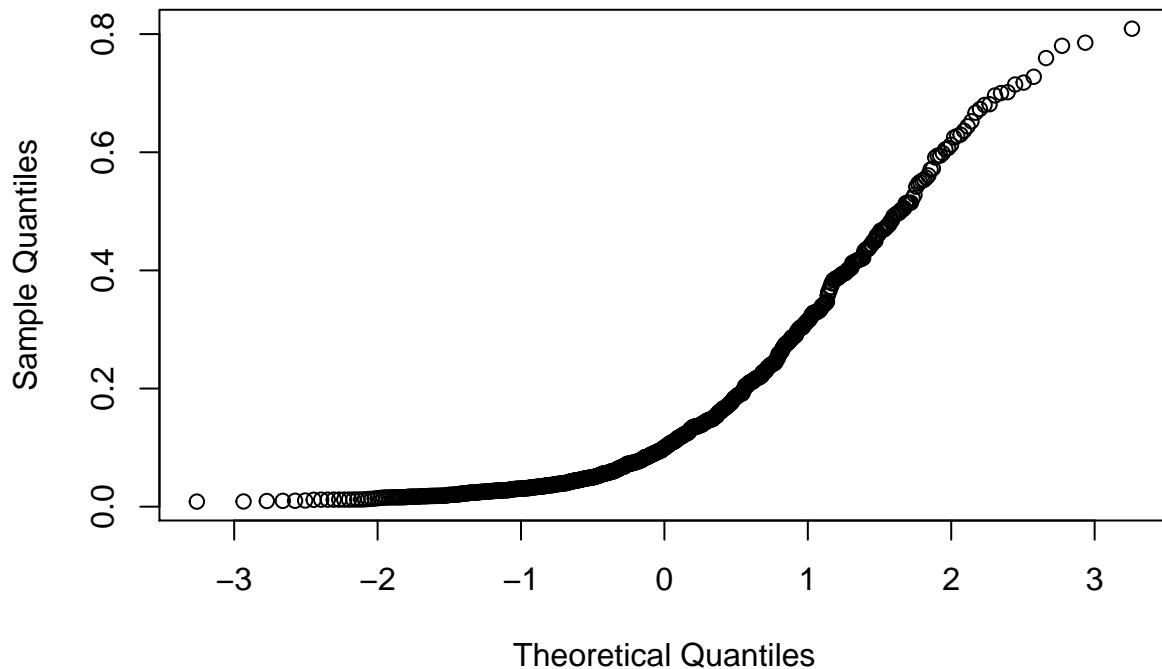
```
### UMBS ####
hist(comp_umbs_spp$relabun) # skewed to the right
```

Histogram of comp_umbs_spp\$relabun



```
qqnorm(comp_umbs_spp$relabun)
```

Normal Q-Q Plot



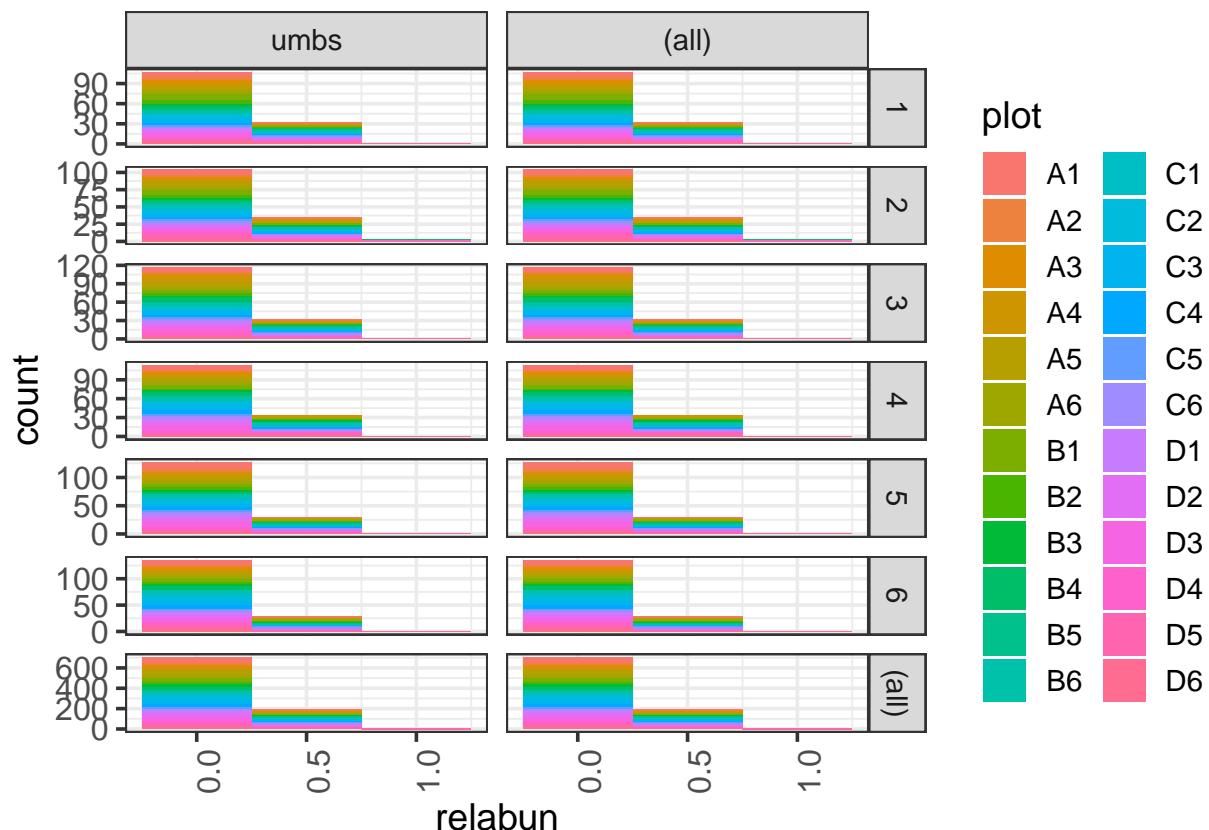
```

shapiro.test(comp_umbs_spp$relabun) # pvalue is < 0.05 so we reject the null hypothesis that the data

##
## Shapiro-Wilk normality test
##
## data: comp_umbs_spp$relabun
## W = 0.81681, p-value < 2.2e-16

# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(comp_umbs_spp, aes(relabun, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")

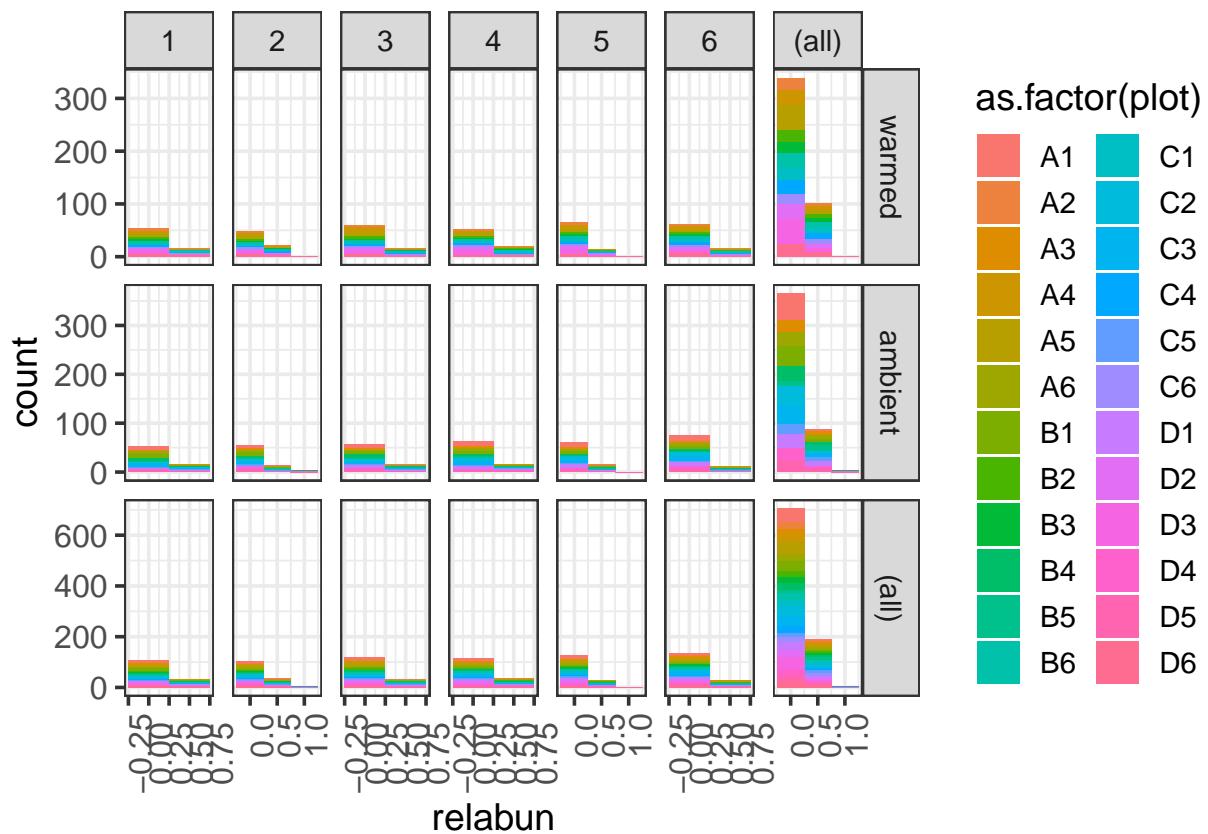
```



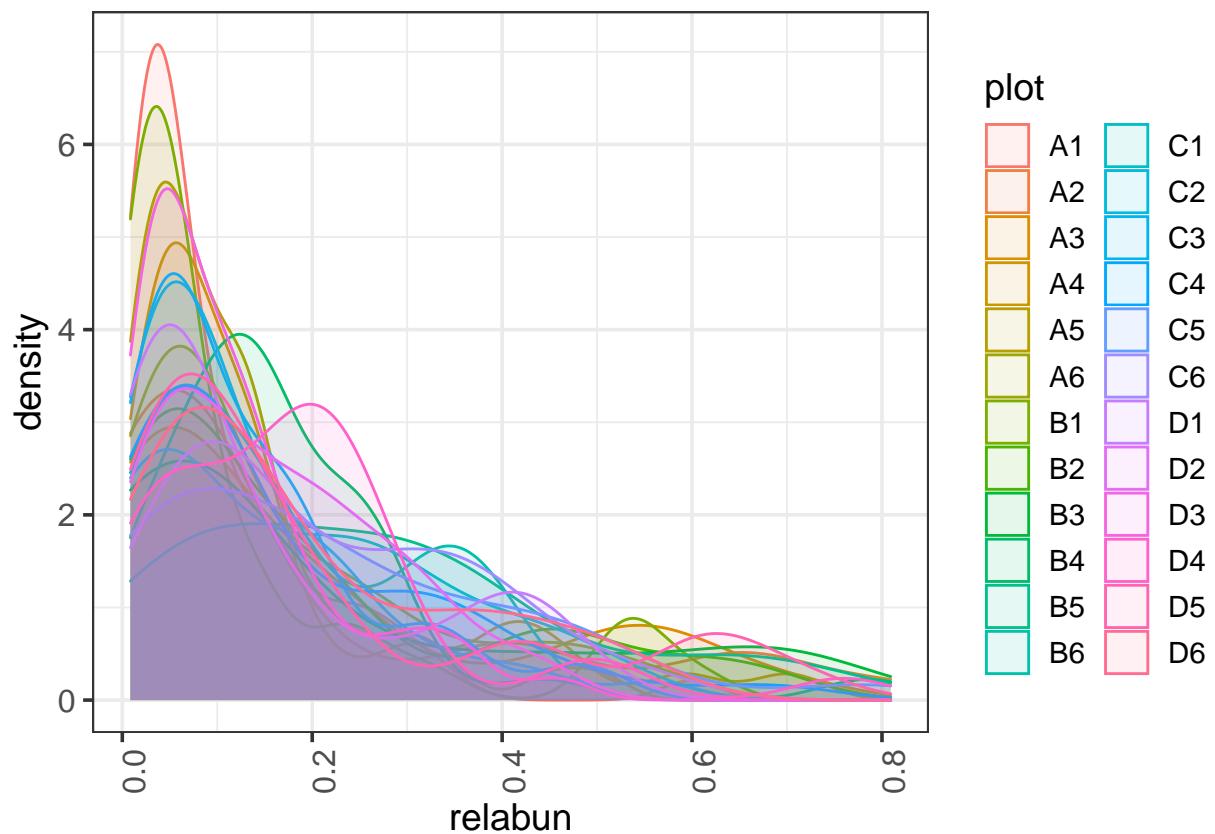
```

ggplot(comp_umbs_spp, aes(relabun, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year_factor, margins = TRUE, scales = "free")

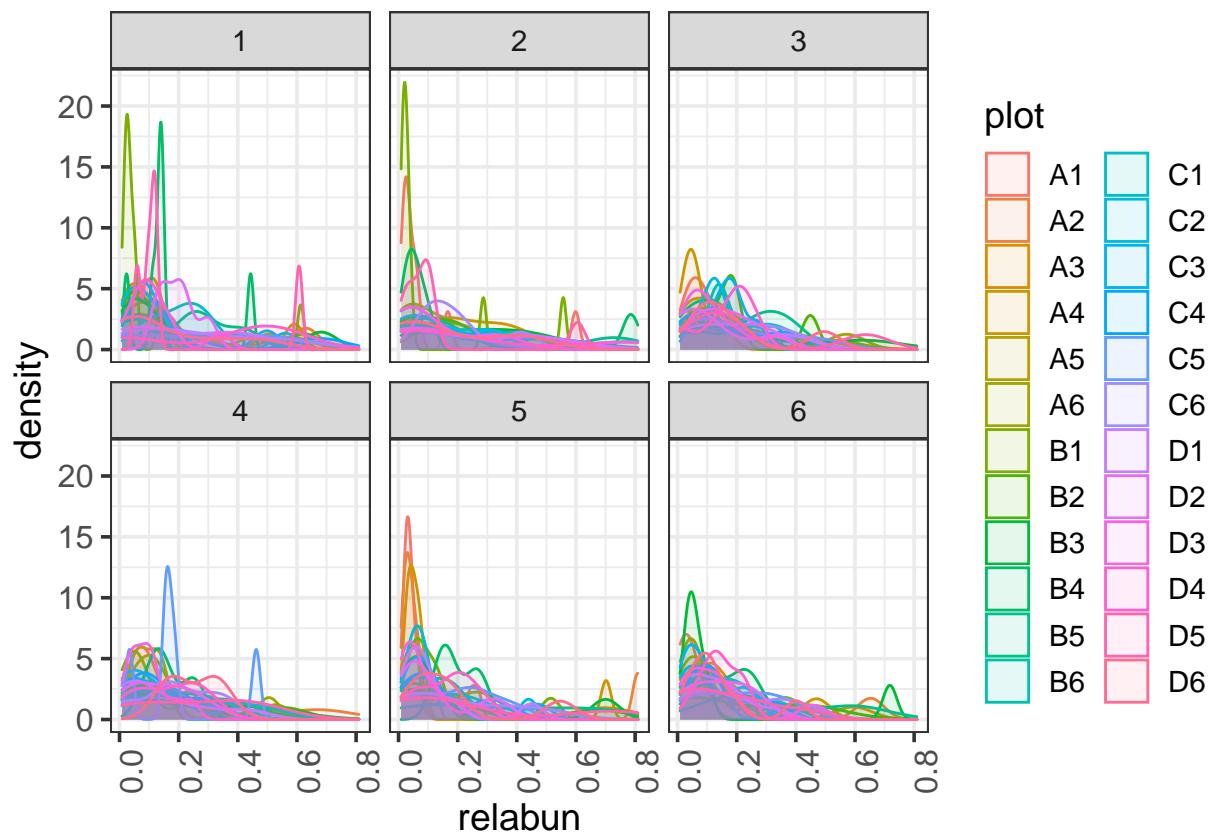
```



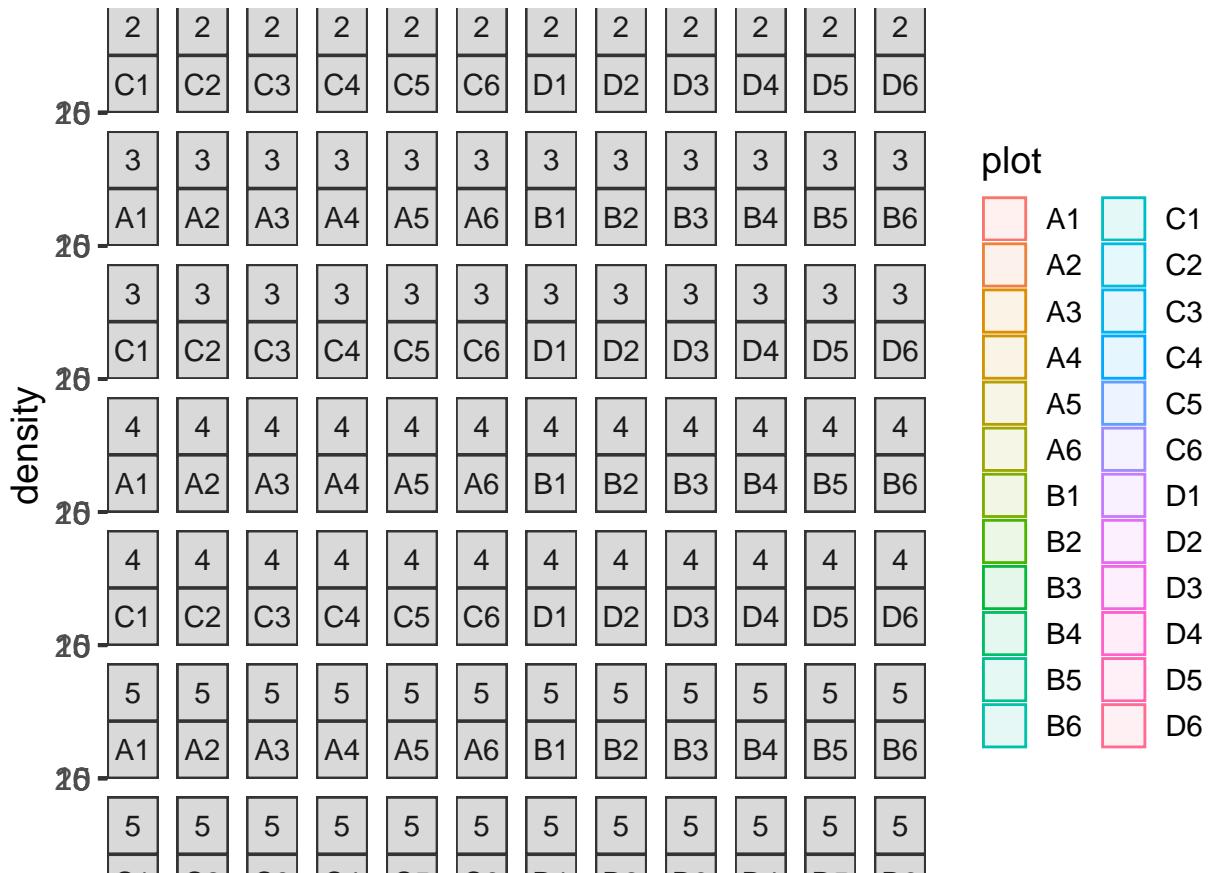
```
ggplot(comp_umbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(comp_umbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor)
```

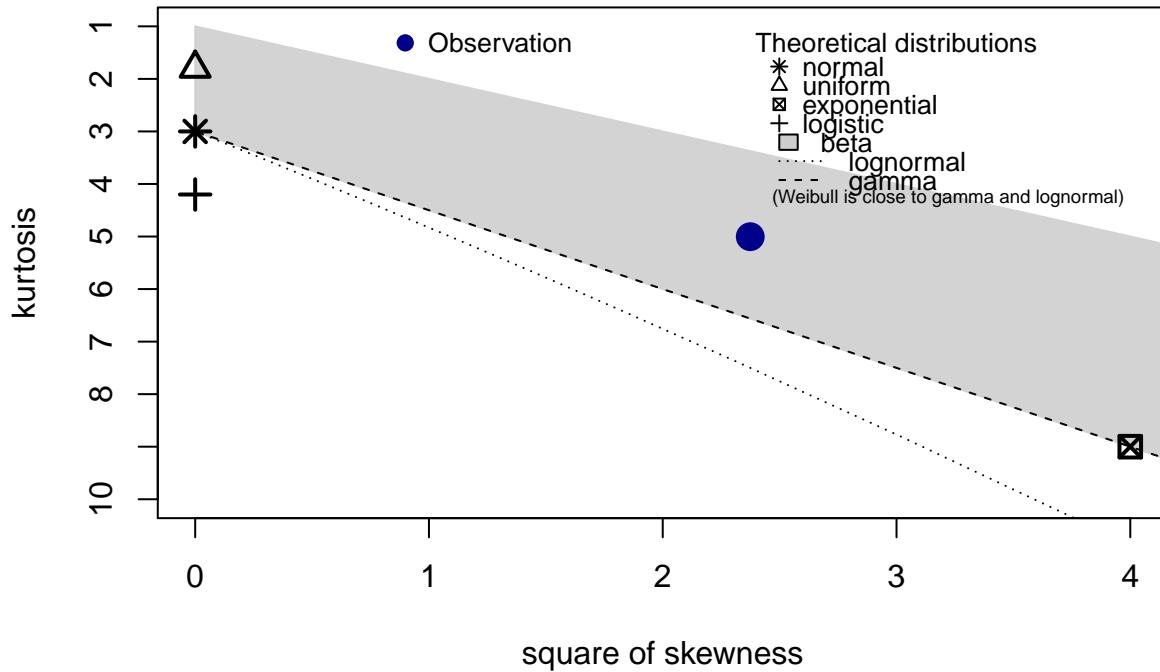


```
ggplot(comp_umbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor + plot)
```



```
# Exploring distributions for these right-skewed data:  
descdist(comp_umbs_spp$relabun, discrete = FALSE)
```

Cullen and Frey graph



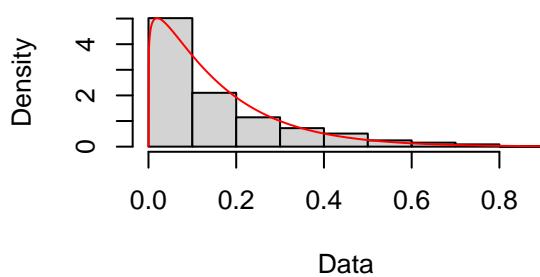
```

## summary statistics
## -----
## min:  0.008576329  max:  0.8091703
## median:  0.09957567
## mean:  0.160178
## estimated sd:  0.1594335
## estimated skewness:  1.540918
## estimated kurtosis:  5.003079

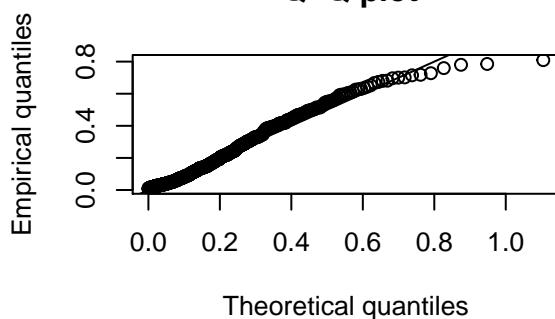
# Gamma distribution
fit.gamma <- fitdist(comp_umbs_spp$relabun, "gamma")
plot(fit.gamma)

```

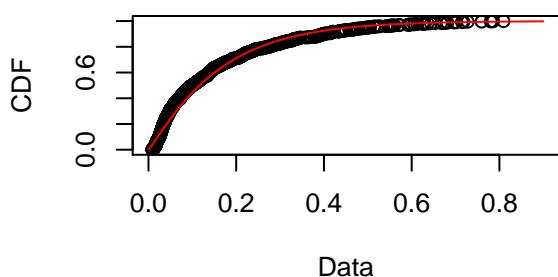
Empirical and theoretical dens.



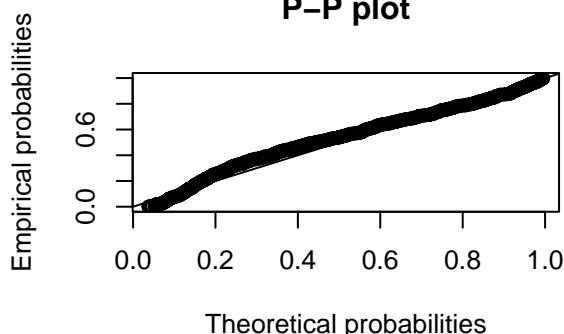
Q-Q plot



Empirical and theoretical CDFs

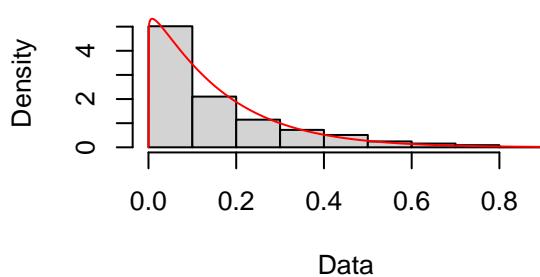


P-P plot

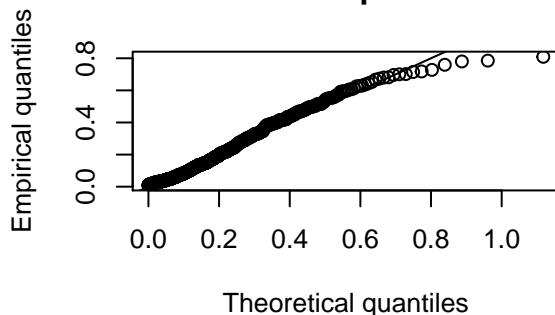


```
# Weibull distribution
fit.weibull <- fitdist(comp_umbs_spp$relabun, "weibull")
plot(fit.weibull)
```

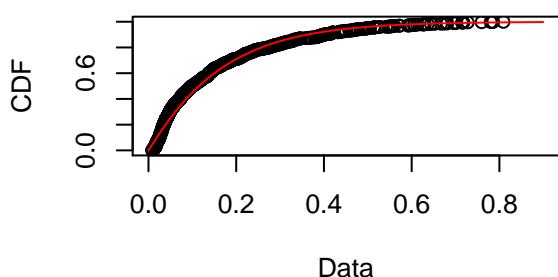
Empirical and theoretical dens.



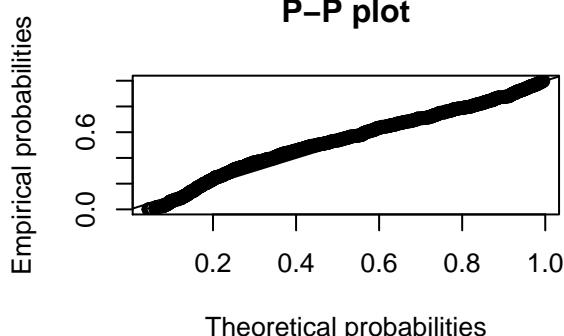
Q-Q plot



Empirical and theoretical CDFs

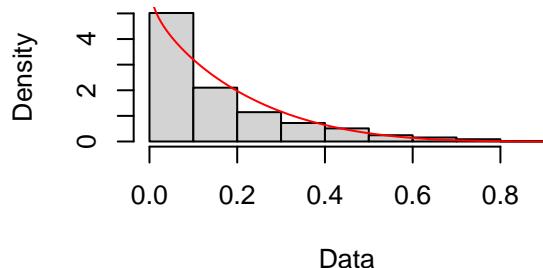


P-P plot

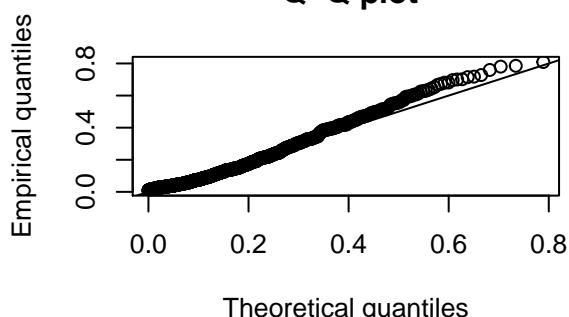


```
# Beta
fit.beta <- fitdist(comp_umbs_spp$relabun, "beta")
plot(fit.beta)
```

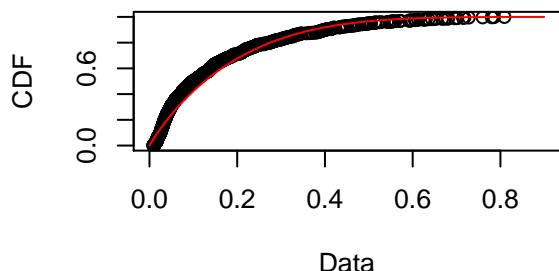
Empirical and theoretical dens.



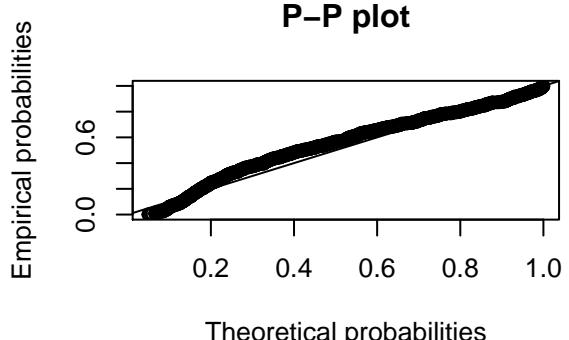
Q–Q plot



Empirical and theoretical CDFs

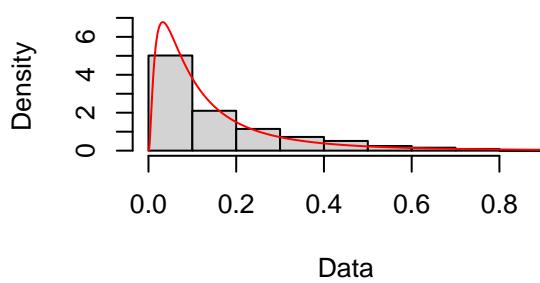


P–P plot

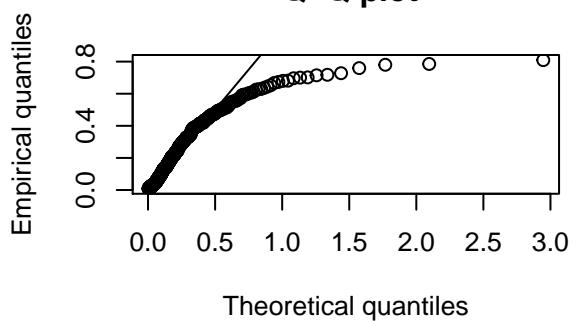


```
# Lognormal distribution
fit.ln <- fitdist(comp_umbs_spp$relabun, "lnorm")
plot(fit.ln)
```

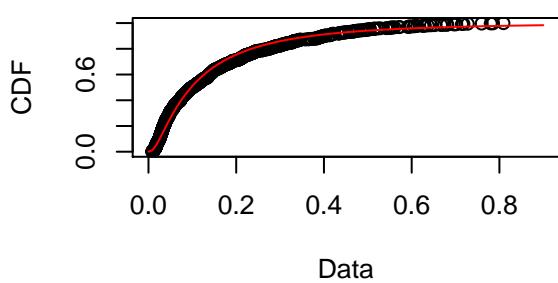
Empirical and theoretical dens.



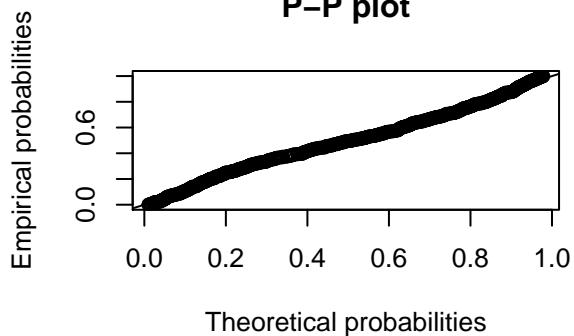
Q-Q plot



Empirical and theoretical CDFs

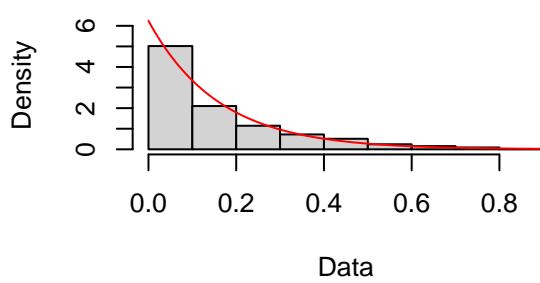


P-P plot

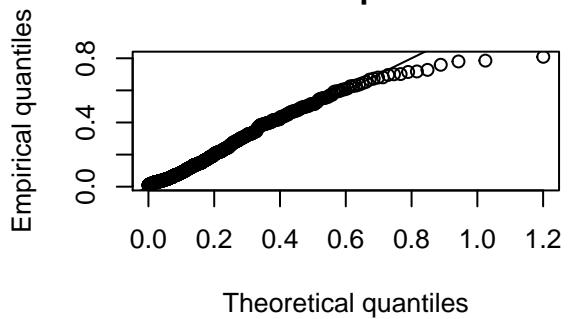


```
# Exponential distribution is another option  
fit.exp <- fitdist(comp_umbs_spp$relabun, "exp")  
plot(fit.exp)
```

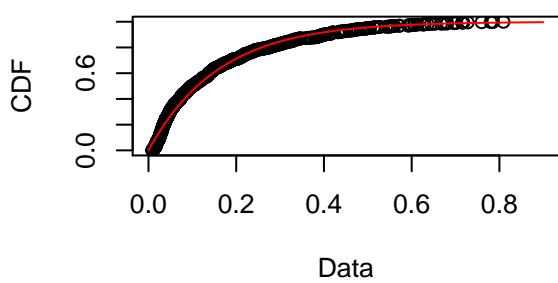
Empirical and theoretical dens.



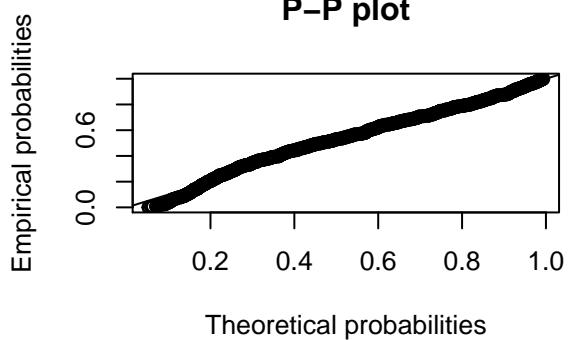
Q-Q plot



Empirical and theoretical CDFs



P-P plot

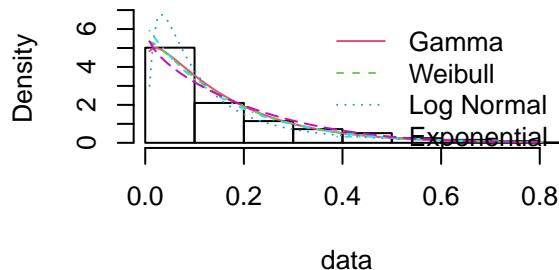


```

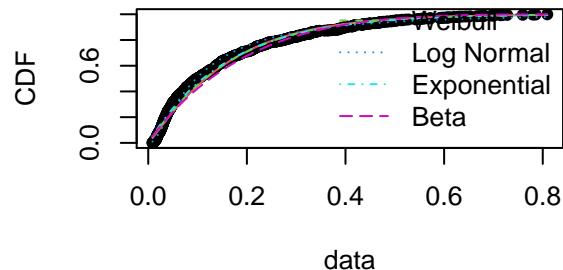
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal", "Exponential", "Beta")
denscomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)

```

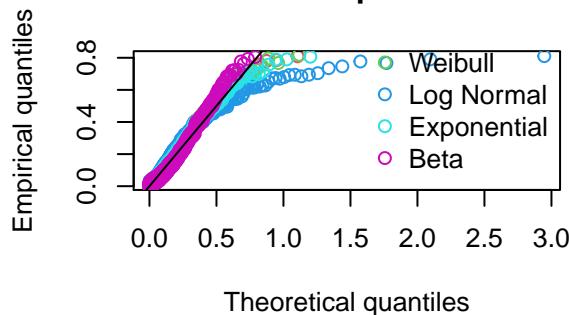
Histogram and theoretical densities



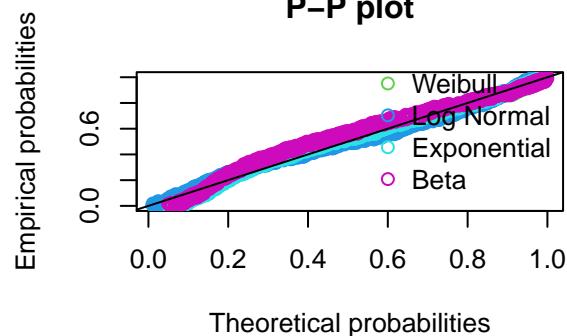
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```

# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), fitnames = c("Gamma",
    "Weibull", "Log Normal", "Exp", "Beta"))

```

```

## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal      Exp
## Kolmogorov-Smirnov statistic 0.07776196 0.06720039 0.05018519 0.0666861
## Cramer-von Mises statistic   1.50231036 1.20082631 0.74429208 0.8263555
## Anderson-Darling statistic   9.33691935 8.24847329 4.80014789 7.1414656
##                                     Beta
## Kolmogorov-Smirnov statistic  0.0857168
## Cramer-von Mises statistic   2.3253269
## Anderson-Darling statistic   13.7081247
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal      Exp
## Akaike's Information Criterion -1500.418 -1494.224 -1553.369 -1492.983
## Bayesian Information Criterion -1490.815 -1484.622 -1543.767 -1488.181
##                                     Beta

```

```

## Akaike's Information Criterion -1459.308
## Bayesian Information Criterion -1449.705

# Beta and exp distributions look to be the best based on AIC and BIC values

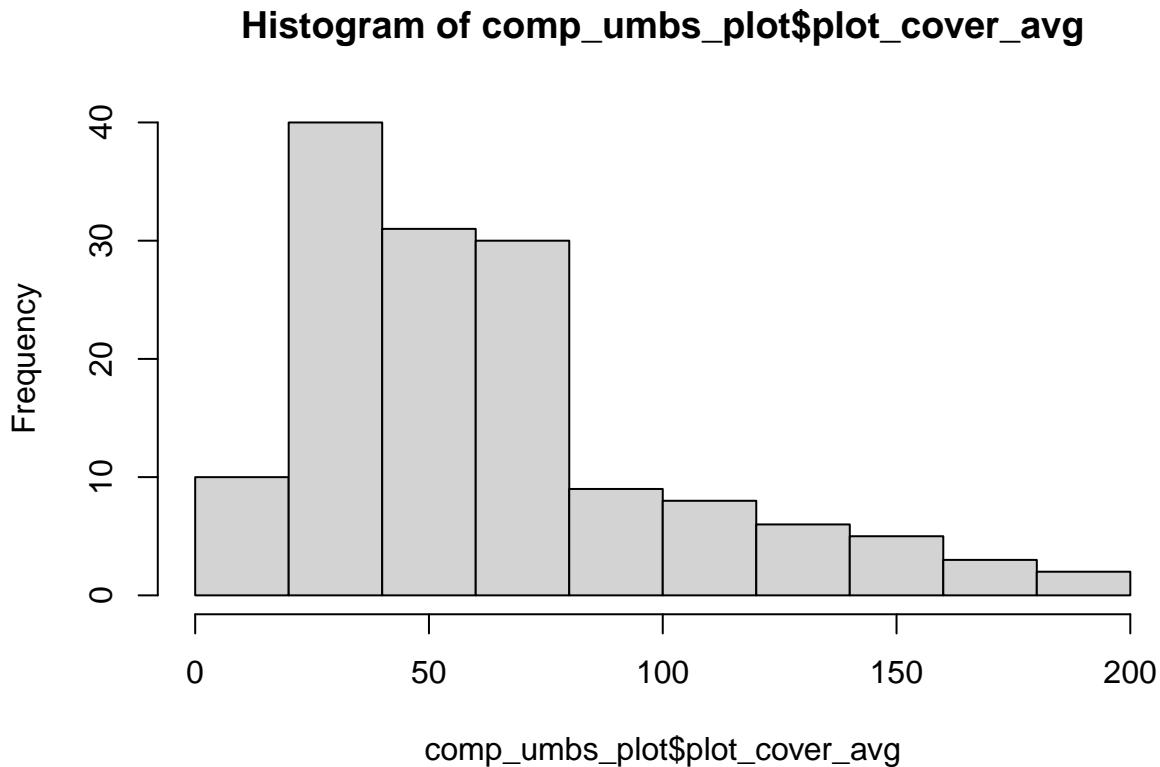
```

UMBS PLOT LEVEL - Looking at PLOT AVG TOTALS

```

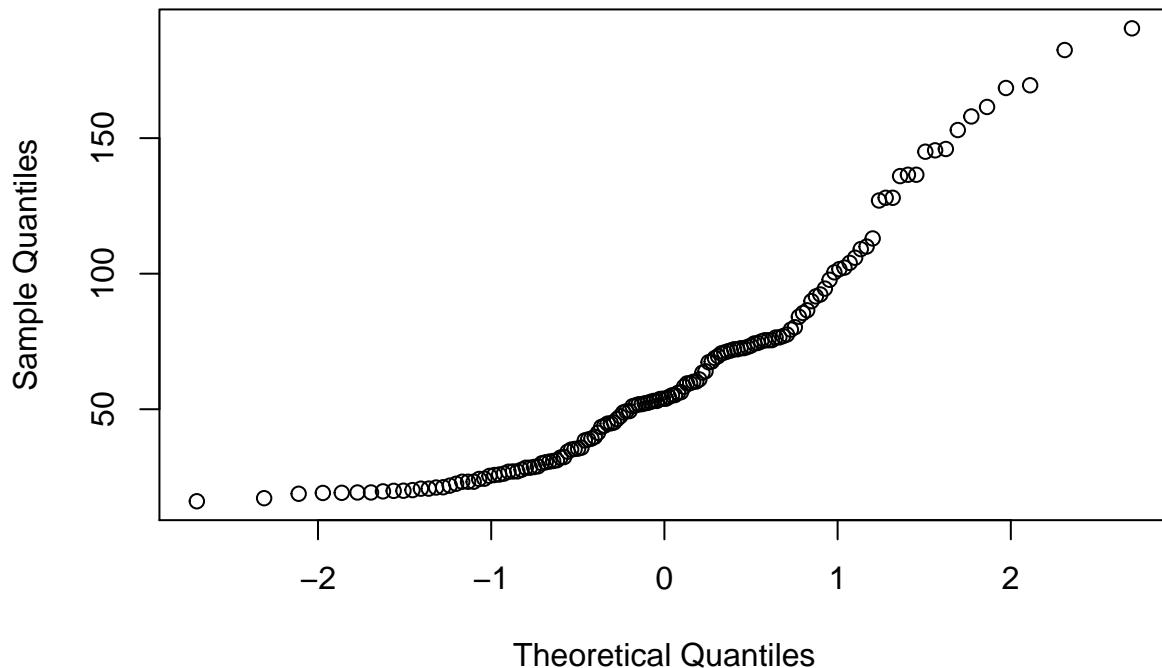
### UMBS ####
hist(comp_umbs_plot$plot_cover_avg) # skewed to the right

```



```
qqnorm(comp_umbs_plot$plot_cover_avg)
```

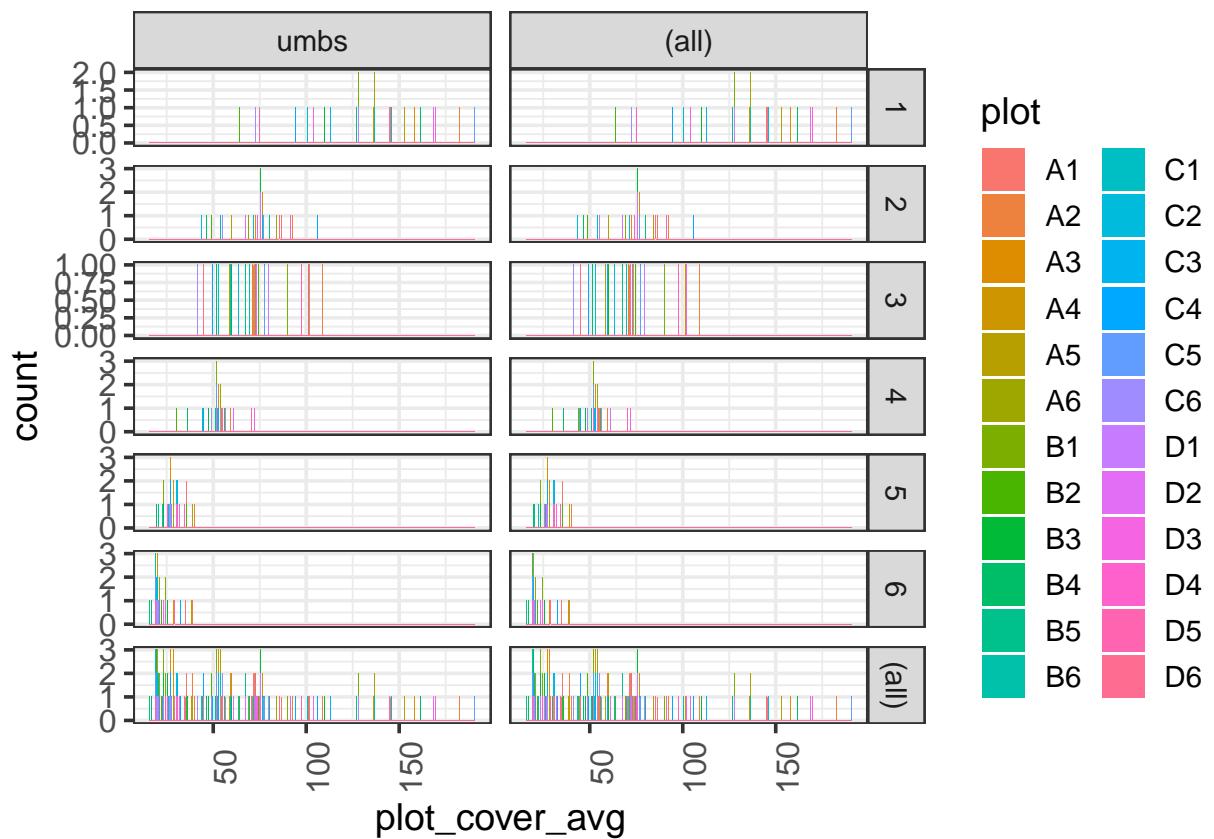
Normal Q-Q Plot



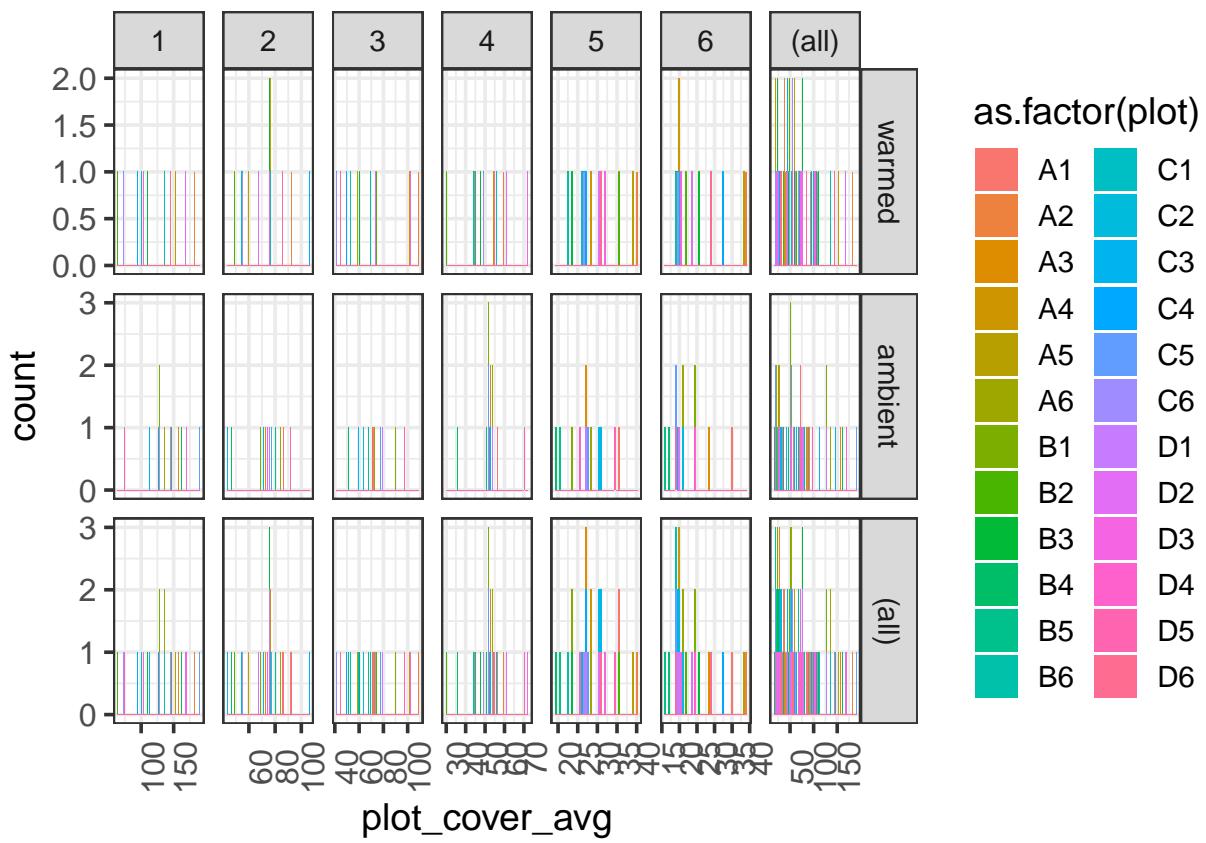
```
shapiro.test(comp_umbs_plot$plot_cover_avg) # pvalue is < 0.05 so we reject the null hypothesis that the data is normally distributed

## 
## Shapiro-Wilk normality test
##
## data: comp_umbs_plot$plot_cover_avg
## W = 0.888888, p-value = 5.615e-09

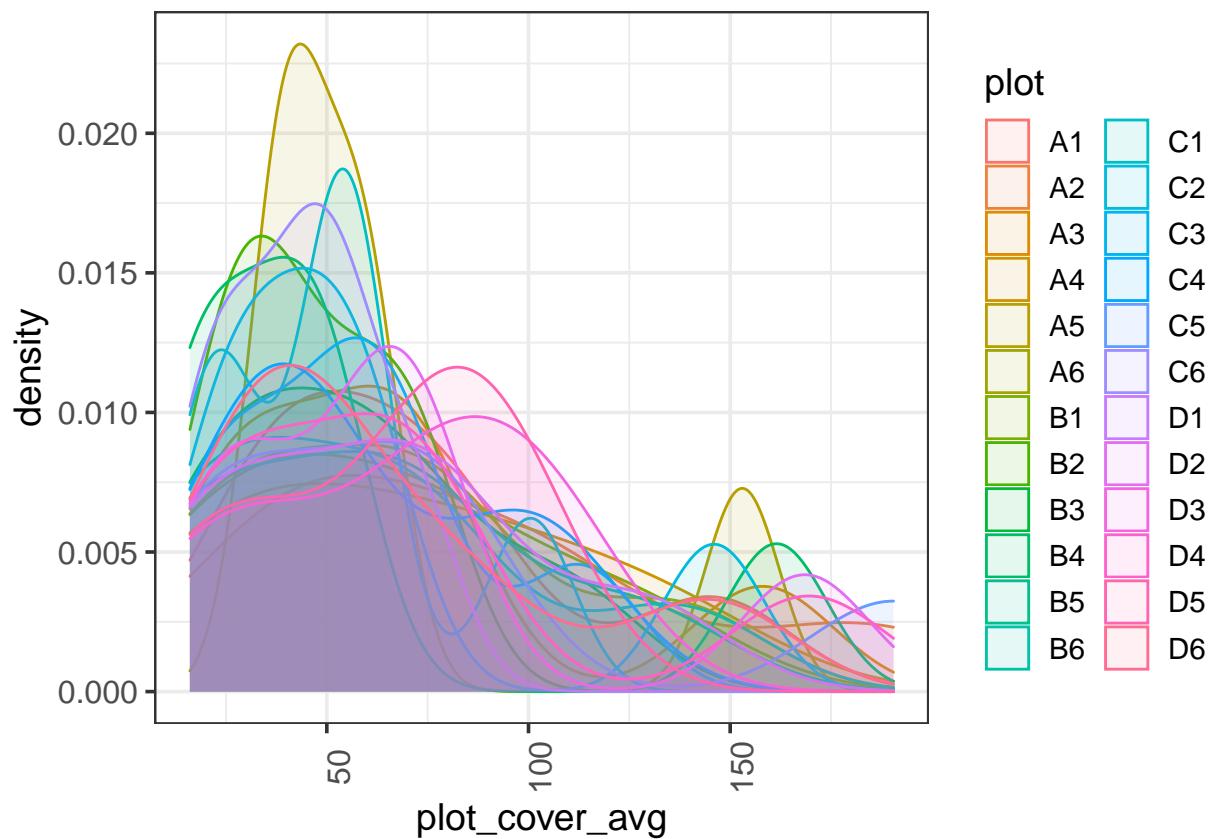
# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(comp_umbs_plot, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")
```



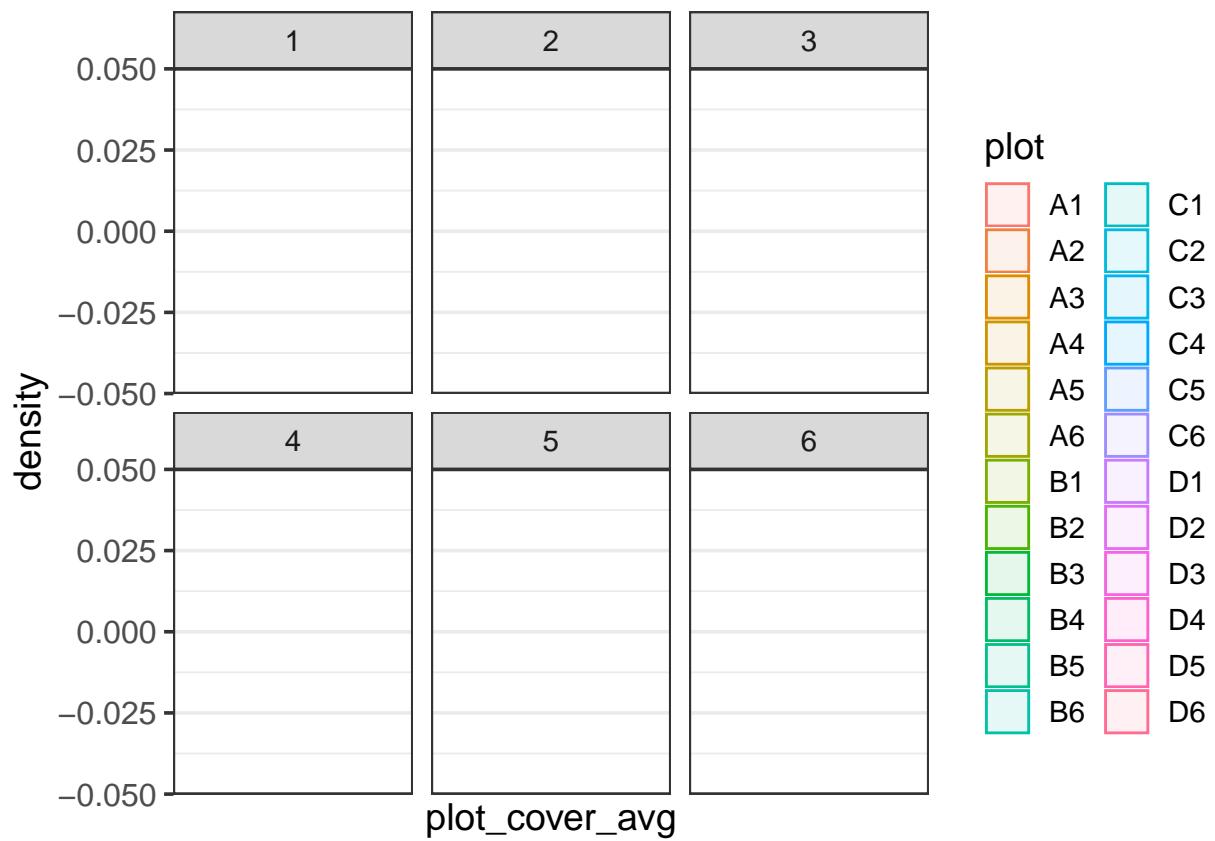
```
ggplot(comp_umbs_plot, aes(plot_cover_avg, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year_factor, margins = TRUE, scales = "free")
```



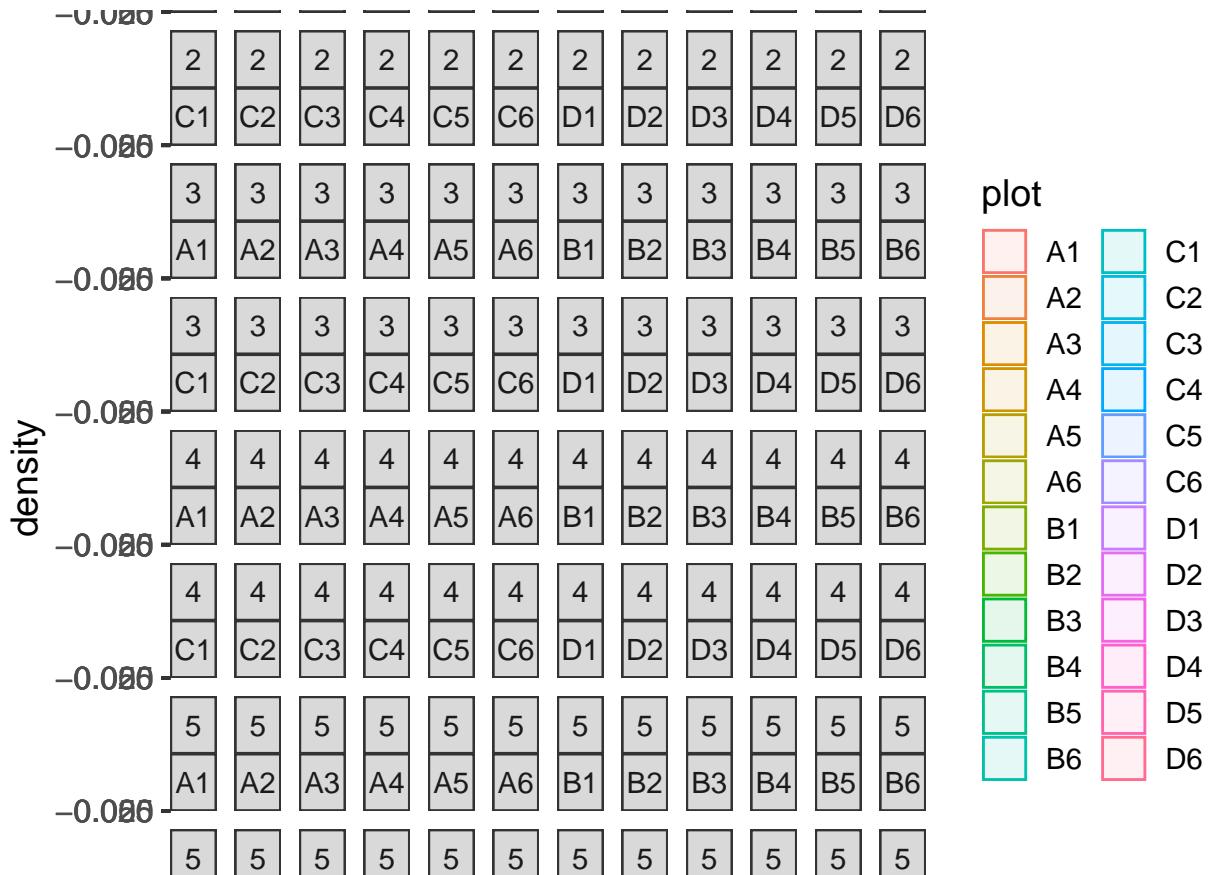
```
ggplot(comp_umbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
ggplot(comp_umbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor)
```

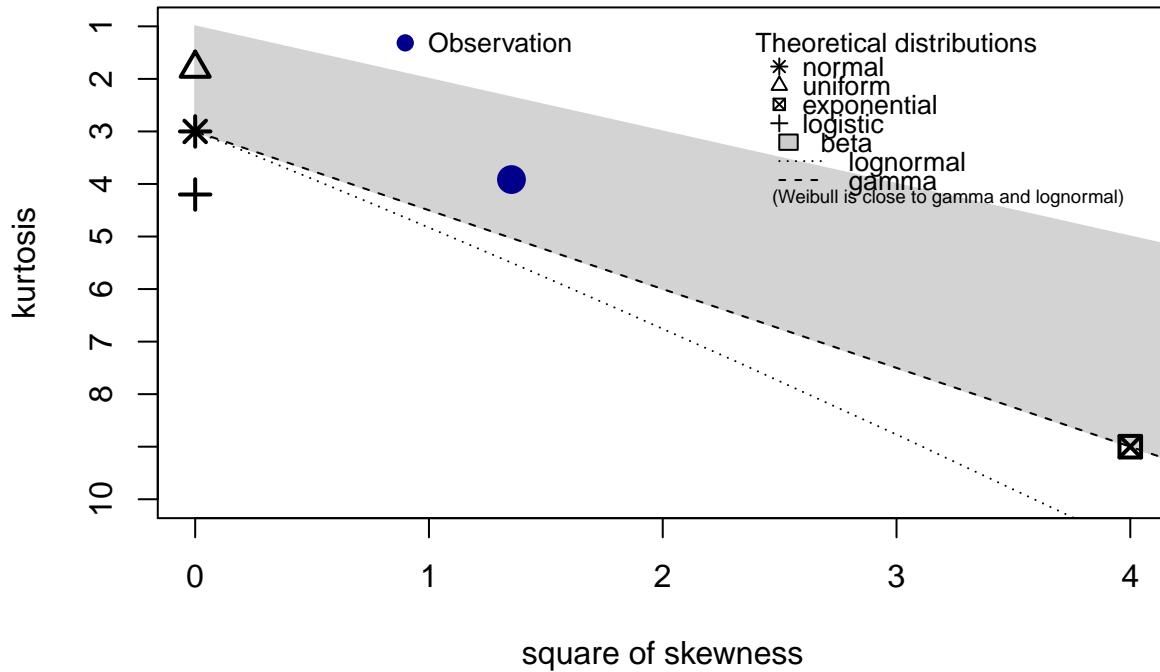


