warmXtrophic Project: CN Analyses

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Load in packages & data

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

# Load packages
library(tidyverse)
library(bbmle)
library(lmerTest)

# Set working directory to Google Drive
setwd("/Volumes/GoogleDrive/Shared drives/SpaCE_Lab_warmXtrophic/data/")

# Read in data
cn <- read.csv("L1/final_CN_L1.csv")

# create dataframes for kbs and umbs
cn_kbs <- subset(cn, site == "kbs")
cn_umbs <- subset(cn, site == "umbs")
```

Check what species are measured at each site

```
unique(cn_kbs$species)
```

```
## [1] "Soca"
```

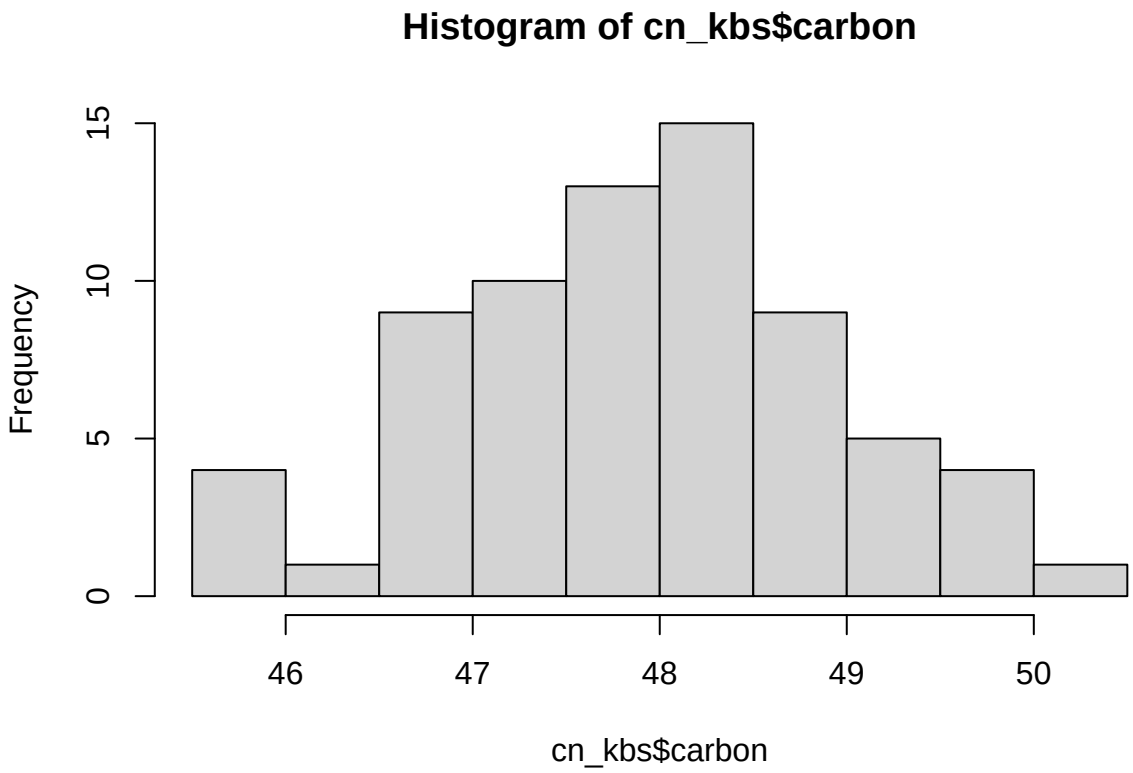
```
unique(cn_umbs$species)
```

