

# 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_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

# 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")

```

```

# create dataframes for kbs and umbs
comp_kbs_plot <- subset(comp_plot, site == "kbs")
comp_umbs_plot <- subset(comp_plot, site == "umbs")

# read in meta data
meta <- read.csv(file.path(L0_dir, "plot.csv")) # dataframe above already has meta data in it

```

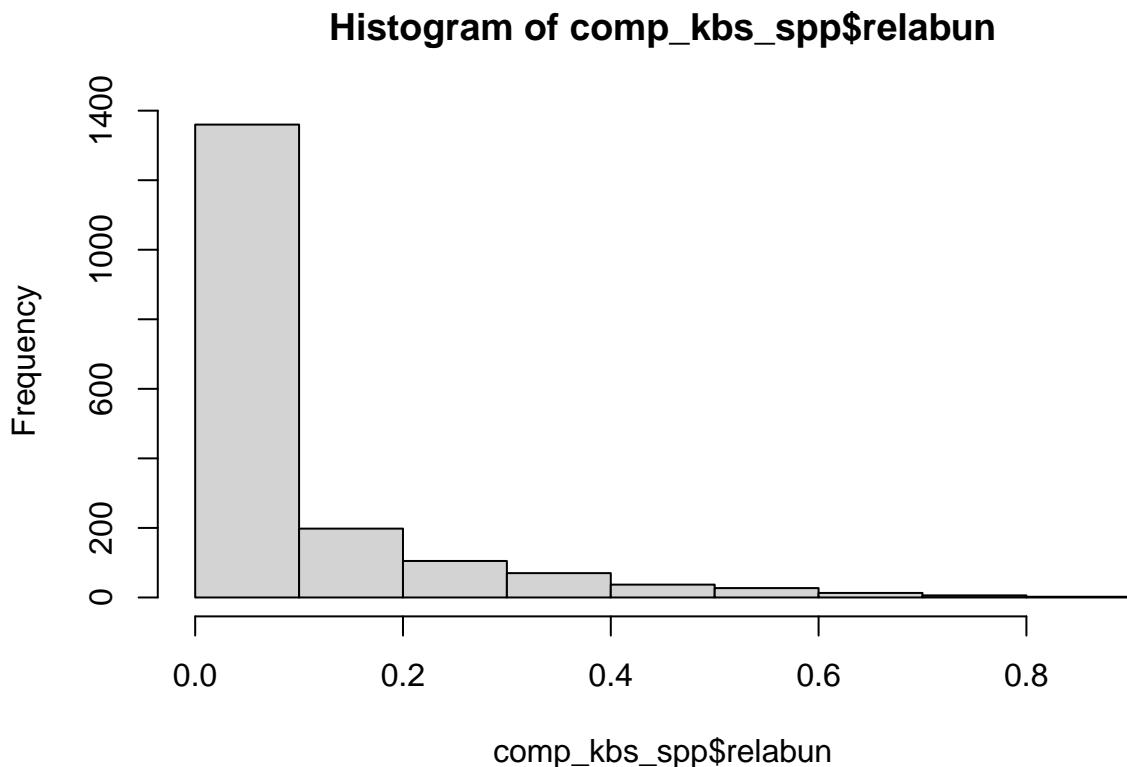
Data exploration - some different ways of visualizing these data

## KBS SPECIES LEVEL - Looking at RELATIVE ABUNDANCE

```

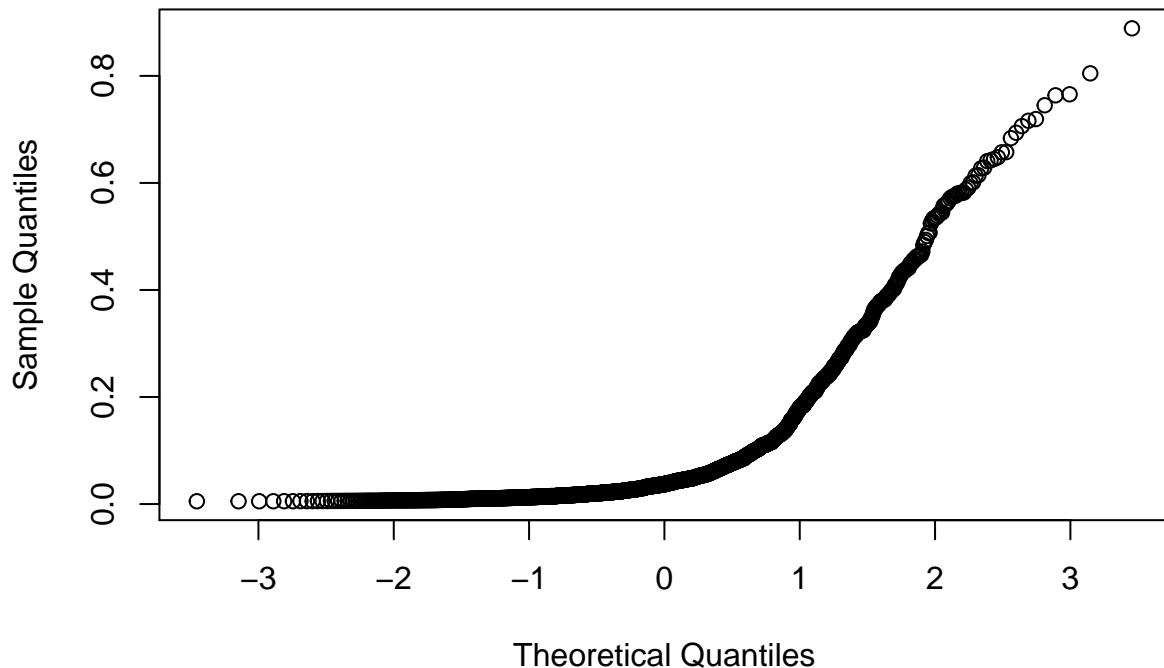
### KBS ####
hist(comp_kbs_spp$relabun)

```



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

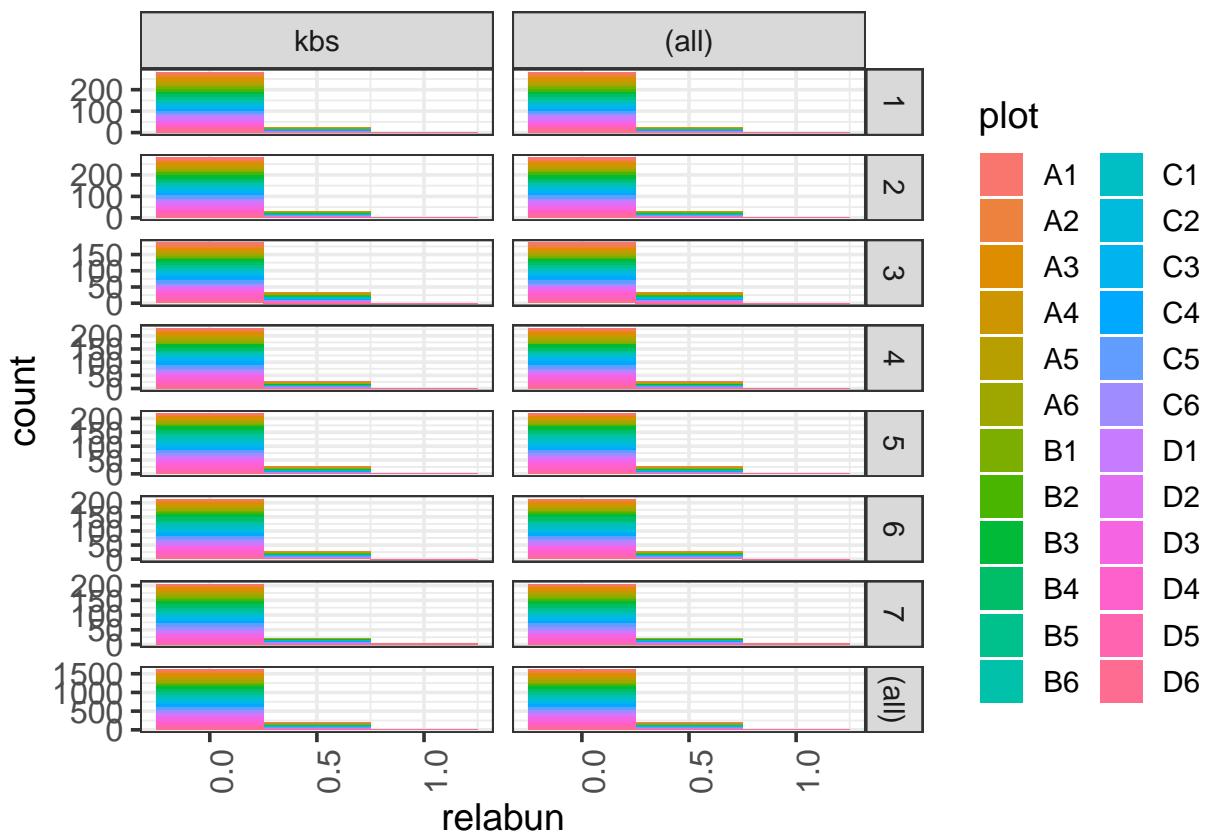
## Normal Q-Q Plot



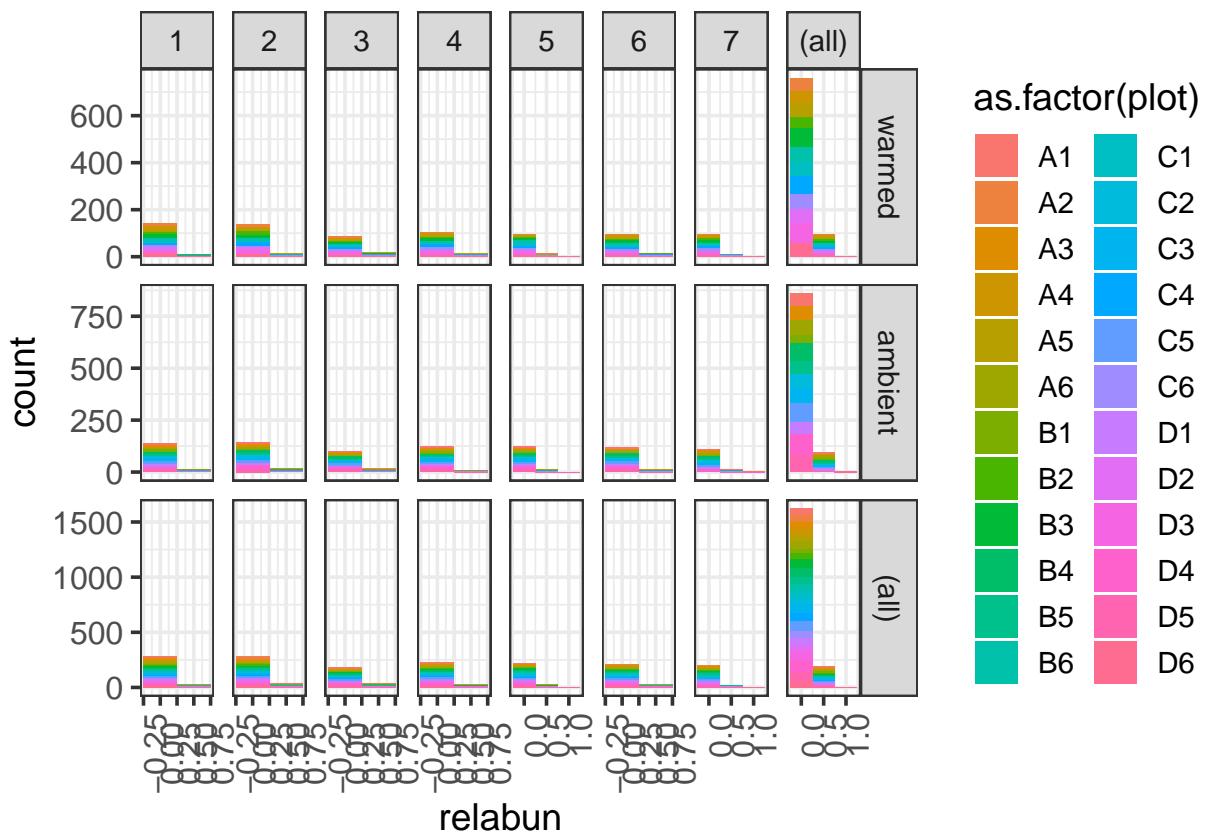
```
shapiro.test(comp_kbs_spp$relabun) # pvalue is < 0.05 so we reject the null hypothesis that the data is normally distributed

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

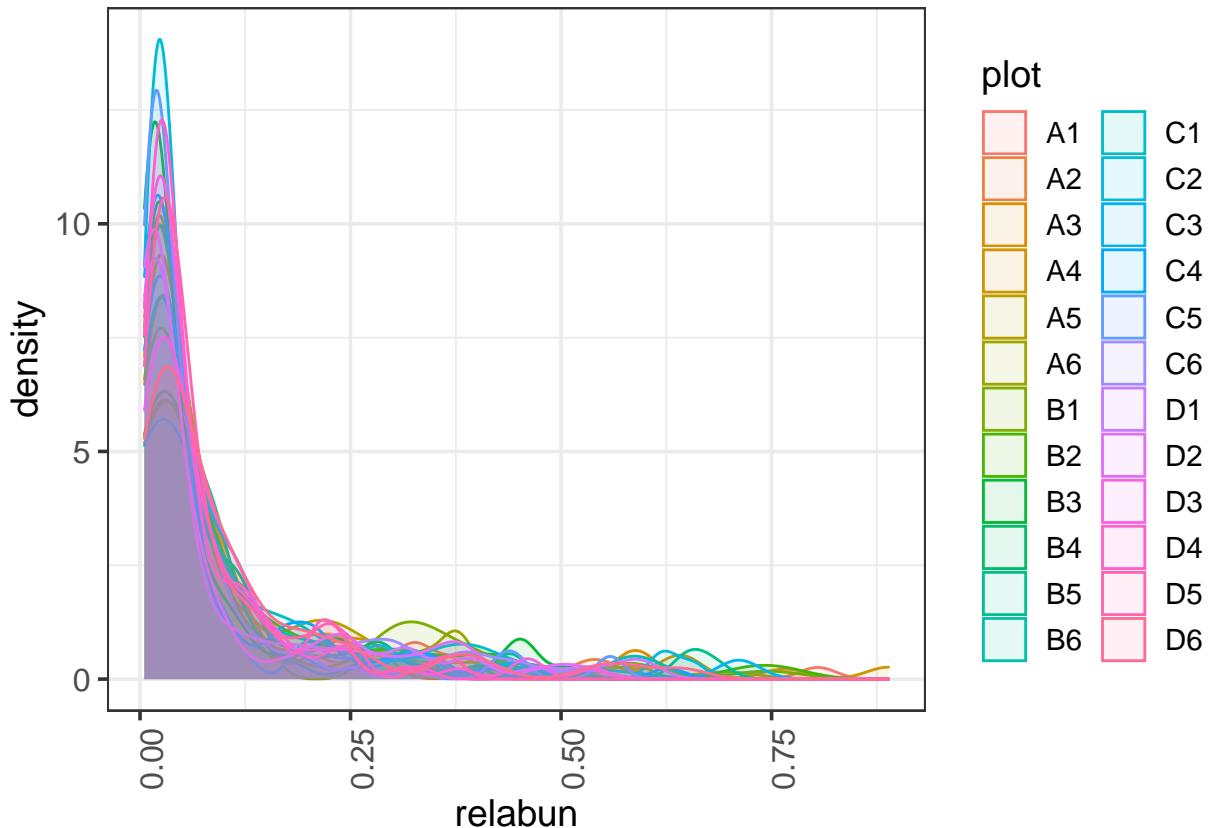
# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(comp_kbs_spp, aes(relabun, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")
```



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



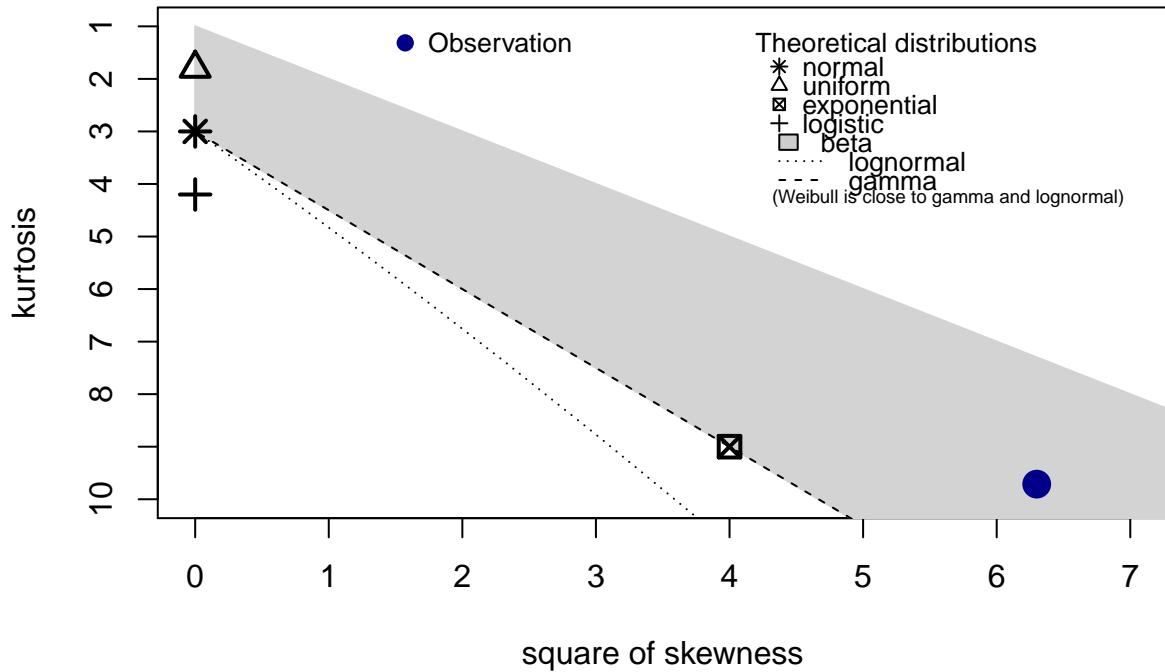
```
ggplot(comp_kbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
# ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color=plot)) +
# geom_density(alpha = 0.1) + facet_wrap(~year)
ggplot(umbs_flwr_plot,
# aes(julian_median, fill = plot, color=plot)) + geom_density(alpha = 0.1) +
# facet_wrap(~year + plot)
```

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

## Cullen and Frey graph



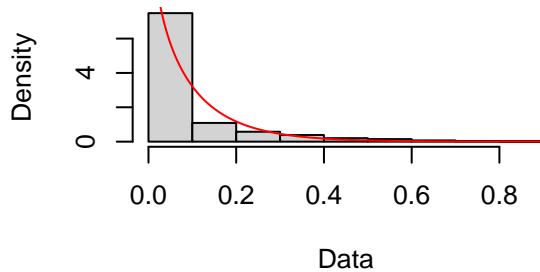
```

## 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

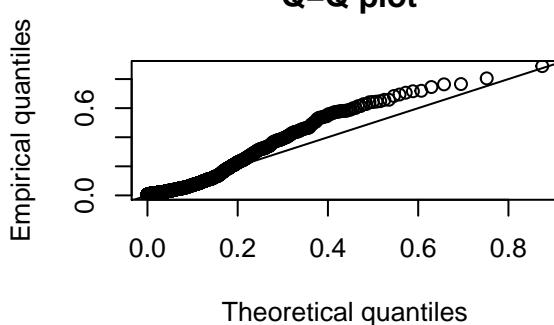
# Gamma distribution
fit.gamma <- fitdist(comp_kbs_spp$relabun, "gamma")
plot(fit.gamma)

```

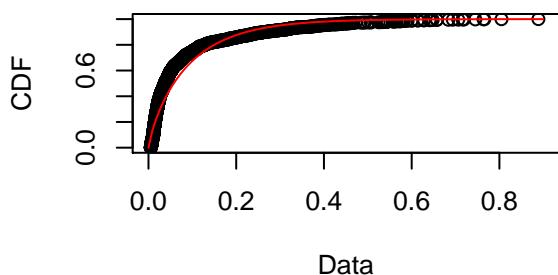
**Empirical and theoretical dens.**



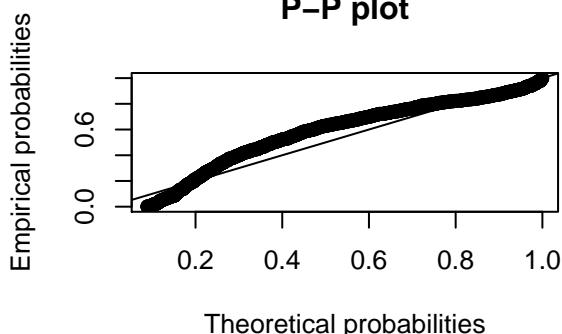
**Q-Q plot**



**Empirical and theoretical CDFs**

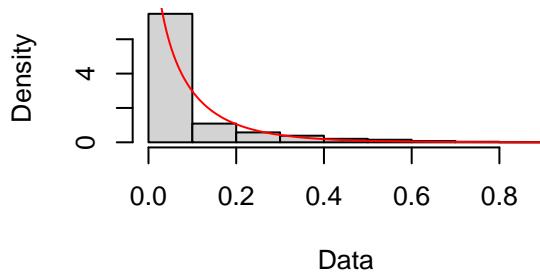


**P-P plot**

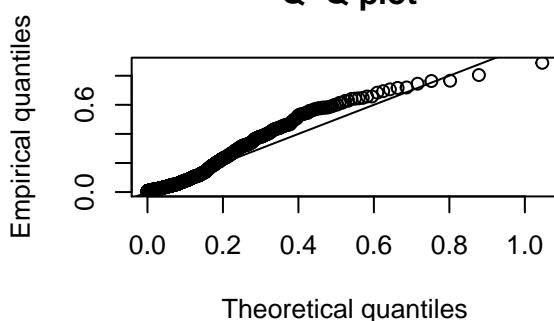


```
# Weibull distribution
fit.weibull <- fitdist(comp_kbs_spp$relabun, "weibull")
plot(fit.weibull)
```

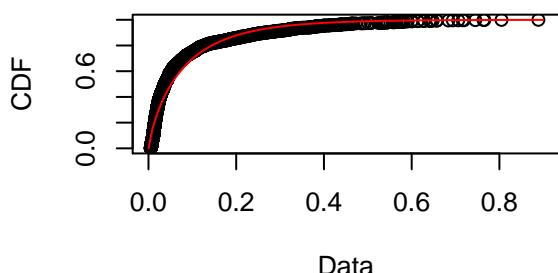
**Empirical and theoretical dens.**



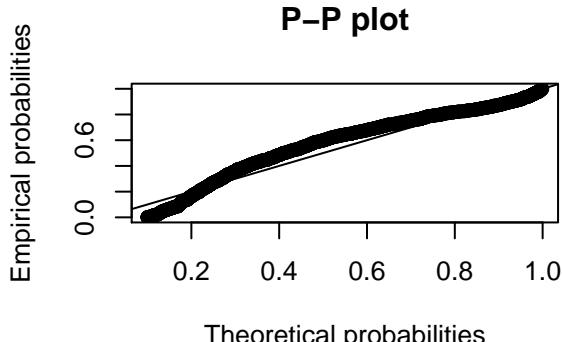
**Q-Q plot**



**Empirical and theoretical CDFs**

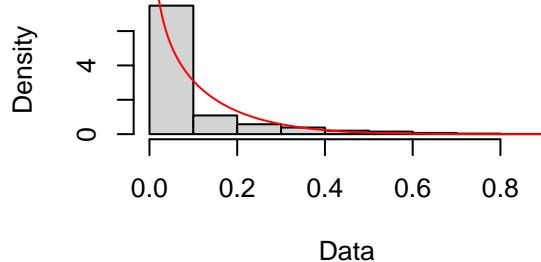


**P-P plot**

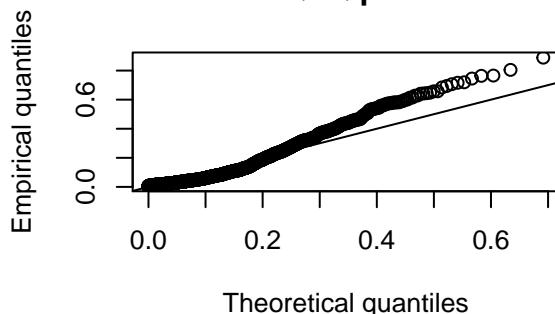


```
fit.beta <- fitdist(comp_kbs_spp$relabun, "beta")
plot(fit.beta)
```

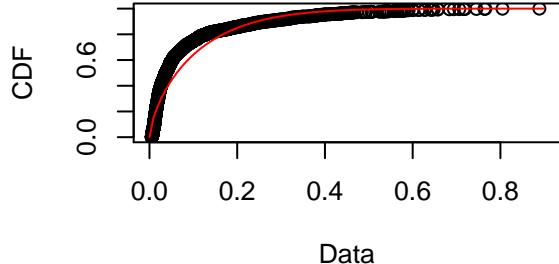
Empirical and theoretical dens.



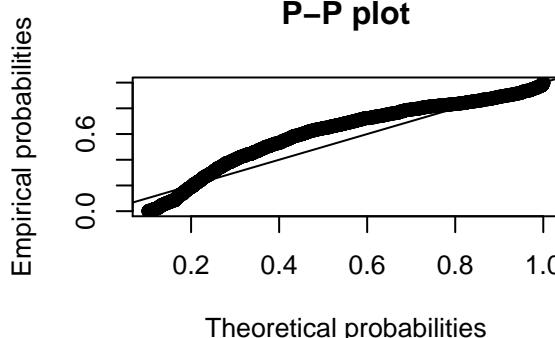
Q–Q plot



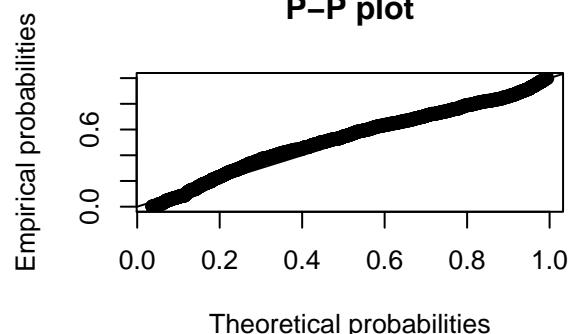
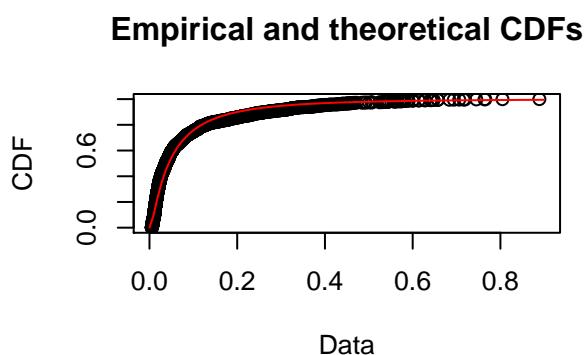
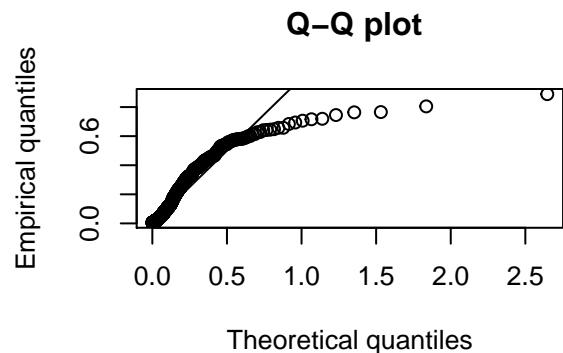
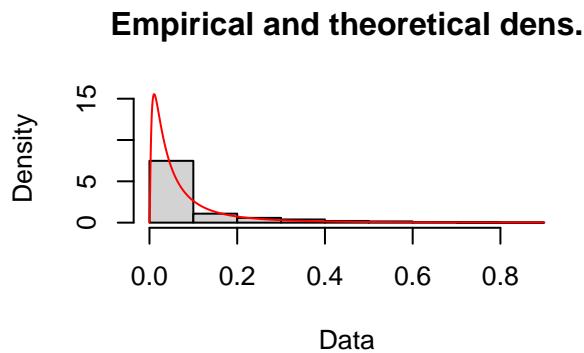
Empirical and theoretical CDFs



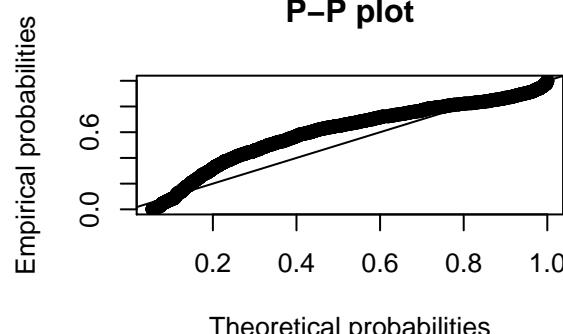
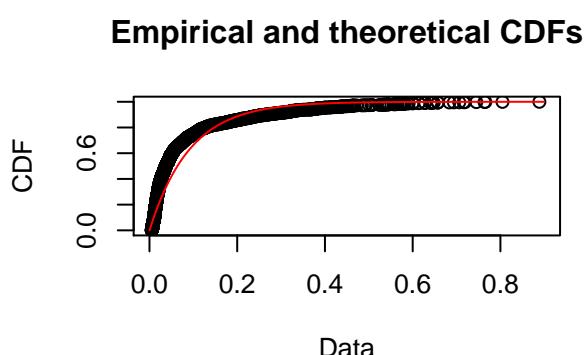
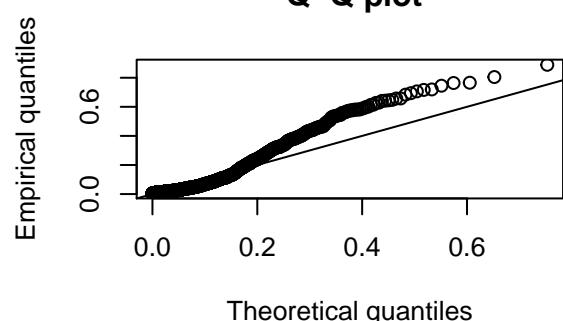
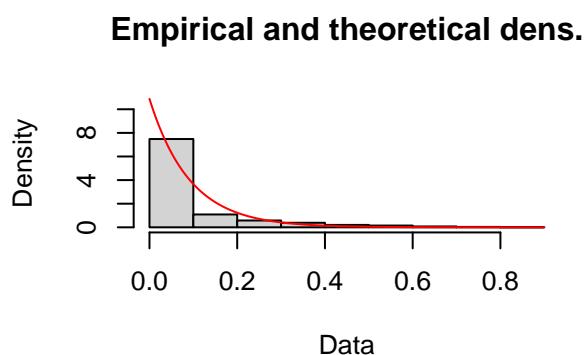
P–P plot



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



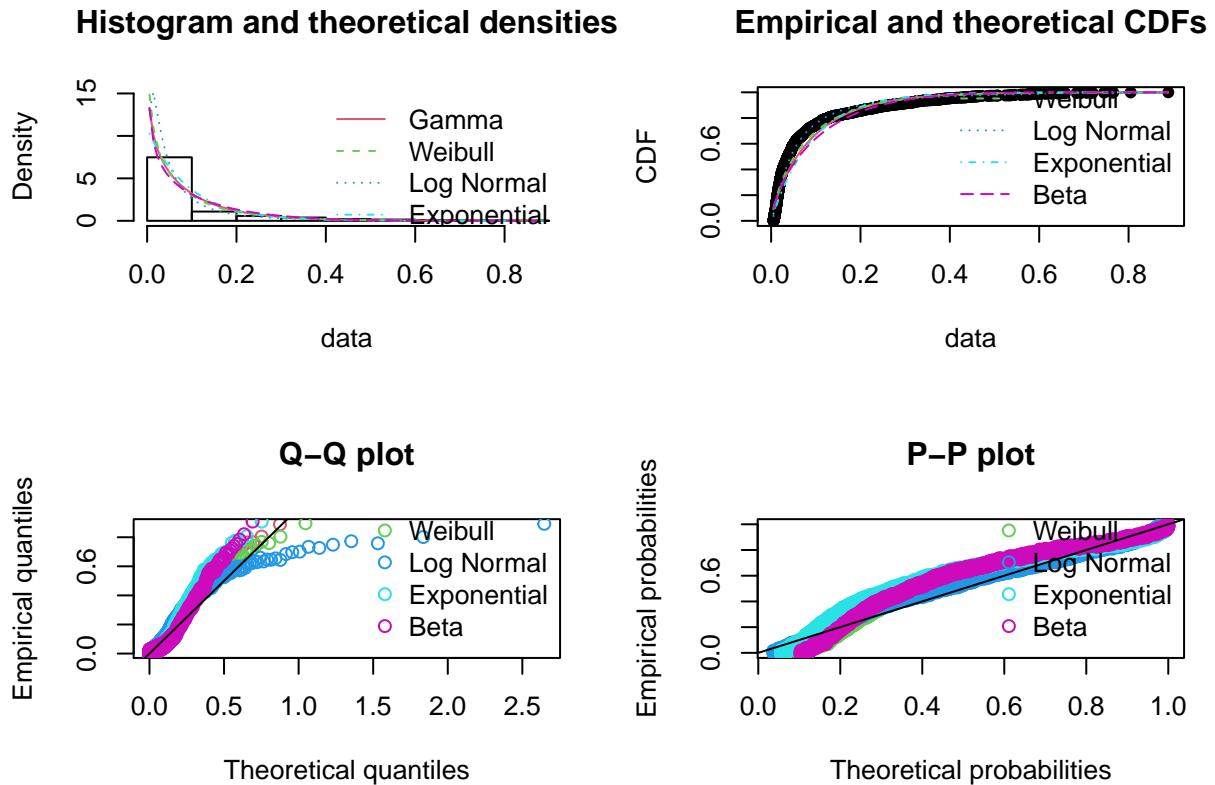
```
# Exponential distribution is another option
fit.exp <- fitdist(comp_kbs_spp$relabun, "exp")
plot(fit.exp)
```



```

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

```

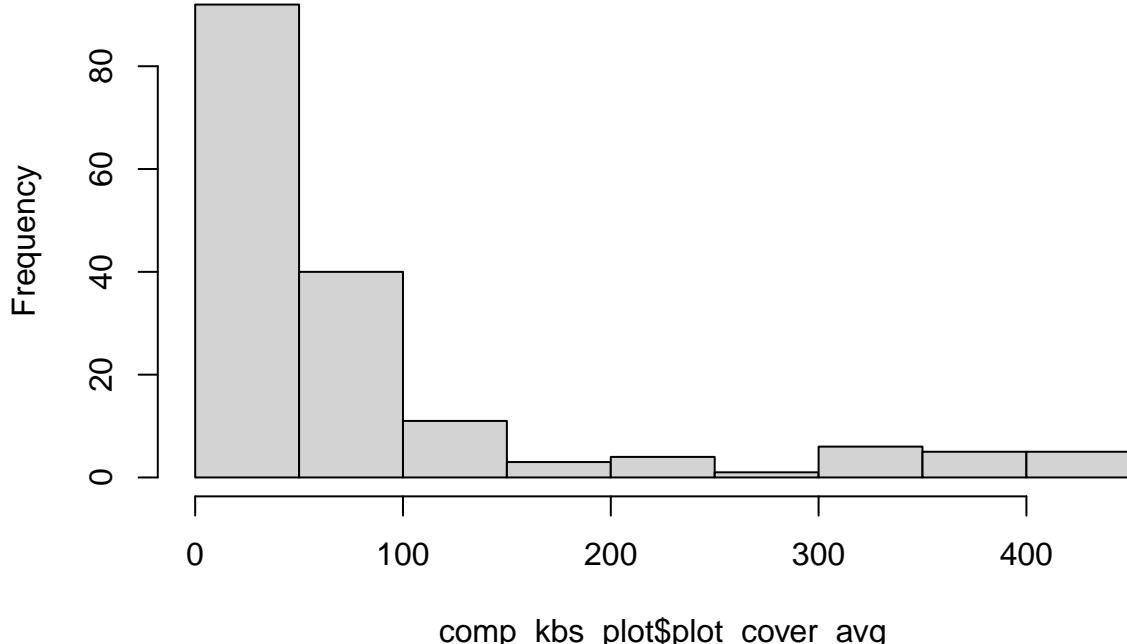
```
## Akaike's Information Criterion -4939.073
## Bayesian Information Criterion -4928.062

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

## KBS PLOT LEVEL - Looking at PLOT AVG TOTALS

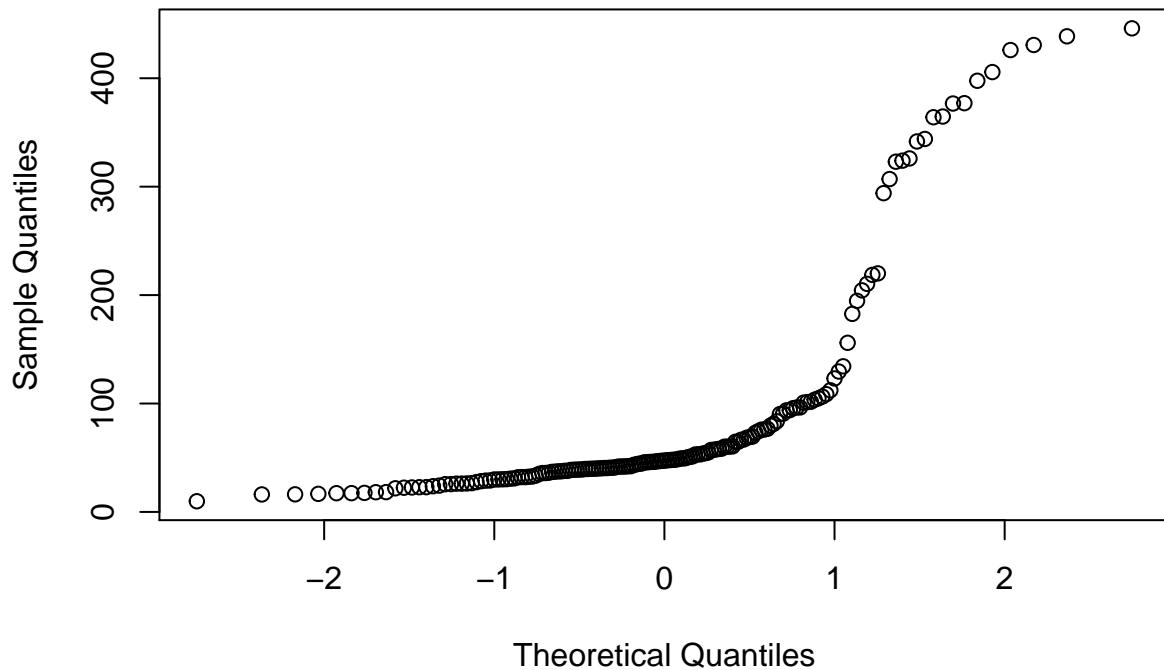
```
### KBS ####
hist(comp_kbs_plot$plot_cover_avg)
```

Histogram of comp\_kbs\_plot\$plot\_cover\_avg



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

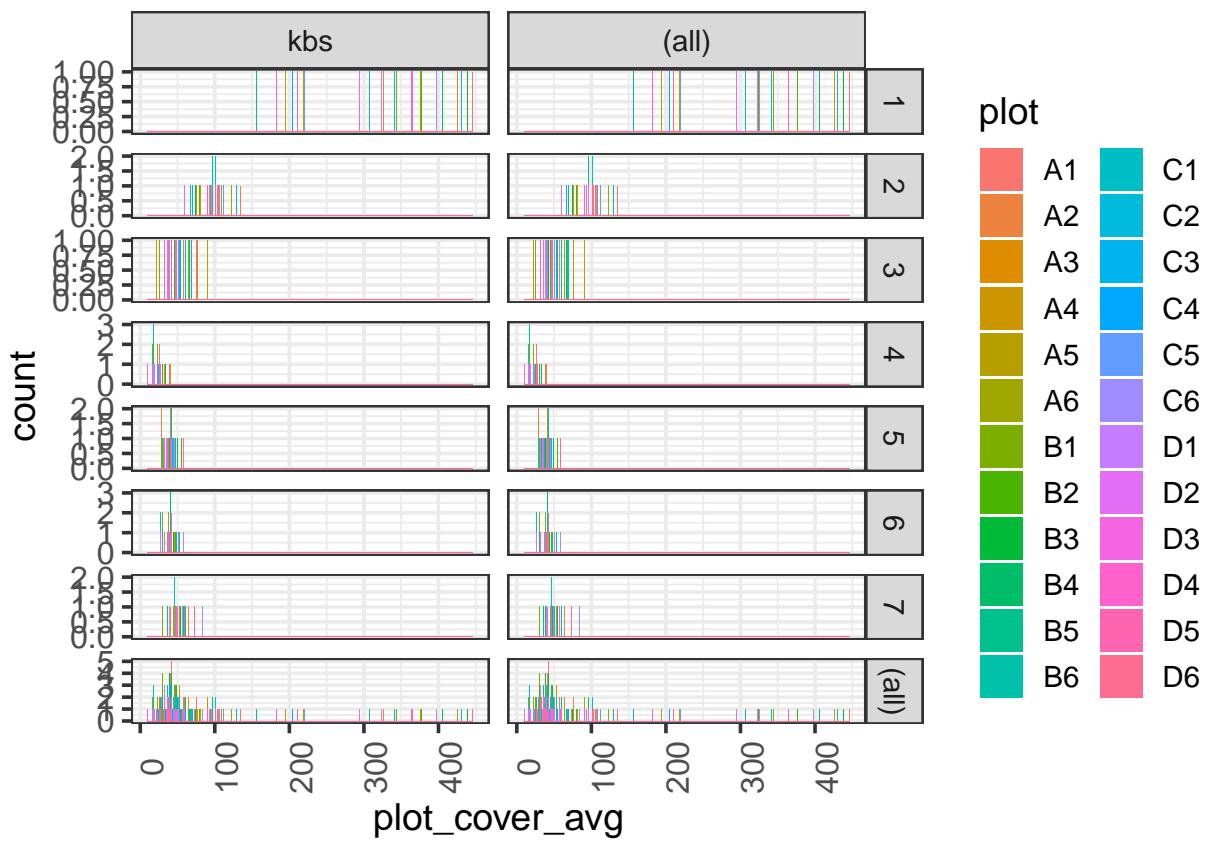
## Normal Q-Q Plot



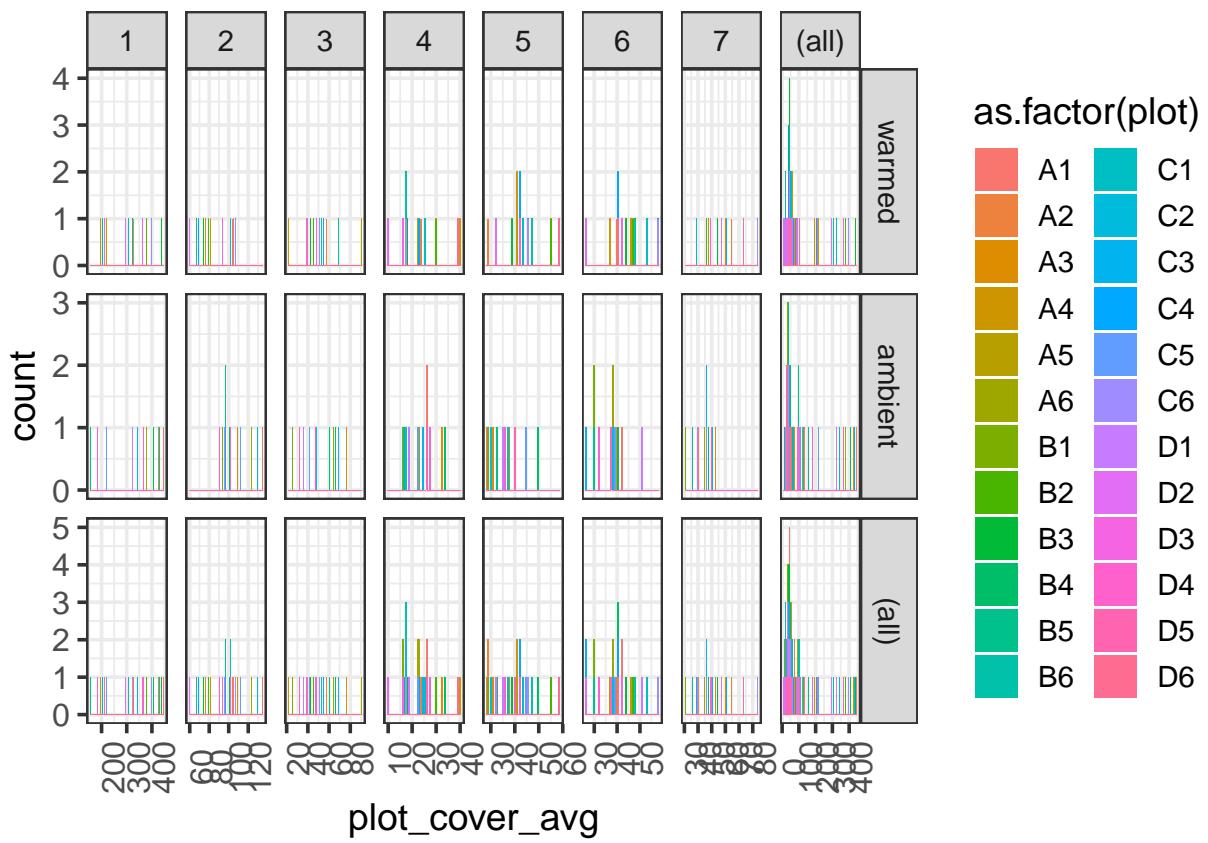
```
shapiro.test(comp_kbs_plot$plot_cover_avg) # pvalue is < 0.05 so we reject the null hypothesis that the data is normally distributed

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

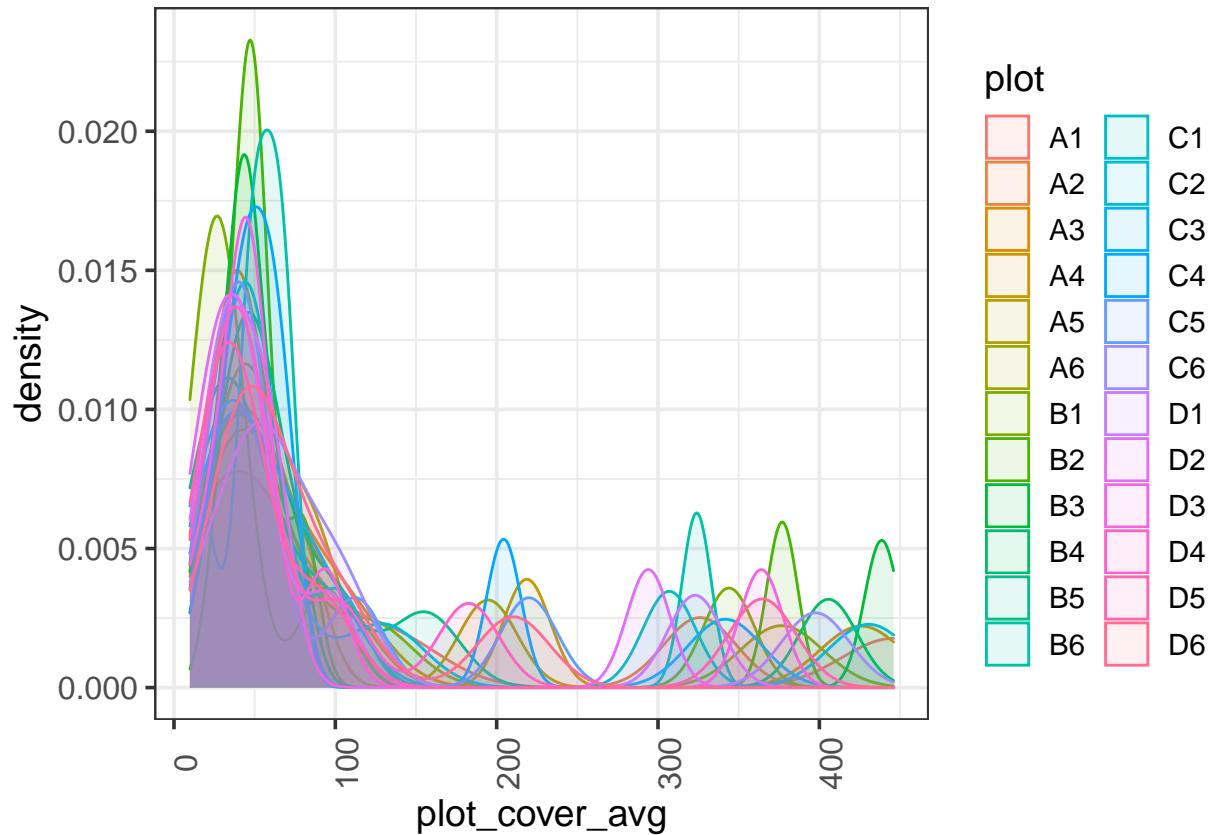
# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(comp_kbs_plot, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")
```



```
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")
```