```
ggplot(comp_umbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1) +
  facet_wrap(~year_factor + plot)
```



```
# Exploring distributions for these right-skewed data:  
descdist(comp_umbs_plot$plot_cover_avg, discrete = FALSE)
```

Cullen and Frey graph

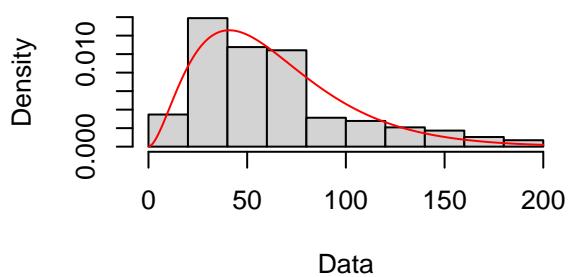
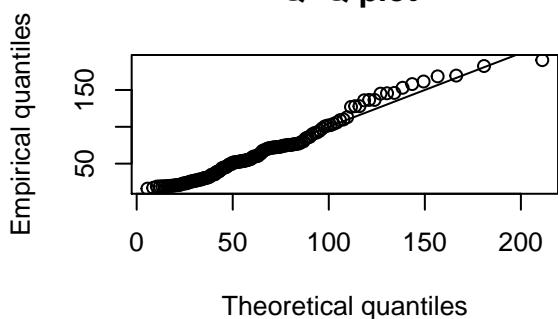
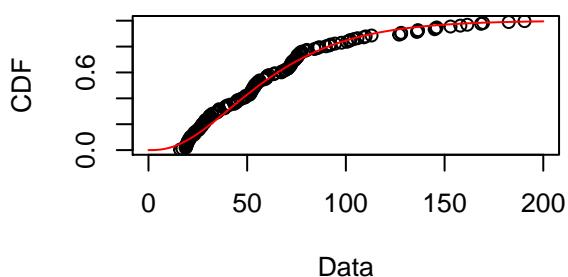
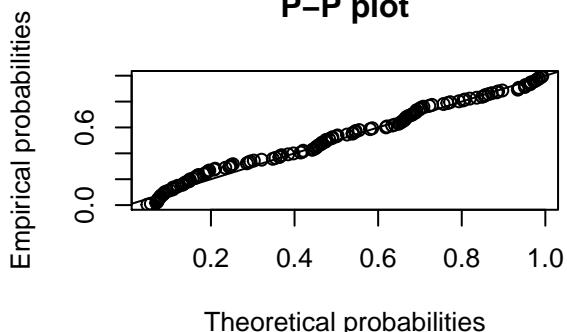


```

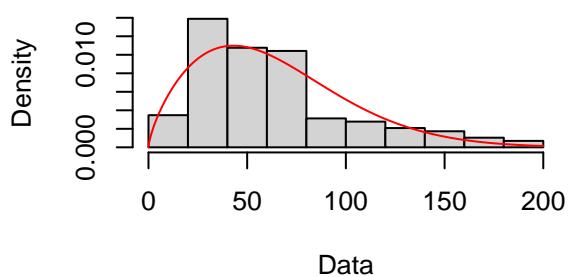
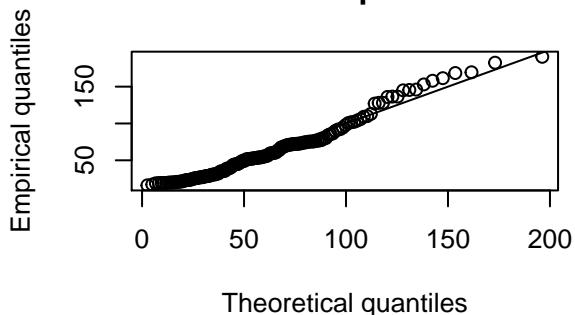
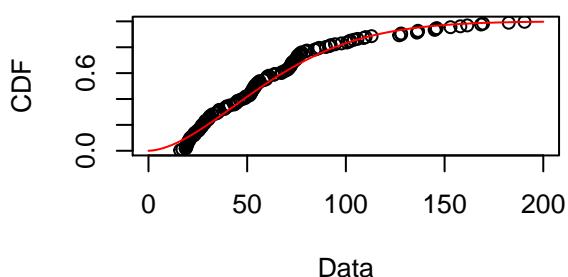
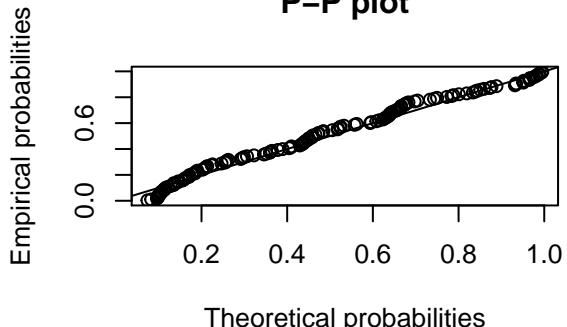
## summary statistics
## -----
## min: 16.05882  max: 190.5
## median: 53.88562
## mean: 63.35173
## estimated sd: 39.75901
## estimated skewness: 1.163142
## estimated kurtosis: 3.915878

# Gamma distribution
fit.gamma <- fitdist(comp_umbs_plot$plot_cover_avg, "gamma")
plot(fit.gamma)

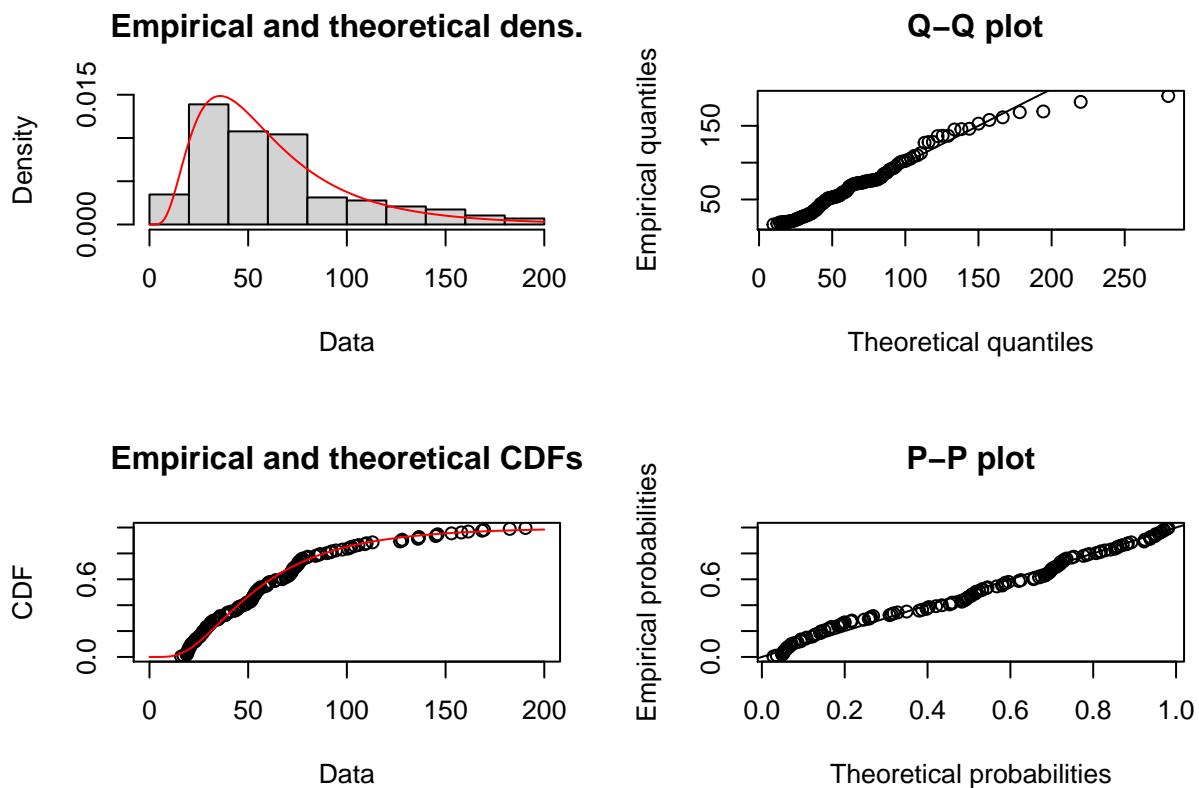
```

Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

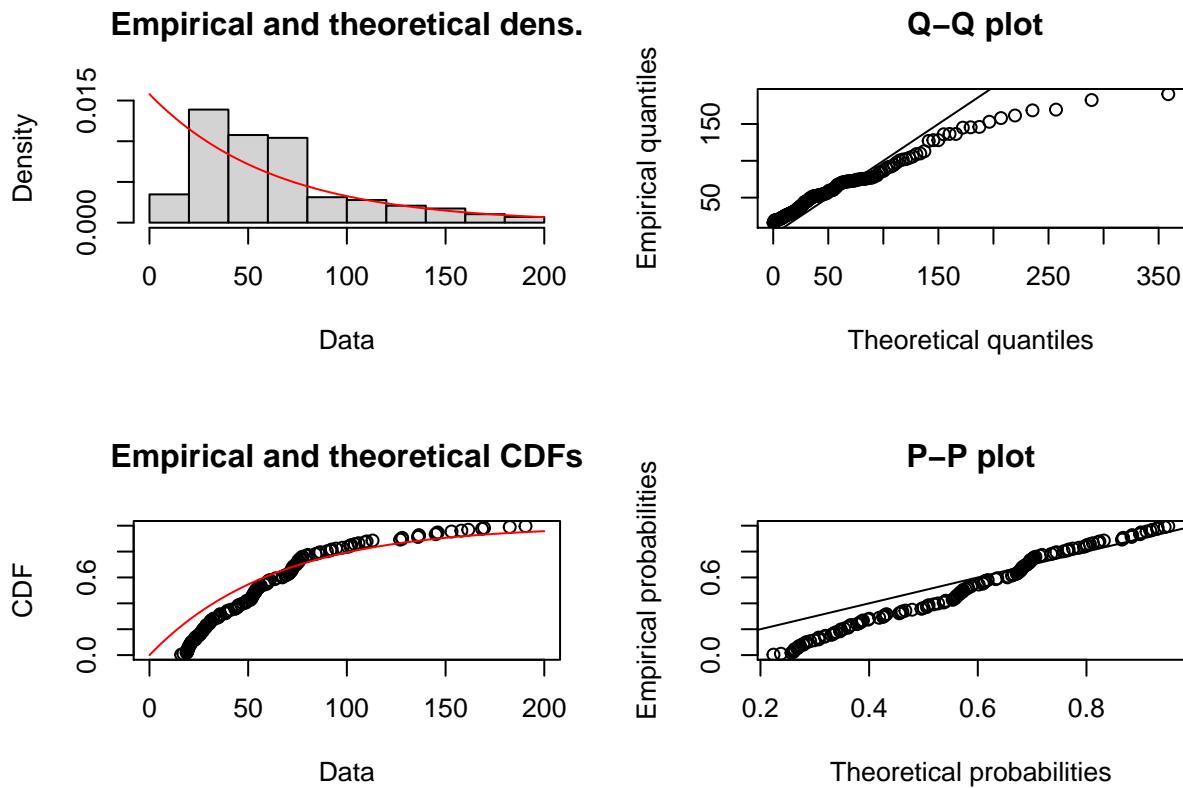
```
# Weibull distribution
fit.weibull <- fitdist(comp_umbs_plot$plot_cover_avg, "weibull")
plot(fit.weibull)
```

Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

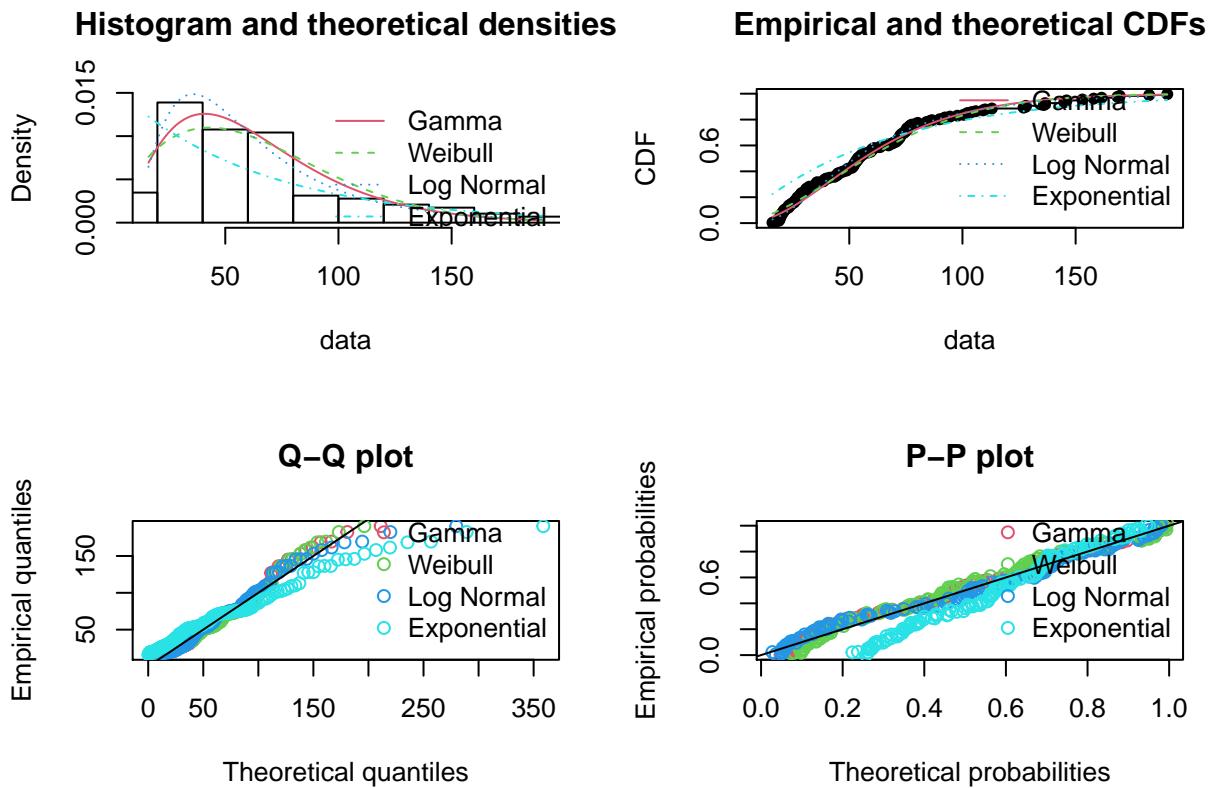
```
# Lognormal distribution
fit.ln <- fitdist(comp_umbs_plot$plot_cover_avg, "lnorm")
plot(fit.ln)
```



```
# Exponential distribution is another option
fit.exp <- fitdist(comp_umbs_plot$plot_cover_avg, "exp")
plot(fit.exp)
```



```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal", "Exponential")
denscomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp), legendtext = plot.legend)
```



```
# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln, fit.exp), fitnames = c("Gamma", "Weibull",
  "Log Normal", "Exp"))
```

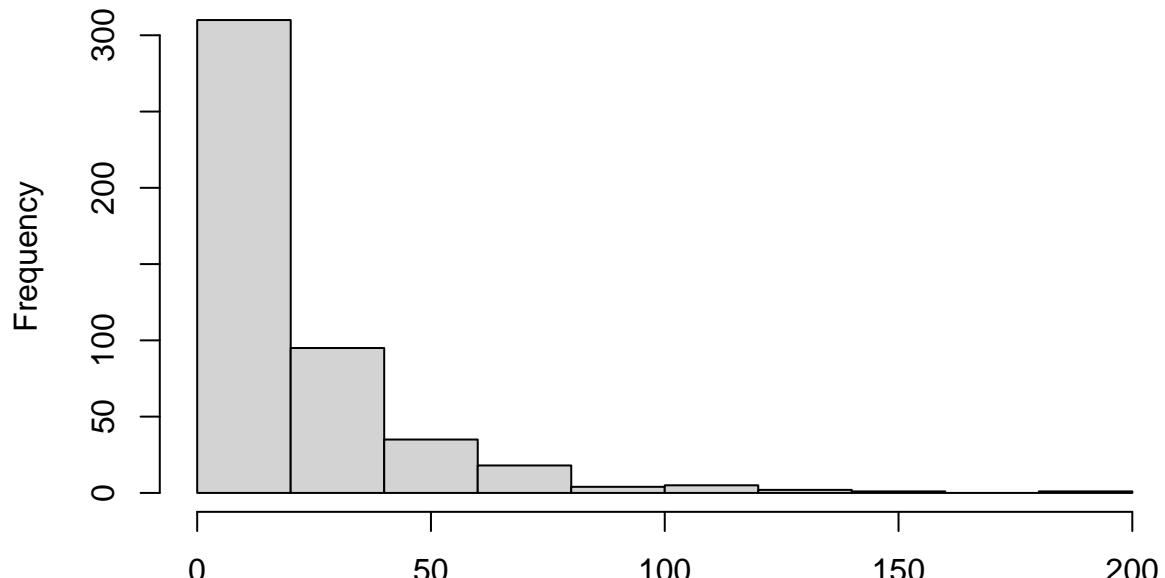
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal      Exp
## Kolmogorov-Smirnov statistic 0.07479574 0.08203544 0.07074297 0.2431617
## Cramer-von Mises statistic  0.13935488 0.19248423 0.14807679 1.8922613
## Anderson-Darling statistic  1.16877890 1.59146091 1.03119165 10.9587774
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal      Exp
## Akaike's Information Criterion 1421.071 1429.938 1415.615 1484.826
## Bayesian Information Criterion 1427.011 1435.878 1421.555 1487.796

# log normal distribution looks to be the best based on AIC and BIC values
```

UMBS PLOT LEVEL ORIGIN - Looking at PLOT AVG TOTALS

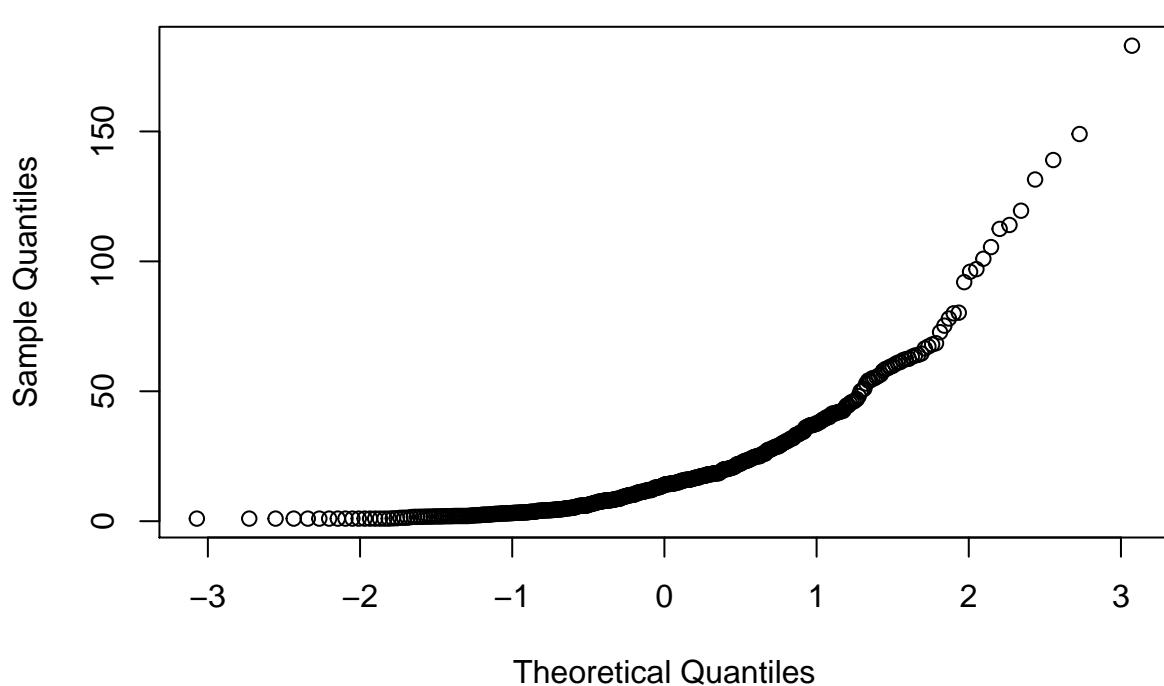
```
### UMBS ####
hist(umbs_comp_plot_origin$plot_cover_avg) # skewed to the right
```

Histogram of umbs_comp_plot_origin\$plot_cover_avg



```
qqnorm(umbc_comp_plot_origin$plot_cover_avg)
```

Normal Q-Q Plot



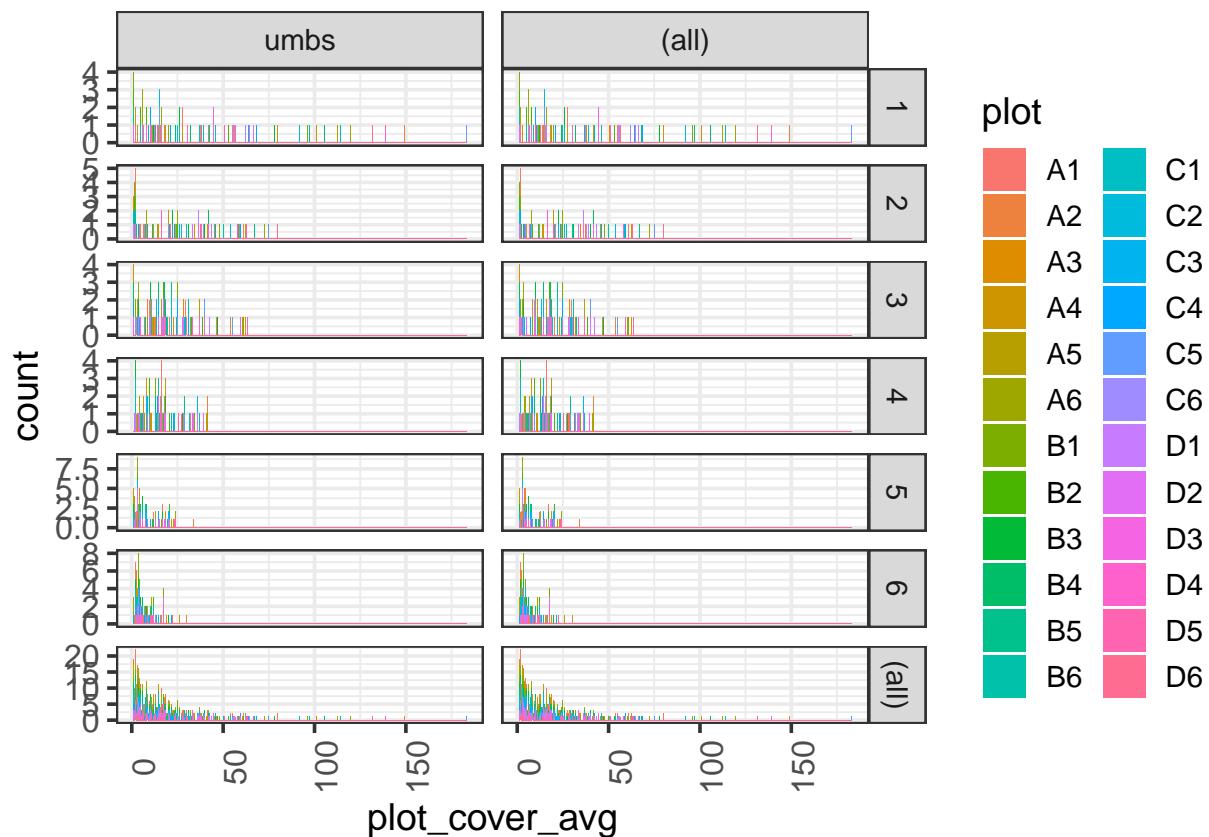
```

shapiro.test(umbs_comp_plot_origin$plot_cover_avg) # pvalue is < 0.05 so we reject the null hypothesis

## 
## Shapiro-Wilk normality test
## 
## data: umbs_comp_plot_origin$plot_cover_avg
## W = 0.73533, p-value < 2.2e-16

# Visualizing plot average totals for umbs at the PLOT LEVEL
ggplot(umbs_comp_plot_origin, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")

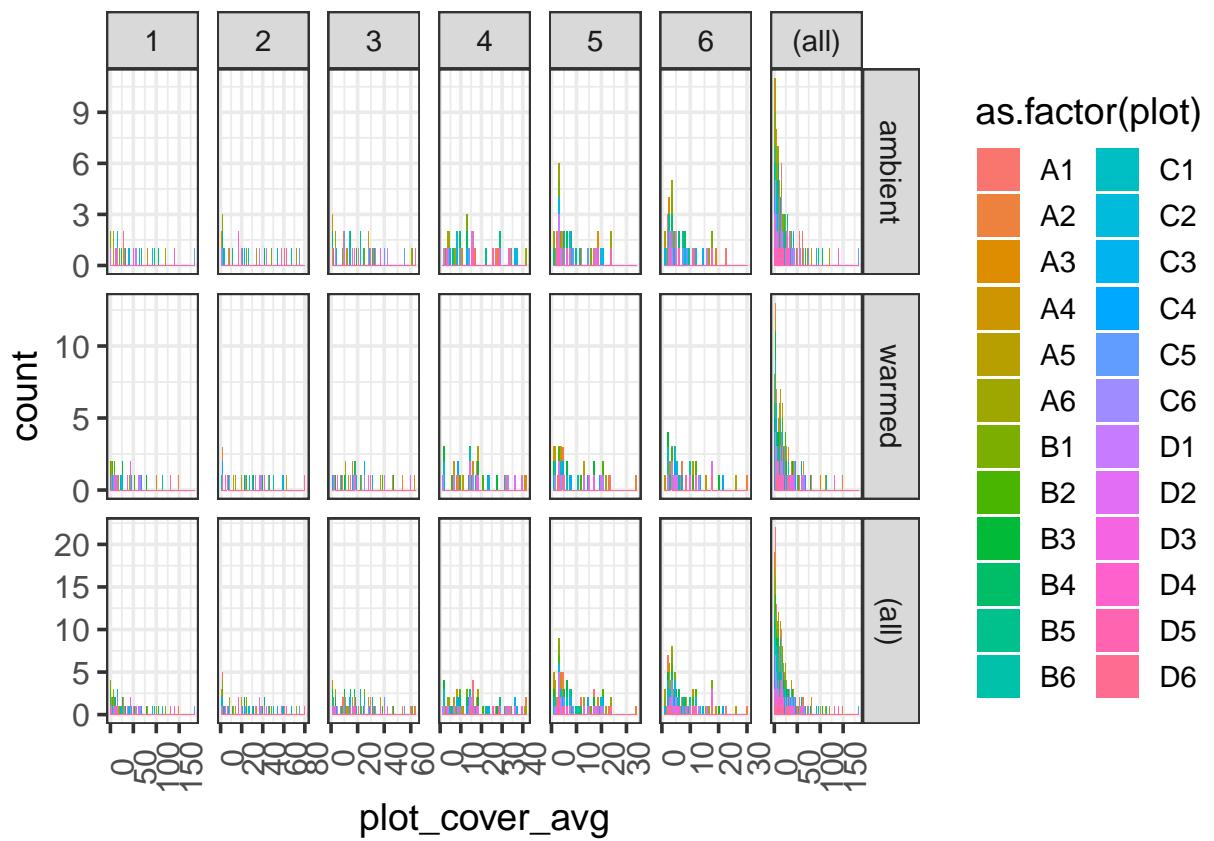
```



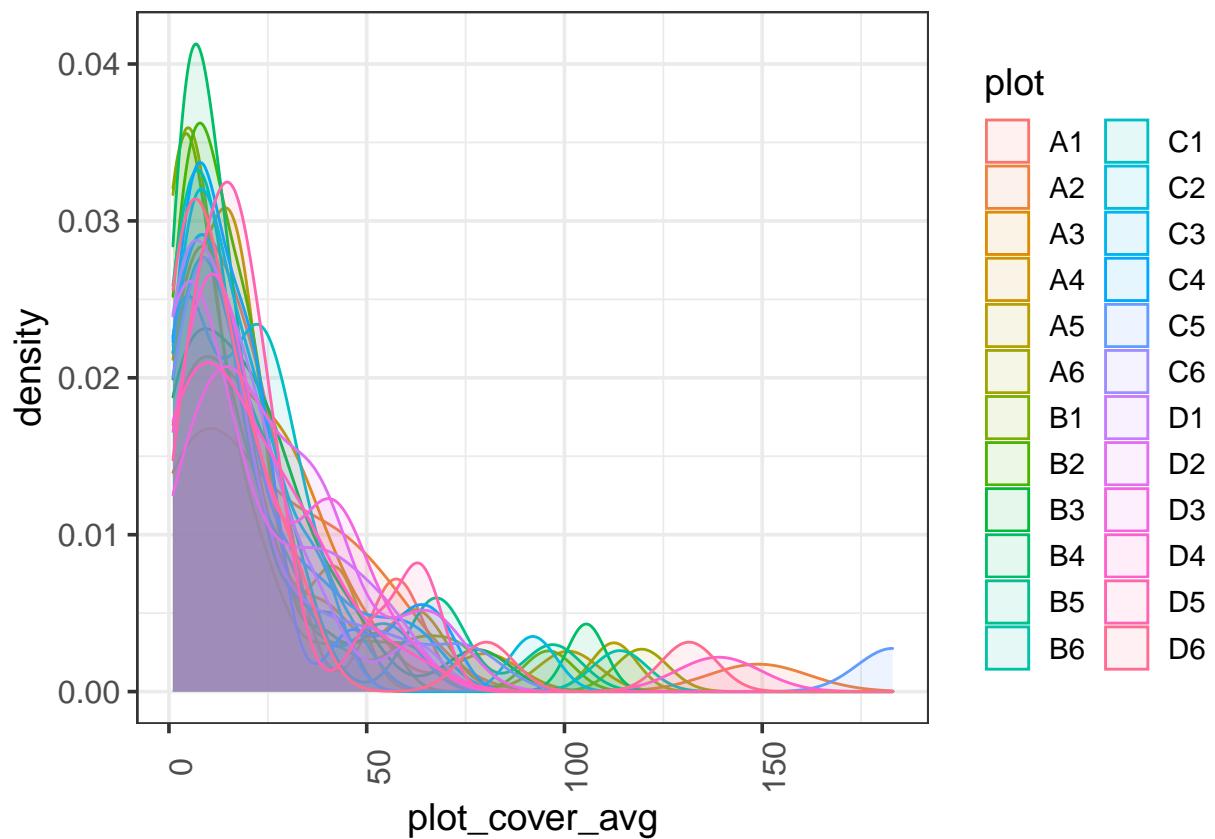
```

ggplot(umbs_comp_plot_origin, aes(plot_cover_avg, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year_factor, margins = TRUE, scales = "free")

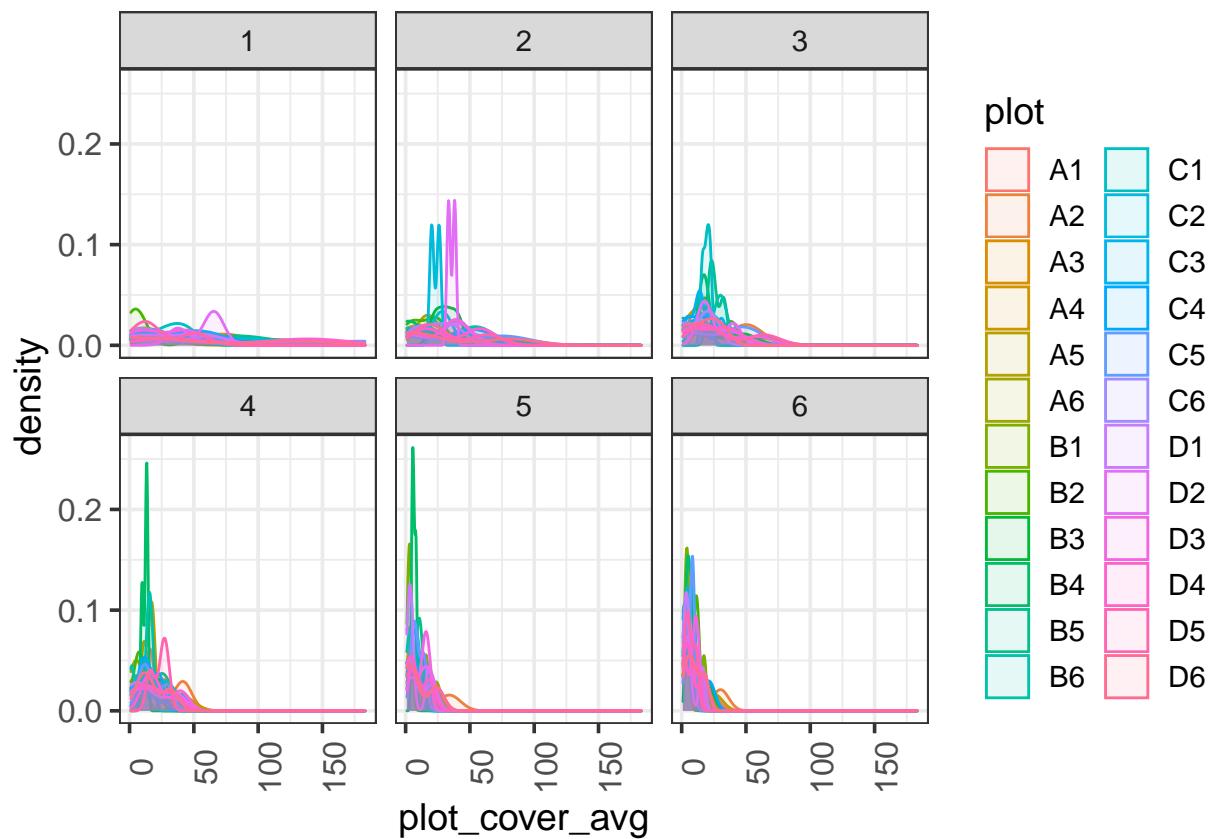
```



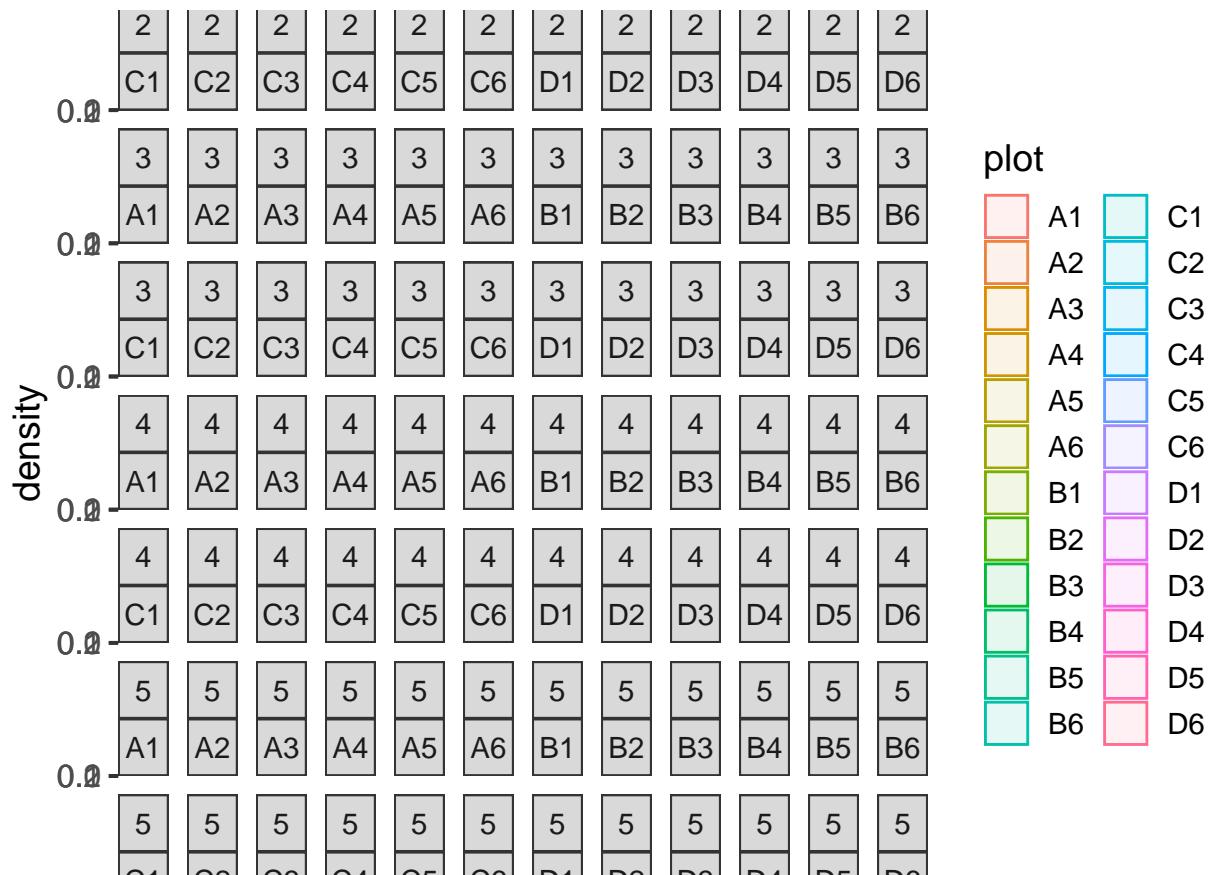
```
ggplot(umbc_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.5)
```



```
ggplot(umbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.5)
  facet_wrap(~year_factor)
```

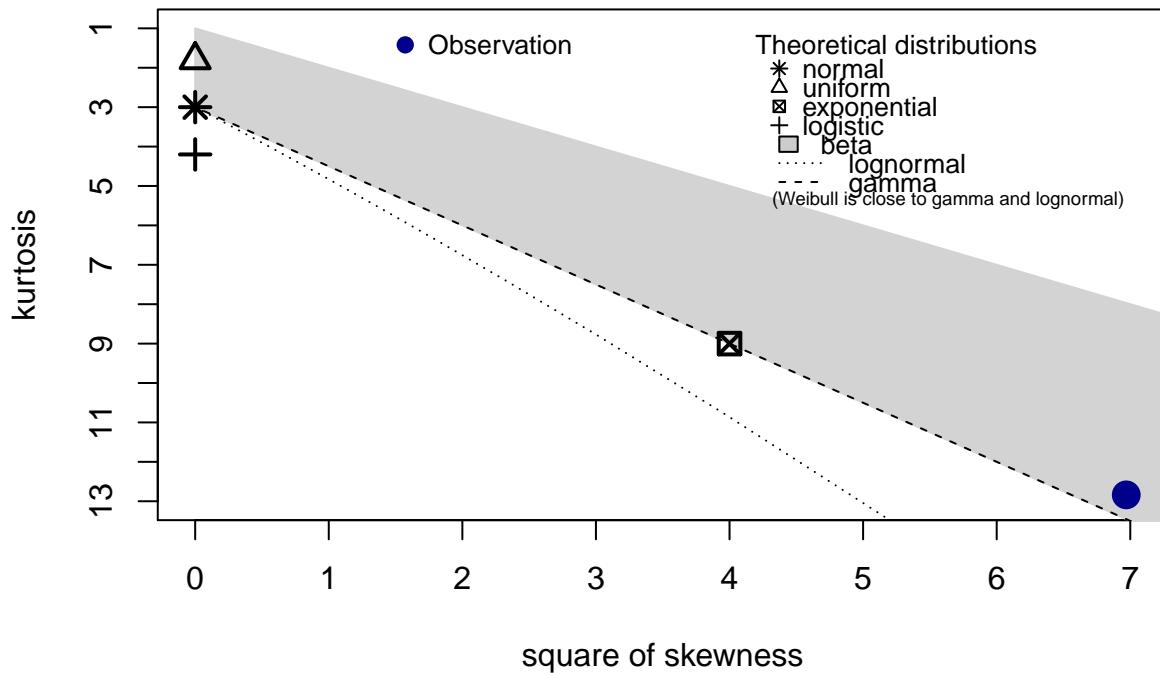


```
ggplot(umbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.5)
  facet_wrap(~year_factor + plot)
```



```
# Exploring distributions for these data:  
descdist(umbs_comp_plot_origin$plot_cover_avg, discrete = FALSE)
```

Cullen and Frey graph

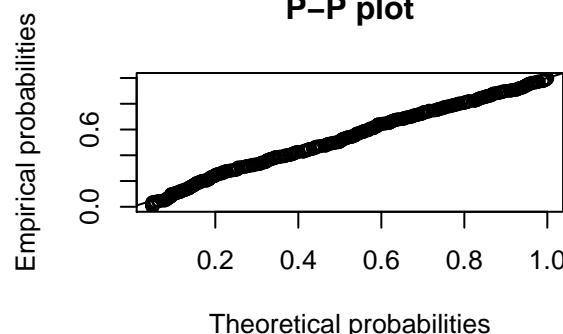
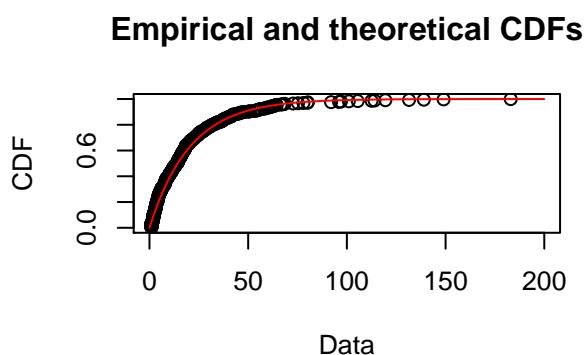
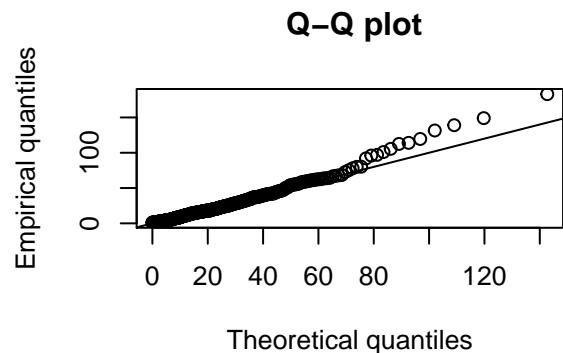
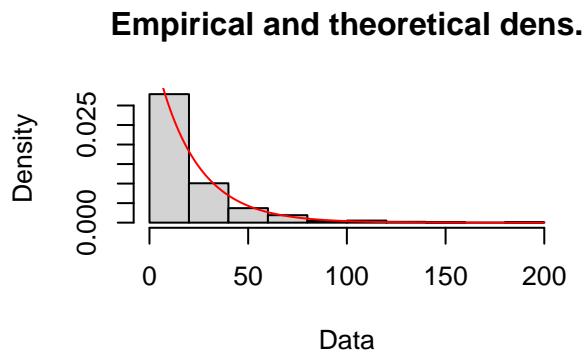


```

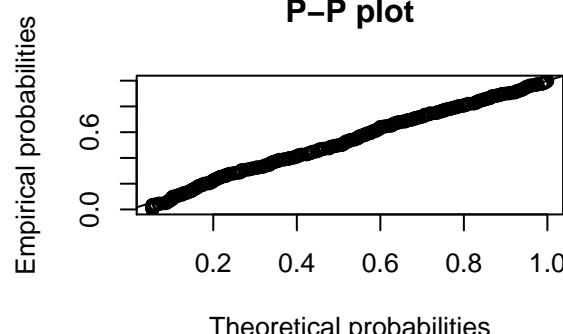
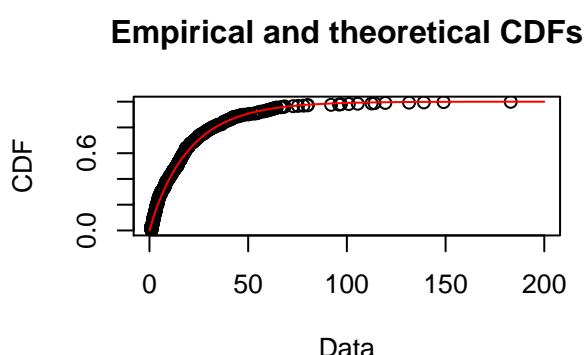
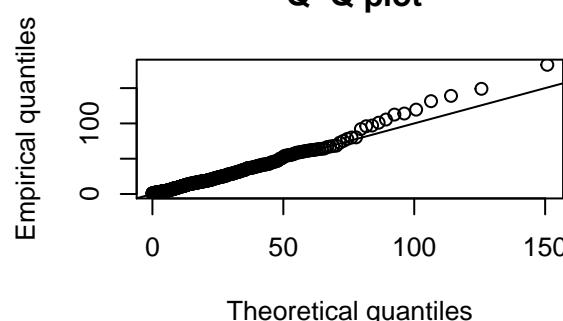
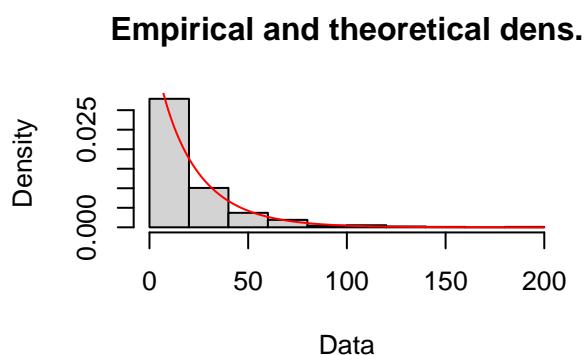
## summary statistics
## -----
## min: 1   max: 183
## median: 14
## mean: 20.69013
## estimated sd: 23.71993
## estimated skewness: 2.640043
## estimated kurtosis: 12.83848

# Gamma distribution
fit.gamma <- fitdist(umbs_comp_plot_origin$plot_cover_avg, "gamma")
plot(fit.gamma)

```

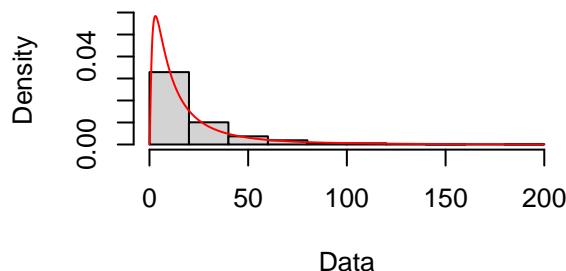


```
# Weibull distribution
fit.weibull <- fitdist(umbc_comp_plot_origin$plot_cover_avg, "weibull")
plot(fit.weibull)
```

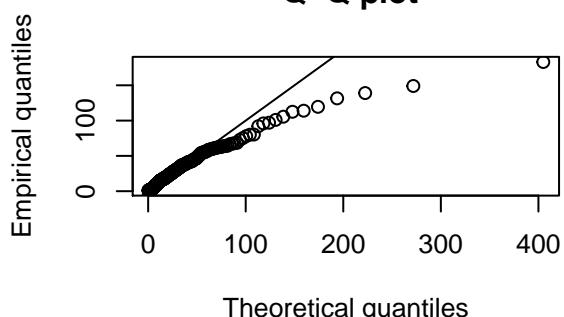


```
# Lognormal distribution
fit.ln <- fitdist(umbs_comp_plot_origin$plot_cover_avg, "lnorm")
plot(fit.ln)
```

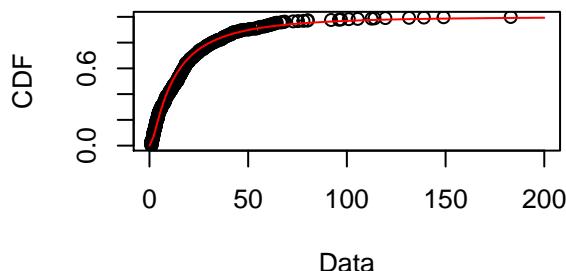
Empirical and theoretical dens.



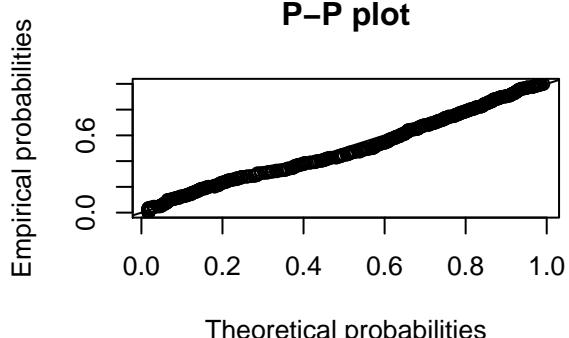
Q–Q plot



Empirical and theoretical CDFs

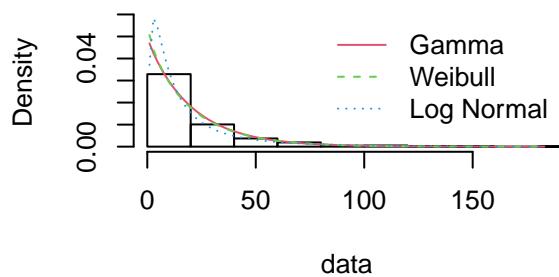


P–P plot

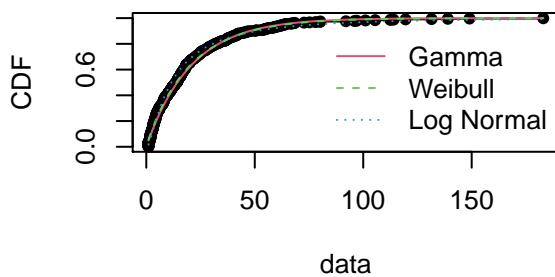


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```

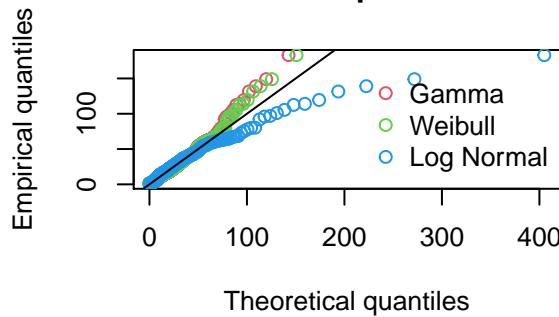
Histogram and theoretical densities



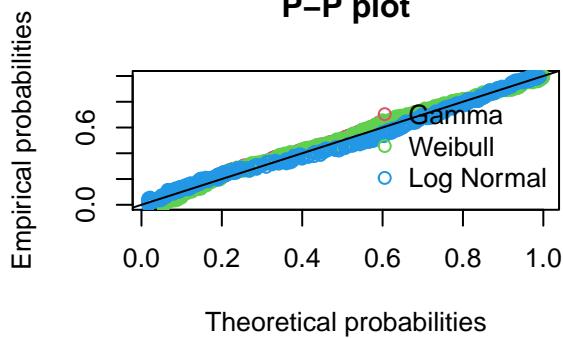
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
# Goodness of fit comparisons across fits
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

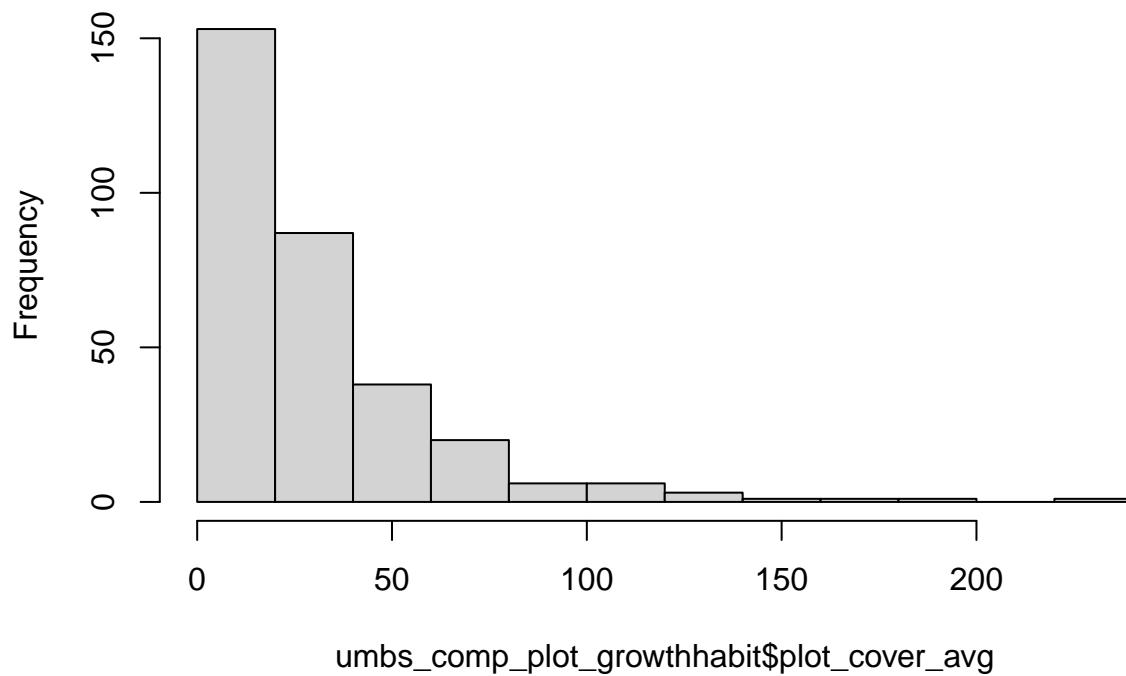
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.05144002 0.05435059 0.06972493
## Cramer-von Mises statistic   0.31034696 0.18376774 0.42240938
## Anderson-Darling statistic   2.26233406 1.74799931 2.44661427
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 3799.896 3798.425 3782.243
## Bayesian Information Criterion 3808.206 3806.735 3790.553
```

```
# log normal looks like it's the best fit
```

UMBS PLOT LEVEL GROWTH HABIT - Looking at PLOT AVG TOTALS

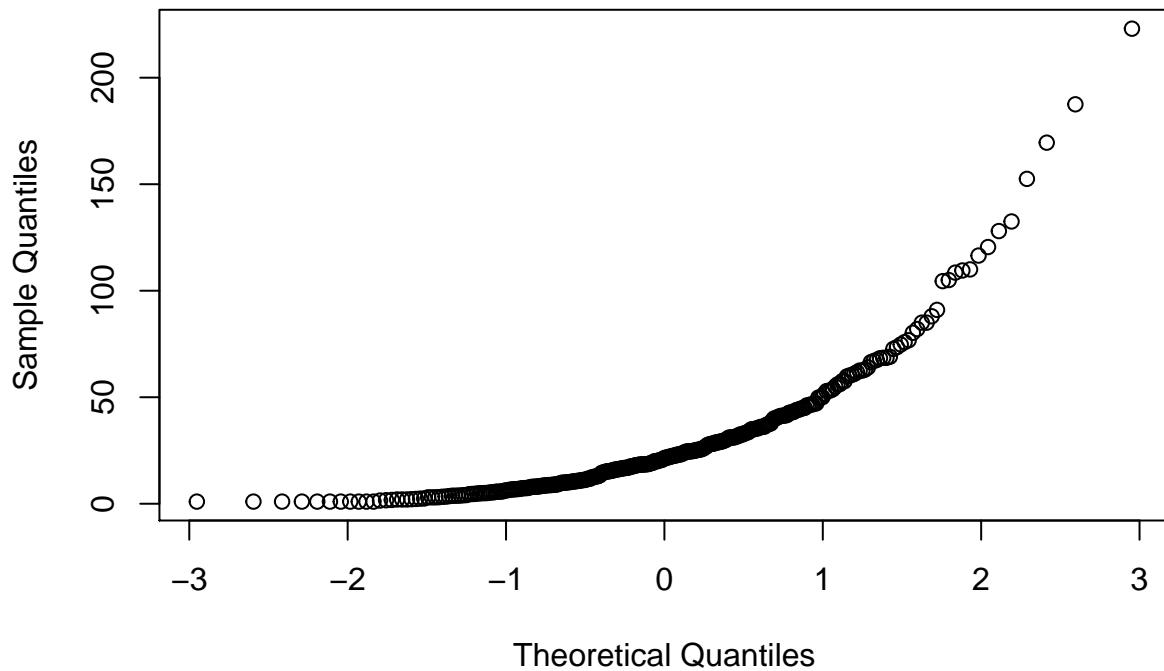
```
### UMBS ####
hist(umbs_comp_plot_growthhabit$plot_cover_avg)
```

Histogram of umbs_comp_plot_growthhabit\$plot_cover_avg



```
qqnorm(umbc_comp_plot_growthhabit$plot_cover_avg)
```

Normal Q-Q Plot



```

shapiro.test(umbs_comp_plot_growthhabit$plot_cover_avg)  # pvalue is < 0.05 so we reject the null hypothesis

##
## Shapiro-Wilk normality test
##
## data: umbs_comp_plot_growthhabit$plot_cover_avg
## W = 0.76384, p-value < 2.2e-16

# Visualizing plot average totals for umbs at the PLOT LEVEL
ggplot(umbs_comp_plot_growthhabit, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year ~ site, margins = TRUE, scales = "free")

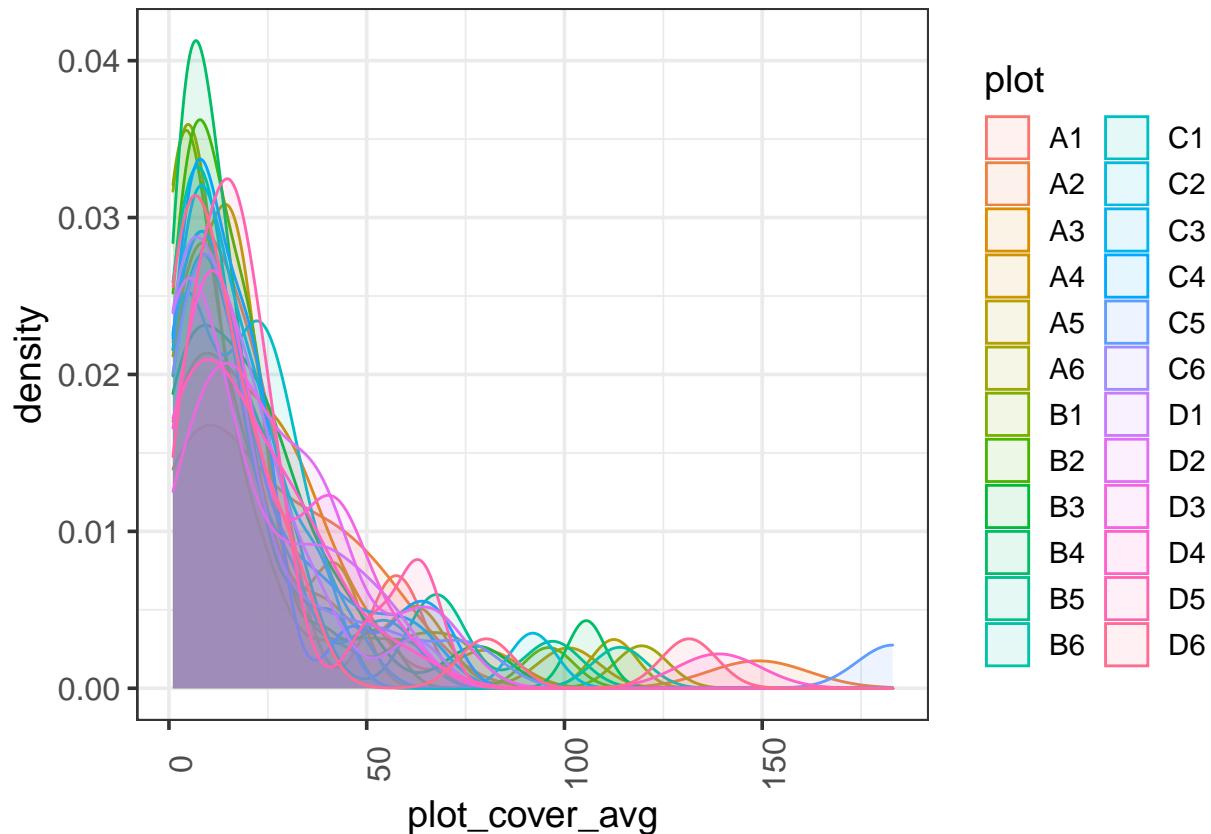
## Error: At least one layer must contain all facetting variables: 'year'.
## * Plot is missing 'year'
## * Layer 1 is missing 'year'

ggplot(umbs_comp_plot_origin, aes(plot_cover_avg, fill = as.factor(plot))) + geom_histogram(binwidth = 0.5) +
  facet_grid(state ~ year, margins = TRUE, scales = "free")

## Error: At least one layer must contain all facetting variables: 'year'.
## * Plot is missing 'year'
## * Layer 1 is missing 'year'

ggplot(umbs_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.5)

```



```
ggplot(umbc_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.5)
      facet_wrap(~year)

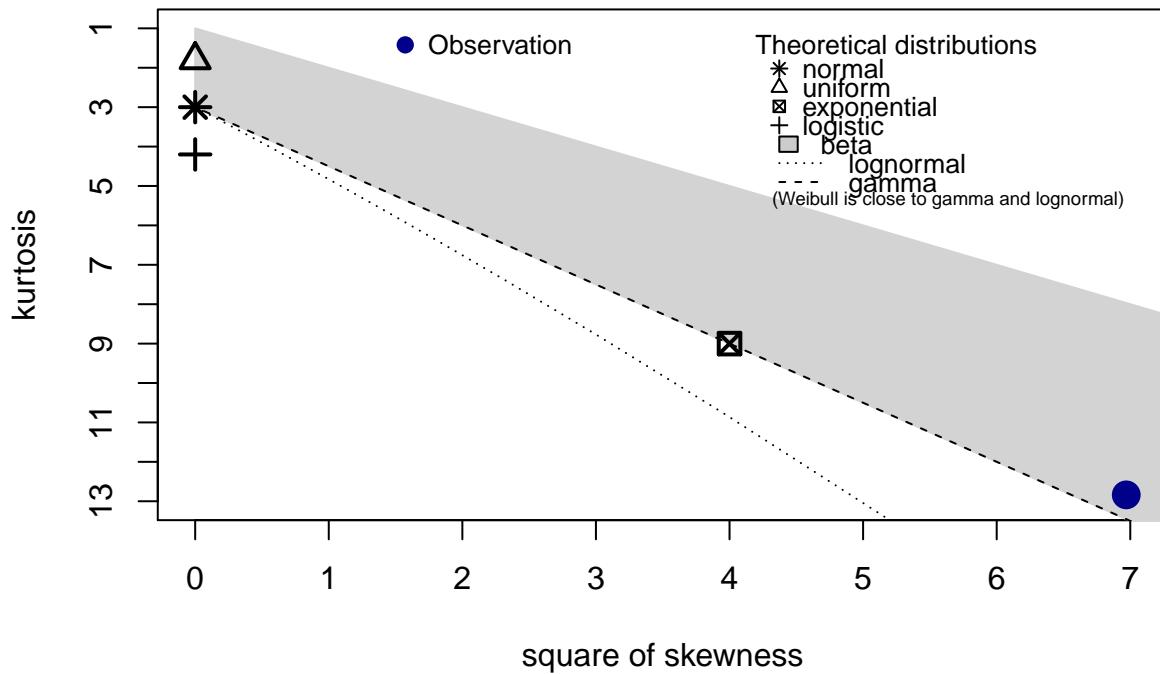
## Error: At least one layer must contain all faceting variables: 'year'.
## * Plot is missing 'year'
## * Layer 1 is missing 'year'

ggplot(umbc_comp_plot_origin, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.5)
      facet_wrap(~year + plot)

## Error: At least one layer must contain all faceting variables: 'year', 'plot'.
## * Plot is missing 'year'
## * Layer 1 is missing 'year'

# Exploring distributions for these data:
descdist(umbc_comp_plot_origin$plot_cover_avg, discrete = FALSE)
```

Cullen and Frey graph

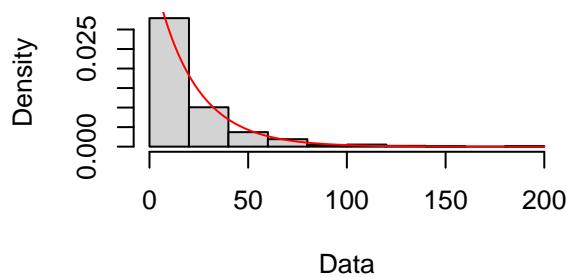
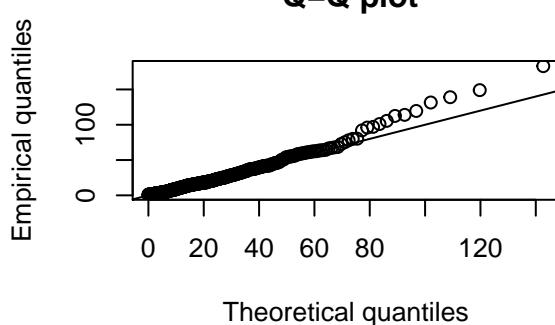
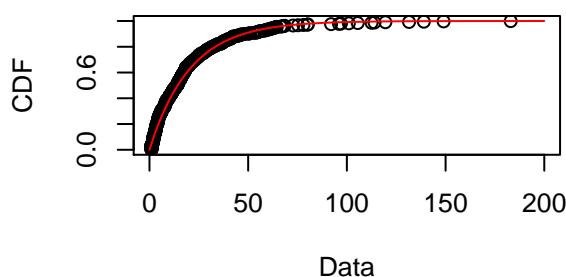
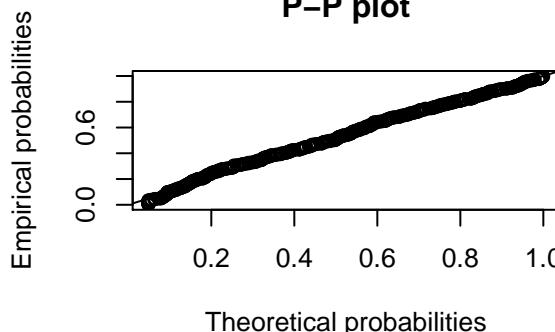


```

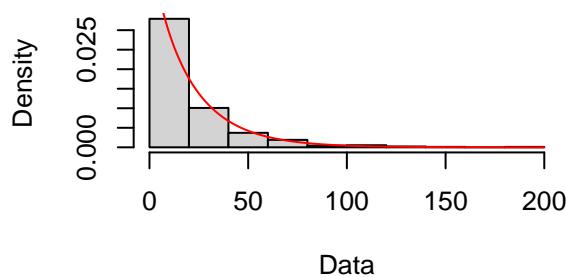
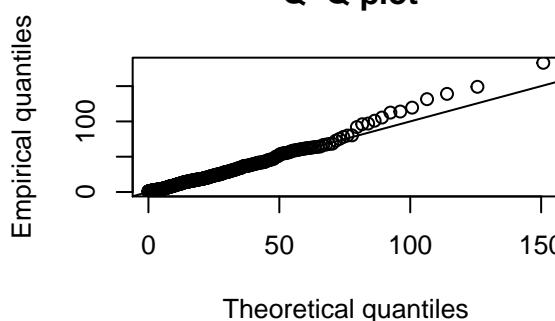
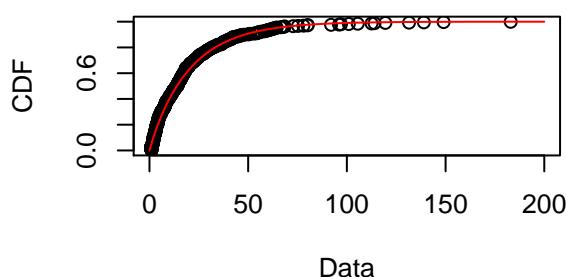
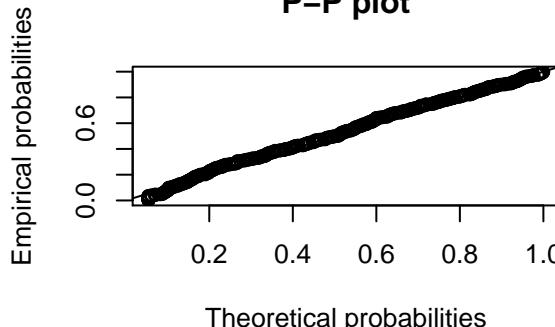
## summary statistics
## -----
## min: 1   max: 183
## median: 14
## mean: 20.69013
## estimated sd: 23.71993
## estimated skewness: 2.640043
## estimated kurtosis: 12.83848

# Gamma distribution
fit.gamma <- fitdist(umbs_comp_plot_origin$plot_cover_avg, "gamma")
plot(fit.gamma)

```

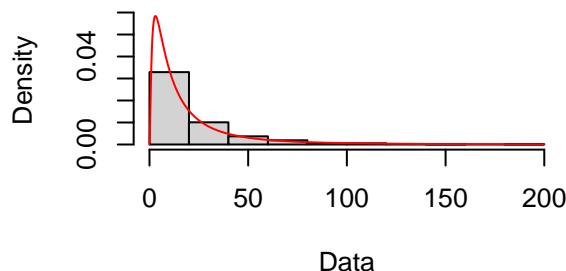
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Weibull distribution
fit.weibull <- fitdist(umbc_comp_plot_origin$plot_cover_avg, "weibull")
plot(fit.weibull)
```

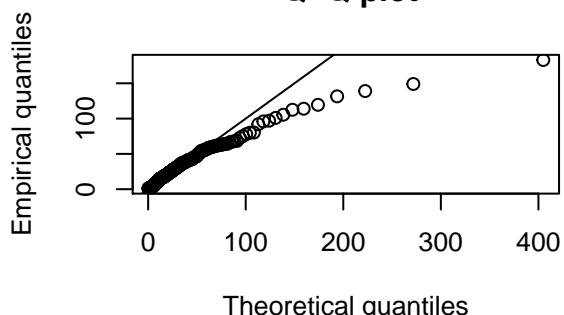
Empirical and theoretical dens.**Q-Q plot****Empirical and theoretical CDFs****P-P plot**

```
# Lognormal distribution
fit.ln <- fitdist(umbs_comp_plot_origin$plot_cover_avg, "lnorm")
plot(fit.ln)
```

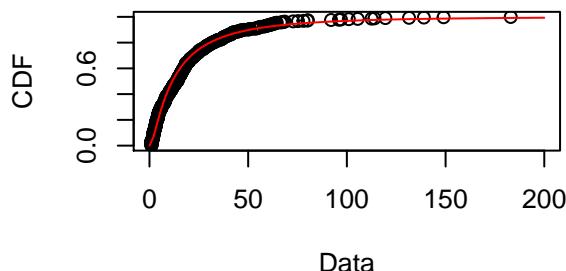
Empirical and theoretical dens.