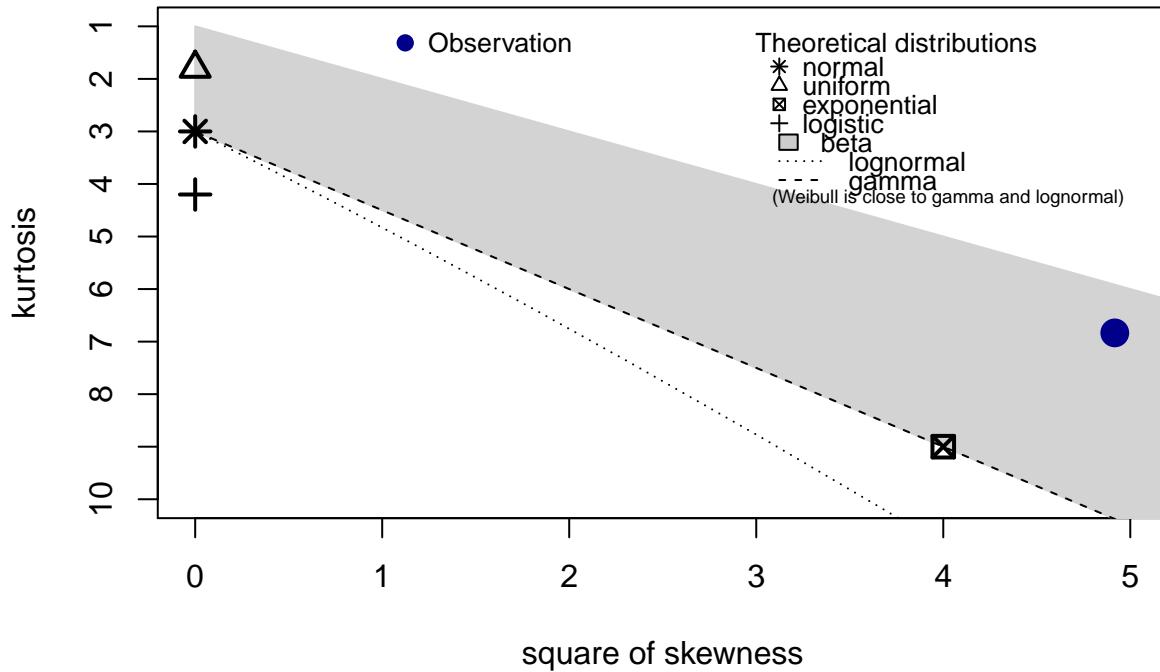
```
ggplot(comp_kbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
# ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color=plot)) +
# geom_density(alpha = 0.1) + facet_wrap(~year) ggplot(umbs_flwr_plot,
# aes(julian_median, fill = plot, color=plot)) + geom_density(alpha = 0.1) +
# facet_wrap(~year + plot)
```

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

## Cullen and Frey graph

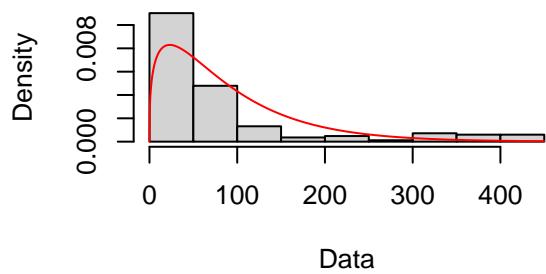
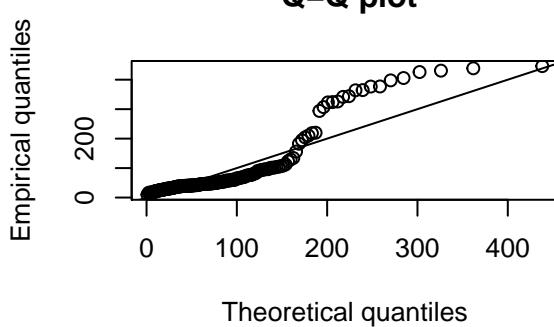
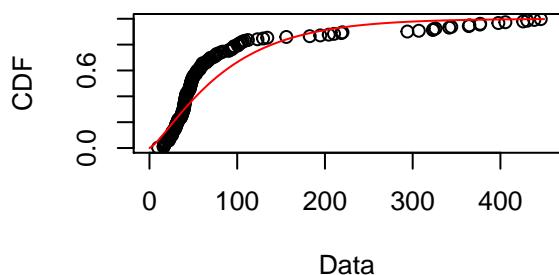
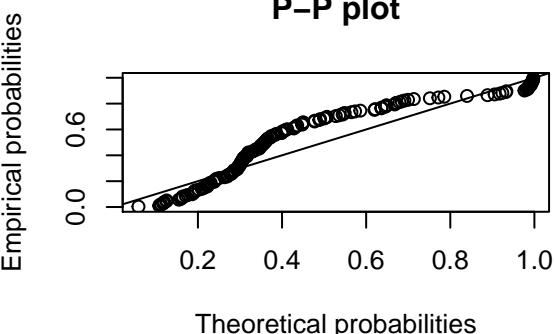


```

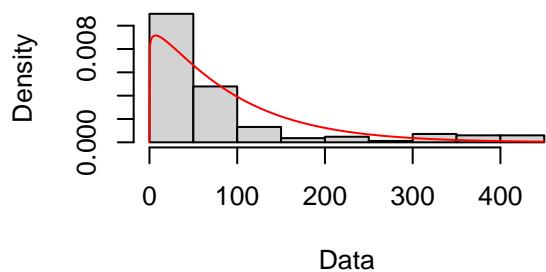
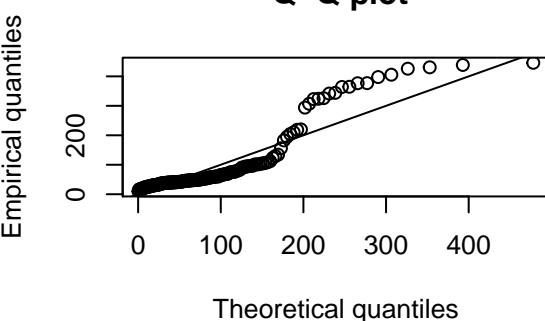
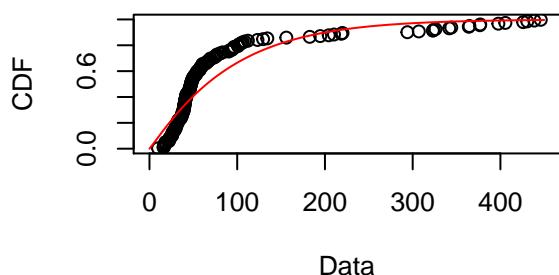
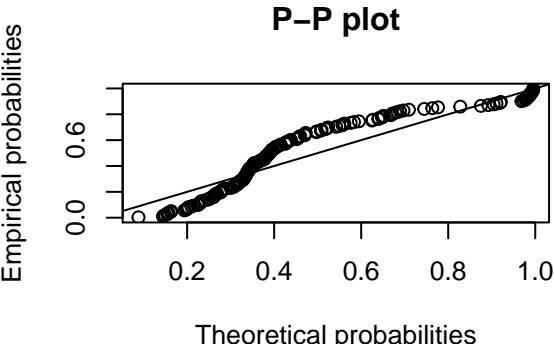
## summary statistics
## -----
## min:  9.857143  max:  446
## median: 47.23077
## mean:  89.1331
## estimated sd: 103.2916
## estimated skewness: 2.217462
## estimated kurtosis: 6.834041

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

```

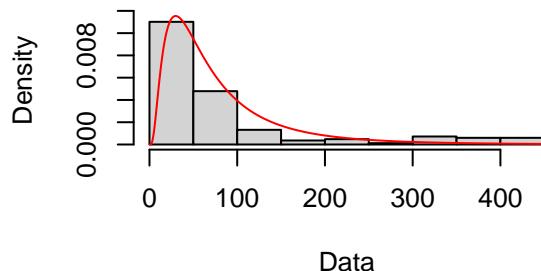
**Empirical and theoretical dens.****Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

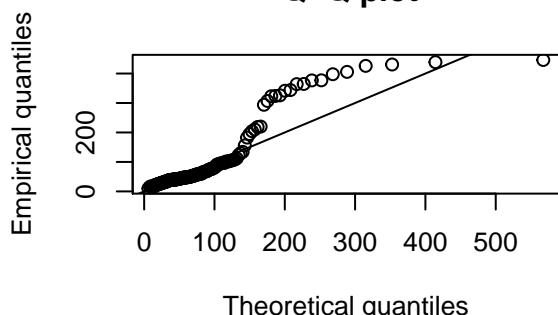
**Empirical and theoretical dens.****Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

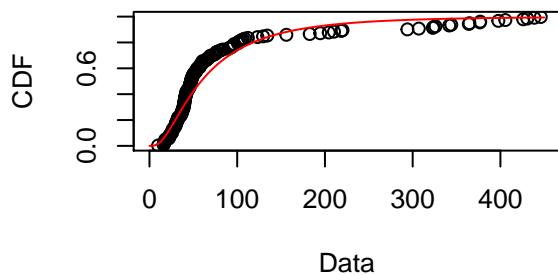
**Empirical and theoretical dens.**



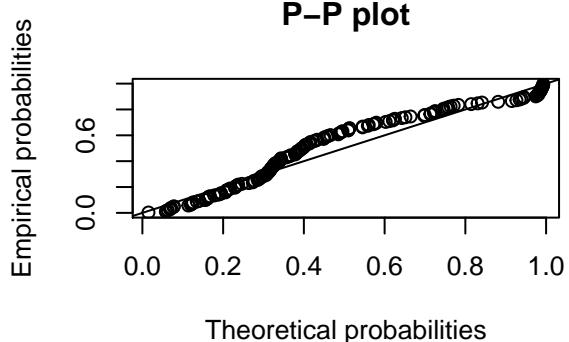
**Q–Q plot**



**Empirical and theoretical CDFs**

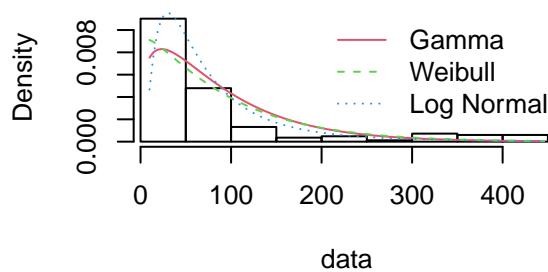


**P–P plot**

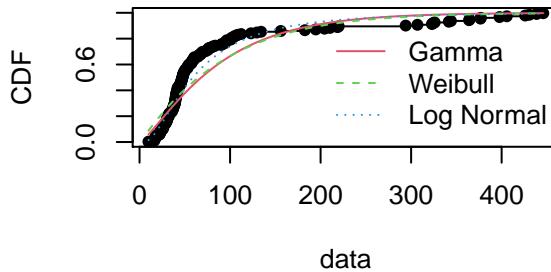


```
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal")
denscomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
qqcomp(list(fit.gamma, fit.weibull, fit.ln), legendtext = plot.legend)
ppcomp(list(fit.gamma,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

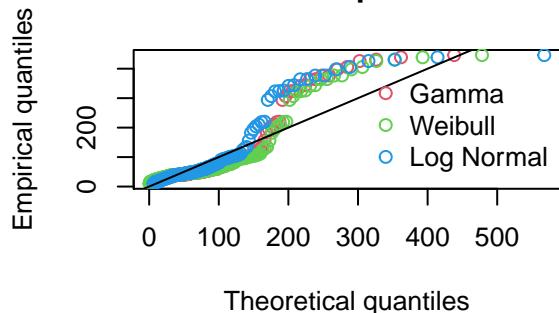
### Histogram and theoretical densities



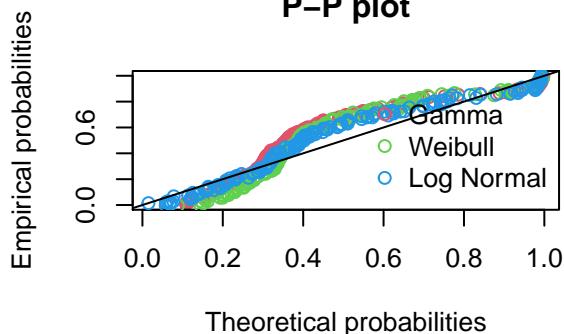
### Empirical and theoretical CDFs



### 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"))
```

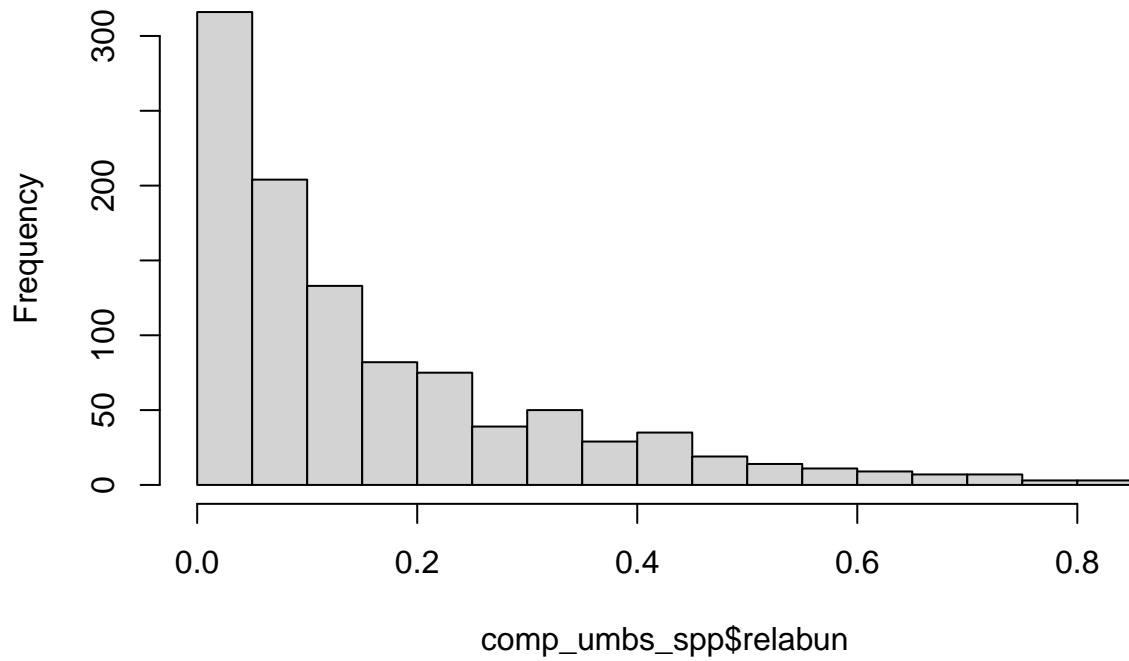
```
## Goodness-of-fit statistics
##                                     Gamma   Weibull Log Normal
## Kolmogorov-Smirnov statistic 0.2084312 0.1860727 0.1457357
## Cramer-von Mises statistic   2.1039134 1.9334703 0.9063833
## Anderson-Darling statistic  11.5222610 10.9721217 5.3825803
##
## Goodness-of-fit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

```
# Log Normal the best...
```

## UMBS SPECIES LEVEL - Looking at RELATIVE ABUNDANCE

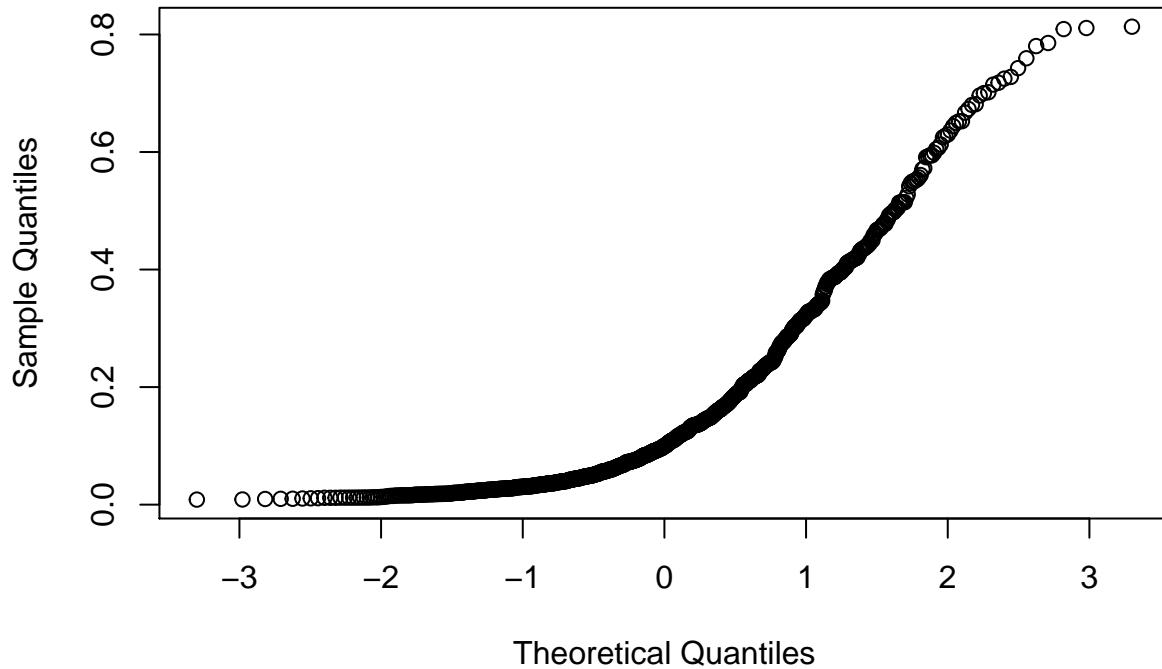
```
### UMBS ####
hist(comp_umbs_spp$relabun)
```

### Histogram of comp\_umbs\_spp\$relabun



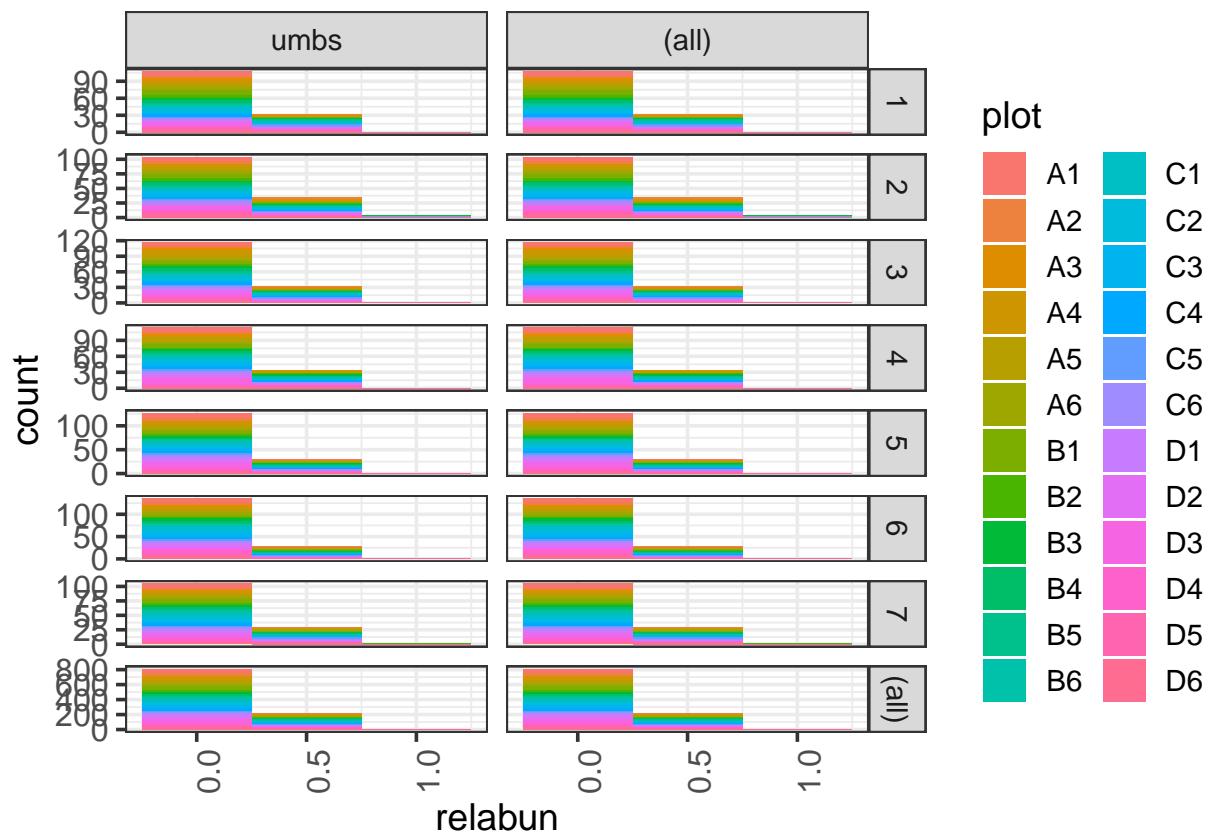
```
qqnorm(comp_umbs_spp$relabun)
```

### Normal Q-Q Plot

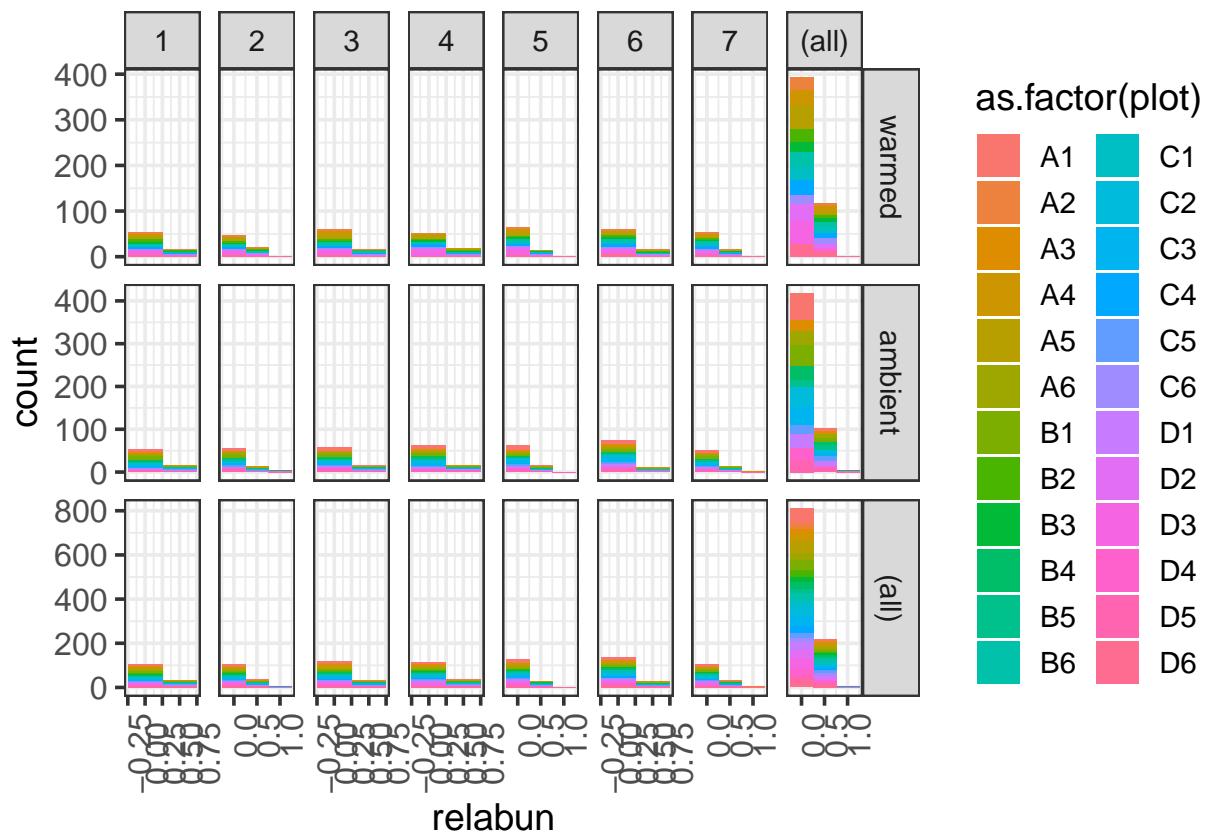


```
shapiro.test(comp_umbs_spp$relabun) # pvalue is < 0.05 so we reject the null hypothesis that the data
```

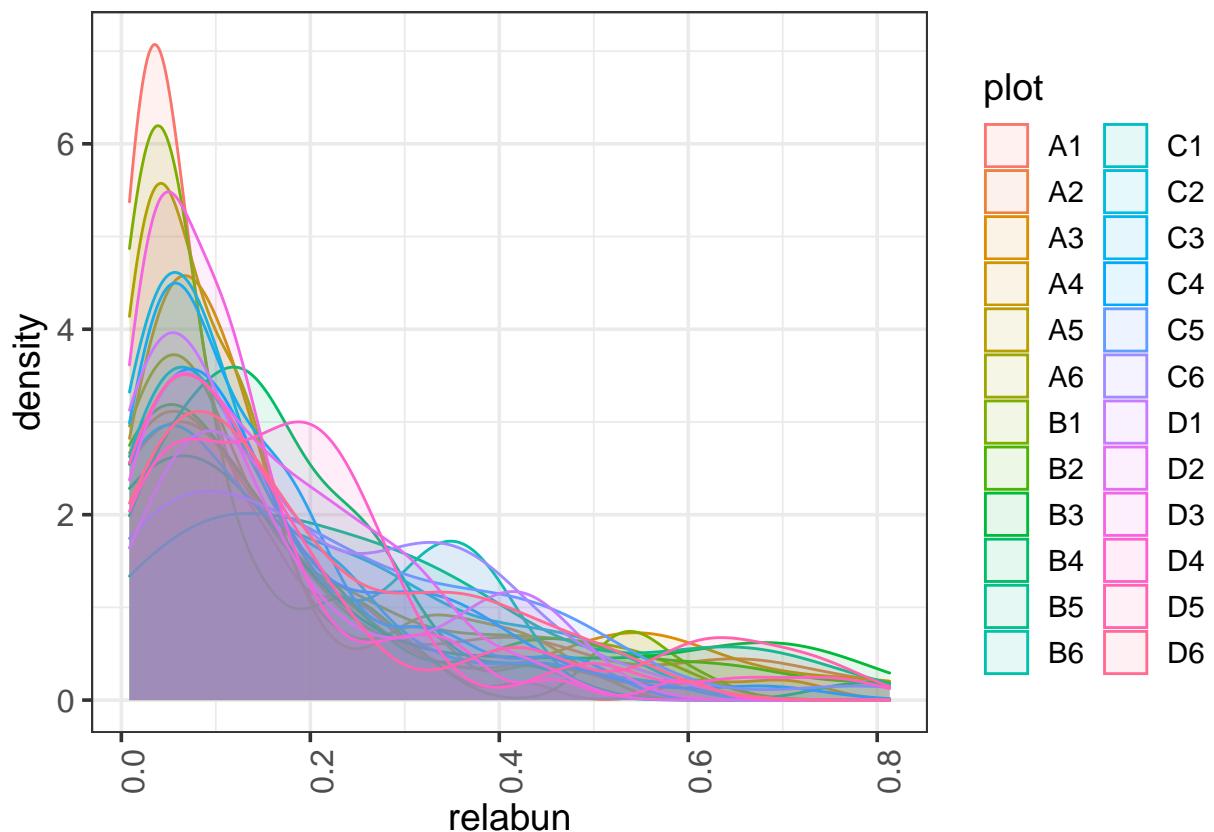
```
##  
## Shapiro-Wilk normality test  
##  
## data: comp_umbs_spp$relabun  
## W = 0.81457, p-value < 2.2e-16  
  
# Visualizing median Julian date for umbs at the PLOT LEVEL  
ggplot(comp_umbs_spp, aes(relabun, fill = plot)) + geom_histogram(binwidth = 0.5) +  
  facet_grid(year_factor ~ site, margins = 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")
```



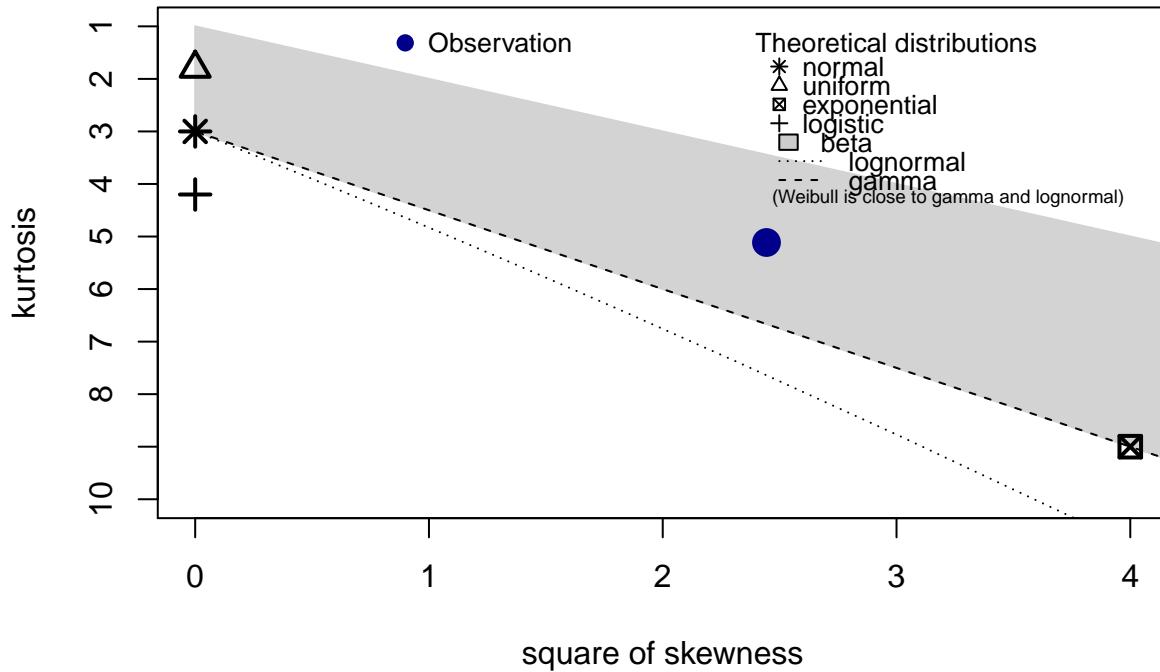
```
ggplot(comp_umbs_spp, aes(relabun, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
# ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color=plot)) +
# geom_density(alpha = 0.1) + facet_wrap(~year) ggplot(umbs_flwr_plot,
# aes(julian_median, fill = plot, color=plot)) + geom_density(alpha = 0.1) +
# facet_wrap(~year + plot)
```

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

## Cullen and Frey graph

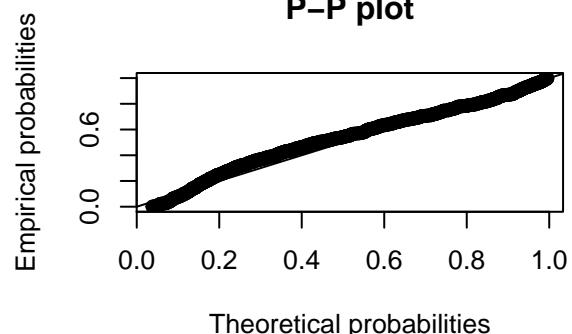
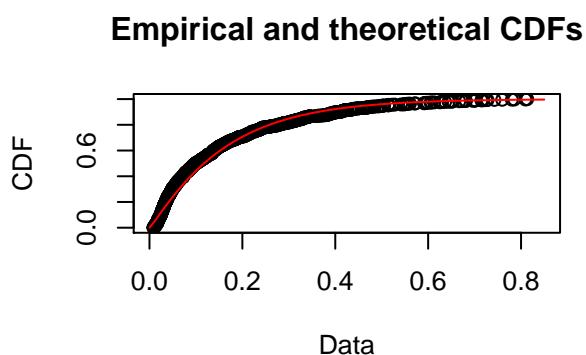
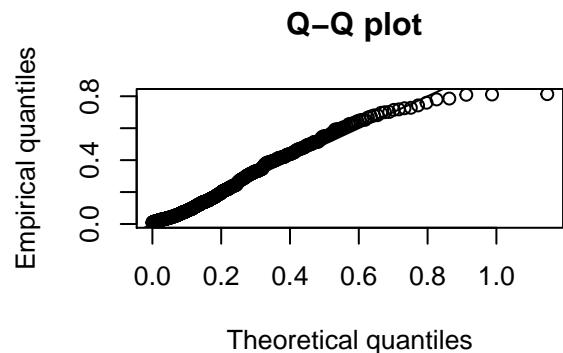
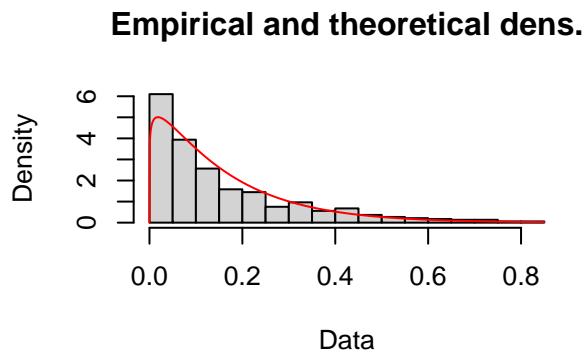


```

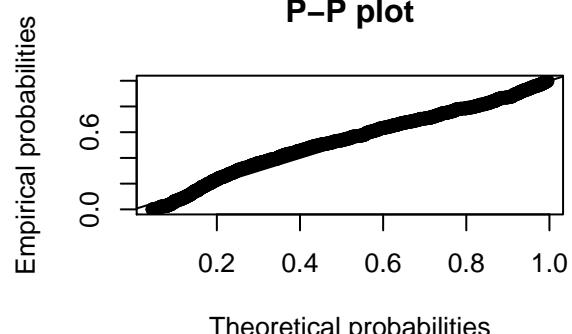
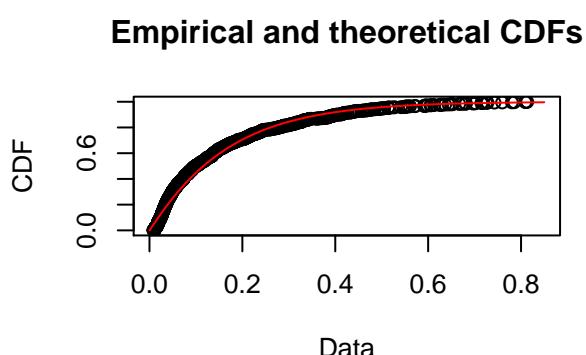
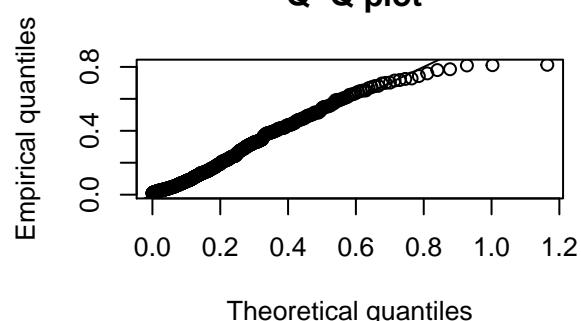
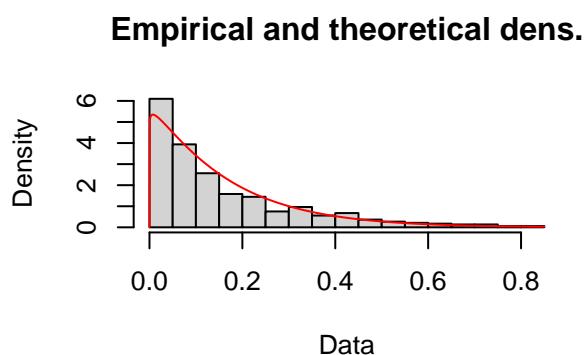
## summary statistics
## -----
## min:  0.008576329  max:  0.8132261
## median:  0.09942812
## mean:  0.1621622
## estimated sd:  0.1625539
## estimated skewness:  1.563266
## estimated kurtosis:  5.113612

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

```

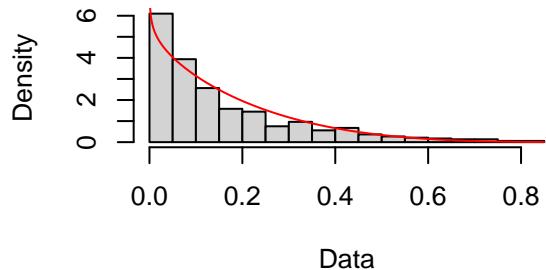


```
# Weibull distribution
fit.weibull <- fitdist(comp_umbs_spp$relabun, "weibull")
plot(fit.weibull)
```

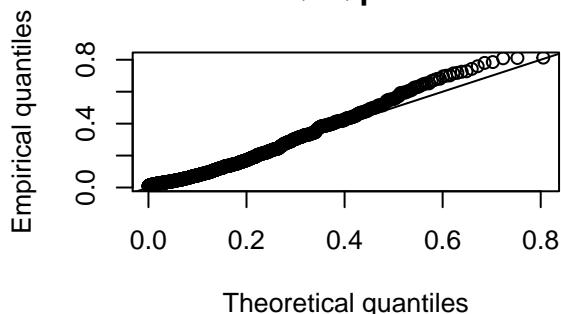


```
fit.beta <- fitdist(comp_umbs_spp$relabun, "beta")
plot(fit.beta)
```

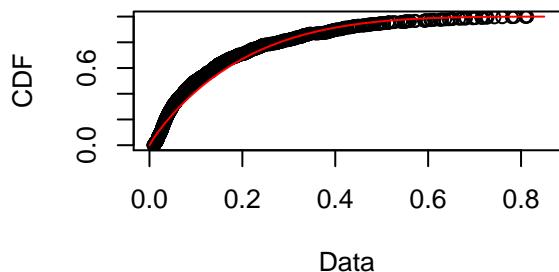
**Empirical and theoretical dens.**



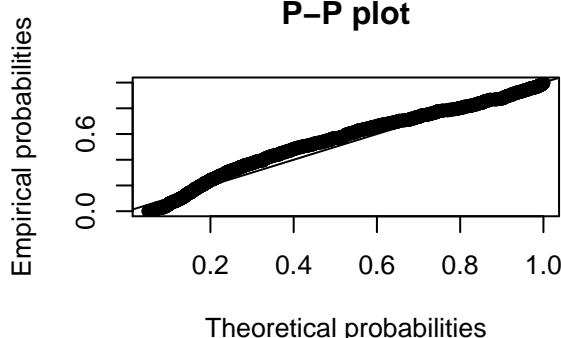
**Q–Q plot**



**Empirical and theoretical CDFs**

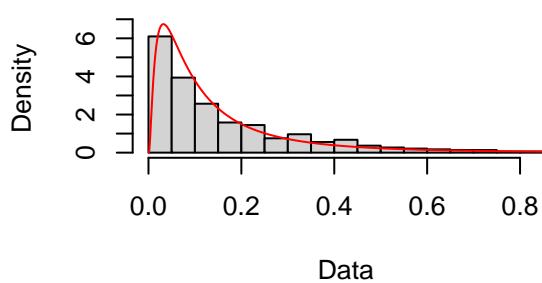


**P–P plot**

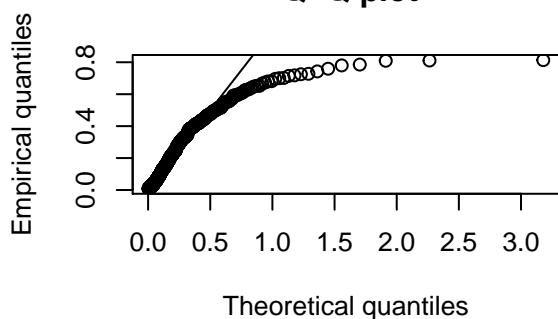


```
# Lognormal distribution
fit.ln <- fitdist(comp_umbs_spp$relabun, "lnorm")
plot(fit.ln)
```

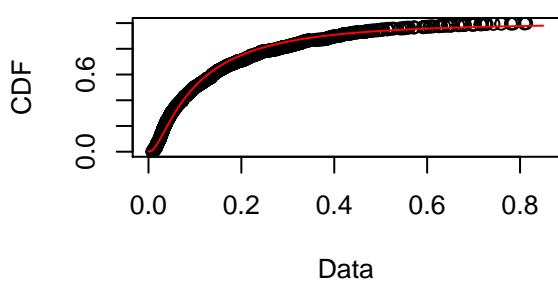
### Empirical and theoretical dens.



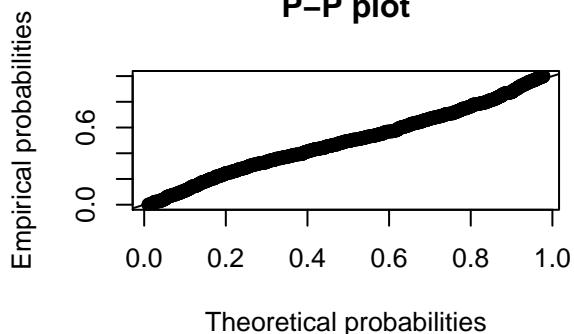
### Q-Q plot



### Empirical and theoretical CDFs

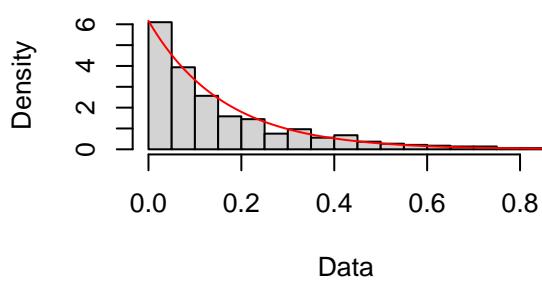


### P-P plot

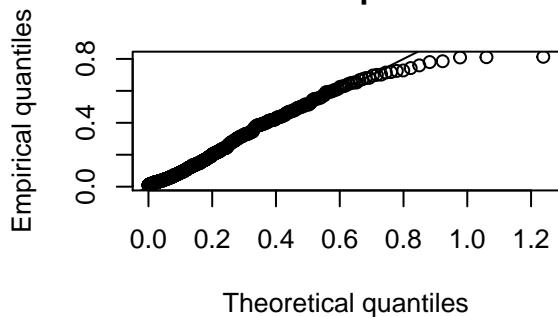


```
# Exponential distribution is another option  
fit.exp <- fitdist(comp_umbs_spp$relabun, "exp")  
plot(fit.exp)
```

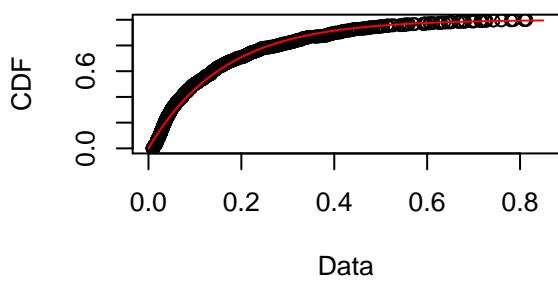
### Empirical and theoretical dens.



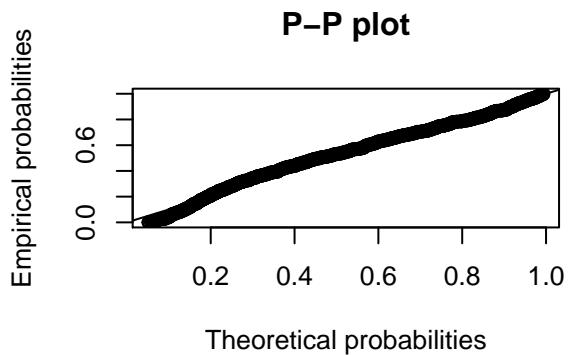
### Q-Q plot



### Empirical and theoretical CDFs



### P-P plot

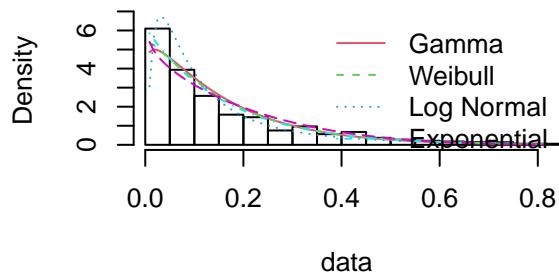


```

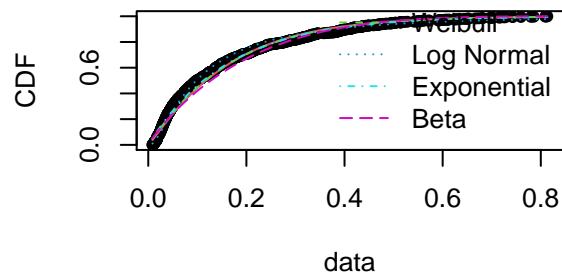
par(mfrow = c(2, 2))
plot.legend <- c("Gamma", "Weibull", "Log Normal", "Exponential", "Beta")
denscomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
cdfcomp(list(fit.gamma, fit.weibull, fit.ln, fit.exp, fit.beta), legendtext = plot.legend)
qqcomp(list(fit.gamma,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

```

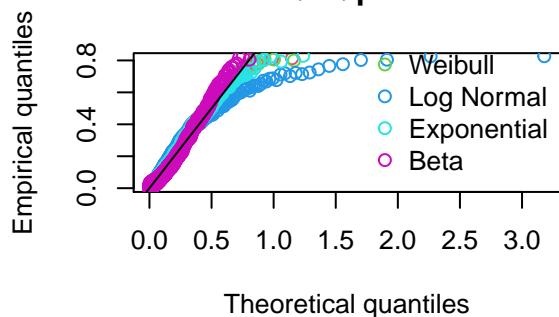
**Histogram and theoretical densities**



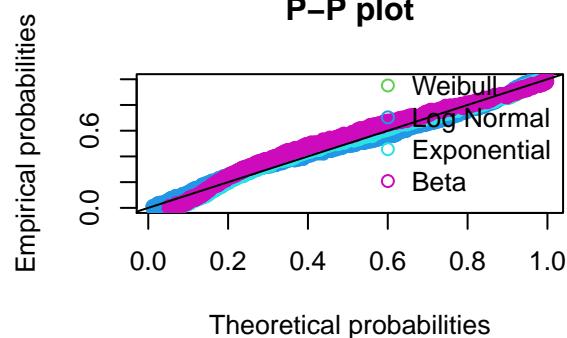
**Empirical and theoretical CDFs**



**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 0.07172526 0.06110881 0.04609401 0.06223669
## Cramer-von Mises statistic  1.66643014 1.31861355 0.76941523 0.93790091
## Anderson-Darling statistic 10.33276363 9.06809325 5.11490389 7.90136228
##                                     Beta
## Kolmogorov-Smirnov statistic 0.08549927
## Cramer-von Mises statistic  2.68792583
## Anderson-Darling statistic 15.69170653
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal      Exp
## Akaike's Information Criterion -1702.294 -1695.979 -1762.153 -1695.296
## Bayesian Information Criterion -1692.407 -1686.093 -1752.267 -1690.353
##                                     Beta

```

```

## Akaike's Information Criterion -1651.385
## Bayesian Information Criterion -1641.499

# Beta distribution looks to be the best based on AIC and BIC values

```

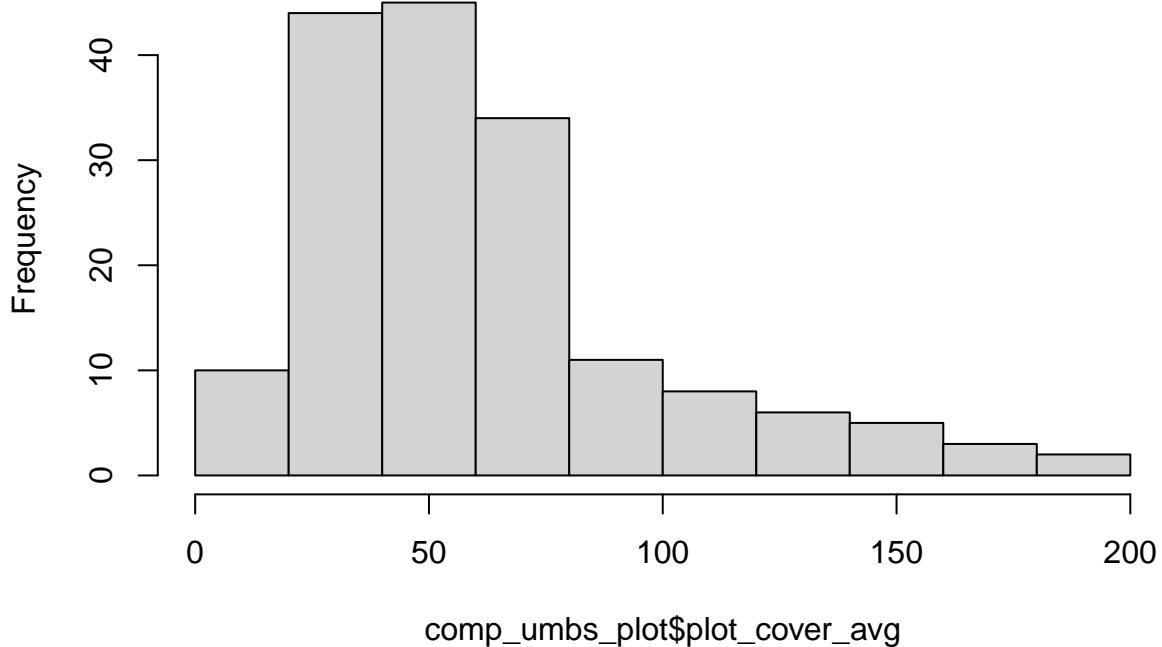
## UMBS PLOT LEVEL - Looking at PLOT AVG TOTALS

```

### UMBS ###
hist(comp_umbs_plot$plot_cover_avg)

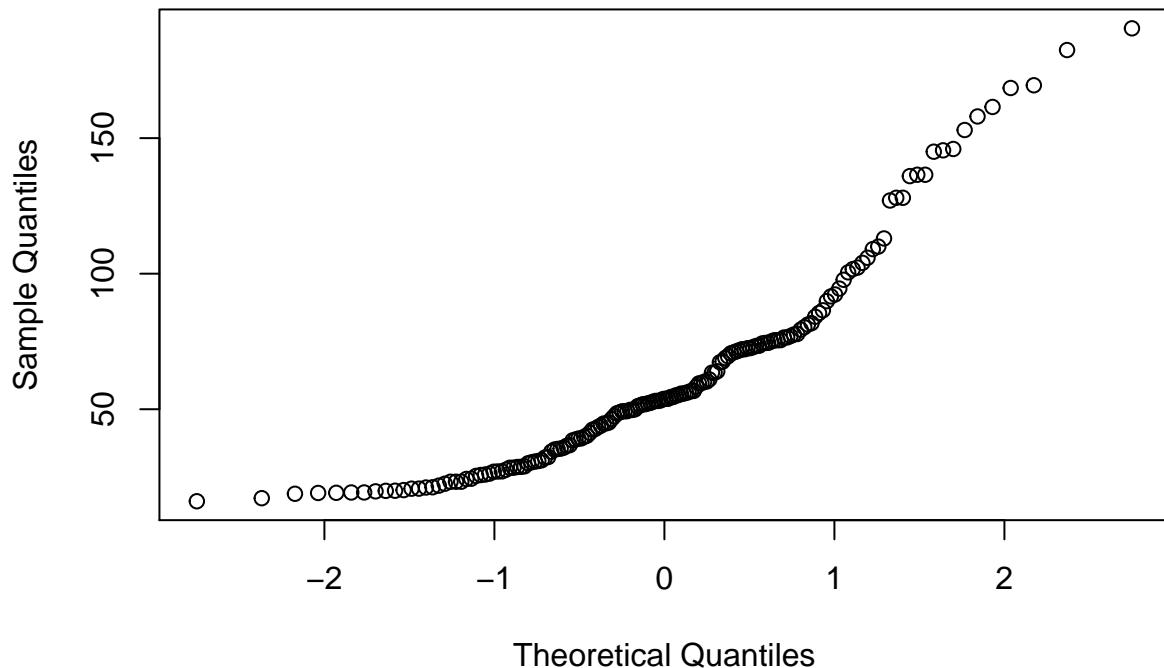
```

**Histogram of comp\_umbs\_plot\$plot\_cover\_avg**



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

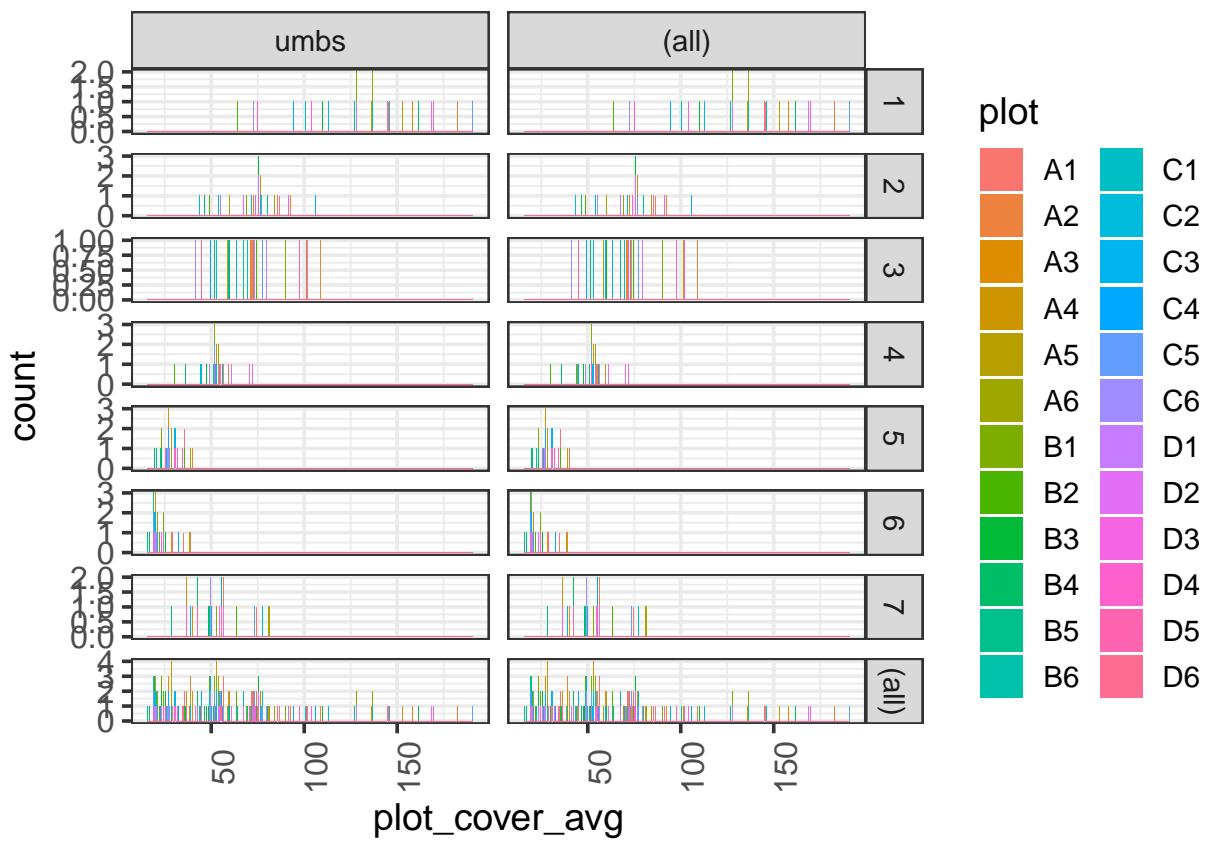
## Normal Q-Q Plot



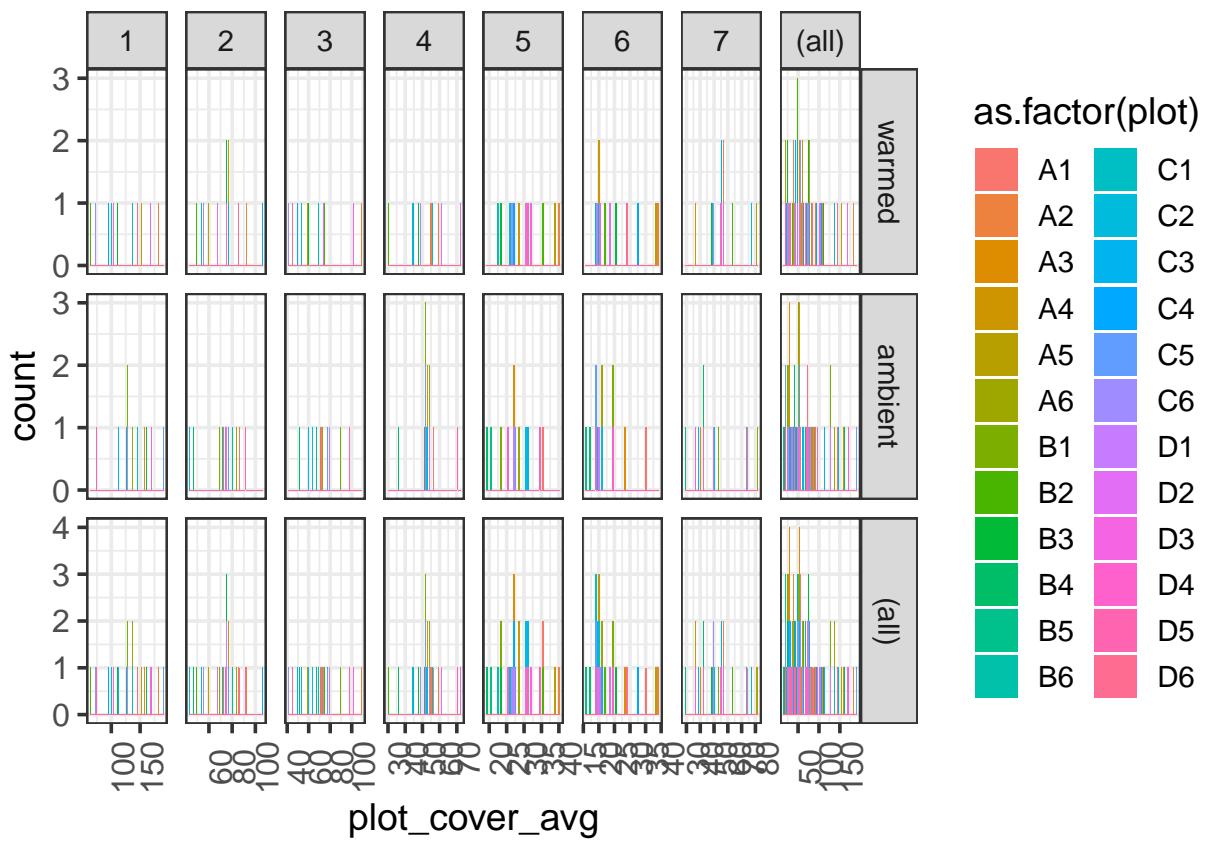
```
shapiro.test(comp_umbs_plot$plot_cover_avg) # pvalue is < 0.05 so we reject the null hypothesis that the data is normally distributed

## 
## Shapiro-Wilk normality test
##
## data: comp_umbs_plot$plot_cover_avg
## W = 0.88376, p-value = 3.599e-10

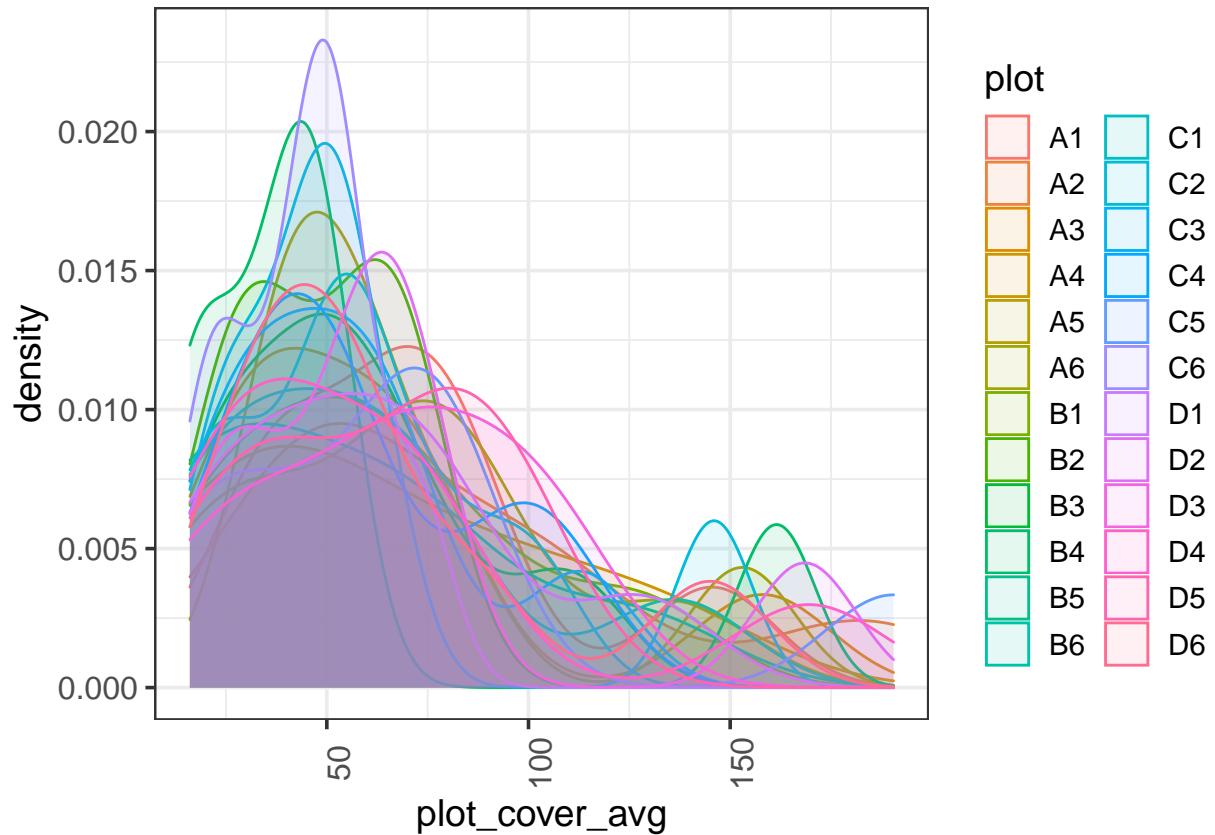
# Visualizing median Julian date for umbs at the PLOT LEVEL
ggplot(comp_umbs_plot, aes(plot_cover_avg, fill = plot)) + geom_histogram(binwidth = 0.5) +
  facet_grid(year_factor ~ site, margins = TRUE, scales = "free")
```



```
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")
```



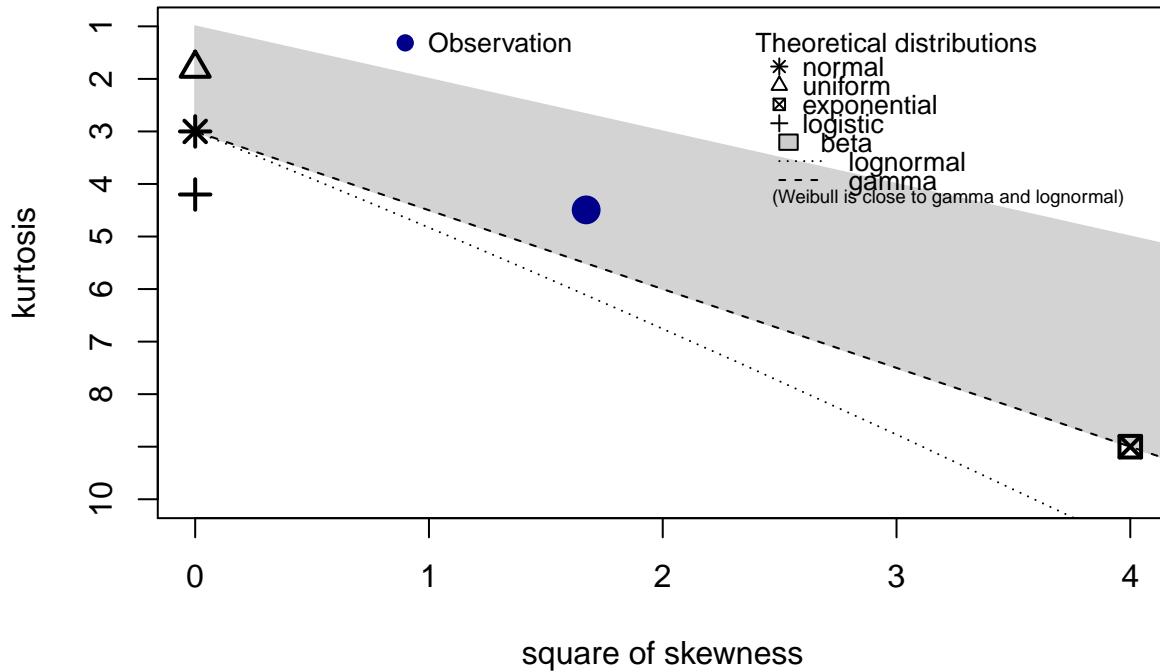
```
ggplot(comp_umbs_plot, aes(plot_cover_avg, fill = plot, color = plot)) + geom_density(alpha = 0.1)
```



```
# ggplot(umbs_flwr_plot, aes(julian_median, fill = plot, color=plot)) +
# geom_density(alpha = 0.1) + facet_wrap(~year) ggplot(umbs_flwr_plot,
# aes(julian_median, fill = plot, color=plot)) + geom_density(alpha = 0.1) +
# facet_wrap(~year + plot)
```

*# Exploring distributions for these right-skewed data:  
descdist(comp\_umbs\_plot\$plot\_cover\_avg, discrete = FALSE)*

## Cullen and Frey graph

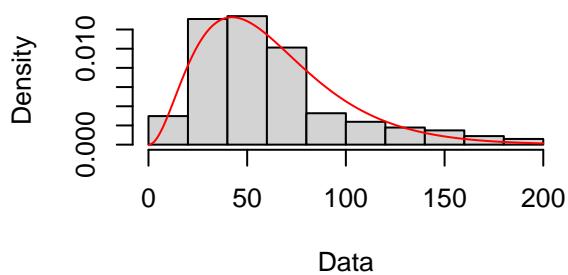
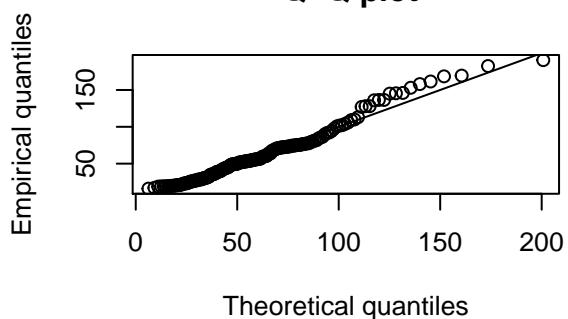
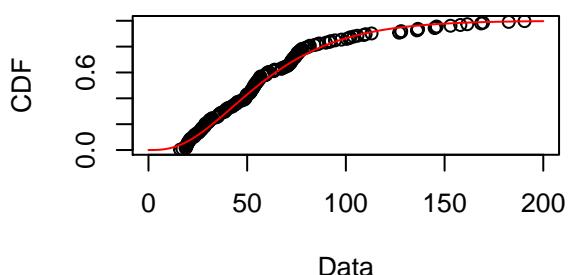
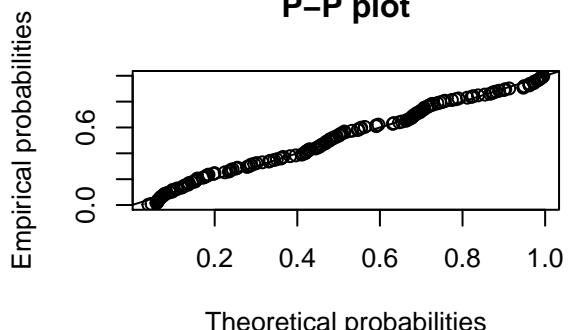


```

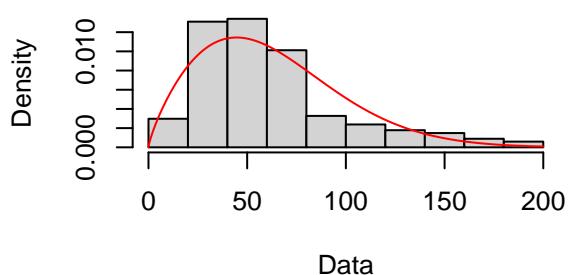
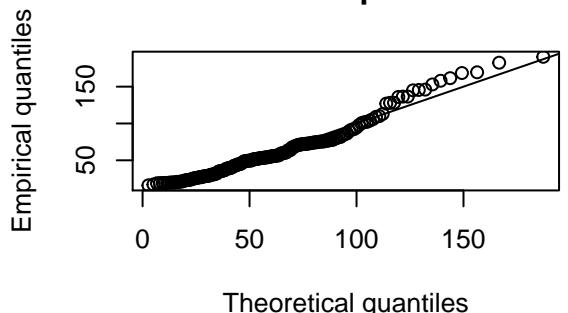
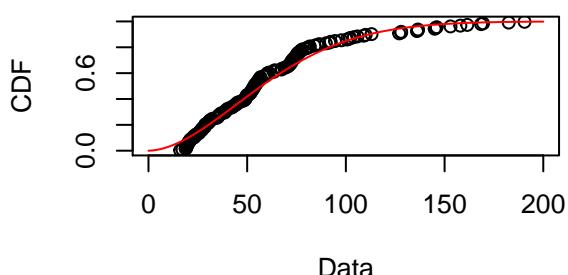
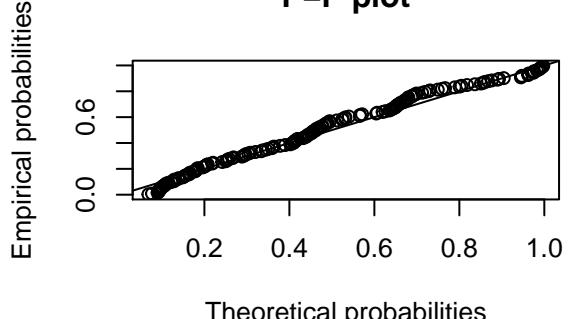
## summary statistics
## -----
## min: 16.05882  max: 190.5
## median: 53.82353
## mean: 62.03263
## estimated sd: 37.33645
## estimated skewness: 1.293271
## estimated kurtosis: 4.493284

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

```

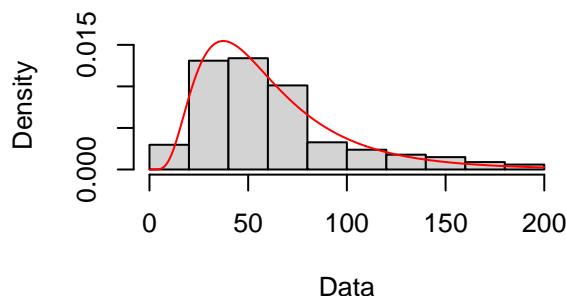
**Empirical and theoretical dens.****Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

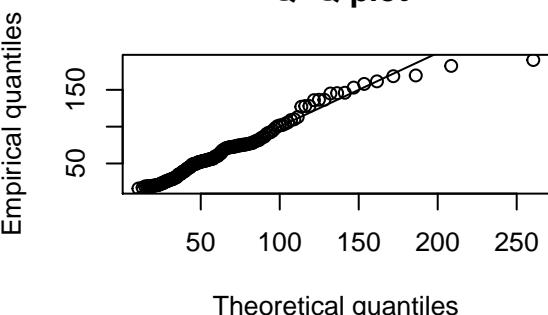
**Empirical and theoretical dens.****Q-Q plot****Empirical and theoretical CDFs****P-P plot**

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

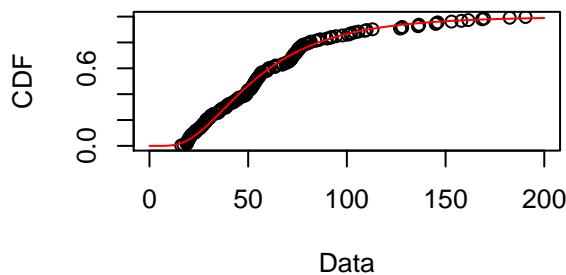
**Empirical and theoretical dens.**



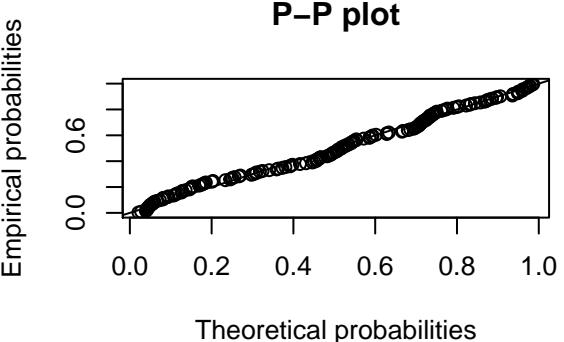
**Q–Q plot**



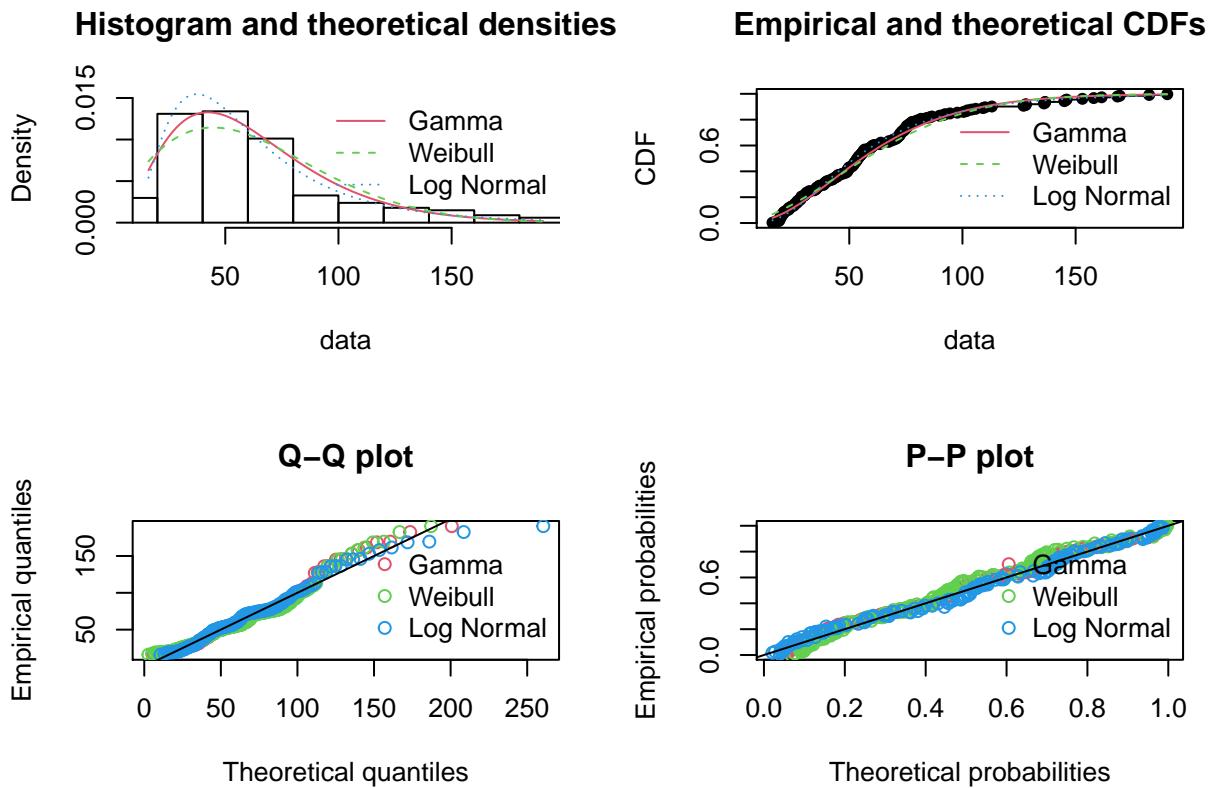
**Empirical and theoretical CDFs**



**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)
```



```
# 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 0.05954516 0.08671333 0.05939556
## Cramer-von Mises statistic   0.12661502 0.24900792 0.11266902
## Anderson-Darling statistic   1.07862351 1.94296016 0.80317754
##
## Goodness-of-fit criteria
##                                     Gamma   Weibull Log Normal
## Akaike's Information Criterion 1636.711 1649.765 1629.868
## Bayesian Information Criterion 1642.959 1656.013 1636.115

# Log Normal the best based on AIC and BIC values
```

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

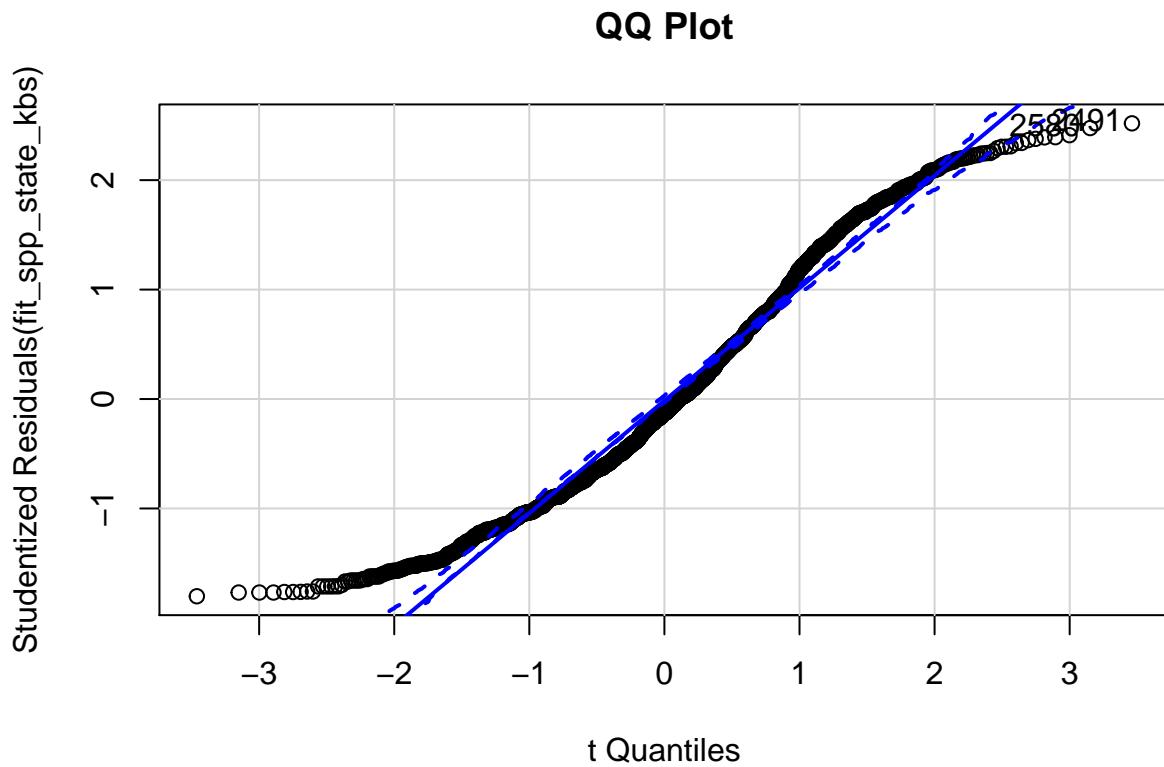
These illustrate whether certain data points have more leverage (more influence), and thus could be outliers. It's a way of detecting outliers. Leverage plots can help identify whether a point has high or low influence, based on its leverage and residual and determining model fit with and without the 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

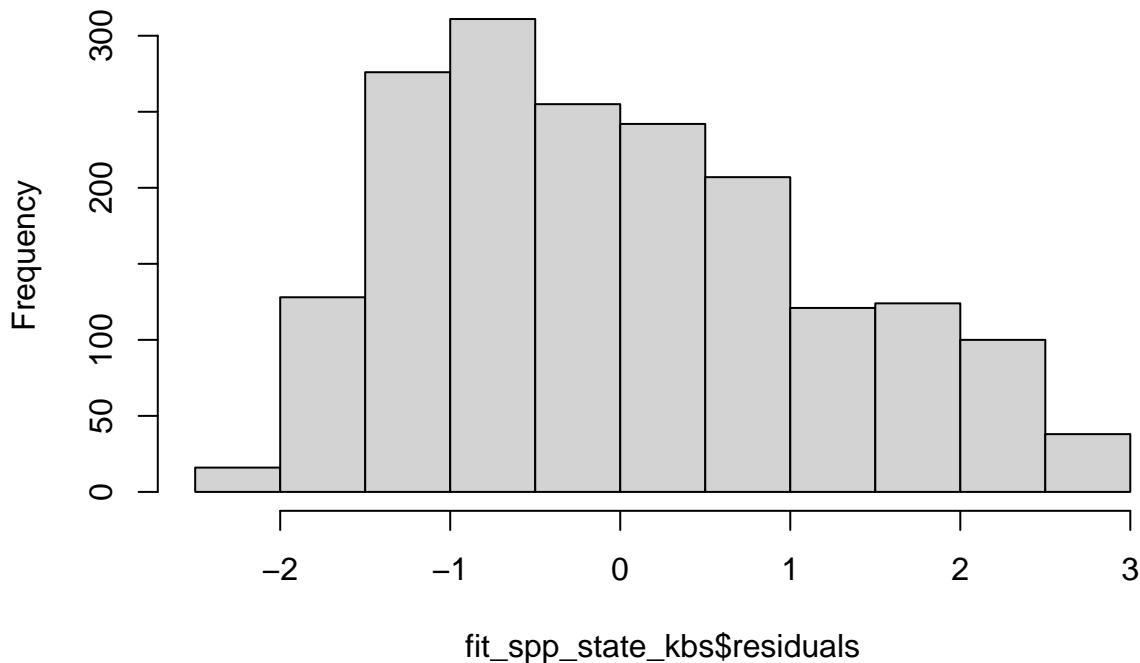
qqPlot(fit_spp_state_kbs, main = "QQ Plot")
```



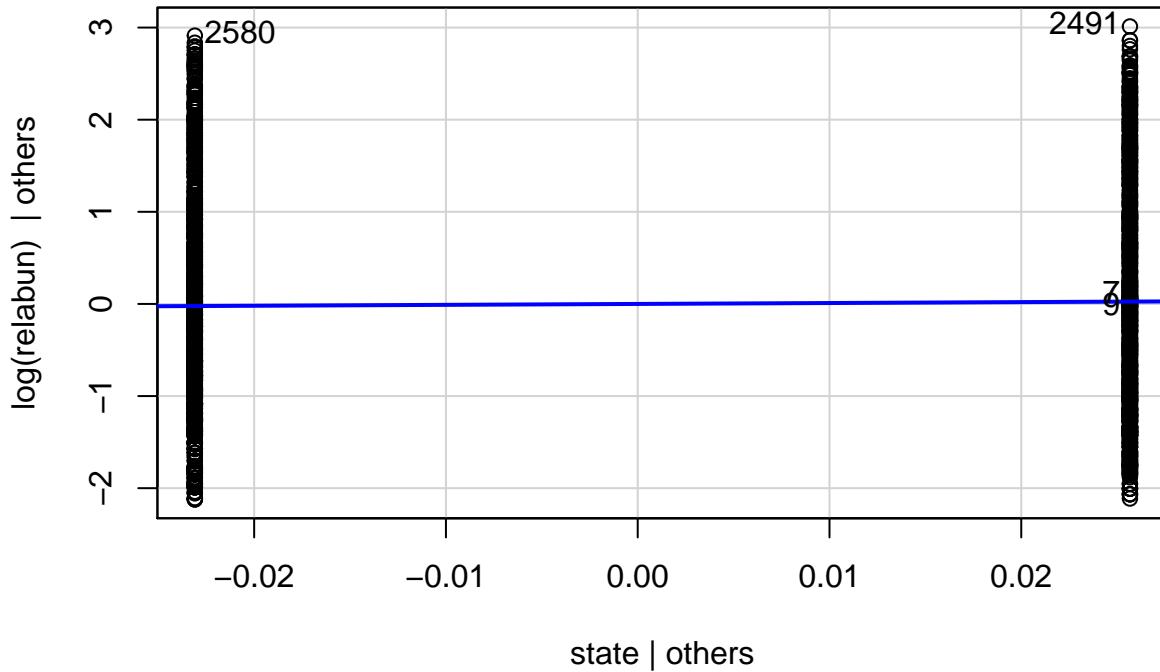
```
## 2491 2580
## 1491 1580
```

```
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)
```