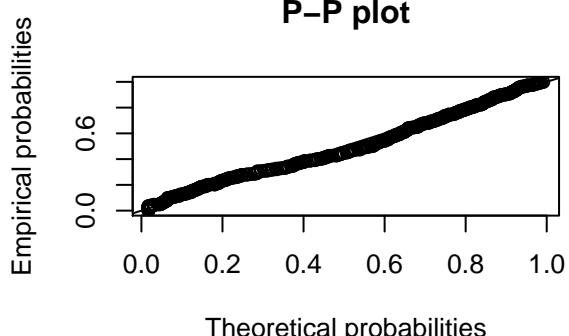
Q–Q plot



Empirical and theoretical CDFs

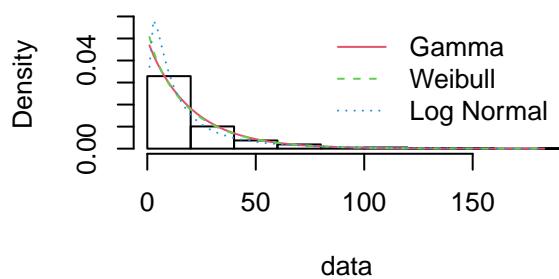


P–P plot

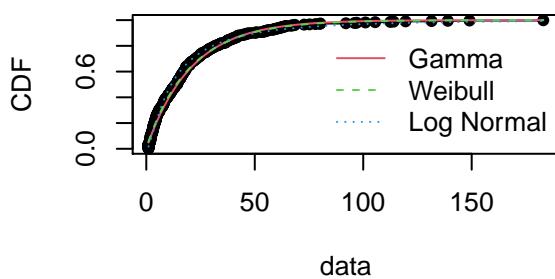


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
```

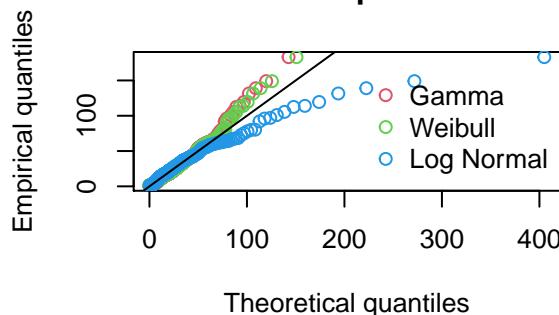
Histogram and theoretical densities



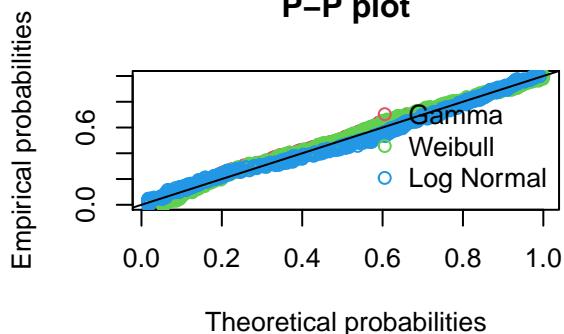
Empirical and theoretical CDFs



Q-Q plot



P-P plot



```
# Goodness of fit comparisons across fits (can't include the sqrt normal bc it
# becomes diff response values)
gofstat(list(fit.gamma, fit.weibull, fit.ln), fitnames = c("Gamma", "Weibull", "Log Normal"))
```

```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.05144002 0.05435059 0.06972493
## Cramer-von Mises statistic  0.31034696 0.18376774 0.42240938
## Anderson-Darling statistic  2.26233406 1.74799931 2.44661427
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 3799.896 3798.425 3782.243
## Bayesian Information Criterion 3808.206 3806.735 3790.553
```

```
# log normal looks like it's the best fit
```

Leverage plots and detecting Outliers. <https://www.statmethods.net/stats/rdiagnostics.html>

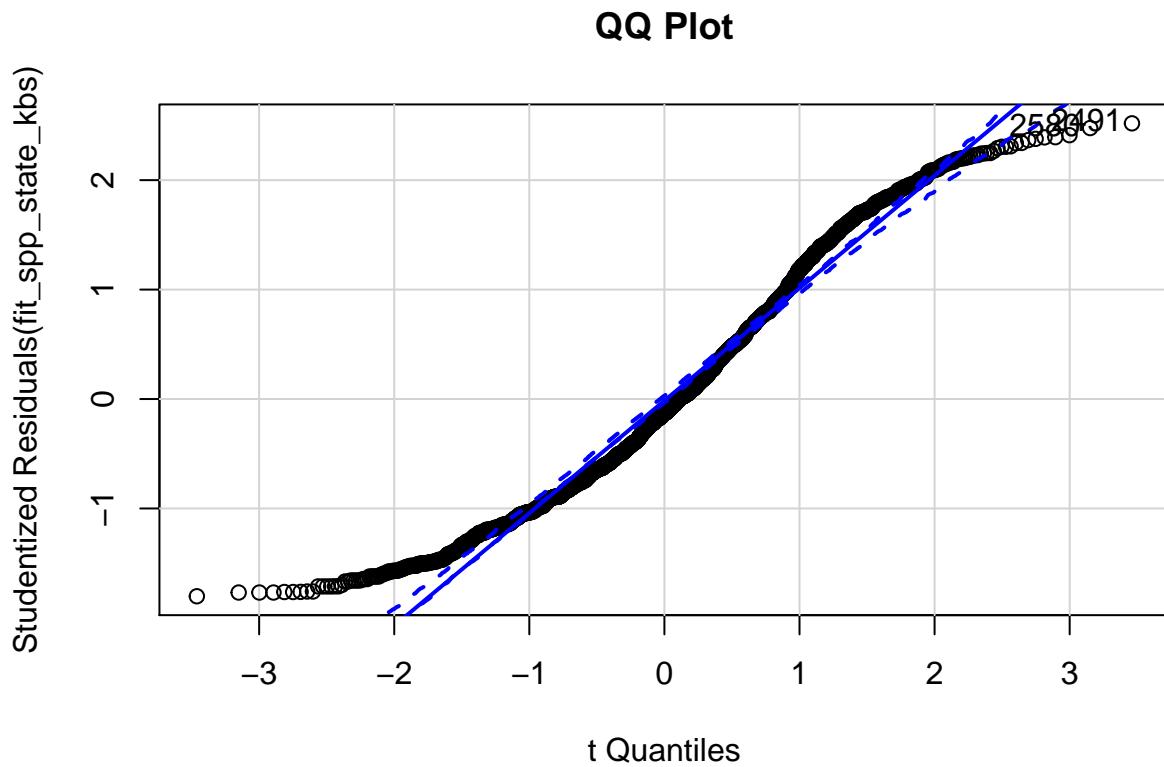
These illustrate whether certain data points have more leverage (more influence), and thus could be outliers. It's a way of detecting outliers. Leverage plots can help identify whether a point has high or low influence, based on its leverage and residual and determining model fit with and without the point in question. Ultimately you decide whether the points are outliers or not, based on the knowledge of the system and how much it changes the model when included vs. excluded from the data used to fit the model. Here is a good overview of the combination of leverage and residual: scroll down to sections beginning at “13.3 Unusual Observations”: <https://daviddalpiaz.github.io/appliedstats/model-diagnostics.html>

KBS

```
# species level data KBS State-only model
fit_spp_state_kbs <- lm(log(relabun) ~ state, data = comp_kbs_spp)
outlierTest(fit_spp_state_kbs) # outliers - row 449

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 2491  2.518923          0.011857         NA

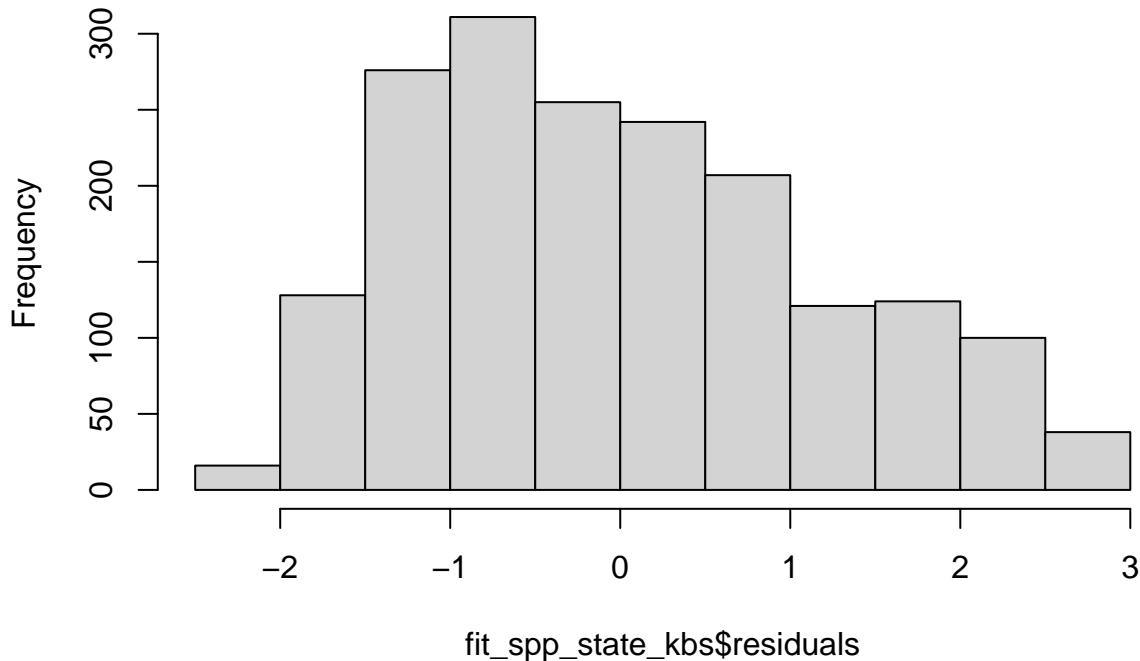
qqPlot(fit_spp_state_kbs, main = "QQ Plot")
```



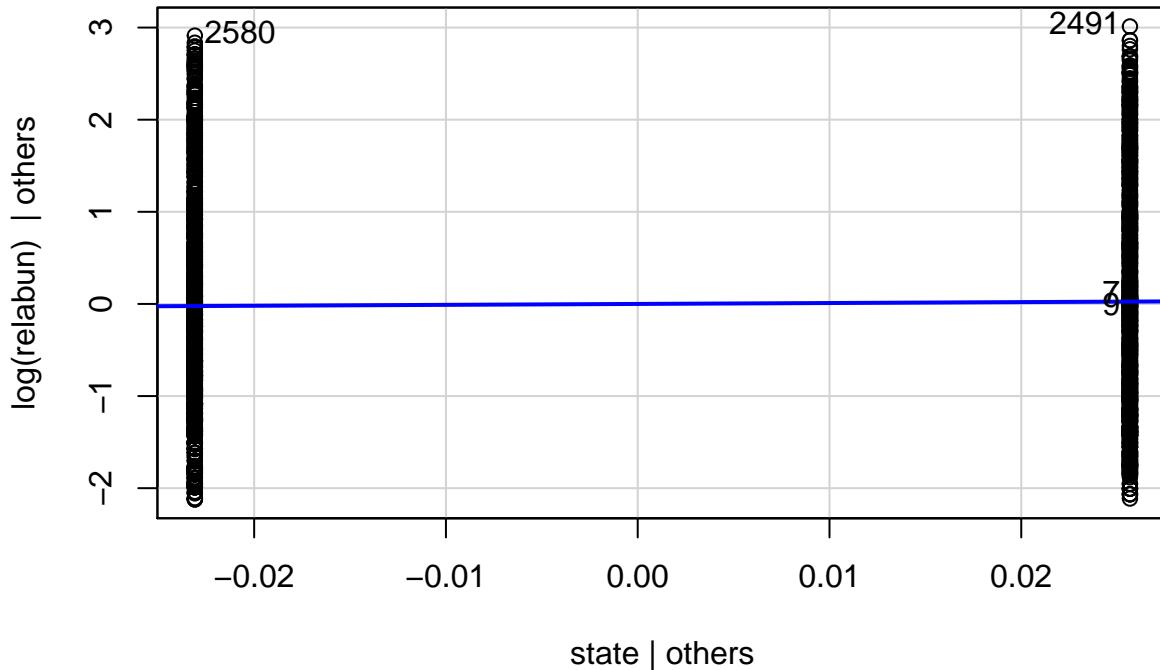
```
## 2491 2580
## 1491 1580
```

```
hist(fit_spp_state_kbs$residuals)
```

Histogram of fit_spp_state_kbs\$residuals



```
leveragePlots(fit_spp_state_kbs)
```



```
ols_test_normality(fit_spp_state_kbs)
```

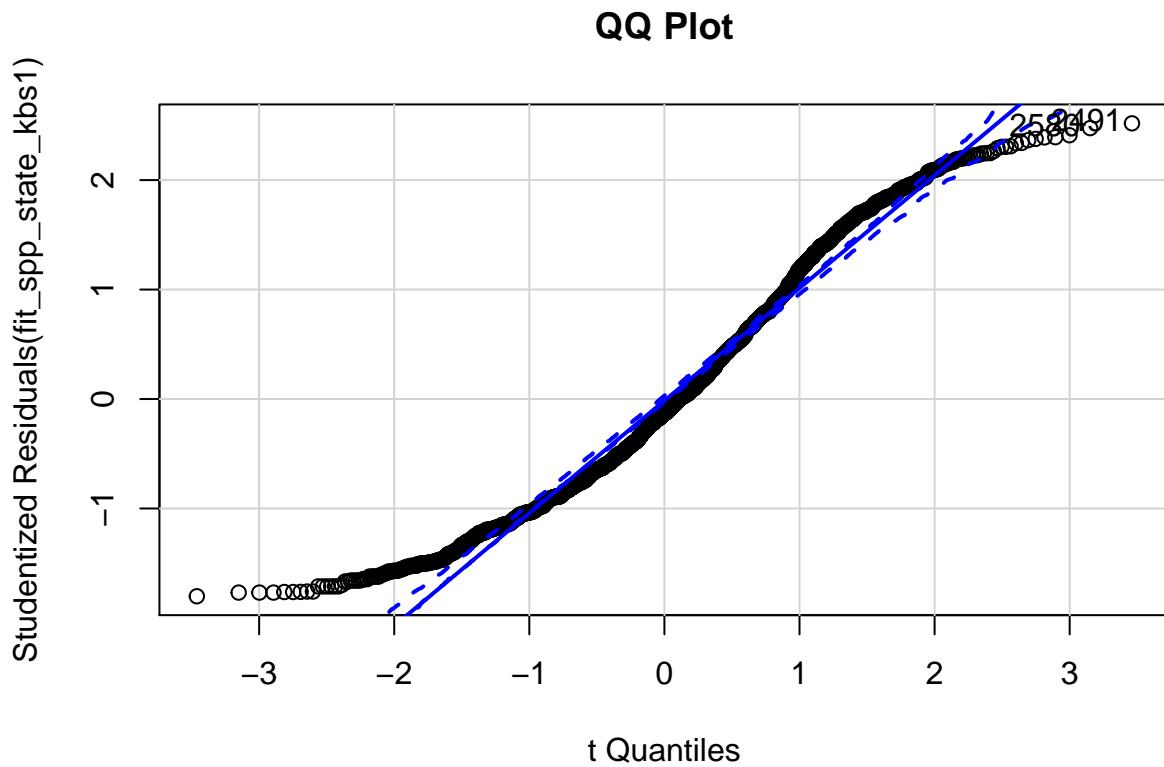
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9664       0.0000
## Kolmogorov-Smirnov 0.0678       0.0000
## Cramer-von Mises 144.9267      0.0000
## Anderson-Darling 16.7536       0.0000
## -----
```

```
comp_kbs_spp_no_outliers <- comp_kbs_spp[-449, ] # remove outliers
fit_spp_state_kbs1 <- lm(log(relabun) ~ state, data = comp_kbs_spp_no_outliers)
outlierTest(fit_spp_state_kbs1) # outliers - row 449
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 2491 2.518341        0.011876           NA
```

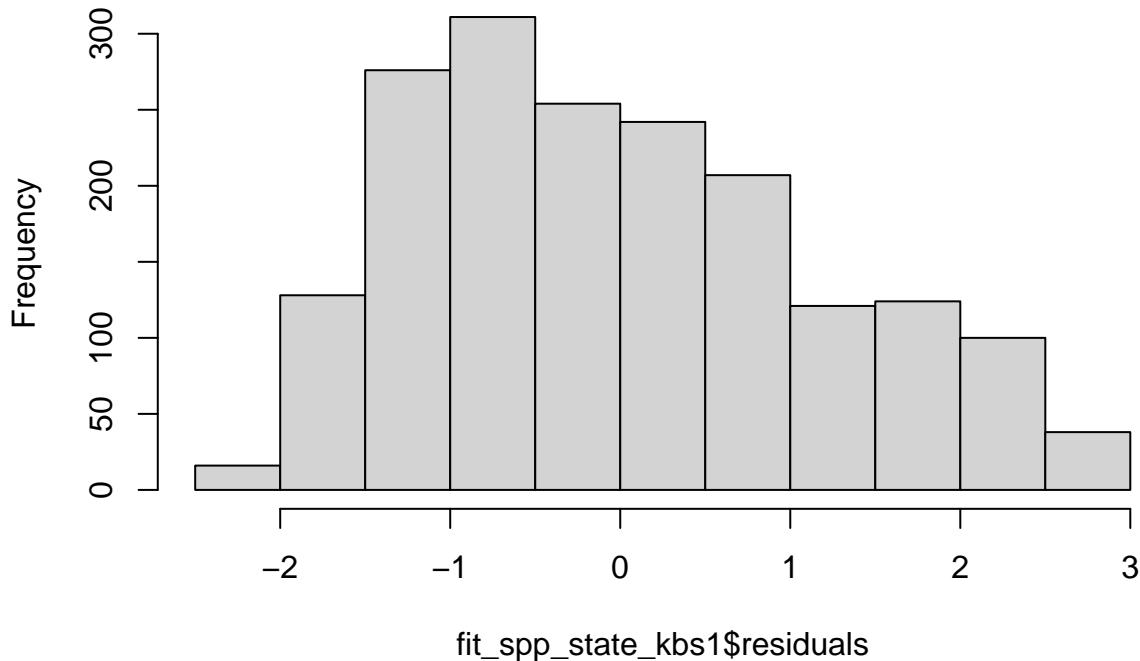
```
qqPlot(fit_spp_state_kbs1, main = "QQ Plot")
```



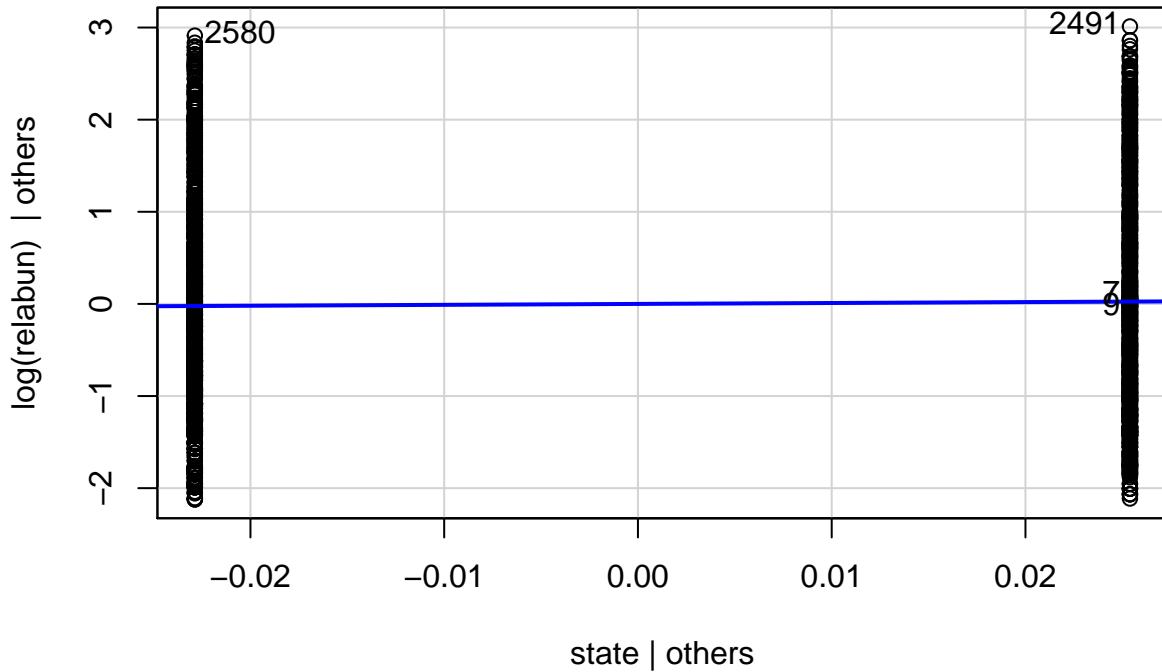
```
## 2491 2580
## 1490 1579
```

```
hist(fit_spp_state_kbs1$residuals)
```

Histogram of fit_spp_state_kbs1\$residuals



```
leveragePlots(fit_spp_state_kbs1)
```



```
ols_test_normality(fit_spp_state_kbs1)
```

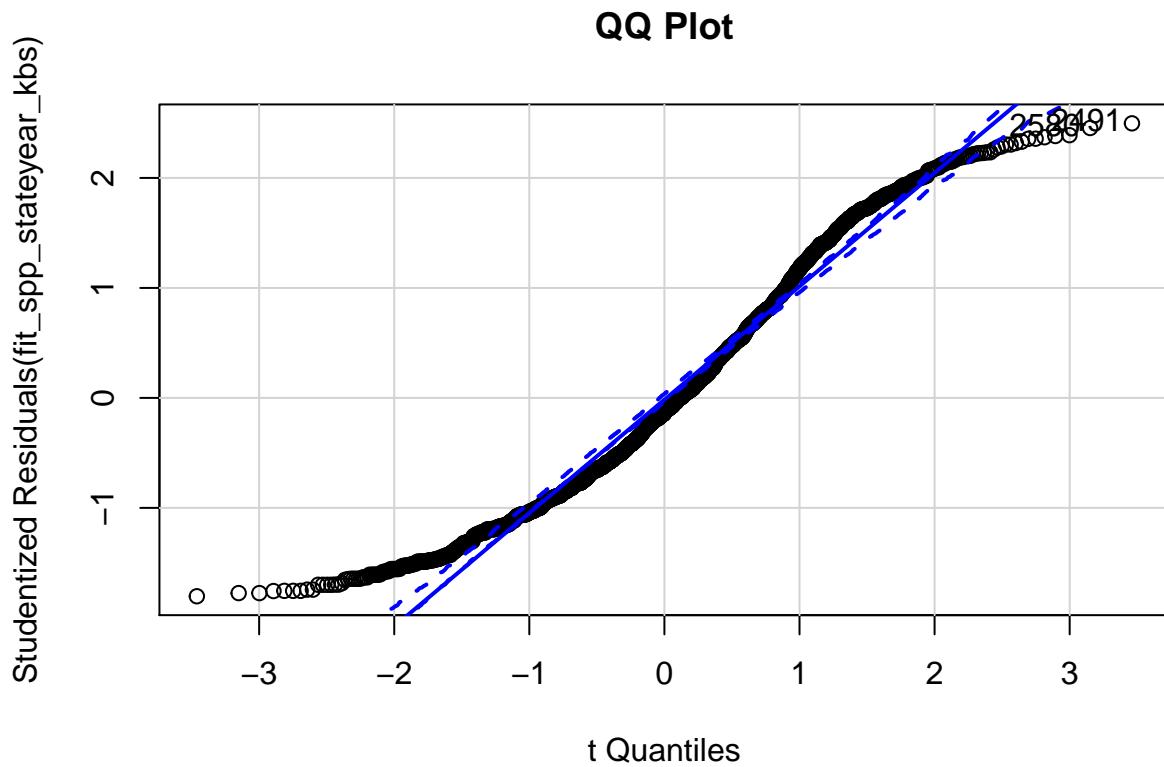
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9664       0.0000
## Kolmogorov-Smirnov 0.0675       0.0000
## Cramer-von Mises 144.7554      0.0000
## Anderson-Darling 16.7367       0.0000
## -----
```

```
# KBS State and year model
fit_spp_stateyear_kbs <- lm(log(relabun) ~ state + year_factor, data = comp_kbs_spp)
outlierTest(fit_spp_stateyear_kbs) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 2491 2.496313           0.012637        NA
```

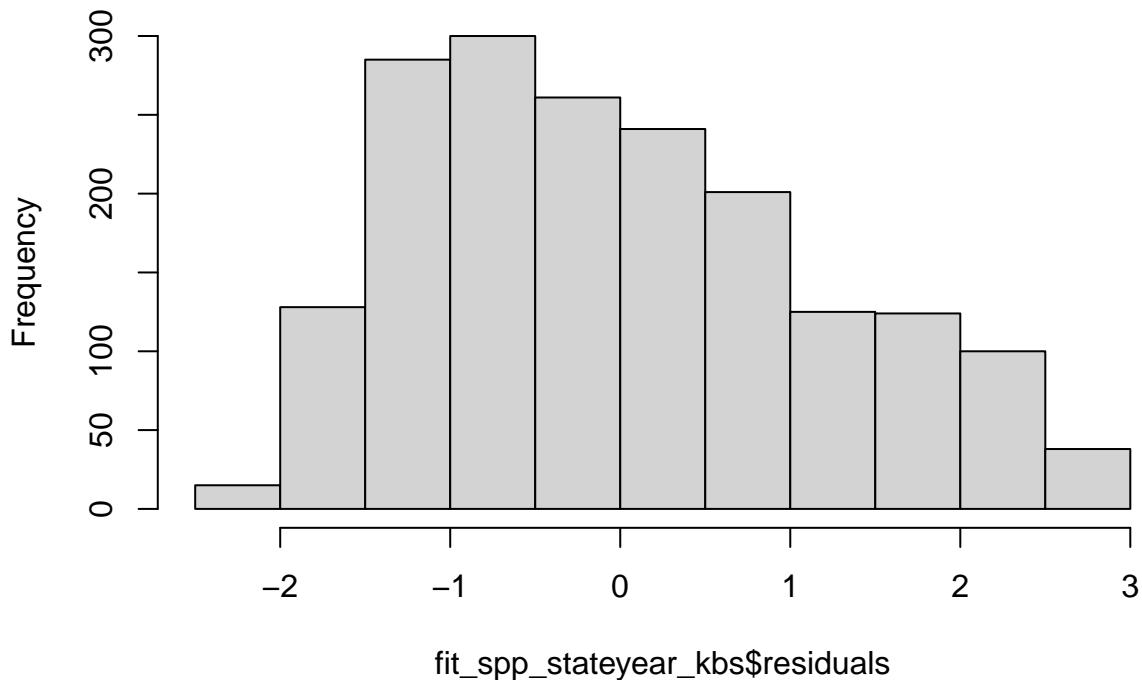
```
qqPlot(fit_spp_stateyear_kbs, main = "QQ Plot")
```



```
## 2491 2580
## 1491 1580
```

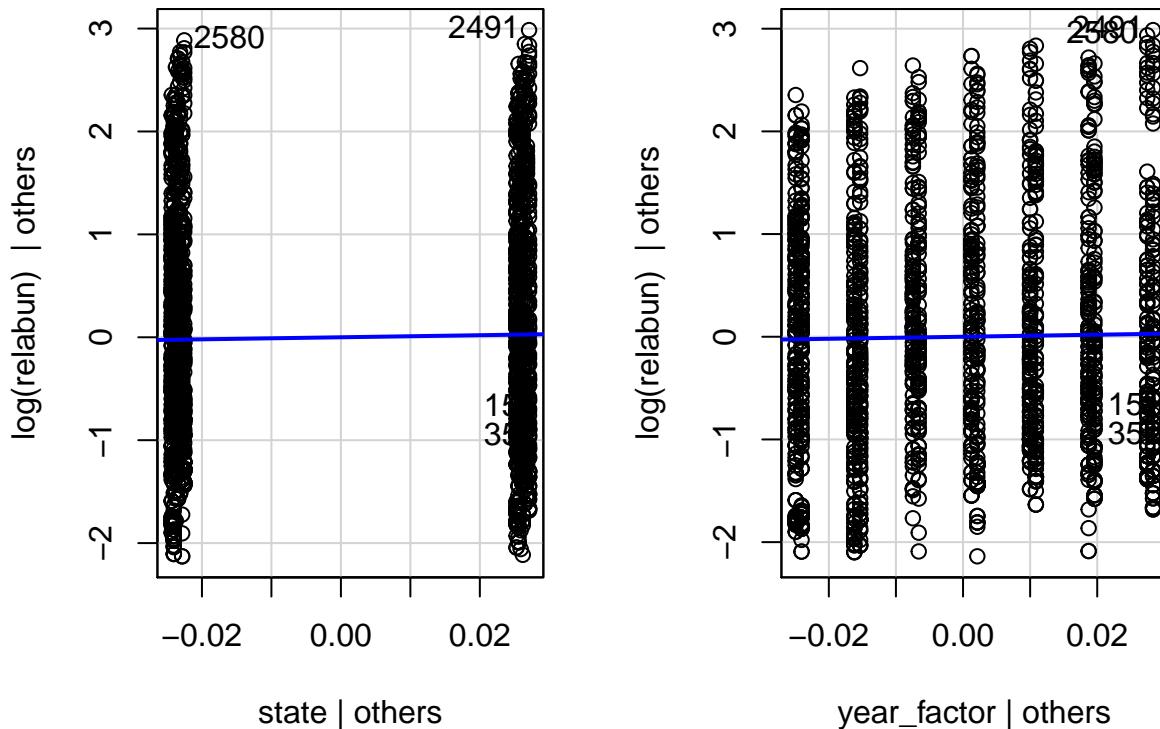
```
hist(fit_spp_stateyear_kbs$residuals)
```

Histogram of fit_spp_stateyear_kbs\$residuals



```
leveragePlots(fit_spp_stateyear_kbs)
```

Leverage Plots



```
ols_test_normality(fit_spp_stateyear_kbs)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

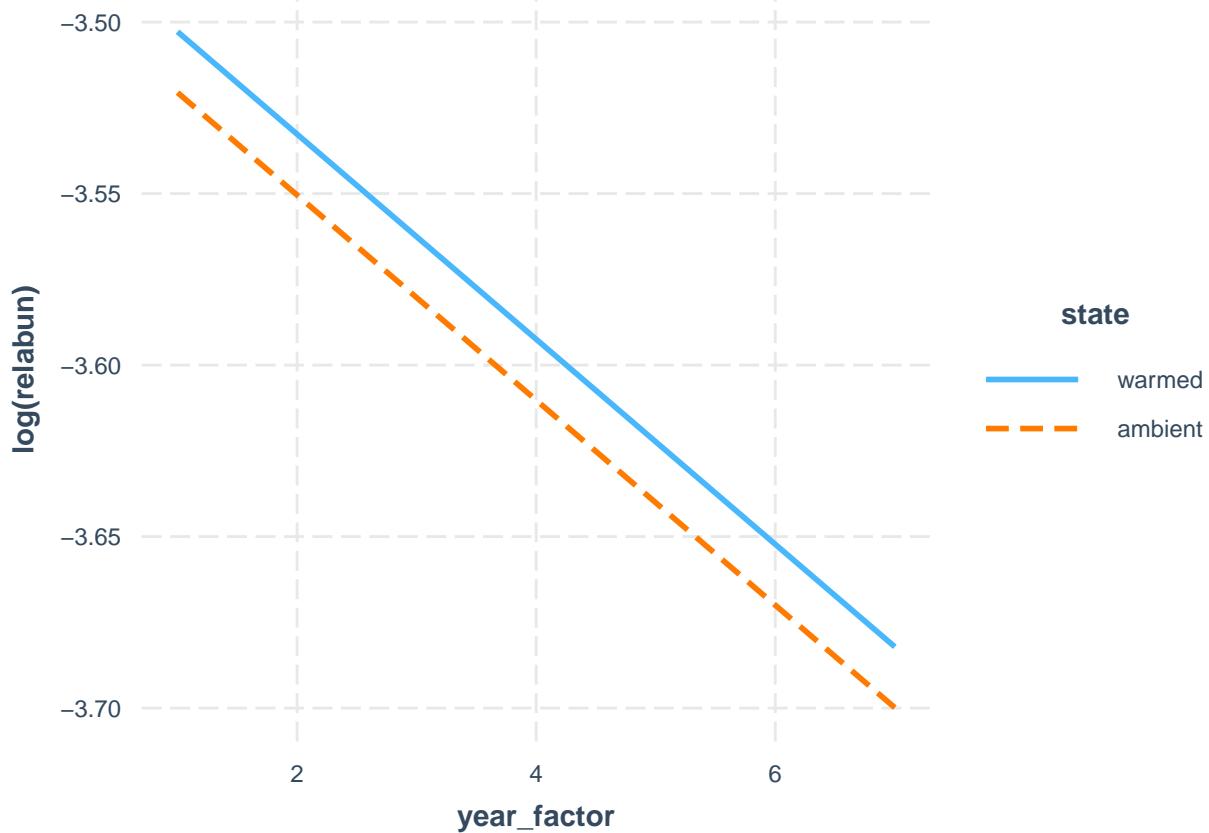
```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9656       0.0000
## Kolmogorov-Smirnov 0.0685       0.0000
## Cramer-von Mises 144.8202      0.0000
## Anderson-Darling 17.0611       0.0000
## -----
```

```
# Interaction plot (ignore for now the repeated measures with species); see:
# https://cran.r-project.org/web/packages/interactions/vignettes/interactions.html
# and: https://interactions.jacob-long.com/
```

```
fit3 <- lm(log(relabun) ~ state + year_factor + species, data = comp_kbs_spp)
interact_plot(fit3, pred = year_factor, modx = state)
```

```
## Using data comp_kbs_spp from global environment. This could cause incorrect
## results if comp_kbs_spp has been altered since the model was fit. You can
## manually provide the data to the "data =" argument.
```

```
## Warning: year_factor and state are not included in an interaction with one another
## in the model.
```



```
fit4 <- lm(log(relabun) ~ state * year_factor + species, data = comp_kbs_spp)
interact_plot(fit4, pred = year_factor, modx = state, mod2 = species)
```

```
## Using data comp_kbs_spp from global environment. This could cause incorrect
## results if comp_kbs_spp has been altered since the model was fit. You can
## manually provide the data to the "data =" argument.
```

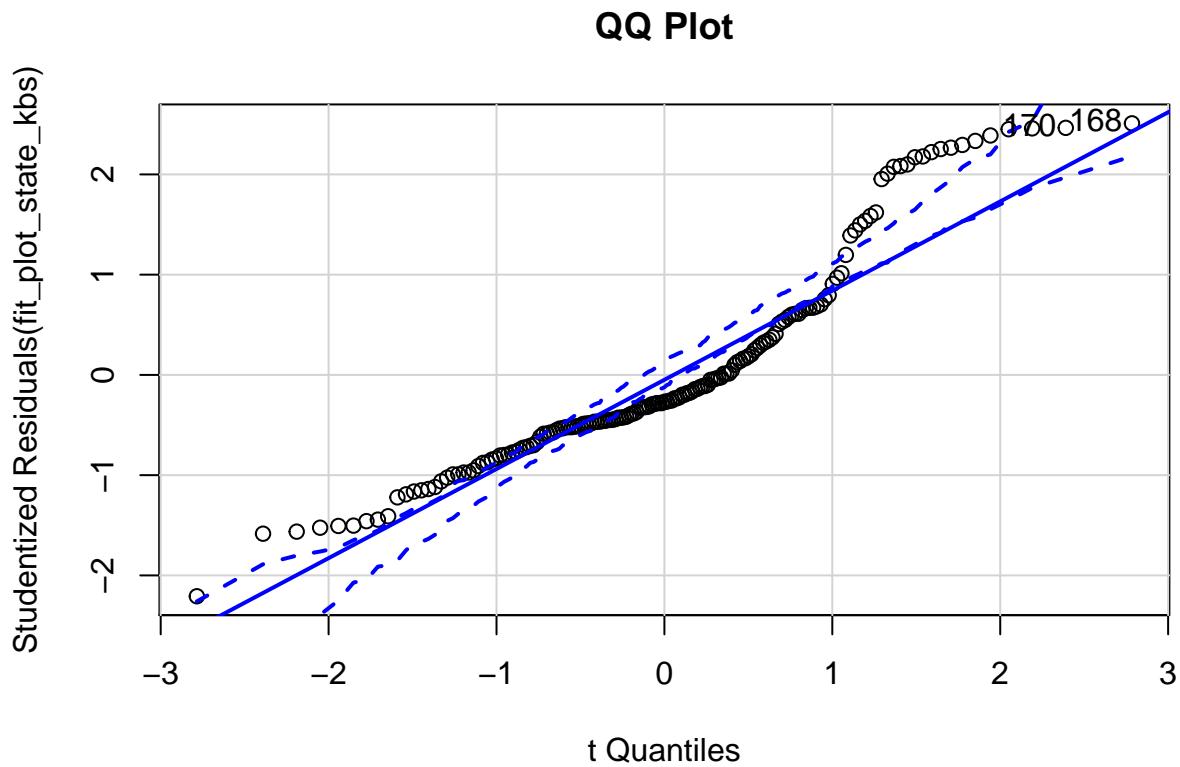
```
## Warning: year_factor and state and species are not included in an interaction with
## one another in the model.
```



```
# Plot level data KBS State-only model
fit_plot_state_kbs <- lm(log(plot_cover_avg) ~ state, data = comp_kbs_plot)
outlierTest(fit_plot_state_kbs) # outlier - row 252
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 168 2.509288          0.013068        NA
```

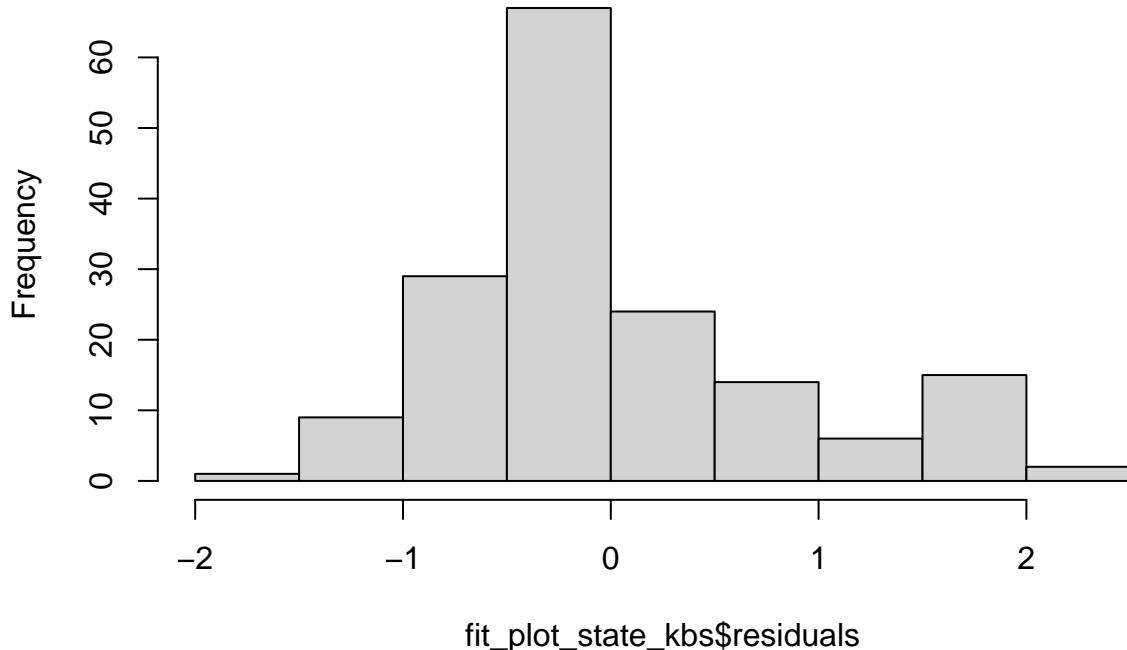
```
comp_kbs_plot_no_outliers <- comp_kbs_plot[-252, ] # remove outliers
qqPlot(fit_plot_state_kbs, main = "QQ Plot")
```



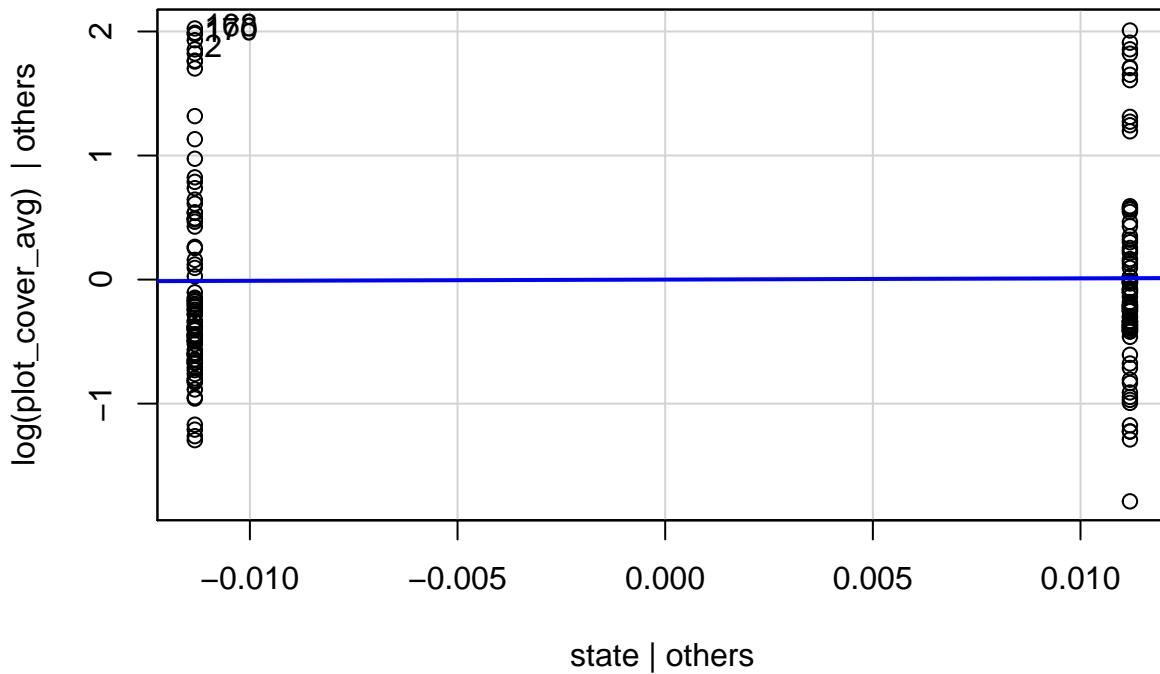
```
## 168 170
## 84 86
```

```
hist(fit_plot_state_kbs$residuals)
```

Histogram of fit_plot_state_kbs\$residuals



```
leveragePlots(fit_plot_state_kbs)
```



```
ols_test_normality(fit_plot_state_kbs)
```

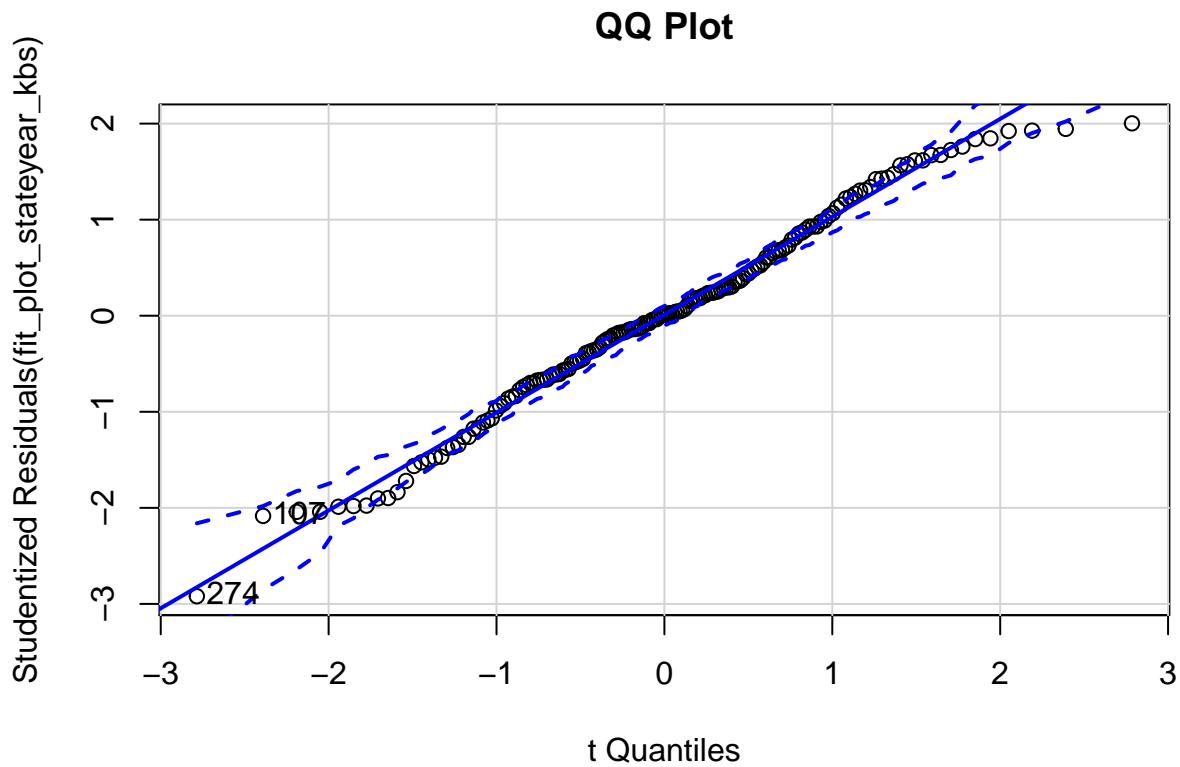
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9122       0.0000
## Kolmogorov-Smirnov 0.1469       0.0015
## Cramer-von Mises 20.8792       0.0000
## Anderson-Darling  5.4727       0.0000
## -----
```

```
# KBS State and year model
fit_plot_stateyear_kbs <- lm(log(plot_cover_avg) ~ state + year_factor, data = comp_kbs_plot)
outlierTest(fit_plot_stateyear_kbs) # outlier - row 190
```

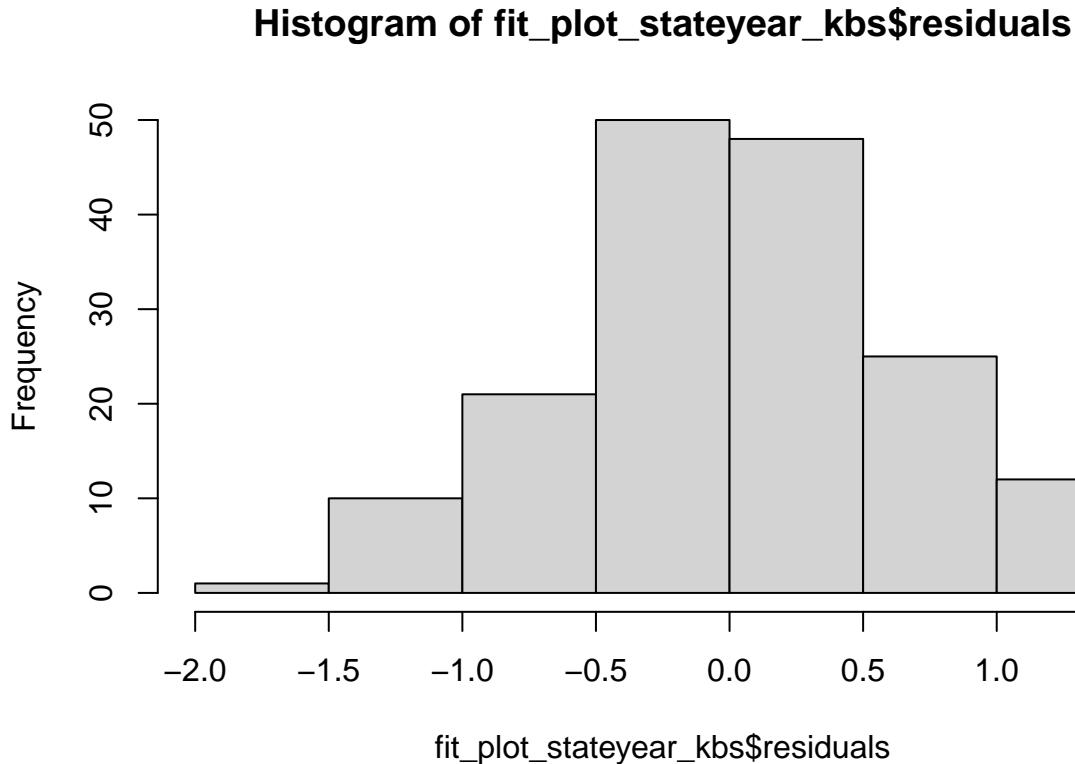
```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 274 -2.920104      0.0039949      0.66716
```

```
comp_kbs_plot_no_outliers <- comp_kbs_plot[-190, ] # remove outliers
qqPlot(fit_plot_stateyear_kbs, main = "QQ Plot")
```



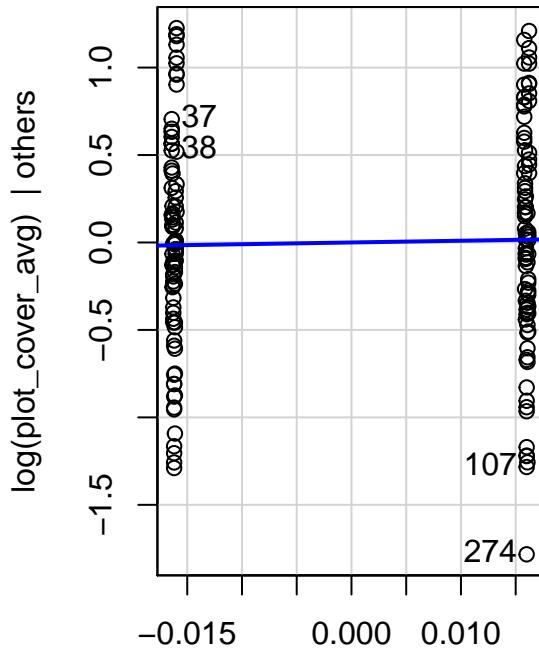
```
## 107 274
## 65 148
```

```
hist(fit_plot_stateyear_kbs$residuals)
```

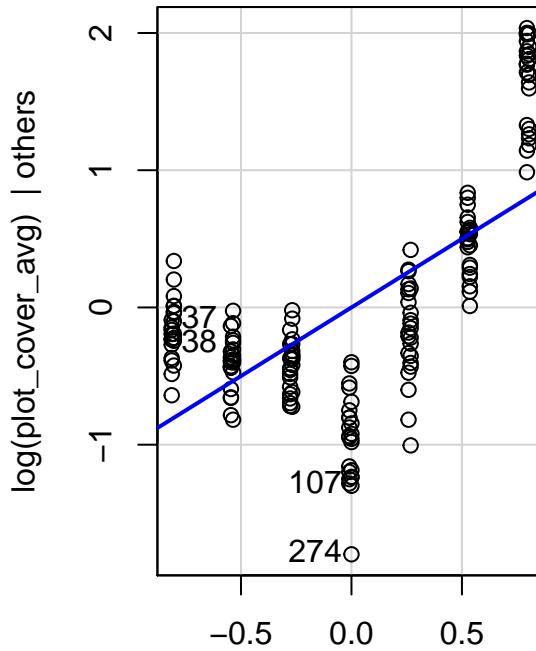


```
leveragePlots(fit_plot_stateyear_kbs)
```

Leverage Plots



state | others



year_factor | others

```
ols_test_normality(fit_plot_stateyear_kbs) # not all are under 0.05 but I think we can move forward wi
```

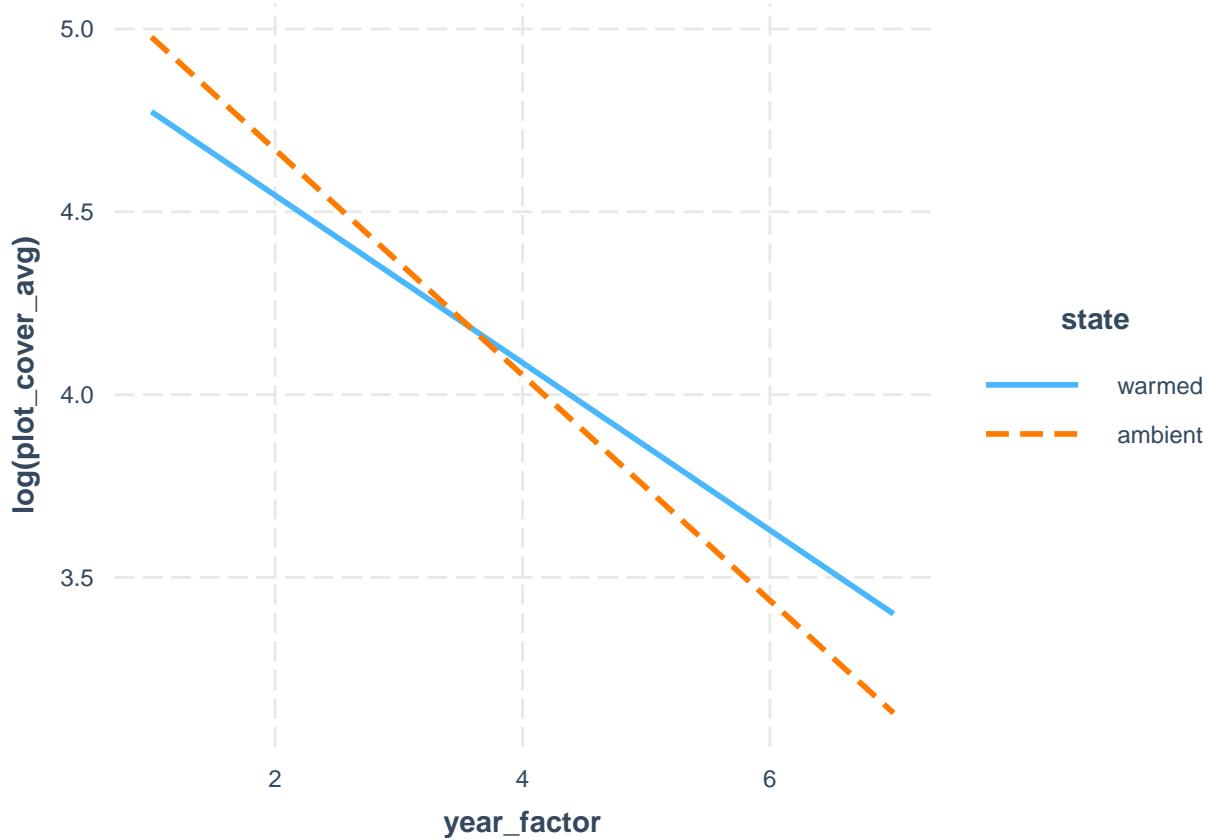
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9869      0.1200
## Kolmogorov-Smirnov 0.0413      0.9387
## Cramer-von Mises   16.4303      0.0000
## Anderson-Darling     0.4221      0.3183
## -----
```

```
# Interaction plot (ignore for now the repeated measures with species); see:
# https://cran.r-project.org/web/packages/interactions/vignettes/interactions.html
# and: https://interactions.jacob-long.com/
```

```
fit3 <- lm(log(plot_cover_avg) ~ state * year_factor, data = comp_kbs_plot)
interact_plot(fit3, pred = year_factor, modx = state)
```

```
## Using data comp_kbs_plot from global environment. This could cause
## incorrect results if comp_kbs_plot has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.
```