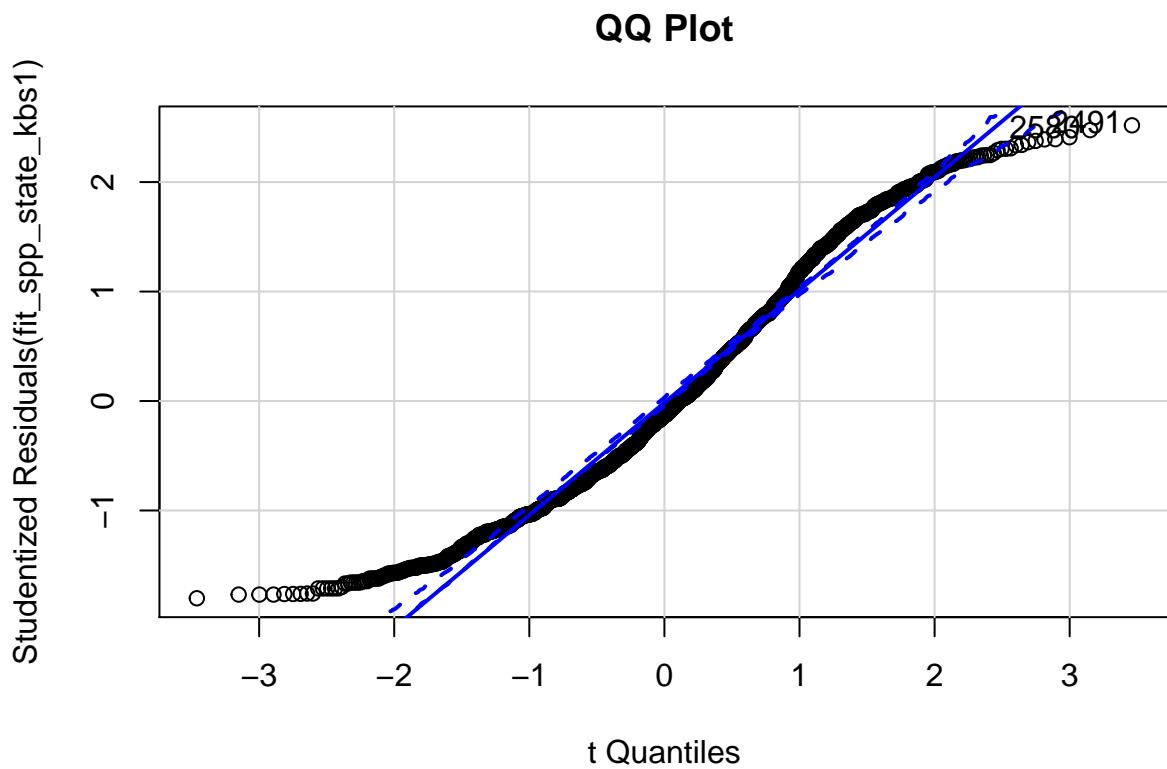
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      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
```

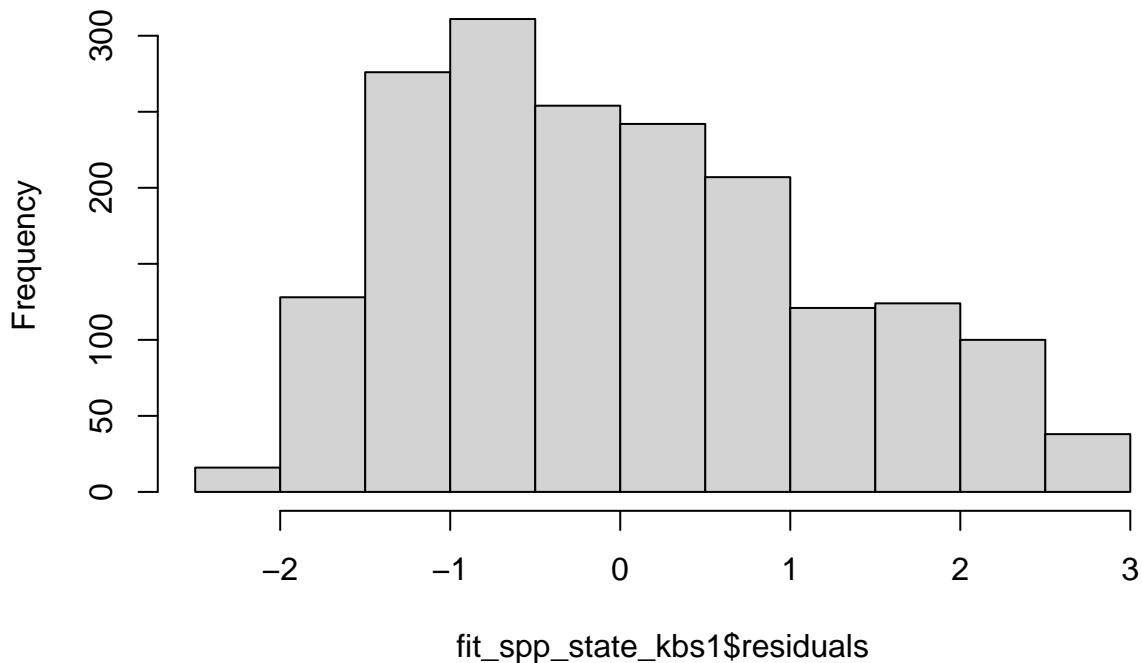
```
qqPlot(fit_spp_state_kbs1, main = "QQ Plot")
```



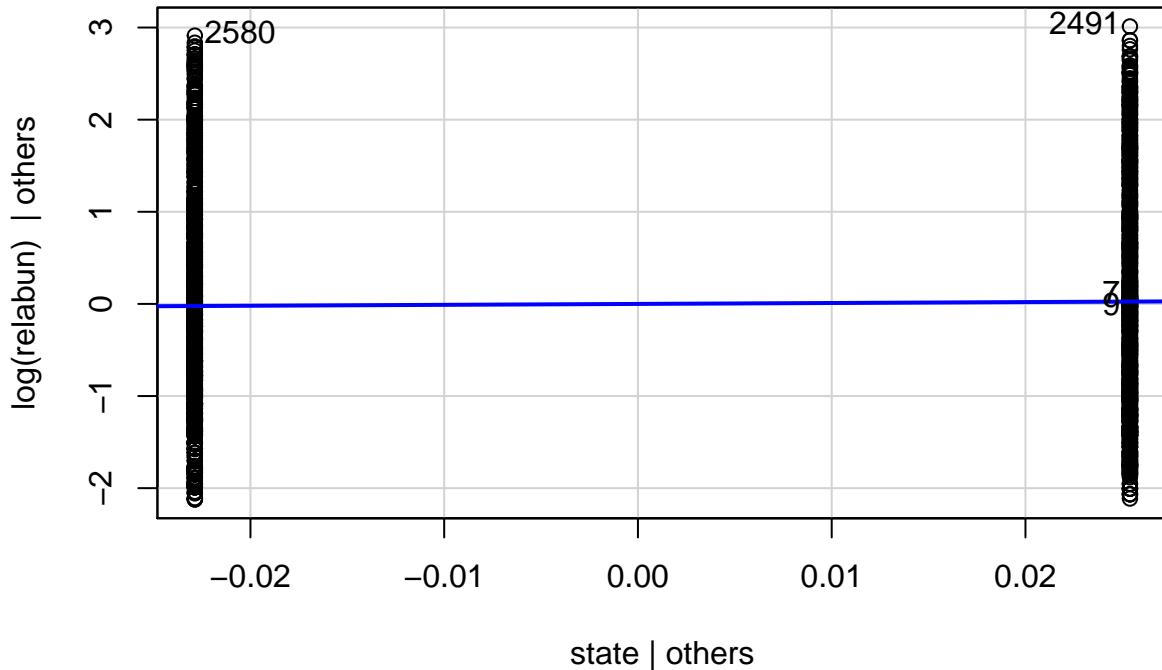
```
## 2491 2580  
## 1490 1579
```

```
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)
```

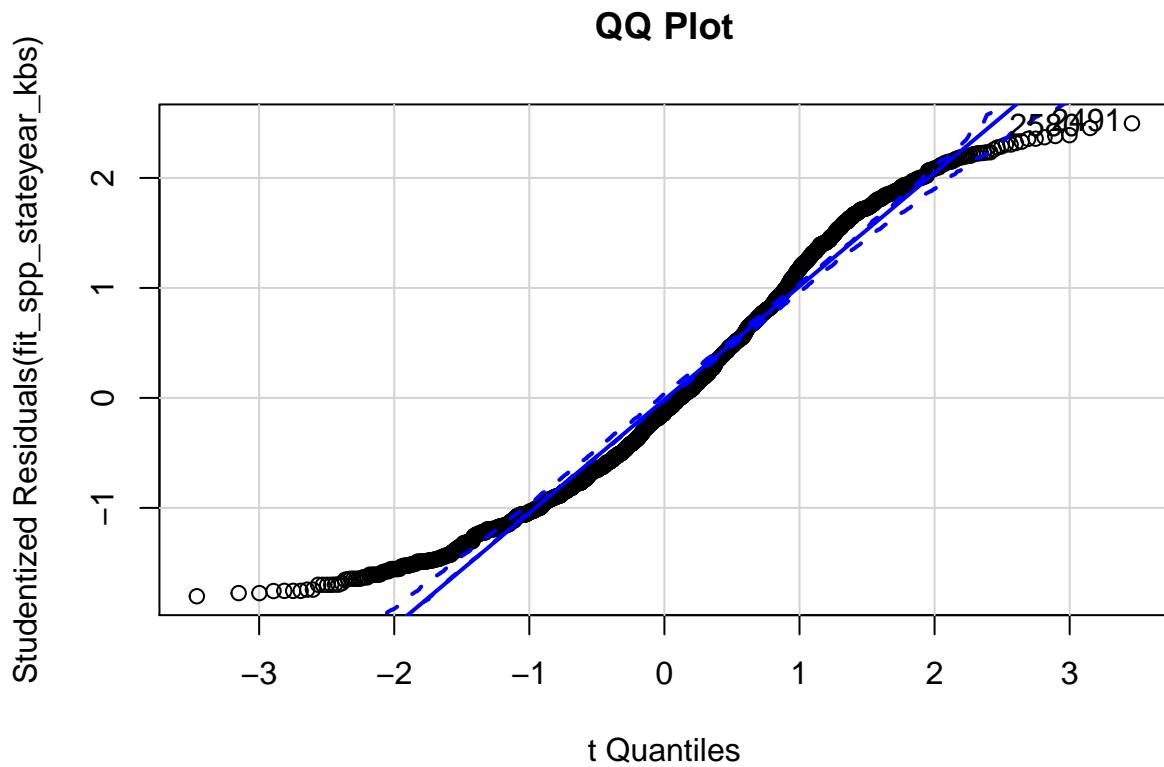
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      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
```

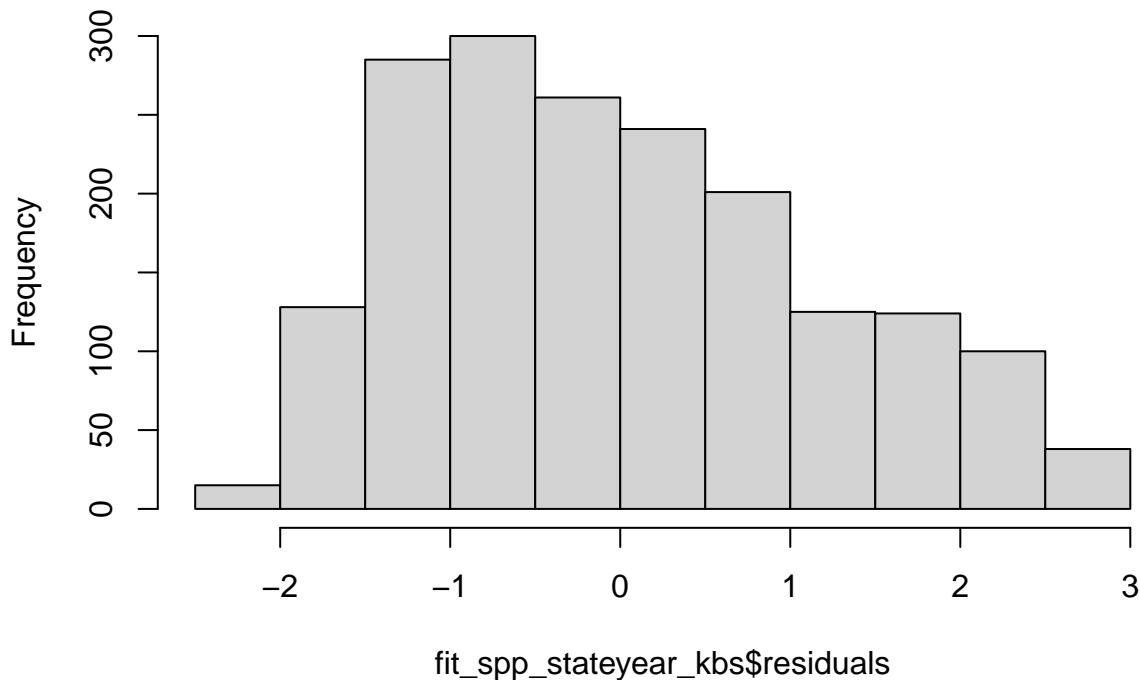
```
qqPlot(fit_spp_stateyear_kbs, main = "QQ Plot")
```



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

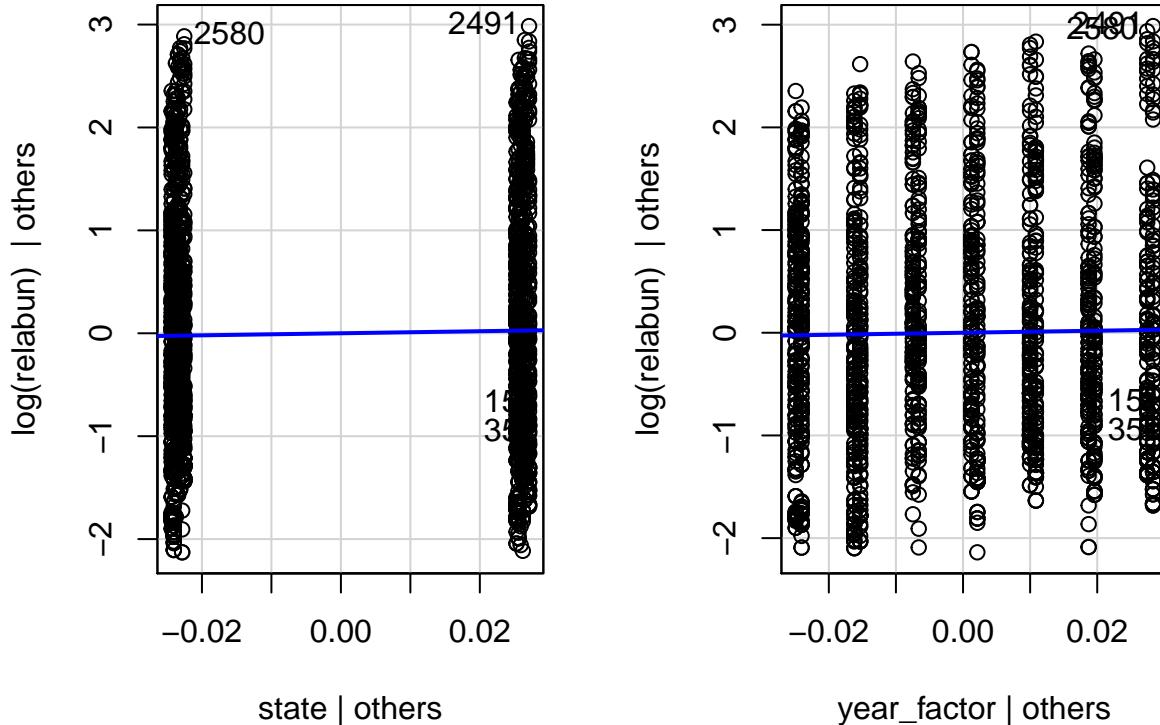
```
hist(fit_spp_stateyear_kbs$residuals)
```

**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
```

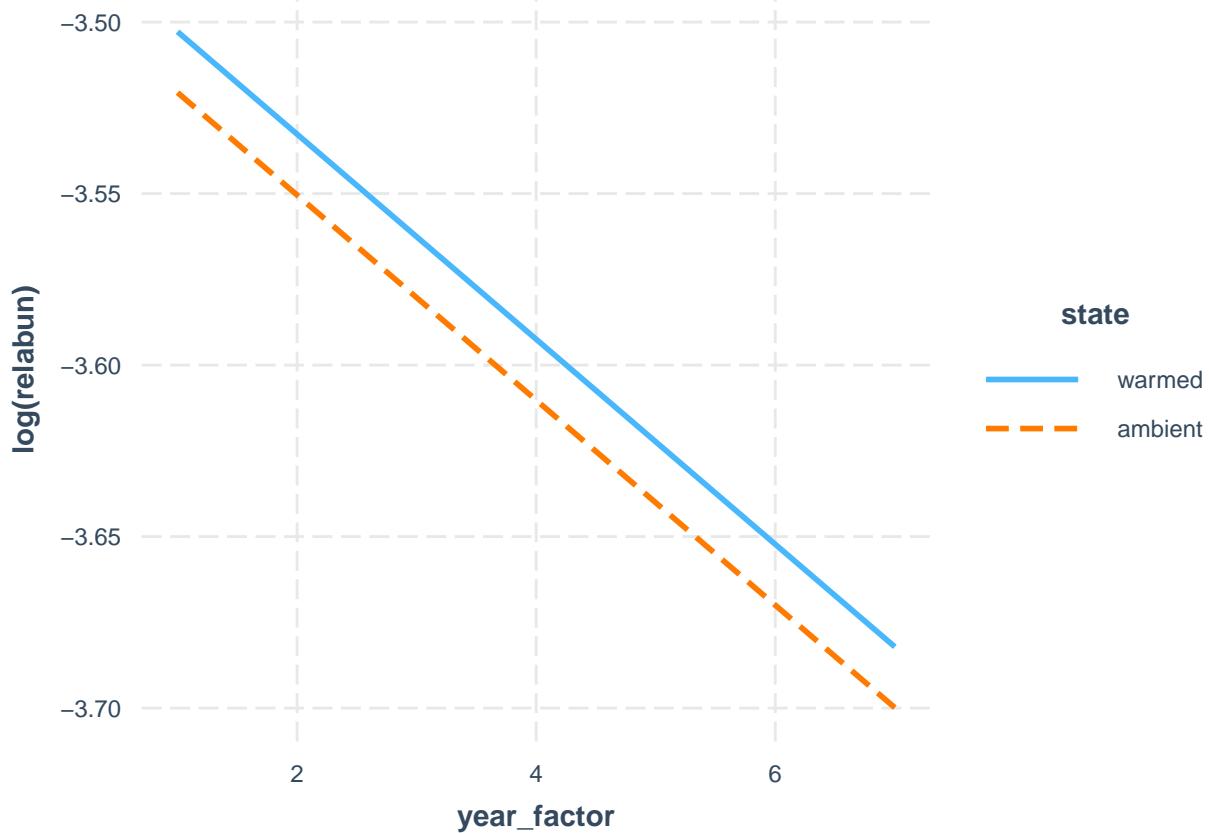
```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9656       0.0000
## Kolmogorov-Smirnov 0.0685       0.0000
## Cramer-von Mises 144.8202      0.0000
## Anderson-Darling 17.0611       0.0000
## -----
```

```
# 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.
```

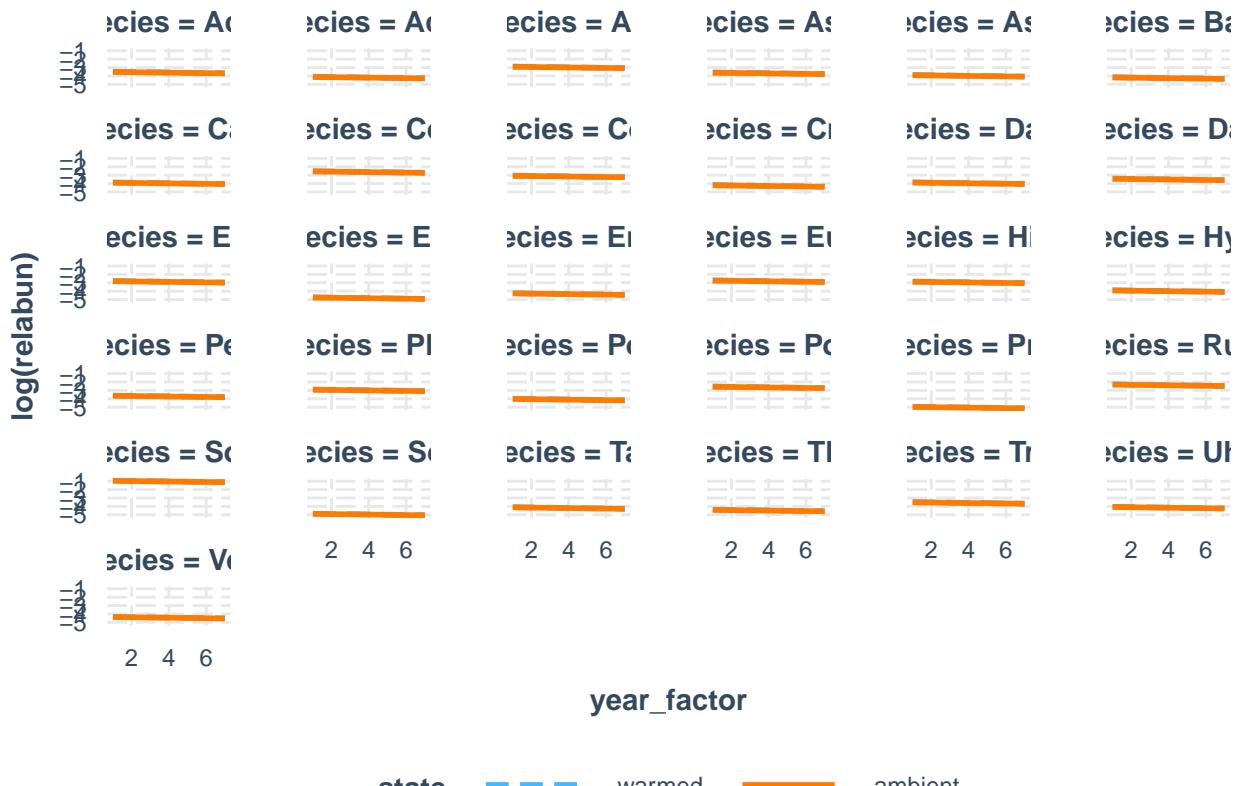
```
## Warning: year_factor and state are not included in an interaction with one another
## in the model.
```



```
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.
```

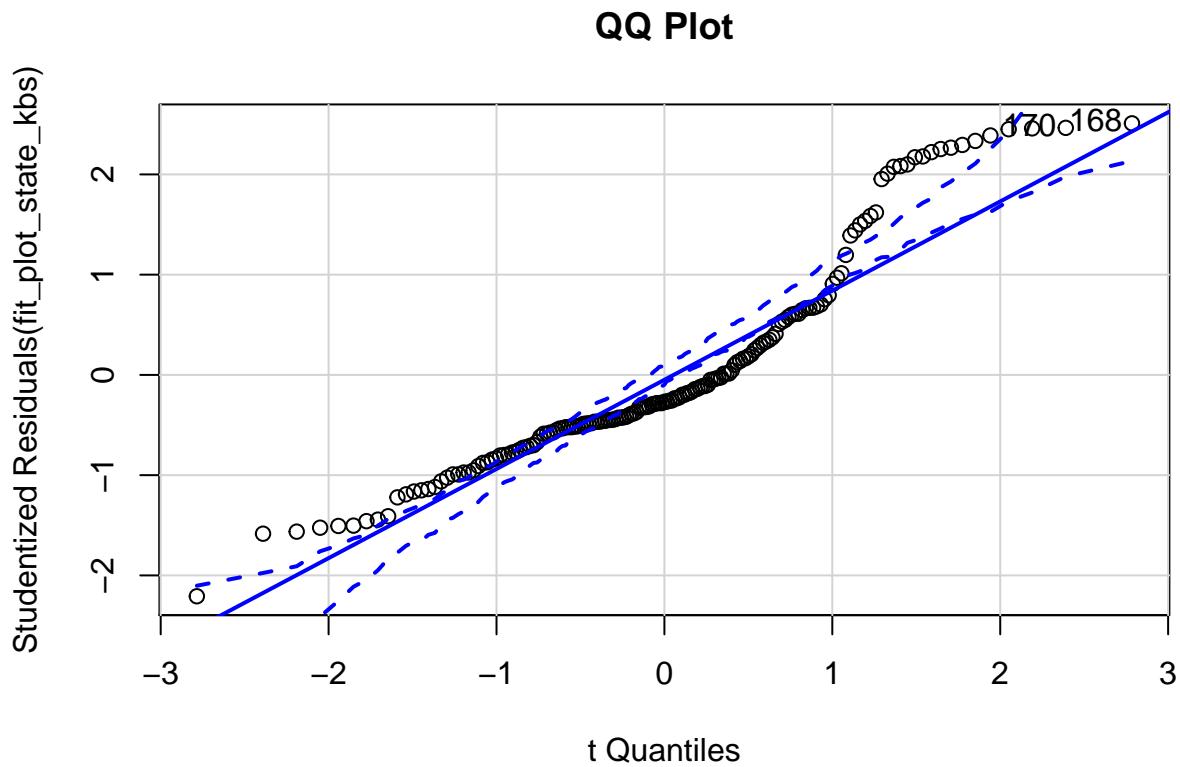
```
## Warning: year_factor and state and species are not included in an interaction with
## one another in the model.
```



```
# 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
```

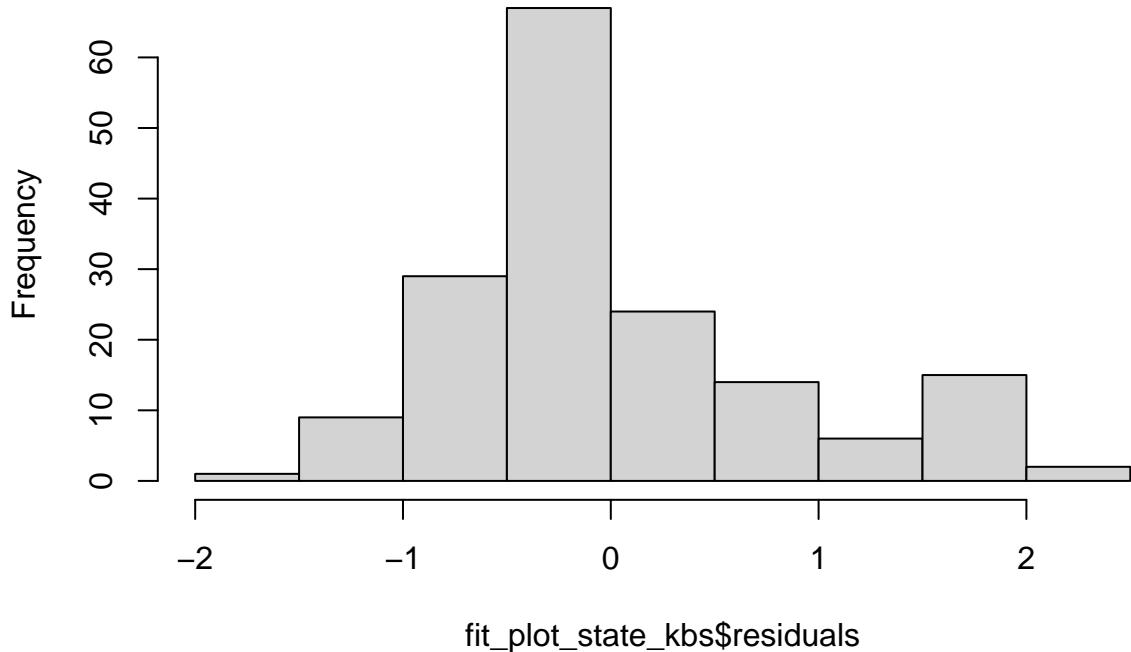
```
comp_kbs_plot_no_outliers <- comp_kbs_plot[-252, ] # remove outliers
qqPlot(fit_plot_state_kbs, main = "QQ Plot")
```



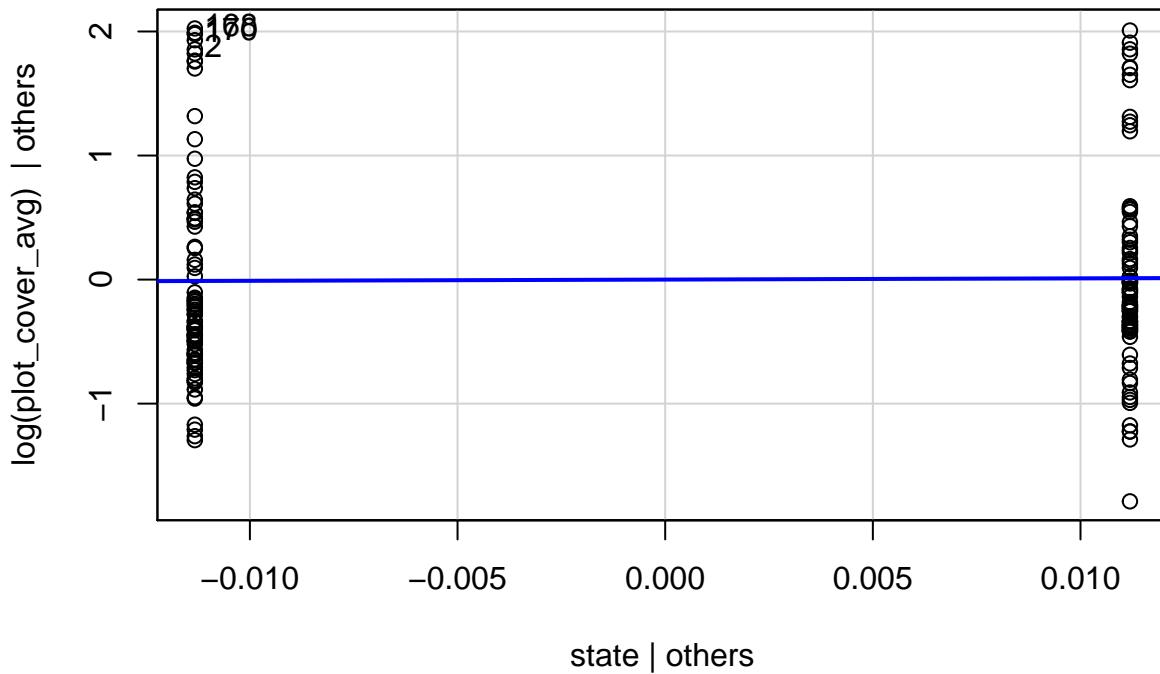
```
## 168 170
## 84 86
```

```
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)
```

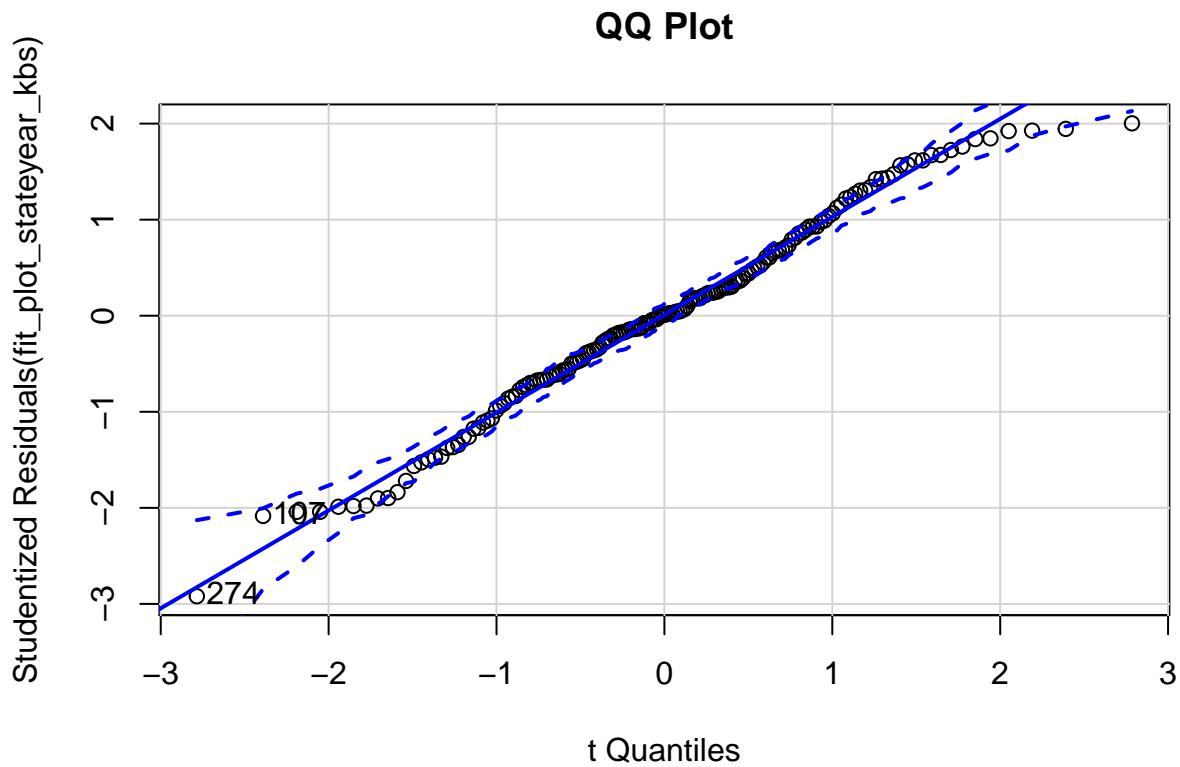
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      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
```

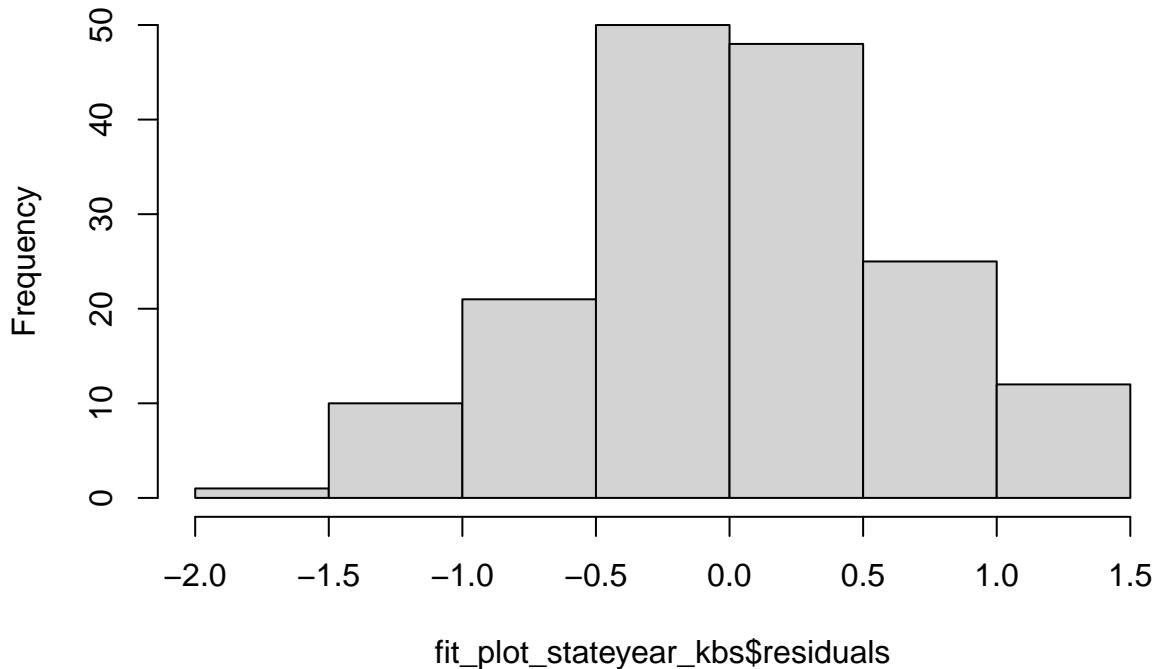
```
comp_kbs_plot_no_outliers <- comp_kbs_plot[-190, ] # remove outliers
qqPlot(fit_plot_stateyear_kbs, main = "QQ Plot")
```



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

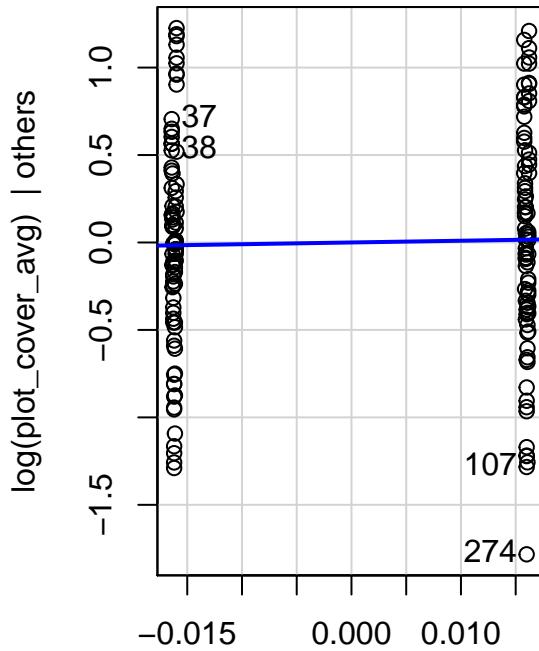
```
hist(fit_plot_stateyear_kbs$residuals)
```

**Histogram of fit\_plot\_stateyear\_kbs\$residuals**

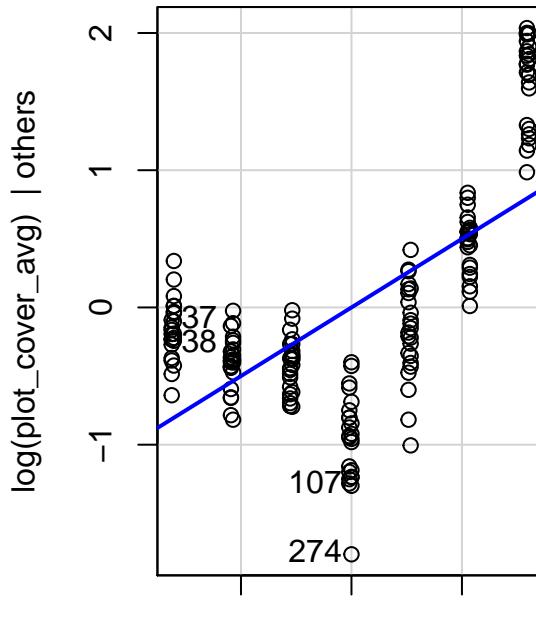


```
leveragePlots(fit_plot_stateyear_kbs)
```

## 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
```

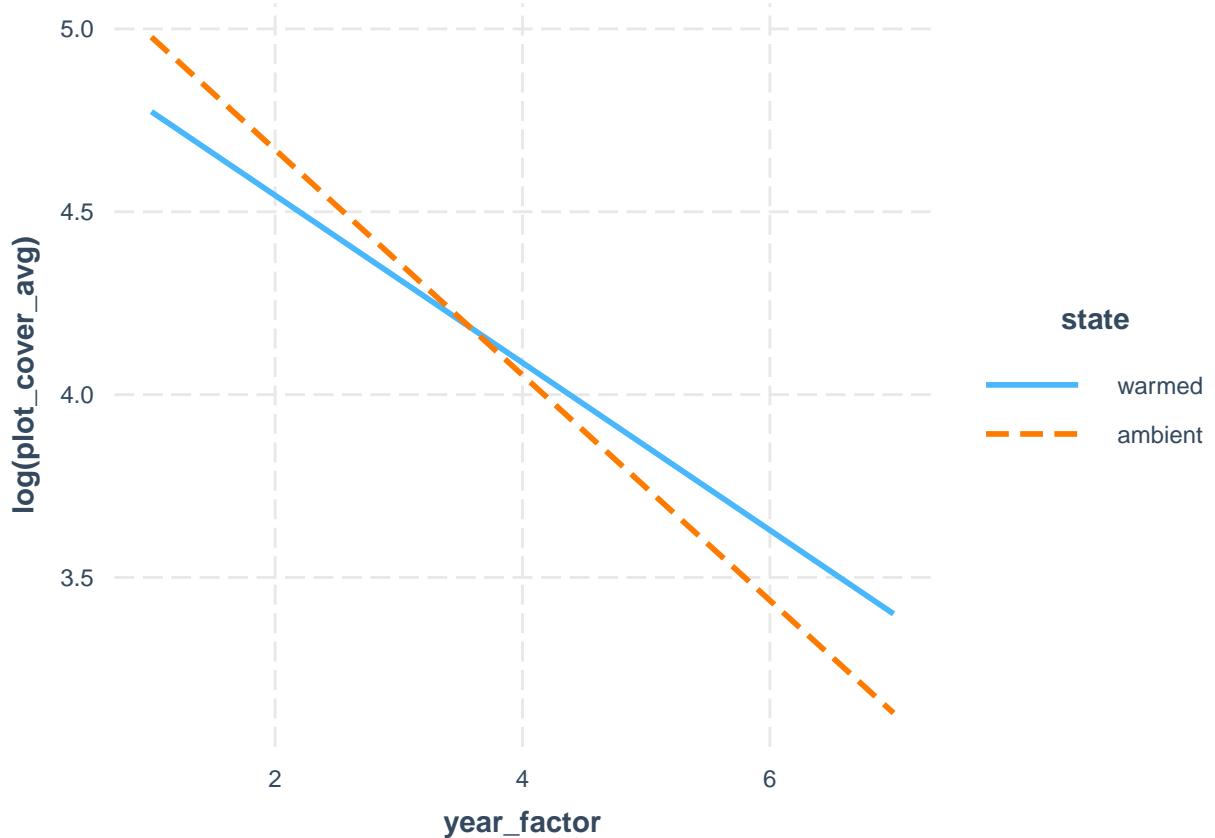
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##      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.
```