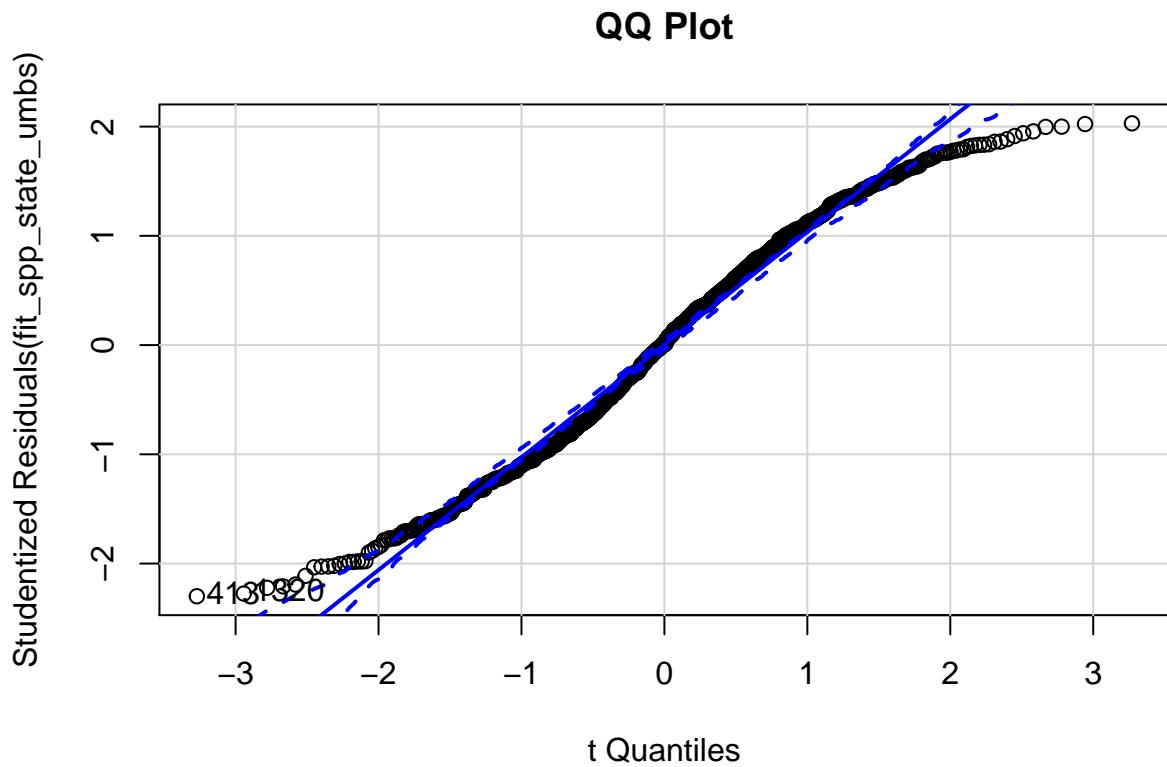


UMBS

```
# species level data UMBS State-only model
fit_spp_state_umbs <- lm(log(relabun) ~ state, data = comp_umbs_spp)
outlierTest(fit_spp_state_umbs) # outliers - row 449
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 413 -2.299237          0.021721           NA
```

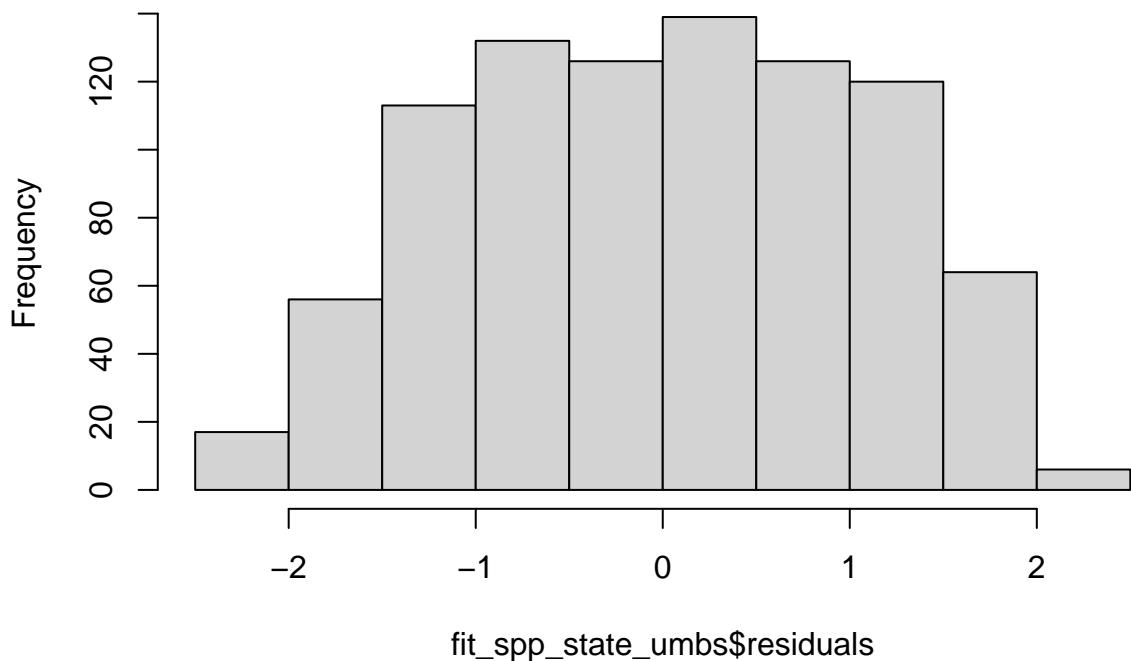
```
qqPlot(fit_spp_state_umbs, main = "QQ Plot")
```



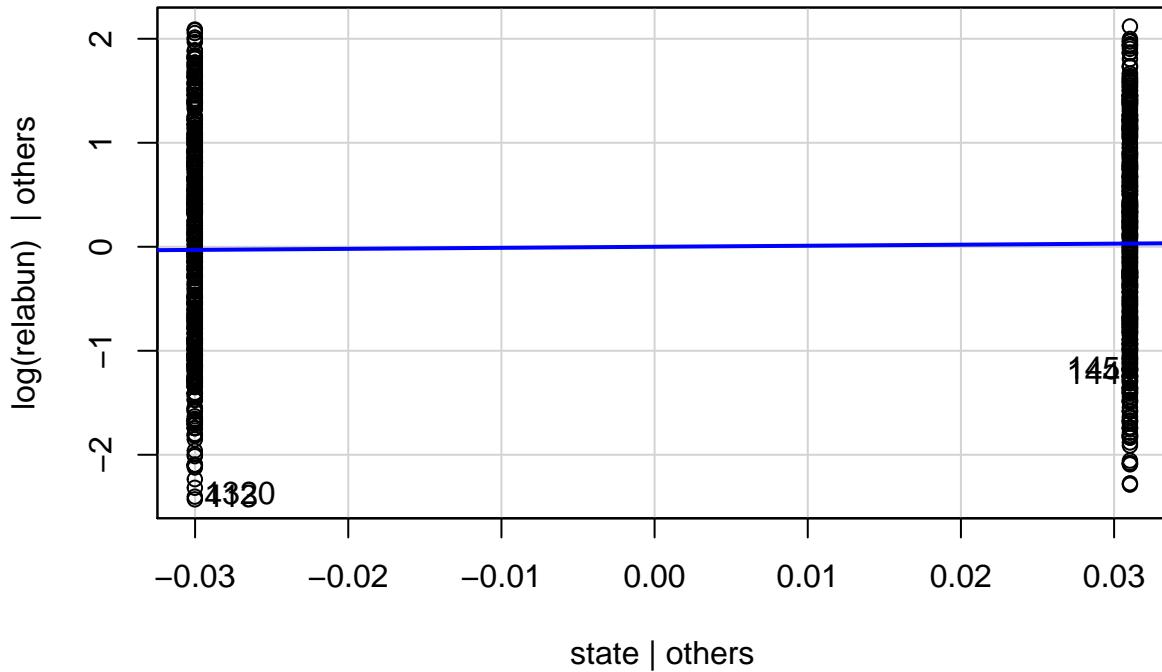
```
##   413 1320
##    64  425
```

```
hist(fit_spp_state_umbs$residuals)
```

Histogram of fit_spp_state_umbs\$residuals



```
leveragePlots(fit_spp_state_umbs)
```



```
ols_test_normality(fit_spp_state_umbs)
```

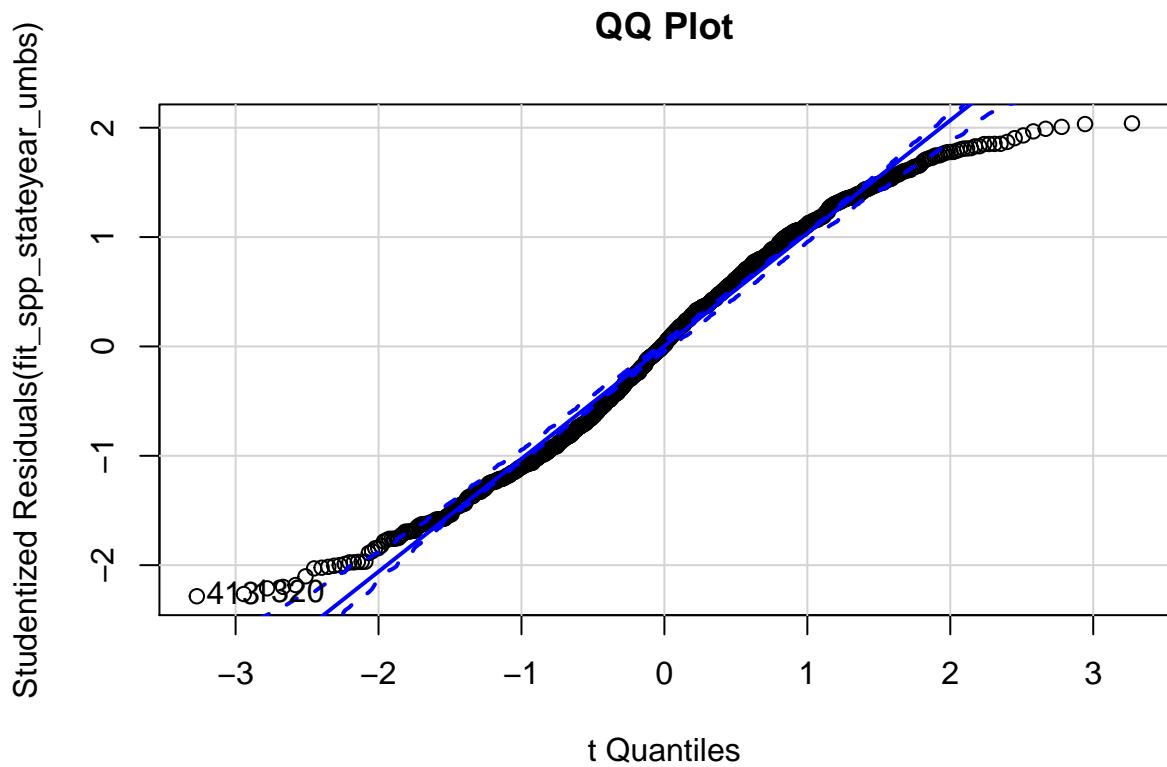
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9795       0.0000
## Kolmogorov-Smirnov 0.0487       0.0279
## Cramer-von Mises  54.5597       0.0000
## Anderson-Darling   4.7484       0.0000
## -----
```

```
# UMBS State and year model
fit_spp_stateyear_umbs <- lm(log(relabun) ~ state + year_factor, data = comp_umbs_spp)
outlierTest(fit_spp_stateyear_umbs) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 413 -2.284325           0.022586        NA
```

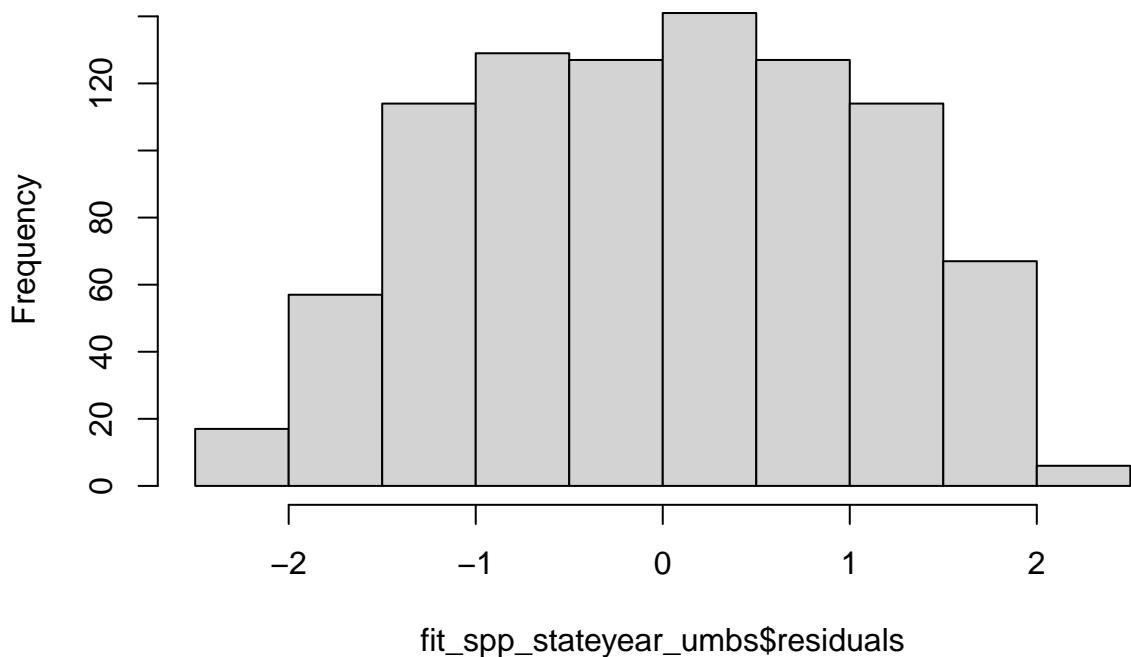
```
qqPlot(fit_spp_stateyear_umbs, main = "QQ Plot")
```



```
##   413 1320
##    64   425
```

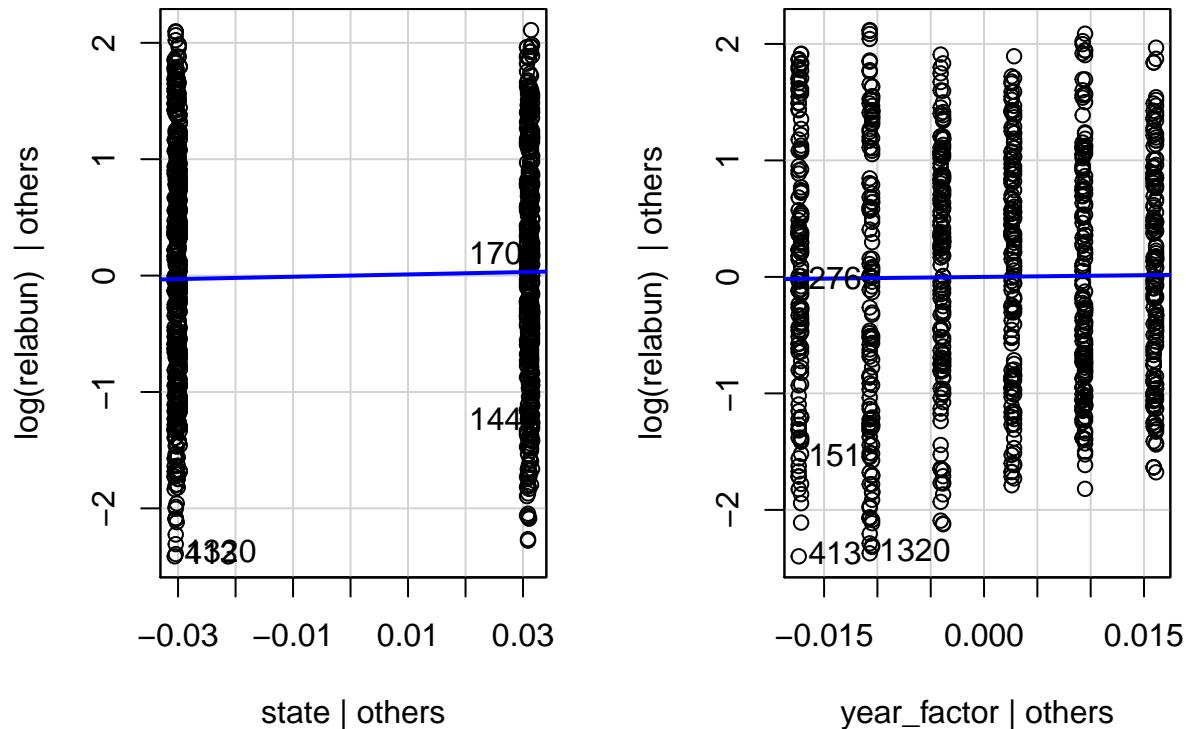
```
hist(fit_spp_stateyear_umbs$residuals)
```

Histogram of fit_spp_stateyear_umbs\$residuals



```
leveragePlots(fit_spp_stateyear_umbs)
```

Leverage Plots



```
ols_test_normality(fit_spp_stateyear_umbs)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

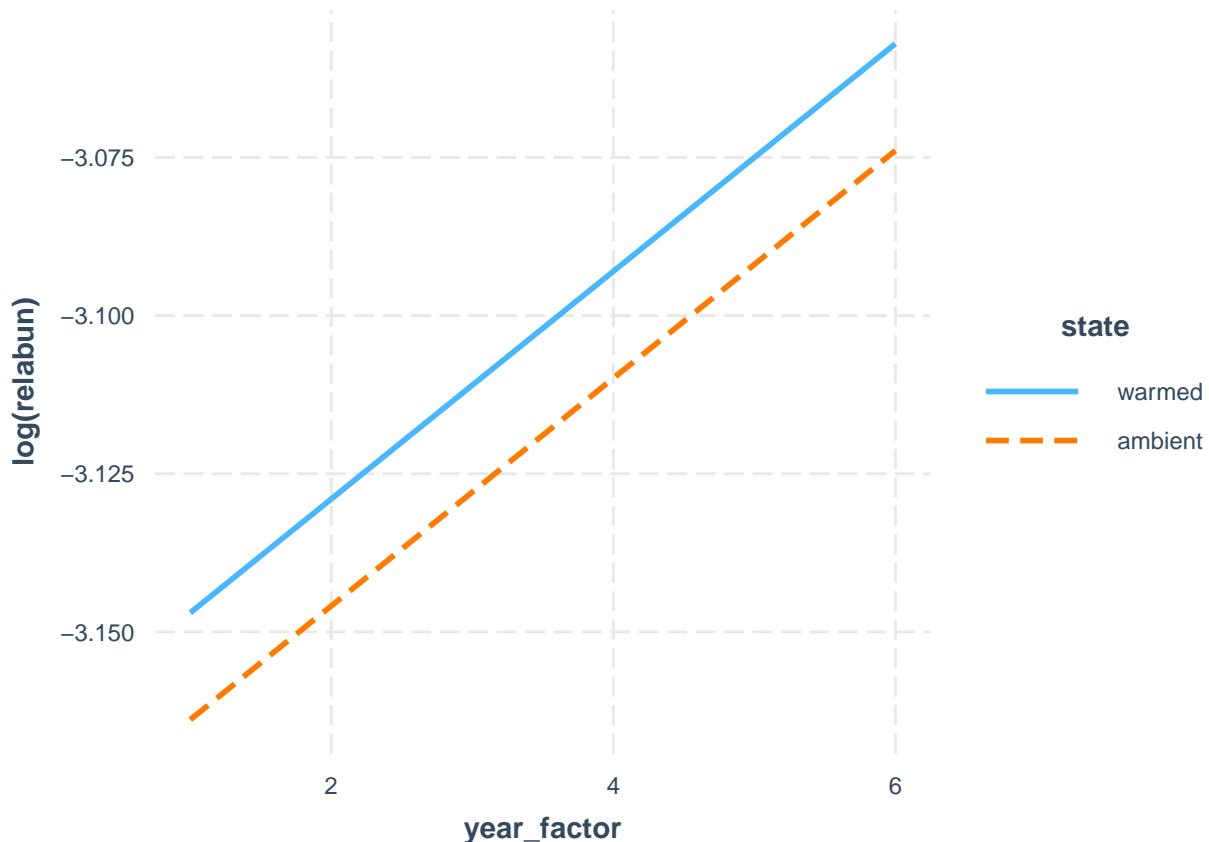
```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9794      0.0000
## Kolmogorov-Smirnov   0.05      0.0225
## Cramer-von Mises    54.4927      0.0000
## Anderson-Darling     4.7891      0.0000
## -----
```

```
# Interaction plot (ignore for now the repeated measures with species); see:
# https://cran.r-project.org/web/packages/interactions/vignettes/interactions.html
# and: https://interactions.jacob-long.com/
```

```
fit3 <- lm(log(relabun) ~ state + year_factor + species, data = comp_umbs_spp)
interact_plot(fit3, pred = year_factor, modx = state)
```

```
## Using data comp_umbs_spp from global environment. This could cause
## incorrect results if comp_umbs_spp has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.
```

```
## Warning: year_factor and state are not included in an interaction with one another
## in the model.
```



```
fit4 <- lm(log(relabun) ~ state * year_factor + species, data = comp_umbs_spp)
interact_plot(fit4, pred = year_factor, modx = state, mod2 = species)
```

```
## Using data comp_umbs_spp from global environment. This could cause
## incorrect results if comp_umbs_spp has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.
```

```
## Warning: year_factor and state and species are not included in an interaction with
## one another in the model.
```

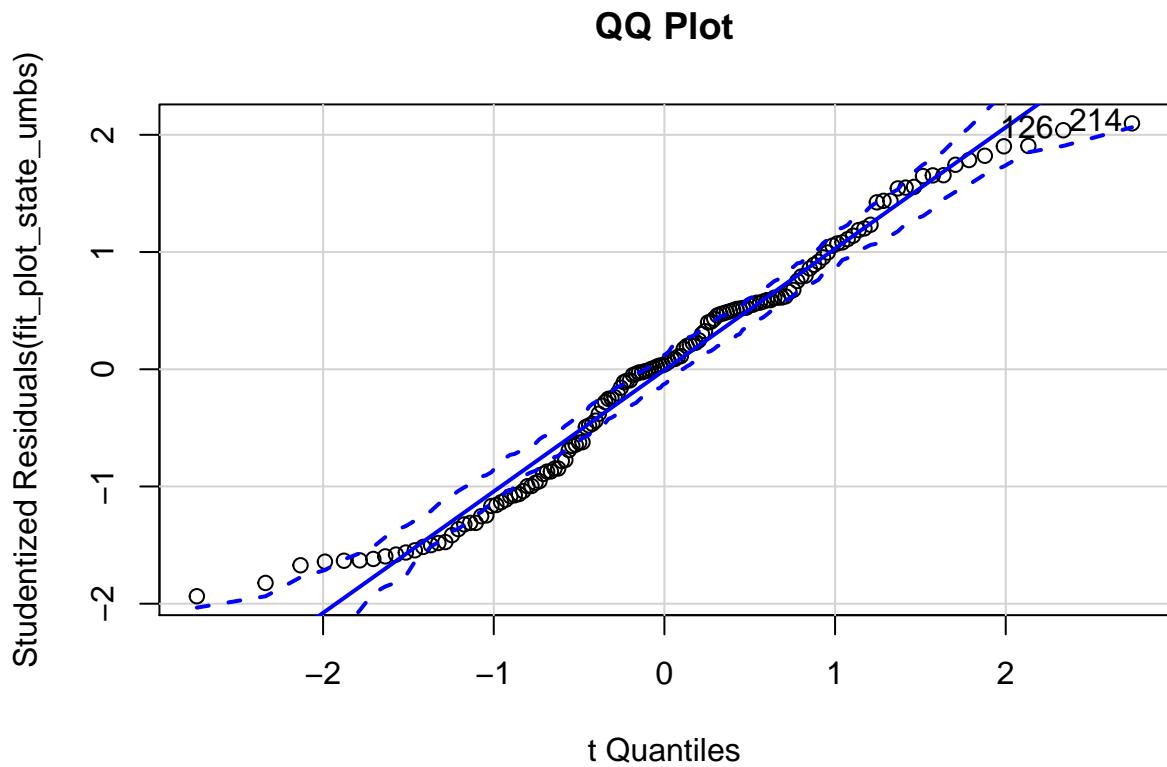


state ——— warmed ——— ambient

```
# Plot level data UMBS State-only model
fit_plot_state_umbs <- lm(log(plot_cover_avg) ~ state, data = comp_umbs_plot)
outlierTest(fit_plot_state_umbs) # outlier - row 252
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 214 2.097798          0.037707         NA
```

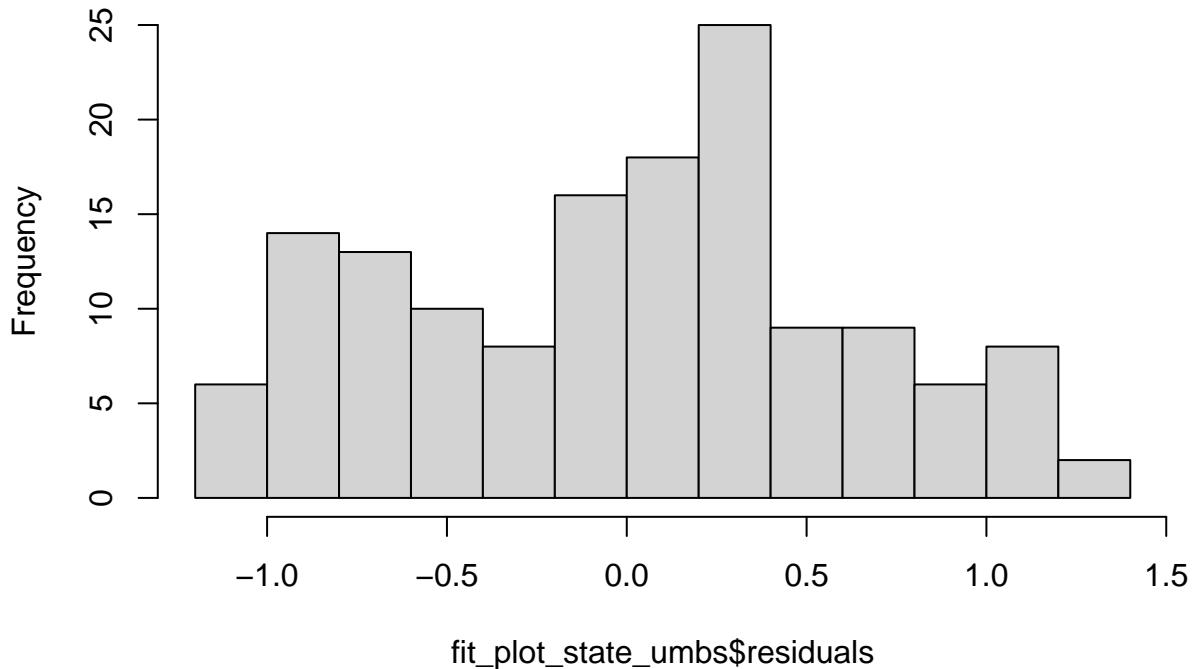
```
qqPlot(fit_plot_state_umbs, main = "QQ Plot")
```



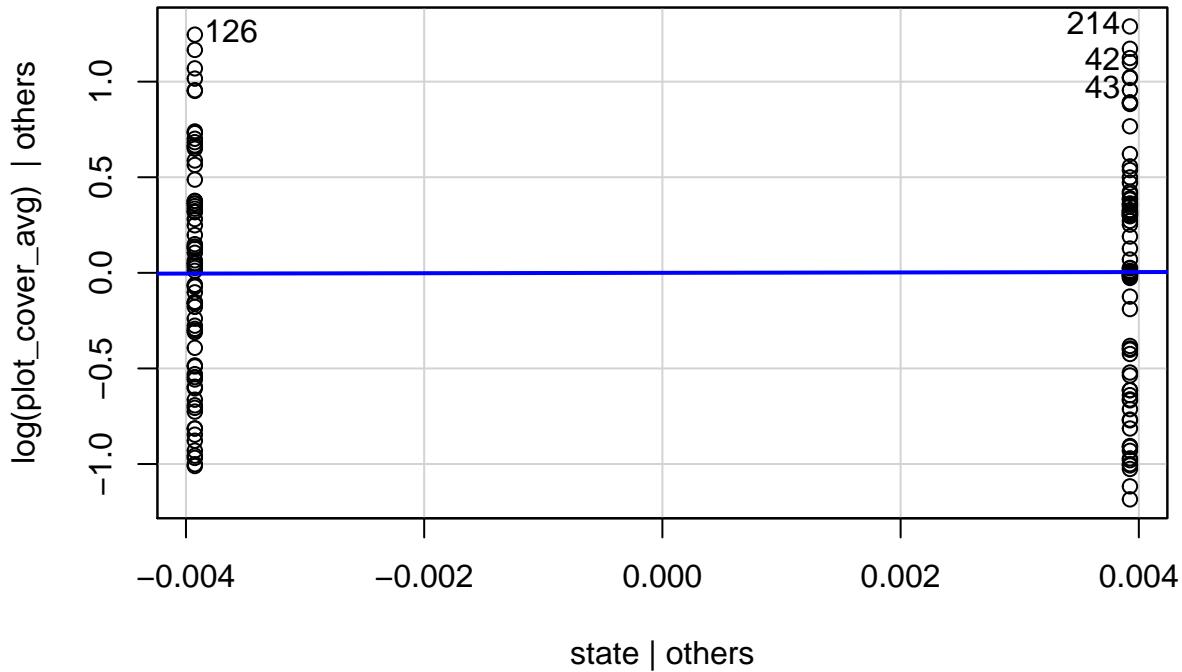
```
## 126 214
## 37 77
```

```
hist(fit_plot_state_umbs$residuals)
```

Histogram of fit_plot_state_umbs\$residuals



```
leveragePlots(fit_plot_state_umbs)
```



```
ols_test_normality(fit_plot_state_umbs)
```

```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

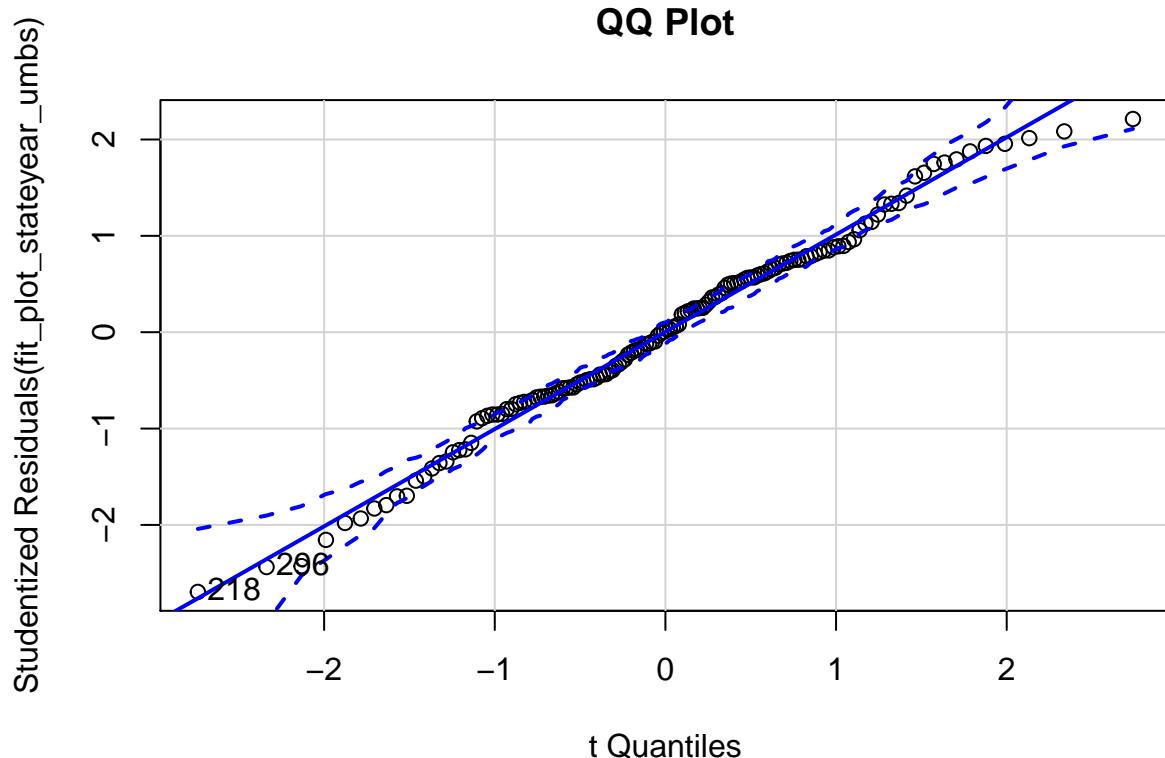
```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9722      0.0049
## Kolmogorov-Smirnov 0.0717      0.4498
## Cramer-von Mises 12.7256      0.0000
## Anderson-Darling   1.0016      0.0118
## -----
```

```
comp_umbs_plot_no_outliers <- comp_umbs_plot[-298, ] # remove outliers
```

```
# KBS State and year model
fit_plot_stateyear_umbs <- lm(log(plot_cover_avg) ~ state + year_factor, data = comp_umbs_plot)
outlierTest(fit_plot_stateyear_umbs) # outlier - row 190
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 218 -2.695146           0.0078978        NA
```

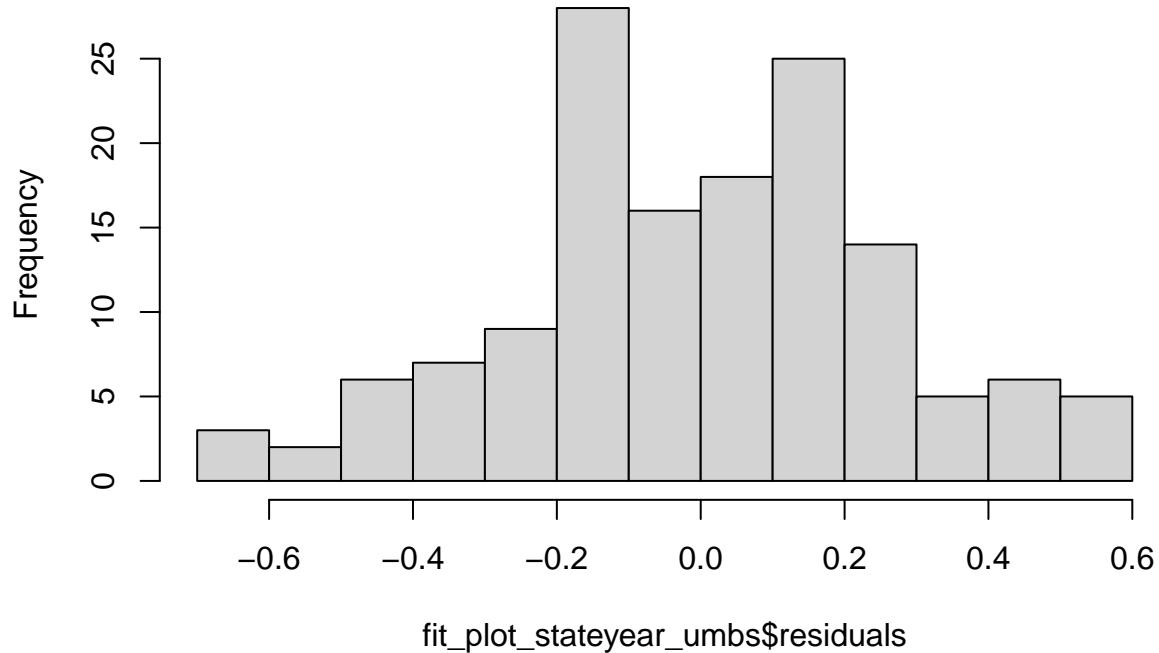
```
comp_umbs_plot_no_outliers <- comp_umbs_plot[-190, ] # remove outliers  
qqPlot(fit_plot_stateyear_umbs, main = "QQ Plot")
```



```
## 218 296  
## 81 111
```

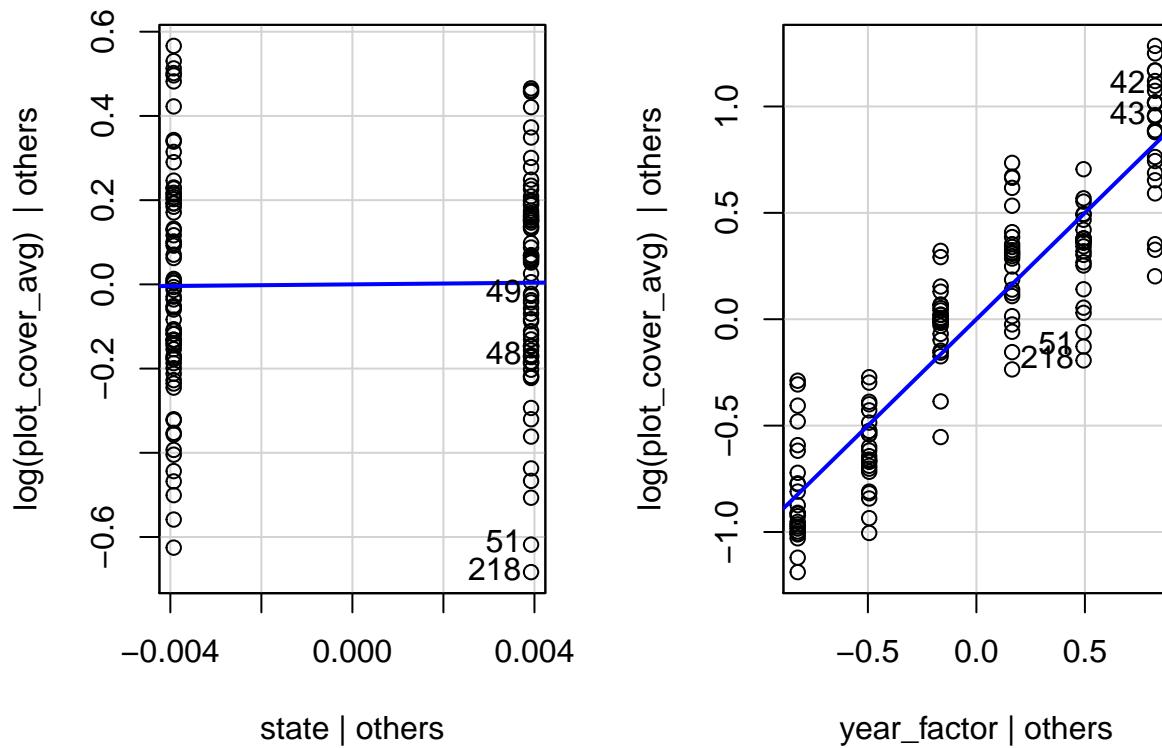
```
hist(fit_plot_stateyear_umbs$residuals)
```

Histogram of fit_plot_stateyear_umbs\$residuals



```
leveragePlots(fit_plot_stateyear_umbs)
```

Leverage Plots



```

ols_test_normality(fit_plot_stateyear_umbs) # not all are under 0.05 but I think we can move forward w

## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test

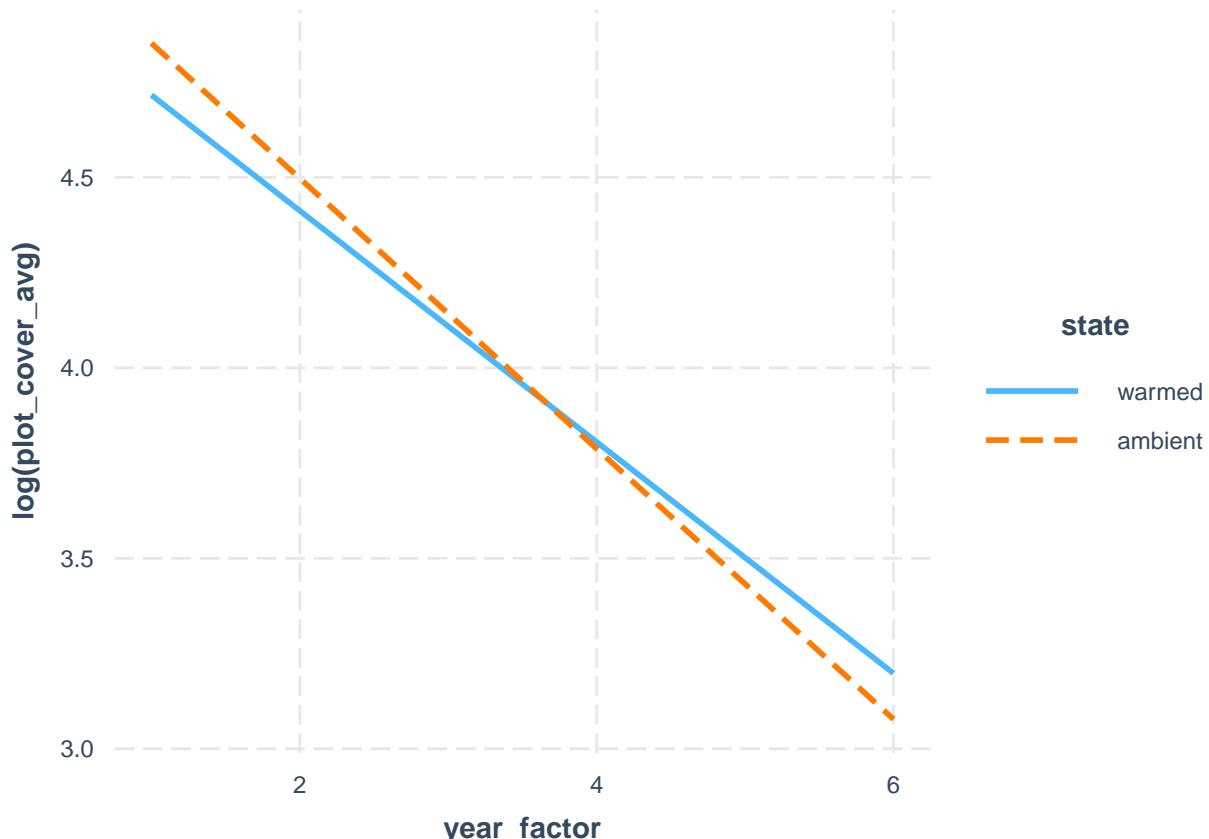
## -----
##          Test      Statistic     pvalue
## -----
## Shapiro-Wilk      0.9893    0.3354
## Kolmogorov-Smirnov 0.0493    0.8753
## Cramer-von Mises   27.072    0.0000
## Anderson-Darling    0.4069    0.3452
## -----


# Interaction plot (ignore for now the repeated measures with species); see:
# https://cran.r-project.org/web/packages/interactions/vignettes/interactions.html
# and: https://interactions.jacob-long.com/


fit3 <- lm(log(plot_cover_avg) ~ state * year_factor, data = comp_umbs_plot)
interact_plot(fit3, pred = year_factor, modx = state)

## Using data comp_umbs_plot from global environment. This could cause
## incorrect results if comp_umbs_plot has been altered since the model was
## fit. You can manually provide the data to the "data =" argument.

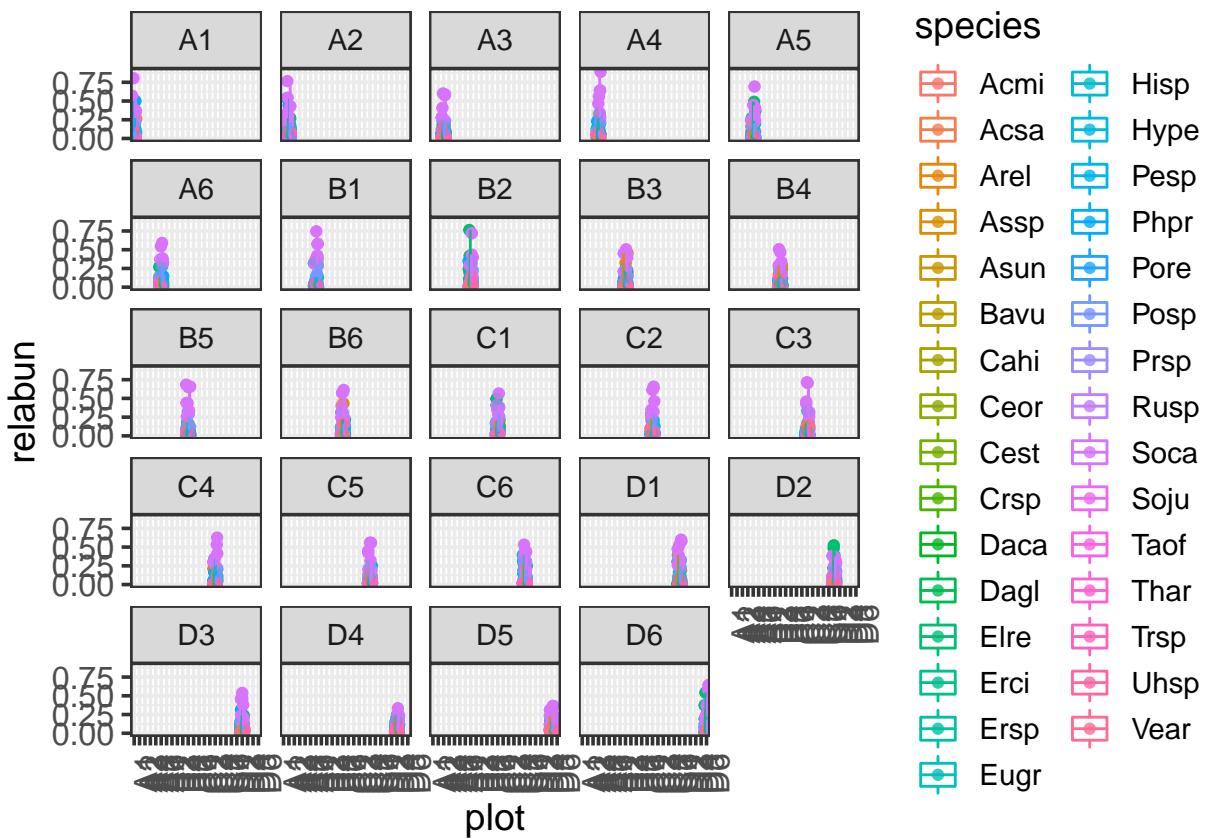
```



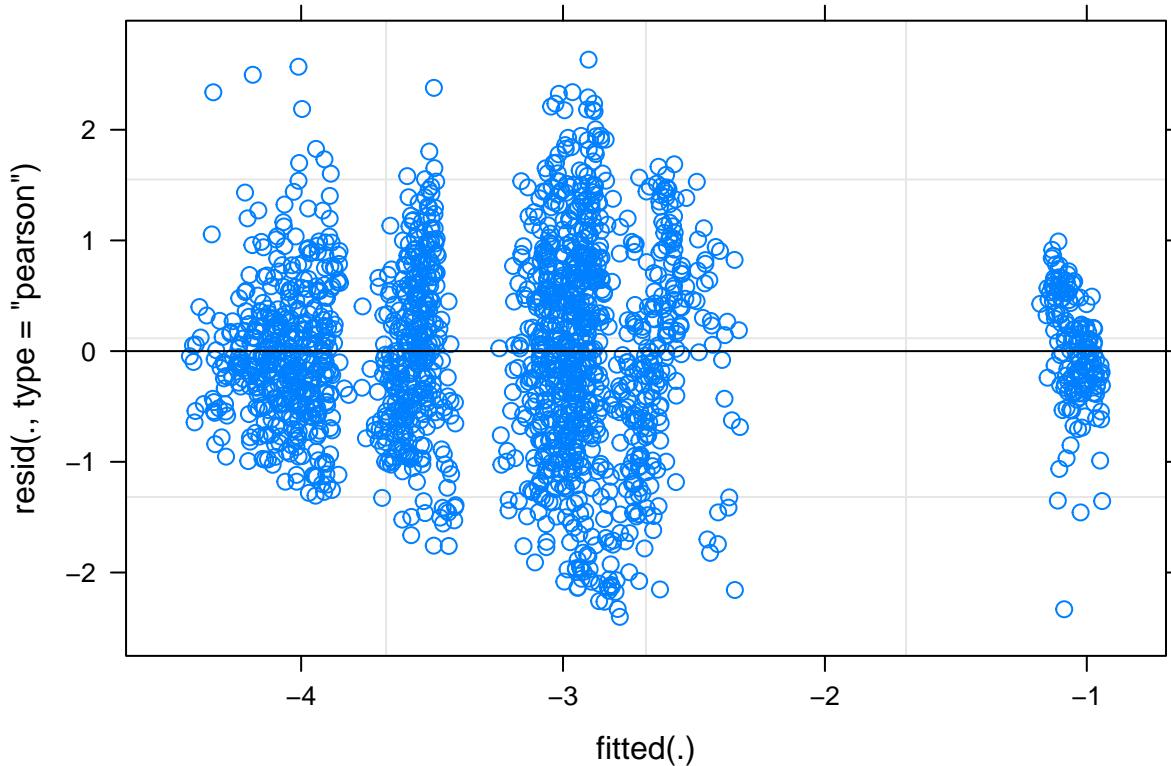
MIXED EFFECT MODELS

KBS species level data

```
# KBS SPECIES LEVEL - Looking at RELATIVE ABUNDANCE
mod1 <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 | species) + (1 | plot), comp_kbs_spp, REML = FALSE)
ggplot(comp_kbs_spp, aes(x = plot, y = relabun, col = species)) + geom_jitter() +
  geom_boxplot(alpha = 0.2) + facet_wrap(~plot)
```



```
# Check Assumptions: (1) Linearity: if covariates are not categorical (year # isn't) (2) Homogeneity: Need to Check by plotting residuals vs predicted # values.
par(mfrow = c(1, 2))
plot(mod1)
```



```
# Homogeneity of variance is ok here (increasing variance in resids is not
# increasing with fitted values) Check for homogeneity of variances (true if
# p>0.05). If the result is not significant, the assumption of equal variances
# (homoscedasticity) is met (no significant difference between the group
# variances). *****Levene's Test - tests whether or not the variance among two
# or more groups is equal - If the p-value is less than our chosen significance
# level, we can reject the null hypothesis and conclude that we have enough
# evidence to state that the variance among the groups is not equal (which we
# want).
```

```
leveneTest(residuals(mod1) ~ comp_kbs_spp$state)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value    Pr(>F)
## group     1 8.1274 0.004409 **
##          1816
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Assumption met
leveneTest(residuals(mod1) ~ comp_kbs_spp$species)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value    Pr(>F)
```

```

## group    30  9.5894 < 2.2e-16 ***
##          1787
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Assumption met
leveneTest(residuals(mod1) ~ comp_kbs_spp$insecticide)

## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.

## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group      1  0.7224 0.3955
##             1816

# Assumption not met - this seems weird
leveneTest(residuals(mod1) ~ comp_kbs_spp$plot)

## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.

## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value   Pr(>F)
## group     23  1.7568 0.01463 *
##             1794
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Assumption met

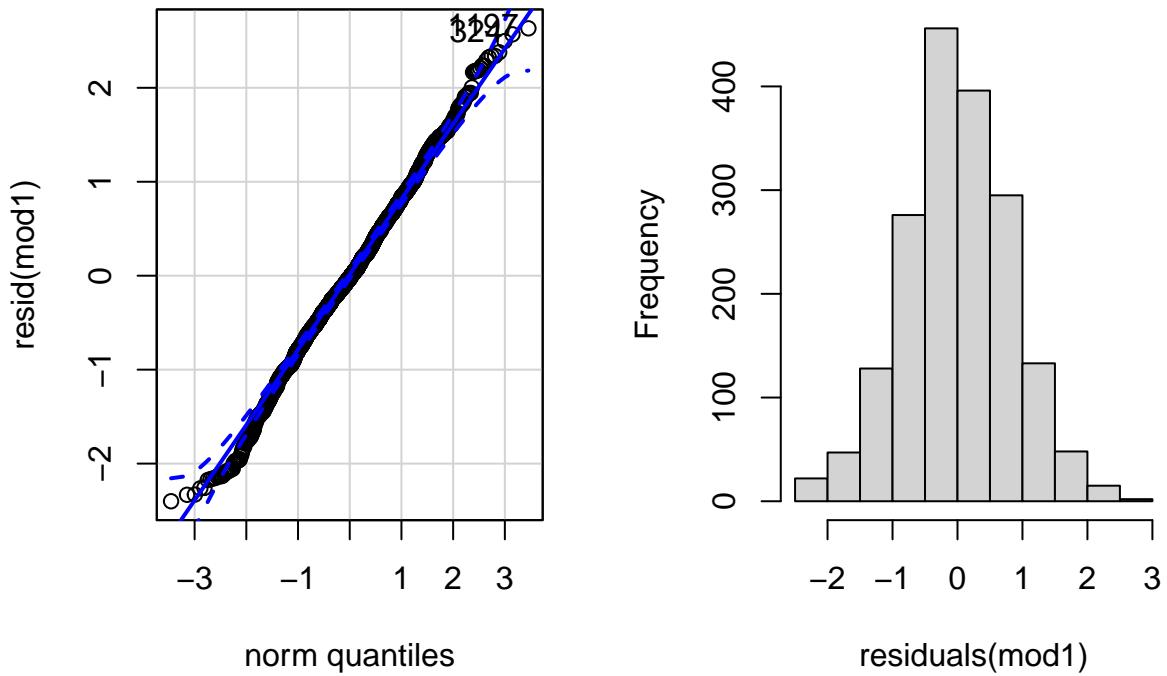
# (3) Normality of error term: need to check by histogram, QQplot of residuals,
# could do Kolmogorov-Smirnov test. Check for normal residuals
qqPlot(resid(mod1))

## 1197  324
##  713  257

hist(residuals(mod1))

```

Histogram of residuals(mod1)



```
shapiro.test(resid(mod1)) # not normally distributed resids bc p<0.05
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: resid(mod1)  
## W = 0.99775, p-value = 0.01176
```

```
outlierTest(mod1) # no outliers
```

```
## No Studentized residuals with Bonferroni p < 0.05  
## Largest |rstudent|:  
##      rstudent unadjusted p-value Bonferroni p  
## 324 3.182167          0.0014866       NA
```

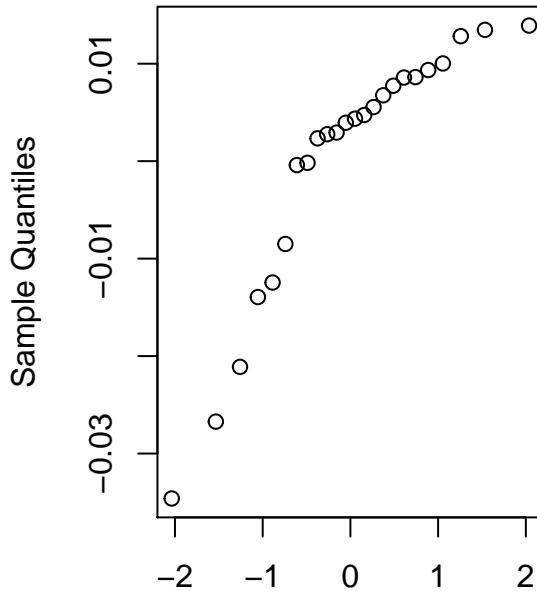
(4) Normality of random effect: Get the estimate of random effect (e.g., random intercepts), and check them as you would check the residual.

```
require(lme4)  
r_int <- ranef(mod1)$plot$`Intercept`  
qnorm(r_int)  
# qqline(r_int) doesn't work  
shapiro.test(r_int)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: r_int  
## W = 0.84158, p-value = 0.001532
```

```
# Not normally distributed random effect - p-value = 0.0015
```

Normal Q–Q Plot



Theoretical Quantiles

```
# Do we need to include plot as a random effect with the KBS models?
mod1 <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |
  species) + (1 | plot), comp_kbs_spp, REML = FALSE)
mod2 <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |
  species), comp_kbs_spp, REML = FALSE)
# Run analysis of variance on each model (see this for more explanation on how
# anova on a linear mixed effects model is similar to an anova on a regular
# linear model: https://m-clark.github.io/docs/mixedModels/anovamixed.html)
anova(mod1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                     Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state                           0.0745 0.0745     1   346.29  0.1057 0.745233
## year_factor                     5.1615 5.1615     1 1803.74  7.3298 0.006846 **
## insecticide                      0.0028 0.0028     1   352.08  0.0040 0.949833
## state:year_factor                0.0108 0.0108     1 1795.30  0.0154 0.901364
## year_factor:insecticide          0.0232 0.0232     1 1797.80  0.0329 0.856061
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mod2)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                     Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state                           0.0756 0.0756     1 1798.8  0.1072 0.743362
```

```

## year_factor      5.2202  5.2202      1 1803.8  7.3994 0.006587 **
## insecticide     0.0048  0.0048      1 1804.0  0.0068 0.934314
## state:year_factor 0.0126  0.0126      1 1796.4  0.0179 0.893691
## year_factor:insecticide 0.0254  0.0254      1 1800.3  0.0359 0.849641
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
anova(mod1, mod2) # Go with model 2 since pvalue >0.05, aka more complex model does not have something
```

```

## Data: comp_kbs_spp
## Models:
## mod2: log(relabun) ~ state * year_factor + insecticide * year_factor +
## mod2:          (1 | species)
## mod1: log(relabun) ~ state * year_factor + insecticide * year_factor +
## mod1:          (1 | species) + (1 | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod2    8 4636.7 4680.7 -2310.3   4620.7
## mod1    9 4638.4 4688.0 -2310.2   4620.4 0.2303  1     0.6313

```

```
summ(mod1)
```

Observations	1818
Dependent variable	log(relabun)
Type	Mixed effects linear regression

AIC	4638.44
BIC	4687.99
Pseudo-R ² (fixed effects)	0.00
Pseudo-R ² (total)	0.47

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	-3.42	0.17	-20.24	43.88	0.00
stateambient	-0.03	0.09	-0.33	346.29	0.75
year_factor	-0.03	0.02	-1.78	1800.47	0.08
insecticideno_insects	-0.01	0.09	-0.06	352.08	0.95
stateambient:year_factor	0.00	0.02	0.12	1795.30	0.90
year_factor:insecticideno_insects	0.00	0.02	0.18	1797.80	0.86

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
species	(Intercept)	0.79
plot	(Intercept)	0.04
Residual		0.84

Grouping Variables		
Group	# groups	ICC
species	31	0.47
plot	24	0.00

```
summ(mod2)
```

Observations	1818
Dependent variable	log(relabun)
Type	Mixed effects linear regression
AIC	4636.67
BIC	4680.71
Pseudo-R ² (fixed effects)	0.00
Pseudo-R ² (total)	0.47

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	-3.42	0.17	-20.31	43.61	0.00
stateambient	-0.03	0.08	-0.33	1798.79	0.74
year_factor	-0.03	0.02	-1.80	1800.92	0.07
insecticideno_insects	-0.01	0.08	-0.08	1804.05	0.93
stateambient:year_factor	0.00	0.02	0.13	1796.41	0.89
year_factor:insecticideno_insects	0.00	0.02	0.19	1800.29	0.85

p values calculated using Satterthwaite d.f.

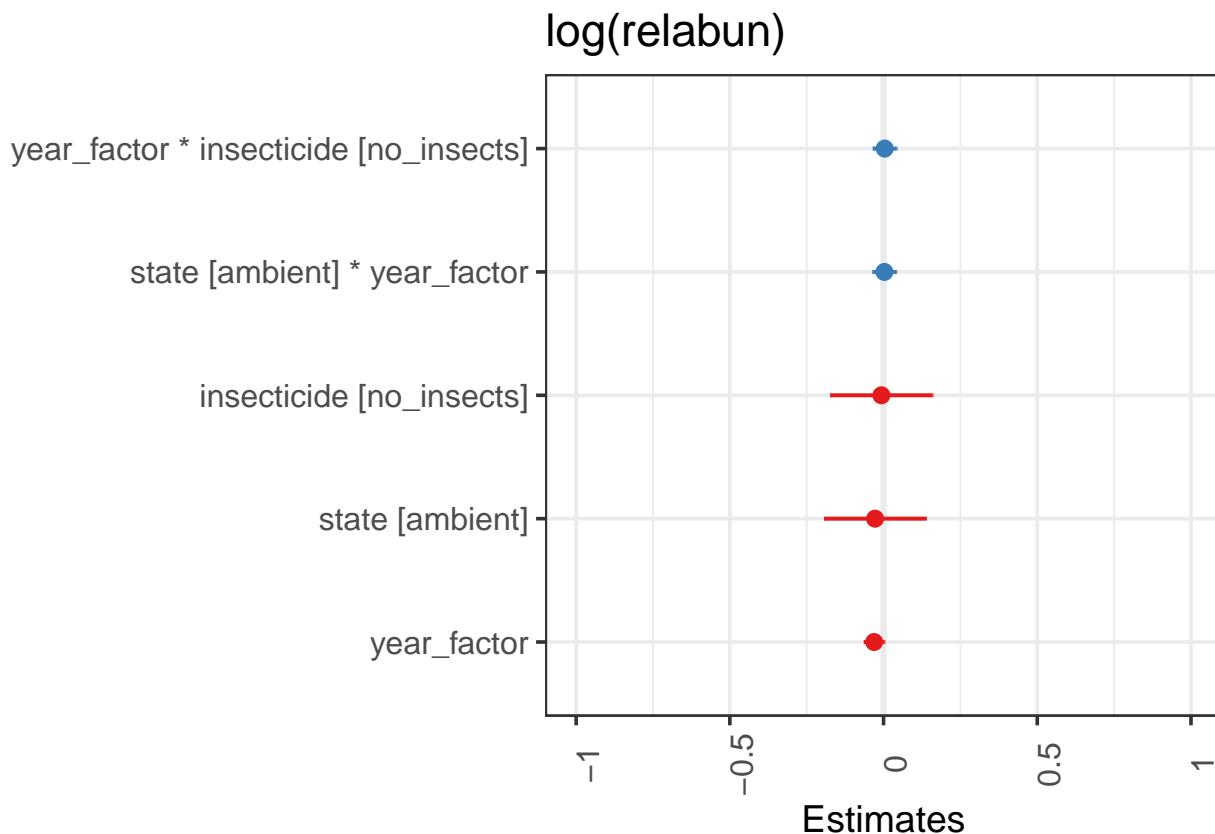
Random Effects		
Group	Parameter	Std. Dev.
species	(Intercept)	0.79
	Residual	0.84

Grouping Variables		
Group	# groups	ICC
species	31	0.47

```
AICctab(mod1, mod2, weights = T)
```

```
##      dAICc df weight
## mod2 0.0   8  0.71
## mod1 1.8   9  0.29
```

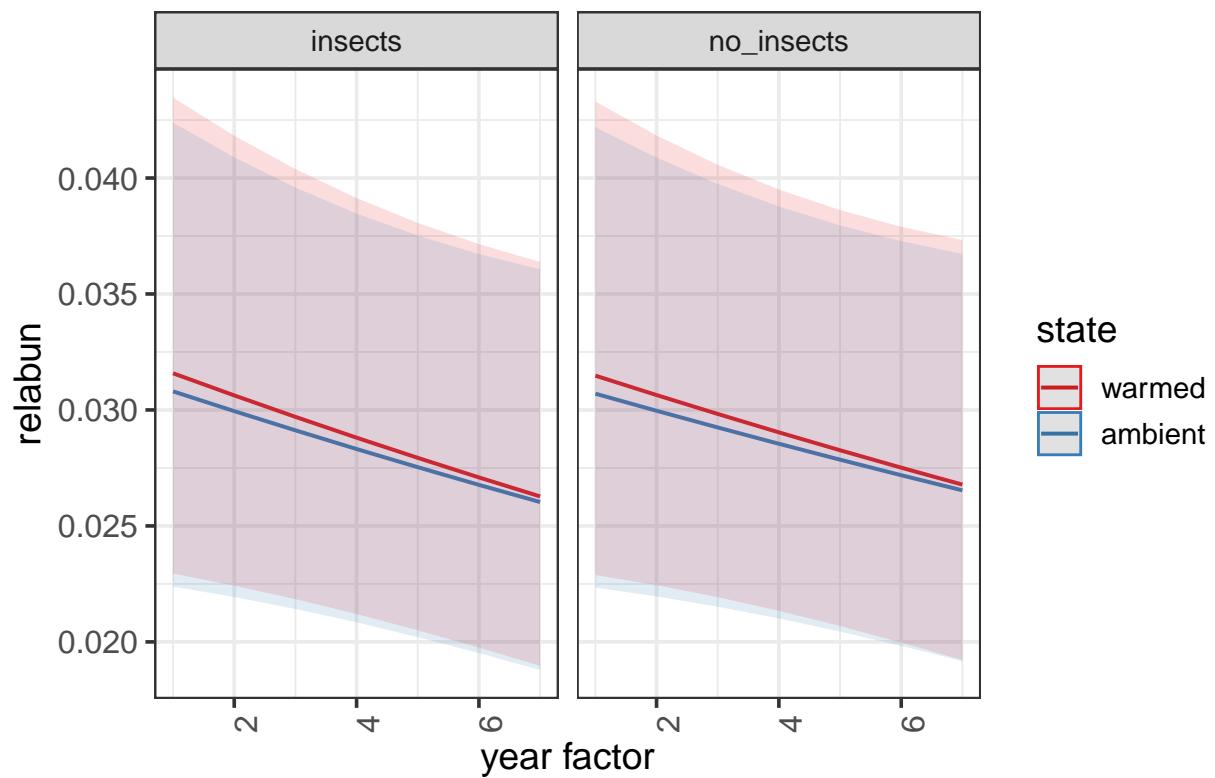
```
# Plot the fixed effects estimates for different models these are the fixed  
# effects estimates from summary(mod1)  
plot_model(mod2, sort.est = TRUE)
```



```
# these are the fixed predicted values:  
plot_model(mod2, type = "pred", terms = c("year_factor", "state", "insecticide"))
```

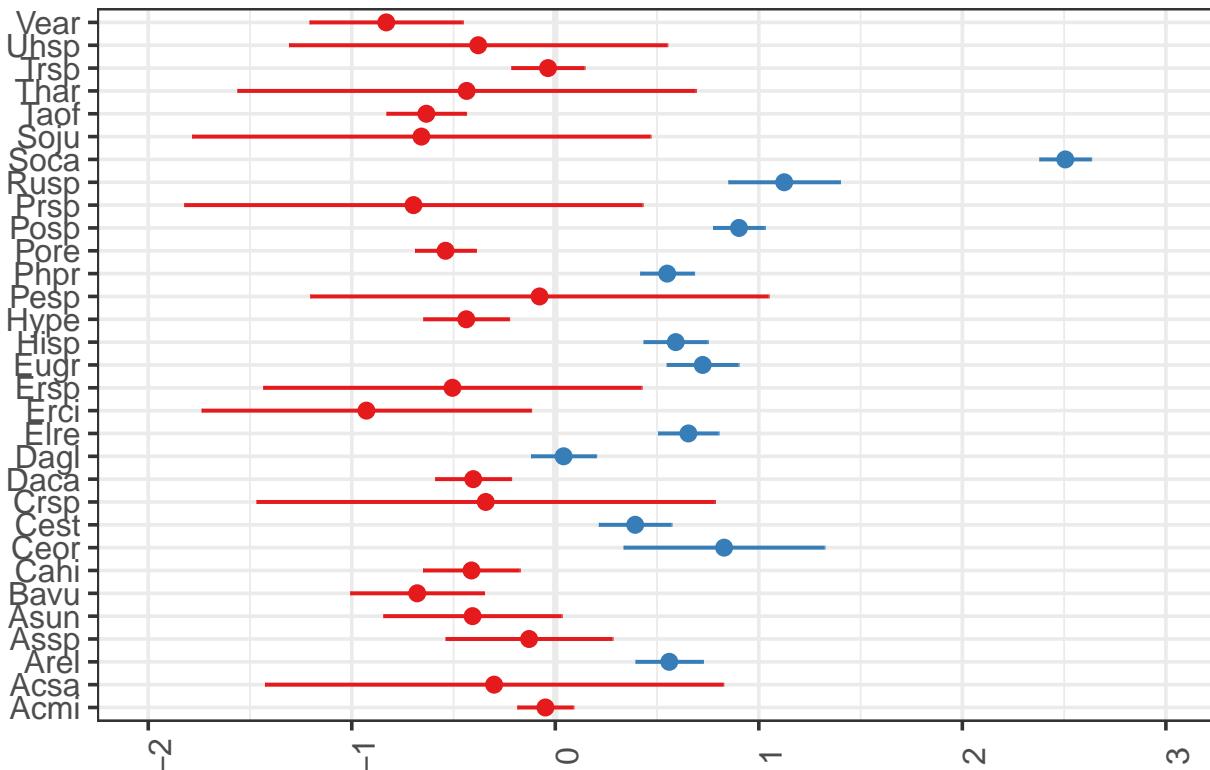
Model has log-transformed response. Back-transforming predictions to original response scale. Standard

Predicted values of relabun



```
# these are the random effects estimates
plot_model(mod2, type = "re", terms = c("species"))
```

Random effects



```
# Do we need to include insecticide? (dropping insecticide from the model) mod2
# <- lmer(log(relabun) ~ state*year_factor + insecticide*year_factor +
# (1/species), comp_kbs_spp, REML=FALSE)
mod3 <- lmer(log(relabun) ~ state * year_factor + (1 | species), comp_kbs_spp, REML = FALSE)
anova(mod2, mod3)
```

```
## Data: comp_kbs_spp
## Models:
## mod3: log(relabun) ~ state * year_factor + (1 | species)
## mod2: log(relabun) ~ state * year_factor + insecticide * year_factor +
## mod2: (1 | species)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod3     6 4632.7 4665.8 -2310.4    4620.7
## mod2     8 4636.7 4680.7 -2310.3    4620.7 0.0684  2      0.9664
```

```
AICctab(mod2, mod3, weights = T)
```

```
##      dAICc df weight
## mod3  0.0   6  0.88
## mod2  4.0   8  0.12
```

```
# Looks like no, pvalue > 0.05, so insecticide does not improve model fit so we
# will go with mod 3
```

```
# Does year need to be interactive with insecticide? - already removed
```

```

# insecticide mod4 <- lmer(log(julian_median) ~ state*year_factor + insecticide +
# (1/species) + (1/plot), umbs_flwr_spp, REML=FALSE)

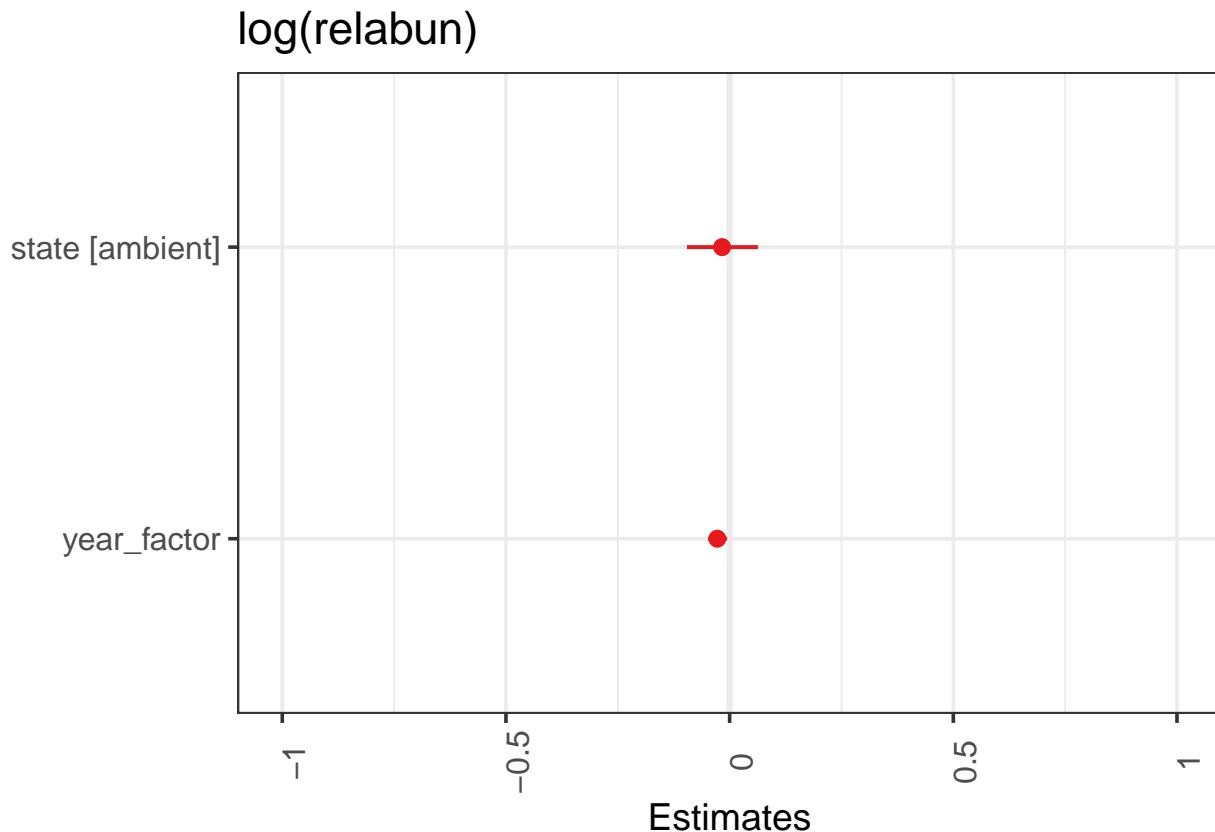
# Does year need to be interactive with state?
mod5 <- lmer(log(relabun) ~ state + year_factor + (1 | species), comp_kbs_spp, REML = FALSE)
anova(mod3, mod5)

## Data: comp_kbs_spp
## Models:
## mod5: log(relabun) ~ state + year_factor + (1 | species)
## mod3: log(relabun) ~ state * year_factor + (1 | species)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5     5 4630.8 4658.3 -2310.4    4620.8
## mod3     6 4632.7 4665.8 -2310.4    4620.7  0.0244  1    0.8758

# No, P>0.05 so state*year_factor doesn't strongly improve model fit so we will
# shift to mod5, but AIC values are super close!!

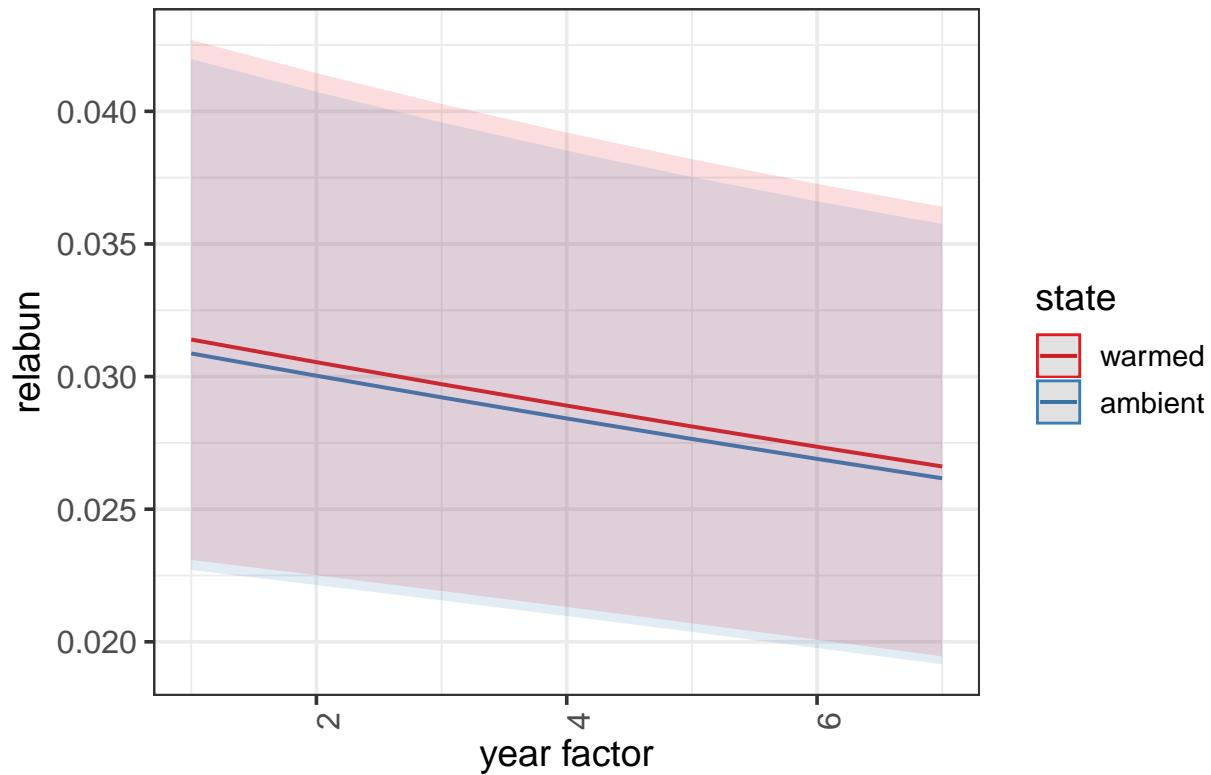
# Plot the fixed effects estimates for different models these are the fixed
# effects estimates from summary(mod5)
plot_model(mod5, sort.est = TRUE)

```



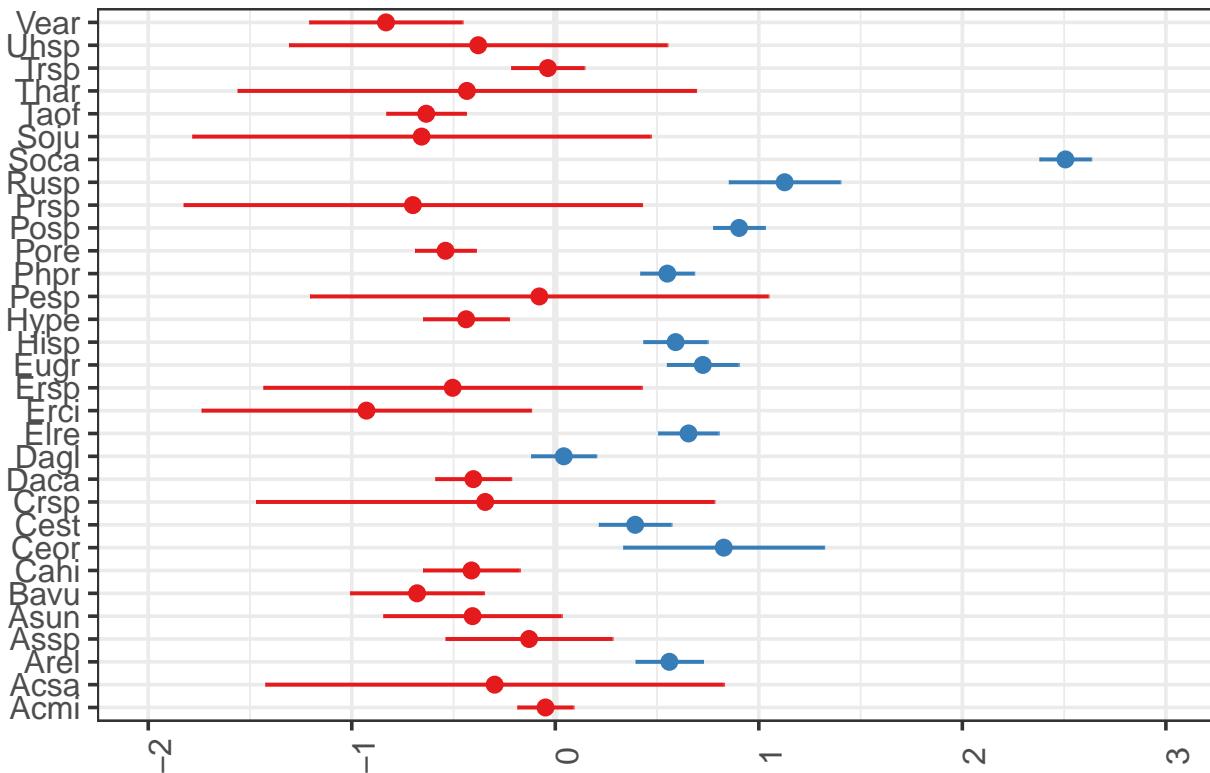
Model has log-transformed response. Back-transforming predictions to original response scale. Standardized residuals.

Predicted values of relabun



```
# these are the random effects estimates
plot_model(mod5, type = "re", terms = c("species"))
```

Random effects



```
# If we wanted to include plots nested within year it would look like this:
mod6 <- lmer(log(relabun) ~ state + year_factor + (1 | species) + (1 + year_factor |
  plot), comp_kbs_spp, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.9e+01
```

```
# Model failed to converge with 1 negative eigenvalue: -1.9e+00
anova(mod5, mod6)
```

```
## Data: comp_kbs_spp
## Models:
## mod5: log(relabun) ~ state + year_factor + (1 | species)
## mod6: log(relabun) ~ state + year_factor + (1 | species) + (1 + year_factor |
##   mod6:   plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5     5 4630.8 4658.3 -2310.4    4620.8
## mod6     8 4636.5 4680.5 -2310.2    4620.5 0.2722  3    0.9652
```

```
anova(mod5)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state     0.1259  0.1259     1 1794.9  0.1784 0.672798
```

```

## year_factor 5.2852 5.2852      1 1803.5 7.4912 0.006261 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# mod4 (and mod5) are pretty complex in terms of interpretation (they actually
# don't have many parameters though). We could consider an alternative model
# that's simpler to understand and also one that provides more insight about the
# species. That would be something like this:
mod7 <- lmer(log(relabun) ~ state + species + (1 + factor(year_factor) | plot), comp_kbs_spp,
              REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7a <- lmer(log(relabun) ~ state + species + factor(year_factor) + (1 | plot),
               comp_kbs_spp, REML = FALSE)
mod7b <- lmer(log(relabun) ~ state * factor(year_factor) + species + (1 | plot),
               comp_kbs_spp, REML = FALSE)
mod7c <- lmer(log(relabun) ~ state + species + factor(year_factor) + insecticide +
               (1 | plot), comp_kbs_spp, REML = FALSE)
anova(mod5, mod7) # model 7 is a better fit to data

## Data: comp_kbs_spp
## Models:
## mod5: log(relabun) ~ state + year_factor + (1 | species)
## mod7: log(relabun) ~ state + species + (1 + factor(year_factor) | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5    5 4630.8 4658.3 -2310.4   4620.8
## mod7   61 4599.4 4935.2 -2238.7  4477.4 143.4 56  1.326e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod7, mod7a) #mod 7a

## Data: comp_kbs_spp
## Models:
## mod7a: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## mod7b: log(relabun) ~ state * factor(year_factor) + species + (1 | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7a   40 4526.0 4746.2 -2223.0   4446.0
## mod7b   61 4599.4 4935.2 -2238.7  4477.4      0 21           1

anova(mod7a, mod7b) #mod 7a - interaction between state and year does not improve model go with simple

## Data: comp_kbs_spp
## Models:
## mod7a: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## mod7b: log(relabun) ~ state * factor(year_factor) + species + (1 | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7a   40 4526 4746.2 -2223.0   4446
## mod7b   46 4533 4786.2 -2220.5  4441 4.9698  6     0.5477

```

```

anova(mod7a, mod7c)  #models are not different than one another, go with simpler model = mod7a

## Data: comp_kbs_spp
## Models:
## mod7a: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## mod7c: log(relabun) ~ state + species + factor(year_factor) + insecticide +
## mod7c:      (1 | plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7a    40 4526.0 4746.2 -2223.0   4446.0
## mod7c    41 4527.9 4753.6 -2222.9   4445.9  0.0743  1     0.7852

summary(mod7a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## Data: comp_kbs_spp
##
##      AIC      BIC  logLik deviance df.resid
## 4526.0 4746.2 -2223.0   4446.0     1778
## 
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.8999 -0.6322 -0.0266  0.6582  3.2129
## 
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.001051 0.03242
## Residual           0.674474 0.82126
## Number of obs: 1818, groups: plot, 24
## 
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) -3.49208  0.08482 991.66088 -41.170 < 2e-16 ***
## stateambient -0.02111  0.04132 25.14843 -0.511 0.613795  
## speciesAcsa  -0.58737  0.82609 1817.09558 -0.711 0.477160  
## speciesArel   0.63389  0.10833 1811.85043  5.852 5.76e-09 ***
## speciesAssp  -0.12894  0.22370 1768.43494 -0.576 0.564410  
## speciesAsun  -0.40312  0.24020 1808.16036 -1.678 0.093466 .
## speciesBavu  -0.66849  0.18219 1816.18706 -3.669 0.000250 ***
## speciesCahi  -0.34196  0.13928 1812.42590 -2.455 0.014176 *  
## speciesCeor   1.05516  0.26968 1718.47460  3.913 9.48e-05 ***
## speciesCest   0.46134  0.11357 1808.59624  4.062 5.07e-05 ***
## speciesCrsp  -0.71193  0.82605 1816.56947 -0.862 0.388890  
## speciesDaca  -0.34892  0.11645 1812.41139 -2.996 0.002770 ** 
## speciesDagl   0.09496  0.10594 1811.04506  0.896 0.370162  
## speciesElre   0.69972  0.10197 1806.27959  6.862 9.31e-12 ***
## speciesErci  -1.25286  0.48151 1817.00942 -2.602 0.009345 ** 
## speciesErsp  -0.74372  0.58684 1817.36081 -1.267 0.205201  
## speciesEugr   0.80724  0.11258 1817.99980  7.170 1.08e-12 ***
## speciesHisp   0.69927  0.10532 1803.72462  6.640 4.15e-11 ***
## speciesHype  -0.39850  0.12673 1816.45240 -3.144 0.001691 **
```

```

## speciesPesp      -0.14053   0.82609 1817.55278 -0.170 0.864939
## speciesPhpr      0.60546   0.09565 1802.00193  6.330 3.09e-10 ***
## speciesPore     -0.48846   0.10192 1808.38590 -4.793 1.78e-06 ***
## speciesPosp      0.95873   0.09383 1799.61063 10.218 < 2e-16 ***
## speciesPrsp     -1.43795   0.82605 1816.56091 -1.741 0.081895 .
## speciesRusp      1.21613   0.15554 1718.13879  7.819 9.24e-15 ***
## speciesSoca      2.57299   0.09383 1799.61063 27.421 < 2e-16 ***
## speciesSoju     -1.38323   0.82612 1817.56258 -1.674 0.094229 .
## speciesTaof     -0.55969   0.12036 1817.98387 -4.650 3.56e-06 ***
## speciesThar     -0.88670   0.82609 1816.97798 -1.073 0.283248
## speciesTrsp      0.06316   0.11413 1806.83812  0.553 0.580073
## speciesUhsp     -0.57186   0.58683 1817.23884 -0.974 0.329945
## speciesVear     -0.76051   0.20647 1817.54411 -3.683 0.000237 ***
## factor(year_factor)2 -0.25667   0.06719 1799.77733 -3.820 0.000138 ***
## factor(year_factor)3  0.19701   0.07426 1807.20791  2.653 0.008046 **
## factor(year_factor)4 -0.10085   0.07125 1808.64692 -1.415 0.157108
## factor(year_factor)5 -0.12596   0.07150 1814.15732 -1.762 0.078301 .
## factor(year_factor)6 -0.10747   0.07254 1815.10992 -1.482 0.138644
## factor(year_factor)7 -0.30491   0.07361 1817.31191 -4.142 3.60e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 38 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

anova(mod7a) # investigates whether at least one of the levels within each factor is significantly different
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state                      0.18   0.176     1    25.15  0.2611  0.6138
## species                   1287.05 42.902    30 1807.33 63.6078 < 2.2e-16 ***
## factor(year_factor)    39.41   6.568     6 1809.89  9.7383 1.401e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

# Yes, at least one of the species is different (they do not all have the same
# relative abundances).
emmeans(mod7c, list(pairwise ~ state + year_factor), adjust = "tukey")
```

```

## $`emmeans of state, year_factor`
##   state  year_factor emmean    SE  df lower.CL upper.CL
##   warmed          1  -3.55 0.0853 996   -3.72   -3.39
##   ambient         1  -3.58 0.0854 1012   -3.74   -3.41
##   warmed         2  -3.81 0.0923 1146   -3.99   -3.63
##   ambient         2  -3.83 0.0919 1156   -4.01   -3.65
##   warmed         3  -3.36 0.0979 1249   -3.55   -3.17
##   ambient         3  -3.38 0.0971 1245   -3.57   -3.19
##   warmed         4  -3.66 0.0951 1185   -3.84   -3.47
##   ambient         4  -3.68 0.0945 1196   -3.86   -3.49
##   warmed         5  -3.68 0.0959 1207   -3.87   -3.49
```

```

## ambient      5 -3.70 0.0947 1199    -3.89    -3.52
## warmed      6 -3.66 0.0967 1215    -3.85    -3.47
## ambient      6 -3.68 0.0957 1209    -3.87    -3.50
## warmed      7 -3.86 0.0975 1207    -4.05    -3.67
## ambient      7 -3.88 0.0966 1217    -4.07    -3.69
##
## Results are averaged over the levels of: species, insecticide
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $'pairwise differences of state, year_factor'
##   1           estimate      SE     df t.ratio p.value
## warmed 1 - ambient 1  0.02174 0.0446   28.6  0.488  1.0000
## warmed 1 - warmed 2  0.25653 0.0679 1835.7  3.779  0.0119
## warmed 1 - ambient 2  0.27827 0.0807  331.9  3.447  0.0405
## warmed 1 - warmed 3 -0.19739 0.0751 1843.3 -2.630  0.3220
## warmed 1 - ambient 3 -0.17565 0.0864  412.7 -2.033  0.7462
## warmed 1 - warmed 4  0.10036 0.0720 1844.1  1.393  0.9828
## warmed 1 - ambient 4  0.12210 0.0840  378.5  1.453  0.9747
## warmed 1 - warmed 5  0.12493 0.0724 1846.8  1.726  0.9067
## warmed 1 - ambient 5  0.14667 0.0836  367.7  1.754  0.8945
## warmed 1 - warmed 6  0.10638 0.0734 1847.8  1.448  0.9759
## warmed 1 - ambient 6  0.12812 0.0848  383.7  1.511  0.9651
## warmed 1 - warmed 7  0.30420 0.0745 1855.0  4.083  0.0037
## warmed 1 - ambient 7  0.32594 0.0857  395.3  3.801  0.0120
## ambient 1 - warmed 2  0.23479 0.0817  344.0  2.874  0.1943
## ambient 1 - ambient 2  0.25653 0.0679 1835.7  3.779  0.0119
## ambient 1 - warmed 3 -0.21913 0.0882  443.6 -2.485  0.4209
## ambient 1 - ambient 3 -0.19739 0.0751 1843.3 -2.630  0.3220
## ambient 1 - warmed 4  0.07862 0.0854  393.5  0.921  0.9997
## ambient 1 - ambient 4  0.10036 0.0720 1844.1  1.393  0.9828
## ambient 1 - warmed 5  0.10319 0.0864  409.0  1.195  0.9957
## ambient 1 - ambient 5  0.12493 0.0724 1846.8  1.726  0.9067
## ambient 1 - warmed 6  0.08464 0.0870  419.6  0.973  0.9995
## ambient 1 - ambient 6  0.10638 0.0734 1847.8  1.448  0.9759
## ambient 1 - warmed 7  0.28246 0.0879  418.3  3.214  0.0802
## ambient 1 - ambient 7  0.30420 0.0745 1855.0  4.083  0.0037
## warmed 2 - ambient 2  0.02174 0.0446   28.6  0.488  1.0000
## warmed 2 - warmed 3 -0.45392 0.0740 1841.2 -6.133 <.0001
## warmed 2 - ambient 3 -0.43218 0.0860  405.9 -5.027  0.0001
## warmed 2 - warmed 4 -0.15617 0.0710 1843.9 -2.200  0.6298
## warmed 2 - ambient 4 -0.13443 0.0836  371.0 -1.608  0.9433
## warmed 2 - warmed 5 -0.13160 0.0713 1845.5 -1.846  0.8546
## warmed 2 - ambient 5 -0.10986 0.0831  360.5 -1.321  0.9889
## warmed 2 - warmed 6 -0.15015 0.0729 1844.8 -2.061  0.7281
## warmed 2 - ambient 6 -0.12841 0.0847  384.5 -1.515  0.9643
## warmed 2 - warmed 7  0.04767 0.0739 1854.1  0.645  1.0000
## warmed 2 - ambient 7  0.06941 0.0857  394.9  0.810  0.9999
## ambient 2 - warmed 3 -0.47566 0.0868  424.5 -5.478 <.0001
## ambient 2 - ambient 3 -0.45392 0.0740 1841.2 -6.133 <.0001
## ambient 2 - warmed 4 -0.17791 0.0841  373.9 -2.117  0.6894
## ambient 2 - ambient 4 -0.15617 0.0710 1843.9 -2.200  0.6298
## ambient 2 - warmed 5 -0.15334 0.0850  389.5 -1.804  0.8734

```

```

## ambient 2 - ambient 5 -0.13160 0.0713 1845.5 -1.846 0.8546
## ambient 2 - warmed 6 -0.17189 0.0861 408.3 -1.997 0.7690
## ambient 2 - ambient 6 -0.15015 0.0729 1844.8 -2.061 0.7281
## ambient 2 - warmed 7 0.02593 0.0869 405.9 0.298 1.0000
## ambient 2 - ambient 7 0.04767 0.0739 1854.1 0.645 1.0000
## warmed 3 - ambient 3 0.02174 0.0446 28.6 0.488 1.0000
## warmed 3 - warmed 4 0.29775 0.0770 1839.8 3.865 0.0086
## warmed 3 - ambient 4 0.31949 0.0892 468.1 3.581 0.0255
## warmed 3 - warmed 5 0.32233 0.0774 1840.3 4.164 0.0026
## warmed 3 - ambient 5 0.34406 0.0889 459.0 3.872 0.0092
## warmed 3 - warmed 6 0.30377 0.0783 1843.1 3.881 0.0081
## warmed 3 - ambient 6 0.32551 0.0899 471.9 3.622 0.0222
## warmed 3 - warmed 7 0.50159 0.0790 1854.5 6.348 <.0001
## warmed 3 - ambient 7 0.52333 0.0905 473.9 5.780 <.0001
## ambient 3 - warmed 4 0.27602 0.0888 451.4 3.108 0.1071
## ambient 3 - ambient 4 0.29775 0.0770 1839.8 3.865 0.0086
## ambient 3 - warmed 5 0.30059 0.0898 469.8 3.348 0.0537
## ambient 3 - ambient 5 0.32233 0.0774 1840.3 4.164 0.0026
## ambient 3 - warmed 6 0.28204 0.0903 477.3 3.123 0.1026
## ambient 3 - ambient 6 0.30377 0.0783 1843.1 3.881 0.0081
## ambient 3 - warmed 7 0.47985 0.0909 465.5 5.279 <.0001
## ambient 3 - ambient 7 0.50159 0.0790 1854.5 6.348 <.0001
## warmed 4 - ambient 4 0.02174 0.0446 28.6 0.488 1.0000
## warmed 4 - warmed 5 0.02457 0.0746 1839.9 0.330 1.0000
## warmed 4 - ambient 5 0.04631 0.0862 410.4 0.537 1.0000
## warmed 4 - warmed 6 0.00602 0.0752 1843.9 0.080 1.0000
## warmed 4 - ambient 6 0.02776 0.0869 418.1 0.319 1.0000
## warmed 4 - warmed 7 0.20384 0.0764 1853.0 2.668 0.2984
## warmed 4 - ambient 7 0.22558 0.0881 431.6 2.562 0.3684
## ambient 4 - warmed 5 0.00283 0.0876 437.5 0.032 1.0000
## ambient 4 - ambient 5 0.02457 0.0746 1839.9 0.330 1.0000
## ambient 4 - warmed 6 -0.01572 0.0878 439.7 -0.179 1.0000
## ambient 4 - ambient 6 0.00602 0.0752 1843.9 0.080 1.0000
## ambient 4 - warmed 7 0.18210 0.0889 439.8 2.049 0.7353
## ambient 4 - ambient 7 0.20384 0.0764 1853.0 2.668 0.2984
## warmed 5 - ambient 5 0.02174 0.0446 28.6 0.488 1.0000
## warmed 5 - warmed 6 -0.01855 0.0755 1836.4 -0.246 1.0000
## warmed 5 - ambient 6 0.00319 0.0879 442.1 0.036 1.0000
## warmed 5 - warmed 7 0.17927 0.0765 1846.5 2.344 0.5219
## warmed 5 - ambient 7 0.20100 0.0888 454.3 2.264 0.5828
## ambient 5 - warmed 6 -0.04029 0.0874 436.7 -0.461 1.0000
## ambient 5 - ambient 6 -0.01855 0.0755 1836.4 -0.246 1.0000
## ambient 5 - warmed 7 0.15753 0.0882 435.4 1.785 0.8818
## ambient 5 - ambient 7 0.17927 0.0765 1846.5 2.344 0.5219
## warmed 6 - ambient 6 0.02174 0.0446 28.6 0.488 1.0000
## warmed 6 - warmed 7 0.19782 0.0768 1845.7 2.575 0.3570
## warmed 6 - ambient 7 0.21956 0.0888 457.5 2.471 0.4305
## ambient 6 - warmed 7 0.17608 0.0888 443.8 1.983 0.7774
## ambient 6 - ambient 7 0.19782 0.0768 1845.7 2.575 0.3570
## warmed 7 - ambient 7 0.02174 0.0446 28.6 0.488 1.0000
##
## Results are averaged over the levels of: species, insecticide
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.

```

```

## P value adjustment: tukey method for comparing a family of 14 estimates

emmeans(mod7c, list(pairwise ~ year_factor), adjust = "tukey")

## $`emmeans of year_factor`
##   year_factor emmean      SE  df lower.CL upper.CL
##       1     -3.57 0.0824 1532    -3.73    -3.40
##       2     -3.82 0.0894 1618    -4.00    -3.65
##       3     -3.37 0.0949 1663    -3.55    -3.18
##       4     -3.67 0.0921 1633    -3.85    -3.49
##       5     -3.69 0.0926 1641    -3.87    -3.51
##       6     -3.67 0.0936 1642    -3.86    -3.49
##       7     -3.87 0.0945 1634    -4.06    -3.68
##
## Results are averaged over the levels of: state, species, insecticide
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor`
##   1 estimate      SE  df t.ratio p.value
##   1 - 2  0.25653 0.0679 1836  3.779  0.0031
##   1 - 3 -0.19739 0.0751 1843 -2.630  0.1177
##   1 - 4  0.10036 0.0720 1844  1.393  0.8057
##   1 - 5  0.12493 0.0724 1847  1.726  0.5984
##   1 - 6  0.10638 0.0734 1848  1.448  0.7752
##   1 - 7  0.30420 0.0745 1855  4.083  0.0009
##   2 - 3 -0.45392 0.0740 1841 -6.133 <.0001
##   2 - 4 -0.15617 0.0710 1844 -2.200  0.2960
##   2 - 5 -0.13160 0.0713 1845 -1.846  0.5167
##   2 - 6 -0.15015 0.0729 1845 -2.061  0.3766
##   2 - 7  0.04767 0.0739 1854  0.645  0.9953
##   3 - 4  0.29775 0.0770 1840  3.865  0.0022
##   3 - 5  0.32233 0.0774 1840  4.164  0.0006
##   3 - 6  0.30377 0.0783 1843  3.881  0.0021
##   3 - 7  0.50159 0.0790 1855  6.348 <.0001
##   4 - 5  0.02457 0.0746 1840  0.330  0.9999
##   4 - 6  0.00602 0.0752 1844  0.080  1.0000
##   4 - 7  0.20384 0.0764 1853  2.668  0.1070
##   5 - 6 -0.01855 0.0755 1836 -0.246  1.0000
##   5 - 7  0.17927 0.0765 1847  2.344  0.2235
##   6 - 7  0.19782 0.0768 1846  2.575  0.1341
##
## Results are averaged over the levels of: state, species, insecticide
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 7 estimates
```

```
emmeans(mod7c, list(pairwise ~ species), adjust = "tukey")
```

```
## $`emmeans of species`
##   species emmean      SE  df lower.CL upper.CL
##   Acmi     -3.60 0.0705 1349    -3.74    -3.464
```

```

##   Acsa    -4.18 0.8331 1856    -5.82    -2.550
##   Arel    -2.97 0.0849 1530    -3.14    -2.802
##   Assp    -3.73 0.2164 1760    -4.16    -3.307
##   Asun    -4.00 0.2328 1858    -4.46    -3.548
##   Bavu    -4.27 0.1710 1799    -4.61    -3.936
##   Cahi    -3.94 0.1230 1796    -4.19    -3.703
##   Ceor    -2.55 0.2653 1730    -3.07    -2.025
##   Cest    -3.14 0.0924 1649    -3.32    -2.959
##   Crsp    -4.32 0.8331 1855    -5.95    -2.685
##   Daca    -3.95 0.0958 1651    -4.14    -3.764
##   Dagl    -3.51 0.0819 1516    -3.67    -3.347
##   Elre    -2.90 0.0762 1477    -3.05    -2.753
##   Erci    -4.85 0.4827 1855    -5.80    -3.903
##   Ersp    -4.34 0.5901 1857    -5.50    -3.183
##   Eugr    -2.80 0.0906 1512    -2.97    -2.618
##   Hisp    -2.90 0.0813 1555    -3.06    -2.743
##   Hype    -4.00 0.1082 1632    -4.21    -3.789
##   Pesp    -3.74 0.8332 1857    -5.37    -2.103
##   Phpr    -3.00 0.0677 1288    -3.13    -2.865
##   Pore    -4.09 0.0767 1445    -4.24    -3.940
##   Posp    -2.64 0.0650 1221    -2.77    -2.516
##   Prsp    -5.04 0.8330 1855    -6.68    -3.411
##   Rusp    -2.39 0.1424 1625    -2.67    -2.110
##   Soca    -1.03 0.0650 1221    -1.16    -0.902
##   Soju    -4.99 0.8331 1857    -6.62    -3.357
##   Taof    -4.16 0.1006 1641    -4.36    -3.964
##   Thar    -4.49 0.8330 1856    -6.13    -2.860
##   Trsp    -3.54 0.0928 1677    -3.72    -3.356
##   Uhsp    -4.17 0.5898 1857    -5.33    -3.017
##   Vear    -4.36 0.1973 1850    -4.75    -3.975
##
## Results are averaged over the levels of: state, year_factor, insecticide
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $'pairwise differences of species'
##   1          estimate   SE   df t.ratio p.value
##   Acmi - Acsa  0.582108 0.8359 1855   0.696 1.0000
##   Acmi - Arel -0.633467 0.1095 1849  -5.784 <.0001
##   Acmi - Assp  0.128765 0.2271 1825   0.567 1.0000
##   Acmi - Asun  0.402109 0.2428 1844   1.656 0.9991
##   Acmi - Bavu  0.669236 0.1845 1858   3.627 0.0800
##   Acmi - Cahi  0.341751 0.1408 1850   2.427 0.8401
##   Acmi - Ceor -1.057298 0.2741 1777  -3.858 0.0370
##   Acmi - Cest -0.461745 0.1148 1845  -4.022 0.0203
##   Acmi - Crsp  0.716188 0.8358 1854   0.857 1.0000
##   Acmi - Daca  0.349205 0.1177 1850   2.966 0.4265
##   Acmi - Dagl -0.094473 0.1071 1848  -0.882 1.0000
##   Acmi - Elre -0.699406 0.1031 1843  -6.786 <.0001
##   Acmi - Erci  1.247405 0.4874 1853   2.559 0.7536
##   Acmi - Ersp  0.738157 0.5940 1855   1.243 1.0000
##   Acmi - Eugr -0.806820 0.1139 1858  -7.081 <.0001
##   Acmi - Hisp -0.700174 0.1065 1837  -6.577 <.0001

```

```

##  Acmi - Hype  0.398653 0.1283 1858   3.107 0.3215
##  Acmi - Pesp  0.134709 0.8359 1857   0.161 1.0000
##  Acmi - Phpr  -0.604969 0.0967 1837  -6.259 <.0001
##  Acmi - Pore  0.488170 0.1030 1845   4.739 0.0010
##  Acmi - Posp  -0.958538 0.0948 1835 -10.111 <.0001
##  Acmi - Prsp  1.442073 0.8358 1854   1.725 0.9981
##  Acmi - Rusp  -1.213359 0.1583 1803  -7.666 <.0001
##  Acmi - Soca  -2.572800 0.0948 1835 -27.139 <.0001
##  Acmi - Soju  1.388351 0.8359 1857   1.661 0.9990
##  Acmi - Taof  0.559274 0.1218 1858   4.591 0.0019
##  Acmi - Thar  0.891495 0.8358 1855   1.067 1.0000
##  Acmi - Trsp  -0.063942 0.1154 1842  -0.554 1.0000
##  Acmi - Uhsp  0.571607 0.5937 1856   0.963 1.0000
##  Acmi - Vear  0.760036 0.2089 1856   3.638 0.0772
##  Acsa - Arel  -1.215575 0.8375 1855  -1.451 0.9999
##  Acsa - Assp  -0.453343 0.8606 1858  -0.527 1.0000
##  Acsa - Asun  -0.179999 0.8653 1854  -0.208 1.0000
##  Acsa - Bavu  0.087128 0.8503 1856   0.102 1.0000
##  Acsa - Cahi  -0.240357 0.8423 1856  -0.285 1.0000
##  Acsa - Ceor  -1.639406 0.8741 1858  -1.875 0.9927
##  Acsa - Cest  -1.043853 0.8379 1856  -1.246 1.0000
##  Acsa - Crsp  0.134080 1.1767 1854   0.114 1.0000
##  Acsa - Daca  -0.232904 0.8384 1856  -0.278 1.0000
##  Acsa - Dagl  -0.676581 0.8371 1856  -0.808 1.0000
##  Acsa - Elre  -1.281514 0.8368 1856  -1.532 0.9998
##  Acsa - Erci  0.665297 0.9604 1856   0.693 1.0000
##  Acsa - Ersp  0.156049 1.0186 1857   0.153 1.0000
##  Acsa - Eugr  -1.388928 0.8377 1855  -1.658 0.9990
##  Acsa - Hisp  -1.282282 0.8366 1855  -1.533 0.9998
##  Acsa - Hype  -0.183455 0.8397 1856  -0.218 1.0000
##  Acsa - Pesp  -0.447399 1.1765 1857  -0.380 1.0000
##  Acsa - Phpr  -1.187077 0.8358 1856  -1.420 1.0000
##  Acsa - Pore  -0.093938 0.8365 1856  -0.112 1.0000
##  Acsa - Posp  -1.540646 0.8355 1856  -1.844 0.9944
##  Acsa - Prsp  0.859965 1.1767 1854   0.731 1.0000
##  Acsa - Rusp  -1.795467 0.8453 1856  -2.124 0.9604
##  Acsa - Soca  -3.154909 0.8355 1856  -3.776 0.0491
##  Acsa - Soju  0.806243 1.1765 1857   0.685 1.0000
##  Acsa - Taof  -0.022834 0.8386 1854  -0.027 1.0000
##  Acsa - Thar  0.309387 1.1764 1856   0.263 1.0000
##  Acsa - Trsp  -0.646050 0.8376 1856  -0.771 1.0000
##  Acsa - Uhsp  -0.010501 1.0187 1857  -0.010 1.0000
##  Acsa - Vear  0.177927 0.8560 1857   0.208 1.0000
##  Arel - Assp  0.762232 0.2322 1815   3.282 0.2132
##  Arel - Asun  1.035576 0.2474 1847   4.185 0.0108
##  Arel - Bavu  1.302702 0.1902 1858   6.848 <.0001
##  Arel - Cahi  0.975218 0.1492 1857   6.535 <.0001
##  Arel - Ceor  -0.423831 0.2782 1779  -1.523 0.9998
##  Arel - Cest  0.171722 0.1252 1857   1.372 1.0000
##  Arel - Crsp  1.349654 0.8373 1854   1.612 0.9994
##  Arel - Daca  0.982671 0.1274 1856   7.715 <.0001
##  Arel - Dagl  0.538994 0.1168 1849   4.613 0.0017
##  Arel - Elre  -0.065939 0.1129 1852  -0.584 1.0000
##  Arel - Erci  1.880872 0.4901 1853   3.837 0.0397

```

```

##  Arel - Ersp  1.371623 0.5961 1854   2.301 0.9035
##  Arel - Eugr -0.173353 0.1232 1857  -1.407 1.0000
##  Arel - Hisp -0.066707 0.1168 1850  -0.571 1.0000
##  Arel - Hype  1.032120 0.1368 1858   7.544 <.0001
##  Arel - Pesp  0.768176 0.8377 1857   0.917 1.0000
##  Arel - Phpr  0.028498 0.1076 1852   0.265 1.0000
##  Arel - Pore  1.121636 0.1135 1853   9.880 <.0001
##  Arel - Posp -0.325071 0.1060 1852  -3.067 0.3493
##  Arel - Prsp  2.075540 0.8372 1853   2.479 0.8082
##  Arel - Rusp -0.579892 0.1649 1827  -3.518 0.1119
##  Arel - Soca -1.939334 0.1060 1852 -18.300 <.0001
##  Arel - Soju  2.021818 0.8375 1857   2.414 0.8473
##  Arel - Taof  1.192741 0.1309 1858   9.111 <.0001
##  Arel - Thar  1.524962 0.8373 1855   1.821 0.9954
##  Arel - Trsp  0.569525 0.1251 1850   4.552 0.0023
##  Arel - Uhsp  1.205074 0.5960 1857   2.022 0.9788
##  Arel - Vear  1.393502 0.2146 1856   6.495 <.0001
##  Assp - Asun  0.273343 0.3188 1853   0.858 1.0000
##  Assp - Bavu  0.540470 0.2753 1843   1.963 0.9859
##  Assp - Cahi  0.212985 0.2480 1853   0.859 1.0000
##  Assp - Ceor -1.186063 0.3423 1768  -3.465 0.1305
##  Assp - Cest -0.590511 0.2348 1828  -2.515 0.7842
##  Assp - Crsp  0.587422 0.8595 1848   0.683 1.0000
##  Assp - Daca  0.220439 0.2355 1852   0.936 1.0000
##  Assp - Dagl -0.223239 0.2310 1828  -0.966 1.0000
##  Assp - Elre -0.828171 0.2291 1820  -3.614 0.0834
##  Assp - Erci  1.118639 0.5284 1857   2.117 0.9619
##  Assp - Ersp  0.609391 0.6283 1858   0.970 1.0000
##  Assp - Eugr -0.935585 0.2339 1841  -3.999 0.0221
##  Assp - Hisp -0.828939 0.2308 1836  -3.592 0.0894
##  Assp - Hype  0.269888 0.2415 1831   1.118 1.0000
##  Assp - Pesp  0.005943 0.8607 1858   0.007 1.0000
##  Assp - Phpr -0.733734 0.2262 1825  -3.243 0.2350
##  Assp - Pore  0.359404 0.2290 1836   1.570 0.9996
##  Assp - Posp -1.087303 0.2255 1821  -4.821 0.0007
##  Assp - Prsp  1.313308 0.8606 1857   1.526 0.9998
##  Assp - Rusp -1.342124 0.2583 1839  -5.196 0.0001
##  Assp - Soca -2.701566 0.2255 1821 -11.979 <.0001
##  Assp - Soju  1.259586 0.8606 1858   1.464 0.9999
##  Assp - Taof  0.430508 0.2382 1833   1.808 0.9959
##  Assp - Thar  0.762730 0.8603 1856   0.887 1.0000
##  Assp - Trsp -0.192707 0.2347 1844  -0.821 1.0000
##  Assp - Uhsp  0.442842 0.6280 1858   0.705 1.0000
##  Assp - Vear  0.631270 0.2916 1857   2.165 0.9503
##  Asun - Bavu  0.267127 0.2888 1858   0.925 1.0000
##  Asun - Cahi -0.060358 0.2631 1849  -0.229 1.0000
##  Asun - Ceor -1.459407 0.3525 1844  -4.140 0.0129
##  Asun - Cest -0.863854 0.2499 1844  -3.456 0.1336
##  Asun - Crsp  0.314079 0.8653 1855   0.363 1.0000
##  Asun - Daca -0.052904 0.2518 1848  -0.210 1.0000
##  Asun - Dagl -0.496582 0.2462 1850  -2.017 0.9795
##  Asun - Elre -1.101515 0.2444 1847  -4.508 0.0028
##  Asun - Erci  0.845296 0.5361 1853   1.577 0.9996
##  Asun - Ersp  0.336048 0.6344 1853   0.530 1.0000

```

```

##  Asun - Eogr -1.208929 0.2495 1849 -4.845 0.0006
##  Asun - Hisp -1.102283 0.2458 1845 -4.484 0.0031
##  Asun - Hype -0.003456 0.2564 1857 -0.013 1.0000
##  Asun - Pesp -0.267400 0.8650 1856 -0.309 1.0000
##  Asun - Phpr -1.007078 0.2422 1846 -4.157 0.0120
##  Asun - Pore  0.086061 0.2447 1847  0.352 1.0000
##  Asun - Posp -1.360646 0.2413 1845 -5.639 <.0001
##  Asun - Prsp  1.039964 0.8653 1855  1.202 1.0000
##  Asun - Rusp -1.615468 0.2726 1856 -5.926 <.0001
##  Asun - Soca -2.974909 0.2413 1845 -12.328 <.0001
##  Asun - Soju  0.986242 0.8656 1856  1.139 1.0000
##  Asun - Taof  0.157165 0.2531 1850  0.621 1.0000
##  Asun - Thar  0.489386 0.8653 1852  0.566 1.0000
##  Asun - Trsp -0.466051 0.2507 1847 -1.859 0.9936
##  Asun - Uhsp  0.169498 0.6344 1856  0.267 1.0000
##  Asun - Vear  0.357927 0.3054 1851  1.172 1.0000
##  Bavu - Cah -0.327485 0.2101 1858 -1.559 0.9997
##  Bavu - Ceor -1.726533 0.3160 1795 -5.464 <.0001
##  Bavu - Cest -1.130981 0.1946 1855 -5.812 <.0001
##  Bavu - Crsp  0.046952 0.8501 1850  0.055 1.0000
##  Bavu - Daca -0.320031 0.1958 1858 -1.635 0.9993
##  Bavu - Dagl -0.763709 0.1889 1857 -4.042 0.0188
##  Bavu - Elre -1.368642 0.1864 1854 -7.343 <.0001
##  Bavu - Erci  0.578169 0.5126 1857  1.128 1.0000
##  Bavu - Ersp  0.068921 0.6145 1856  0.112 1.0000
##  Bavu - Eogr -1.476056 0.1928 1858 -7.658 <.0001
##  Bavu - Hisp -1.369410 0.1892 1857 -7.239 <.0001
##  Bavu - Hype -0.270582 0.2018 1854 -1.341 1.0000
##  Bavu - Pesp -0.534527 0.8511 1858 -0.628 1.0000
##  Bavu - Phpr -1.274205 0.1833 1856 -6.951 <.0001
##  Bavu - Pore -0.181066 0.1873 1853 -0.967 1.0000
##  Bavu - Posp -1.627773 0.1824 1855 -8.924 <.0001
##  Bavu - Prsp  0.772837 0.8508 1855  0.908 1.0000
##  Bavu - Rusp -1.882595 0.2222 1827 -8.471 <.0001
##  Bavu - Soca -3.242036 0.1824 1855 -17.774 <.0001
##  Bavu - Soju  0.719116 0.8505 1858  0.846 1.0000
##  Bavu - Taof -0.109962 0.1986 1847 -0.554 1.0000
##  Bavu - Thar  0.222259 0.8502 1855  0.261 1.0000
##  Bavu - Trsp -0.733177 0.1945 1858 -3.769 0.0502
##  Bavu - Uhsp -0.097628 0.6144 1858 -0.159 1.0000
##  Bavu - Vear  0.090800 0.2612 1858  0.348 1.0000
##  Cah - Ceor -1.399049 0.2916 1826 -4.797 0.0007
##  Cah - Cest -0.803496 0.1525 1853 -5.270 0.0001
##  Cah - Crsp  0.374437 0.8424 1853  0.444 1.0000
##  Cah - Daca  0.007454 0.1548 1847  0.048 1.0000
##  Cah - Dagl -0.436224 0.1475 1856 -2.958 0.4323
##  Cah - Elre -1.041157 0.1443 1853 -7.216 <.0001
##  Cah - Erci  0.905654 0.4985 1853  1.817 0.9956
##  Cah - Ersp  0.396406 0.6030 1854  0.657 1.0000
##  Cah - Eogr -1.148571 0.1522 1854 -7.546 <.0001
##  Cah - Hisp -1.041925 0.1466 1852 -7.106 <.0001
##  Cah - Hype  0.056902 0.1631 1854  0.349 1.0000
##  Cah - Pesp -0.207042 0.8427 1857 -0.246 1.0000
##  Cah - Phpr -0.946720 0.1397 1852 -6.779 <.0001

```

```

## Cahi - Pore 0.146419 0.1443 1856  1.014 1.0000
## Cahi - Posp -1.300288 0.1384 1852 -9.398 <.0001
## Cahi - Prsp  1.100322 0.8424 1854  1.306 1.0000
## Cahi - Rusp -1.555110 0.1880 1845 -8.272 <.0001
## Cahi - Soca -2.914551 0.1384 1852 -21.066 <.0001
## Cahi - Soju  1.046600 0.8423 1857  1.243 1.0000
## Cahi - Taof  0.217523 0.1580 1858  1.377 1.0000
## Cahi - Thar  0.549744 0.8422 1855  0.653 1.0000
## Cahi - Trsp  -0.405693 0.1529 1844 -2.653 0.6830
## Cahi - Uhsp  0.229856 0.6029 1857  0.381 1.0000
## Cahi - Vear  0.418285 0.2307 1849  1.813 0.9957
## Ceor - Cest  0.595552 0.2801 1781  2.126 0.9599
## Ceor - Crsp  1.773485 0.8741 1858  2.029 0.9778
## Ceor - Daca  1.406502 0.2815 1781  4.997 0.0003
## Ceor - Dagl  0.962824 0.2774 1775  3.471 0.1283
## Ceor - Elre  0.357892 0.2758 1800  1.298 1.0000
## Ceor - Erci  2.304702 0.5500 1857  4.190 0.0105
## Ceor - Ersp  1.795454 0.6450 1848  2.784 0.5758
## Ceor - Eugr  0.250478 0.2800 1770  0.895 1.0000
## Ceor - Hisp  0.357124 0.2765 1785  1.292 1.0000
## Ceor - Hype  1.455951 0.2865 1746  5.081 0.0002
## Ceor - Pesp  1.192006 0.8740 1858  1.364 1.0000
## Ceor - Phpr  0.452329 0.2736 1771  1.653 0.9991
## Ceor - Pore  1.545467 0.2757 1759  5.605 <.0001
## Ceor - Posp  0.098760 0.2727 1786  0.362 1.0000
## Ceor - Prsp  2.499371 0.8741 1858  2.860 0.5128
## Ceor - Rusp  -0.156061 0.3006 1792 -0.519 1.0000
## Ceor - Soca -1.515503 0.2727 1786 -5.557 <.0001
## Ceor - Soju  2.445649 0.8740 1857  2.798 0.5638
## Ceor - Taof  1.616571 0.2829 1783  5.714 <.0001
## Ceor - Thar  1.948793 0.8743 1858  2.229 0.9309
## Ceor - Trsp  0.993356 0.2799 1802  3.549 0.1019
## Ceor - Uhsp  1.628905 0.6462 1858  2.521 0.7805
## Ceor - Vear  1.817333 0.3298 1817  5.510 <.0001
## Cest - Crsp  1.177933 0.8375 1854  1.406 1.0000
## Cest - Daca  0.810950 0.1313 1849  6.176 <.0001
## Cest - Dagl  0.367272 0.1227 1854  2.992 0.4058
## Cest - Elre -0.237661 0.1197 1849 -1.985 0.9835
## Cest - Erci  1.709150 0.4903 1852  3.486 0.1228
## Cest - Ersp  1.199902 0.5965 1856  2.012 0.9802
## Cest - Eugr -0.345075 0.1288 1858 -2.679 0.6616
## Cest - Hisp -0.238429 0.1214 1842 -1.965 0.9857
## Cest - Hype  0.860399 0.1414 1858  6.083 <.0001
## Cest - Pesp  0.596454 0.8376 1857  0.712 1.0000
## Cest - Phpr -0.143224 0.1136 1847 -1.261 1.0000
## Cest - Pore  0.949915 0.1186 1845  8.010 <.0001
## Cest - Posp -0.496792 0.1120 1846 -4.435 0.0038
## Cest - Prsp  1.903818 0.8375 1854  2.273 0.9148
## Cest - Rusp -0.751614 0.1693 1789 -4.439 0.0037
## Cest - Soca -2.111055 0.1120 1846 -18.847 <.0001
## Cest - Soju  1.850097 0.8379 1857  2.208 0.9377
## Cest - Taof  1.021019 0.1350 1858  7.562 <.0001
## Cest - Thar  1.353240 0.8377 1854  1.615 0.9994
## Cest - Trsp  0.397803 0.1290 1847  3.083 0.3382

```

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##  Cest - Uhsp  1.033353 0.5962 1856   1.733 0.9979
##  Cest - Vear  1.221781 0.2167 1857   5.638 <.0001
##  Crsp - Daca -0.366983 0.8379 1853  -0.438 1.0000
##  Crsp - Dagl -0.810661 0.8368 1853  -0.969 1.0000
##  Crsp - Elre -1.415594 0.8367 1854  -1.692 0.9986
##  Crsp - Erci  0.531217 0.9606 1853   0.553 1.0000
##  Crsp - Ersp  0.021969 1.0189 1854   0.022 1.0000
##  Crsp - Eugr -1.523007 0.8377 1853  -1.818 0.9955
##  Crsp - Hisp -1.416361 0.8366 1853  -1.693 0.9986
##  Crsp - Hype -0.317534 0.8398 1854  -0.378 1.0000
##  Crsp - Pesp -0.581479 1.1764 1856  -0.494 1.0000
##  Crsp - Phpr -1.321157 0.8356 1854  -1.581 0.9996
##  Crsp - Pore -0.228018 0.8362 1853  -0.273 1.0000
##  Crsp - Posp -1.674725 0.8355 1854  -2.005 0.9812
##  Crsp - Prsp  0.725885 1.1760 1856   0.617 1.0000
##  Crsp - Rusp -1.929546 0.8441 1852  -2.286 0.9097
##  Crsp - Soca -3.288988 0.8355 1854  -3.937 0.0279
##  Crsp - Soju  0.672164 1.1764 1856   0.571 1.0000
##  Crsp - Taof -0.156914 0.8386 1853  -0.187 1.0000
##  Crsp - Thar  0.175307 1.1763 1855   0.149 1.0000
##  Crsp - Trsp -0.780129 0.8375 1853  -0.931 1.0000
##  Crsp - Uhsp -0.144580 1.0186 1855  -0.142 1.0000
##  Crsp - Vear  0.043848 0.8558 1853   0.051 1.0000
##  Daca - Dagl -0.443678 0.1252 1851  -3.543 0.1036
##  Daca - Elre -1.048610 0.1221 1854  -8.589 <.0001
##  Daca - Erci  0.898200 0.4914 1853   1.828 0.9951
##  Daca - Ersp  0.388952 0.5973 1856   0.651 1.0000
##  Daca - Eugr -1.156024 0.1311 1858  -8.820 <.0001
##  Daca - Hisp -1.049378 0.1244 1846  -8.436 <.0001
##  Daca - Hype  0.049449 0.1437 1858   0.344 1.0000
##  Daca - Pesp -0.214496 0.8384 1857  -0.256 1.0000
##  Daca - Phpr -0.954174 0.1164 1851  -8.201 <.0001
##  Daca - Pore  0.138965 0.1215 1849   1.144 1.0000
##  Daca - Posp -1.307742 0.1149 1852  -11.385 <.0001
##  Daca - Prsp  1.092869 0.8381 1855   1.304 1.0000
##  Daca - Rusp -1.562563 0.1709 1812  -9.142 <.0001
##  Daca - Soca -2.922005 0.1149 1852  -25.438 <.0001
##  Daca - Soju  1.039147 0.8383 1857   1.240 1.0000
##  Daca - Taof  0.210069 0.1379 1858   1.524 0.9998
##  Daca - Thar  0.542290 0.8380 1854   0.647 1.0000
##  Daca - Trsp -0.413146 0.1319 1842  -3.133 0.3036
##  Daca - Uhsp  0.222403 0.5969 1856   0.373 1.0000
##  Daca - Vear  0.410831 0.2183 1852   1.882 0.9923
##  Dagl - Elre -0.604933 0.1108 1845  -5.459 <.0001
##  Dagl - Erci  1.341878 0.4894 1853   2.742 0.6104
##  Dagl - Ersp  0.832630 0.5956 1856   1.398 1.0000
##  Dagl - Eugr -0.712347 0.1212 1858  -5.876 <.0001
##  Dagl - Hisp -0.605701 0.1145 1846  -5.290 0.0001
##  Dagl - Hype  0.493127 0.1349 1858   3.657 0.0729
##  Dagl - Pesp  0.229182 0.8373 1858   0.274 1.0000
##  Dagl - Phpr -0.510496 0.1052 1843  -4.854 0.0006
##  Dagl - Pore  0.582643 0.1112 1849   5.239 0.0001
##  Dagl - Posp -0.864064 0.1036 1847  -8.344 <.0001
##  Dagl - Prsp  1.536546 0.8368 1854   1.836 0.9947