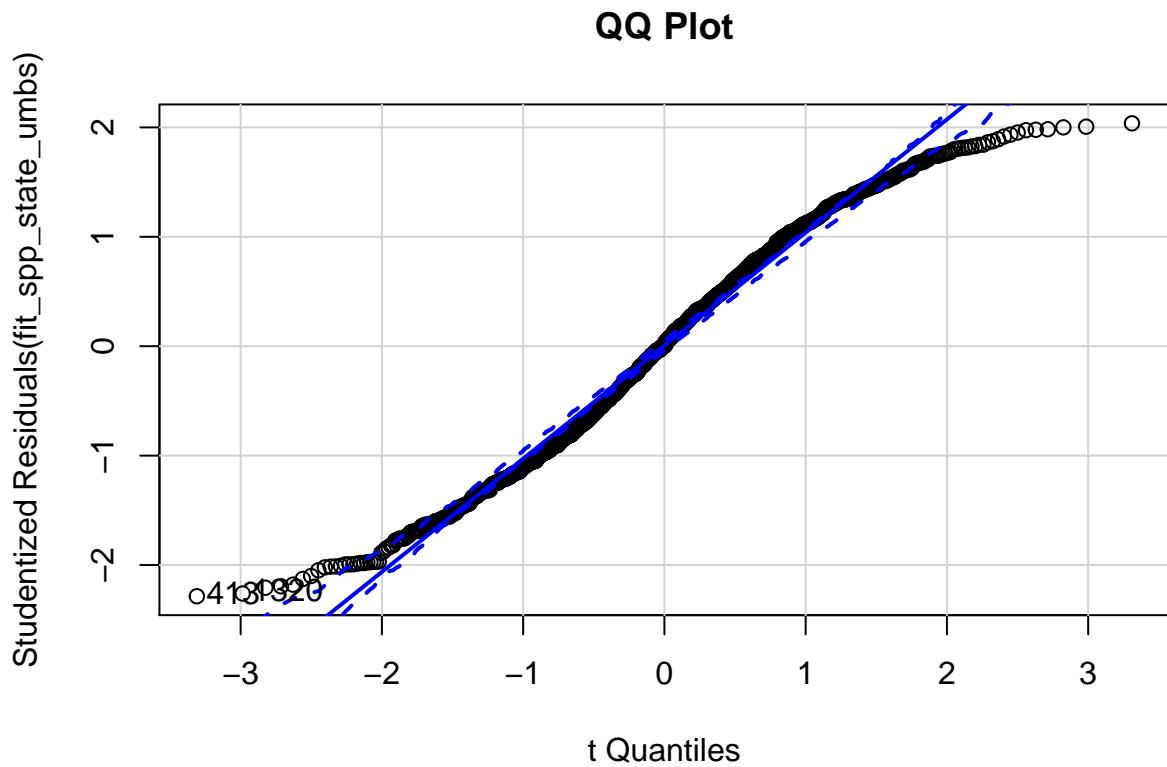


UMBS

```
# 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 -2.285399           0.022491        NA
```

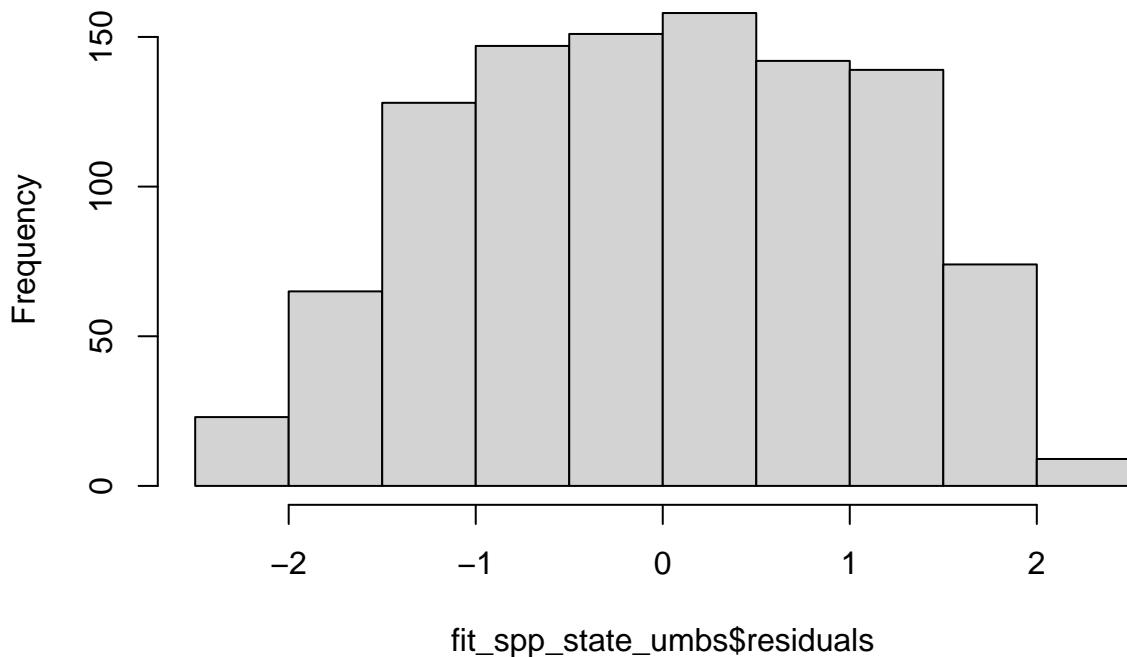
```
qqPlot(fit_spp_state_umbs, main = "QQ Plot")
```



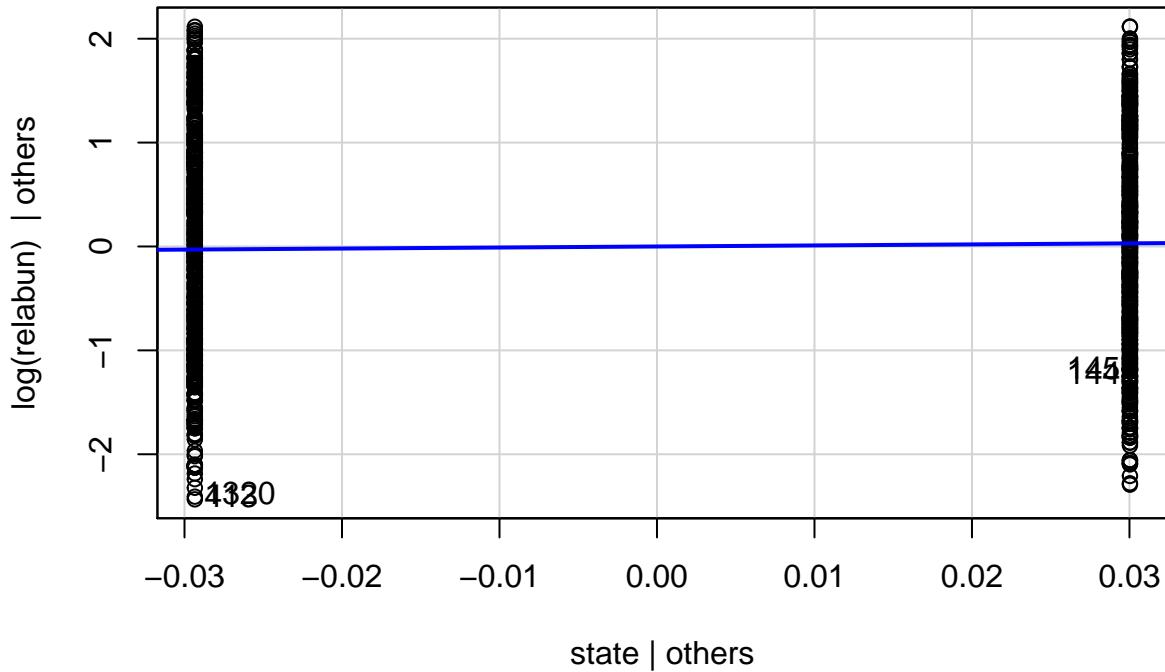
```
##  413 1320
##    73   490
```

```
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)
```

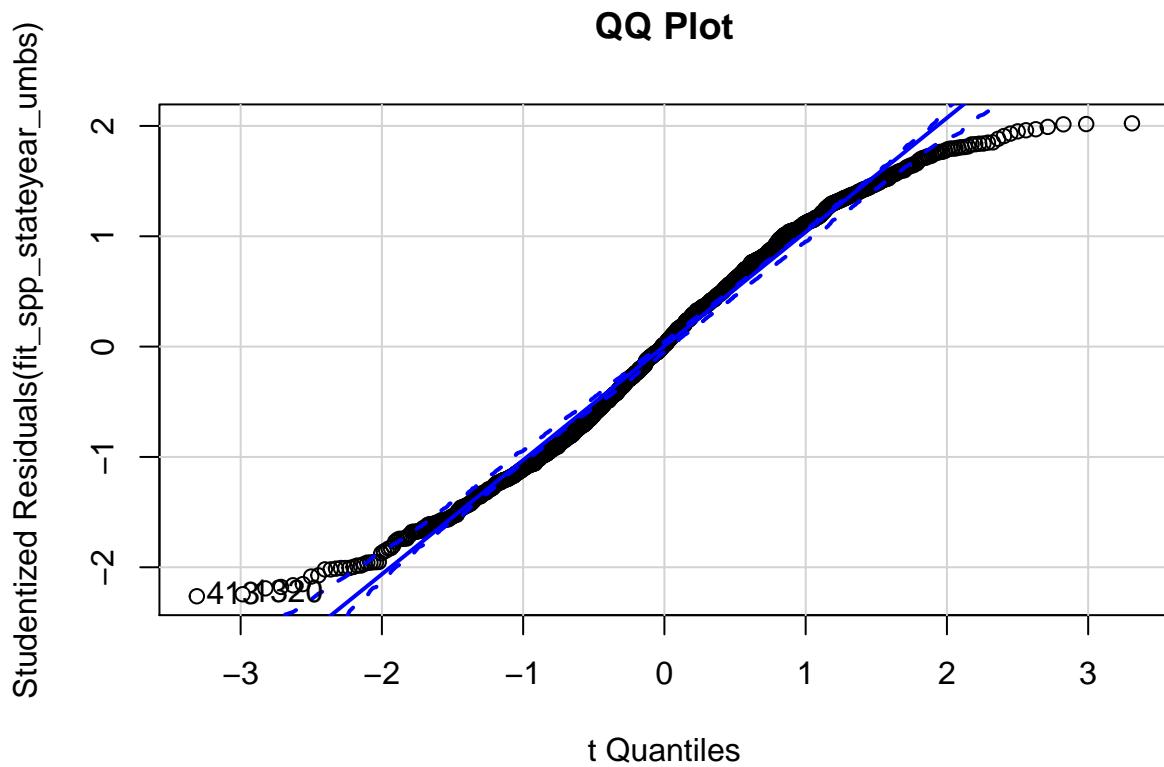
```
## Warning in ks.test(y, "pnorm", mean(y), sd(y)): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
## -----
##          Test           Statistic      pvalue
## -----
## Shapiro-Wilk       0.9803      0.0000
## Kolmogorov-Smirnov 0.0462      0.0241
## Cramer-von Mises   63.4266      0.0000
## Anderson-Darling    5.036       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 -2.262603          0.023867        NA
```

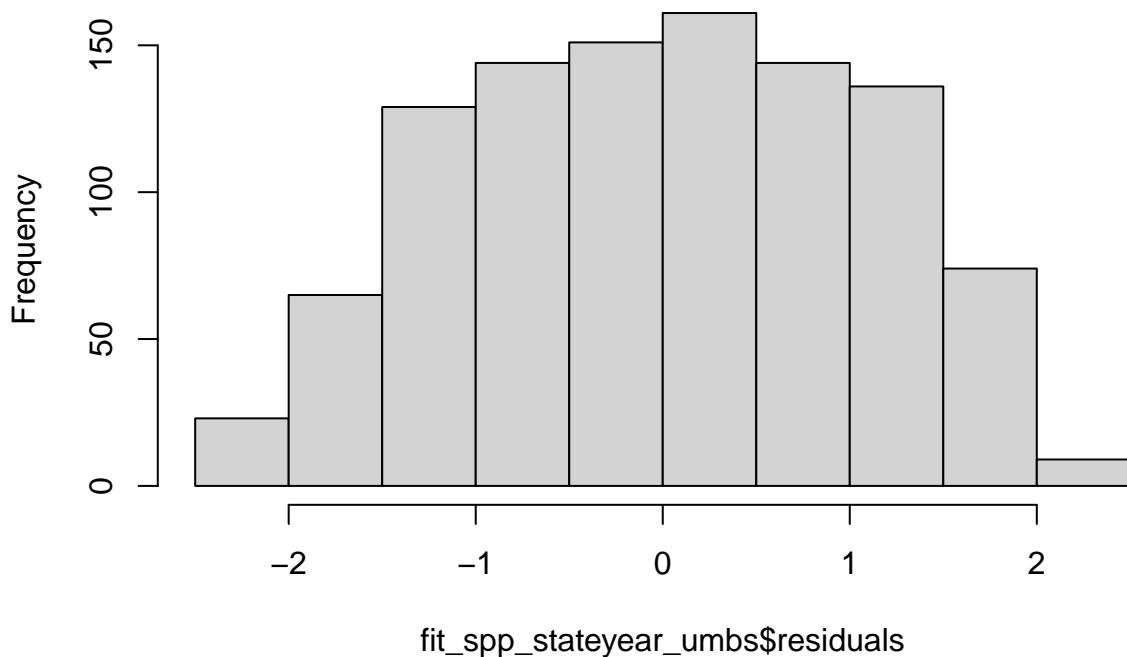
```
qqPlot(fit_spp_stateyear_umbs, main = "QQ Plot")
```



```
##   413 1320
##    73  490
```

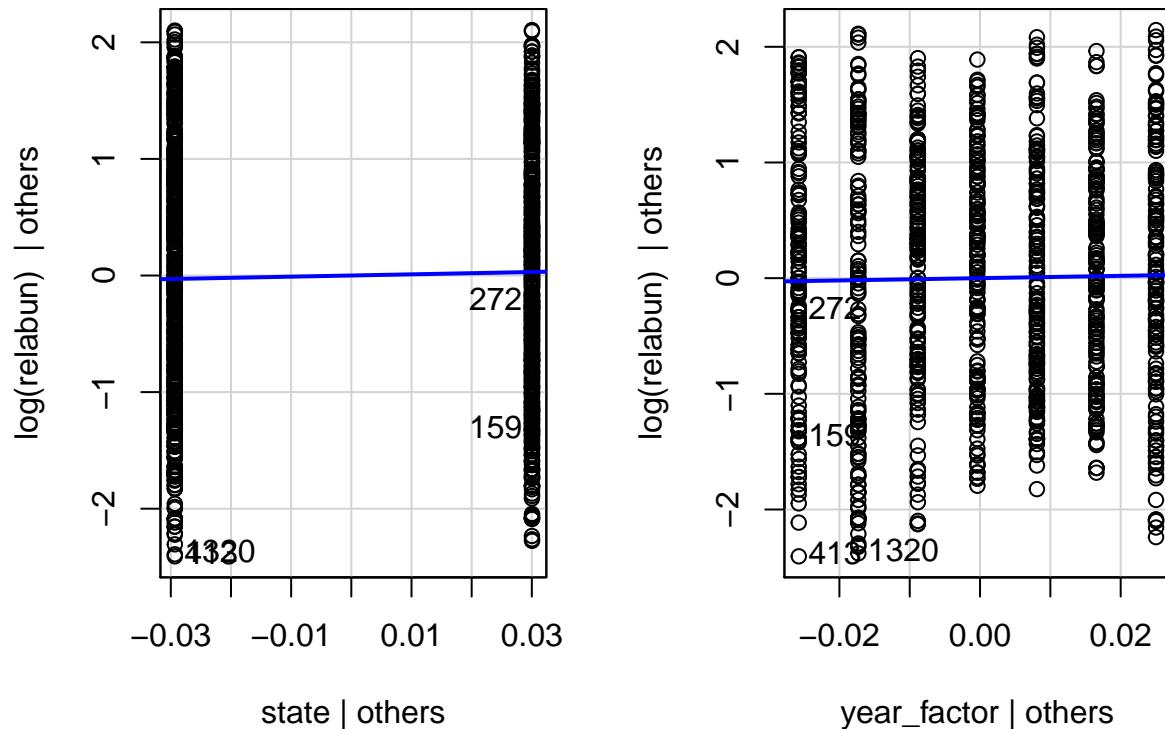
```
hist(fit_spp_stateyear_umbs$residuals)
```

**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
```

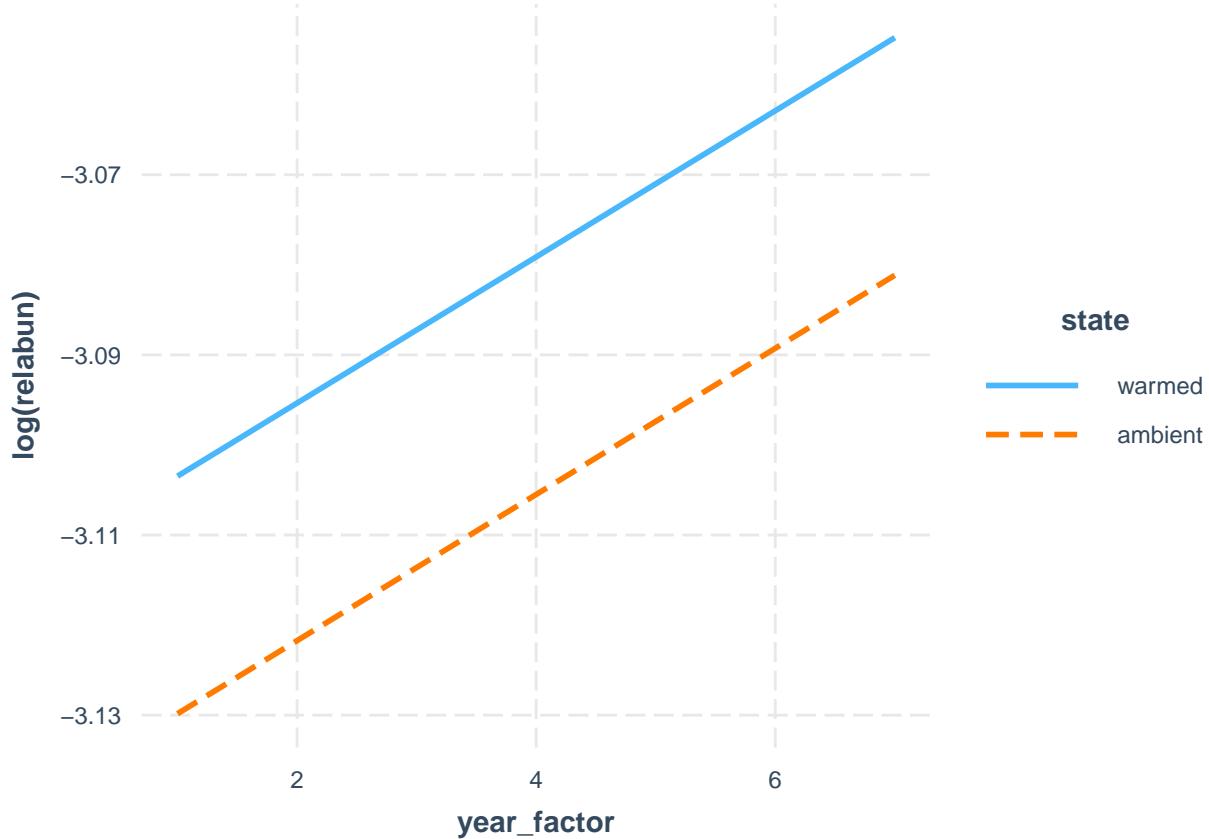
```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk        0.98       0.0000
## Kolmogorov-Smirnov   0.0464     0.0231
## Cramer-von Mises    63.3509     0.0000
## Anderson-Darling     5.0747     0.0000
## -----
```

```
# 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.
```

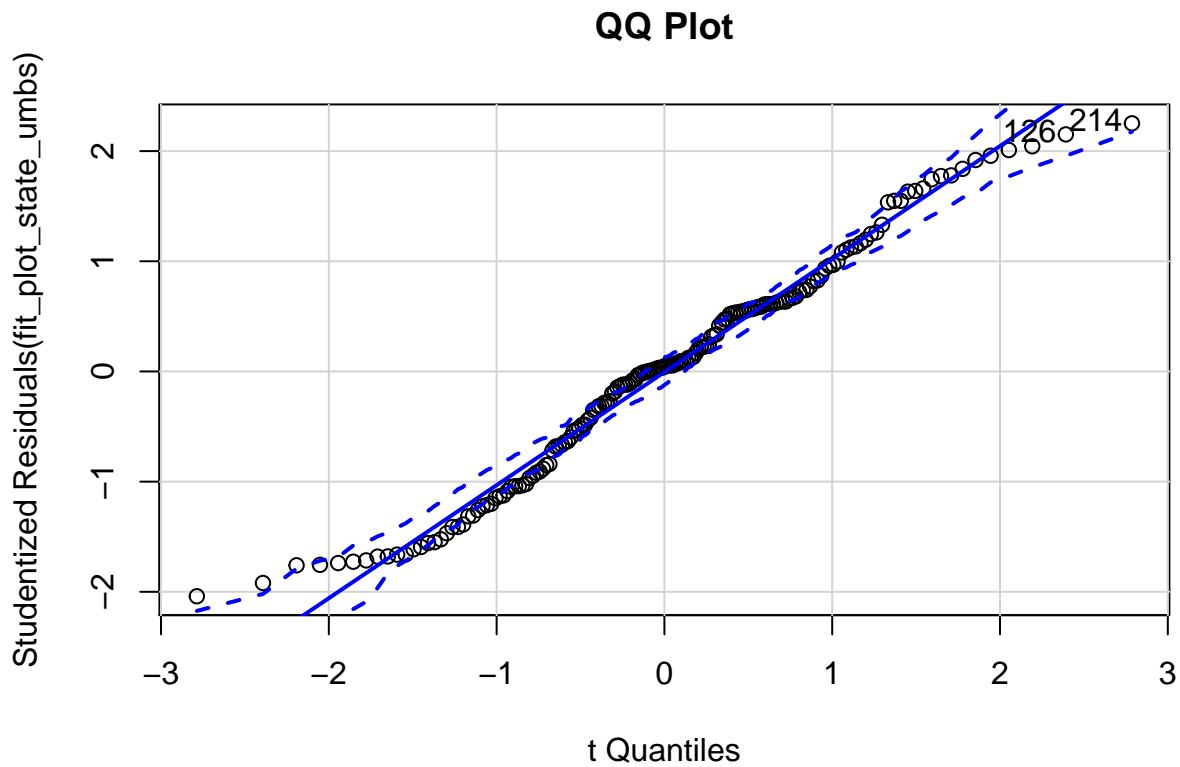
```
## Warning: year_factor and state and species are not included in an interaction with
## one another in the model.
```



```
# 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 2.251762          0.025657        NA
```

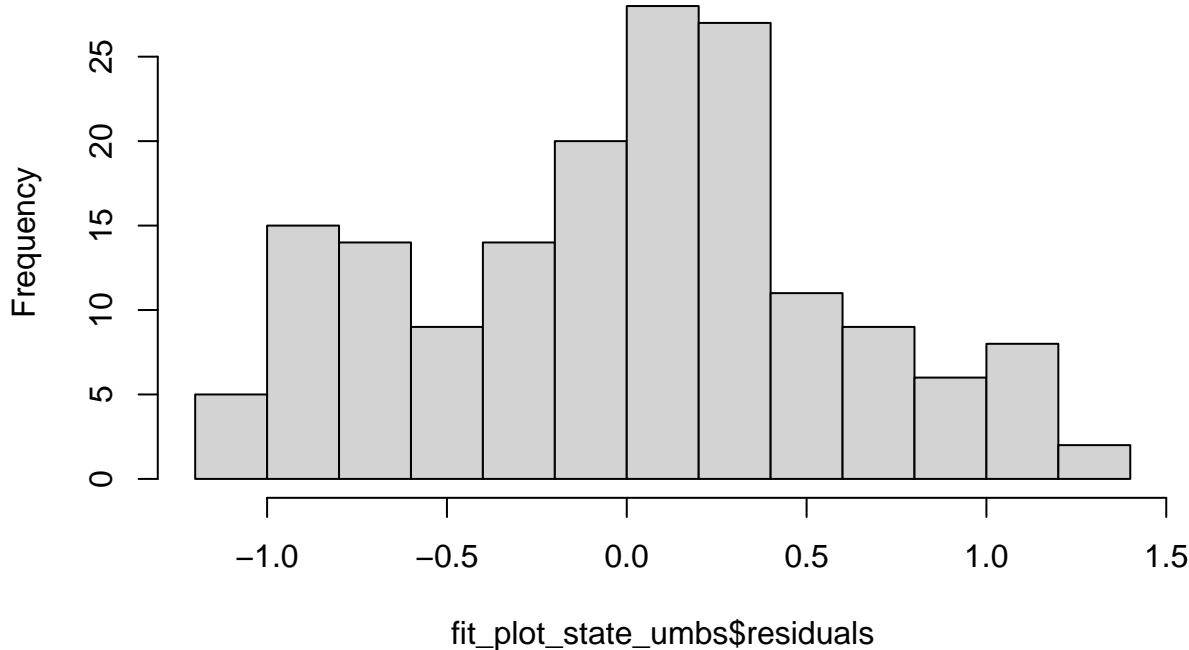
```
qqPlot(fit_plot_state_umbs, main = "QQ Plot")
```



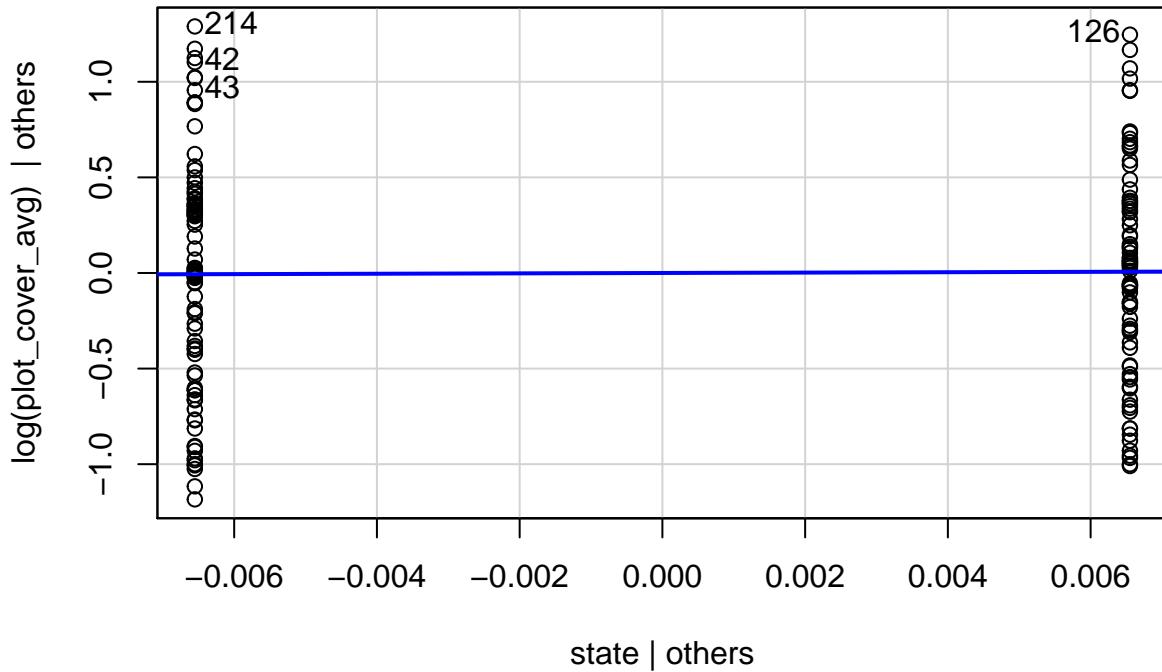
```
## 126 214
## 43 89
```

```
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
```

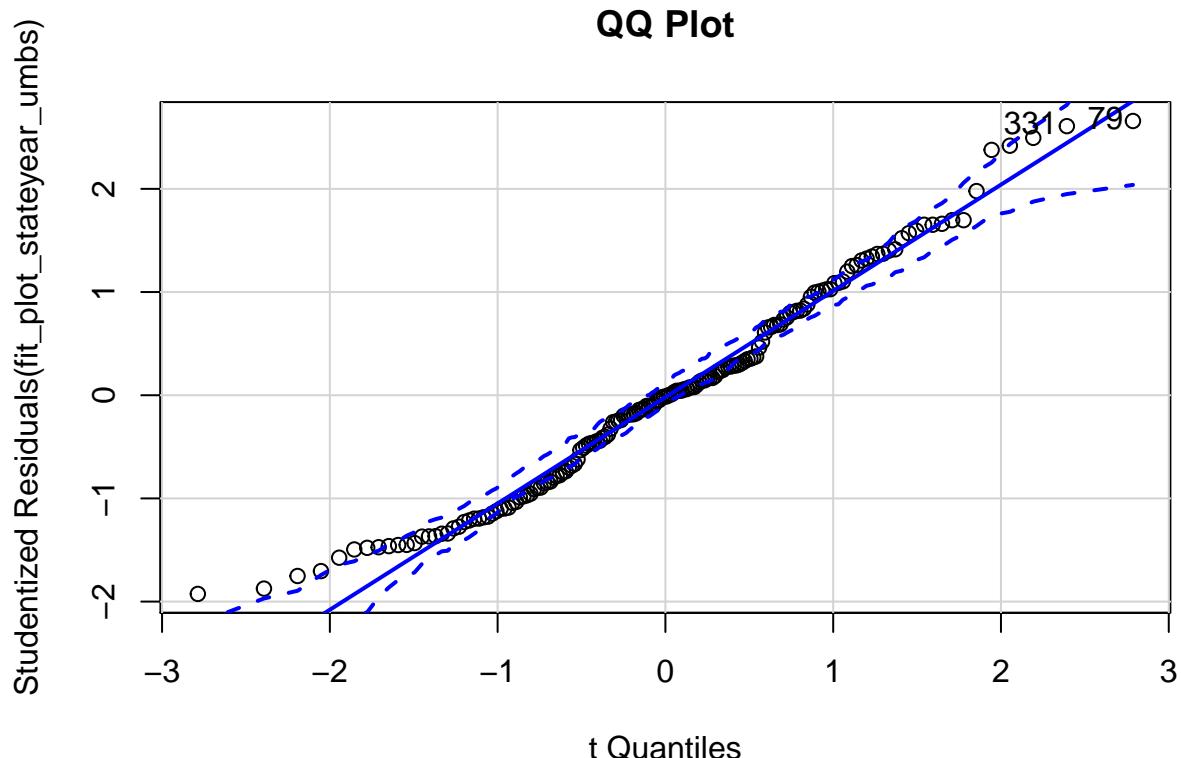
```
## -----
##      Test          Statistic       pvalue
## -----
## Shapiro-Wilk      0.9798     0.0151
## Kolmogorov-Smirnov 0.0551     0.6870
## Cramer-von Mises 16.8246    0.0000
## Anderson-Darling  0.7984     0.0379
## -----
```

```
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
## 79  2.657677           0.0086466        NA
```

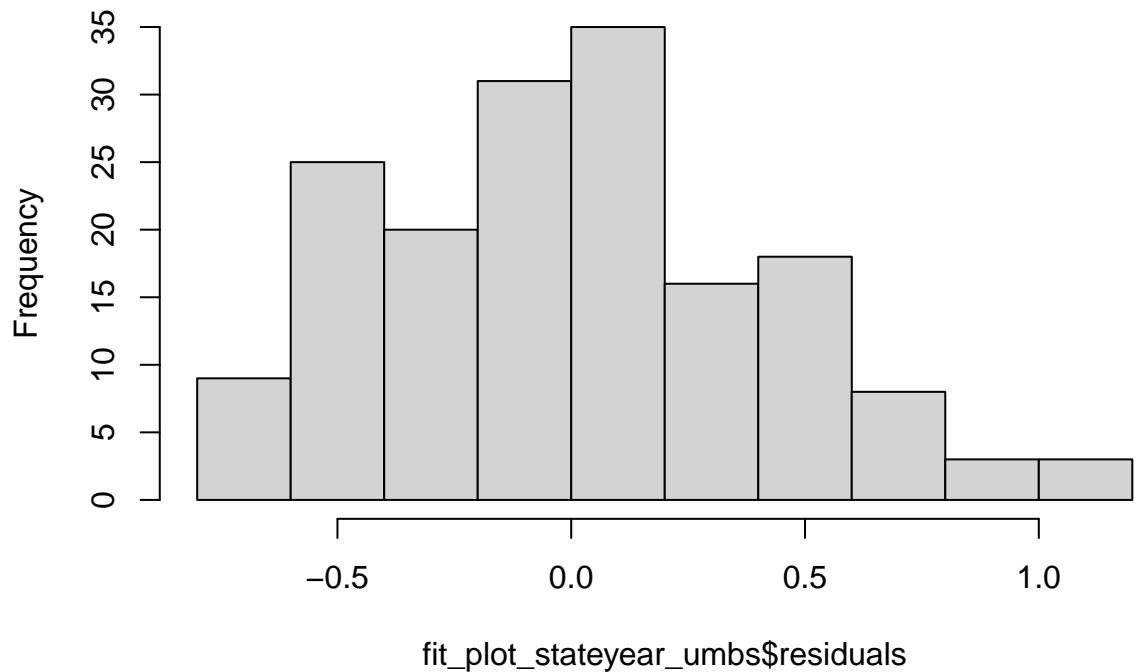
```
comp_umbs_plot_no_outliers <- comp_umbs_plot[-190, ] # remove outliers
qqPlot(fit_plot_stateyear_umbs, main = "QQ Plot")
```



```
## 79 331
## 38 164
```

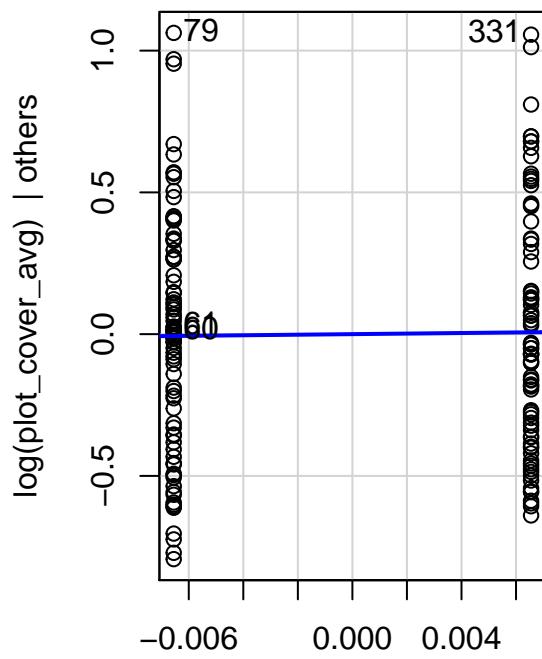
```
hist(fit_plot_stateyear_umbs$residuals)
```

### Histogram of fit\_plot\_stateyear\_umbs\$residuals

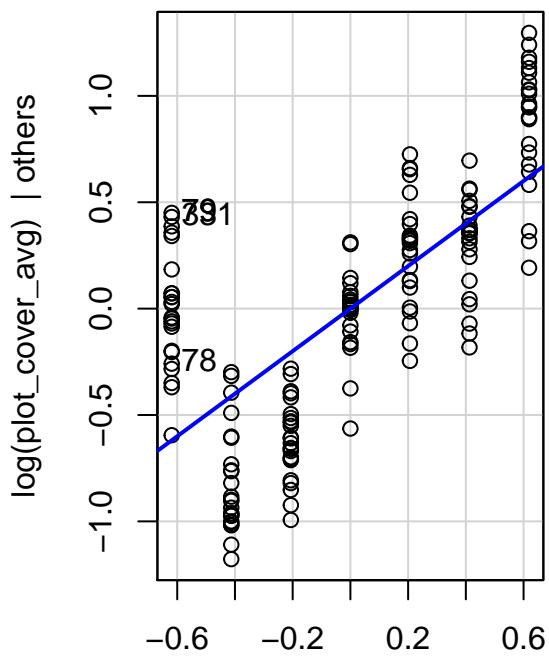


```
leveragePlots(fit_plot_stateyear_umbs)
```

### Leverage Plots



state | others



year\_factor | others

```

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

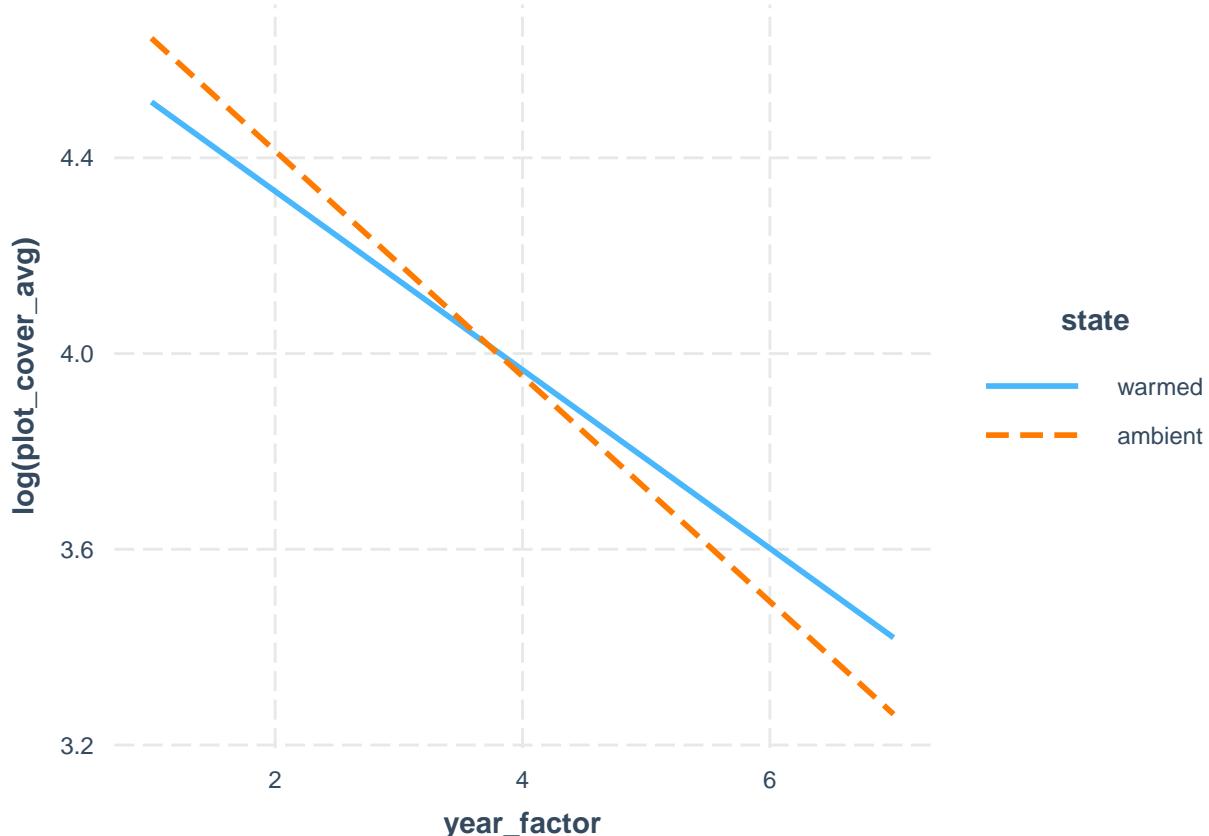
## -----
##          Test      Statistic     pvalue
## -----
## Shapiro-Wilk      0.9785    0.0105
## Kolmogorov-Smirnov   0.0622    0.5350
## Cramer-von Mises    23.6235   0.0000
## Anderson-Darling     0.809    0.0357
## -----


# 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.

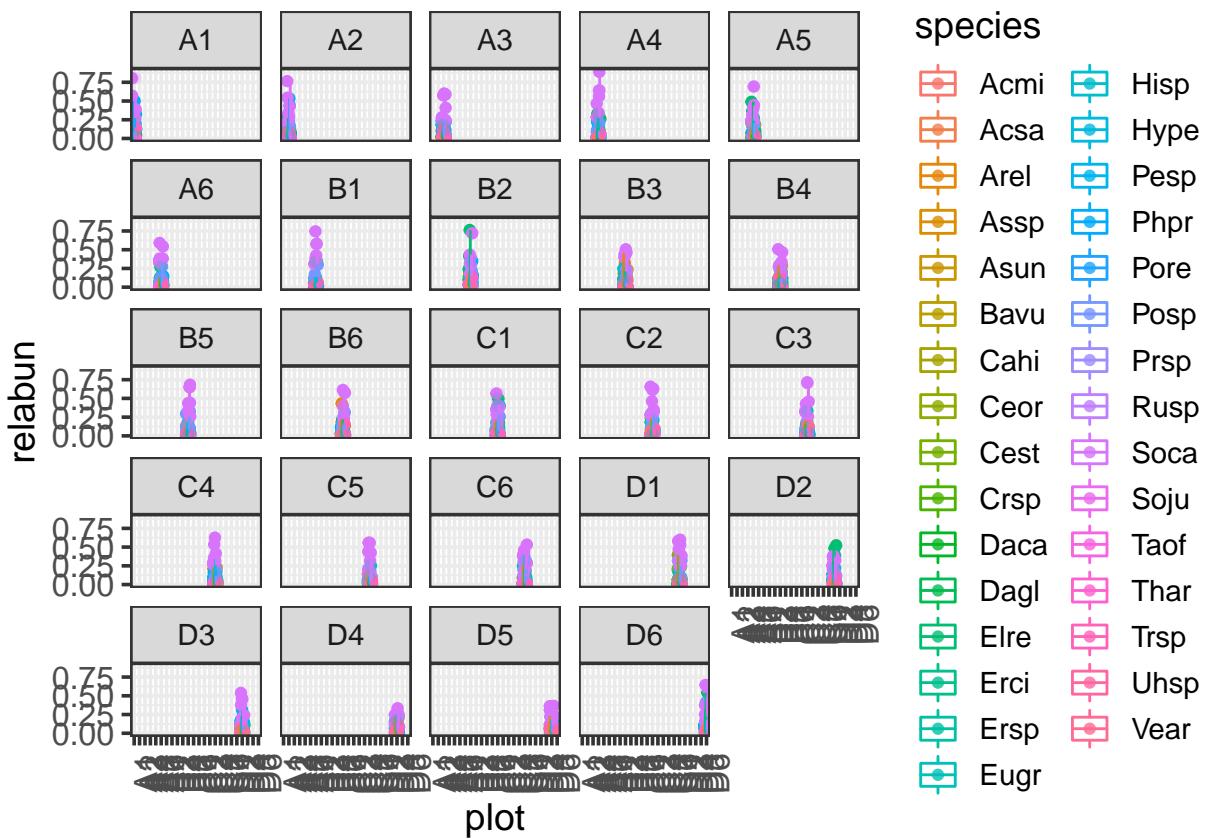
```



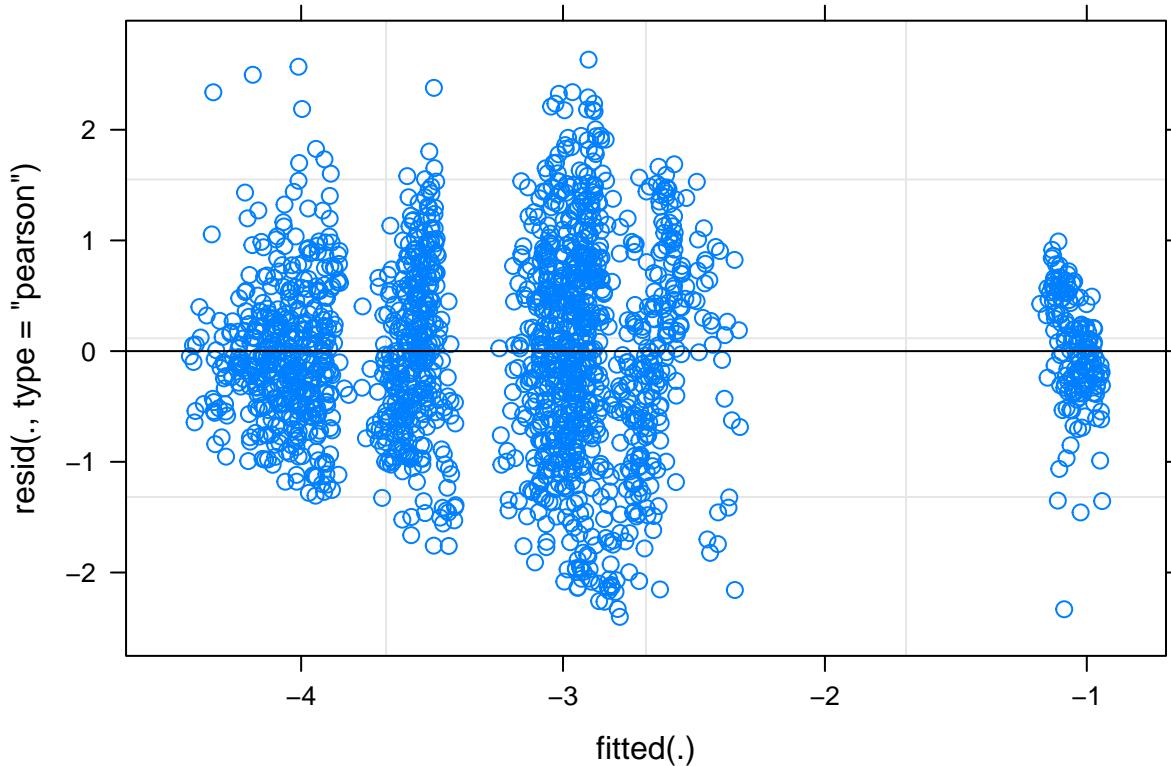
## MIXED EFFECT MODELS

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

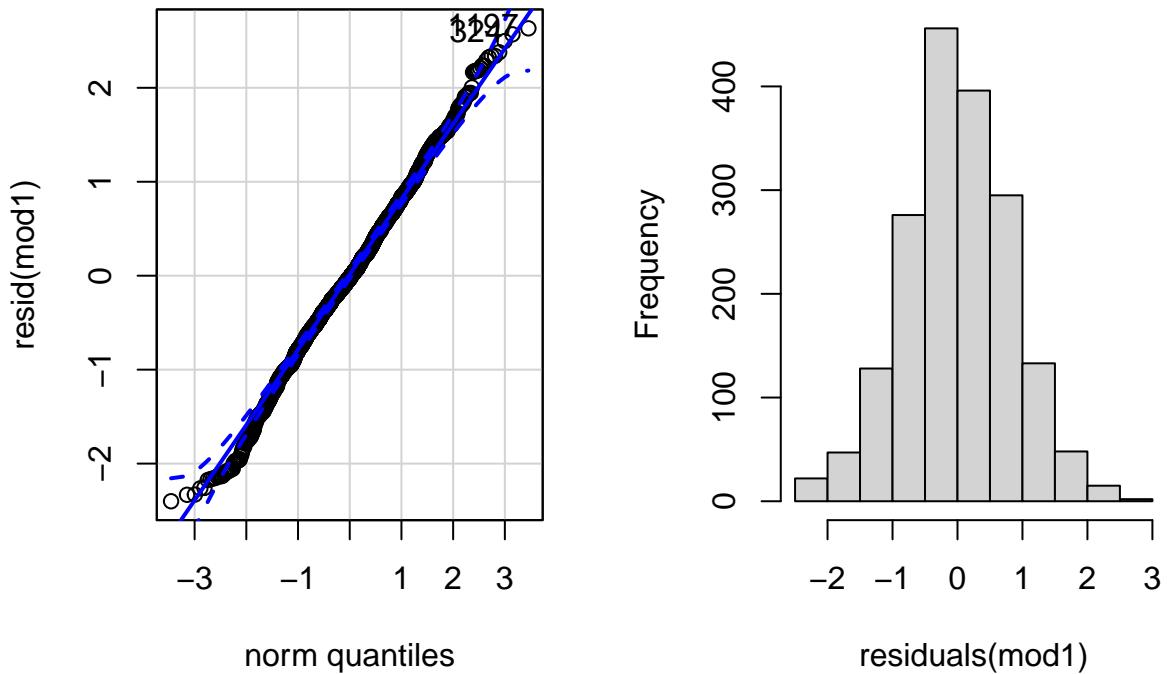
# (3) Normality of error term: need to check by histogram, QQplot of residuals,
# could do Kolmogorov-Smirnov test. Check for normal residuals
qqPlot(resid(mod1))

## 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
```

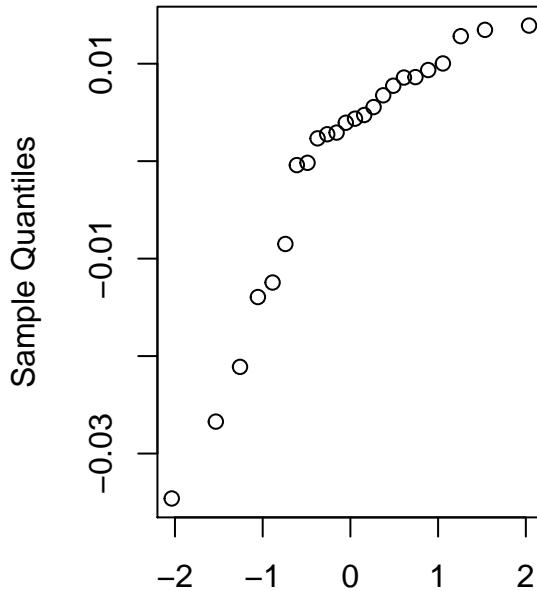
# (4) Normality of random effect: Get the estimate of random effect (e.g., random intercepts), and check them as you would check the residual.

```
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 <sup>2</sup> (fixed effects)	0.00
Pseudo-R <sup>2</sup> (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 <sup>2</sup> (fixed effects)	0.00
Pseudo-R <sup>2</sup> (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.

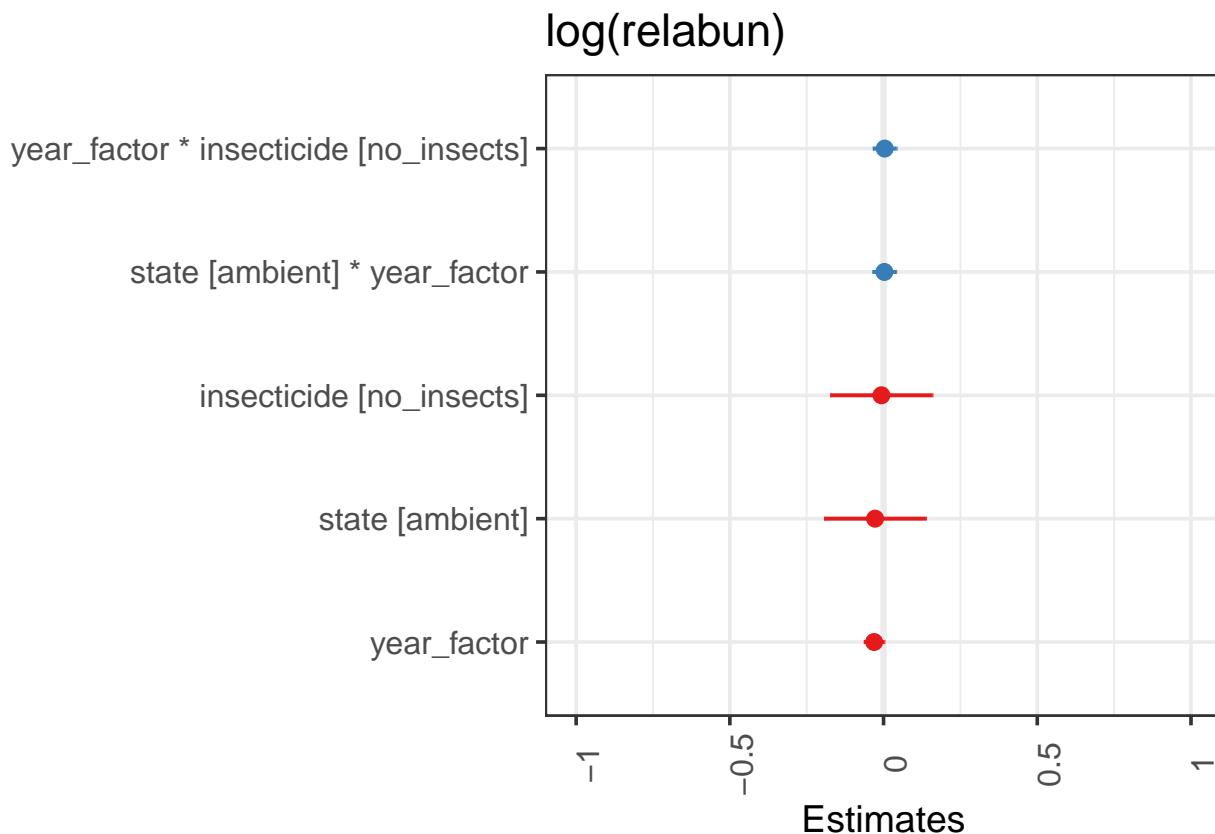
Random Effects		
Group	Parameter	Std. Dev.
species	(Intercept)	0.79
	Residual	0.84

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
```

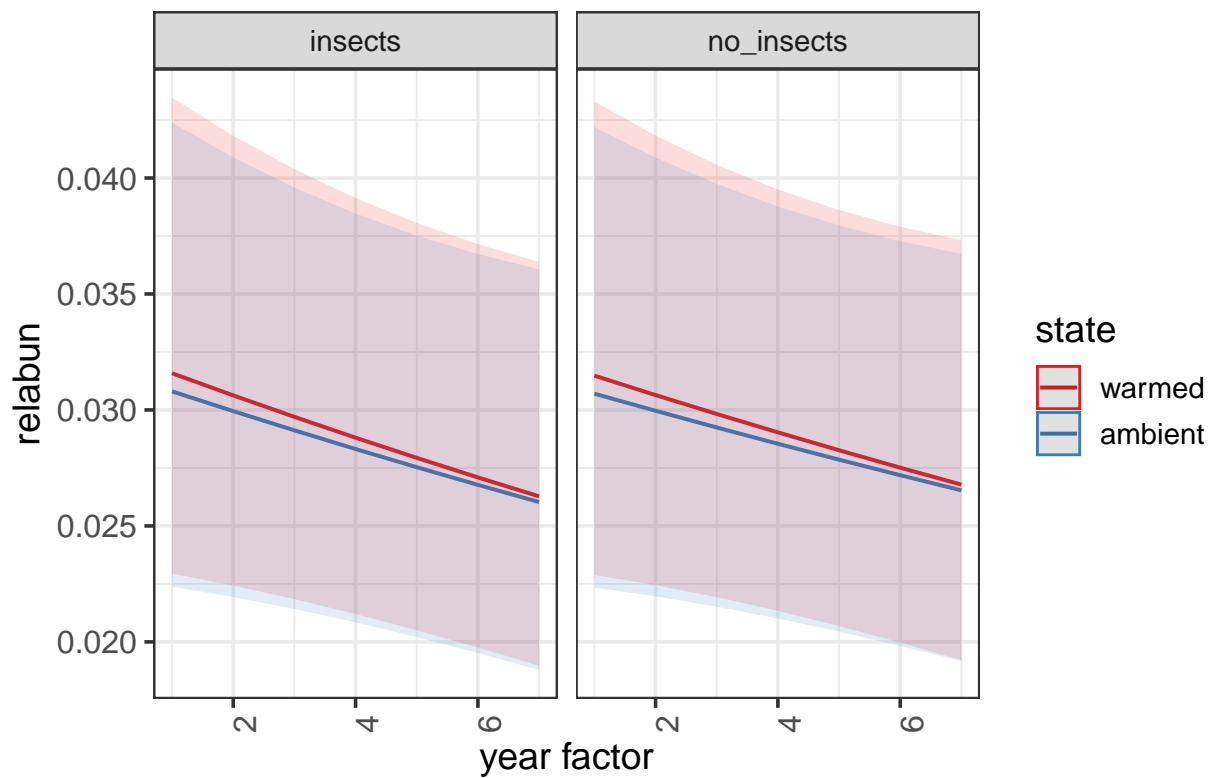
```
# Plot the fixed effects estimates for different models these are the fixed  
# effects estimates from summary(mod1)  
plot_model(mod2, sort.est = TRUE)
```



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

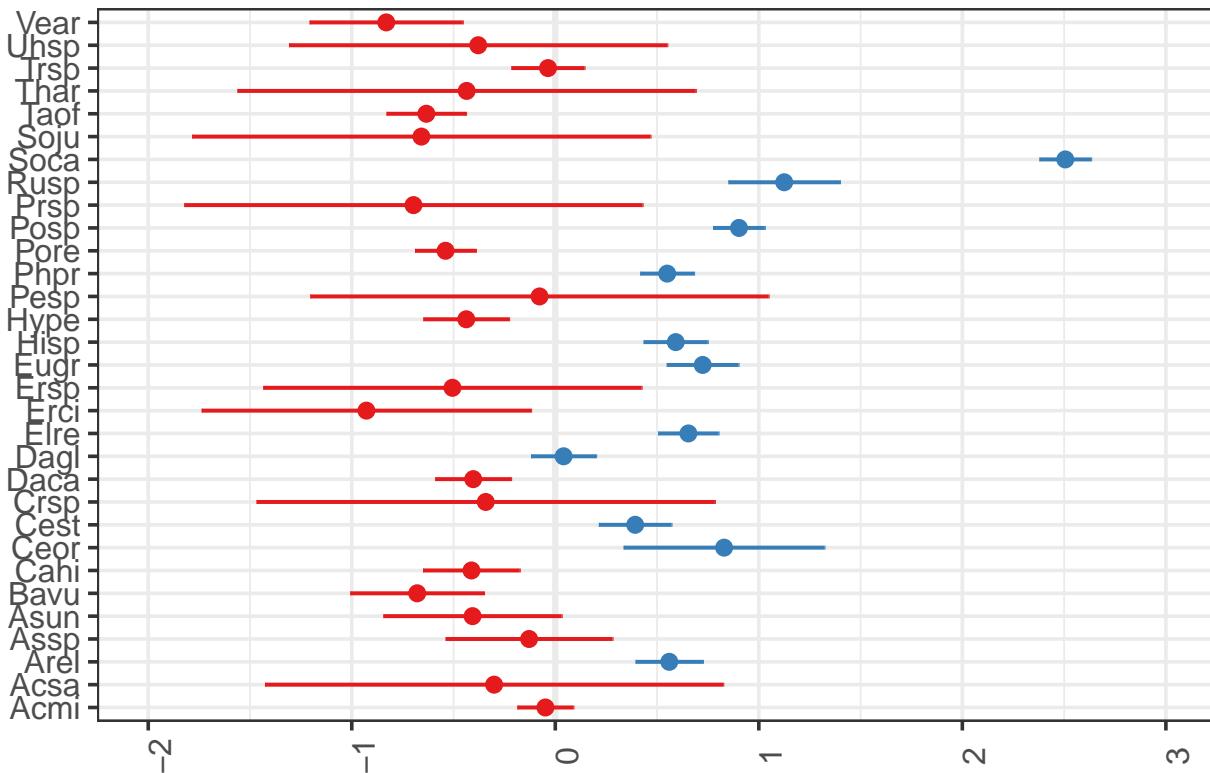
## Model has log-transformed response. Back-transforming predictions to original response scale. Standard

## 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)

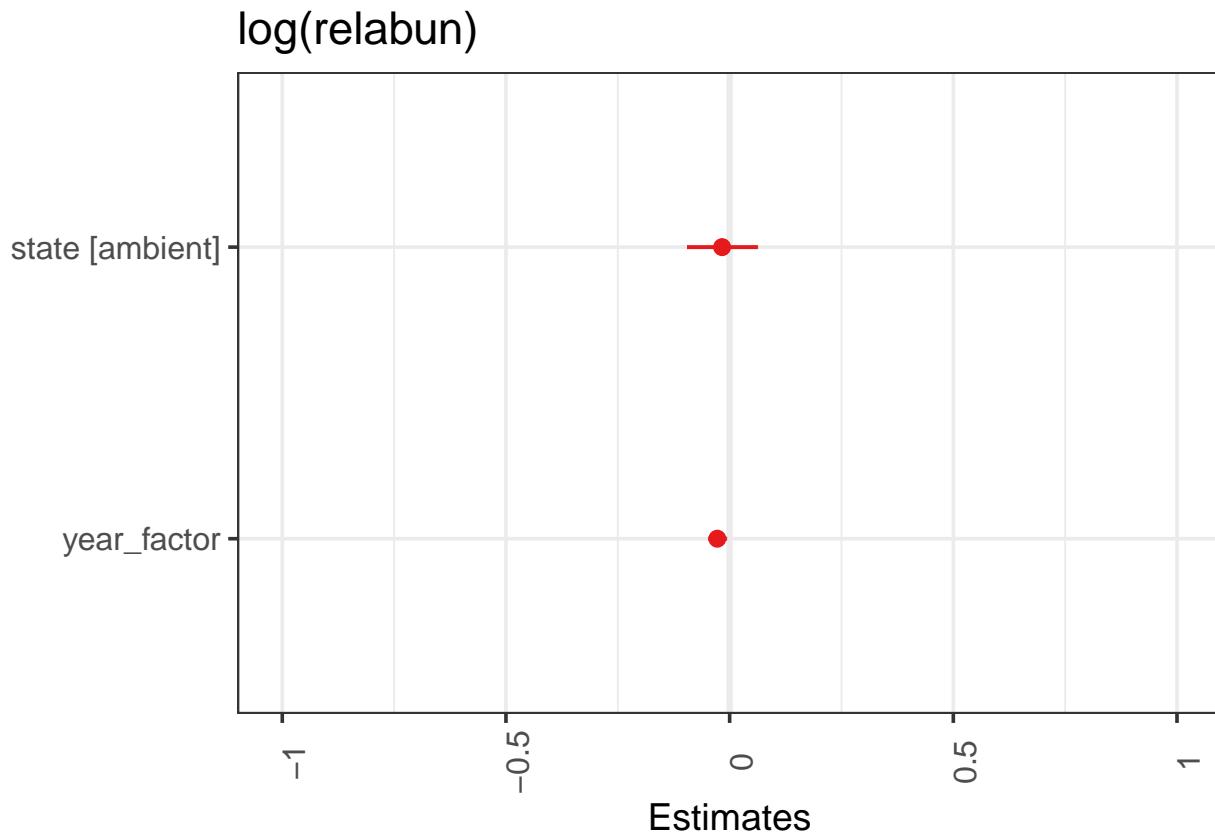
# Does year need to be interactive with state?
mod5 <- lmer(log(relabun) ~ state + year_factor + (1 | species), comp_kbs_spp, REML = FALSE)
anova(mod3, mod5)

## 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!!

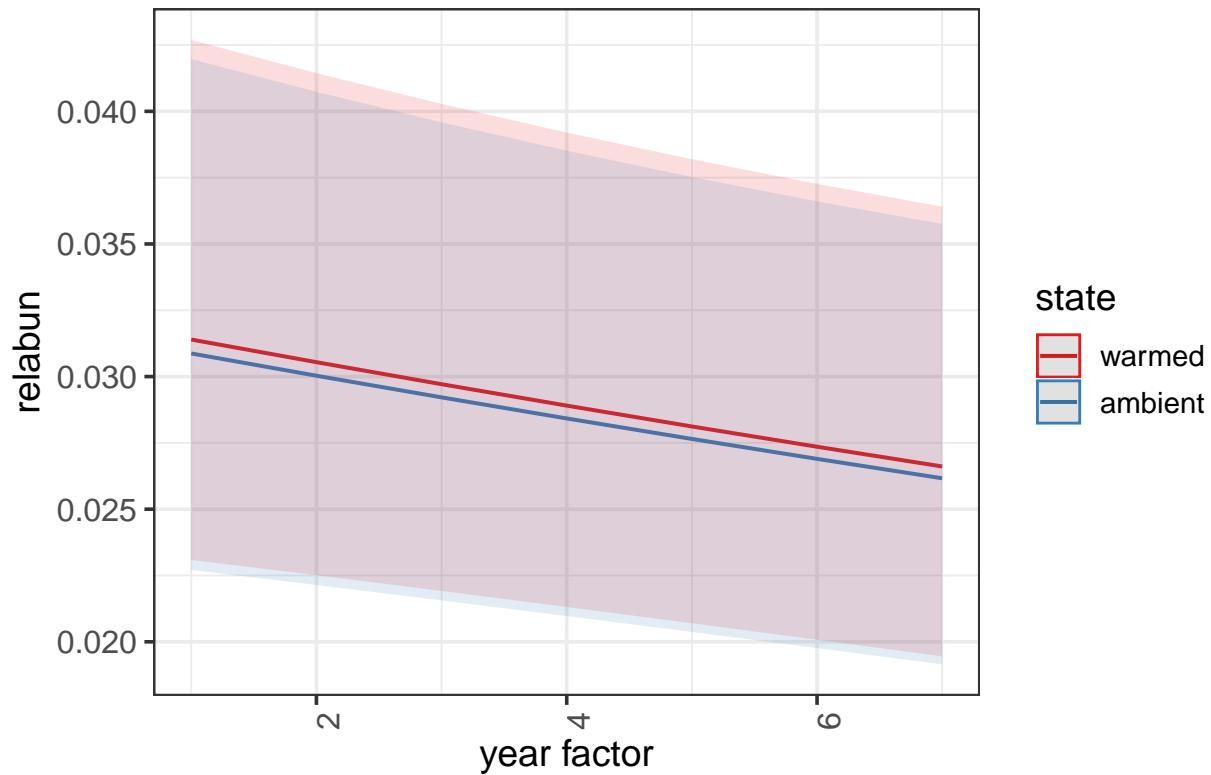
# Plot the fixed effects estimates for different models these are the fixed
# effects estimates from summary(mod5)
plot_model(mod5, sort.est = TRUE)

```



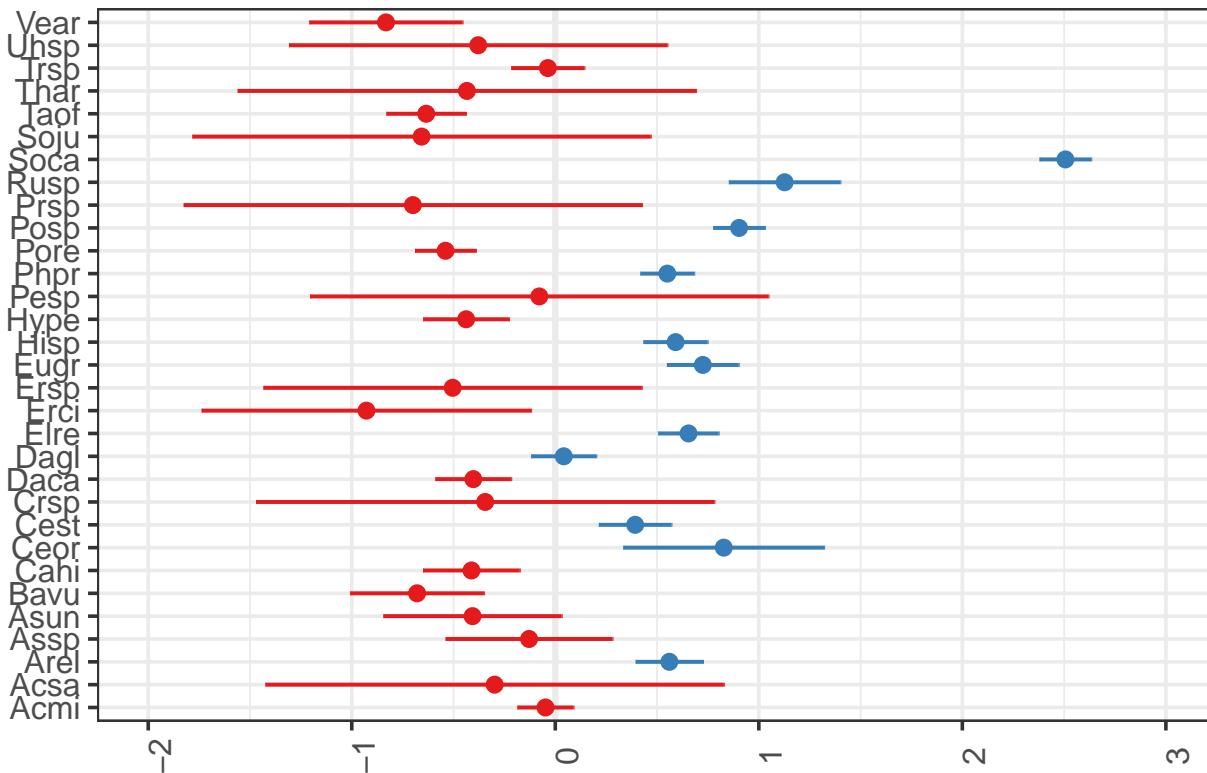
## Model has log-transformed response. Back-transforming predictions to original response scale. Standardized residuals.

## 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'
##   estimate     SE    df t.ratio p.value
## 1      0.02174 0.0446  28.6  0.488  1.0000
##  warmed 1 - ambient 1  0.25653 0.0679 1835.7 3.779  0.0119
##  warmed 1 - warmed 2  0.27827 0.0807  331.9  3.447  0.0405
##  warmed 1 - ambient 2  0.19739 0.0751 1843.3 -2.630  0.3220
##  warmed 1 - warmed 3  -0.17565 0.0864  412.7 -2.033  0.7462
##  warmed 1 - ambient 3  0.10036 0.0720 1844.1  1.393  0.9828
##  warmed 1 - warmed 4  0.12210 0.0840  378.5  1.453  0.9747
##  warmed 1 - ambient 4  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

```

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##  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 - Cahi -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
##  Cahi - Ceor -1.399049 0.2916 1826 -4.797 0.0007
##  Cahi - Cest -0.803496 0.1525 1853 -5.270 0.0001
##  Cahi - Crsp  0.374437 0.8424 1853  0.444 1.0000
##  Cahi - Daca  0.007454 0.1548 1847  0.048 1.0000
##  Cahi - Dagl -0.436224 0.1475 1856 -2.958 0.4323
##  Cahi - Elre -1.041157 0.1443 1853 -7.216 <.0001
##  Cahi - Erci  0.905654 0.4985 1853  1.817 0.9956
##  Cahi - Ersp  0.396406 0.6030 1854  0.657 1.0000
##  Cahi - Eogr -1.148571 0.1522 1854 -7.546 <.0001
##  Cahi - Hisp -1.041925 0.1466 1852 -7.106 <.0001
##  Cahi - Hype  0.056902 0.1631 1854  0.349 1.0000
##  Cahi - Pesp -0.207042 0.8427 1857 -0.246 1.0000
##  Cahi - Phpr -0.946720 0.1397 1852 -6.779 <.0001

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## 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

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## 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")
```

```

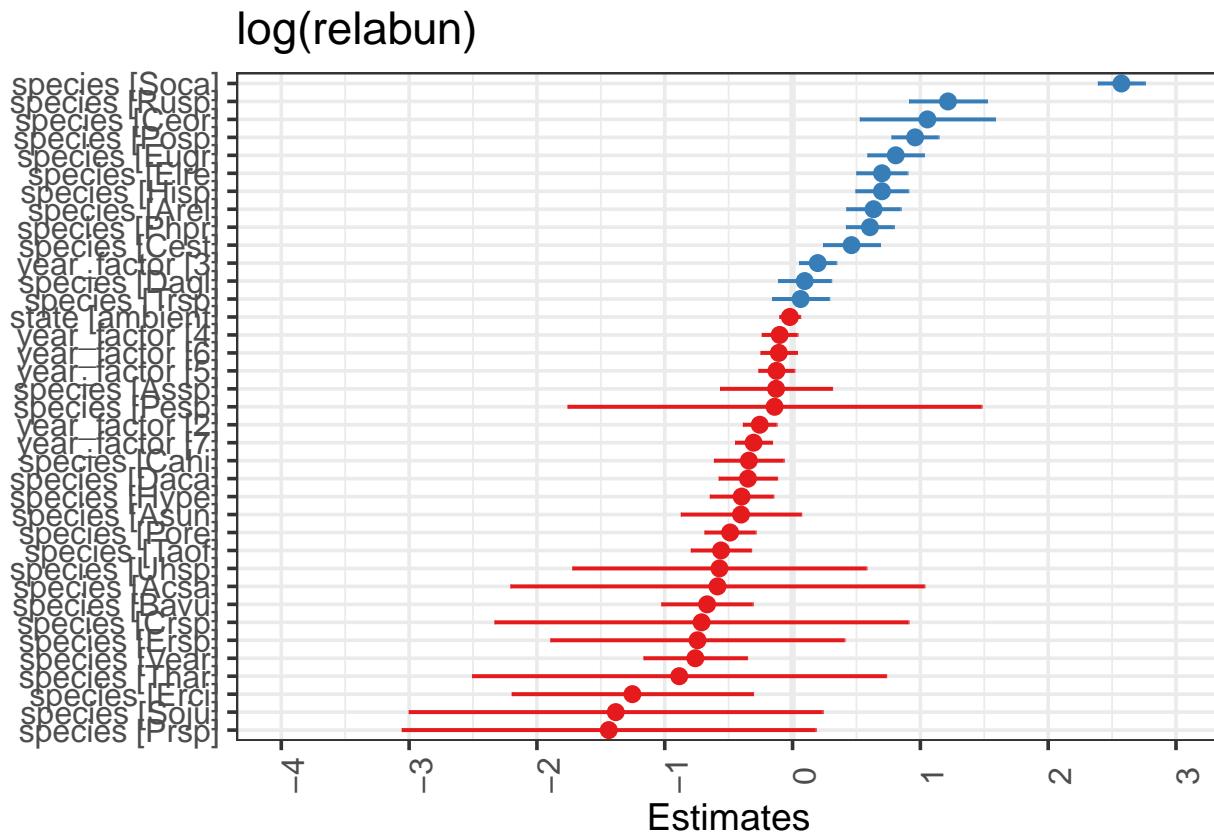
## $`emmeans of insecticide`
##  insecticide emmean    SE  df lower.CL upper.CL
##  insects      -3.67 0.0801 870    -3.83    -3.51
##  no_insects   -3.66 0.0808 852    -3.82    -3.50
##
## Results are averaged over the levels of: state, species, year_factor
## Degrees-of-freedom method: kenward-roger
## 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)

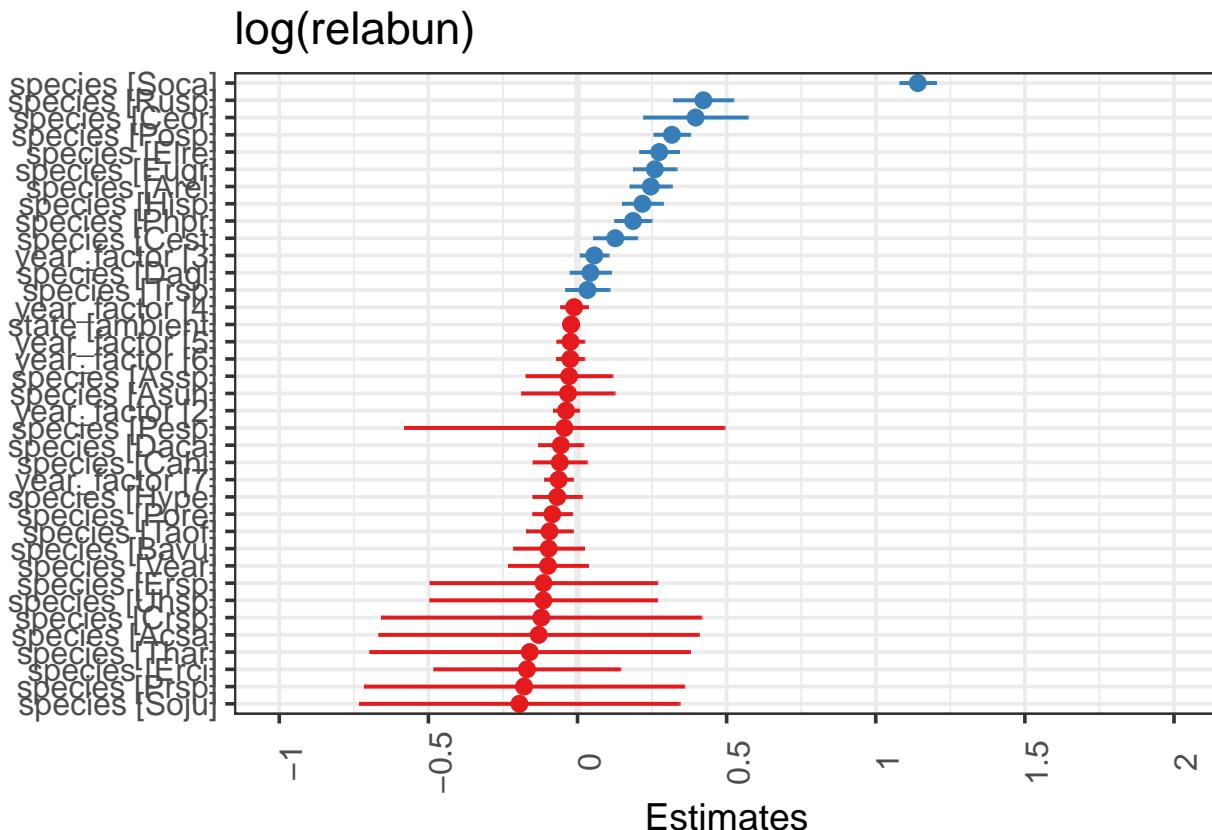
```



```
# 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.

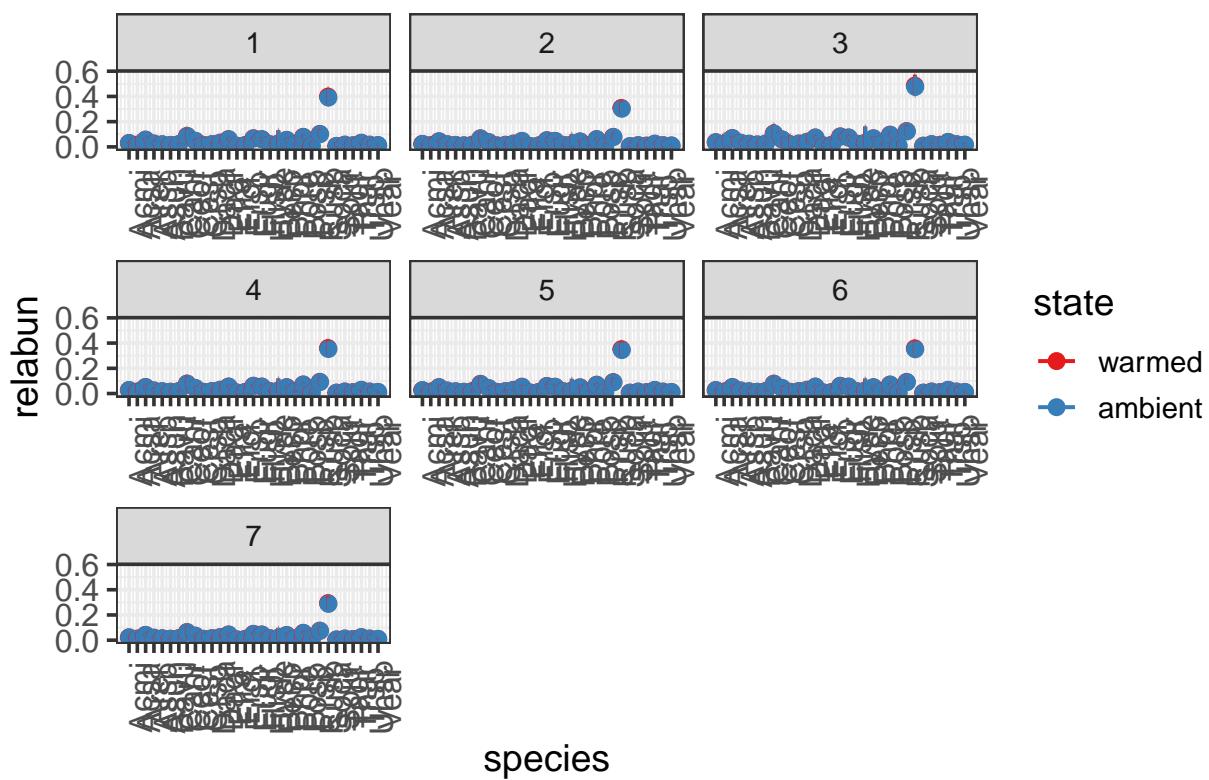
## boundary (singular) fit: see ?isSingular
```



```
# these are the fixed predicted values: - note this is a new plot
plot_model(mod7a, type = "pred", terms = c("species", "state", "year_factor"))
```

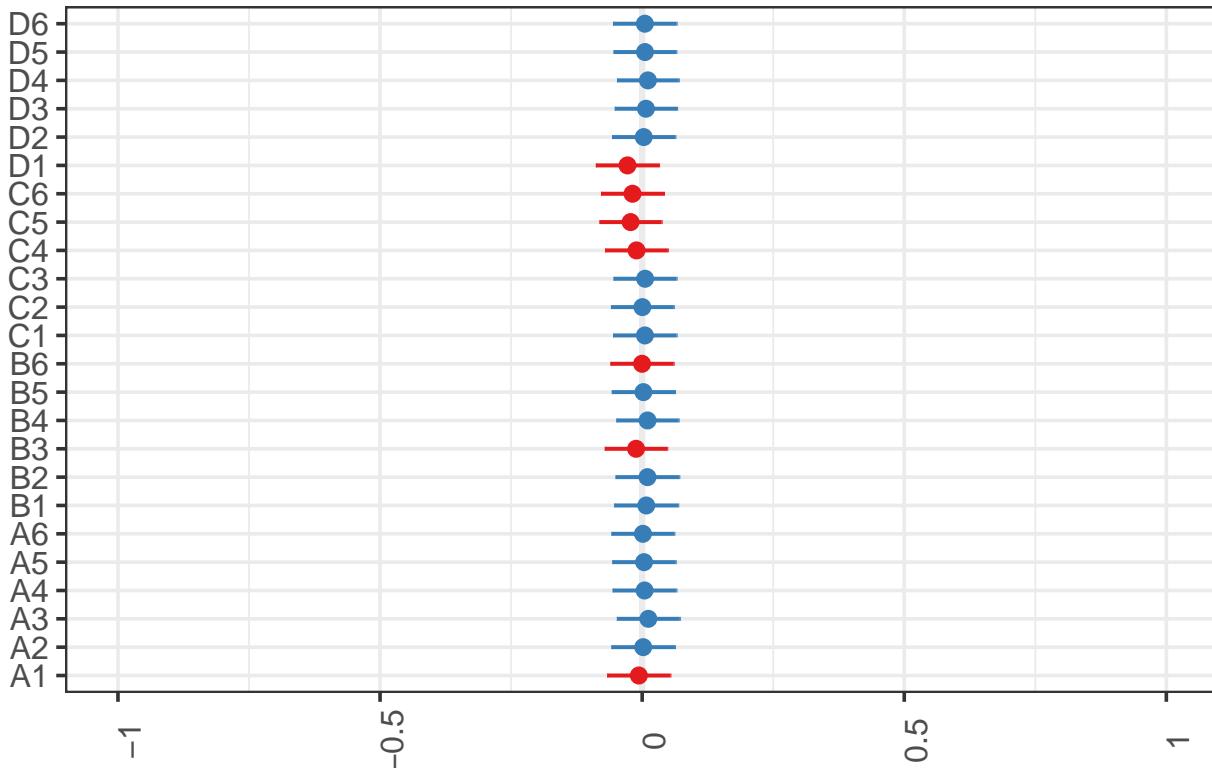
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standardized
```

## 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)
```

```

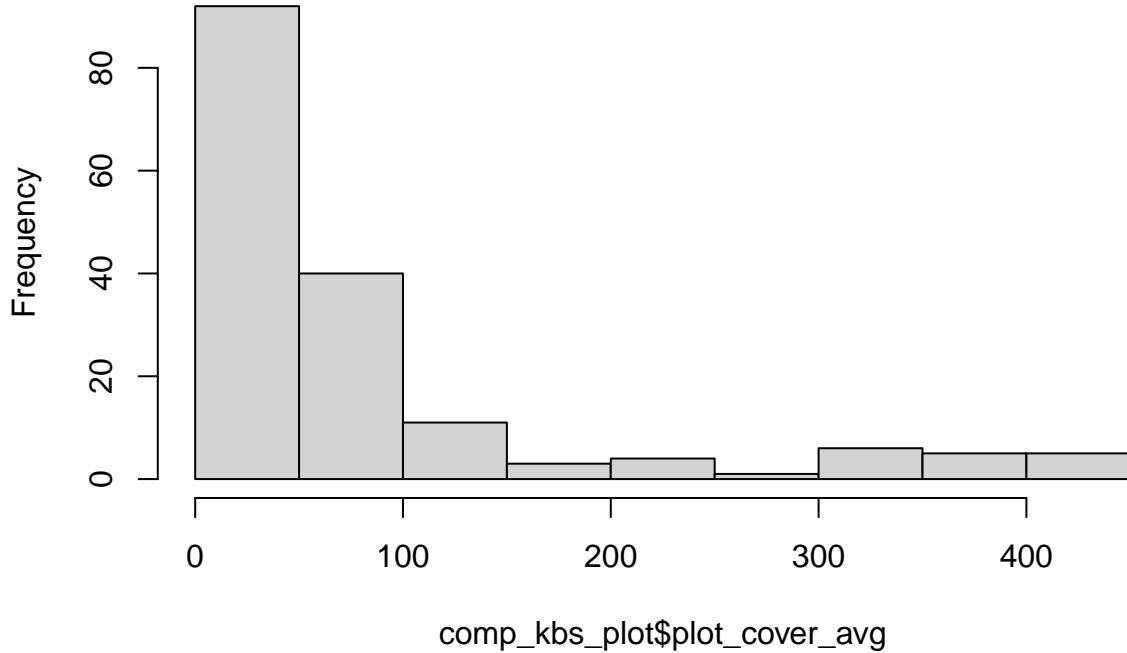
## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## state                      0.18   0.176     1  25.15  0.2611   0.6138
## species                   1287.05  42.902    30 1807.33 63.6078 < 2.2e-16 ***
## 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:

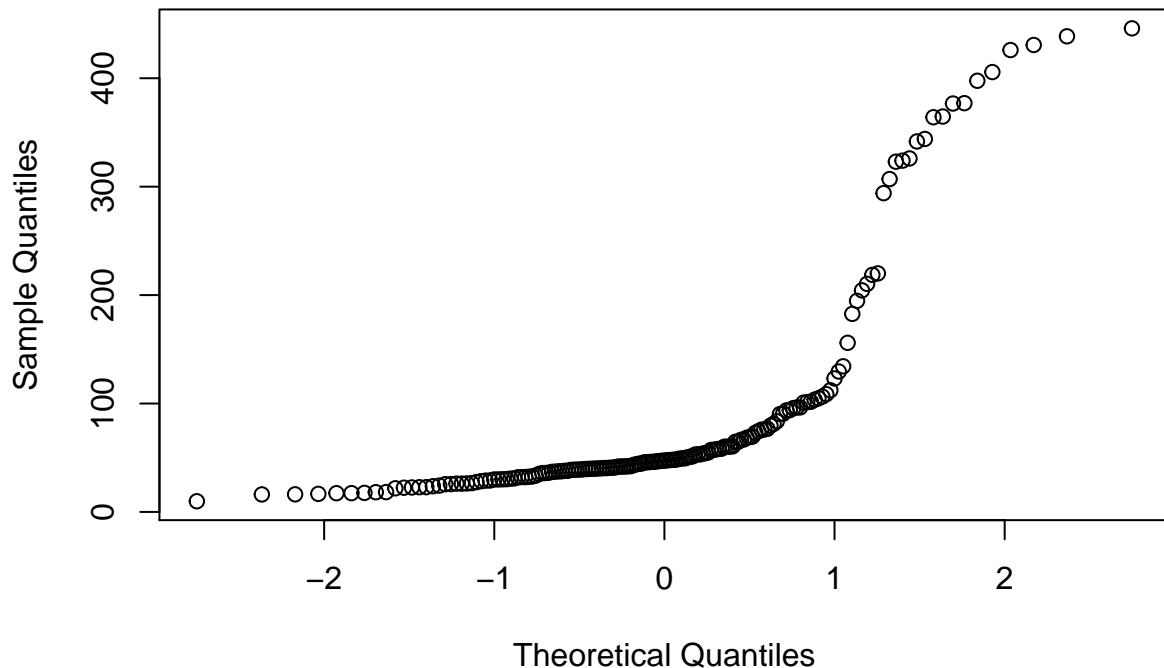
```
hist(comp_kbs_plot$plot_cover_avg) # skewed to the right - positive skew
```

Histogram of comp\_kbs\_plot\$plot\_cover\_avg



```
qqnorm(comp_kbs_plot$plot_cover_avg) # this doesn't look good
```

## Normal Q-Q Plot

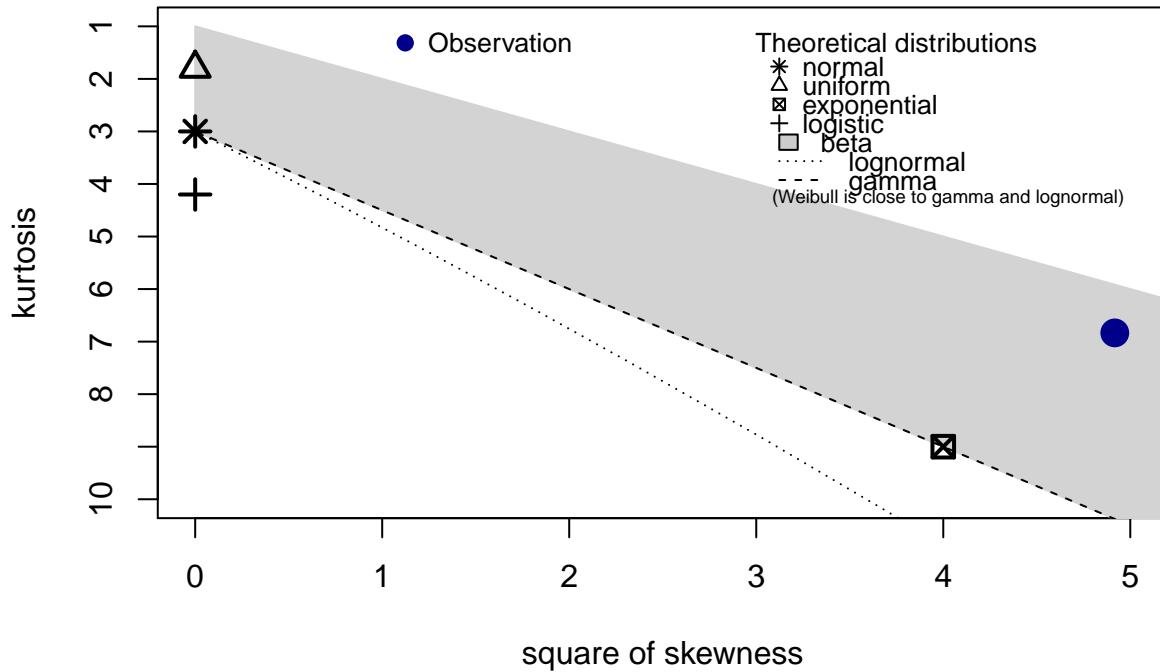


```
shapiro.test(comp_kbs_plot$plot_cover_avg) # not normal

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

# 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

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 <sup>2</sup> (fixed effects)	0.43
Pseudo-R <sup>2</sup> (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

```
emmeans(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'
##  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.