```

```

## Dagl - Rusp -1.118886 0.1633 1824 -6.850 <.0001
## Dagl - Soca -2.478327 0.1036 1847 -23.933 <.0001
## Dagl - Soju 1.482825 0.8370 1856 1.772 0.9970
## Dagl - Taof 0.653747 0.1289 1857 5.074 0.0002
## Dagl - Thar 0.985968 0.8369 1855 1.178 1.0000
## Dagl - Trsp 0.030531 0.1230 1847 0.248 1.0000
## Dagl - Uhsp 0.666080 0.5952 1856 1.119 1.0000
## Dagl - Vear 0.854509 0.2134 1856 4.003 0.0218
## Elre - Erci 1.946811 0.4889 1852 3.982 0.0236
## Elre - Ersp 1.437563 0.5951 1855 2.415 0.8466
## Elre - Eugr -0.107414 0.1175 1858 -0.914 1.0000
## Elre - Hisp -0.000768 0.1109 1843 -0.007 1.0000
## Elre - Hype 1.098059 0.1317 1857 8.339 <.0001
## Elre - Pesp 0.834115 0.8369 1857 0.997 1.0000
## Elre - Phpr 0.094437 0.1009 1837 0.936 1.0000
## Elre - Pore 1.187576 0.1075 1846 11.052 <.0001
## Elre - Posp -0.259132 0.0991 1835 -2.615 0.7123
## Elre - Prsp 2.141479 0.8366 1854 2.560 0.7533
## Elre - Rusp -0.513953 0.1607 1832 -3.197 0.2622
## Elre - Soca -1.873395 0.0991 1835 -18.904 <.0001
## Elre - Soju 2.087757 0.8366 1856 2.496 0.7974
## Elre - Taof 1.258680 0.1257 1856 10.010 <.0001
## Elre - Thar 1.590901 0.8366 1855 1.902 0.9911
## Elre - Trsp 0.635464 0.1198 1844 5.302 0.0001
## Elre - Uhsp 1.271013 0.5948 1856 2.137 0.9574
## Elre - Vear 1.459441 0.2115 1857 6.900 <.0001
## Erci - Ersp -0.509248 0.7591 1857 -0.671 1.0000
## Erci - Eugr -2.054225 0.4909 1855 -4.185 0.0108
## Erci - Hisp -1.947579 0.4886 1853 -3.986 0.0232
## Erci - Hype -0.848751 0.4941 1854 -1.718 0.9982
## Erci - Pesp -1.112696 0.9603 1858 -1.159 1.0000
## Erci - Phpr -1.852374 0.4872 1852 -3.802 0.0449
## Erci - Pore -0.759235 0.4881 1852 -1.555 0.9997
## Erci - Posp -2.205942 0.4868 1853 -4.531 0.0025
## Erci - Prsp 0.194668 0.9607 1854 0.203 1.0000
## Erci - Rusp -2.460764 0.5030 1853 -4.892 0.0005
## Erci - Soca -3.820205 0.4868 1853 -7.847 <.0001
## Erci - Soju 0.140947 0.9610 1856 0.147 1.0000
## Erci - Taof -0.688131 0.4922 1852 -1.398 1.0000
## Erci - Thar -0.355910 0.9609 1854 -0.370 1.0000
## Erci - Trsp -1.311347 0.4903 1852 -2.675 0.6654
## Erci - Uhsp -0.675798 0.7593 1857 -0.890 1.0000
## Erci - Vear -0.487369 0.5208 1850 -0.936 1.0000
## Ersp - Eugr -1.544976 0.5967 1856 -2.589 0.7317
## Ersp - Hisp -1.438331 0.5950 1855 -2.418 0.8454
## Ersp - Hype -0.339503 0.5995 1856 -0.566 1.0000
## Ersp - Pesp -0.603448 1.0186 1858 -0.592 1.0000
## Ersp - Phpr -1.343126 0.5938 1856 -2.262 0.9191
## Ersp - Pore -0.249987 0.5947 1856 -0.420 1.0000
## Ersp - Posp -1.696694 0.5935 1855 -2.859 0.5132
## Ersp - Prsp 0.703916 1.0190 1855 0.691 1.0000
## Ersp - Rusp -1.951515 0.6071 1857 -3.215 0.2517
## Ersp - Soca -3.310957 0.5935 1855 -5.579 <.0001
## Ersp - Soju 0.650195 1.0192 1857 0.638 1.0000

```

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##  Ersp - Taof -0.178883 0.5981 1856 -0.299 1.0000
##  Ersp - Thar  0.153338 1.0191 1855  0.150 1.0000
##  Ersp - Trsp -0.802098 0.5963 1855 -1.345 1.0000
##  Ersp - Uhsp -0.166549 0.8317 1857 -0.200 1.0000
##  Ersp - Vear  0.021879 0.6219 1856  0.035 1.0000
##  Eugr - Hisp  0.106646 0.1207 1858  0.884 1.0000
##  Eugr - Hype  1.205473 0.1402 1856  8.598 <.0001
##  Eugr - Pesp  0.941529 0.8381 1857  1.123 1.0000
##  Eugr - Phpr  0.201851 0.1121 1858  1.801 0.9961
##  Eugr - Pore  1.294989 0.1179 1858 10.987 <.0001
##  Eugr - Posp -0.151718 0.1105 1858 -1.372 1.0000
##  Eugr - Prsp  2.248893 0.8376 1853  2.685 0.6572
##  Eugr - Rusp -0.406539 0.1677 1842 -2.424 0.8419
##  Eugr - Soca -1.765981 0.1105 1858 -15.975 <.0001
##  Eugr - Soju  2.195171 0.8379 1858  2.620 0.7084
##  Eugr - Taof  1.366094 0.1343 1858 10.172 <.0001
##  Eugr - Thar  1.698315 0.8376 1854  2.028 0.9780
##  Eugr - Trsp  0.742878 0.1286 1856  5.778 <.0001
##  Eugr - Uhsp  1.378427 0.5965 1857  2.311 0.8991
##  Eugr - Vear  1.566855 0.2165 1856  7.238 <.0001
##  Hisp - Hype  1.098827 0.1345 1858  8.172 <.0001
##  Hisp - Pesp  0.834883 0.8367 1857  0.998 1.0000
##  Hisp - Phpr  0.095205 0.1049 1840  0.908 1.0000
##  Hisp - Pore  1.188344 0.1105 1839 10.759 <.0001
##  Hisp - Posp -0.258364 0.1031 1838 -2.506 0.7906
##  Hisp - Prsp  2.142247 0.8367 1854  2.560 0.7527
##  Hisp - Rusp -0.513185 0.1635 1816 -3.139 0.2993
##  Hisp - Soca -1.872627 0.1031 1838 -18.163 <.0001
##  Hisp - Soju  2.088525 0.8368 1857  2.496 0.7973
##  Hisp - Taof  1.259448 0.1278 1855  9.852 <.0001
##  Hisp - Thar  1.591669 0.8367 1855  1.902 0.9910
##  Hisp - Trsp  0.636232 0.1215 1840  5.239 0.0001
##  Hisp - Uhsp  1.271781 0.5948 1856  2.138 0.9571
##  Hisp - Vear  1.460209 0.2123 1856  6.877 <.0001
##  Hype - Pesp -0.263945 0.8401 1858 -0.314 1.0000
##  Hype - Phpr -1.003622 0.1268 1858 -7.917 <.0001
##  Hype - Pore  0.089516 0.1319 1857  0.679 1.0000
##  Hype - Posp -1.357191 0.1254 1857 -10.821 <.0001
##  Hype - Prsp  1.043420 0.8394 1852  1.243 1.0000
##  Hype - Rusp -1.612012 0.1782 1824 -9.048 <.0001
##  Hype - Soca -2.971454 0.1254 1857 -23.692 <.0001
##  Hype - Soju  0.989698 0.8398 1857  1.178 1.0000
##  Hype - Taof  0.160620 0.1469 1855  1.093 1.0000
##  Hype - Thar  0.492842 0.8398 1856  0.587 1.0000
##  Hype - Trsp -0.462595 0.1415 1858 -3.268 0.2209
##  Hype - Uhsp  0.172954 0.5993 1858  0.289 1.0000
##  Hype - Vear  0.361382 0.2244 1856  1.610 0.9994
##  Pesp - Phpr -0.739678 0.8359 1857 -0.885 1.0000
##  Pesp - Pore  0.353461 0.8364 1857  0.423 1.0000
##  Pesp - Posp -1.093246 0.8357 1857 -1.308 1.0000
##  Pesp - Prsp  1.307364 1.1764 1856  1.111 1.0000
##  Pesp - Rusp -1.348068 0.8454 1858 -1.595 0.9995
##  Pesp - Soca -2.707509 0.8357 1857 -3.240 0.2368
##  Pesp - Soju  1.253643 1.1771 1857  1.065 1.0000

```

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##  Pesp - Taof  0.424565  0.8390  1857   0.506 1.0000
##  Pesp - Thar  0.756786  1.1769  1856   0.643 1.0000
##  Pesp - Trsp -0.198651  0.8378  1857  -0.237 1.0000
##  Pesp - Uhsp  0.436898  1.0188  1858   0.429 1.0000
##  Pesp - Vear  0.625327  0.8562  1858   0.730 1.0000
##  Phpr - Pore  1.093139  0.1013  1841  10.793 <.0001
##  Phpr - Posp -0.353569  0.0927  1833  -3.813 0.0432
##  Phpr - Prsp  2.047042  0.8356  1854   2.450 0.8265
##  Phpr - Rusp -0.608390  0.1569  1819  -3.878 0.0345
##  Phpr - Soca -1.967831  0.0927  1833 -21.224 <.0001
##  Phpr - Soju  1.993320  0.8357  1857   2.385 0.8631
##  Phpr - Taof  1.164243  0.1204  1858   9.672 <.0001
##  Phpr - Thar  1.496464  0.8356  1855   1.791 0.9965
##  Phpr - Trsp  0.541027  0.1139  1842   4.750 0.0009
##  Phpr - Uhsp  1.176576  0.5934  1856   1.983 0.9838
##  Phpr - Vear  1.365005  0.2081  1856   6.559 <.0001
##  Pore - Posp -1.446707  0.0995  1843 -14.537 <.0001
##  Pore - Prsp  0.953903  0.8362  1854   1.141 1.0000
##  Pore - Rusp -1.701528  0.1609  1825 -10.572 <.0001
##  Pore - Soca -3.060970  0.0995  1843 -30.757 <.0001
##  Pore - Soju  0.900182  0.8365  1857   1.076 1.0000
##  Pore - Taof  0.071104  0.1253  1856   0.568 1.0000
##  Pore - Thar  0.403325  0.8363  1854   0.482 1.0000
##  Pore - Trsp -0.552111  0.1191  1844 -4.637 0.0015
##  Pore - Uhsp  0.083438  0.5944  1857   0.140 1.0000
##  Pore - Vear  0.271866  0.2110  1855   1.288 1.0000
##  Posp - Prsp  2.400611  0.8354  1854   2.873 0.5012
##  Posp - Rusp -0.254821  0.1558  1813  -1.635 0.9992
##  Posp - Soca -1.614263  0.0908  1830 -17.782 <.0001
##  Posp - Soju  2.346889  0.8355  1857   2.809 0.5548
##  Posp - Taof  1.517811  0.1189  1857  12.769 <.0001
##  Posp - Thar  1.850033  0.8354  1855   2.214 0.9357
##  Posp - Trsp  0.894596  0.1123  1843   7.963 <.0001
##  Posp - Uhsp  1.530145  0.5931  1856   2.580 0.7387
##  Posp - Vear  1.718573  0.2073  1857   8.291 <.0001
##  Prsp - Rusp -2.655432  0.8441  1852 -3.146 0.2949
##  Prsp - Soca -4.014874  0.8354  1854 -4.806 0.0007
##  Prsp - Soju -0.053722  1.1764  1856 -0.046 1.0000
##  Prsp - Taof -0.882799  0.8385  1852 -1.053 1.0000
##  Prsp - Thar -0.550578  1.1764  1855 -0.468 1.0000
##  Prsp - Trsp -1.506015  0.8376  1854 -1.798 0.9962
##  Prsp - Uhsp -0.870466  1.0186  1856 -0.855 1.0000
##  Prsp - Vear -0.682038  0.8561  1855 -0.797 1.0000
##  Rusp - Soca -1.359442  0.1558  1813 -8.723 <.0001
##  Rusp - Soju  2.601710  0.8451  1858   3.079 0.3412
##  Rusp - Taof  1.772633  0.1733  1854  10.231 <.0001
##  Rusp - Thar  2.104854  0.8450  1857   2.491 0.8005
##  Rusp - Trsp  1.149417  0.1694  1842   6.787 <.0001
##  Rusp - Uhsp  1.784966  0.6066  1858   2.942 0.4451
##  Rusp - Vear  1.973394  0.2430  1858   8.121 <.0001
##  Soca - Soju  3.961152  0.8355  1857   4.741 0.0010
##  Soca - Taof  3.132074  0.1189  1857  26.349 <.0001
##  Soca - Thar  3.464295  0.8354  1855   4.147 0.0125
##  Soca - Trsp  2.508859  0.1123  1843  22.332 <.0001

```

```

##  Soca - Uhsp  3.144408 0.5931 1856   5.301 0.0001
##  Soca - Vear  3.332836 0.2073 1857  16.080 <.0001
##  Soju - Taof -0.829078 0.8390 1857  -0.988 1.0000
##  Soju - Thar -0.496856 1.1760 1857  -0.422 1.0000
##  Soju - Trsp -1.452293 0.8378 1857  -1.734 0.9979
##  Soju - Uhsp -0.816744 1.0171 1842  -0.803 1.0000
##  Soju - Vear -0.628316 0.8558 1856  -0.734 1.0000
##  Taof - Thar  0.332221 0.8389 1855   0.396 1.0000
##  Taof - Trsp -0.623216 0.1351 1857  -4.612 0.0017
##  Taof - Uhsp  0.012334 0.5979 1857   0.021 1.0000
##  Taof - Vear  0.200762 0.2204 1858   0.911 1.0000
##  Thar - Trsp -0.955437 0.8375 1854  -1.141 1.0000
##  Thar - Uhsp -0.319888 1.0186 1856  -0.314 1.0000
##  Thar - Vear -0.131459 0.8555 1853  -0.154 1.0000
##  Trsp - Uhsp  0.635549 0.5962 1856   1.066 1.0000
##  Trsp - Vear  0.823977 0.2165 1853   3.807 0.0442
##  Uhsp - Vear  0.188428 0.6216 1857   0.303 1.0000
##
## Results are averaged over the levels of: state, year_factor, insecticide
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 31 estimates

```

```
emmeans(mod7c, list(pairwise ~ insecticide), adjust = "tukey")
```

```

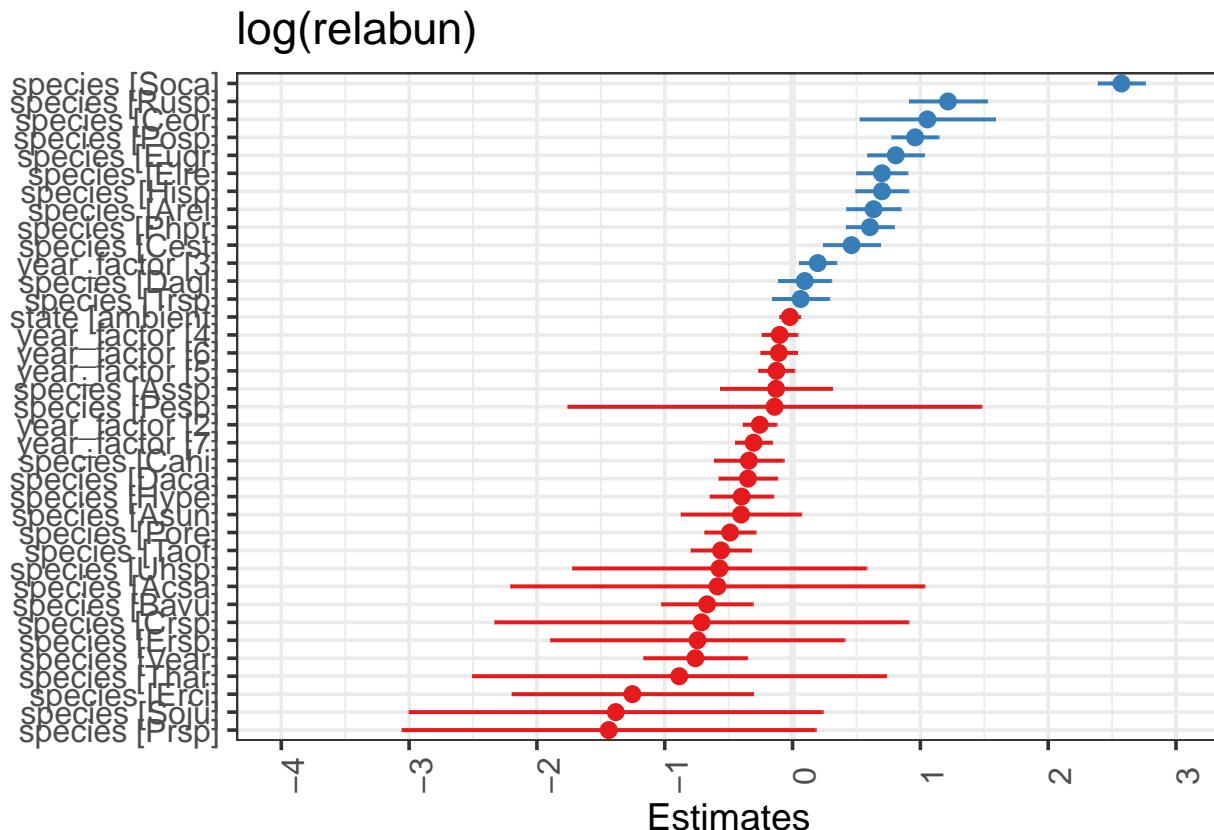
## $`emmeans of insecticide`
##  insecticide emmean    SE  df lower.CL upper.CL
##  insects      -3.67 0.0801 870    -3.83    -3.51
##  no_insects   -3.66 0.0808 852    -3.82    -3.50
##
## Results are averaged over the levels of: state, species, year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of insecticide`
##  1                  estimate     SE  df t.ratio p.value
##  insects - no_insects -0.0113 0.0445 28.2 -0.253  0.8021
## 
## Results are averaged over the levels of: state, species, year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.

```

```

# Take a look at the estimates for each fixed effect. These are the estimates
# from summary(mod7a). You'll see that species vary a lot - and many of them are
# different from zero (meaning their half cover date is significantly different
# from zero).
plot_model(mod7a, sort.est = TRUE)

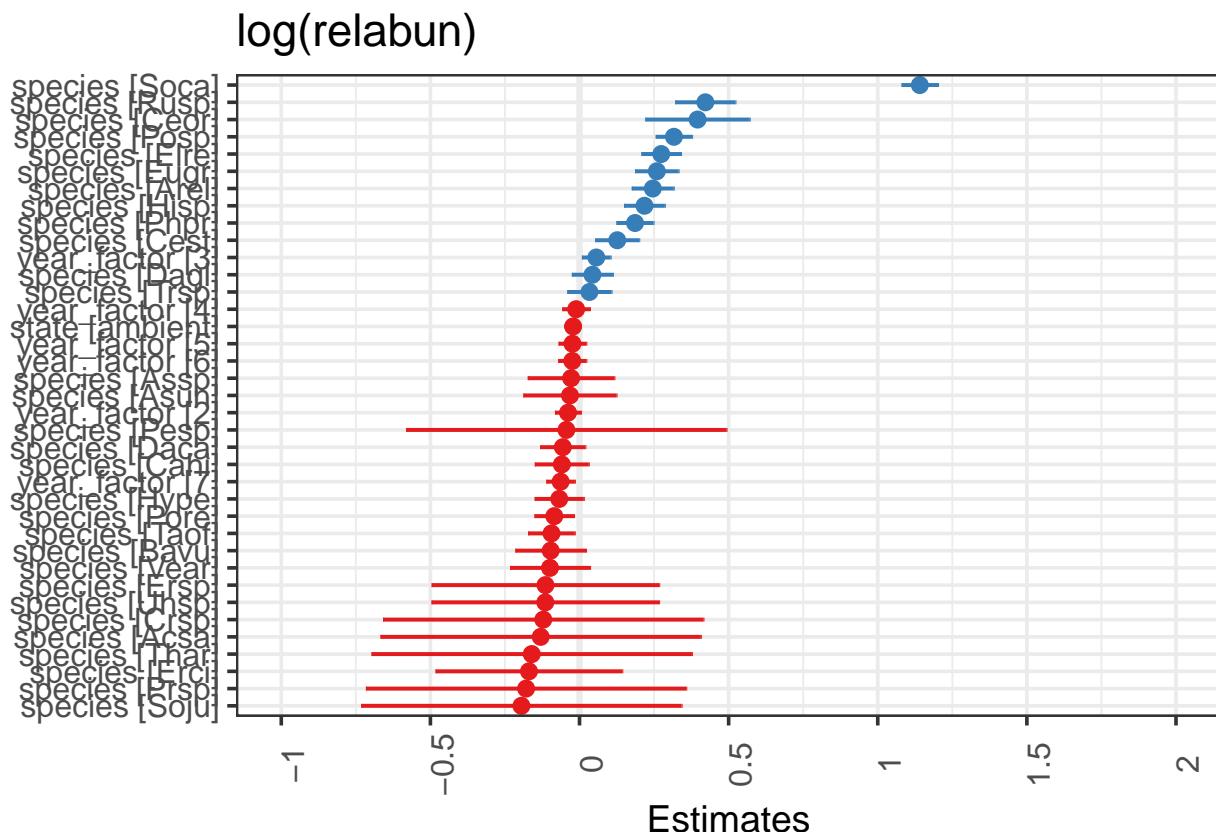
```



```
# if you want to standardize the estimates:
plot_model(mod7a, sort.est = TRUE, type = "std")
```

```
## Formula contains log- or sqrt-terms. See help("standardize") for how such terms are standardized.
```

```
## boundary (singular) fit: see ?isSingular
```

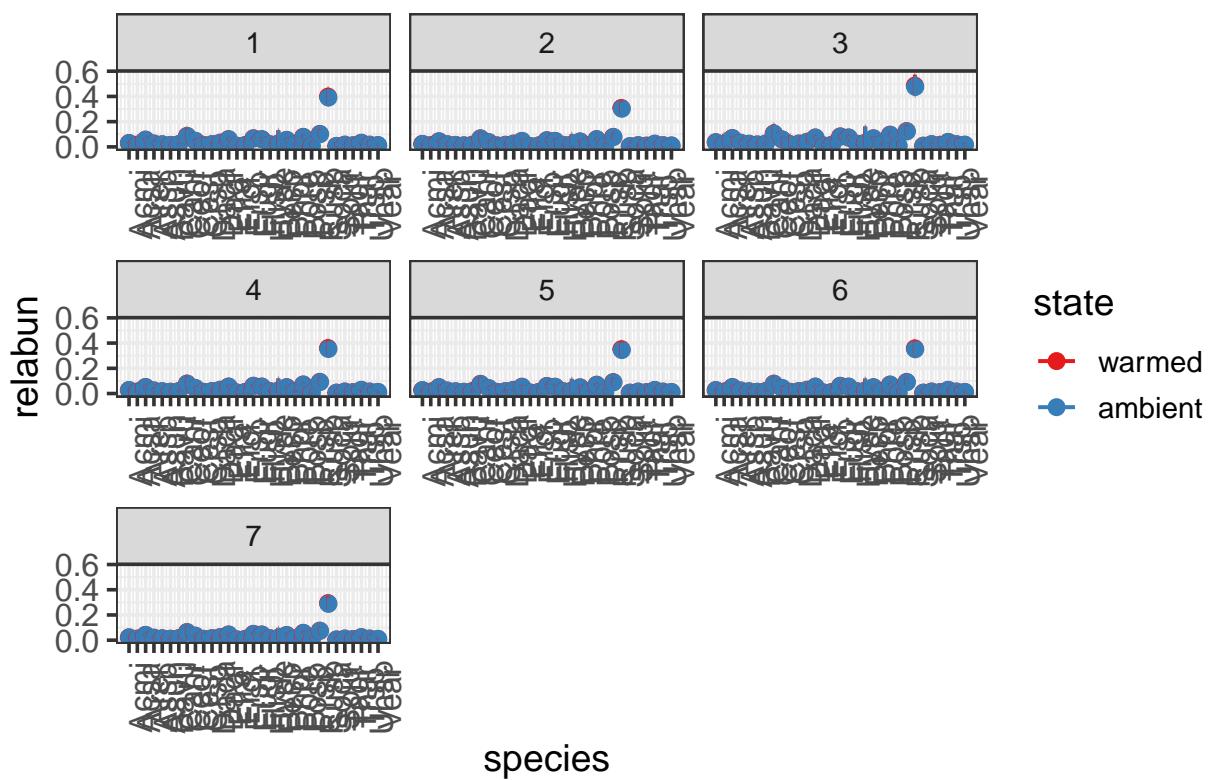


```
# these are the fixed predicted values: - note this is a new plot
```

```
plot_model(mod7a, type = "pred", terms = c("species", "state", "year_factor"))
```

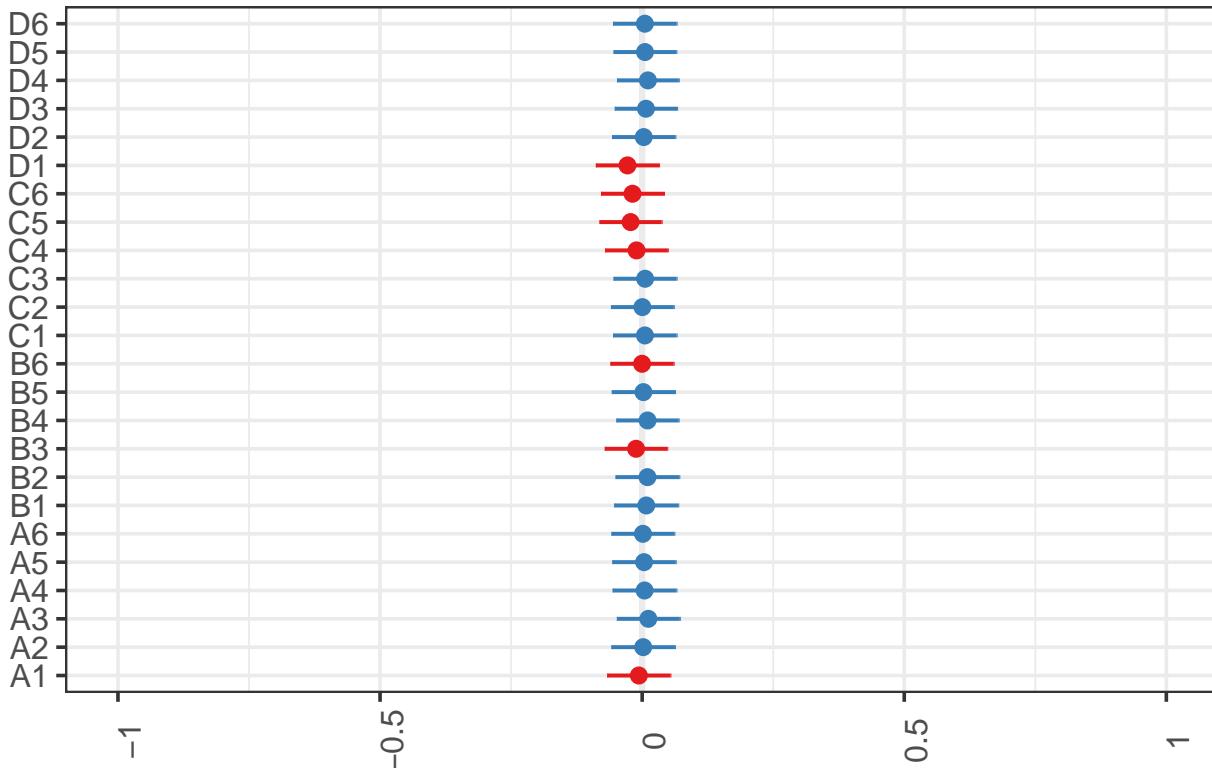
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standardized
```

Predicted values of relabun



```
# these are the random effects estimates  
plot_model(mod7a, type = "re")
```

Random effects



```
# including native vs. exotic
comp_kbs_spp <- within(comp_kbs_spp, origin <- relevel(factor(origin), ref = "Native")) # releveling s
mod8 <- lmer(log(relabun) ~ state * origin + (1 + factor(year_factor) | plot), comp_kbs_spp,
             REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -1.5e+01

mod9 <- lmer(log(relabun) ~ state + origin + (1 + factor(year_factor) | plot), comp_kbs_spp,
              REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -7.4e+00

mod9a <- lmer(log(relabun) ~ state + origin + factor(year_factor) + (1 | plot), comp_kbs_spp,
               REML = FALSE)
anova(mod8, mod9) # model 8 is a better fit to data

## Data: comp_kbs_spp
## Models:
## mod9: log(relabun) ~ state + origin + (1 + factor(year_factor) | plot)
## mod8: log(relabun) ~ state * origin + (1 + factor(year_factor) | plot)
```

```

##      npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9    34 5536.0 5723.2 -2734.0    5468.0
## mod8    37 5533.3 5737.0 -2729.6    5459.3 8.7886  3    0.03224 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod8, mod9a)  # mod 8

## Data: comp_kbs_spp
## Models:
## mod9a: log(relabun) ~ state + origin + factor(year_factor) + (1 | plot)
## mod8: log(relabun) ~ state * origin + (1 + factor(year_factor) | plot)
##      npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## mod9a    13 5463.6 5535.2 -2718.8    5437.6
## mod8     37 5533.3 5737.0 -2729.6    5459.3      0 24             1

summary(mod8)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(relabun) ~ state * origin + (1 + factor(year_factor) | plot)
## Data: comp_kbs_spp
##
##      AIC     BIC logLik deviance df.resid
## 5533.3 5737.0 -2729.6    5459.3      1781
##
## Scaled residuals:
##      Min     1Q Median     3Q     Max
## -2.67336 -0.79469 -0.08668  0.81810  2.85984
##
## Random effects:
## Groups   Name        Variance Std.Dev. Corr
## plot     (Intercept) 2.934e-07 0.0005417
##          factor(year_factor)2 2.321e-02 0.1523378 -1.00
##          factor(year_factor)3 5.661e-02 0.2379337  0.95 -0.95
##          factor(year_factor)4 4.836e-03 0.0695403 -0.59  0.59 -0.31
##          factor(year_factor)5 5.431e-03 0.0736949  0.13 -0.13  0.43  0.73
##          factor(year_factor)6 9.586e-03 0.0979057  0.49 -0.49  0.73  0.41
##          factor(year_factor)7 1.356e-02 0.1164594 -0.93  0.93 -0.77  0.85
## Residual           1.168e+00 1.0806123
##
## 
## 
## 
## 
## 
## 
## 
## 
##      0.93
##      0.25 -0.13
## 
## Number of obs: 1818, groups: plot, 24
## 
## Fixed effects:
##                  Estimate Std. Error      df t value Pr(>|t|)


```

```

## (Intercept)           -2.36885   0.07826  521.17921 -30.270 < 2e-16 ***
## stateambient          0.03527   0.11005  490.02417   0.320   0.749
## origin                -0.54123   0.13816 1773.01682  -3.917  9.29e-05 ***
## originBoth             -0.83563   0.12992 1801.99563  -6.432  1.61e-10 ***
## originExotic           -1.04693   0.09204 1785.75152 -11.375 < 2e-16 ***
## stateambient:origin     0.19590   0.19222 1773.08824   1.019   0.308
## stateambient:originBoth  0.12946   0.17742 1801.88122   0.730   0.466
## stateambient:originExotic -0.19984   0.12856 1789.15296  -1.554   0.120
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn origin orgnBt orgnEx sttmB: sttm:B
## stateambint -0.711
## origin      -0.551  0.392
## originBoth   -0.589  0.419  0.332
## originExotic -0.828  0.589  0.469  0.500
## sttmbnt:rgn  0.396 -0.557 -0.719 -0.239 -0.337
## sttmbnt:rgB  0.431 -0.606 -0.243 -0.732 -0.366  0.345
## sttmbnt:rgE  0.593 -0.833 -0.336 -0.358 -0.716  0.477  0.518
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
anova(mod8)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state       1.25   1.250     1   80.4  1.0705 0.30394
## origin     394.60 131.532     3 1791.6 112.6396 < 2e-16 ***
## state:origin 10.29   3.431     3 1791.6   2.9380 0.03215 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
emmeans(mod8, list(pairwise ~ state * origin), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Model failed to converge with 2 negative eigenvalues: -5.3e-02 -1.4e+01
```

```

## $`emmeans of state, origin`
##    state  origin emmean      SE    df lower.CL upper.CL
##    warmed Native -2.37 0.0842  357.4   -2.53   -2.20
##    ambient Native -2.33 0.0838  361.4   -2.50   -2.17
##    warmed        -2.91 0.1194 1023.9   -3.14   -2.68
##    ambient        -2.68 0.1153  941.9   -2.91   -2.45
##    warmed Both    -3.20 0.1110  681.5   -3.42   -2.99
##    ambient Both    -3.04 0.1012  550.0   -3.24   -2.84
##    warmed Exotic -3.42 0.0603   78.6   -3.54   -3.30
##    ambient Exotic -3.58 0.0590   64.4   -3.70   -3.46
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.

```

```

## Confidence level used: 0.95
##
## $'pairwise differences of state, origin'
## 1
## warmed Native - ambient Native      estimate      SE      df t.ratio p.value
## warmed Native - warmed             0.5412 0.1388 1688.7  3.900  0.0025
## warmed Native - ambient            0.3101 0.1428  673.0  2.172  0.3703
## warmed Native - warmed Both       0.8356 0.1316 1735.9  6.349 <.0001
## warmed Native - ambient Both     0.6709 0.1316  470.0  5.097 <.0001
## warmed Native - warmed Exotic   1.0469 0.0927 1707.4 11.291 <.0001
## warmed Native - ambient Exotic  1.2115 0.1028  191.5 11.785 <.0001
## ambient Native - warmed          0.5765 0.1458  728.3  3.953  0.0021
## ambient Native - ambient         0.3453 0.1343 1693.0  2.571  0.1674
## ambient Native - warmed Both    0.8709 0.1390  560.8  6.264 <.0001
## ambient Native - ambient Both   0.7062 0.1224 1736.8  5.769 <.0001
## ambient Native - warmed Exotic 1.0822 0.1032  201.8 10.487 <.0001
## ambient Native - ambient Exotic 1.2468 0.0905 1709.8 13.784 <.0001
## warmed - ambient                -0.2312 0.1660  986.7 -1.393  0.8607
## warmed - warmed Both            0.2944 0.1568 1732.2  1.877  0.5670
## warmed - ambient Both           0.1297 0.1565  817.8  0.829  0.9915
## warmed - warmed Exotic         0.5057 0.1258 1700.3  4.021  0.0016
## warmed - ambient Exotic        0.6703 0.1332  546.5  5.034 <.0001
## ambient - warmed Both          0.5256 0.1600  840.8  3.284  0.0236
## ambient - ambient Both          0.3608 0.1460 1728.5  2.472  0.2082
## ambient - warmed Exotic        0.7369 0.1301  505.9  5.663 <.0001
## ambient - ambient Exotic       0.9014 0.1205 1712.6  7.483 <.0001
## warmed Both - ambient Both    -0.1647 0.1502  622.3 -1.097  0.9574
## warmed Both - warmed Exotic   0.2113 0.1173 1742.0  1.802  0.6189
## warmed Both - ambient Exotic  0.3759 0.1257  382.6  2.991  0.0587
## ambient Both - warmed Exotic  0.3760 0.1178  308.4  3.193  0.0330
## ambient Both - ambient Exotic 0.5406 0.1063 1737.4  5.085 <.0001
## warmed Exotic - ambient Exotic 0.1646 0.0843  71.5  1.951  0.5213
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 8 estimates

# including growth form - first with interaction term
comp_kbs_spp <- within(comp_kbs_spp, growth_habit <- relevel(factor(growth_habit),
  ref = "Forb")) # releveling so forb is the reference
mod10 <- lmer(log(relabun) ~ state * growth_habit + (1 + factor(year_factor) | plot),
  comp_kbs_spp, REML = FALSE)

## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -1.3e+00

mod11 <- lmer(log(relabun) ~ state + growth_habit + (1 + factor(year_factor) | plot),
  comp_kbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

## Warning: Model failed to converge with 1 negative eigenvalue: -1.0e+01

mod11a <- lmer(log(relabun) ~ state + growth_habit + factor(year_factor) + (1 | plot),
  comp_kbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod10, mod11) # model 10 is a better fit to data

## Data: comp_kbs_spp
## Models:
## mod11: log(relabun) ~ state + growth_habit + (1 + factor(year_factor) |
## mod11:     plot)
## mod10: log(relabun) ~ state * growth_habit + (1 + factor(year_factor) |
## mod10:     plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod11   35 5830.1 6022.8 -2880.0    5760.1
## mod10   38 5827.5 6036.7 -2875.8    5751.5 8.5415  3    0.03605 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod10, mod11a) # model 10 is still a better fit to data

## Data: comp_kbs_spp
## Models:
## mod11a: log(relabun) ~ state + growth_habit + factor(year_factor) + (1 |
## mod11a:     plot)
## mod10: log(relabun) ~ state * growth_habit + (1 + factor(year_factor) |
## mod10:     plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod11a  14 5760.3 5837.3 -2866.1    5732.3
## mod10   38 5827.5 6036.7 -2875.8    5751.5      0 24           1

summary(mod10)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(relabun) ~ state * growth_habit + (1 + factor(year_factor) |
## plot)
## Data: comp_kbs_spp
##
##      AIC      BIC  logLik deviance df.resid
## 5827.5  6036.7 -2875.8    5751.5     1780
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -1.9959 -0.7887 -0.1565  0.6277  2.7346
##
## Random effects:
## Groups   Name            Variance Std.Dev. Corr
## plot     (Intercept) 6.715e-05 0.008194

```

```

##          factor(year_factor)2 3.378e-02 0.183782 -1.00
##          factor(year_factor)3 4.967e-02 0.222869  1.00 -1.00
##          factor(year_factor)4 3.481e-03 0.058997 -1.00  1.00 -1.00
##          factor(year_factor)5 1.110e-03 0.033322 -1.00  1.00 -1.00  1.00
##          factor(year_factor)6 1.753e-03 0.041870 -1.00  1.00 -1.00  1.00  1.00
##          factor(year_factor)7 2.608e-02 0.161501 -1.00  1.00 -1.00  1.00  1.00
##  Residual                      1.374e+00 1.172164
##
##
##
##
##
##
##
##
##      1.00
##
## Number of obs: 1818, groups: plot, 24
##
## Fixed effects:
##                               Estimate Std. Error        df t value
## (Intercept)                -3.21771  0.05692 411.69740 -56.533
## stateambient                 0.01503  0.07841 416.97102   0.192
## growth_habit                  0.02385  0.12775 1802.54595   0.187
## growth_habitGraminoid       0.35613  0.08650 1790.67370   4.117
## growth_habitTree              -0.88473  1.17357 1787.85588  -0.754
## growth_habitVine              -0.46767  0.68172 1768.17413  -0.686
## stateambient:growth_habit      0.09152  0.17019 1801.76954   0.538
## stateambient:growth_habitGraminoid -0.21287  0.12052 1792.90021  -1.766
## stateambient:growth_habitVine     1.63367  0.81608 1747.38696   2.002
##                               Pr(>|t|)
## (Intercept)                < 2e-16 ***
## stateambient                   0.8481
## growth_habit                     0.8519
## growth_habitGraminoid        4.01e-05 ***
## growth_habitTree                  0.4510
## growth_habitVine                  0.4928
## stateambient:growth_habit        0.5908
## stateambient:growth_habitGraminoid 0.0775 .
## stateambient:growth_habitVine      0.0455 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn grwth_ grwt_G grwt_T grwt_V sttm:_ stt:_G
## stateambint -0.726
## growth_habt -0.432  0.314
## grwth_hbtGr -0.648  0.470  0.288
## grwth_hbtTr -0.049  0.035  0.021  0.031
## grwth_hbtVn -0.079  0.057  0.037  0.054  0.004
## sttmbnt:gr_  0.324 -0.447 -0.751 -0.216 -0.016 -0.028
## sttmbnt:g_G  0.465 -0.640 -0.207 -0.718 -0.023 -0.039  0.295
## sttmbnt:g_V  0.066 -0.091 -0.031 -0.045 -0.003 -0.835  0.045  0.062
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient

```

```

## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

anova(mod10)

## Missing cells for: stateambient:growth_habitTree.
## Interpret type III hypotheses with care.

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state        4.8413  4.8413     1 1343.4  3.5236 0.060718 .
## growth_habit 24.9430  6.2358     4 1782.7  4.5385 0.001195 **
## state:growth_habit 11.9517  3.9839     3 1780.8  2.8996 0.033863 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(mod10, list(pairwise ~ factor(year_factor) * growth_habit), adjust = "tukey")

## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -2.4e+01

## Error in emmeans(object = object, specs = specs[[i]], name = contr.name, : No variable named year_fa

# New version of our model incorporating interaction term and species within year
# so that there is a separate intercept and slope for each species. The issue
# here is that there are some species that are not found each year. Easiest to
# remove those from another version of this dataframe before running below.
# Otherwise, it's not a balanced design. updated mod4
mod12 <- lmer(log(relabun) ~ state * factor(year_factor) + (1 + factor(year_factor) |
  species), comp_kbs_spp)

## boundary (singular) fit: see ?isSingular

# So another version of this model would include the interaction but not include
# the nesting (and thus would assume that species aren't observed ea yr) updated
# mod5
mod13 <- lmer(log(relabun) ~ state * factor(year_factor) + (1 | species), comp_kbs_spp)

# All the models ran:
mod1 <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |
  species) + (1 | plot), comp_kbs_spp, REML = FALSE)
mod2 <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |
  species), comp_kbs_spp, REML = FALSE)
mod3 <- lmer(log(relabun) ~ state * year_factor + (1 | species), comp_kbs_spp, REML = FALSE)
mod4 <- lmer(log(relabun) ~ state * year_factor + insecticide + (1 | species) + (1 |
  plot), comp_kbs_spp, REML = FALSE)
mod5 <- lmer(log(relabun) ~ state + year_factor + (1 | species), comp_kbs_spp, REML = FALSE)
mod6 <- lmer(log(relabun) ~ state + year_factor + (1 | species) + (1 + year | plot),
  comp_kbs_spp, REML = FALSE)

```

```

## Error in eval(predvars, data, env): object 'year' not found

mod7 <- lmer(log(relabun) ~ state + species + (1 + factor(year_factor) | plot), comp_kbs_spp,
             REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7a <- lmer(log(relabun) ~ state + species + factor(year_factor) + (1 | plot),
               comp_kbs_spp, REML = FALSE)
mod7b <- lmer(log(relabun) ~ state * factor(year_factor) + species + (1 | plot),
               comp_kbs_spp, REML = FALSE)
mod7c <- lmer(log(relabun) ~ state + species + factor(year_factor) + insecticide +
               (1 | plot), comp_kbs_spp, REML = FALSE)
mod8 <- lmer(log(relabun) ~ state * origin + (1 + factor(year_factor) | plot), comp_kbs_spp,
             REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -1.5e+01

mod9 <- lmer(log(relabun) ~ state + origin + (1 + factor(year_factor) | plot), comp_kbs_spp,
              REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -7.4e+00

mod9a <- lmer(log(relabun) ~ state + origin + factor(year_factor) + (1 | plot), comp_kbs_spp,
               REML = FALSE)
mod10 <- lmer(log(relabun) ~ state * growth_habit + (1 + factor(year_factor) | plot),
               comp_kbs_spp, REML = FALSE)

## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -1.3e+00

mod11 <- lmer(log(relabun) ~ state + growth_habit + (1 + factor(year_factor) | plot),
               comp_kbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -1.0e+01

mod11a <- lmer(log(relabun) ~ state + growth_habit + factor(year_factor) + (1 | plot),
                comp_kbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

mod12 <- lmer(log(relabun) ~ state * factor(year_factor) + (1 + factor(year_factor) | 
  species), comp_kbs_spp)

## boundary (singular) fit: see ?isSingular

mod13 <- lmer(log(relabun) ~ state * factor(year_factor) + (1 | species), comp_kbs_spp)
AICctab(mod1, mod2, mod3, mod5, mod6, mod7, mod7a, mod7b, mod7c, mod8, mod9, mod9a,
  mod10, mod11, mod11a, mod13, weights = T) #mod7a is the best fitting model (took out mod12 bc it w

##          dAICc   df weight
## mod7a      0.0  40  0.721
## mod7c      2.0  41  0.263
## mod7b      7.6  46  0.016
## mod7      75.9  61 <0.001
## mod5     103.0  5  <0.001
## mod3     105.0  6  <0.001
## mod6     108.8  8  <0.001
## mod2     108.9  8  <0.001
## mod1     110.7  9  <0.001
## mod13    115.8 16 <0.001
## mod9a    936.0 13 <0.001
## mod8    1007.0 37 <0.001
## mod9    1009.6 34 <0.001
## mod11a  1232.7 14 <0.001
## mod10   1301.4 38 <0.001
## mod11   1303.7 35 <0.001

summary(mod7a)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## Data: comp_kbs_spp
##
##          AIC      BIC      logLik deviance df.resid
## 4526.0  4746.2 -2223.0   4446.0     1778
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.8999 -0.6322 -0.0266  0.6582  3.2129
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.001051 0.03242
## Residual           0.674474 0.82126
## Number of obs: 1818, groups: plot, 24
##
## Fixed effects:
##                   Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)     -3.49208   0.08482 991.66088 -41.170 < 2e-16 ***
## stateambient   -0.02111   0.04132  25.14843 -0.511  0.613795

```

```

## speciesAcsa      -0.58737   0.82609 1817.09558 -0.711 0.477160
## speciesArel      0.63389   0.10833 1811.85043  5.852 5.76e-09 ***
## speciesAssp     -0.12894   0.22370 1768.43494 -0.576 0.564410
## speciesAsun     -0.40312   0.24020 1808.16036 -1.678 0.093466 .
## speciesBavu     -0.66849   0.18219 1816.18706 -3.669 0.000250 ***
## speciesCahi      -0.34196   0.13928 1812.42590 -2.455 0.014176 *
## speciesCeor       1.05516   0.26968 1718.47460  3.913 9.48e-05 ***
## speciesCest       0.46134   0.11357 1808.59624  4.062 5.07e-05 ***
## speciesCrsp     -0.71193   0.82605 1816.56947 -0.862 0.388890
## speciesDaca     -0.34892   0.11645 1812.41139 -2.996 0.002770 **
## speciesDagl       0.09496   0.10594 1811.04506  0.896 0.370162
## speciesElre      0.69972   0.10197 1806.27959  6.862 9.31e-12 ***
## speciesErci     -1.25286   0.48151 1817.00942 -2.602 0.009345 **
## speciesErsp     -0.74372   0.58684 1817.36081 -1.267 0.205201
## speciesEugr      0.80724   0.11258 1817.99980  7.170 1.08e-12 ***
## speciesHisp      0.69927   0.10532 1803.72462  6.640 4.15e-11 ***
## speciesHype     -0.39850   0.12673 1816.45240 -3.144 0.001691 **
## speciesPesp     -0.14053   0.82609 1817.55278 -0.170 0.864939
## speciesPhpr      0.60546   0.09565 1802.00193  6.330 3.09e-10 ***
## speciesPore     -0.48846   0.10192 1808.38590 -4.793 1.78e-06 ***
## speciesPosp      0.95873   0.09383 1799.61063 10.218 < 2e-16 ***
## speciesPrsp     -1.43795   0.82605 1816.56091 -1.741 0.081895 .
## speciesRusp      1.21613   0.15554 1718.13879  7.819 9.24e-15 ***
## speciesSoca      2.57299   0.09383 1799.61063 27.421 < 2e-16 ***
## speciesSoju     -1.38323   0.82612 1817.56258 -1.674 0.094229 .
## speciesTaof      -0.55969   0.12036 1817.98387 -4.650 3.56e-06 ***
## speciesThar     -0.88670   0.82609 1816.97798 -1.073 0.283248
## speciesTrsp      0.06316   0.11413 1806.83812  0.553 0.580073
## speciesUhsp     -0.57186   0.58683 1817.23884 -0.974 0.329945
## speciesVear     -0.76051   0.20647 1817.54411 -3.683 0.000237 ***
## factor(year_factor)2 -0.25667   0.06719 1799.77733 -3.820 0.000138 ***
## factor(year_factor)3  0.19701   0.07426 1807.20791  2.653 0.008046 **
## factor(year_factor)4 -0.10085   0.07125 1808.64692 -1.415 0.157108
## factor(year_factor)5 -0.12596   0.07150 1814.15732 -1.762 0.078301 .
## factor(year_factor)6 -0.10747   0.07254 1815.10992 -1.482 0.138644
## factor(year_factor)7 -0.30491   0.07361 1817.31191 -4.142 3.60e-05 ***

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

## 
## Correlation matrix not shown by default, as p = 38 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

```

```
anova(mod7a)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state                      0.18   0.176     1  25.15  0.2611   0.6138
## species                   1287.05  42.902    30 1807.33 63.6078 < 2.2e-16 ***
## factor(year_factor)    39.41    6.568     6 1809.89  9.7383 1.401e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

KBS Plot-level Mixed Effects Models:

```
mod1p <- lmer(log(plot_cover_avg) ~ state + (1 | plot), comp_kbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod2p <- lmer(log(plot_cover_avg) ~ insecticide + (1 | plot), comp_kbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod3p <- lmer(log(plot_cover_avg) ~ insecticide + state + (1 | plot), comp_kbs_plot,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod4p <- lmer(log(plot_cover_avg) ~ insecticide * state + (1 | plot), comp_kbs_plot,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod5p <- lmer(log(plot_cover_avg) ~ state + year_factor + (1 | plot), comp_kbs_plot,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod6p <- lmer(log(plot_cover_avg) ~ state + year_factor + insecticide + (1 | plot),
comp_kbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7p <- lmer(log(plot_cover_avg) ~ state * year_factor + (1 | plot), comp_kbs_plot,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod8p <- lmer(log(plot_cover_avg) ~ state * year_factor + insecticide + (1 | plot),
comp_kbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9p <- lmer(log(plot_cover_avg) ~ state * insecticide + year_factor + (1 | plot),
comp_kbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular
```

```

mod10p <- lmer(log(plot_cover_avg) ~ state + insecticide * year_factor + (1 | plot),
  comp_kbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11p <- lmer(log(plot_cover_avg) ~ state * year_factor * insecticide + (1 | plot),
  comp_kbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

AICctab(mod1p, mod2p, mod3p, mod4p, mod5p, mod6p, mod7p, mod8p, mod9p, mod10p, mod11p,
  weights = T) # model 11p and 10p the same

##          dAICc df weight
## mod7p     0.0   6  0.3654
## mod5p     0.5   5  0.2841
## mod8p    1.9   7  0.1419
## mod6p    2.4   6  0.1125
## mod10p   4.0   7  0.0495
## mod9p    4.5   7  0.0394
## mod11p   7.9  10  0.0071
## mod2p   88.9   4 <0.001
## mod1p   89.2   4 <0.001
## mod3p   91.0   5 <0.001
## mod4p   93.2   6 <0.001

anova(mod7p, mod5p) #7p just barely better

## Data: comp_kbs_plot
## Models:
## mod5p: log(plot_cover_avg) ~ state + year_factor + (1 | plot)
## mod7p: log(plot_cover_avg) ~ state * year_factor + (1 | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5p     5 328.58 344.17 -159.29    318.58
## mod7p     6 327.93 346.64 -157.97    315.93 2.6553  1     0.1032

summ(mod7p)

```

Observations	167
Dependent variable	log(plot_cover_avg)
Type	Mixed effects linear regression

AIC	327.93
BIC	346.64
Pseudo-R ² (fixed effects)	0.43
Pseudo-R ² (total)	0.43

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	5.00	0.15	32.91	167.00	0.00
stateambient	0.28	0.22	1.31	167.00	0.19
year_factor	-0.23	0.03	-6.73	167.00	0.00
stateambient:year_factor	-0.08	0.05	-1.64	167.00	0.10

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
Residual		0.62

Grouping Variables		
Group	# groups	ICC
plot	24	0.00

```
emmmeans(mod7p, list(pairwise ~ state * year_factor), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular

## $`emmeans of state, year_factor`
##   state    year_factor emmean      SE   df lower.CL upper.CL
##   warmed      3.98  4.09 0.0688 22.8     3.95    4.23
##   ambient      3.98  4.06 0.0692 23.3     3.92    4.20
## 
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
## 
## $`pairwise differences of state, year_factor`
##   1                               estimate      SE   df
##   warmed 3.98203592814371 - ambient 3.98203592814371  0.0322 0.0976 23.1
##   t.ratio p.value
##   0.330   0.7443
## 
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.

# including native vs. exotic
kbs_comp_plot_origin <- within(kbs_comp_plot_origin, origin <- relevel(factor(origin),
  ref = "Native")) # releveling so native is the reference
mod12p <- lmer(log(plot_cover_avg) ~ state * origin + (1 + year_factor | plot), kbs_comp_plot_origin,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular
```

```

mod13p <- lmer(log(plot_cover_avg) ~ state + origin + (1 + year_factor | plot), kbs_comp_plot_origin,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod14p <- lmer(log(plot_cover_avg) ~ state + origin + year_factor + (1 | plot), kbs_comp_plot_origin,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod12p, mod13p) # go with model 12pu

## Data: kbs_comp_plot_origin
## Models:
## mod13p: log(plot_cover_avg) ~ state + origin + (1 + year_factor | plot)
## mod12p: log(plot_cover_avg) ~ state * origin + (1 + year_factor | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod13p     9 1730.3 1770.3 -856.14    1712.3
## mod12p    12 1722.5 1775.8 -849.23    1698.5 13.825  3  0.003154 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod12p, mod14p) # mod 14pu

## Data: kbs_comp_plot_origin
## Models:
## mod14p: log(plot_cover_avg) ~ state + origin + year_factor + (1 | plot)
## mod12p: log(plot_cover_avg) ~ state * origin + (1 + year_factor | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod14p     8 1660.7 1696.2 -822.32    1644.7
## mod12p    12 1722.5 1775.8 -849.23    1698.5     0  4           1

summ(mod14p)

```

Observations	631
Dependent variable	log(plot_cover_avg)
Type	Mixed effects linear regression

AIC	1660.65
BIC	1696.22
Pseudo-R ² (fixed effects)	0.48
Pseudo-R ² (total)	0.48

```
anova(mod14p)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value Pr(>F)

```

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	4.80	0.11	45.66	631.00	0.00
statewarmed	-0.06	0.07	-0.79	631.00	0.43
origin	-1.38	0.10	-14.17	631.00	0.00
originBoth	-1.53	0.10	-14.68	631.00	0.00
originExotic	-0.78	0.10	-8.03	631.00	0.00
year_factor	-0.32	0.02	-17.89	631.00	0.00

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
Residual		0.89

Grouping Variables		
Group	# groups	ICC
plot	24	0.00

```
## state      0.50   0.500     1   631    0.6307 0.4274
## origin    227.63  75.878     3   631   95.6399 <2e-16 ***
## year_factor 253.91 253.915     1   631  320.0458 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod14p, list(pairwise ~ state + origin + year_factor), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```
## $`emmeans of state, origin, year_factor`
## state origin year_factor emmean     SE  df lower.CL upper.CL
## ambient Native     3.94  3.55 0.0780 120     3.39    3.70
## warmed  Native     3.94  3.49 0.0778 119     3.34    3.65
## ambient          3.94  2.17 0.0780 120     2.01    2.32
## warmed           3.94  2.11 0.0778 119     1.96    2.27
## ambient Both      3.94  2.02 0.0852 156     1.85    2.19
## warmed  Both      3.94  1.96 0.0876 166     1.79    2.13
## ambient Exotic    3.94  2.77 0.0780 120     2.61    2.92
## warmed  Exotic    3.94  2.71 0.0778 119     2.56    2.86
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin, year_factor`
```

	estimate
## 1	0.0564
## ambient Native 3.93660855784469 - warmed Native 3.93660855784469	0.0564
## ambient Native 3.93660855784469 - ambient 3.93660855784469	1.3808

```

## ambient Native 3.93660855784469 - warmed 3.93660855784469      1.4371
## ambient Native 3.93660855784469 - ambient Both 3.93660855784469    1.5311
## ambient Native 3.93660855784469 - warmed Both 3.93660855784469    1.5874
## ambient Native 3.93660855784469 - ambient Exotic 3.93660855784469   0.7829
## ambient Native 3.93660855784469 - warmed Exotic 3.93660855784469   0.8393
## warmed Native 3.93660855784469 - ambient 3.93660855784469      1.3244
## warmed Native 3.93660855784469 - warmed 3.93660855784469      1.3808
## warmed Native 3.93660855784469 - ambient Both 3.93660855784469   1.4747
## warmed Native 3.93660855784469 - warmed Both 3.93660855784469   1.5311
## warmed Native 3.93660855784469 - ambient Exotic 3.93660855784469   0.7266
## warmed Native 3.93660855784469 - warmed Exotic 3.93660855784469   0.7829
## ambient 3.93660855784469 - warmed 3.93660855784469      0.0564
## ambient 3.93660855784469 - ambient Both 3.93660855784469      0.1503
## ambient 3.93660855784469 - warmed Both 3.93660855784469      0.2067
## ambient 3.93660855784469 - ambient Exotic 3.93660855784469   -0.5979
## ambient 3.93660855784469 - warmed Exotic 3.93660855784469   -0.5415
## warmed 3.93660855784469 - ambient Both 3.93660855784469      0.0939
## warmed 3.93660855784469 - warmed Both 3.93660855784469      0.1503
## warmed 3.93660855784469 - ambient Exotic 3.93660855784469   -0.6542
## warmed 3.93660855784469 - warmed Exotic 3.93660855784469   -0.5979
## ambient Both 3.93660855784469 - warmed Both 3.93660855784469   0.0564
## ambient Both 3.93660855784469 - ambient Exotic 3.93660855784469   -0.7481
## ambient Both 3.93660855784469 - warmed Exotic 3.93660855784469   -0.6918
## warmed Both 3.93660855784469 - ambient Exotic 3.93660855784469   -0.8045
## warmed Both 3.93660855784469 - warmed Exotic 3.93660855784469   -0.7481
## ambient Exotic 3.93660855784469 - warmed Exotic 3.93660855784469   0.0564
##      SE df t.ratio p.value
## 0.0713 22.4 0.790 0.9920
## 0.0979 614.7 14.098 <.0001
## 0.1212 165.0 11.862 <.0001
## 0.1049 622.9 14.600 <.0001
## 0.1285 191.5 12.352 <.0001
## 0.0979 614.7 7.994 <.0001
## 0.1212 165.0 6.927 <.0001
## 0.1212 165.0 10.931 <.0001
## 0.0979 614.7 14.098 <.0001
## 0.1251 180.8 11.788 <.0001
## 0.1049 622.9 14.600 <.0001
## 0.1212 165.0 5.997 <.0001
## 0.0979 614.7 7.994 <.0001
## 0.0713 22.4 0.790 0.9920
## 0.1049 622.9 1.433 0.8416
## 0.1285 191.5 1.608 0.7450
## 0.0979 614.7 -6.104 <.0001
## 0.1212 165.0 -4.469 0.0004
## 0.1251 180.8 0.751 0.9952
## 0.1049 622.9 1.433 0.8416
## 0.1212 165.0 -5.400 <.0001
## 0.0979 614.7 -6.104 <.0001
## 0.0713 22.4 0.790 0.9920
## 0.1049 622.9 -7.134 <.0001
## 0.1251 180.8 -5.530 <.0001
## 0.1285 191.5 -6.260 <.0001
## 0.1049 622.9 -7.134 <.0001

```

```

##  0.0713 22.4 0.790 0.9920
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 8 estimates

# including growth form - first with interaction term
kbs_comp_plot_growthhabit <- within(kbs_comp_plot_growthhabit, growth_habit <- relevel(factor(growth_habit,
  ref = "Forb")) # releveling so forb is the reference
mod15p <- lmer(log(plot_cover_avg) ~ state * growth_habit + (1 + year_factor | plot),
  kbs_comp_plot_growthhabit, REML = FALSE)

## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
## boundary (singular) fit: see ?isSingular

mod16p <- lmer(log(plot_cover_avg) ~ state + growth_habit + (1 + year_factor | plot),
  kbs_comp_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod17p <- lmer(log(plot_cover_avg) ~ state + growth_habit + year_factor + (1 | plot),
  kbs_comp_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod15p, mod16p) # go with model 15pu

## Data: kbs_comp_plot_growthhabit
## Models:
## mod16p: log(plot_cover_avg) ~ state + growth_habit + (1 + year_factor | plot)
## mod15p: log(plot_cover_avg) ~ state * growth_habit + (1 + year_factor | plot)
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod15p, mod17p) # mod 17pu

## Data: kbs_comp_plot_growthhabit
## Models:
## mod17p: log(plot_cover_avg) ~ state + growth_habit + year_factor + (1 | plot)
## mod15p: log(plot_cover_avg) ~ state * growth_habit + (1 + year_factor | plot)
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
summ(mod17p)
```

Observations	474				
Dependent variable	log(plot_cover_avg)				
Type	Mixed effects linear regression				
AIC	1216.45				
BIC	1253.90				
Pseudo-R ² (fixed effects)	0.47				
Pseudo-R ² (total)	0.47				
Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	4.64	0.11	42.04	474.00	0.00
statewarmed	-0.07	0.08	-0.84	474.00	0.40
growth_habit	-1.48	0.10	-14.76	474.00	0.00
growth_habitGraminoid	-0.40	0.09	-4.24	474.00	0.00
growth_habitTree	-3.20	0.86	-3.71	474.00	0.00
growth_habitVine	-1.38	0.28	-4.94	474.00	0.00
year_factor	-0.28	0.02	-14.38	474.00	0.00

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
Residual		0.86

Grouping Variables		
Group	# groups	ICC
plot	24	0.00

```
anova(mod17p)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state      0.523   0.523     1    474   0.7123 0.3991
## growth_habit 179.550  44.888     4    474  61.1700 <2e-16 ***
## year_factor  151.719  151.719     1    474 206.7528 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod17p, list(pairwise ~ state + growth_habit + year_factor), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```

## $`emmeans of state, growth_habit, year_factor`
##   state   growth_habit year_factor emmean      SE    df lower.CL upper.CL
## ambient     Forb          3.91  3.540 0.0779  79.1     3.38    3.69
## warmed     Forb          3.91  3.473 0.0776  78.2     3.32    3.63
## ambient           3.91  2.056 0.0846 102.6     1.89    2.22
## warmed           3.91  1.989 0.0873 110.7     1.82    2.16
## ambient  Graminoid       3.91  3.142 0.0779  79.1     2.99    3.30
## warmed  Graminoid       3.91  3.075 0.0776  78.2     2.92    3.23
## ambient     Tree          3.91  0.344 0.8724 481.0    -1.37    2.06
## warmed     Tree          3.91  0.277 0.8689 480.9    -1.43    1.98
## ambient     Vine          3.91  2.158 0.2792 284.2     1.61    2.71
## warmed     Vine          3.91  2.092 0.2835 304.9     1.53    2.65
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, growth_habit, year_factor`
## 1
## ambient Forb 3.91350210970464 - warmed Forb 3.91350210970464
## ambient Forb 3.91350210970464 - ambient   3.91350210970464
## ambient Forb 3.91350210970464 - warmed   3.91350210970464
## ambient Forb 3.91350210970464 - ambient Graminoid 3.91350210970464
## ambient Forb 3.91350210970464 - warmed Graminoid 3.91350210970464
## ambient Forb 3.91350210970464 - ambient Tree 3.91350210970464
## ambient Forb 3.91350210970464 - warmed Tree 3.91350210970464
## ambient Forb 3.91350210970464 - ambient Vine 3.91350210970464
## ambient Forb 3.91350210970464 - warmed Vine 3.91350210970464
## warmed Forb 3.91350210970464 - ambient   3.91350210970464
## warmed Forb 3.91350210970464 - warmed   3.91350210970464
## warmed Forb 3.91350210970464 - ambient Graminoid 3.91350210970464
## warmed Forb 3.91350210970464 - warmed Graminoid 3.91350210970464
## warmed Forb 3.91350210970464 - ambient Tree 3.91350210970464
## warmed Forb 3.91350210970464 - warmed Tree 3.91350210970464
## warmed Forb 3.91350210970464 - ambient Vine 3.91350210970464
## warmed Forb 3.91350210970464 - warmed Vine 3.91350210970464
## ambient   3.91350210970464 - warmed   3.91350210970464
## ambient   3.91350210970464 - ambient Graminoid 3.91350210970464
## ambient   3.91350210970464 - warmed Graminoid 3.91350210970464
## ambient   3.91350210970464 - ambient Tree 3.91350210970464
## ambient   3.91350210970464 - warmed Tree 3.91350210970464
## ambient   3.91350210970464 - ambient Vine 3.91350210970464
## ambient   3.91350210970464 - warmed Vine 3.91350210970464
## warmed   3.91350210970464 - ambient Graminoid 3.91350210970464
## warmed   3.91350210970464 - warmed Graminoid 3.91350210970464
## warmed   3.91350210970464 - ambient Tree 3.91350210970464
## warmed   3.91350210970464 - warmed Tree 3.91350210970464
## warmed   3.91350210970464 - ambient Vine 3.91350210970464
## warmed   3.91350210970464 - warmed Vine 3.91350210970464
## ambient Graminoid 3.91350210970464 - warmed Graminoid 3.91350210970464
## ambient Graminoid 3.91350210970464 - ambient Tree 3.91350210970464
## ambient Graminoid 3.91350210970464 - warmed Tree 3.91350210970464
## ambient Graminoid 3.91350210970464 - ambient Vine 3.91350210970464
## ambient Graminoid 3.91350210970464 - warmed Vine 3.91350210970464

```

```

## warmed Graminoid 3.91350210970464 - ambient Tree 3.91350210970464
## warmed Graminoid 3.91350210970464 - warmed Tree 3.91350210970464
## warmed Graminoid 3.91350210970464 - ambient Vine 3.91350210970464
## warmed Graminoid 3.91350210970464 - warmed Vine 3.91350210970464
## ambient Tree 3.91350210970464 - warmed Tree 3.91350210970464
## ambient Tree 3.91350210970464 - ambient Vine 3.91350210970464
## ambient Tree 3.91350210970464 - warmed Vine 3.91350210970464
## warmed Tree 3.91350210970464 - ambient Vine 3.91350210970464
## warmed Tree 3.91350210970464 - warmed Vine 3.91350210970464
## ambient Vine 3.91350210970464 - warmed Vine 3.91350210970464
## estimate SE df t.ratio p.value
## 0.0667 0.0796 22.3 0.837 0.9970
## 1.4838 0.1014 466.3 14.638 <.0001
## 1.5504 0.1308 137.1 11.851 <.0001
## 0.3979 0.0944 458.6 4.213 0.0012
## 0.4645 0.1235 118.2 3.761 0.0096
## 3.1959 0.8724 481.1 3.663 0.0103
## 3.2626 0.8725 480.4 3.739 0.0078
## 1.3815 0.2865 363.0 4.822 0.0001
## 1.4482 0.3015 293.6 4.804 0.0001
## 1.4171 0.1269 128.2 11.165 <.0001
## 1.4838 0.1014 466.3 14.638 <.0001
## 0.3312 0.1235 118.2 2.681 0.1935
## 0.3979 0.0944 458.6 4.213 0.0012
## 3.1293 0.8795 480.6 3.558 0.0148
## 3.1959 0.8724 481.1 3.663 0.0103
## 1.3149 0.2932 257.4 4.485 0.0005
## 1.3815 0.2865 363.0 4.822 0.0001
## 0.0667 0.0796 22.3 0.837 0.9970
## -1.0859 0.1014 466.3 -10.713 <.0001
## -1.0193 0.1269 128.2 -8.030 <.0001
## 1.7121 0.8730 481.1 1.961 0.6267
## 1.7788 0.8728 480.5 2.038 0.5725
## -0.1023 0.2885 365.2 -0.354 1.0000
## -0.0356 0.3026 295.6 -0.118 1.0000
## -1.1526 0.1308 137.1 -8.810 <.0001
## -1.0859 0.1014 466.3 -10.713 <.0001
## 1.6455 0.8803 480.7 1.869 0.6900
## 1.7121 0.8730 481.1 1.961 0.6267
## -0.1689 0.2960 261.3 -0.571 0.9999
## -0.1023 0.2885 365.2 -0.354 1.0000
## 0.0667 0.0796 22.3 0.837 0.9970
## 2.7981 0.8724 481.1 3.207 0.0459
## 2.8647 0.8725 480.4 3.283 0.0364
## 0.9837 0.2865 363.0 3.434 0.0230
## 1.0503 0.3015 293.6 3.484 0.0199
## 2.7314 0.8795 480.6 3.106 0.0618
## 2.7981 0.8724 481.1 3.207 0.0459
## 0.9170 0.2932 257.4 3.128 0.0601
## 0.9837 0.2865 363.0 3.434 0.0230
## 0.0667 0.0796 22.3 0.837 0.9970
## -1.8144 0.9135 479.2 -1.986 0.6092
## -1.7477 0.9216 477.3 -1.896 0.6716
## -1.8811 0.9123 475.9 -2.062 0.5555

```

```

##   -1.8144 0.9135 479.2  -1.986 0.6092
##   0.0667 0.0796  22.3   0.837 0.9970
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 10 estimates

```

UMBS species level mixed effects models

```

# UMBS SPECIES LEVEL - Looking at RELATIVE ABUNDANCE
mod1u <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |
  species) + (1 | plot), comp_umbs_spp, REML = FALSE)

```

```

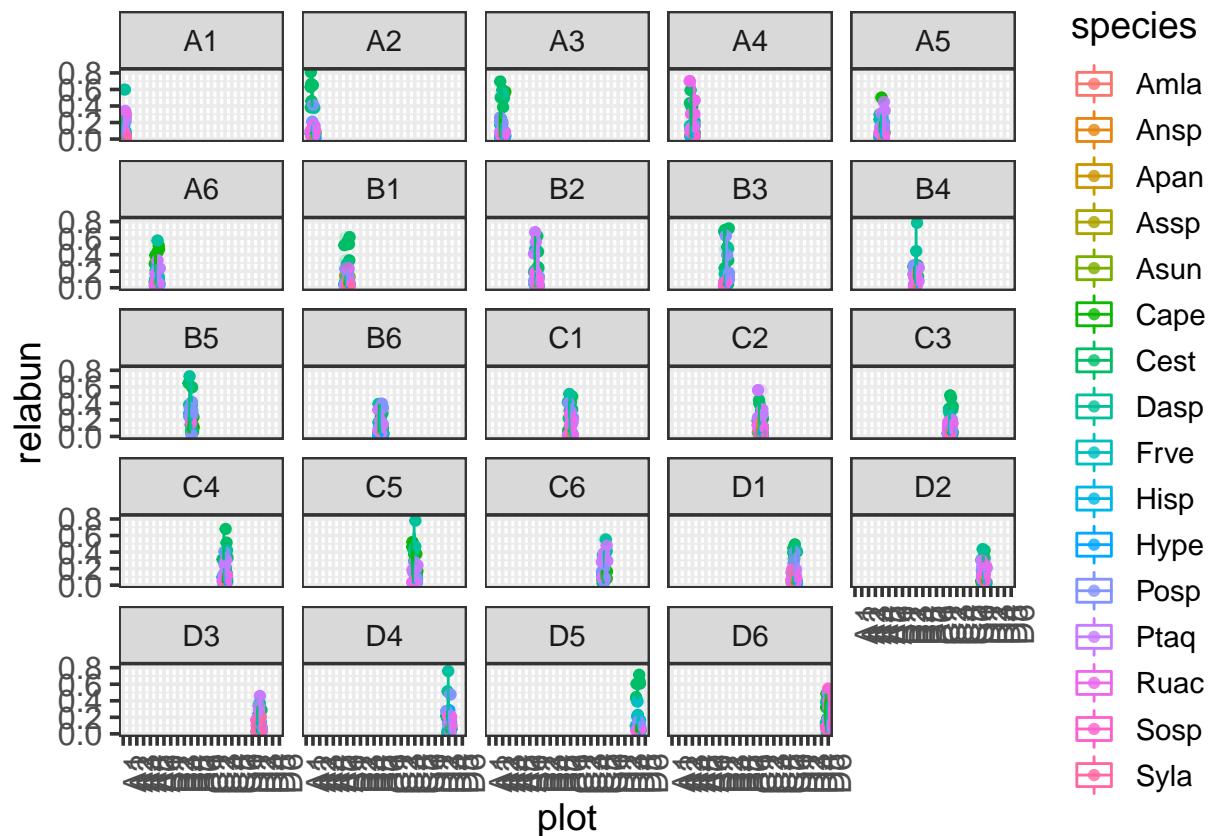
## boundary (singular) fit: see ?isSingular

```

```

ggplot(comp_umbs_spp, aes(x = plot, y = relabun, col = species)) + geom_jitter() +
  geom_boxplot(alpha = 0.2) + facet_wrap(~plot)

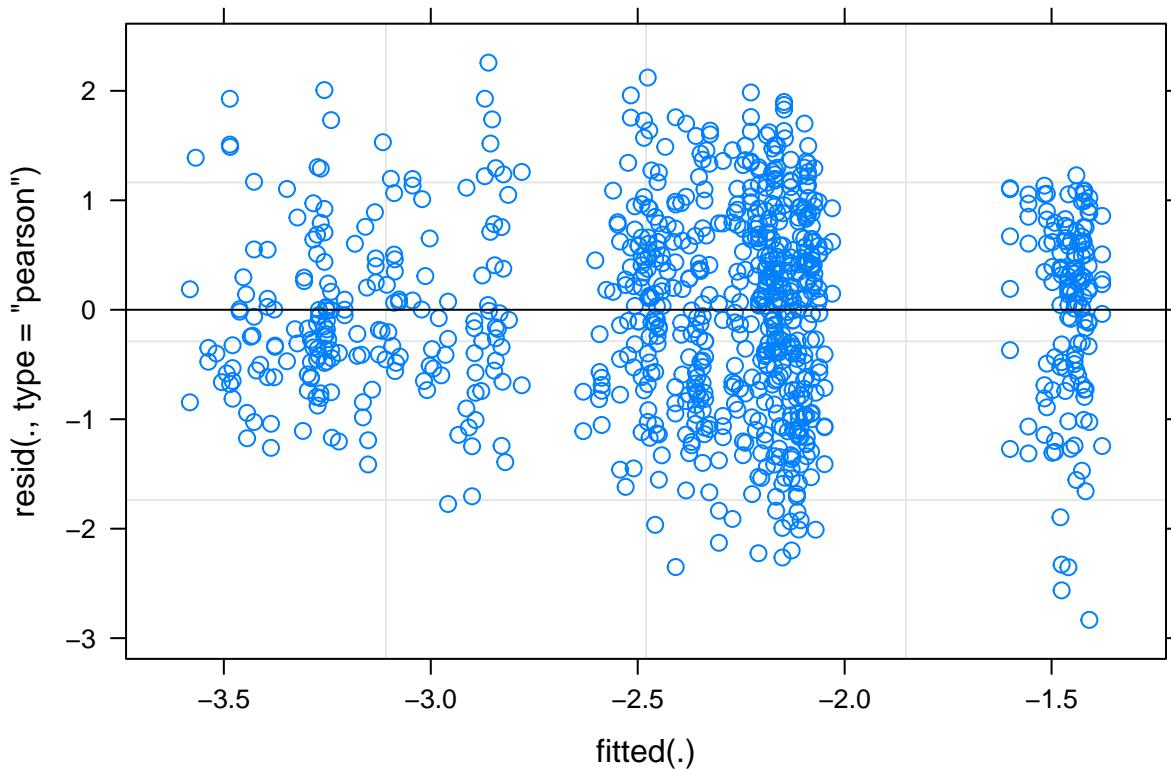
```



```

# Check Assumptions: (1) Linearity: if covariates are not categorical (year
# isn't) (2) Homogeneity: Need to Check by plotting residuals vs predicted
# values.
par(mfrow = c(1, 2))
plot(mod1u)

```



```
# Homogeneity of variance is ok here (increasing variance in resids is not
# increasing with fitted values) Check for homogeneity of variances (true if
# p>0.05). If the result is not significant, the assumption of equal variances
# (homoscedasticity) is met (no significant difference between the group
# variances). *****Levene's Test - tests whether or not the variance among two
# or more groups is equal - If the p-value is less than our chosen significance
# level, we can reject the null hypothesis and conclude that we have enough
# evidence to state that the variance among the groups is not equal (which we
# want).
```

```
leveneTest(residuals(modiu) ~ comp_umbs_spp$state)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value Pr(>F)
## group     1  0.0505  0.8222
##          897
```

```
# Assumption not met
leveneTest(residuals(modiu) ~ comp_umbs_spp$species)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value    Pr(>F)
## group    15  2.8451 0.0002262 ***
##          883
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

# Assumption met
leveneTest(residuals(mod1u) ~ comp_umbs_spp$insecticide)

## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.

## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value Pr(>F)
## group    1  1.9758 0.1602
##          897

# Assumption not met - this seems weird
leveneTest(residuals(mod1u) ~ comp_umbs_spp$plot)

## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.

## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value     Pr(>F)
## group   23  2.3561 0.0003437 ***
##          875
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

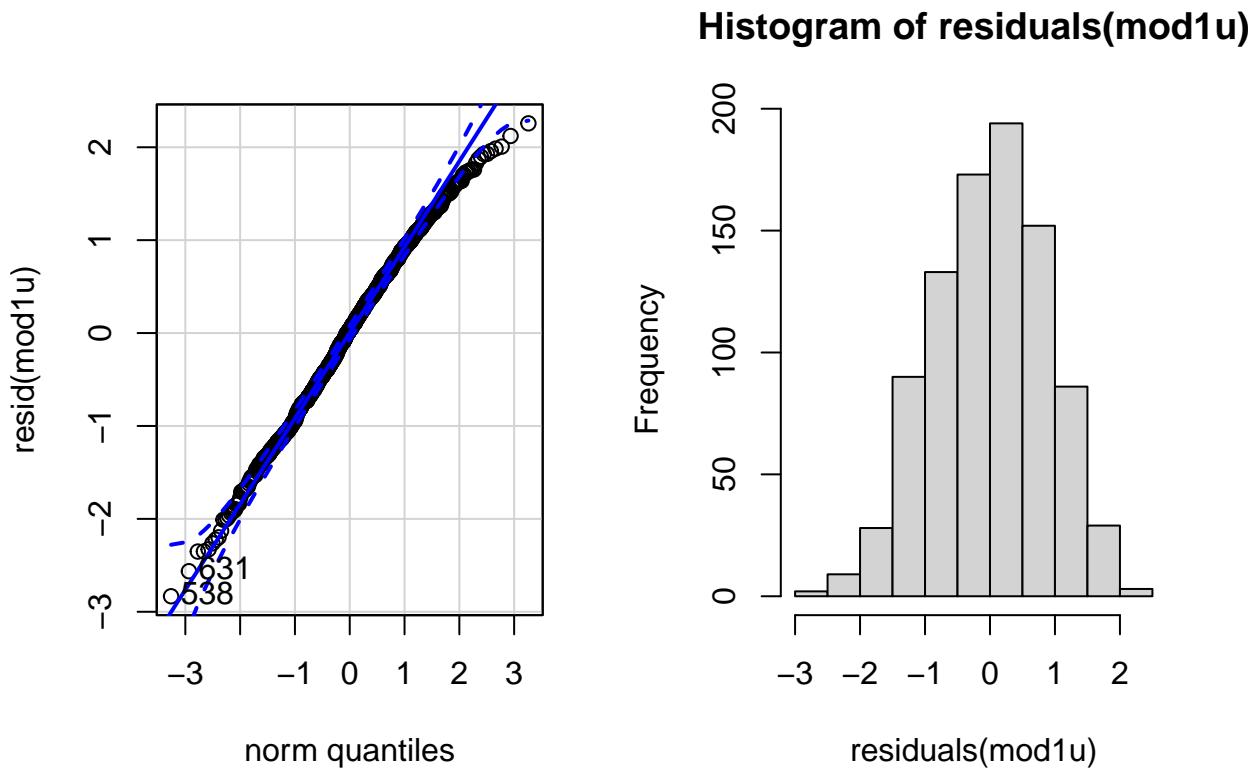
# Assumption met

# (3) Normality of error term: need to check by histogram, QQplot of residuals,
# could do Kolmogorov-Smirnov test. Check for normal residuals
qqPlot(resid(mod1u))

## 538 631
## 160 210

hist(residuals(mod1u))

```



```
shapiro.test(resid(mod1u)) # not normally distributed resids bc p<0.05
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: resid(mod1u)  
## W = 0.99584, p-value = 0.01617
```

```
outlierTest(mod1u) # no outliers
```

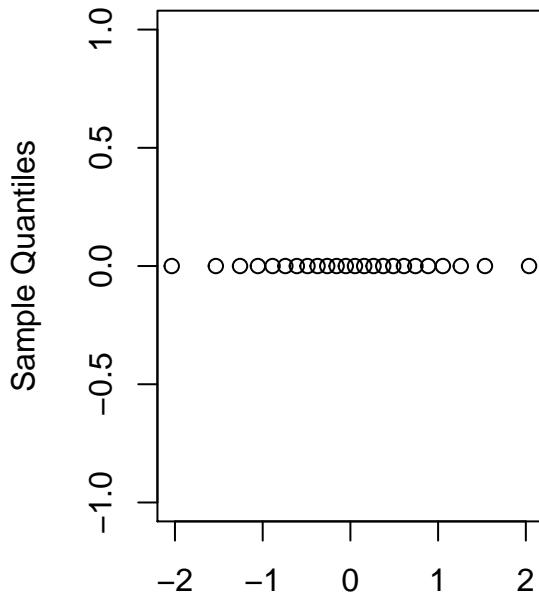
```
## No Studentized residuals with Bonferroni p < 0.05  
## Largest |rstudent|:  
##      rstudent unadjusted p-value Bonferroni p  
## 538 -3.236539          0.0012546        NA
```

```
# (4) Normality of random effect: Get the estimate of random effect (e.g., random  
# intercepts), and check them as you would check the residual.  
require(lme4)  
r_int <- ranef(mod1u)$plot$`  
qqnorm(r_int)  
# qline(r_int) #doesn't work  
shapiro.test(r_int)
```

```
## Error in shapiro.test(r_int): all 'x' values are identical
```

```
# Normally distributed random effect - p-value > 0.05
```

Normal Q–Q Plot



Theoretical Quantiles

```
# Do we need to include plot as a random effect with the KBS models?  
modiu <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |  
  species) + (1 | plot), comp_umbs_spp, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
mod2u <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |  
  species), comp_umbs_spp, REML = FALSE)  
# Run analysis of variance on each model (see this for more explanation on how  
# anova on a linear mixed effects model is similar to an anova on a regular  
# linear model: https://m-clark.github.io/docs/mixedModels/anovamixed.html)  
anova(modiu)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method  
##  
##             Sum Sq Mean Sq NumDF DenDF F value Pr(>F)  
## state          0.48531 0.48531     1  885.25  0.6229 0.4302  
## year_factor    0.80199 0.80199     1  890.55  1.0293 0.3106  
## insecticide    0.77081 0.77081     1  885.27  0.9893 0.3202  
## state:year_factor 0.41633 0.41633     1  885.26  0.5343 0.4650  
## year_factor:insecticide 0.51853 0.51853     1  886.95  0.6655 0.4148
```

```
anova(mod2u)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
```

```

##                                     Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state                           0.48531 0.48531      1 885.25  0.6229 0.4302
## year_factor                     0.80199 0.80199      1 890.55  1.0293 0.3106
## insecticide                      0.77081 0.77081      1 885.27  0.9893 0.3202
## state:year_factor               0.41633 0.41633      1 885.26  0.5343 0.4650
## year_factor:insecticide          0.51853 0.51853      1 886.95  0.6655 0.4148

```

```
anova(mod1u, mod2u) # Go with model 2 since pvalue >0.05, aka more complex model does not have something
```

```

## Data: comp_umbs_spp
## Models:
## mod2u: log(relabun) ~ state * year_factor + insecticide * year_factor +
## mod2u: (1 | species)
## mod1u: log(relabun) ~ state * year_factor + insecticide * year_factor +
## mod1u: (1 | species) + (1 | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod2u     8 2386.7 2425.1 -1185.4   2370.7
## mod1u     9 2388.7 2431.9 -1185.4   2370.7     0  1           1

```

```
summ(mod1u)
```

Observations	899
Dependent variable	log(relabun)
Type	Mixed effects linear regression

AIC	2388.72
BIC	2431.93
Pseudo-R ² (fixed effects)	0.00
Pseudo-R ² (total)	0.30

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	-2.80	0.19	-14.41	41.89	0.00
stateambient	-0.11	0.14	-0.79	885.25	0.43
year_factor	0.02	0.03	0.63	886.84	0.53
insecticideno_insects	0.14	0.14	0.99	885.27	0.32
stateambient:year_factor	0.03	0.03	0.73	885.26	0.46
year_factor:insecticideno_insects	-0.03	0.03	-0.82	886.95	0.41

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
species	(Intercept)	0.58
Residual		0.88

Grouping Variables		
Group	# groups	ICC
plot	24	0.00
species	16	0.30

```
summ(mod2u)
```

Observations	899
Dependent variable	log(relabun)
Type	Mixed effects linear regression

AIC	2386.72
BIC	2425.13
Pseudo-R ² (fixed effects)	0.00
Pseudo-R ² (total)	0.30

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	-2.80	0.19	-14.41	41.89	0.00
stateambient	-0.11	0.14	-0.79	885.25	0.43
year_factor	0.02	0.03	0.63	886.84	0.53
insecticideno_insects	0.14	0.14	0.99	885.27	0.32
stateambient:year_factor	0.03	0.03	0.73	885.26	0.46
year_factor:insecticideno_insects	-0.03	0.03	-0.82	886.95	0.41

p values calculated using Satterthwaite d.f.

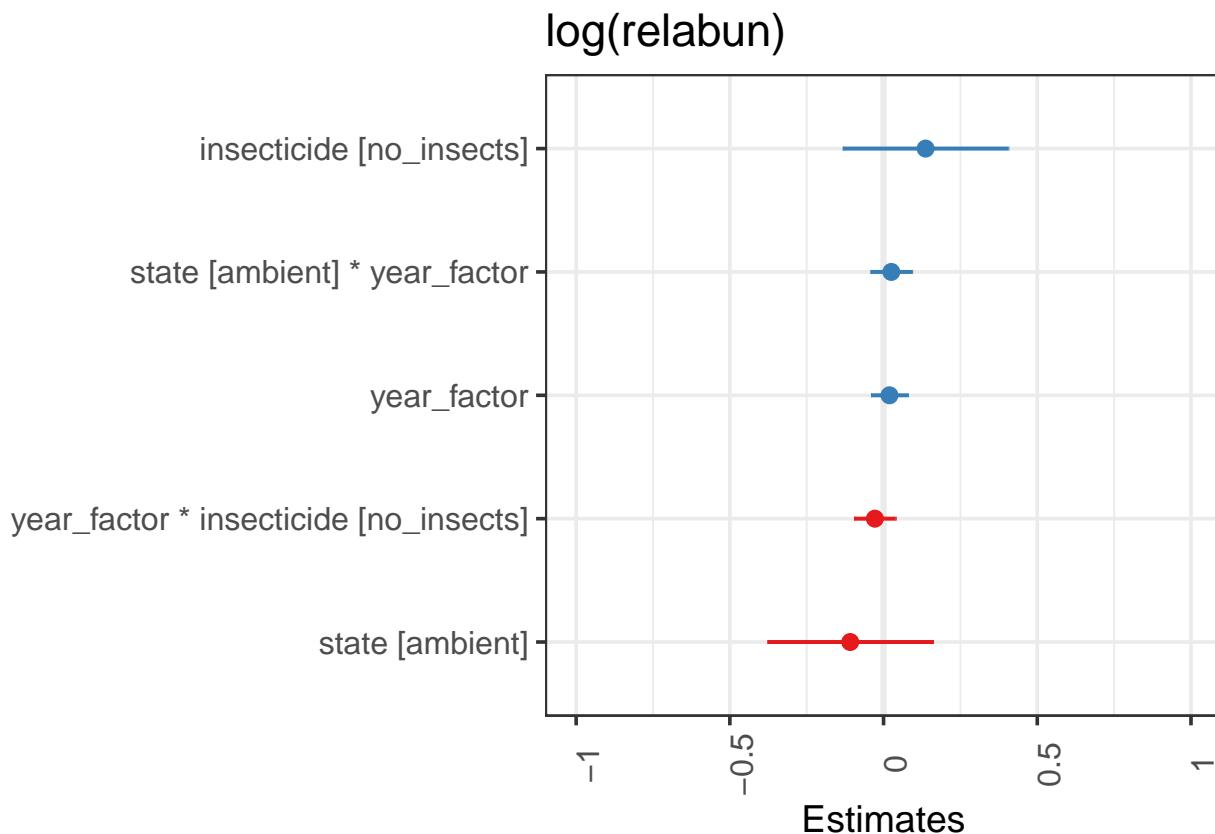
Random Effects		
Group	Parameter	Std. Dev.
species	(Intercept)	0.58
Residual		0.88

Grouping Variables		
Group	# groups	ICC
species	16	0.30

```
AICctab(mod1u, mod2u, weights = T)
```

```
##      dAICc df weight
## mod2u  0.0   8  0.74
## mod1u  2.0   9  0.26
```

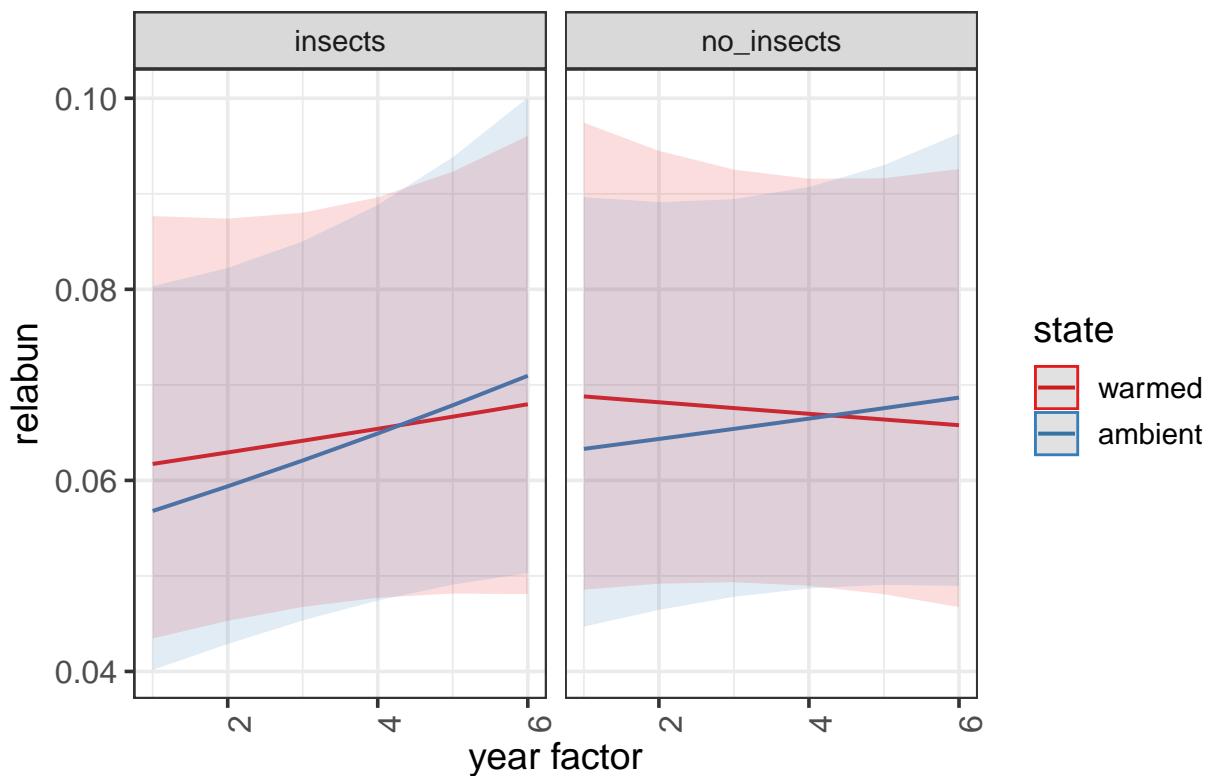
```
# Plot the fixed effects estimates for different models these are the fixed
# effects estimates from summary(mod1)
plot_model(mod2u, sort.est = TRUE)
```



```
# these are the fixed predicted values:
plot_model(mod2u, type = "pred", terms = c("year_factor", "state", "insecticide"))
```

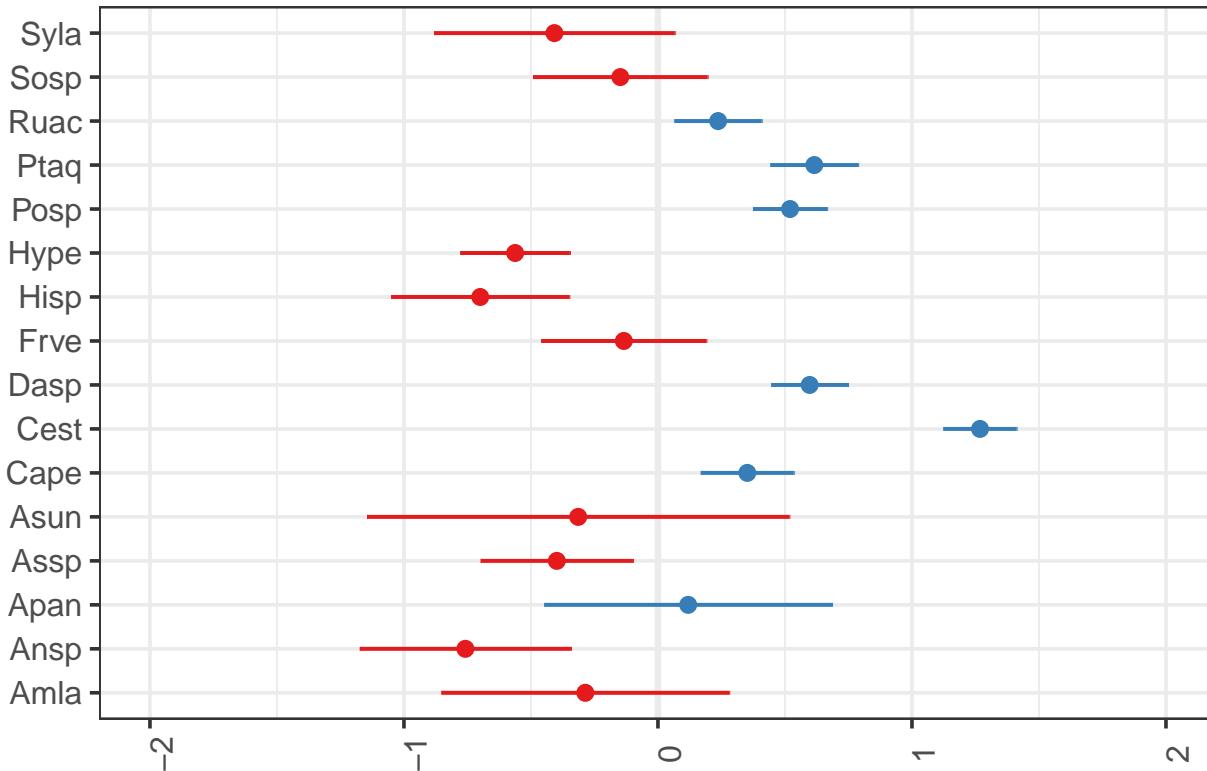
Model has log-transformed response. Back-transforming predictions to original response scale. Standard

Predicted values of relabun



```
# these are the random effects estimates
plot_model(mod2u, type = "re", terms = c("species"))
```

Random effects



```

# Does year need to be interactive with insecticide? - already removed
# insecticide
mod3 <- lmer(log(relabun) ~ state * year_factor + insecticide + (1 | species) + (1 |
  plot), comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod2u, mod3u) # Looks like no, pvalue > 0.05, so year interactive with insecticide does not improve model fit so we will drop it

## Error in anova.lmerModLmerTest(mod2u, mod3u): object 'mod3u' not found

# Do we need to include insecticide? (dropping insecticide from the model)
mod4u <- lmer(log(relabun) ~ state * year_factor + (1 | species), comp_umbs_spp,
  REML = FALSE)
anova(mod2u, mod4u) # Looks like no, pvalue > 0.05, so insecticide does not improve model fit so we will drop it

## Data: comp_umbs_spp
## Models:
## mod4u: log(relabun) ~ state * year_factor + (1 | species)
## mod2u: log(relabun) ~ state * year_factor + insecticide * year_factor +
## mod2u:      (1 | species)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod4u     6 2383.7 2412.6 -1185.9    2371.7
## mod2u     8 2386.7 2425.1 -1185.4    2370.7 1.0233  2      0.5995

```

```

AICctab(mod2u, mod4u, weights = T)

##      dAICc df weight
## mod4u 0.0   6  0.82
## mod2u 3.0   8  0.18

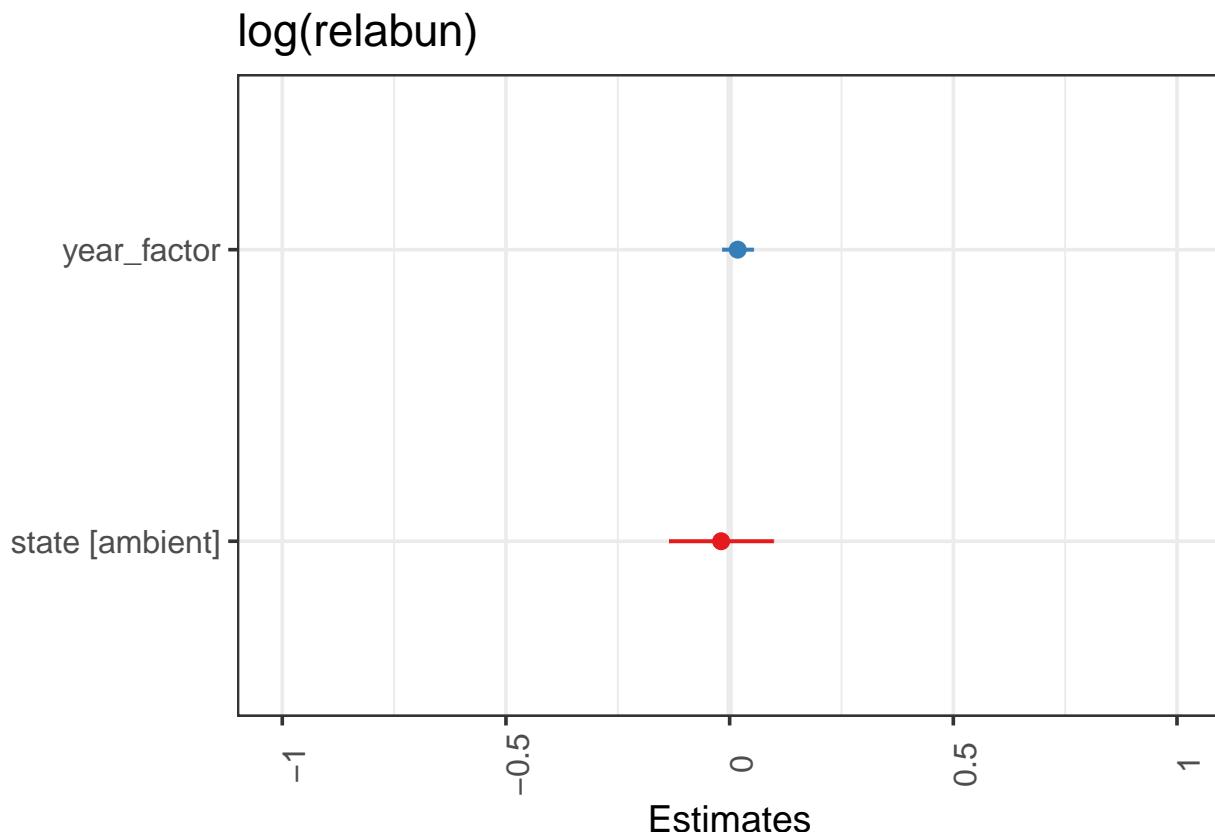
# Does year need to be interactive with state?
mod5u <- lmer(log(relabun) ~ state + year_factor + (1 | species), comp_umbs_spp,
               REML = FALSE)
anova(mod4u, mod5u)

## Data: comp_umbs_spp
## Models:
## mod5u: log(relabun) ~ state + year_factor + (1 | species)
## mod4u: log(relabun) ~ state * year_factor + (1 | species)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5u     5 2382.3 2406.3 -1186.2    2372.3
## mod4u     6 2383.7 2412.6 -1185.9    2371.7 0.5743  1     0.4486

# No, P>0.05 so state*year_factor doesn't strongly improve model fit so we will
# shift to mod5u, but AIC values are close!!

# Plot the fixed effects estimates for different models these are the fixed
# effects estimates from summary(mod5)
plot_model(mod5u, sort.est = TRUE)

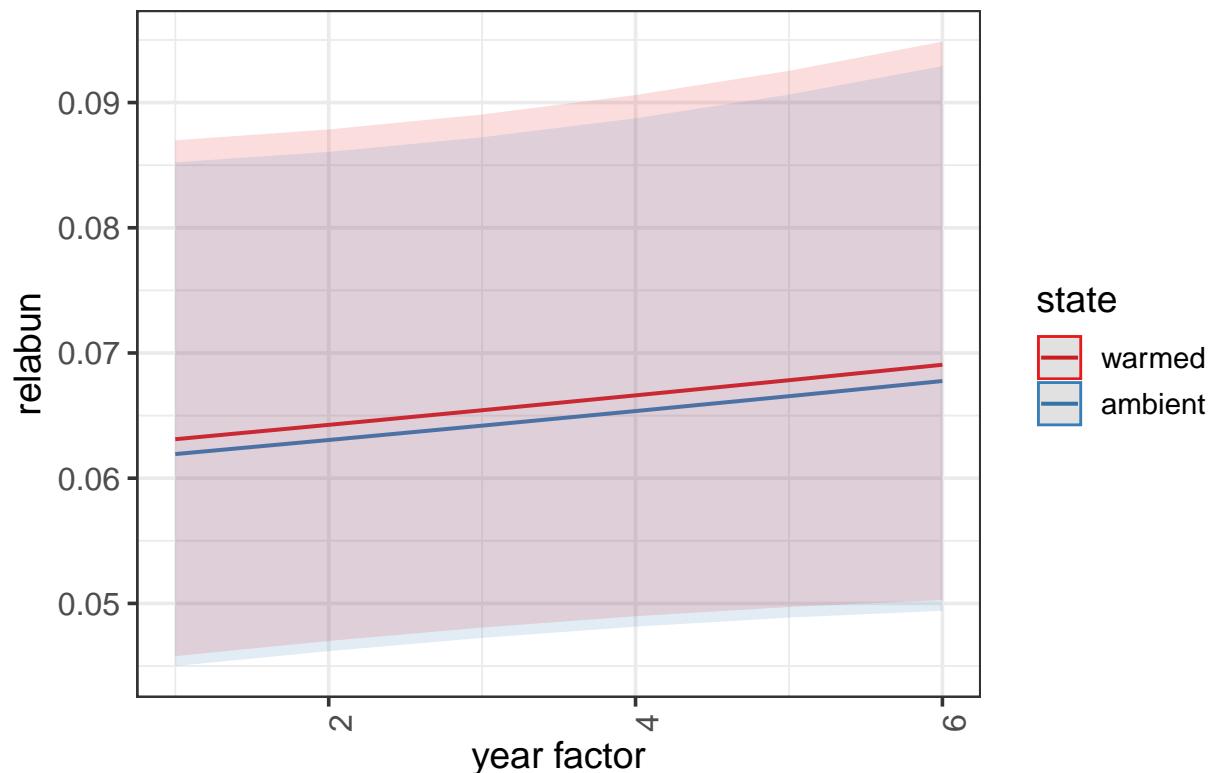
```



```
# these are the fixed predicted values:  
plot_model(mod5u, type = "pred", terms = c("year_factor", "state"))
```

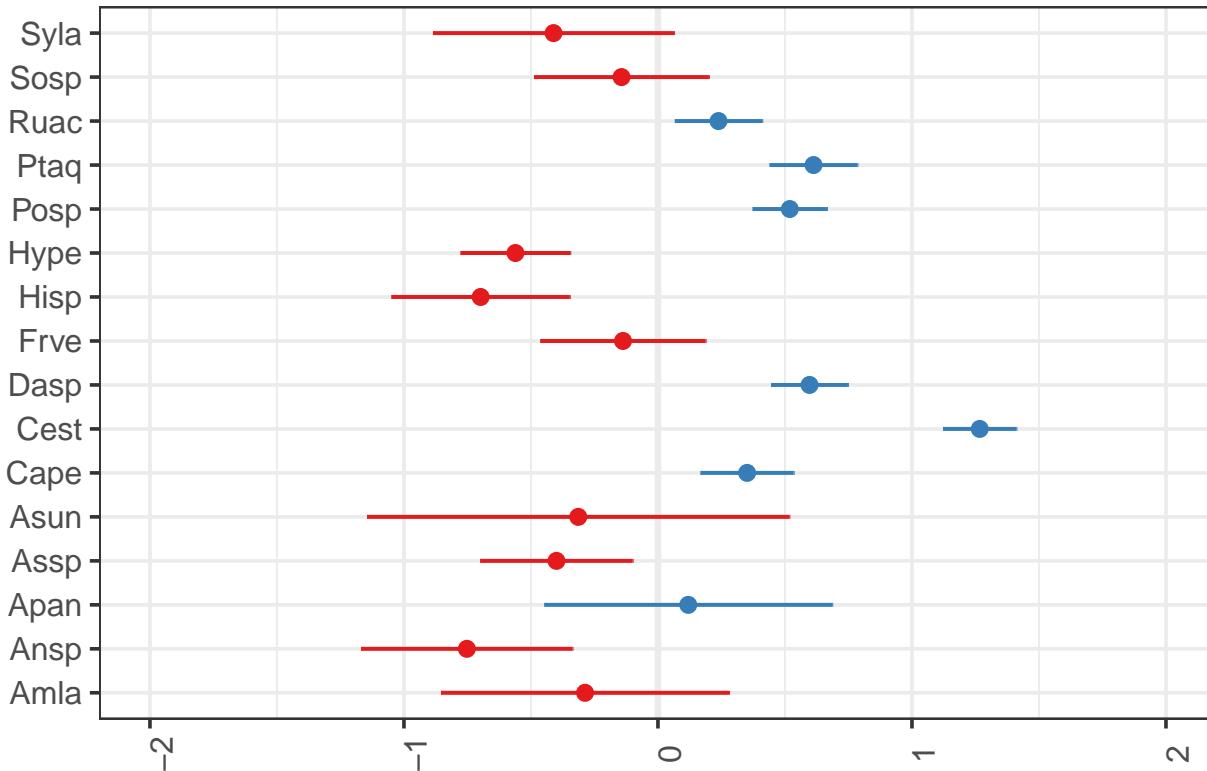
Model has log-transformed response. Back-transforming predictions to original response scale. Standard errors are back-transformed and so do not sum to zero.

Predicted values of relabun



```
# these are the random effects estimates  
plot_model(mod5u, type = "re", terms = c("species"))
```

Random effects



```
# If we wanted to include plots nested within year it would look like this:
mod6u <- lmer(log(relabun) ~ state + year_factor + (1 | species) + (1 + year_factor |
  plot), comp_umbs_spp, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```
anova(mod5u, mod6u) # go with simpler model = mod5u
```

```
## Data: comp_umbs_spp
## Models:
## mod5u: log(relabun) ~ state + year_factor + (1 | species)
## mod6u: log(relabun) ~ state + year_factor + (1 | species) + (1 + year_factor |
## mod6u:   plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5u     5 2382.3 2406.3 -1186.2    2372.3
## mod6u     8 2388.3 2426.7 -1186.2    2372.3      0  3          1
```

```
anova(mod5u)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state       0.08011 0.08011      1  885.97  0.1026 0.7488
## year_factor 0.82358 0.82358      1  890.68  1.0550 0.3046
```

```

# reminder what model 5u is: mod5u <- lmer(log(relabun) ~ state + year_factor +
# (1/species), comp_umbs_spp, REML=FALSE)

# mod5u (and mod6u) are pretty complex in terms of interpretation (they actually
# don't have many parameters though). We could consider an alternative model
# that's simpler to understand and also one that provides more insight about the
# species. That would be something like this:
mod7u <- lmer(log(relabun) ~ state + species + (1 + factor(year_factor) | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -8.0e+00

mod7au <- lmer(log(relabun) ~ state + species + factor(year_factor) + (1 | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7bu <- lmer(log(relabun) ~ state * factor(year_factor) + species + (1 | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7cu <- lmer(log(relabun) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod5u, mod7u) # model 7u is a better fit to data

## Data: comp_umbs_spp
## Models:
## mod5u: log(relabun) ~ state + year_factor + (1 | species)
## mod7u: log(relabun) ~ state + species + (1 + factor(year_factor) | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod5u    5 2382.3 2406.3 -1186.2   2372.3
## mod7u   39 2392.0 2579.3 -1157.0   2314.0 58.297 34   0.005881 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

anova(mod7u, mod7au) #mod 7au

## Data: comp_umbs_spp
## Models:
## mod7au: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## mod7u: log(relabun) ~ state + species + (1 + factor(year_factor) | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7au   24 2346.9 2462.2 -1149.5   2298.9
## mod7u   39 2392.0 2579.3 -1157.0   2314.0      0 15           1

```

```

anova(mod7au, mod7bu)  #mod 7au - interaction between state and year does not improve model go with simpe

## Data: comp_umbs_spp
## Models:
## mod7au: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## mod7bu: log(relabun) ~ state * factor(year_factor) + species + (1 | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7au    24 2346.9 2462.2 -1149.5   2298.9
## mod7bu    29 2352.8 2492.1 -1147.4   2294.8 4.1234  5     0.5318

anova(mod7au, mod7cu)  #models are not different than one another, go with simpler model = mod7au

## Data: comp_umbs_spp
## Models:
## mod7au: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## mod7cu: log(relabun) ~ state + species + factor(year_factor) + insecticide +
## mod7cu:      (1 | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7au    24 2346.9 2462.2 -1149.5   2298.9
## mod7cu    25 2348.5 2468.6 -1149.3   2298.5 0.4019  1     0.5261

summary(mod7au)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## Data: comp_umbs_spp
##
##      AIC      BIC  logLik deviance df.resid
##  2346.9  2462.2 -1149.5   2298.9     875
##
## Scaled residuals:
##    Min     1Q   Median     3Q    Max
## -3.2474 -0.7044  0.0280  0.7063  2.6539
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0000   0.0000
## Residual           0.7553   0.8691
## Number of obs: 899, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) -3.10745  0.34107 899.00000 -9.111 < 2e-16 ***
## stateambient -0.01567  0.05839 899.00000 -0.268 0.78846  
## speciesAnsp  -0.49583  0.40091 899.00000 -1.237 0.21649  
## speciesApan   0.55769  0.46483 899.00000  1.200 0.23054  
## speciesAssp  -0.01418  0.36498 899.00000 -0.039 0.96903  
## speciesAsun  -0.22506  0.69954 899.00000 -0.322 0.74773  
## speciesCape   0.75918  0.34226 899.00000  2.218 0.02680 *   
## speciesCest   1.68795  0.33791 899.00000  4.995 7.06e-07 ***

```

```

## speciesDasp      1.00785   0.33901 899.00000  2.973  0.00303 **
## speciesFrve    0.27617   0.37191 899.00000  0.743  0.45793
## speciesHisp    -0.45271   0.38135 899.00000 -1.187  0.23549
## speciesHype    -0.17211   0.34724 899.00000 -0.496  0.62027
## speciesPosp     0.91835   0.33807 899.00000  2.716  0.00673 **
## speciesPtaq     1.03503   0.34184 899.00000  3.028  0.00253 **
## speciesRuac     0.64773   0.34103 899.00000  1.899  0.05784 .
## speciesSosp     0.23844   0.37741 899.00000  0.632  0.52770
## speciesSyla    -0.08720   0.42122 899.00000 -0.207  0.83605
## factor(year_factor)2 -0.24404  0.10419 899.00000 -2.342  0.01939 *
## factor(year_factor)3  0.11660   0.10324 899.00000  1.129  0.25905
## factor(year_factor)4  0.08689   0.10373 899.00000  0.838  0.40245
## factor(year_factor)5 -0.04077   0.10238 899.00000 -0.398  0.69055
## factor(year_factor)6  0.01253   0.10117 899.00000  0.124  0.90145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Correlation matrix not shown by default, as p = 22 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)       if you need it

```

```

## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
anova(mod7au) # investigates whether at least one of the levels within each factor is significantly di
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state                      0.054  0.0544     1     899  0.0720  0.788461
## species                    295.084 19.6722    15     899 26.0460 < 2.2e-16 ***
## factor(year_factor)     11.599  2.3197     5     899  3.0713  0.009337 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
# Yes, at least one of the species is different (they do not all have the same
# relative abundances).
```

```
emmeans(mod7au, list(pairwise ~ state + year_factor), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```

## $`emmeans of state, year_factor`
##   state  year_factor emmean      SE  df lower.CL upper.CL
##   warmed          1 -2.75 0.0987 338    -2.95   -2.56
##   ambient         1 -2.77 0.0973 303    -2.96   -2.58
##   warmed          2 -3.00 0.0981 331    -3.19   -2.80
##   ambient         2 -3.01 0.0964 300    -3.20   -2.82
##   warmed          3 -2.64 0.0961 326    -2.82   -2.45
##   ambient         3 -2.65 0.0951 301    -2.84   -2.46
##   warmed          4 -2.67 0.0956 301    -2.85   -2.48
##   ambient         4 -2.68 0.0937 272    -2.87   -2.50
##   warmed          5 -2.79 0.0911 253    -2.97   -2.61

```

```

## ambient          5 -2.81 0.0903 223    -2.99    -2.63
## warmed          6 -2.74 0.0933 295    -2.92    -2.56
## ambient          6 -2.76 0.0911 248    -2.94    -2.58
##
## Results are averaged over the levels of: species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $'pairwise differences of state, year_factor'
##   1           estimate      SE   df t.ratio p.value
## warmed 1 - ambient 1  0.01567 0.0594 20.9  0.264  1.0000
## warmed 1 - warmed 2  0.24404 0.1055 903.2  2.313  0.4680
## warmed 1 - ambient 2  0.25971 0.1208 295.7  2.149  0.5879
## warmed 1 - warmed 3 -0.11660 0.1046 906.0 -1.115  0.9940
## warmed 1 - ambient 3 -0.10092 0.1207 291.4 -0.836  0.9995
## warmed 1 - warmed 4 -0.08689 0.1051 906.3 -0.827  0.9996
## warmed 1 - ambient 4 -0.07121 0.1204 290.9 -0.592  1.0000
## warmed 1 - warmed 5  0.04077 0.1037 908.3  0.393  1.0000
## warmed 1 - ambient 5  0.05644 0.1201 278.4  0.470  1.0000
## warmed 1 - warmed 6 -0.01253 0.1025 908.2 -0.122  1.0000
## warmed 1 - ambient 6  0.00314 0.1180 262.4  0.027  1.0000
## ambient 1 - warmed 2  0.22836 0.1214 292.3  1.882  0.7697
## ambient 1 - ambient 2  0.24404 0.1055 903.2  2.313  0.4680
## ambient 1 - warmed 3 -0.13227 0.1199 279.8 -1.103  0.9944
## ambient 1 - ambient 3 -0.11660 0.1046 906.0 -1.115  0.9940
## ambient 1 - warmed 4 -0.10256 0.1210 286.0 -0.847  0.9995
## ambient 1 - ambient 4 -0.08689 0.1051 906.3 -0.827  0.9996
## ambient 1 - warmed 5  0.02510 0.1190 278.1  0.211  1.0000
## ambient 1 - ambient 5  0.04077 0.1037 908.3  0.393  1.0000
## ambient 1 - warmed 6 -0.02820 0.1190 279.4 -0.237  1.0000
## ambient 1 - ambient 6 -0.01253 0.1025 908.2 -0.122  1.0000
## warmed 2 - ambient 2  0.01567 0.0594 20.9  0.264  1.0000
## warmed 2 - warmed 3 -0.36063 0.1047 908.5 -3.444  0.0294
## warmed 2 - ambient 3 -0.34496 0.1210 288.2 -2.850  0.1653
## warmed 2 - warmed 4 -0.33092 0.1043 906.1 -3.174  0.0678
## warmed 2 - ambient 4 -0.31525 0.1199 284.3 -2.628  0.2690
## warmed 2 - warmed 5 -0.20326 0.1033 910.2 -1.968  0.7152
## warmed 2 - ambient 5 -0.18759 0.1200 272.4 -1.563  0.9206
## warmed 2 - warmed 6 -0.25657 0.1020 907.0 -2.514  0.3321
## warmed 2 - ambient 6 -0.24089 0.1179 259.3 -2.044  0.6629
## ambient 2 - warmed 3 -0.37630 0.1197 280.0 -3.143  0.0778
## ambient 2 - ambient 3 -0.36063 0.1047 908.5 -3.444  0.0294
## ambient 2 - warmed 4 -0.34660 0.1201 282.8 -2.886  0.1515
## ambient 2 - ambient 4 -0.33092 0.1043 906.1 -3.174  0.0678
## ambient 2 - warmed 5 -0.21894 0.1183 275.1 -1.850  0.7886
## ambient 2 - ambient 5 -0.20326 0.1033 910.2 -1.968  0.7152
## ambient 2 - warmed 6 -0.27224 0.1183 279.4 -2.301  0.4784
## ambient 2 - ambient 6 -0.25657 0.1020 907.0 -2.514  0.3321
## warmed 3 - ambient 3  0.01567 0.0594 20.9  0.264  1.0000
## warmed 3 - warmed 4  0.02971 0.1042 905.1  0.285  1.0000
## warmed 3 - ambient 4  0.04538 0.1193 280.9  0.381  1.0000
## warmed 3 - warmed 5  0.15737 0.1031 906.0  1.526  0.9332
## warmed 3 - ambient 5  0.17304 0.1192 271.0  1.452  0.9517

```

```

##  warmed 3 - warmed 6  0.10407 0.1018 908.0  1.022  0.9972
##  warmed 3 - ambient 6 0.11974 0.1170 253.2  1.023  0.9971
##  ambient 3 - warmed 4 0.01404 0.1207 287.6  0.116  1.0000
##  ambient 3 - ambient 4 0.02971 0.1042 905.1  0.285  1.0000
##  ambient 3 - warmed 5 0.14170 0.1188 282.1  1.192  0.9892
##  ambient 3 - ambient 5 0.15737 0.1031 906.0  1.526  0.9332
##  ambient 3 - warmed 6 0.08839 0.1188 281.5  0.744  0.9999
##  ambient 3 - ambient 6 0.10407 0.1018 908.0  1.022  0.9972
##  warmed 4 - ambient 4 0.01567 0.0594 20.9   0.264  1.0000
##  warmed 4 - warmed 5 0.12766 0.1014 903.3  1.259  0.9838
##  warmed 4 - ambient 5 0.14333 0.1185 266.4  1.210  0.9878
##  warmed 4 - warmed 6 0.07436 0.1001 904.8  0.743  0.9999
##  warmed 4 - ambient 6 0.09003 0.1163 249.1  0.774  0.9998
##  ambient 4 - warmed 5 0.11199 0.1166 270.5  0.960  0.9983
##  ambient 4 - ambient 5 0.12766 0.1014 903.3  1.259  0.9838
##  ambient 4 - warmed 6 0.05868 0.1166 270.3  0.503  1.0000
##  ambient 4 - ambient 6 0.07436 0.1001 904.8  0.743  0.9999
##  warmed 5 - ambient 5 0.01567 0.0594 20.9   0.264  1.0000
##  warmed 5 - warmed 6 -0.05330 0.0987 904.5 -0.540  1.0000
##  warmed 5 - ambient 6 -0.03763 0.1141 242.4 -0.330  1.0000
##  ambient 5 - warmed 6 -0.06897 0.1163 259.8 -0.593  1.0000
##  ambient 5 - ambient 6 -0.05330 0.0987 904.5 -0.540  1.0000
##  warmed 6 - ambient 6 0.01567 0.0594 20.9   0.264  1.0000
##
## Results are averaged over the levels of: species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 12 estimates

```

```
emmeans(mod7au, list(pairwise ~ year_factor), adjust = "tukey")
```

```

## boundary (singular) fit: see ?isSingular

## $`emmeans of year_factor`
##  year_factor emmean    SE  df lower.CL upper.CL
##  1      -2.76 0.0934 539     -2.94    -2.58
##  2      -3.00 0.0926 534     -3.19    -2.82
##  3      -2.64 0.0909 540     -2.82    -2.47
##  4      -2.67 0.0898 493     -2.85    -2.50
##  5      -2.80 0.0857 414     -2.97    -2.63
##  6      -2.75 0.0873 475     -2.92    -2.58
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of year_factor`
##  1      estimate    SE  df t.ratio p.value
##  1 - 2     0.2440 0.1055 903   2.313  0.1898
##  1 - 3    -0.1166 0.1046 906  -1.115  0.8752
##  1 - 4    -0.0869 0.1051 906  -0.827  0.9625
##  1 - 5     0.0408 0.1037 908   0.393  0.9988

```

```

## 1 - 6 -0.0125 0.1025 908 -0.122 1.0000
## 2 - 3 -0.3606 0.1047 908 -3.444 0.0079
## 2 - 4 -0.3309 0.1043 906 -3.174 0.0193
## 2 - 5 -0.2033 0.1033 910 -1.968 0.3617
## 2 - 6 -0.2566 0.1020 907 -2.514 0.1209
## 3 - 4 0.0297 0.1042 905 0.285 0.9997
## 3 - 5 0.1574 0.1031 906 1.526 0.6473
## 3 - 6 0.1041 0.1018 908 1.022 0.9106
## 4 - 5 0.1277 0.1014 903 1.259 0.8073
## 4 - 6 0.0744 0.1001 905 0.743 0.9765
## 5 - 6 -0.0533 0.0987 905 -0.540 0.9945
##
## Results are averaged over the levels of: state, species
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 6 estimates

emmeans(mod7au, list(pairwise ~ species), adjust = "tukey")

## boundary (singular) fit: see ?isSingular

## $`emmeans of species`
##   species emmean    SE df lower.CL upper.CL
##   Amla     -3.13 0.3364 840    -3.79    -2.47
##   Ansp     -3.62 0.2291 912    -4.07    -3.17
##   Apan     -2.57 0.3361 870    -3.23    -1.91
##   Assp     -3.14 0.1598 705    -3.45    -2.83
##   Asun     -3.35 0.6273 922    -4.58    -2.12
##   Cape     -2.37 0.0950 657    -2.55    -2.18
##   Cest     -1.44 0.0738 525    -1.58    -1.29
##   Dasp     -2.12 0.0776 560    -2.27    -1.97
##   Frve     -2.85 0.1746 652    -3.19    -2.51
##   Hisp     -3.58 0.1913 887    -3.95    -3.20
##   Hype     -3.30 0.1130 714    -3.52    -3.08
##   Posp     -2.21 0.0750 539    -2.36    -2.06
##   Ptaq     -2.09 0.0893 603    -2.27    -1.92
##   Ruac     -2.48 0.0888 595    -2.65    -2.30
##   Sosp     -2.89 0.1856 664    -3.25    -2.52
##   Syla     -3.21 0.2683 734    -3.74    -2.69
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of species`
##   1           estimate    SE df t.ratio p.value
##   Amla - Ansp  0.4958 0.409 876  1.214  0.9981
##   Amla - Apan -0.5577 0.473 906 -1.179  0.9986
##   Amla - Assp  0.0142 0.373 815  0.038  1.0000
##   Amla - Asun  0.2251 0.710 920  0.317  1.0000
##   Amla - Cape -0.7592 0.349 859 -2.175  0.7144
##   Amla - Cest -1.6880 0.344 871 -4.901  0.0001