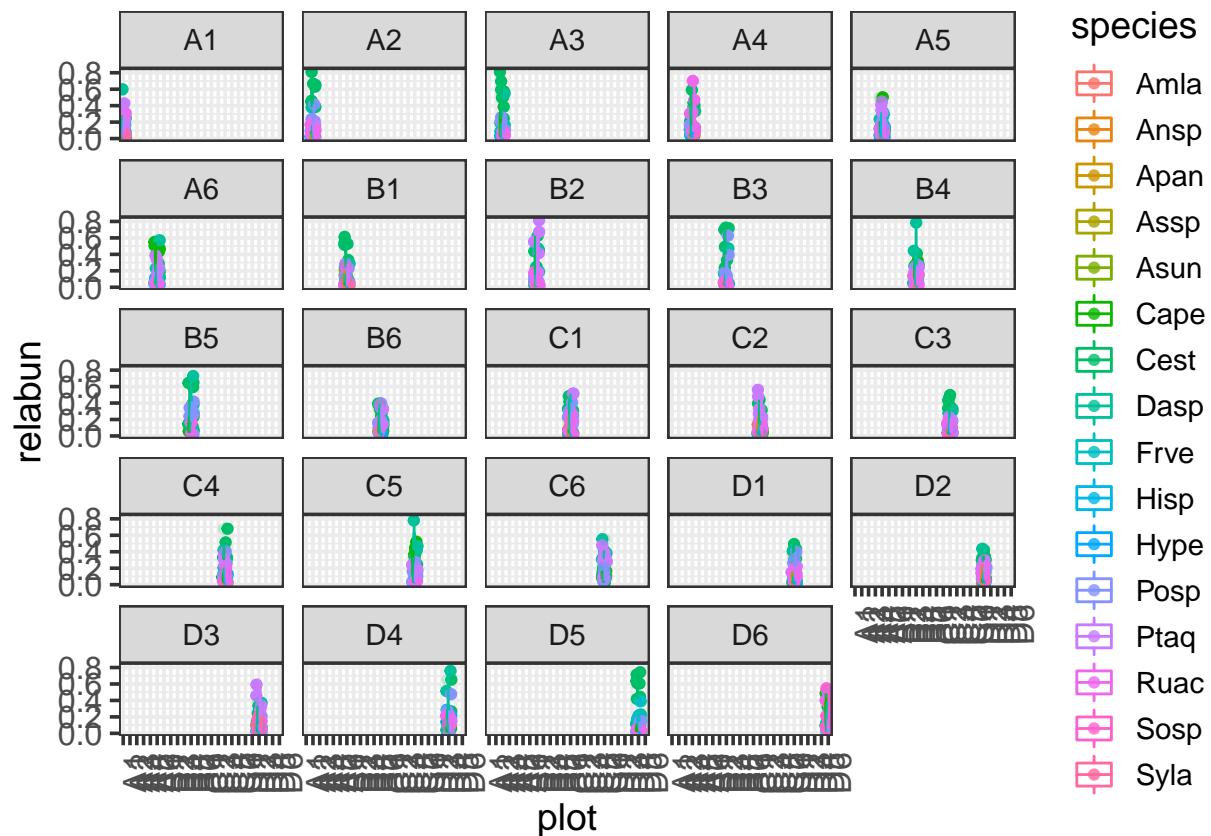
```

UMBS species level mixed effects models

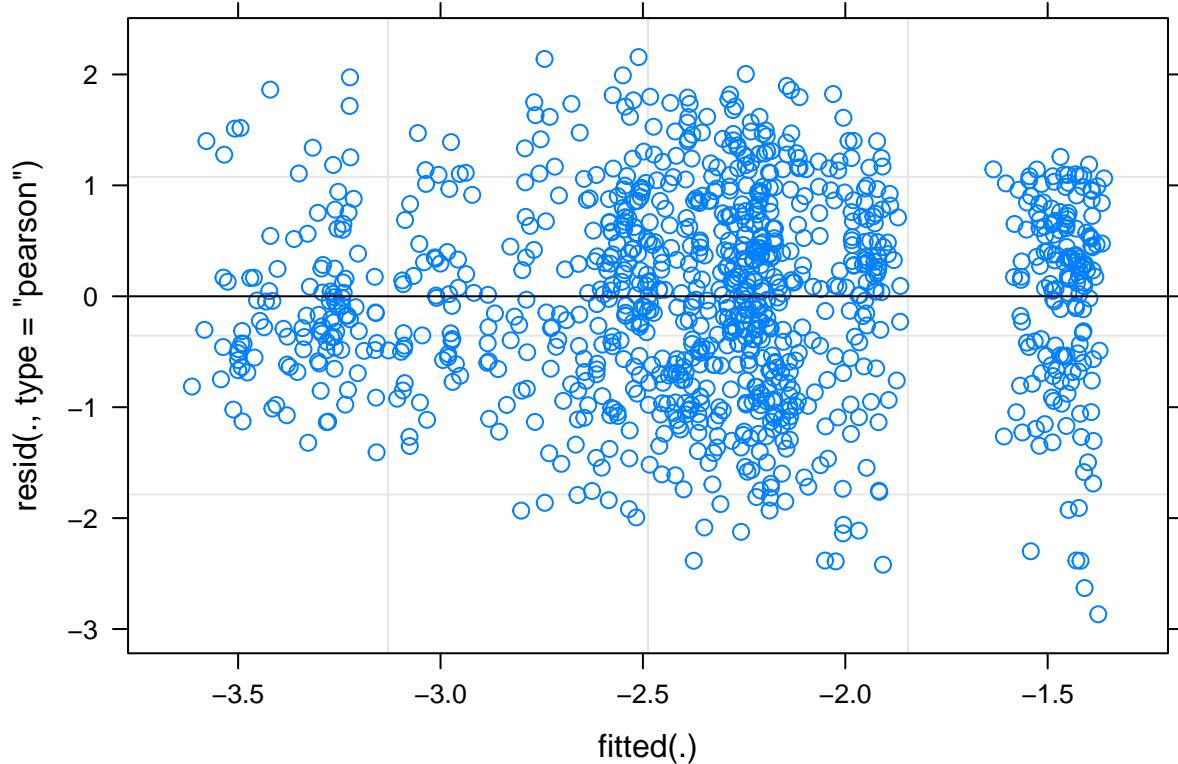
```

# 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)
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(mod1u) ~ comp_umbs_spp$state)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value Pr(>F)
## group     1  0.0841 0.7719
##          1034
```

```
# Assumption not met
leveneTest(residuals(mod1u) ~ 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 2.9377 0.0001358 ***
##           1020
## ---
## 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  1.5053 0.2201
##           1034

# 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 3.0618 1.874e-06 ***
##           1012
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Assumption met

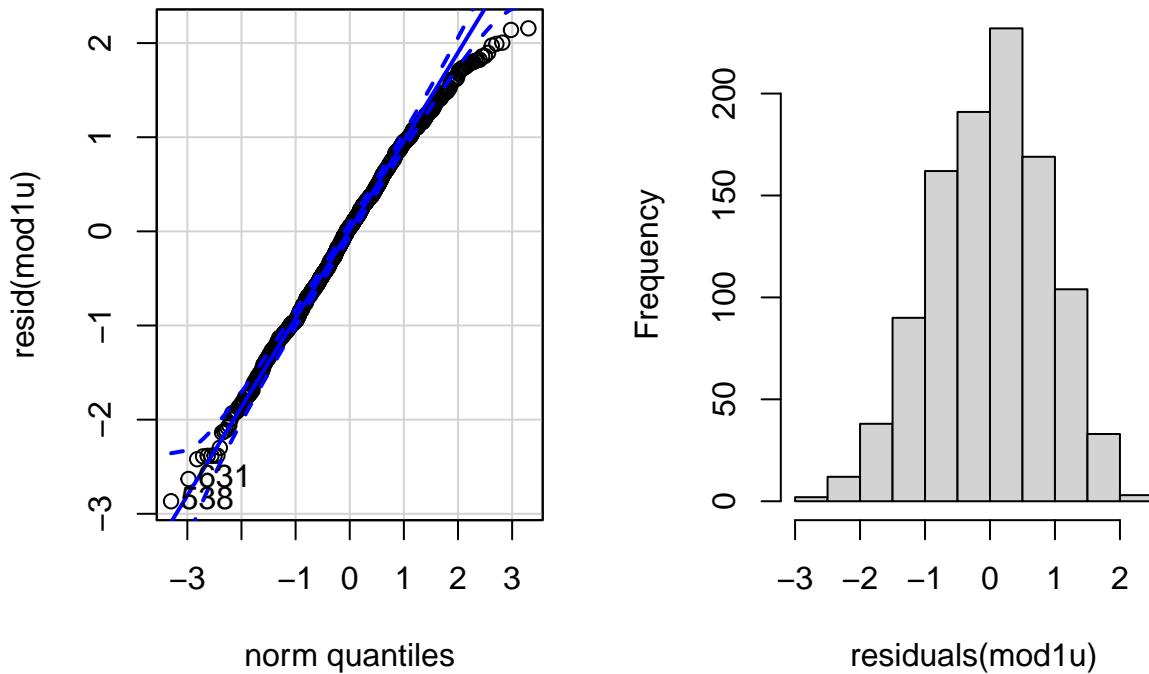
# (3) Normality of error term: need to check by histogram, QQplot of residuals,
# could do Kolmogorov-Smirnov test. Check for normal residuals
qqPlot(resid(mod1u))

## 538 631
## 185 244

hist(residuals(mod1u))

```

## Histogram of residuals(mod1u)



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

```
##  
## Shapiro-Wilk normality test  
##  
## data: resid(mod1u)  
## W = 0.99478, p-value = 0.001195
```

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

```
## No Studentized residuals with Bonferroni p < 0.05  
## Largest |rstudent|:  
##      rstudent unadjusted p-value Bonferroni p  
## 538 -3.232035          0.0012683       NA
```

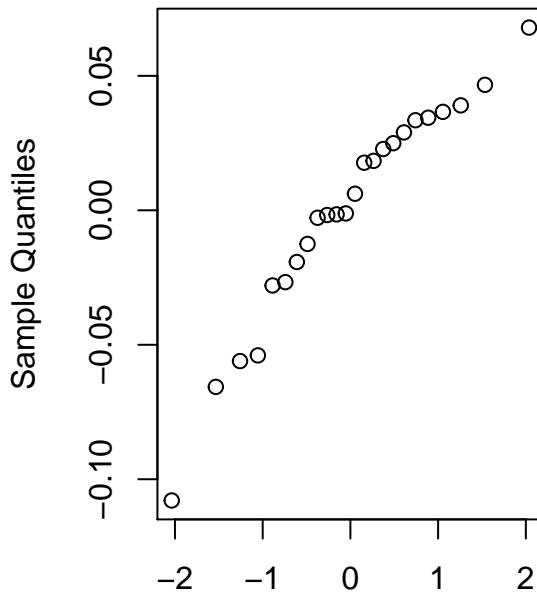
# (4) Normality of random effect: Get the estimate of random effect (e.g., random intercepts), and check them as you would check the residual.

```
require(lme4)  
r_int <- ranef(mod1u)$plot$`'(Intercept)`'  
qnorm(r_int)  
# qline(r_int) #doesn't work  
shapiro.test(r_int)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: r_int  
## W = 0.94659, p-value = 0.2283
```

```
# 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?
mod1u <- lmer(log(relabun) ~ state * year_factor + insecticide * year_factor + (1 |
  species) + (1 | plot), comp_umbs_spp, REML = FALSE)
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(mod1u)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                     Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state                           0.20362 0.20362     1   302.74 0.2535 0.6150
## year_factor                     0.32111 0.32111     1  1012.98 0.3998 0.5273
## insecticide                      1.14161 1.14161     1   301.14 1.4215 0.2341
## state:year_factor               0.13829 0.13829     1  1008.19 0.1722 0.6783
## year_factor:insecticide         1.00559 1.00559     1  1008.83 1.2522 0.2634
```

```
anova(mod2u)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                     Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state                           0.25077 0.25077     1   1022.0 0.3099 0.5778
## year_factor                     0.31790 0.31790     1  1027.5 0.3929 0.5309
## insecticide                      1.10666 1.10666     1   1022.0 1.3677 0.2425
```

```
## state:year_factor      0.12144 0.12144      1 1022.0  0.1501 0.6985
## year_factor:insecticide 1.01482 1.01482      1 1023.4  1.2542 0.2630
```

```
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 2781.1 2820.6 -1382.5   2765.1
## mod1u     9 2781.9 2826.4 -1382.0   2763.9 1.1698  1     0.2794
```

```
summ(mod1u)
```

Observations	1036
Dependent variable	log(relabun)
Type	Mixed effects linear regression

AIC	2781.90
BIC	2826.39
Pseudo-R <sup>2</sup> (fixed effects)	0.00
Pseudo-R <sup>2</sup> (total)	0.29

Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	-2.76	0.19	-14.70	41.27	0.00
stateambient	-0.07	0.13	-0.50	302.74	0.61
year_factor	0.02	0.03	0.76	1010.18	0.45
insecticideno_insects	0.16	0.13	1.19	301.14	0.23
stateambient:year_factor	0.01	0.03	0.41	1008.19	0.68
year_factor:insecticideno_insects	-0.03	0.03	-1.12	1008.83	0.26

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
plot	(Intercept)	0.08
species	(Intercept)	0.56
Residual		0.90

```
summ(mod2u)
```

Grouping Variables					
Group	# groups	ICC			
plot	24	0.01			
species	16	0.28			
Observations			1036		
Dependent variable			log(relabun)		
Type			Mixed effects linear regression		
AIC			2781.07		
BIC			2820.62		
Pseudo-R <sup>2</sup> (fixed effects)			0.00		
Pseudo-R <sup>2</sup> (total)			0.29		
Fixed Effects					
	Est.	S.E.	t val.	d.f.	p
(Intercept)	-2.77	0.19	-14.82	39.10	0.00
stateambient	-0.07	0.13	-0.56	1022.01	0.58
year_factor	0.02	0.03	0.77	1024.66	0.44
insecticideno_insects	0.15	0.13	1.17	1022.05	0.24
stateambient:year_factor	0.01	0.03	0.39	1021.96	0.70
year_factor:insecticideno_insects	-0.03	0.03	-1.12	1023.44	0.26

p values calculated using Satterthwaite d.f.

Random Effects		
Group	Parameter	Std. Dev.
species	(Intercept)	0.57
Residual		0.90

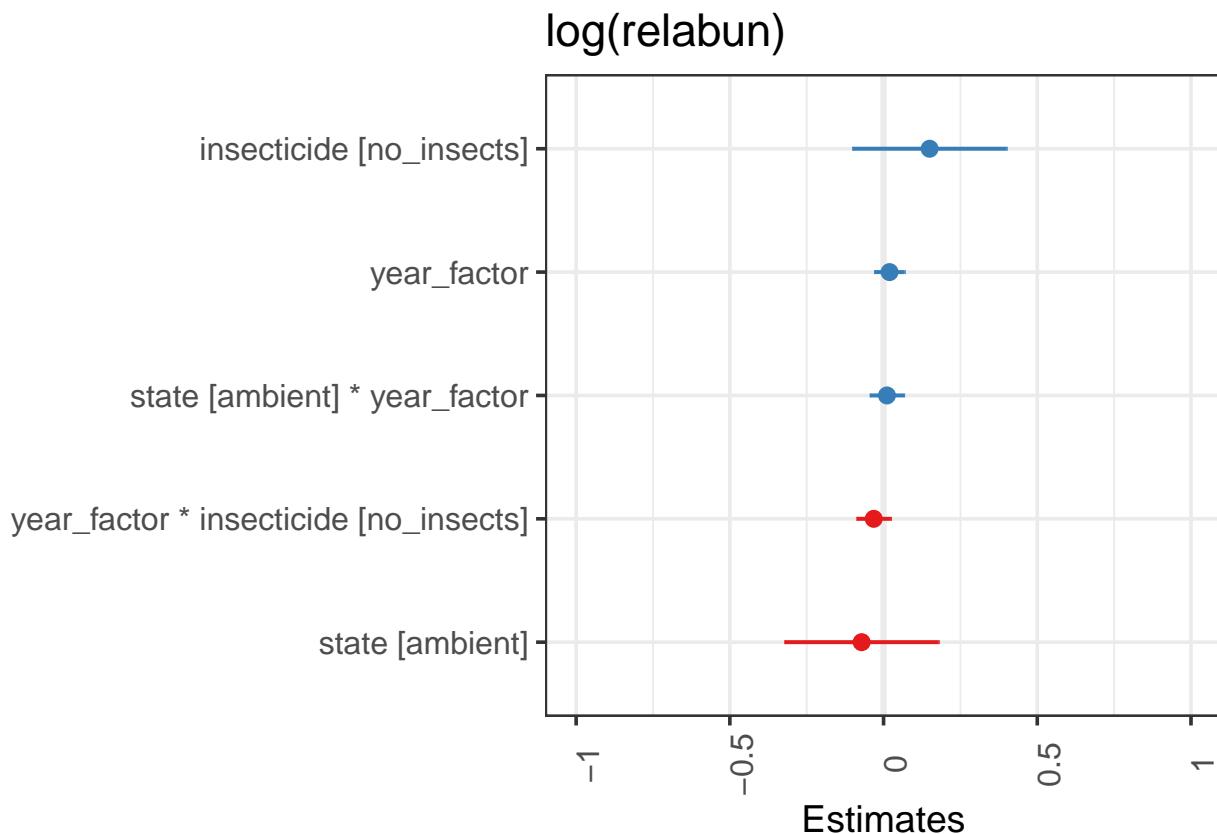
  

Grouping Variables			
Group	# groups	ICC	
species	16	0.28	

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

```
##      dAICc df weight
## mod2u 0.0   8  0.61
## mod1u 0.9   9  0.39
```

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

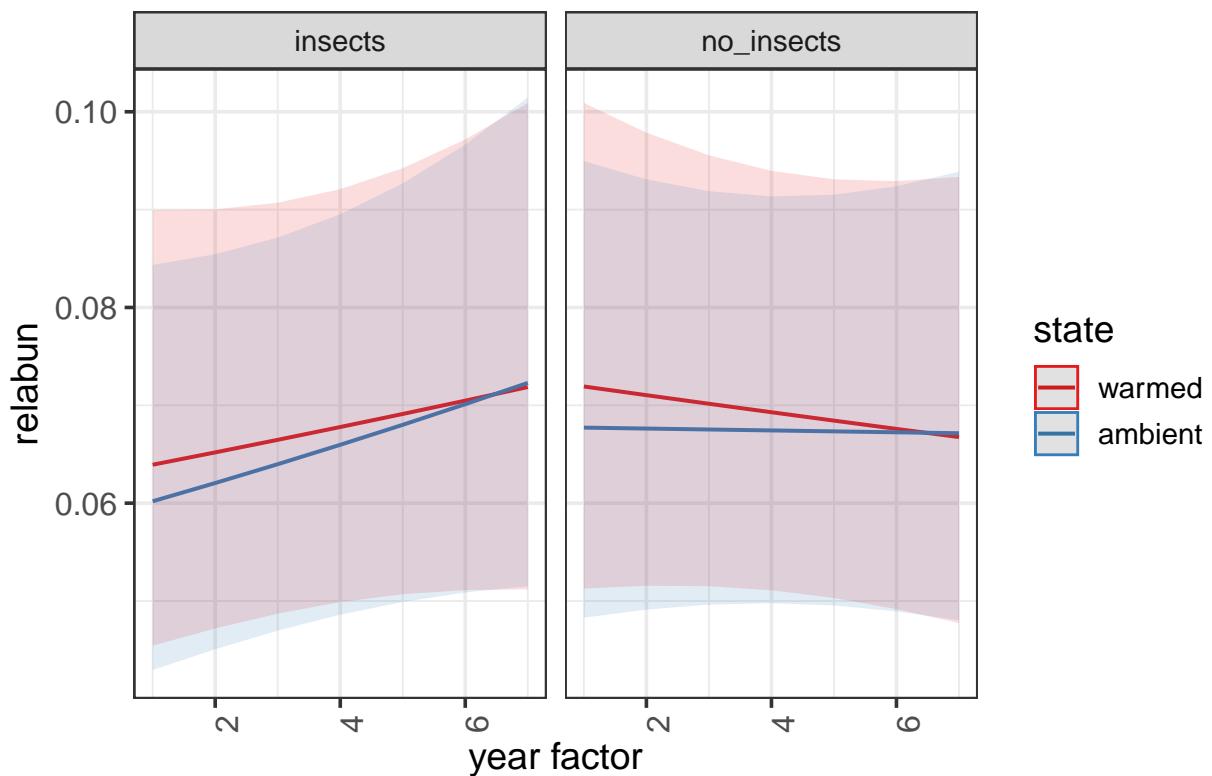


```
# these are the fixed predicted values:
```

```
plot_model(mod2u, type = "pred", terms = c("year_factor", "state", "insecticide"))
```

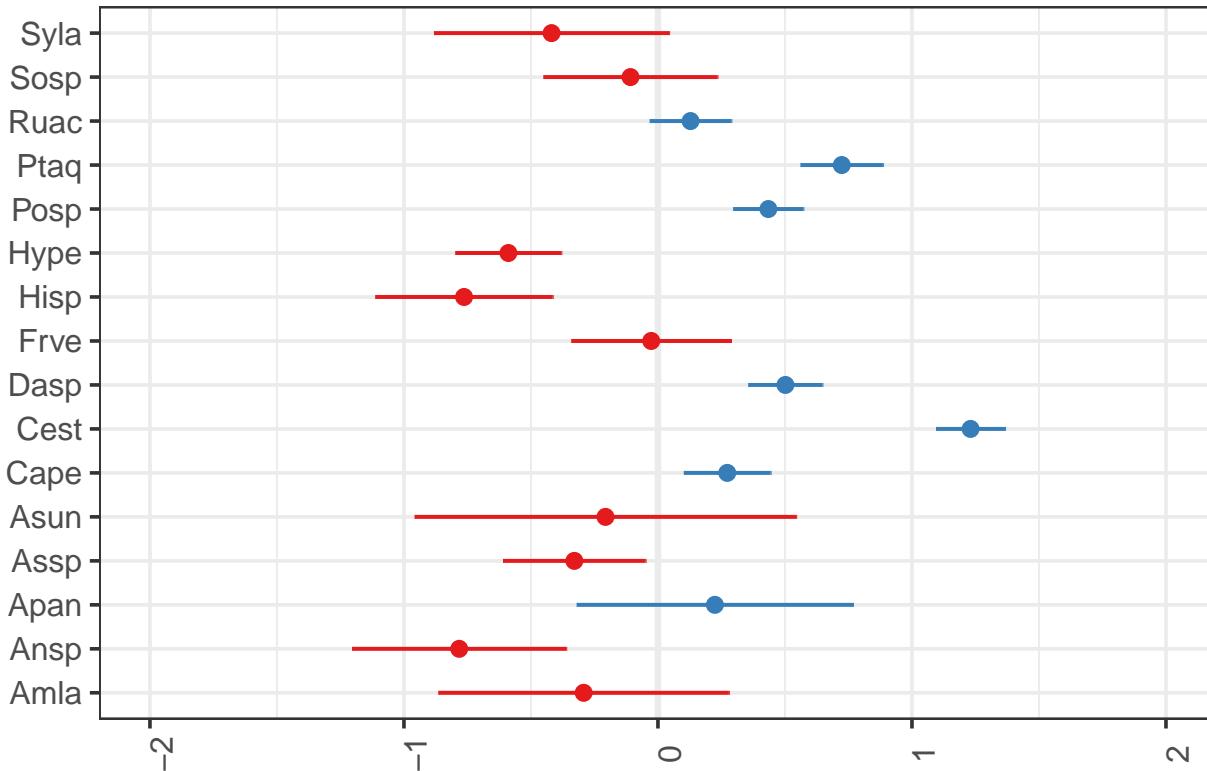
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standard
```

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

```
## 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 +
##        (1 | species)
##          npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## mod4u     6 2778.5 2808.1 -1383.2    2766.5
## mod2u     8 2781.1 2820.6 -1382.5    2765.1 1.392  2      0.4986
```

```
AICctab(mod2u, mod4u, weights = T)
```

```
##          dAICc df weight
```

```

## mod4u 0.0   6   0.79
## mod2u 2.7   8   0.21

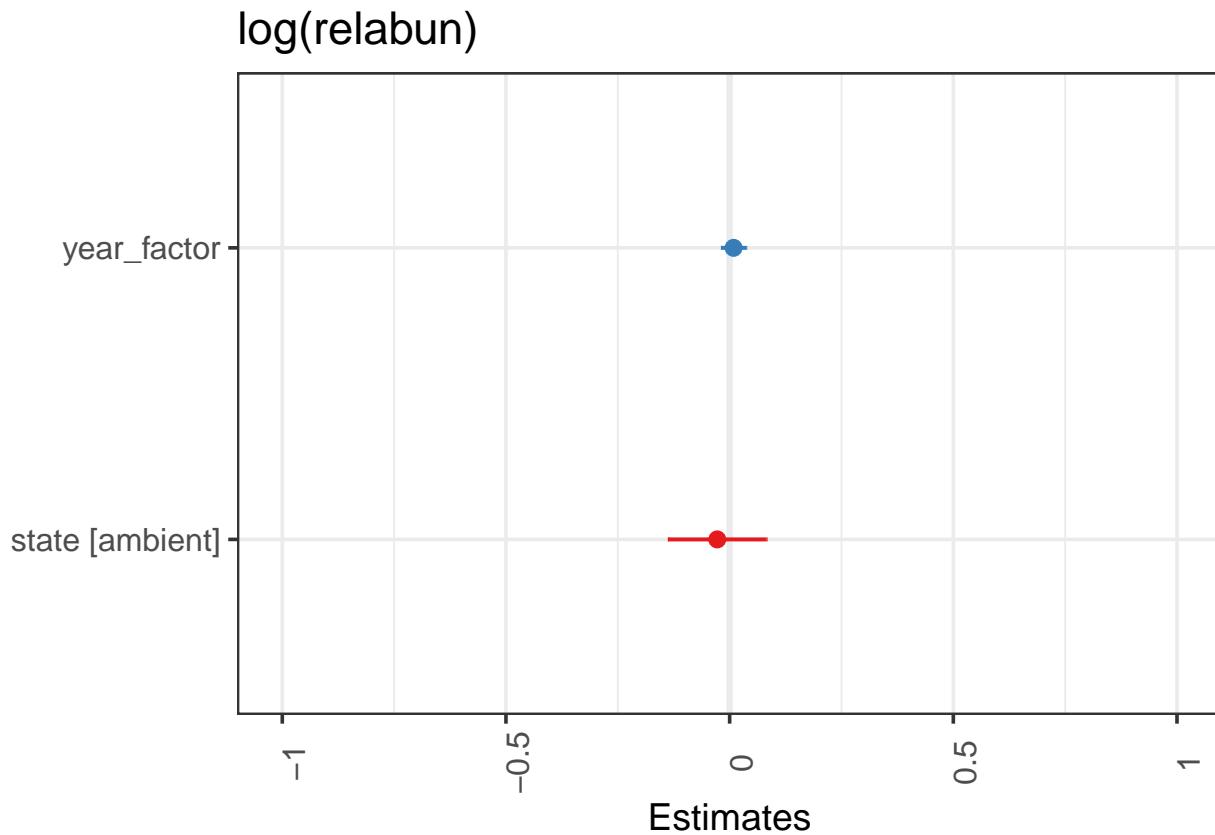
# Does year need to be interactive with state?
mod5u <- lmer(log(relabun) ~ state + year_factor + (1 | species), comp_umbs_spp,
               REML = FALSE)
anova(mod4u, mod5u)

## 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 2776.6 2801.4 -1383.3    2766.6
## mod4u     6 2778.5 2808.1 -1383.2    2766.5 0.1766  1      0.6743

# 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)

```



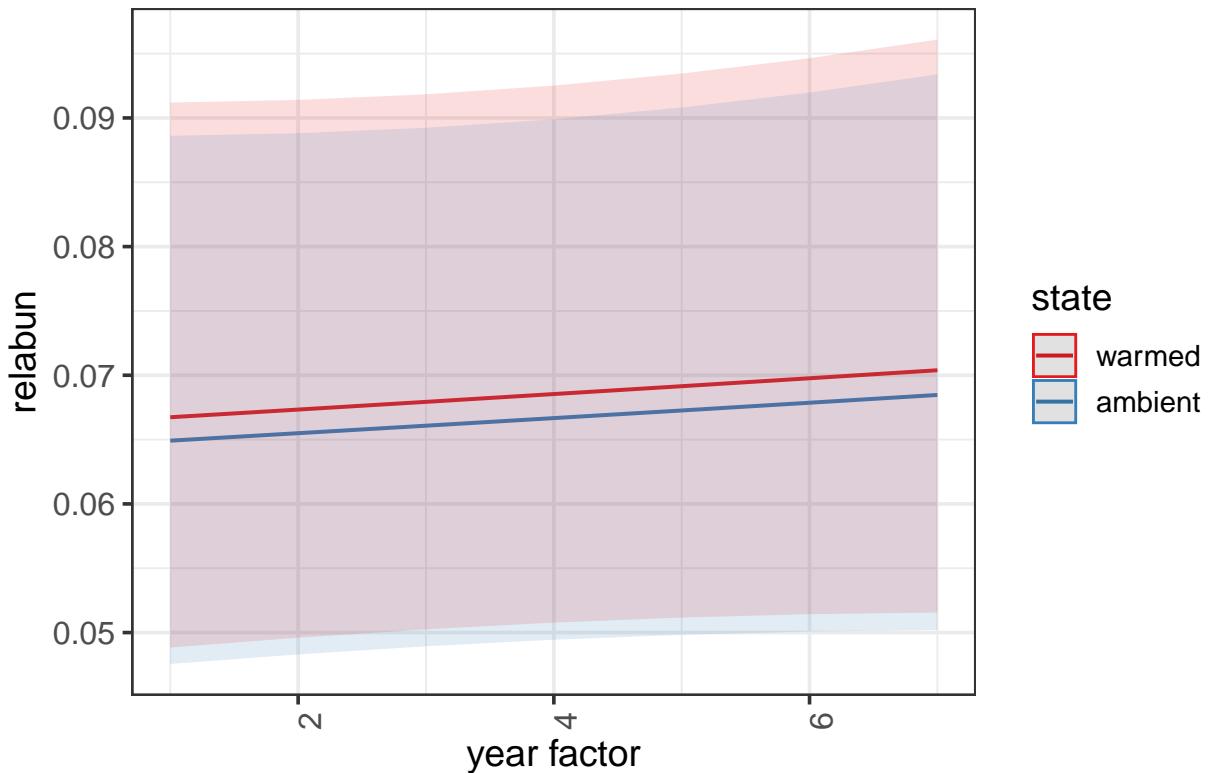
```

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

```

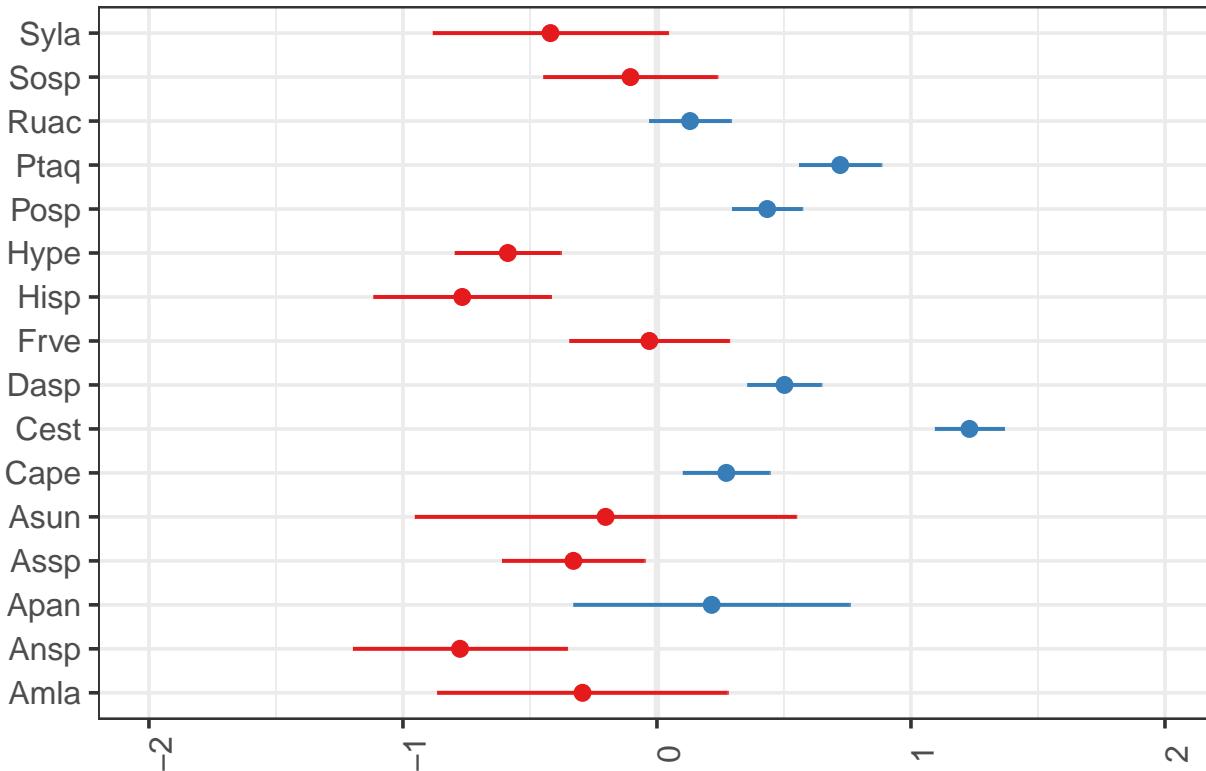
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standard
```

## 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
```

```
## Warning: Model failed to converge with 1 negative eigenvalue: -3.1e+02
```

```
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 2776.6 2801.4 -1383.3    2766.6
## mod6u     8 2781.2 2820.8 -1382.6    2765.2 1.4181  3     0.7013
```

```
anova(mod5u)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state      0.19548 0.19548     1 1023.2  0.2412 0.6234
## year_factor 0.30648 0.30648     1 1027.5  0.3782 0.5387
```

```

# 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

```

mod7au <- lmer(log(relabun) ~ state + species + factor(year_factor) + (1 | plot),
  comp_umbs_spp, REML = FALSE)
mod7bu <- lmer(log(relabun) ~ state * factor(year_factor) + species + (1 | plot),
  comp_umbs_spp, REML = FALSE)
mod7cu <- lmer(log(relabun) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), comp_umbs_spp, REML = FALSE)
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 2776.6 2801.4 -1383.3    2766.6
## mod7u    46 2796.8 3024.2 -1352.4    2704.8 61.808 41     0.01942 *
## ---
## 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    25 2740.6 2864.2 -1345.3    2690.6
## mod7u    46 2796.8 3024.2 -1352.4    2704.8      0 21          1

```

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

```

## 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    25 2740.6 2864.2 -1345.3    2690.6
## mod7bu   31 2748.2 2901.5 -1343.1    2686.2 4.3422  6     0.6305

```

```

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    25 2740.6 2864.2 -1345.3   2690.6
## mod7cu    26 2742.4 2870.9 -1345.2   2690.4  0.1921   1     0.6611

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
## 2740.6  2864.2 -1345.3   2690.6      1011
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -3.2110 -0.7123  0.0433  0.7239  2.4807
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## plot     (Intercept) 0.003751 0.06124
## Residual           0.782614 0.88466
## Number of obs: 1036, groups: plot, 24
##
## Fixed effects:
##                               Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept)             -3.11389  0.34894 982.89721 -8.924 < 2e-16 ***
## stateambient          -0.02130  0.06098 22.72192 -0.349 0.730152  
## speciesAnsp            -0.49198  0.40985 1021.29094 -1.200 0.230259  
## speciesApan            0.70839  0.45989 1029.38094  1.540 0.123787  
## speciesAssp            0.12999  0.36835  987.91990  0.353 0.724246  
## speciesAsun            0.14286  0.61371 1031.56236  0.233 0.815975  
## speciesCape            0.71522  0.34830 1011.15876  2.053 0.040285 *
## speciesCest            1.69374  0.34451 1019.18676  4.916 1.03e-06 ***
## speciesDasp            0.95677  0.34576 1018.86770  2.767 0.005757 ** 
## speciesFrve            0.45691  0.37668  987.23255  1.213 0.225422  
## speciesHisp            -0.47353  0.38729 1032.69936 -1.223 0.221732  
## speciesHype            -0.15921  0.35317 1027.37955 -0.451 0.652220  
## speciesPosp            0.87654  0.34465 1019.88336  2.543 0.011129 *  
## speciesPtaq            1.19656  0.34774 1024.46360  3.441 0.000603 *** 
## speciesRuac            0.58520  0.34698 1025.14338  1.687 0.091993 .  
## speciesSosp            0.33550  0.38381 1026.29847  0.874 0.382253  
## speciesSyla            -0.01776  0.42355 1027.30567 -0.042 0.966561  
## factor(year_factor)2   -0.24679  0.10603 1014.91542 -2.327 0.020136 * 
## factor(year_factor)3   0.12481  0.10508 1017.42936  1.188 0.235184

```

```

## factor(year_factor)4    0.09849   0.10552 1017.34710   0.933 0.350853
## factor(year_factor)5   -0.03859   0.10407 1019.10257  -0.371 0.710849
## factor(year_factor)6    0.01625   0.10292 1019.10813   0.158 0.874562
## factor(year_factor)7   -0.04883   0.10728 1015.93590  -0.455 0.649060
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Correlation matrix not shown by default, as p = 23 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)       if you need it

```

```
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                      0.10  0.0954     1    22.72 0.1219 0.73015
## species                   321.15 21.4099    15 1010.12 27.3569 < 2e-16 ***
## factor(year_factor)  12.65  2.1079     6 1017.27  2.6935 0.01341 *
## ---
## 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")
```

```

## $`emmeans of state, year_factor`
##   state  year_factor emmean      SE df lower.CL upper.CL
##   warmed          1  -2.70 0.0989 393    -2.89   -2.50
##   ambient          1  -2.72 0.0982 374    -2.91   -2.53
##   warmed          2  -2.94 0.0983 385    -3.14   -2.75
##   ambient          2  -2.97 0.0973 367    -3.16   -2.77
##   warmed          3  -2.57 0.0962 373    -2.76   -2.38
##   ambient          3  -2.59 0.0959 361    -2.78   -2.41
##   warmed          4  -2.60 0.0957 353    -2.79   -2.41
##   ambient          4  -2.62 0.0946 335    -2.81   -2.43
##   warmed          5  -2.74 0.0924 311    -2.92   -2.55
##   ambient          5  -2.76 0.0922 295    -2.94   -2.58
##   warmed          6  -2.68 0.0934 338    -2.87   -2.50
##   ambient          6  -2.70 0.0921 308    -2.88   -2.52
##   warmed          7  -2.75 0.0988 396    -2.94   -2.55
##   ambient          7  -2.77 0.0988 382    -2.96   -2.57
##
## 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  0.02130 0.0648  26.2  0.329  1.0000
##   warmed 1 - warmed 2  0.24679 0.1071 1036.0  2.303  0.5528

```

```

## warmed 1 - ambient 2  0.26808 0.1250  343.2  2.145  0.6694
## warmed 1 - warmed 3 -0.12481 0.1062 1038.6 -1.175  0.9964
## warmed 1 - ambient 3 -0.10352 0.1247  338.1 -0.830  0.9999
## warmed 1 - warmed 4 -0.09849 0.1066 1038.5 -0.924  0.9997
## warmed 1 - ambient 4 -0.07719 0.1244  337.6 -0.620  1.0000
## warmed 1 - warmed 5  0.03859 0.1052 1040.2  0.367  1.0000
## warmed 1 - ambient 5 0.05989 0.1239  326.1  0.483  1.0000
## warmed 1 - warmed 6 -0.01625 0.1040 1040.2 -0.156  1.0000
## warmed 1 - ambient 6 0.00504 0.1221  310.8  0.041  1.0000
## warmed 1 - warmed 7  0.04883 0.1084 1037.0  0.450  1.0000
## warmed 1 - ambient 7 0.07013 0.1268  354.3  0.553  1.0000
## ambient 1 - warmed 2 0.22549 0.1254  341.8  1.798  0.8759
## ambient 1 - ambient 2 0.24679 0.1071 1036.0  2.303  0.5528
## ambient 1 - warmed 3 -0.14611 0.1241  329.0 -1.177  0.9963
## ambient 1 - ambient 3 -0.12481 0.1062 1038.6 -1.175  0.9964
## ambient 1 - warmed 4 -0.11978 0.1251  336.0 -0.957  0.9996
## ambient 1 - ambient 4 -0.09849 0.1066 1038.5 -0.924  0.9997
## ambient 1 - warmed 5  0.01729 0.1231  324.1  0.140  1.0000
## ambient 1 - ambient 5 0.03859 0.1052 1040.2  0.367  1.0000
## ambient 1 - warmed 6 -0.03755 0.1230  323.4 -0.305  1.0000
## ambient 1 - ambient 6 -0.01625 0.1040 1040.2 -0.156  1.0000
## ambient 1 - warmed 7  0.02754 0.1258  347.1  0.219  1.0000
## ambient 1 - ambient 7 0.04883 0.1084 1037.0  0.450  1.0000
## warmed 2 - ambient 2  0.02130 0.0648  26.2   0.329  1.0000
## warmed 2 - warmed 3 -0.37160 0.1063 1041.0 -3.495  0.0326
## warmed 2 - ambient 3 -0.35030 0.1250  336.2 -2.802  0.2284
## warmed 2 - warmed 4 -0.34527 0.1058 1038.3 -3.262  0.0676
## warmed 2 - ambient 4 -0.32398 0.1240  331.4 -2.613  0.3360
## warmed 2 - warmed 5 -0.20820 0.1048 1041.9 -1.987  0.7756
## warmed 2 - ambient 5 -0.18690 0.1238  321.1 -1.510  0.9652
## warmed 2 - warmed 6 -0.26304 0.1036 1039.1 -2.540  0.3816
## warmed 2 - ambient 6 -0.24174 0.1219  308.1 -1.983  0.7774
## warmed 2 - warmed 7 -0.19795 0.1079 1039.5 -1.834  0.8602
## warmed 2 - ambient 7 -0.17666 0.1266  348.0 -1.396  0.9820
## ambient 2 - warmed 3 -0.39289 0.1240  328.4 -3.169  0.0919
## ambient 2 - ambient 3 -0.37160 0.1063 1041.0 -3.495  0.0326
## ambient 2 - warmed 4 -0.36657 0.1242  331.2 -2.952  0.1618
## ambient 2 - ambient 4 -0.34527 0.1058 1038.3 -3.262  0.0676
## ambient 2 - warmed 5 -0.22949 0.1225  320.3 -1.873  0.8395
## ambient 2 - ambient 5 -0.20820 0.1048 1041.9 -1.987  0.7756
## ambient 2 - warmed 6 -0.28433 0.1224  321.9 -2.323  0.5391
## ambient 2 - ambient 6 -0.26304 0.1036 1039.1 -2.540  0.3816
## ambient 2 - warmed 7 -0.21925 0.1252  342.1 -1.752  0.8954
## ambient 2 - ambient 7 -0.19795 0.1079 1039.5 -1.834  0.8602
## warmed 3 - ambient 3  0.02130 0.0648  26.2   0.329  1.0000
## warmed 3 - warmed 4  0.02632 0.1058 1037.8  0.249  1.0000
## warmed 3 - ambient 4  0.04762 0.1234  327.4  0.386  1.0000
## warmed 3 - warmed 5  0.16340 0.1045 1038.4  1.563  0.9550
## warmed 3 - ambient 5  0.18470 0.1231  318.4  1.501  0.9668
## warmed 3 - warmed 6  0.10856 0.1033 1040.7  1.051  0.9989
## warmed 3 - ambient 6  0.12986 0.1212  301.3  1.071  0.9985
## warmed 3 - warmed 7  0.17365 0.1078 1037.0  1.611  0.9433
## warmed 3 - ambient 7  0.19494 0.1260  345.3  1.548  0.9576
## ambient 3 - warmed 4 0.00503 0.1247  334.9  0.040  1.0000

```

```

## ambient 3 - ambient 4  0.02632 0.1058 1037.8  0.249  1.0000
## ambient 3 - warmed 5  0.14211 0.1228  325.5  1.157  0.9968
## ambient 3 - ambient 5  0.16340 0.1045 1038.4  1.563  0.9550
## ambient 3 - warmed 6  0.08726 0.1227  322.8  0.711  1.0000
## ambient 3 - ambient 6  0.10856 0.1033 1040.7  1.051  0.9989
## ambient 3 - warmed 7  0.15235 0.1255  347.2  1.213  0.9950
## ambient 3 - ambient 7  0.17365 0.1078 1037.0  1.611  0.9433
## warmed 4 - ambient 4  0.02130 0.0648   26.2  0.329  1.0000
## warmed 4 - warmed 5  0.13708 0.1029 1036.4  1.332  0.9884
## warmed 4 - ambient 5  0.15837 0.1224  312.7  1.294  0.9908
## warmed 4 - warmed 6  0.08224 0.1017 1037.5  0.809  0.9999
## warmed 4 - ambient 6  0.10353 0.1205  296.5  0.860  0.9999
## warmed 4 - warmed 7  0.14732 0.1067 1036.9  1.381  0.9840
## warmed 4 - ambient 7  0.16862 0.1256  341.2  1.342  0.9872
## ambient 4 - warmed 5  0.11578 0.1208  311.9  0.958  0.9996
## ambient 4 - ambient 5  0.13708 0.1029 1036.4  1.332  0.9884
## ambient 4 - warmed 6  0.06094 0.1207  310.2  0.505  1.0000
## ambient 4 - ambient 6  0.08224 0.1017 1037.5  0.809  0.9999
## ambient 4 - warmed 7  0.12602 0.1240  335.6  1.017  0.9992
## ambient 4 - ambient 7  0.14732 0.1067 1036.9  1.381  0.9840
## warmed 5 - ambient 5  0.02130 0.0648   26.2  0.329  1.0000
## warmed 5 - warmed 6  -0.05484 0.1001 1037.2 -0.548  1.0000
## warmed 5 - ambient 6  -0.03355 0.1183  285.5 -0.283  1.0000
## warmed 5 - warmed 7  0.01024 0.1050 1037.0  0.098  1.0000
## warmed 5 - ambient 7  0.03154 0.1234  328.9  0.256  1.0000
## ambient 5 - warmed 6  -0.07614 0.1202  300.2 -0.634  1.0000
## ambient 5 - ambient 6 -0.05484 0.1001 1037.2 -0.548  1.0000
## ambient 5 - warmed 7  -0.01105 0.1233  323.5 -0.090  1.0000
## ambient 5 - ambient 7  0.01024 0.1050 1037.0  0.098  1.0000
## warmed 6 - ambient 6  0.02130 0.0648   26.2  0.329  1.0000
## warmed 6 - warmed 7  0.06509 0.1039 1037.2  0.626  1.0000
## warmed 6 - ambient 7  0.08638 0.1234  328.9  0.700  1.0000
## ambient 6 - warmed 7  0.04379 0.1215  308.9  0.360  1.0000
## ambient 6 - ambient 7  0.06509 0.1039 1037.2  0.626  1.0000
## warmed 7 - ambient 7  0.02130 0.0648   26.2  0.329  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 14 estimates

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

## $`emmeans of year_factor`
##    year_factor emmean      SE  df lower.CL upper.CL
##    1     -2.71 0.0931 662    -2.89    -2.53
##    2     -2.96 0.0923 655    -3.14    -2.77
##    3     -2.58 0.0904 651    -2.76    -2.41
##    4     -2.61 0.0895 612    -2.79    -2.43
##    5     -2.75 0.0865 546    -2.92    -2.58
##    6     -2.69 0.0869 588    -2.86    -2.52
##    7     -2.76 0.0934 671    -2.94    -2.57
##
## 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    0.2468 0.107 1036   2.303  0.2432
## 1 - 3   -0.1248 0.106 1039  -1.175  0.9034
## 1 - 4   -0.0985 0.107 1038  -0.924  0.9688
## 1 - 5    0.0386 0.105 1040   0.367  0.9998
## 1 - 6   -0.0163 0.104 1040  -0.156  1.0000
## 1 - 7    0.0488 0.108 1037   0.450  0.9994
## 2 - 3   -0.3716 0.106 1041  -3.495  0.0089
## 2 - 4   -0.3453 0.106 1038  -3.262  0.0195
## 2 - 5   -0.2082 0.105 1042  -1.987  0.4233
## 2 - 6   -0.2630 0.104 1039  -2.540  0.1464
## 2 - 7   -0.1980 0.108 1039  -1.834  0.5251
## 3 - 4    0.0263 0.106 1038   0.249  1.0000
## 3 - 5    0.1634 0.105 1038   1.563  0.7059
## 3 - 6    0.1086 0.103 1041   1.051  0.9419
## 3 - 7    0.1736 0.108 1037   1.611  0.6753
## 4 - 5    0.1371 0.103 1036   1.332  0.8368
## 4 - 6    0.0822 0.102 1038   0.809  0.9841
## 4 - 7    0.1473 0.107 1037   1.381  0.8121
## 5 - 6   -0.0548 0.100 1037  -0.548  0.9981
## 5 - 7    0.0102 0.105 1037   0.098  1.0000
## 6 - 7    0.0651 0.104 1037   0.626  0.9960
##
## 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 7 estimates

```

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

```

## $`emmeans of species`
##   species emmean      SE   df lower.CL upper.CL
##   Amla    -3.14 0.3435 1033    -3.81   -2.46
##   Ansp    -3.63 0.2340 1056    -4.09   -3.17
##   Apan    -2.43 0.3210 1029    -3.06   -1.80
##   Assp    -3.01 0.1505  854    -3.30   -2.71
##   Asun    -3.00 0.5219 1059    -4.02   -1.97
##   Cape    -2.42 0.0899  692    -2.60   -2.25
##   Cest    -1.44 0.0712  508    -1.58   -1.30
##   Dasp    -2.18 0.0764  575    -2.33   -2.03
##   Frve    -2.68 0.1702  822    -3.02   -2.35
##   Hisp    -3.61 0.1913 1034    -3.99   -3.24
##   Hype    -3.30 0.1103  827    -3.51   -3.08
##   Posp    -2.26 0.0722  525    -2.40   -2.12
##   Ptaq    -1.94 0.0851  632    -2.11   -1.77
##   Ruac    -2.55 0.0844  629    -2.72   -2.39
##   Sosp    -2.80 0.1869  875    -3.17   -2.44
##   Syla    -3.16 0.2631  959    -3.67   -2.64
##
```

```

## 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  0.49198 0.4164 1051  1.182  0.9986
## Amla - Apan -0.70839 0.4668 1056 -1.517  0.9805
## Amla - Assp -0.12999 0.3750 1025 -0.347  1.0000
## Amla - Asun -0.14286 0.6212 1053 -0.230  1.0000
## Amla - Cape -0.71522 0.3541 1043 -2.020  0.8139
## Amla - Cest -1.69374 0.3501 1049 -4.838  0.0002
## Amla - Dasp -0.95677 0.3513 1049 -2.723  0.3169
## Amla - Frve -0.45691 0.3835 1024 -1.192  0.9984
## Amla - Hisp  0.47353 0.3930 1059  1.205  0.9982
## Amla - Hype  0.15921 0.3586 1055  0.444  1.0000
## Amla - Posp -0.87654 0.3502 1050 -2.503  0.4700
## Amla - Ptaq -1.19656 0.3532 1053 -3.388  0.0578
## Amla - Ruac -0.58520 0.3524 1054 -1.661  0.9563
## Amla - Sosp -0.33550 0.3897 1054 -0.861  1.0000
## Amla - Syla  0.01776 0.4301 1056  0.041  1.0000
## Ansp - Apan -1.20037 0.3968 1059 -3.025  0.1602
## Ansp - Assp -0.62197 0.2774 1060 -2.242  0.6668
## Ansp - Asun -0.63485 0.5735 1060 -1.107  0.9993
## Ansp - Cape -1.20720 0.2504 1058 -4.822  0.0002
## Ansp - Cest -2.18572 0.2436 1056 -8.974 <.0001
## Ansp - Dasp -1.44876 0.2447 1055 -5.921 <.0001
## Ansp - Frve -0.94890 0.2878 1058 -3.297  0.0761
## Ansp - Hisp -0.01846 0.2994 1057 -0.062  1.0000
## Ansp - Hype -0.33277 0.2583 1053 -1.288  0.9963
## Ansp - Posp -1.36852 0.2440 1056 -5.608 <.0001
## Ansp - Ptaq -1.68855 0.2483 1058 -6.801 <.0001
## Ansp - Ruac -1.07719 0.2476 1052 -4.351  0.0016
## Ansp - Sosp -0.82748 0.2979 1046 -2.777  0.2837
## Ansp - Syla -0.47422 0.3519 1042 -1.348  0.9940
## Apan - Assp  0.57840 0.3540 1027  1.634  0.9619
## Apan - Asun  0.56553 0.6122 1057  0.924  0.9999
## Apan - Cape -0.00683 0.3322 1042 -0.021  1.0000
## Apan - Cest -0.98535 0.3280 1049 -3.004  0.1688
## Apan - Dasp -0.24838 0.3293 1050 -0.754  1.0000
## Apan - Frve  0.25148 0.3637 1008  0.691  1.0000
## Apan - Hisp  1.18192 0.3741 1052  3.160  0.1125
## Apan - Hype  0.86760 0.3373 1054  2.572  0.4196
## Apan - Posp -0.16815 0.3282 1047 -0.512  1.0000
## Apan - Ptaq -0.48817 0.3311 1054 -1.474  0.9852
## Apan - Ruac  0.12318 0.3305 1054  0.373  1.0000
## Apan - Sosp  0.37289 0.3715 1036  1.004  0.9998
## Apan - Syla  0.72615 0.4145 1026  1.752  0.9321
## Assp - Asun -0.01287 0.5425 1060 -0.024  1.0000
## Assp - Cape -0.58523 0.1739 1008 -3.366  0.0620
## Assp - Cest -1.56375 0.1650 1034 -9.480 <.0001
## Assp - Dasp -0.82678 0.1672 1042 -4.945  0.0001
## Assp - Frve -0.32692 0.2251 1009 -1.453  0.9872

```

```

## Assp - Hisp  0.60352 0.2427 1057  2.487  0.4821
## Assp - Hype  0.28920 0.1850 1044  1.564  0.9743
## Assp - Posp -0.74655 0.1655 1031 -4.510  0.0008
## Assp - Ptaq -1.06657 0.1712 1046 -6.232 <.0001
## Assp - Ruac -0.45522 0.1707 1043 -2.666  0.3540
## Assp - Sosp -0.20551 0.2389 1013 -0.860  1.0000
## Assp - Syla  0.14775 0.3004 1044  0.492  1.0000
## Asun - Cape -0.57235 0.5290 1060 -1.082  0.9995
## Asun - Cest -1.55087 0.5262 1060 -2.947  0.1939
## Asun - Dasp -0.81391 0.5272 1060 -1.544  0.9771
## Asun - Frve -0.31405 0.5479 1060 -0.573  1.0000
## Asun - Hisp  0.61639 0.5554 1058  1.110  0.9993
## Asun - Hype  0.30207 0.5321 1060  0.568  1.0000
## Asun - Posp -0.73367 0.5263 1060 -1.394  0.9915
## Asun - Ptaq -1.05370 0.5280 1060 -1.996  0.8276
## Asun - Ruac -0.44234 0.5279 1060 -0.838  1.0000
## Asun - Sosp -0.19264 0.5520 1055 -0.349  1.0000
## Asun - Syla  0.16062 0.5800 1042  0.277  1.0000
## Cape - Cest -0.97852 0.1124 1054 -8.705 <.0001
## Cape - Dasp -0.24155 0.1161 1058 -2.080  0.7778
## Cape - Frve  0.25831 0.1910 1006  1.352  0.9938
## Cape - Hisp  1.18875 0.2106 1060  5.644 <.0001
## Cape - Hype  0.87443 0.1402 1057  6.238 <.0001
## Cape - Posp -0.16132 0.1130 1053 -1.427  0.9892
## Cape - Ptaq -0.48134 0.1220 1060 -3.946  0.0083
## Cape - Ruac  0.13001 0.1214 1053  1.071  0.9995
## Cape - Sosp  0.37972 0.2068 1001  1.836  0.9027
## Cape - Syla  0.73298 0.2775 994  2.642  0.3707
## Cest - Dasp  0.73696 0.1020 1039  7.228 <.0001
## Cest - Frve  1.23682 0.1831 992  6.754 <.0001
## Cest - Hisp  2.16726 0.2029 1059 10.681 <.0001
## Cest - Hype  1.85295 0.1293 1060 14.327 <.0001
## Cest - Posp  0.81720 0.0989 1033  8.263 <.0001
## Cest - Ptaq  0.49717 0.1086 1055  4.576  0.0006
## Cest - Ruac  1.10853 0.1080 1054 10.262 <.0001
## Cest - Sosp  1.35824 0.1987 1004  6.836 <.0001
## Cest - Syla  1.71150 0.2717 1012  6.300 <.0001
## Dasp - Frve  0.49986 0.1851 988  2.700  0.3317
## Dasp - Hisp  1.43030 0.2043 1058  7.001 <.0001
## Dasp - Hype  1.11598 0.1324 1059  8.431 <.0001
## Dasp - Posp  0.08024 0.1028 1041  0.781  1.0000
## Dasp - Ptaq -0.23979 0.1120 1054 -2.141  0.7383
## Dasp - Ruac  0.37157 0.1116 1050  3.330  0.0690
## Dasp - Sosp  0.62127 0.2004 998  3.100  0.1323
## Dasp - Syla  0.97453 0.2730 1015  3.570  0.0322
## Frve - Hisp  0.93044 0.2535 1060  3.670  0.0229
## Frve - Hype  0.61612 0.2017 1006  3.055  0.1484
## Frve - Posp -0.41962 0.1836 994 -2.285  0.6349
## Frve - Ptaq -0.73965 0.1891 976 -3.912  0.0095
## Frve - Ruac -0.12829 0.1886 993 -0.680  1.0000
## Frve - Sosp  0.12141 0.2508 1007  0.484  1.0000
## Frve - Syla  0.47467 0.3102 1046  1.530  0.9789
## Hisp - Hype -0.31432 0.2200 1054 -1.429  0.9891
## Hisp - Posp -1.35006 0.2031 1059 -6.648 <.0001

```

```

##  Hisp - Ptaq -1.67009 0.2079 1059 -8.032 <.0001
##  Hisp - Ruac -1.05873 0.2079 1058 -5.092 <.0001
##  Hisp - Sosp -0.80903 0.2649 1051 -3.054 0.1488
##  Hisp - Syla -0.45577 0.3236 1057 -1.409 0.9905
##  Hype - Posp -1.03575 0.1299 1059 -7.975 <.0001
##  Hype - Ptaq -1.35577 0.1375 1060 -9.861 <.0001
##  Hype - Ruac -0.74442 0.1365 1057 -5.453 <.0001
##  Hype - Sosp -0.49471 0.2163 1002 -2.288 0.6332
##  Hype - Syla -0.14145 0.2839 1029 -0.498 1.0000
##  Posp - Ptaq -0.32003 0.1094 1056 -2.925 0.2043
##  Posp - Ruac  0.29133 0.1088 1054  2.677 0.3465
##  Posp - Sosp  0.54104 0.1991 1006  2.717 0.3206
##  Posp - Syla  0.89430 0.2719 1013  3.288 0.0781
##  Ptaq - Ruac  0.61136 0.1177 1058  5.195 <.0001
##  Ptaq - Sosp  0.86106 0.2039 1010  4.224 0.0027
##  Ptaq - Syla  1.21432 0.2753 1026  4.411 0.0012
##  Ruac - Sosp  0.24971 0.2038 1009  1.225 0.9978
##  Ruac - Syla  0.60296 0.2750 1027  2.193 0.7024
##  Sosp - Syla  0.35326 0.3185 1060  1.109 0.9993
##
## 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

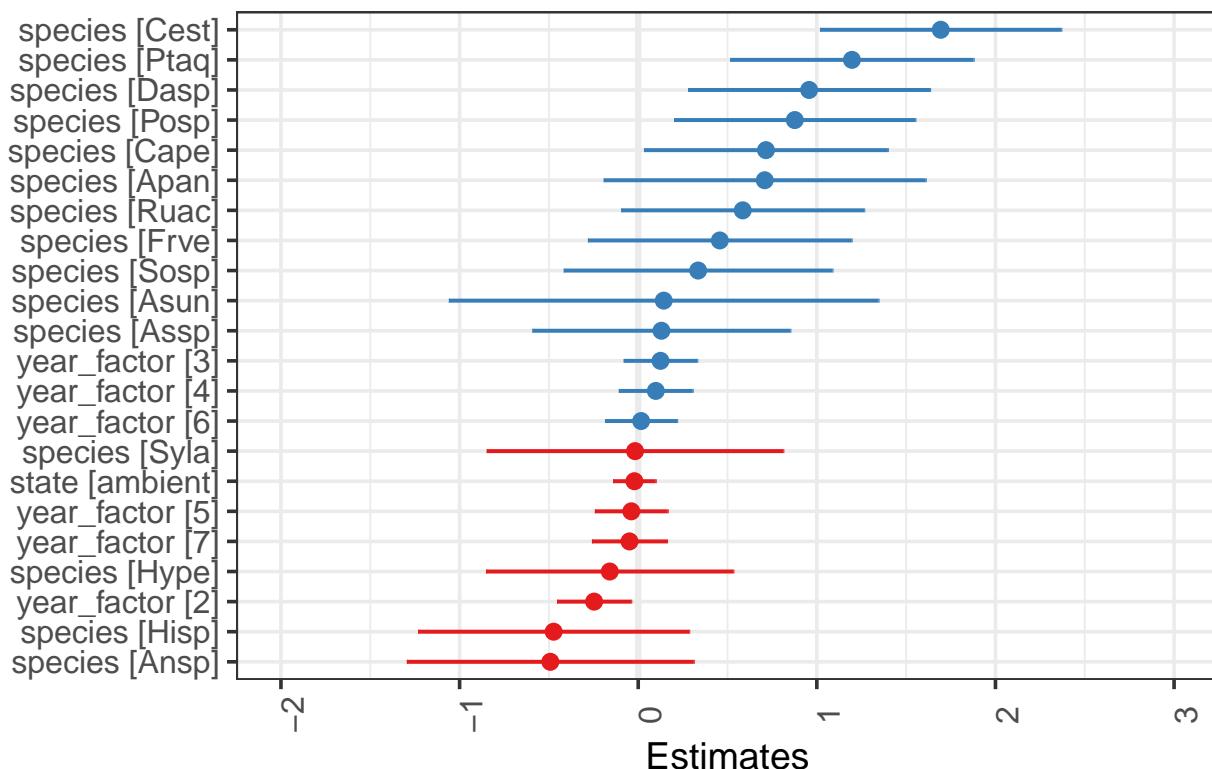
emmeans(mod7au, list(pairwise ~ insecticide), adjust = "tukey")

## 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)

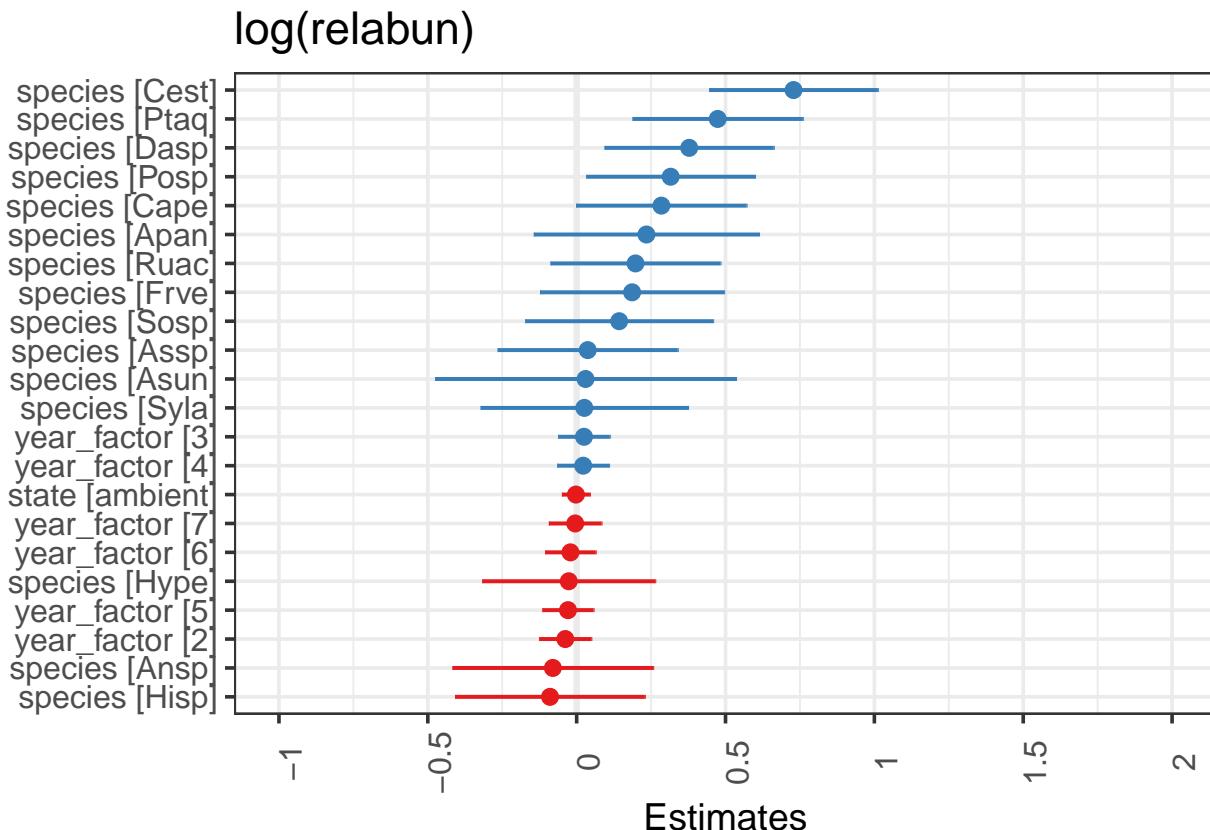
```

## log(relabun)



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

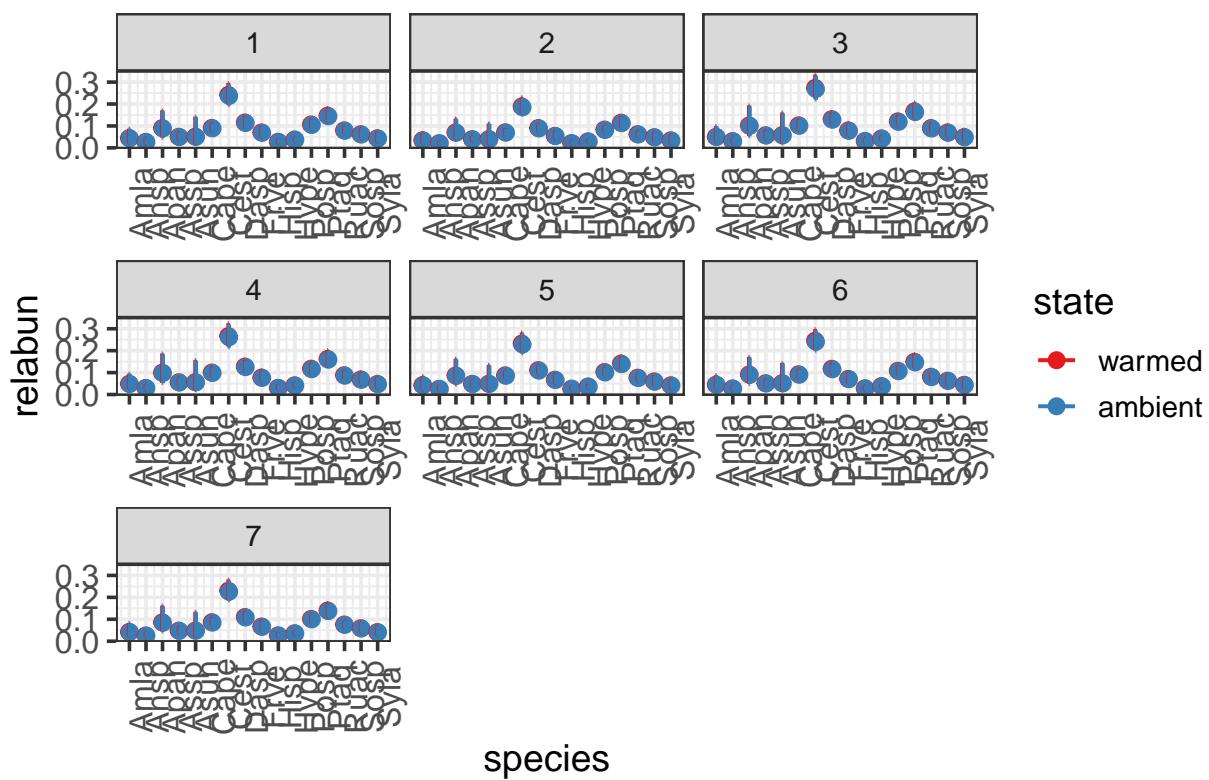
```
## Formula contains log- or sqrt-terms. See help("standardize") for how such terms are standardized.
```



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

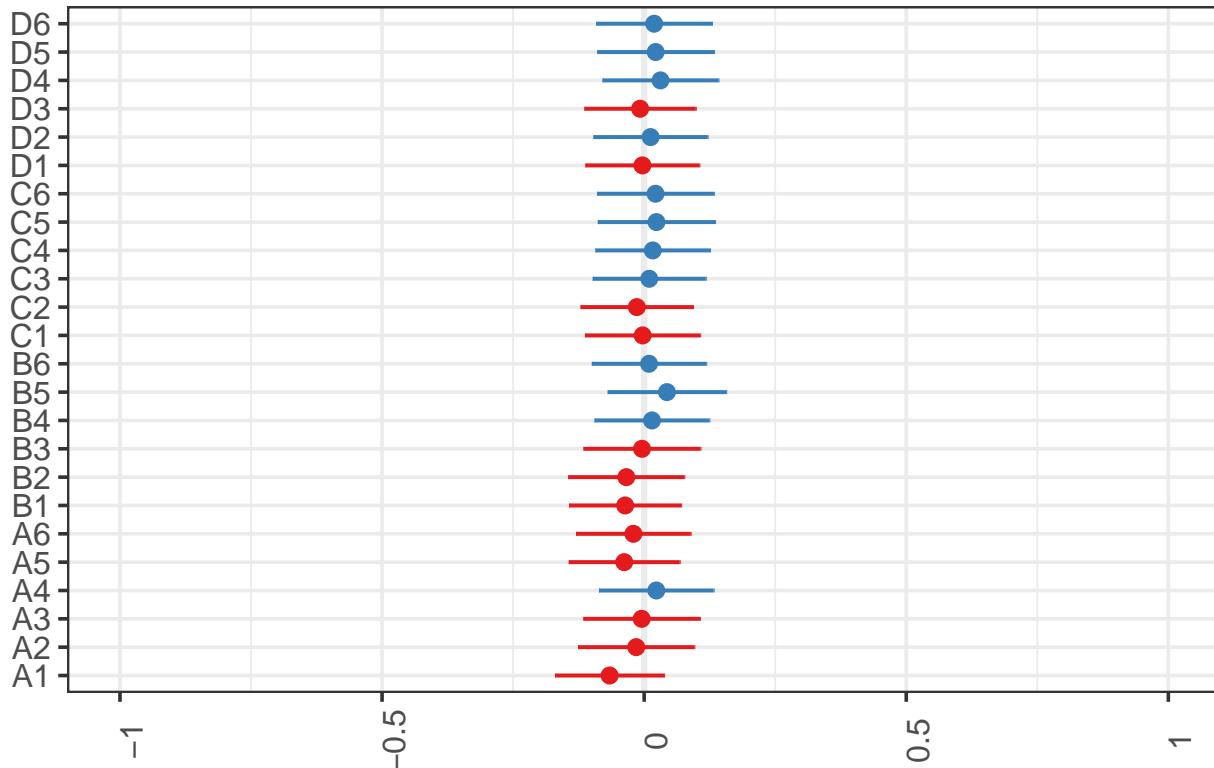
```
## Model has log-transformed response. Back-transforming predictions to original response scale. Standardized
```

## 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    34 3056.2 3224.3 -1494.1    2988.2
## mod8u    37 3060.5 3243.4 -1493.2    2986.5 1.7774  3      0.6199
```

```

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    13 3006.4 3070.7 -1490.2   2980.4
## mod8u     37 3060.5 3243.4 -1493.2   2986.5      0 24          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
##  3060.5   3243.4  -1493.2    2986.5      999
##
## Scaled residuals:
##    Min      1Q  Median      3Q      Max
## -2.50988 -0.79288  0.05386  0.80675  2.23945
##
## Random effects:
##   Groups   Name        Variance Std.Dev. Corr
##   plot     (Intercept) 0.0214322 0.14640
##           factor(year_factor)2 0.0112125 0.10589  1.00
##           factor(year_factor)3 0.0105996 0.10295 -1.00 -1.00
##           factor(year_factor)4 0.0018626 0.04316 -1.00 -1.00  1.00
##           factor(year_factor)5 0.0017895 0.04230  1.00  1.00 -1.00 -1.00
##           factor(year_factor)6 0.0002094 0.01447  1.00  1.00 -1.00 -1.00  1.00
##           factor(year_factor)7 0.0001138 0.01067 -1.00 -1.00  1.00  1.00 -1.00
##   Residual             1.0286150 1.01421
##
## 
## 
## 
## 
## 
## 
## 
## 
## 
## -1.00
##
## Number of obs: 1036, groups: plot, 24
##
## Fixed effects:
##               Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) -2.25615   0.07862 83.07522 -28.698 < 2e-16 ***
## stateambient -0.06030   0.11095 80.28902 -0.544   0.588  
## origin       0.04341   0.12997 1019.30552  0.334   0.738  
## originBoth   -1.04194   0.22866 1028.37529 -4.557 5.82e-06 ***
## originExotic  0.08615   0.10189 1029.06462  0.846   0.398  
## 
```

```

## stateambient:origin      0.01511   0.18504 1020.52065   0.082   0.935
## stateambient:originBoth 0.29948   0.29058 1031.41445   1.031   0.303
## stateambient:originExotic 0.14087   0.14441 1027.18002   0.975   0.330
## ---
## 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 -0.709
## origin      -0.455  0.322
## originBoth   -0.258  0.183  0.154
## originExotic -0.576  0.408  0.350  0.199
## sttmbnt:rgn  0.319 -0.449 -0.702 -0.108 -0.246
## sttmbnt:rgB  0.203 -0.286 -0.121 -0.787 -0.157  0.166
## sttmbnt:rgE  0.406 -0.567 -0.247 -0.141 -0.706  0.340  0.215
## 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       0.277  0.2770     1   62.32  0.2693   0.6056
## origin      52.177 17.3924     3 1027.21 16.9085 1.003e-10 ***
## state:origin 1.833  0.6109     3 1027.21  0.5939   0.6191
## ---
## 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
```

```

## $`emmeans of state, origin`
##   state  origin emmean      SE   df lower.CL upper.CL
##   warmed Native -2.26 0.0940  71.6   -2.44   -2.07
##   ambient Native -2.32 0.0942  69.6   -2.50   -2.13
##   warmed        -2.21 0.1275 304.1   -2.46   -1.96
##   ambient        -2.26 0.1299 320.8   -2.51   -2.00
##   warmed Both   -3.30 0.2360 746.1   -3.76   -2.83
##   ambient Both   -3.06 0.1847 480.0   -3.42   -2.70
##   warmed Exotic -2.17 0.0995  99.0   -2.37   -1.97
##   ambient Exotic -2.09 0.1016 107.2   -2.29   -1.89
##
## 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  0.06030 0.133  71.0  0.453  0.9998
##   warmed Native - warmed          -0.04341 0.131 916.3 -0.331  1.0000
##   warmed Native - ambient          0.00178 0.160 186.6  0.011  1.0000

```

```

## warmed Native - warmed Both      1.04194 0.236 967.8  4.406  0.0003
## warmed Native - ambient Both    0.80276 0.207 323.4  3.874  0.0032
## warmed Native - warmed Exotic   -0.08615 0.104 942.7 -0.831  0.9913
## warmed Native - ambient Exotic  -0.16672 0.138 89.5 -1.205  0.9285
## ambient Native - warmed          -0.10372 0.159 176.5 -0.654  0.9980
## ambient Native - ambient         -0.05853 0.133 915.5 -0.440  0.9999
## ambient Native - warmed Both     0.98164 0.254 567.2  3.864  0.0031
## ambient Native - ambient Both    0.74246 0.185 947.9  4.020  0.0016
## ambient Native - warmed Exotic   -0.14646 0.137 84.3 -1.069  0.9615
## ambient Native - ambient Exotic  -0.22702 0.104 928.9 -2.188  0.3602
## warmed - ambient                0.04519 0.182 313.1  0.248  1.0000
## warmed - warmed Both             1.08536 0.253 965.5  4.292  0.0005
## warmed - ambient Both            0.84618 0.224 429.4  3.771  0.0046
## warmed - warmed Exotic           -0.04274 0.135 904.0 -0.316  1.0000
## warmed - ambient Exotic          -0.12330 0.163 201.3 -0.756  0.9950
## ambient - warmed Both            1.04017 0.269 644.9  3.862  0.0031
## ambient - ambient Both           0.80099 0.207 942.0  3.862  0.0030
## ambient - warmed Exotic          -0.08793 0.164 204.4 -0.537  0.9994
## ambient - ambient Exotic         -0.16850 0.139 911.7 -1.214  0.9279
## warmed Both - ambient Both       -0.23918 0.300 671.4 -0.798  0.9932
## warmed Both - warmed Exotic      -1.12810 0.239 965.2 -4.717  0.0001
## warmed Both - ambient Exotic     -1.20866 0.257 594.2 -4.705  0.0001
## ambient Both - warmed Exotic     -0.88892 0.210 342.9 -4.238  0.0008
## ambient Both - ambient Exotic    -0.96948 0.189 953.0 -5.116 <.0001
## warmed Exotic - ambient Exotic   -0.08057 0.142 103.2 -0.567  0.9992
##
## 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

```

```

## Warning: Model failed to converge with 1 negative eigenvalue: -2.0e+00

```

```

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   34 3069.9 3237.9 -1500.9   3001.9
## mod10u   37 3075.3 3258.2 -1500.7   3001.3 0.5533  3       0.907

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   13 3018.7 3082.9 -1496.3   2992.7
## mod10u    37 3075.3 3258.2 -1500.7   3001.3      0 24           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
##  3075.3  3258.2 -1500.7   3001.3      999
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -2.53360 -0.79180  0.01417  0.78897  2.23190
##
## Random effects:
## Groups   Name        Variance Std.Dev. Corr
## plot     (Intercept) 2.813e-02 0.1677057
## factor(year_factor)2 1.477e-02 0.1215421  1.00
## factor(year_factor)3 1.279e-02 0.1130714 -1.00 -1.00
## factor(year_factor)4 3.167e-03 0.0562725 -1.00 -1.00  1.00
## factor(year_factor)5 5.315e-07 0.0007290 -1.00 -1.00  1.00  1.00
## factor(year_factor)6 5.356e-07 0.0007319  1.00  1.00 -1.00 -1.00
## factor(year_factor)7 2.836e-07 0.0005325 -1.00 -1.00  1.00  1.00
## Residual             1.042e+00 1.0205500
##
## 
## 
## 
## 
## 
## -0.99
##  1.00 -0.99

```

```

## 
## Number of obs: 1036, groups: plot, 24
## 
## Fixed effects:
##                                     Estimate Std. Error      df t value
## (Intercept)                  -2.20662   0.07382 52.56873 -29.890
## stateambient                 -0.04388   0.10489 51.78804 -0.418
## growth_habit                 -1.15461   0.29144 1010.53113 -3.962
## growth_habitGraminoid        -0.05281   0.09401 1028.88866 -0.562
## growth_habitTree              -0.95159   0.59834 967.42905 -1.590
## stateambient:growth_habit    -0.02605   0.41129 1022.21240 -0.063
## stateambient:growth_habitGraminoid 0.08825   0.13245 1030.08858 0.666
## stateambient:growth_habitTree 0.27095   0.79164 975.92094 0.342
##                                     Pr(>|t|)
## (Intercept)                  < 2e-16 ***
## stateambient                 0.677
## growth_habit                 7.96e-05 ***
## growth_habitGraminoid        0.574
## growth_habitTree              0.112
## stateambient:growth_habit    0.950
## stateambient:growth_habitGraminoid 0.505
## stateambient:growth_habitTree 0.732
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation of Fixed Effects:
##          (Intr) sttmbn grwth_G grwt_T sttm:_G
## stateambint -0.704
## growth_habt -0.174  0.122
## grwth_hbtGr -0.527  0.371  0.126
## grwth_hbtTr -0.076  0.054  0.028  0.054
## sttmbnt:gr_  0.123 -0.184 -0.709 -0.089 -0.020
## sttmbnt:g_G  0.374 -0.531 -0.089 -0.710 -0.039  0.127
## sttmbnt:g_T  0.058 -0.087 -0.021 -0.041 -0.756  0.027  0.063
## 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       0.030  0.0303     1  528.01  0.0291  0.8646
## growth_habit 37.898 12.6327     3 1008.57 12.1290 8.401e-08 ***
## state:growth_habit 0.582  0.1938     3 1008.57  0.1861  0.9059
## ---
## 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

## Warning: Model failed to converge with 1 negative eigenvalue: -6.3e-01

# 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)
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)
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

mod7au <- lmer(log(relabun) ~ state + species + factor(year_factor) + (1 | plot),
  comp_umbs_spp, REML = FALSE)
mod7bu <- lmer(log(relabun) ~ state * factor(year_factor) + species + (1 | plot),
  comp_umbs_spp, REML = FALSE)
mod7cu <- lmer(log(relabun) ~ state + species + factor(year_factor) + insecticide +
  (1 | plot), comp_umbs_spp, REML = FALSE)
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

## Warning: Model failed to converge with 1 negative eigenvalue: -2.0e+00

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

## Warning: Model failed to converge with 1 negative eigenvalue: -6.3e-01

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 25  0.714
## mod7cu    1.9 26  0.275
## mod7bu    8.3 31  0.011
## mod5u    34.8 5  <0.001
## mod3u    36.7 6  <0.001
## mod2u    39.3 8  <0.001
## mod6u    39.5 8  <0.001
## mod1u    40.2 9  <0.001
## mod7u    59.3 46 <0.001
## mod13u   72.2 16 <0.001
## mod9au   264.9 13 <0.001
## mod11au  277.2 13 <0.001
## mod9u    316.7 34 <0.001
## mod8u    321.4 37 <0.001
## mod11u   330.4 34 <0.001
## mod10u   336.2 37 <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
## 2740.6   2864.2 -1345.3   2690.6     1011
##
## Scaled residuals:
##       Min     1Q Median     3Q    Max
## -3.2110 -0.7123  0.0433  0.7239  2.4807
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   plot     (Intercept) 0.003751 0.06124
##   Residual           0.782614 0.88466
## Number of obs: 1036, groups: plot, 24
##
## Fixed effects:
##             Estimate Std. Error    df t value Pr(>|t|)    
## (Intercept) -3.11389  0.34894 982.89721 -8.924 < 2e-16 ***
## stateambient -0.02130  0.06098 22.72192 -0.349 0.730152
## speciesAnsp  -0.49198  0.40985 1021.29094 -1.200 0.230259
## speciesApan  0.70839  0.45989 1029.38094  1.540 0.123787
## speciesAssp  0.12999  0.36835  987.91990  0.353 0.724246
## speciesAsun  0.14286  0.61371 1031.56236  0.233 0.815975
## speciesCape  0.71522  0.34830 1011.15876  2.053 0.040285 *
## speciesCest  1.69374  0.34451 1019.18676  4.916 1.03e-06 ***
## speciesDasp  0.95677  0.34576 1018.86770  2.767 0.005757 ** 
## speciesFrve  0.45691  0.37668  987.23255  1.213 0.225422
## speciesHisp -0.47353  0.38729 1032.69936 -1.223 0.221732
## speciesHype -0.15921  0.35317 1027.37955 -0.451 0.652220
## speciesPosp  0.87654  0.34465 1019.88336  2.543 0.011129 *  
## speciesPtaq  1.19656  0.34774 1024.46360  3.441 0.000603 ***
## speciesRuac  0.58520  0.34698 1025.14338  1.687 0.091993 .
## speciesSosp  0.33550  0.38381 1026.29847  0.874 0.382253
## speciesSyla -0.01776  0.42355 1027.30567 -0.042 0.966561
## factor(year_factor)2 -0.24679  0.10603 1014.91542 -2.327 0.020136 *
## factor(year_factor)3  0.12481  0.10508 1017.42936  1.188 0.235184
## factor(year_factor)4  0.09849  0.10552 1017.34710  0.933 0.350853
## factor(year_factor)5 -0.03859  0.10407 1019.10257 -0.371 0.710849
## factor(year_factor)6  0.01625  0.10292 1019.10813  0.158 0.874562
## factor(year_factor)7 -0.04883  0.10728 1015.93590 -0.455 0.649060
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 23 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)           if you need it
```

```
anova(mod7au)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## state                      0.10  0.0954     1    22.72  0.1219 0.73015
## species                   321.15 21.4099    15 1010.12 27.3569 < 2e-16 ***
## factor(year_factor)   12.65  2.1079     6 1017.27  2.6935 0.01341 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```