```

```

## Amla - Dasp -1.0079 0.346 871 -2.917 0.2088
## Amla - Frve -0.2762 0.380 820 -0.727 1.0000
## Amla - Hisp 0.4527 0.388 907 1.167 0.9988
## Amla - Hype 0.1721 0.354 891 0.487 1.0000
## Amla - Posp -0.9183 0.345 873 -2.665 0.3549
## Amla - Ptaq -1.0350 0.348 883 -2.972 0.1830
## Amla - Ruac -0.6477 0.347 885 -1.864 0.8913
## Amla - Sosp -0.2384 0.384 892 -0.620 1.0000
## Amla - Syla 0.0872 0.429 897 0.203 1.0000
## Ansp - Apan -1.0535 0.408 920 -2.585 0.4107
## Ansp - Assp -0.4817 0.280 916 -1.723 0.9407
## Ansp - Asun -0.2708 0.670 921 -0.404 1.0000
## Ansp - Cape -1.2550 0.249 921 -5.046 0.0001
## Ansp - Cest -2.1838 0.241 921 -9.071 <.0001
## Ansp - Dasp -1.5037 0.242 921 -6.222 <.0001
## Ansp - Frve -0.7720 0.288 908 -2.683 0.3430
## Ansp - Hisp -0.0431 0.297 922 -0.145 1.0000
## Ansp - Hype -0.3237 0.256 920 -1.262 0.9970
## Ansp - Posp -1.4142 0.241 921 -5.863 <.0001
## Ansp - Ptaq -1.5309 0.246 921 -6.219 <.0001
## Ansp - Ruac -1.1436 0.246 919 -4.655 0.0004
## Ansp - Sosp -0.7343 0.294 875 -2.494 0.4771
## Ansp - Syla -0.4086 0.353 856 -1.156 0.9989
## Apan - Assp 0.5719 0.372 844 1.537 0.9779
## Apan - Asun 0.7827 0.711 918 1.101 0.9994
## Apan - Cape -0.2015 0.348 883 -0.578 1.0000
## Apan - Cest -1.1303 0.344 894 -3.285 0.0791
## Apan - Dasp -0.4502 0.345 895 -1.304 0.9957
## Apan - Frve 0.2815 0.379 827 0.742 1.0000
## Apan - Hisp 1.0104 0.388 901 2.605 0.3961
## Apan - Hype 0.7298 0.353 907 2.066 0.7863
## Apan - Posp -0.3607 0.344 891 -1.048 0.9997
## Apan - Ptaq -0.4773 0.348 905 -1.373 0.9927
## Apan - Ruac -0.0900 0.347 903 -0.259 1.0000
## Apan - Sosp 0.3192 0.385 868 0.829 1.0000
## Apan - Syla 0.6449 0.430 843 1.500 0.9825
## Assp - Asun 0.2109 0.647 921 0.326 1.0000
## Assp - Cape -0.7734 0.186 823 -4.162 0.0036
## Assp - Cest -1.7021 0.176 872 -9.668 <.0001
## Assp - Dasp -1.0220 0.178 885 -5.754 <.0001
## Assp - Frve -0.2903 0.236 853 -1.232 0.9977
## Assp - Hisp 0.4385 0.250 910 1.757 0.9306
## Assp - Hype 0.1579 0.196 877 0.808 1.0000
## Assp - Posp -0.9325 0.177 869 -5.281 <.0001
## Assp - Ptaq -1.0492 0.183 888 -5.733 <.0001
## Assp - Ruac -0.6619 0.183 881 -3.624 0.0270
## Assp - Sosp -0.2526 0.245 843 -1.031 0.9997
## Assp - Syla 0.0730 0.311 871 0.235 1.0000
## Asun - Cape -0.9842 0.634 922 -1.552 0.9759
## Asun - Cest -1.9130 0.632 921 -3.029 0.1590
## Asun - Dasp -1.2329 0.632 921 -1.950 0.8516
## Asun - Frve -0.5012 0.651 921 -0.770 1.0000
## Asun - Hisp 0.2276 0.656 919 0.347 1.0000
## Asun - Hype -0.0530 0.637 921 -0.083 1.0000

```

```

##  Asun - Posp -1.1434 0.632 921 -1.810 0.9126
##  Asun - Ptaq -1.2601 0.634 921 -1.989 0.8311
##  Asun - Ruac -0.8728 0.633 921 -1.378 0.9924
##  Asun - Sosp -0.4635 0.653 914 -0.710 1.0000
##  Asun - Syla -0.1379 0.680 902 -0.203 1.0000
##  Cape - Cest -0.9288 0.120 920 -7.719 <.0001
##  Cape - Dasp -0.2487 0.123 921 -2.023 0.8121
##  Cape - Frve 0.4830 0.199 831 2.430 0.5253
##  Cape - Hisp 1.2119 0.214 920 5.661 <.0001
##  Cape - Hype 0.9313 0.147 911 6.337 <.0001
##  Cape - Posp -0.1592 0.121 919 -1.316 0.9953
##  Cape - Ptaq -0.2758 0.131 920 -2.112 0.7572
##  Cape - Ruac 0.1114 0.130 902 0.857 1.0000
##  Cape - Sosp 0.5207 0.209 797 2.489 0.4806
##  Cape - Syla 0.8464 0.285 771 2.972 0.1833
##  Cest - Dasp 0.6801 0.107 904 6.350 <.0001
##  Cest - Frve 1.4118 0.190 818 7.448 <.0001
##  Cest - Hisp 2.1407 0.205 921 10.438 <.0001
##  Cest - Hype 1.8601 0.135 921 13.784 <.0001
##  Cest - Posp 0.7696 0.105 900 7.313 <.0001
##  Cest - Ptaq 0.6529 0.116 919 5.634 <.0001
##  Cest - Ruac 1.0402 0.115 919 9.008 <.0001
##  Cest - Sosp 1.4495 0.200 811 7.256 <.0001
##  Cest - Syla 1.7752 0.278 805 6.379 <.0001
##  Dasp - Frve 0.7317 0.191 814 3.832 0.0130
##  Dasp - Hisp 1.4606 0.206 922 7.084 <.0001
##  Dasp - Hype 1.1800 0.137 922 8.596 <.0001
##  Dasp - Posp 0.0895 0.108 905 0.829 1.0000
##  Dasp - Ptaq -0.0272 0.118 918 -0.230 1.0000
##  Dasp - Ruac 0.3601 0.118 918 3.052 0.1500
##  Dasp - Sosp 0.7694 0.201 807 3.827 0.0132
##  Dasp - Syla 1.0950 0.279 809 3.921 0.0093
##  Frve - Hisp 0.7289 0.258 921 2.823 0.2578
##  Frve - Hype 0.4483 0.208 841 2.154 0.7289
##  Frve - Posp -0.6422 0.190 823 -3.378 0.0600
##  Frve - Ptaq -0.7589 0.196 805 -3.871 0.0112
##  Frve - Ruac -0.3716 0.196 825 -1.898 0.8766
##  Frve - Sosp 0.0377 0.254 840 0.148 1.0000
##  Frve - Syla 0.3634 0.319 879 1.140 0.9990
##  Hisp - Hype -0.2806 0.223 919 -1.258 0.9971
##  Hisp - Posp -1.3711 0.205 921 -6.680 <.0001
##  Hisp - Ptaq -1.4877 0.211 922 -7.054 <.0001
##  Hisp - Ruac -1.1004 0.211 921 -5.213 <.0001
##  Hisp - Sosp -0.6911 0.265 904 -2.605 0.3966
##  Hisp - Syla -0.3655 0.329 905 -1.110 0.9993
##  Hype - Posp -1.0905 0.135 921 -8.048 <.0001
##  Hype - Ptaq -1.2071 0.144 920 -8.382 <.0001
##  Hype - Ruac -0.8198 0.143 921 -5.723 <.0001
##  Hype - Sosp -0.4105 0.218 812 -1.884 0.8829
##  Hype - Syla -0.0849 0.291 835 -0.292 1.0000
##  Posp - Ptaq -0.1167 0.117 920 -1.001 0.9998
##  Posp - Ruac 0.2706 0.116 920 2.328 0.6030
##  Posp - Sosp 0.6799 0.200 814 3.396 0.0569
##  Posp - Syla 1.0055 0.279 806 3.610 0.0285

```

```

##  Ptaq - Ruac  0.3873 0.126 922  3.073  0.1421
##  Ptaq - Sosp  0.7966 0.206 827  3.872  0.0112
##  Ptaq - Syla  1.1222 0.283 833  3.972  0.0076
##  Ruac - Sosp  0.4093 0.206 831  1.989  0.8310
##  Ruac - Syla  0.7349 0.282 835  2.603  0.3978
##  Sosp - Syla  0.3256 0.324 922  1.005  0.9998
##
## Results are averaged over the levels of: state, year_factor
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 16 estimates

```

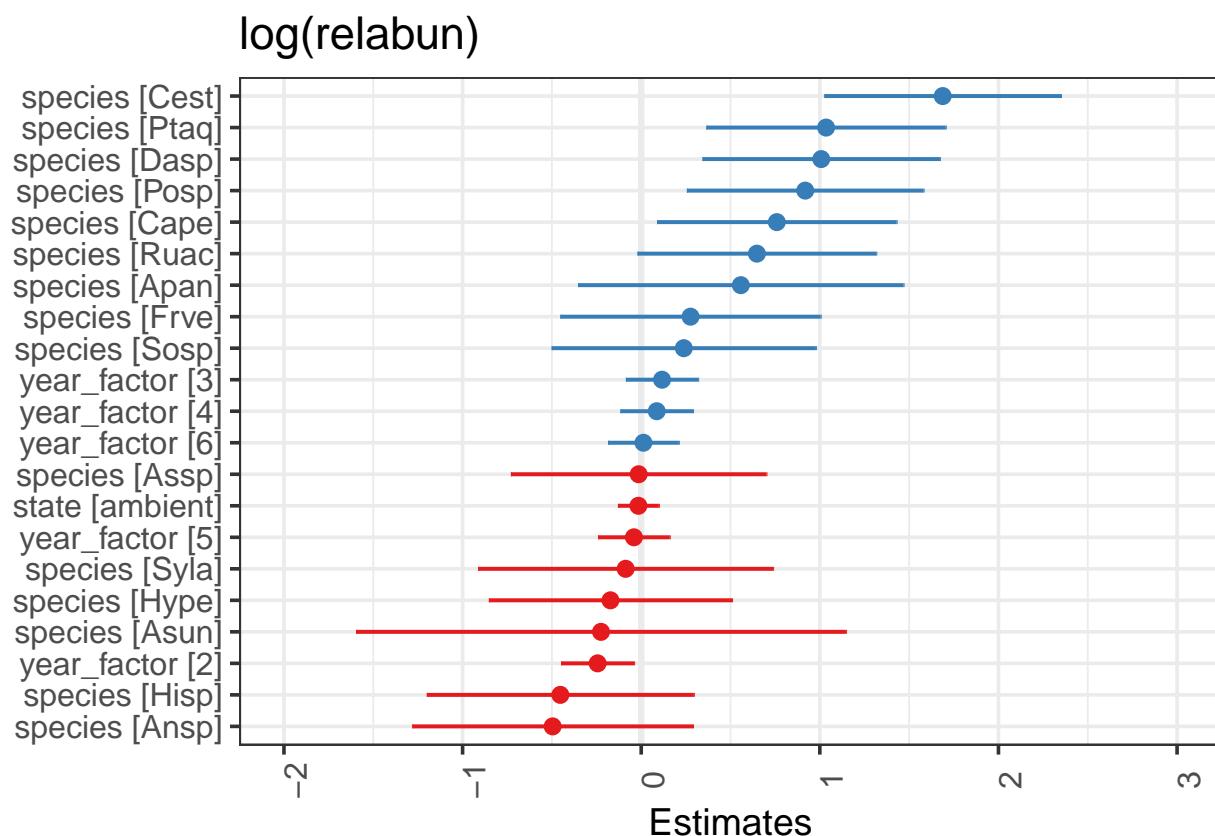
```
emmeans(mod7au, list(pairwise ~ insecticide), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Error in emmeans(object = object, specs = specs[[i]], name = contr.name, : No variable named insecticid
```

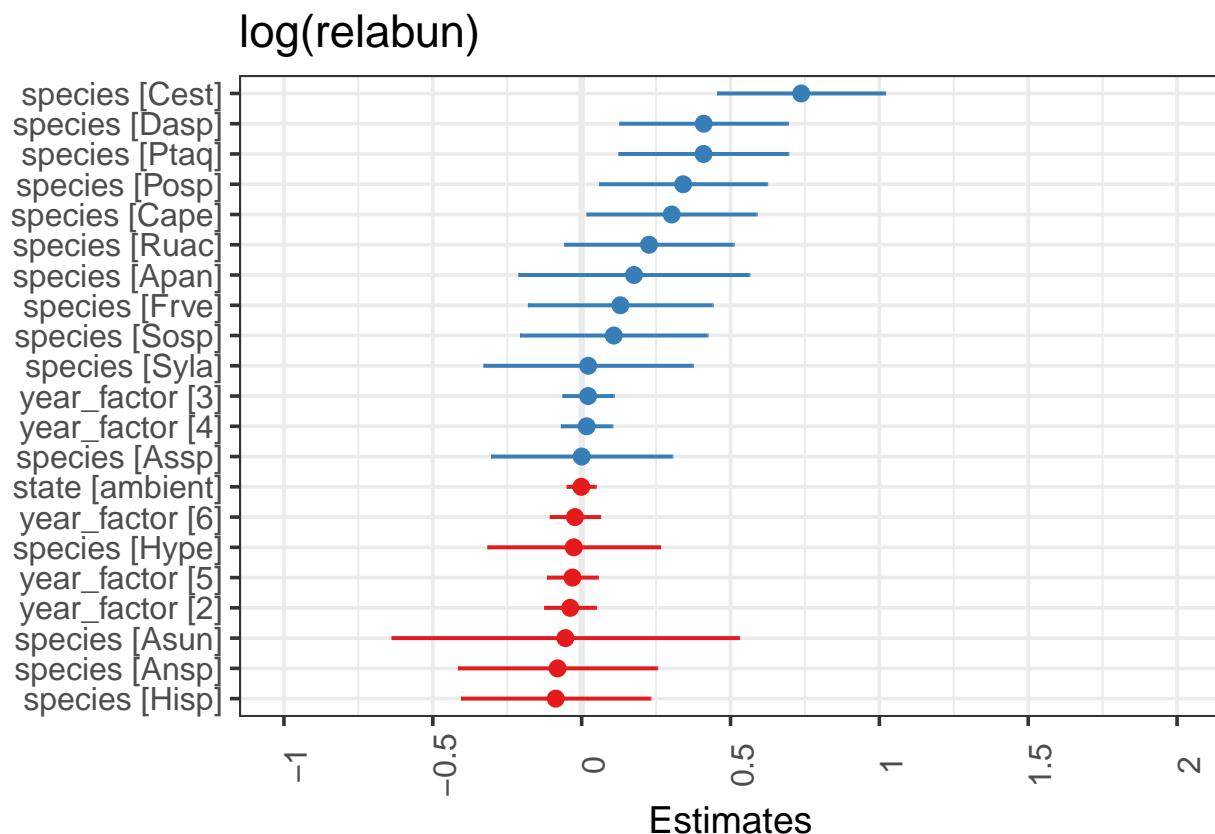
Take a look at the estimates for each fixed effect. These are the estimates from summary(mod7a). You'll see that species vary a lot - and many of them are different from zero (meaning their half cover date is significantly different from zero).

```
plot_model(mod7au, sort.est = TRUE)
```



```
# if you want to standardize the estimates:  
plot_model(mod7au, sort.est = TRUE, type = "std")
```

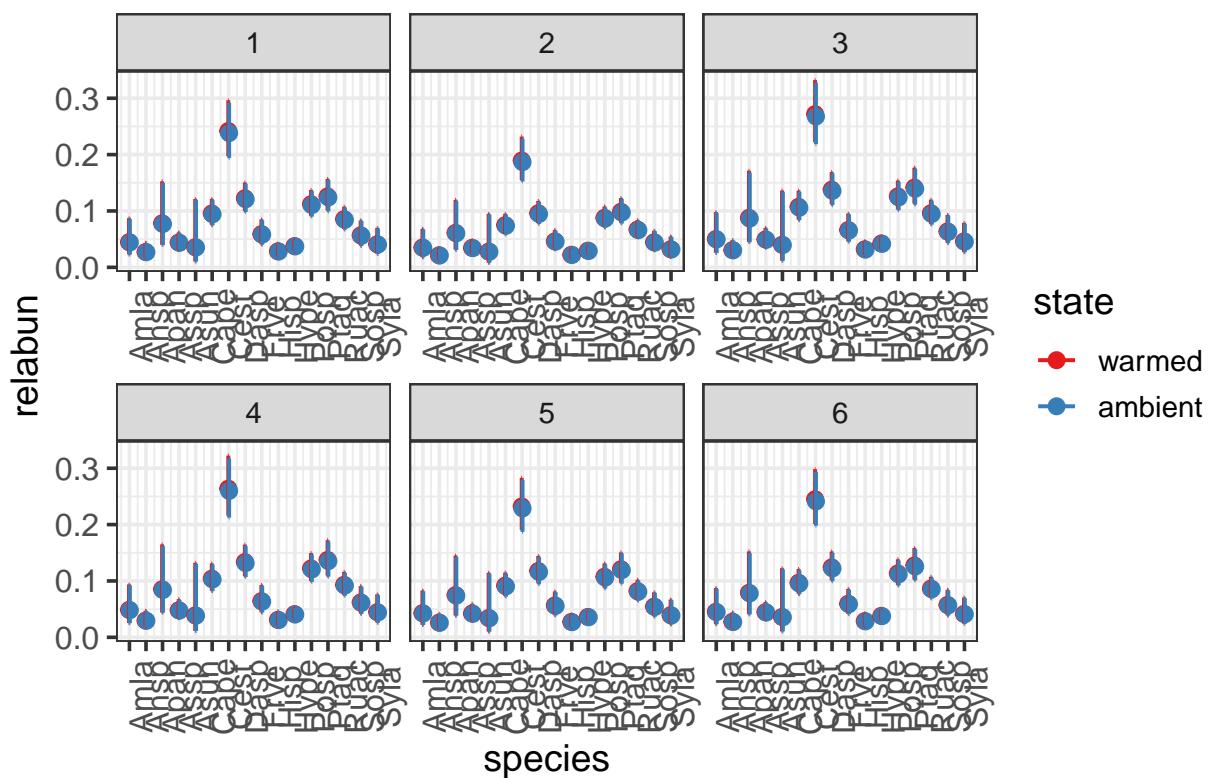
```
## Formula contains log- or sqrt-terms. See help("standardize") for how such terms are standardized.  
## boundary (singular) fit: see ?isSingular
```



```
# these are the fixed predicted values: - note this is a new plot  
plot_model(mod7au, type = "pred", terms = c("species", "state", "year_factor"))
```

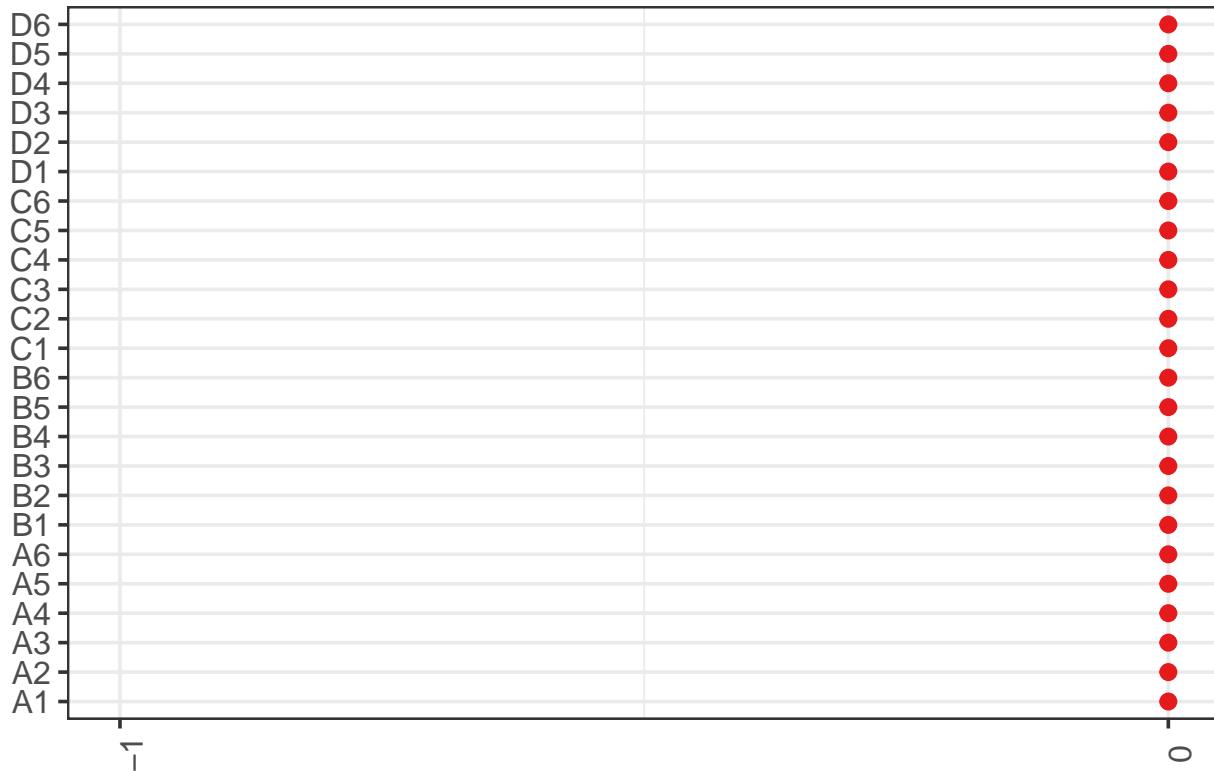
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standard
```

Predicted values of relabun



```
# these are the random effects estimates  
plot_model(mod7au, type = "re")
```

Random effects



```
# including native vs. exotic
comp_umbs_spp <- within(comp_umbs_spp, origin <- relevel(factor(origin), ref = "Native")) # releveling
mod8u <- lmer(log(relabun) ~ state * origin + (1 + factor(year_factor) | plot), comp_umbs_spp,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9u <- lmer(log(relabun) ~ state + origin + (1 + factor(year_factor) | plot), comp_umbs_spp,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9au <- lmer(log(relabun) ~ state + origin + factor(year_factor) + (1 | plot),
comp_umbs_spp, REML = FALSE)
anova(mod8u, mod9u) # model 8 is a better fit to data

## Data: comp_umbs_spp
## Models:
## mod9u: log(relabun) ~ state + origin + (1 + factor(year_factor) | plot)
## mod8u: log(relabun) ~ state * origin + (1 + factor(year_factor) | plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod9u    27 2621.8 2751.4 -1283.9    2567.8
## mod8u    30 2627.0 2771.1 -1283.5    2567.0 0.7828  3      0.8536
```

```

anova(mod8u, mod9au) # mod 8

## Data: comp_umbs_spp
## Models:
## mod9au: log(relabun) ~ state + origin + factor(year_factor) + (1 | plot)
## mod8u: log(relabun) ~ state * origin + (1 + factor(year_factor) | plot)
##      npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod9au    12 2583.7 2641.3 -1279.8   2559.7
## mod8u     30 2627.0 2771.1 -1283.5   2567.0      0 18          1

```

```
summary(mod8u)
```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(relabun) ~ state * origin + (1 + factor(year_factor) | plot)
##   Data: comp_umbs_spp
##
##      AIC      BIC  logLik deviance df.resid
##  2627.0  2771.1 -1283.5   2567.0      869
##
## Scaled residuals:
##    Min      1Q  Median      3Q      Max
## -2.54061 -0.77846  0.04232  0.78209  2.24494
##
## Random effects:
##   Groups   Name        Variance Std.Dev. Corr
##   plot     (Intercept) 2.014e-02 0.141917
##   factor(year_factor)2 1.163e-02 0.107852  1.00
##   factor(year_factor)3 1.131e-02 0.106354 -1.00 -1.00
##   factor(year_factor)4 1.601e-03 0.040017 -1.00 -1.00  1.00
##   factor(year_factor)5 1.676e-03 0.040935  1.00  1.00 -1.00 -1.00
##   factor(year_factor)6 3.975e-05 0.006305  1.00  1.00 -1.00 -1.00  1.00
##   Residual           1.000e+00 1.000115
## Number of obs: 899, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) -2.30401  0.08103 87.70938 -28.435 < 2e-16 ***
## stateambient -0.03656  0.11440 84.65273 -0.320  0.750  
## origin       0.12919  0.13864 881.74943  0.932  0.352  
## originBoth   -1.04643  0.24208 892.65169 -4.323 1.72e-05 ***
## originExotic  0.17270  0.10806 891.01134  1.598  0.110  
## stateambient:origin  0.01978  0.19670 882.49410  0.101  0.920  
## stateambient:originBoth  0.23995  0.30595 894.80086  0.784  0.433  
## stateambient:originExotic  0.08270  0.15286 889.09586  0.541  0.589  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) sttmbn origin orgnBt orgnEx sttmB: sttm:B
## stateambint -0.708
## origin      -0.457  0.323

```

```

## originBoth -0.262 0.186 0.152
## originExotc -0.581 0.412 0.342 0.197
## sttmbnt:rgn 0.322 -0.453 -0.705 -0.107 -0.241
## sttmbnt:rgB 0.208 -0.293 -0.120 -0.791 -0.156 0.165
## sttmbnt:rgE 0.411 -0.574 -0.242 -0.139 -0.707 0.334 0.214
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
anova(mod8u)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state       0.212  0.2125     1   66.53  0.2124    0.6464
## origin      55.747 18.5823     3 889.52 18.5780 1.075e-11 ***
## state:origin 0.785  0.2617     3 889.52  0.2617    0.8530
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
emmeans(mod8u, list(pairwise ~ state * origin), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -1.8e+00
```

```

## $`emmeans of state, origin`
##   state origin emmean    SE   df lower.CL upper.CL
##   warmed Native -2.30 0.0946 73.6   -2.49   -2.12
##   ambient Native -2.34 0.0948 72.3   -2.53   -2.15
##   warmed          -2.17 0.1332 331.4   -2.44   -1.91
##   ambient          -2.19 0.1347 338.2   -2.46   -1.93
##   warmed Both     -3.35 0.2472 692.6   -3.84   -2.86
##   ambient Both    -3.15 0.1897 453.1   -3.52   -2.77
##   warmed Exotic  -2.13 0.1017 108.5   -2.33   -1.93
##   ambient Exotic -2.09 0.1035 113.8   -2.29   -1.88
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin`
##   1                         estimate    SE   df t.ratio p.value
##   warmed Native - ambient Native  0.0366 0.134 73.5  0.273  1.0000
##   warmed Native - warmed          -0.1292 0.140 792.8 -0.924  0.9838
##   warmed Native - ambient          -0.1124 0.165 199.1 -0.683  0.9974
##   warmed Native - warmed Both    1.0464 0.250 852.5  4.189  0.0008
##   warmed Native - ambient Both   0.8430 0.212 317.0  3.978  0.0022
##   warmed Native - warmed Exotic -0.1727 0.110 817.3 -1.575  0.7654
##   warmed Native - ambient Exotic -0.2188 0.140  93.8 -1.561  0.7718
##   ambient Native - warmed         -0.1657 0.163 193.7 -1.014  0.9719
##   ambient Native - ambient        -0.1490 0.141 795.7 -1.058  0.9651
##   ambient Native - warmed Both   1.0099 0.265 556.3  3.814  0.0038
##   ambient Native - ambient Both  0.8065 0.192 828.8  4.192  0.0008

```

```

## ambient Native - warmed Exotic -0.2093 0.139 90.2 -1.505 0.8029
## ambient Native - ambient Exotic -0.2554 0.110 811.1 -2.330 0.2785
## warmed - ambient 0.0168 0.189 335.3 0.089 1.0000
## warmed - warmed Both 1.1756 0.268 848.2 4.391 0.0003
## warmed - ambient Both 0.9722 0.232 422.7 4.195 0.0009
## warmed - warmed Exotic -0.0435 0.145 787.3 -0.300 1.0000
## warmed - ambient Exotic -0.0897 0.169 220.3 -0.532 0.9995
## ambient - warmed Both 1.1588 0.282 621.8 4.116 0.0011
## ambient - ambient Both 0.9555 0.217 824.5 4.406 0.0003
## ambient - warmed Exotic -0.0603 0.169 221.2 -0.357 1.0000
## ambient - ambient Exotic -0.1064 0.147 793.7 -0.723 0.9963
## warmed Both - ambient Both -0.2034 0.312 630.3 -0.653 0.9981
## warmed Both - warmed Exotic -1.2191 0.253 849.5 -4.823 <.0001
## warmed Both - ambient Exotic -1.2653 0.268 581.7 -4.721 0.0001
## ambient Both - warmed Exotic -1.0157 0.215 338.0 -4.719 0.0001
## ambient Both - ambient Exotic -1.0619 0.198 831.9 -5.373 <.0001
## warmed Exotic - ambient Exotic -0.0461 0.145 111.2 -0.318 1.0000
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 8 estimates

# including growth form - first with interaction term
comp_umbs_spp <- within(comp_umbs_spp, growth_habit <- relevel(factor(growth_habit),
  ref = "Forb")) # releveling so forb is the reference
mod10u <- lmer(log(relabun) ~ state * growth_habit + (1 + factor(year_factor) | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11u <- lmer(log(relabun) ~ state + growth_habit + (1 + factor(year_factor) | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11au <- lmer(log(relabun) ~ state + growth_habit + factor(year_factor) + (1 |
  plot), comp_umbs_spp, REML = FALSE)
anova(mod10u, mod11u) # model 10 is a better fit to data

## Data: comp_umbs_spp
## Models:
## mod11u: log(relabun) ~ state + growth_habit + (1 + factor(year_factor) |
## mod11u:      plot)
## mod10u: log(relabun) ~ state * growth_habit + (1 + factor(year_factor) |
## mod10u:      plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod11u   27 2640.3 2770.0 -1293.2   2586.3
## mod10u   30 2645.4 2789.4 -1292.7   2585.4 0.9457  3     0.8144

anova(mod10u, mod11au) # model 10 is still a better fit to data

```

```

## Data: comp_umbs_spp
## Models:
## mod11au: log(relabun) ~ state + growth_habit + factor(year_factor) + (1 |
## mod11au:      plot)
## mod10u: log(relabun) ~ state * growth_habit + (1 + factor(year_factor) | 
## mod10u:      plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod11au   12 2601.0 2658.6 -1288.5   2577.0
## mod10u    30 2645.4 2789.4 -1292.7   2585.4      0 18           1

summary(mod10u)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(relabun) ~ state * growth_habit + (1 + factor(year_factor) | 
##      plot)
## Data: comp_umbs_spp
##
##      AIC      BIC  logLik deviance df.resid
## 2645.4  2789.4 -1292.7   2585.4     869
##
## Scaled residuals:
##    Min     1Q   Median     3Q    Max
## -2.61209 -0.79411  0.01286  0.77480  2.16420
##
## Random effects:
## Groups   Name        Variance Std.Dev. Corr
## plot     (Intercept) 2.235e-02 0.149511
##          factor(year_factor)2 1.460e-02 0.120821  1.00
##          factor(year_factor)3 1.196e-02 0.109348 -1.00 -1.00
##          factor(year_factor)4 2.890e-03 0.053762 -1.00 -1.00  1.00
##          factor(year_factor)5 1.666e-06 0.001291 -1.00 -1.00  1.00  1.00
##          factor(year_factor)6 5.134e-05 0.007165 -1.00 -1.00  1.00  1.00  1.00
## Residual             1.021e+00 1.010624
## Number of obs: 899, groups: plot, 24
##
## Fixed effects:
##                               Estimate Std. Error      df t value
## (Intercept)            -2.251e+00 7.442e-02 6.041e+01 -30.246
## stateambient          -6.641e-02 1.053e-01 5.785e+01 -0.630
## growth_habit          -1.139e+00 3.128e-01 8.797e+02 -3.642
## growth_habitGraminoid  3.689e-02 1.000e-01 8.923e+02  0.369
## growth_habitTree       -9.170e-01 5.923e-01 8.398e+02 -1.548
## stateambient:growth_habit -4.102e-04 4.253e-01 8.861e+02 -0.001
## stateambient:growth_habitGraminoid 1.282e-01 1.409e-01 8.936e+02  0.910
## stateambient:growth_habitTree  3.108e-01 7.838e-01 8.471e+02  0.397
##                               Pr(>|t|)
## (Intercept)            < 2e-16 ***
## stateambient          0.530930
## growth_habit          0.000286 ***
## growth_habitGraminoid 0.712246
## growth_habitTree      0.121965
## stateambient:growth_habit 0.999231
## stateambient:growth_habitGraminoid 0.363124

```

```

## stateambient:growth_habitTree      0.691795
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttmbn grwth_ grwt_G grwt_T sttm:_ stt:_G
## stateambint -0.706
## growth_habit -0.184  0.130
## grwth_hbtGr -0.559  0.395  0.128
## grwth_hbtTr -0.087  0.062  0.026  0.061
## sttmbnt:gr_  0.135 -0.197 -0.735 -0.094 -0.019
## sttmbnt:g_G  0.397 -0.560 -0.091 -0.710 -0.043  0.132
## sttmbnt:g_T  0.066 -0.098 -0.020 -0.046 -0.756  0.027  0.069
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
anova(mod10u)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state        0.036  0.0364     1 502.57  0.0356   0.8504
## growth_habit 37.957 12.6525     3 874.63 12.3879 6.114e-08 ***
## state:growth_habit 0.977  0.3255     3 874.63  0.3187   0.8118
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
emmeans(mod10u, list(pairwise ~ factor(year_factor) * growth_habit), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Error in emmeans(object = object, specs = specs[[i]], name = contr.name, : No variable named year_fa
```

*# New version of our model incorporating interaction term and species within year
so that there is a separate intercept and slope for each species. The issue
here is that there are some species that are not found each year. Easiest to
remove those from another version of this dataframe before running below.
Otherwise, it's not a balanced design. updated mod4*

```
mod12u <- lmer(log(relabun) ~ state * factor(year_factor) + (1 + factor(year_factor) |  

  species), comp_umbs_spp)
```

```
## boundary (singular) fit: see ?isSingular
```

*# So another version of this model would include the interaction but not include
the nesting (and thus would assume that species aren't observed ea yr) updated
mod5*

```
mod13u <- lmer(log(relabun) ~ state * factor(year_factor) + (1 | species), comp_umbs_spp)

# All the models ran:
mod1u <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |  

  species) + (1 | plot), comp_umbs_spp, REML = FALSE)
```

```
## boundary (singular) fit: see ?isSingular
```

```

mod2u <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |
  species), comp_umbs_spp, REML = FALSE)
mod3u <- lmer(log(relabun) ~ state * year_factor + (1 | species), comp_umbs_spp,
  REML = FALSE)
mod4u <- lmer(log(relabun) ~ state * year_factor + insecticide + (1 | species) +
  (1 | plot), comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod5u <- lmer(log(relabun) ~ state + year_factor + (1 | species), comp_umbs_spp,
  REML = FALSE)
mod6u <- lmer(log(relabun) ~ state + year_factor + (1 | species) + (1 + year | plot),
  comp_umbs_spp, REML = FALSE)

## Error in eval(predvars, data, env): object 'year' not found

mod7u <- lmer(log(relabun) ~ state + species + (1 + factor(year_factor) | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

## Warning: Model failed to converge with 1 negative eigenvalue: -8.0e+00

mod7au <- lmer(log(relabun) ~ state + species + factor(year_factor) + (1 | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7bu <- lmer(log(relabun) ~ state * factor(year_factor) + species + (1 | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod7cu <- lmer(log(relabun) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod8u <- lmer(log(relabun) ~ state * origin + (1 + factor(year_factor) | plot), comp_umbs_spp,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod9u <- lmer(log(relabun) ~ state + origin + (1 + factor(year_factor) | plot), comp_umbs_spp,
  REML = FALSE)

## boundary (singular) fit: see ?isSingular

```

```

mod9au <- lmer(log(relabun) ~ state + origin + factor(year_factor) + (1 | plot),
  comp_umbs_spp, REML = FALSE)
mod10u <- lmer(log(relabun) ~ state * growth_habit + (1 + factor(year_factor) | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11u <- lmer(log(relabun) ~ state + growth_habit + (1 + factor(year_factor) | plot),
  comp_umbs_spp, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod11au <- lmer(log(relabun) ~ state + growth_habit + factor(year_factor) + (1 |
  plot), comp_umbs_spp, REML = FALSE)
mod12u <- lmer(log(relabun) ~ state * factor(year_factor) + (1 + factor(year_factor) |
  species), comp_umbs_spp)

## boundary (singular) fit: see ?isSingular

mod13u <- lmer(log(relabun) ~ state * factor(year_factor) + (1 | species), comp_umbs_spp)
AICctab(mod1u, mod2u, mod3u, mod5u, mod6u, mod7u, mod7au, mod7bu, mod7cu, mod8u,
  mod9u, mod9au, mod10u, mod11u, mod11au, mod13u, weights = T) #mod7a is the best fitting model (too

##          dAICc df weight
## mod7au     0.0 24 0.684
## mod7cu    1.7 25 0.290
## mod7bu   6.5 29 0.026
## mod5u   34.1  5 <0.001
## mod3u   35.5  6 <0.001
## mod2u   38.6  8 <0.001
## mod6u   40.2  8 <0.001
## mod1u   40.6  9 <0.001
## mod7u   47.3 39 <0.001
## mod13u  64.2 14 <0.001
## mod9au  235.7 12 <0.001
## mod11au 253.0 12 <0.001
## mod9u   275.2 27 <0.001
## mod8u   280.9 30 <0.001
## mod11u  293.8 27 <0.001
## mod10u  299.2 30 <0.001

summary(mod7au)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
## method [lmerModLmerTest]
## Formula: log(relabun) ~ state + species + factor(year_factor) + (1 | plot)
## Data: comp_umbs_spp
##
##          AIC      BIC      logLik deviance df.resid
## 2346.9  2462.2 -1149.5   2298.9     875

```

```

## Scaled residuals:
##      Min     1Q Median     3Q    Max
## -3.2474 -0.7044  0.0280  0.7063  2.6539
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   plot      (Intercept) 0.0000  0.0000
##   Residual           0.7553  0.8691
## Number of obs: 899, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error       df t value Pr(>|t|)    
## (Intercept) -3.10745  0.34107 899.00000 -9.111 < 2e-16 ***
## stateambient -0.01567  0.05839 899.00000 -0.268 0.78846  
## speciesAnsp  -0.49583  0.40091 899.00000 -1.237 0.21649  
## speciesApan  0.55769  0.46483 899.00000  1.200 0.23054  
## speciesAssp  -0.01418  0.36498 899.00000 -0.039 0.96903  
## speciesAsun  -0.22506  0.69954 899.00000 -0.322 0.74773  
## speciesCape  0.75918  0.34226 899.00000  2.218 0.02680 *   
## speciesCest  1.68795  0.33791 899.00000  4.995 7.06e-07 ***
## speciesDasp  1.00785  0.33901 899.00000  2.973 0.00303 **  
## speciesFrve 0.27617  0.37191 899.00000  0.743 0.45793  
## speciesHisp -0.45271  0.38135 899.00000 -1.187 0.23549  
## speciesHype -0.17211  0.34724 899.00000 -0.496 0.62027  
## speciesPosp  0.91835  0.33807 899.00000  2.716 0.00673 **  
## speciesPtaq  1.03503  0.34184 899.00000  3.028 0.00253 **  
## speciesRuac  0.64773  0.34103 899.00000  1.899 0.05784 .  
## speciesSosp  0.23844  0.37741 899.00000  0.632 0.52770  
## speciesSyla -0.08720  0.42122 899.00000 -0.207 0.83605  
## factor(year_factor)2 -0.24404  0.10419 899.00000 -2.342 0.01939 * 
## factor(year_factor)3  0.11660  0.10324 899.00000  1.129 0.25905  
## factor(year_factor)4  0.08689  0.10373 899.00000  0.838 0.40245  
## factor(year_factor)5 -0.04077  0.10238 899.00000 -0.398 0.69055  
## factor(year_factor)6  0.01253  0.10117 899.00000  0.124 0.90145  
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Correlation matrix not shown by default, as p = 22 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

[anova](#)(mod7au)

```

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state          0.054  0.0544     1    899  0.0720  0.788461
## species        295.084 19.6722    15    899 26.0460 < 2.2e-16 ***
## factor(year_factor) 11.599  2.3197     5    899  3.0713  0.009337 **
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

UBS Plot-level Mixed Effects Models:

```
mod1pu <- lmer(log(plot_cover_avg) ~ state + (1 | plot), comp_umbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod2pu <- lmer(log(plot_cover_avg) ~ insecticide + (1 | plot), comp_umbs_plot, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod3pu <- lmer(log(plot_cover_avg) ~ insecticide + state + (1 | plot), comp_umbs_plot,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod4pu <- lmer(log(plot_cover_avg) ~ insecticide * state + (1 | plot), comp_umbs_plot,
REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod5pu <- lmer(log(plot_cover_avg) ~ state + year_factor + (1 | plot), comp_umbs_plot,
REML = FALSE)
mod6pu <- lmer(log(plot_cover_avg) ~ state + year_factor + insecticide + (1 | plot),
comp_umbs_plot, REML = FALSE)
mod7pu <- lmer(log(plot_cover_avg) ~ state * year_factor + (1 | plot), comp_umbs_plot,
REML = FALSE)
mod8pu <- lmer(log(plot_cover_avg) ~ state * year_factor + insecticide + (1 | plot),
comp_umbs_plot, REML = FALSE)
mod9pu <- lmer(log(plot_cover_avg) ~ state * insecticide + year_factor + (1 | plot),
comp_umbs_plot, REML = FALSE)
mod10pu <- lmer(log(plot_cover_avg) ~ state + insecticide * year_factor + (1 | plot),
comp_umbs_plot, REML = FALSE)
mod11pu <- lmer(log(plot_cover_avg) ~ state * year_factor * insecticide + (1 | plot),
comp_umbs_plot, REML = FALSE)
AICctab(mod1pu, mod2pu, mod3pu, mod4pu, mod5pu, mod6pu, mod7pu, mod8pu, mod9pu, mod10pu,
mod11pu, weights = T) # model 11p and 10p the same

##          dAICc df weight
## mod7pu     0.0 6  0.547
## mod8pu     2.0 7  0.202
## mod5pu     2.6 5  0.149
## mod6pu     4.6 6  0.056
## mod10pu    6.7 7  0.019
## mod9pu     6.8 7  0.019
## mod11pu    8.5 10 0.008
```

```

## mod2pu 254.8 4 <0.001
## mod1pu 254.9 4 <0.001
## mod3pu 257.0 5 <0.001
## mod4pu 259.2 6 <0.001

anova(mod7pu, mod8pu) #7p just barely better

## Data: comp_umbs_plot
## Models:
## mod7pu: log(plot_cover_avg) ~ state * year_factor + (1 | plot)
## mod8pu: log(plot_cover_avg) ~ state * year_factor + insecticide + (1 |
## mod8pu:      plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod7pu     6 23.621 41.440 -5.8104   11.621
## mod8pu     7 25.399 46.188 -5.6996   11.399 0.2216  1      0.6378

summ(mod7pu)

```

Observations	144
Dependent variable	log(plot_cover_avg)
Type	Mixed effects linear regression

AIC	23.62
BIC	41.44
Pseudo-R ² (fixed effects)	0.83
Pseudo-R ² (total)	0.85

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	5.02	0.07	71.99	123.04	0.00
stateambient	0.19	0.10	1.90	123.04	0.06
year_factor	-0.30	0.02	-18.49	120.00	0.00
stateambient:year_factor	-0.05	0.02	-2.21	120.00	0.03

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.10
	Residual	0.24

Grouping Variables		
Group	# groups	ICC
plot	24	0.14

```
summ(mod8pu)
```

Observations	144
Dependent variable	log(plot_cover_avg)
Type	Mixed effects linear regression

AIC	25.40
BIC	46.19
Pseudo-R ² (fixed effects)	0.83
Pseudo-R ² (total)	0.85

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	5.01	0.07	66.79	100.44	0.00
stateambient	0.19	0.10	1.90	123.50	0.06
year_factor	-0.30	0.02	-18.49	120.00	0.00
insecticideno_insects	0.03	0.06	0.47	24.00	0.64
stateambient:year_factor	-0.05	0.02	-2.21	120.00	0.03

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.10
	Residual	0.24

Grouping Variables		
Group	# groups	ICC
plot	24	0.14

```
emmeans(mod8pu, list(pairwise ~ state * year_factor), adjust = "tukey")
```

```
## $`emmeans of state, year_factor`  
##   state    year_factor emmean     SE   df lower.CL upper.CL  
##   warmed      3.5  3.96 0.042 27.4     3.87    4.04  
##   ambient      3.5  3.96 0.042 27.4     3.88    4.05  
##  
## Results are averaged over the levels of: insecticide  
## Degrees-of-freedom method: kenward-roger  
## Results are given on the log (not the response) scale.  
## Confidence level used: 0.95  
##  
## $`pairwise differences of state, year_factor`  
##   1                  estimate     SE   df t.ratio p.value  
##   warmed 3.5 - ambient 3.5 -0.00785 0.0594 27.4 -0.132  0.8958  
##
```

```

## Results are averaged over the levels of: insecticide
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.

# including native vs. exotic
umbc_comp_plot_origin <- within(umbc_comp_plot_origin, origin <- relevel(factor(origin),
  ref = "Native")) # releveling so native is the reference
mod12pu <- lmer(log(plot_cover_avg) ~ state * origin + (1 + year_factor | plot),
  umbc_comp_plot_origin, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod13pu <- lmer(log(plot_cover_avg) ~ state + origin + (1 + year_factor | plot),
  umbc_comp_plot_origin, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod14pu <- lmer(log(plot_cover_avg) ~ state + origin + year_factor + (1 | plot),
  umbc_comp_plot_origin, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod12pu, mod13pu) # go with model 13pu

## Data: umbc_comp_plot_origin
## Models:
## mod13pu: log(plot_cover_avg) ~ state + origin + (1 + year_factor | plot)
## mod12pu: log(plot_cover_avg) ~ state * origin + (1 + year_factor | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod13pu     9 1255.1 1292.5 -618.55    1237.1
## mod12pu    12 1257.9 1307.8 -616.95    1233.9 3.1883  3      0.3635

anova(mod13pu, mod14pu) # mod 14pu

## Data: umbc_comp_plot_origin
## Models:
## mod14pu: log(plot_cover_avg) ~ state + origin + year_factor + (1 | plot)
## mod13pu: log(plot_cover_avg) ~ state + origin + (1 + year_factor | plot)
##       npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod14pu     8 1196.0 1229.3 -590.01    1180.0
## mod13pu     9 1255.1 1292.5 -618.55    1237.1      0  1           1

summary(mod14pu)

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(plot_cover_avg) ~ state + origin + year_factor + (1 | plot)
##   Data: umbc_comp_plot_origin
##

```

```

##      AIC      BIC logLik deviance df.resid
##  1196.0  1229.3 -590.0   1180.0      463
##
## Scaled residuals:
##      Min     1Q Median     3Q    Max
## -3.5201 -0.6139  0.1769  0.7356  2.3020
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.0000  0.0000
## Residual           0.7171  0.8468
## Number of obs: 471, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  3.72572  0.11430 471.00000 32.595 < 2e-16 ***
## statewarmed -0.02655  0.07826 471.00000 -0.339  0.73451
## origin      -0.45014  0.10107 471.00000 -4.454 1.05e-05 ***
## originBoth   -1.90785  0.14151 471.00000 -13.482 < 2e-16 ***
## originExotic  0.26540  0.10033 471.00000  2.645  0.00844 **
## year_factor  -0.29050  0.02279 471.00000 -12.748 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) sttwrm origin orgnBt orgnEx
## statewarmed -0.362
## origin      -0.420 -0.009
## originBoth   -0.344  0.056  0.350
## originExotic -0.428 -0.008  0.495  0.353
## year_factor -0.708  0.031 -0.016  0.021 -0.009
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
summ(mod14pu)
```

Observations	471
Dependent variable	log(plot_cover_avg)
Type	Mixed effects linear regression

AIC	1196.02
BIC	1229.26
Pseudo-R ² (fixed effects)	0.47
Pseudo-R ² (total)	0.47

```
anova(mod14pu)
```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state       0.083  0.083     1    471  0.1151 0.7345

```

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	3.73	0.11	32.60	471.00	0.00
statewarmed	-0.03	0.08	-0.34	471.00	0.73
origin	-0.45	0.10	-4.45	471.00	0.00
originBoth	-1.91	0.14	-13.48	471.00	0.00
originExotic	0.27	0.10	2.65	471.00	0.01
year_factor	-0.29	0.02	-12.75	471.00	0.00

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
Residual		0.85

Grouping Variables		
Group	# groups	ICC
plot	24	0.00

```
## origin      183.400 61.133      3    471  85.2490 <2e-16 ***
## year_factor 116.533 116.533      1    471 162.5035 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

emmeans(mod14pu, list(pairwise ~ state + origin + year_factor), adjust = "tukey")
```

boundary (singular) fit: see ?isSingular

```
## $`emmeans of state, origin, year_factor`
##   state   origin year_factor emmean     SE    df lower.CL upper.CL
##   ambient Native      3.52 2.704 0.0813  96.4    2.543   2.87
##   warmed  Native      3.52 2.678 0.0816  97.4    2.516   2.84
##   ambient          3.52 2.254 0.0829 102.3    2.090   2.42
##   warmed          3.52 2.228 0.0823 100.3    2.064   2.39
##   ambient Both      3.52 0.796 0.1280 210.9    0.544   1.05
##   warmed  Both      3.52 0.770 0.1329 242.9    0.508   1.03
##   ambient Exotic    3.52 2.970 0.0820  98.5    2.807   3.13
##   warmed  Exotic    3.52 2.943 0.0814  97.0    2.782   3.10
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $`pairwise differences of state, origin, year_factor`
```

	estimate
## 1	0.0266
## ambient Native 3.51592356687898 - warmed Native 3.51592356687898	0.4501
## ambient Native 3.51592356687898 - ambient 3.51592356687898	0.4767
## ambient Native 3.51592356687898 - warmed 3.51592356687898	

```

## ambient Native 3.51592356687898 - ambient Both 3.51592356687898      1.9079
## ambient Native 3.51592356687898 - warmed Both 3.51592356687898      1.9344
## ambient Native 3.51592356687898 - ambient Exotic 3.51592356687898     -0.2654
## ambient Native 3.51592356687898 - warmed Exotic 3.51592356687898     -0.2388
## warmed Native 3.51592356687898 - ambient 3.51592356687898      0.4236
## warmed Native 3.51592356687898 - warmed 3.51592356687898      0.4501
## warmed Native 3.51592356687898 - ambient Both 3.51592356687898      1.8813
## warmed Native 3.51592356687898 - warmed Both 3.51592356687898      1.9079
## warmed Native 3.51592356687898 - ambient Exotic 3.51592356687898     -0.2920
## warmed Native 3.51592356687898 - warmed Exotic 3.51592356687898     -0.2654
## ambient 3.51592356687898 - warmed 3.51592356687898      0.0266
## ambient 3.51592356687898 - ambient Both 3.51592356687898      1.4577
## ambient 3.51592356687898 - warmed Both 3.51592356687898      1.4843
## ambient 3.51592356687898 - ambient Exotic 3.51592356687898     -0.7155
## ambient 3.51592356687898 - warmed Exotic 3.51592356687898     -0.6890
## warmed 3.51592356687898 - ambient Both 3.51592356687898      1.4312
## warmed 3.51592356687898 - warmed Both 3.51592356687898      1.4577
## warmed 3.51592356687898 - ambient Exotic 3.51592356687898     -0.7421
## warmed 3.51592356687898 - warmed Exotic 3.51592356687898     -0.7155
## ambient Both 3.51592356687898 - warmed Both 3.51592356687898      0.0266
## ambient Both 3.51592356687898 - ambient Exotic 3.51592356687898     -2.1733
## ambient Both 3.51592356687898 - warmed Exotic 3.51592356687898     -2.1467
## warmed Both 3.51592356687898 - ambient Exotic 3.51592356687898     -2.1998
## warmed Both 3.51592356687898 - warmed Exotic 3.51592356687898     -2.1733
## ambient Exotic 3.51592356687898 - warmed Exotic 3.51592356687898      0.0266
##      SE   df t.ratio p.value
## 0.0788 22.4  0.337 1.0000
## 0.1017 455.7  4.425 0.0003
## 0.1281 138.1  3.720 0.0068
## 0.1433 471.5 13.309 <.0001
## 0.1673 226.7 11.561 <.0001
## 0.1010 455.2 -2.628 0.1485
## 0.1276 136.6 -1.872 0.5722
## 0.1293 141.1  3.277 0.0281
## 0.1017 455.7  4.425 0.0003
## 0.1598 188.7 11.774 <.0001
## 0.1433 471.5 13.309 <.0001
## 0.1287 139.0 -2.269 0.3181
## 0.1010 455.2 -2.628 0.1485
## 0.0788 22.4  0.337 1.0000
## 0.1441 471.8 10.117 <.0001
## 0.1684 229.7  8.815 <.0001
## 0.1019 455.3 -7.023 <.0001
## 0.1288 140.6 -5.347 <.0001
## 0.1600 189.7  8.945 <.0001
## 0.1441 471.8 10.117 <.0001
## 0.1288 139.9 -5.761 <.0001
## 0.1019 455.3 -7.023 <.0001
## 0.0788 22.4  0.337 1.0000
## 0.1435 472.4 -15.142 <.0001
## 0.1595 189.7 -13.458 <.0001
## 0.1679 229.2 -13.103 <.0001
## 0.1435 472.4 -15.142 <.0001
## 0.0788 22.4  0.337 1.0000

```

```

##  

## Degrees-of-freedom method: kenward-roger  

## Results are given on the log (not the response) scale.  

## P value adjustment: tukey method for comparing a family of 8 estimates

# including growth form - first with interaction term
umbs_comp_plot_growthhabit <- within(umbs_comp_plot_growthhabit, growth_habit <- relevel(factor(growth_habit,
  ref = "Forb")) # releveling so forb is the reference
mod15pu <- lmer(log(plot_cover_avg) ~ state * growth_habit + (1 + year_factor | plot),
  umbs_comp_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod16pu <- lmer(log(plot_cover_avg) ~ state + growth_habit + (1 + year_factor | plot),
  umbs_comp_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

mod17pu <- lmer(log(plot_cover_avg) ~ state + growth_habit + year_factor + (1 | plot),
  umbs_comp_plot_growthhabit, REML = FALSE)

## boundary (singular) fit: see ?isSingular

anova(mod15pu, mod16pu) # go with model 16pu

## Data: umbs_comp_plot_growthhabit
## Models:
## mod16pu: log(plot_cover_avg) ~ state + growth_habit + (1 + year_factor |
## mod16pu:      plot)
## mod15pu: log(plot_cover_avg) ~ state * growth_habit + (1 + year_factor |
## mod15pu:      plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod16pu     9 751.42 785.25 -366.71    733.42
## mod15pu    12 756.22 801.32 -366.11    732.22 1.202   3      0.7525

anova(mod16pu, mod17pu) # mod 17pu

## Data: umbs_comp_plot_growthhabit
## Models:
## mod17pu: log(plot_cover_avg) ~ state + growth_habit + year_factor + (1 |
## mod17pu:      plot)
## mod16pu: log(plot_cover_avg) ~ state + growth_habit + (1 + year_factor |
## mod16pu:      plot)
##      npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod17pu     8 688.55 718.62 -336.27    672.55
## mod16pu     9 751.42 785.25 -366.71    733.42      0   1          1

summary(mod17pu)

```

```

## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: log(plot_cover_avg) ~ state + growth_habit + year_factor + (1 |
##   plot)
## Data: umbs_comp_plot_growthhabit
##
##          AIC      BIC  logLik deviance df.resid
##       688.5    718.6   -336.3     672.5     309
##
## Scaled residuals:
##      Min    1Q Median    3Q   Max
## -4.1205 -0.6184  0.1987  0.6956  2.2908
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   plot      (Intercept) 0.0000   0.000
##   Residual           0.4886   0.699
## Number of obs: 317, groups:  plot, 24
##
## Fixed effects:
##                   Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)      4.291700  0.108758 317.000000 39.461 < 2e-16 ***
## statewarmed      0.001112  0.078551 317.000000  0.014  0.9887    
## growth_habit     -2.461517  0.157201 317.000000 -15.658 < 2e-16 ***
## growth_habitGraminoid -0.173923  0.082521 317.000000 -2.108  0.0358 *  
## growth_habitTree   -1.972891  0.272433 317.000000 -7.242 3.38e-12 ***
## year_factor      -0.312931  0.023348 317.000000 -13.403 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) sttwrm grwth_ grwt_G grwt_T
## statewarmed -0.376
## growth_habt -0.238  0.013
## grwth_hbtGr -0.386  0.003  0.264
## grwth_hbtTr -0.036  0.020  0.075  0.151
## year_factor -0.761  0.016  0.045  0.005 -0.114
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

```
summ(mod17pu)
```

Observations	317
Dependent variable	log(plot_cover_avg)
Type	Mixed effects linear regression

AIC	688.55
BIC	718.62
Pseudo-R ² (fixed effects)	0.60
Pseudo-R ² (total)	0.60

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	4.29	0.11	39.46	317.00	0.00
statewarmed	0.00	0.08	0.01	317.00	0.99
growth_habit	-2.46	0.16	-15.66	317.00	0.00
growth_habitGraminoid	-0.17	0.08	-2.11	317.00	0.04
growth_habitTree	-1.97	0.27	-7.24	317.00	0.00
year_factor	-0.31	0.02	-13.40	317.00	0.00

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.00
Residual		0.70

Grouping Variables		
Group	# groups	ICC
plot	24	0.00

```
anova(mod17pu)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state      0.000  0.000     1    317  0.0002 0.9887
## growth_habit 142.153 47.384     3    317 96.9856 <2e-16 ***
## year_factor   87.766  87.766     1    317 179.6389 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans(mod17pu, list(pairwise ~ state + growth_habit + year_factor), adjust = "tukey")
```

```
## boundary (singular) fit: see ?isSingular
```

```
## $`emmeans of state, growth_habit, year_factor`
## state  growth_habit year_factor emmean      SE      df lower.CL upper.CL
## ambient Forb            3.52 3.191 0.0713  56.1    3.048  3.33
## warmed  Forb            3.52 3.192 0.0710  55.3    3.050  3.33
## ambient
## warmed
## ambient Graminoid       3.52 0.729 0.1533 240.7    0.427  1.03
## warmed Graminoid        3.52 0.731 0.1545 229.1    0.426  1.04
## ambient Tree             3.52 3.017 0.0710  55.3    2.875  3.16
## warmed Graminoid        3.52 3.018 0.0710  55.3    2.876  3.16
## ambient Tree             3.52 1.218 0.2758 241.9    0.675  1.76
## warmed Tree              3.52 1.219 0.2775 239.6    0.673  1.77
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
```

```

## 
## $`pairwise differences of state, growth_habit, year_factor`
## 1
## ambient Forb 3.51735015772871 - warmed Forb 3.51735015772871
## ambient Forb 3.51735015772871 - ambient 3.51735015772871
## ambient Forb 3.51735015772871 - warmed 3.51735015772871
## ambient Forb 3.51735015772871 - ambient Graminoid 3.51735015772871
## ambient Forb 3.51735015772871 - warmed Graminoid 3.51735015772871
## ambient Forb 3.51735015772871 - ambient Tree 3.51735015772871
## ambient Forb 3.51735015772871 - warmed Tree 3.51735015772871
## warmed Forb 3.51735015772871 - ambient 3.51735015772871
## warmed Forb 3.51735015772871 - warmed 3.51735015772871
## warmed Forb 3.51735015772871 - ambient Graminoid 3.51735015772871
## warmed Forb 3.51735015772871 - warmed Graminoid 3.51735015772871
## warmed Forb 3.51735015772871 - ambient Tree 3.51735015772871
## warmed Forb 3.51735015772871 - warmed Tree 3.51735015772871
## ambient 3.51735015772871 - warmed 3.51735015772871
## ambient 3.51735015772871 - ambient Graminoid 3.51735015772871
## ambient 3.51735015772871 - warmed Graminoid 3.51735015772871
## ambient 3.51735015772871 - ambient Tree 3.51735015772871
## ambient 3.51735015772871 - warmed Tree 3.51735015772871
## warmed 3.51735015772871 - ambient Graminoid 3.51735015772871
## warmed 3.51735015772871 - warmed Graminoid 3.51735015772871
## warmed 3.51735015772871 - ambient Tree 3.51735015772871
## warmed 3.51735015772871 - warmed Tree 3.51735015772871
## ambient Graminoid 3.51735015772871 - warmed Graminoid 3.51735015772871
## ambient Graminoid 3.51735015772871 - ambient Tree 3.51735015772871
## ambient Graminoid 3.51735015772871 - warmed Tree 3.51735015772871
## warmed Graminoid 3.51735015772871 - ambient Tree 3.51735015772871
## warmed Graminoid 3.51735015772871 - warmed Tree 3.51735015772871
## ambient Tree 3.51735015772871 - warmed Tree 3.51735015772871
## estimate SE df t.ratio p.value
## -0.00111 0.0795 21.8 -0.014 1.0000
## 2.46152 0.1600 322.2 15.384 <.0001
## 2.46041 0.1798 192.7 13.682 <.0001
## 0.17392 0.0833 300.6 2.088 0.4254
## 0.17281 0.1153 89.2 1.498 0.8063
## 1.97289 0.2801 279.1 7.045 <.0001
## 1.97178 0.2927 224.8 6.736 <.0001
## 2.46263 0.1775 207.7 13.876 <.0001
## 2.46152 0.1600 322.2 15.384 <.0001
## 0.17503 0.1149 88.4 1.523 0.7931
## 0.17392 0.0833 300.6 2.088 0.4254
## 1.97400 0.2895 228.6 6.820 <.0001
## 1.97289 0.2801 279.1 7.045 <.0001
## -0.00111 0.0795 21.8 -0.014 1.0000
## -2.28759 0.1599 322.3 -14.305 <.0001
## -2.28871 0.1775 207.8 -12.893 <.0001
## -0.48863 0.3109 313.8 -1.572 0.7670
## -0.48974 0.3217 280.4 -1.522 0.7950
## -2.28648 0.1796 192.4 -12.730 <.0001
## -2.28759 0.1599 322.3 -14.305 <.0001
## -0.48751 0.3201 278.9 -1.523 0.7944
## -0.48863 0.3109 313.8 -1.572 0.7670

```

```
## -0.00111 0.0795 21.8 -0.014 1.0000
## 1.79897 0.2801 278.8 6.423 <.0001
## 1.79786 0.2927 224.6 6.143 <.0001
## 1.80008 0.2895 228.4 6.217 <.0001
## 1.79897 0.2801 278.8 6.423 <.0001
## -0.00111 0.0795 21.8 -0.014 1.0000
##
## Degrees-of-freedom method: kenward-roger
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 8 estimates
```