```
## [1] "Cest" "Popr"
```

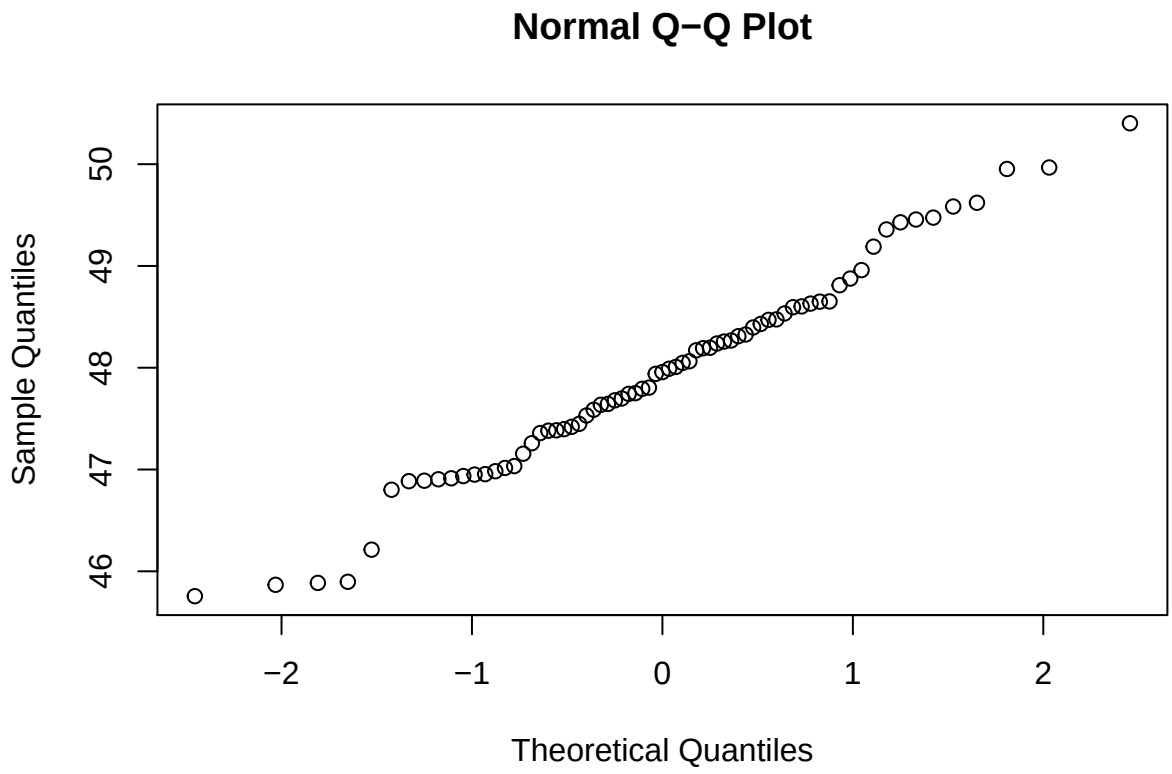
```
# separate dataframes for each species
cn_cest_umbs <- subset(cn_umbs, species == "Cest")
cn_popr_umbs <- subset(cn_umbs, species == "Popr")
```

Data exploration: KBS Soca

```
hist(cn_kbs$carbon)
```




```
qqnorm(cn_kbs$carbon)
```

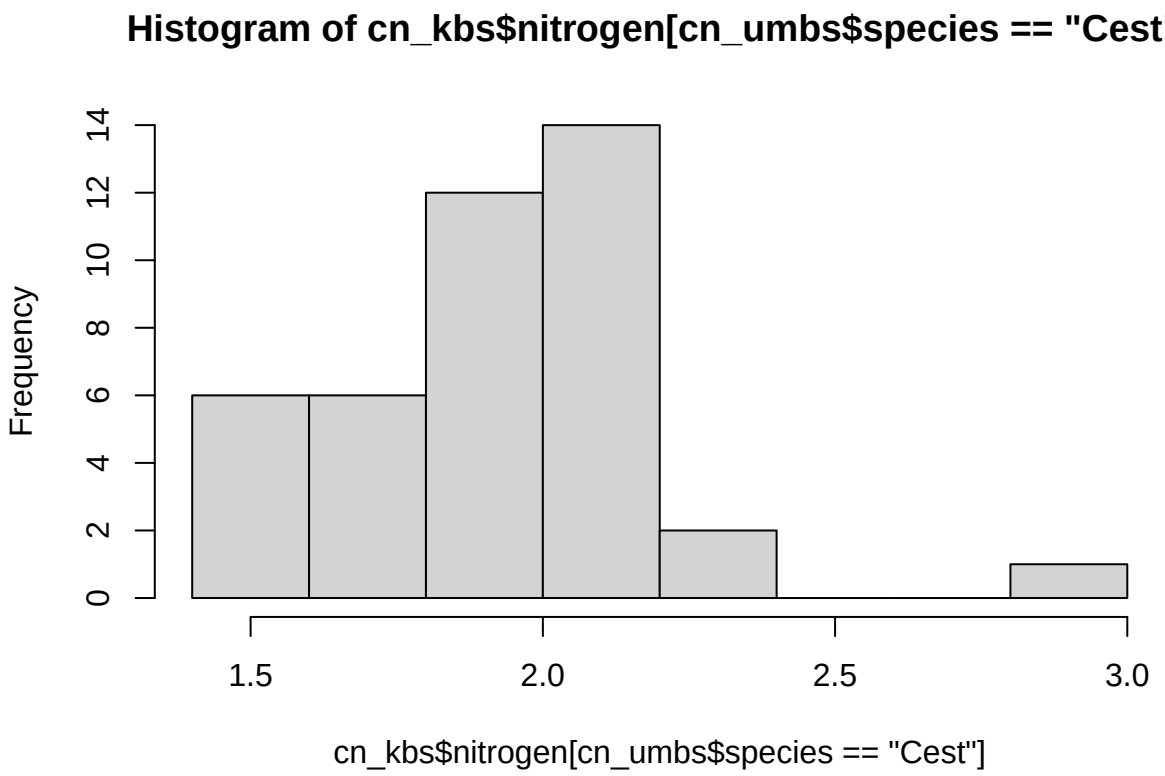


```r
shapiro.test(cn_kbs$carbon)
```

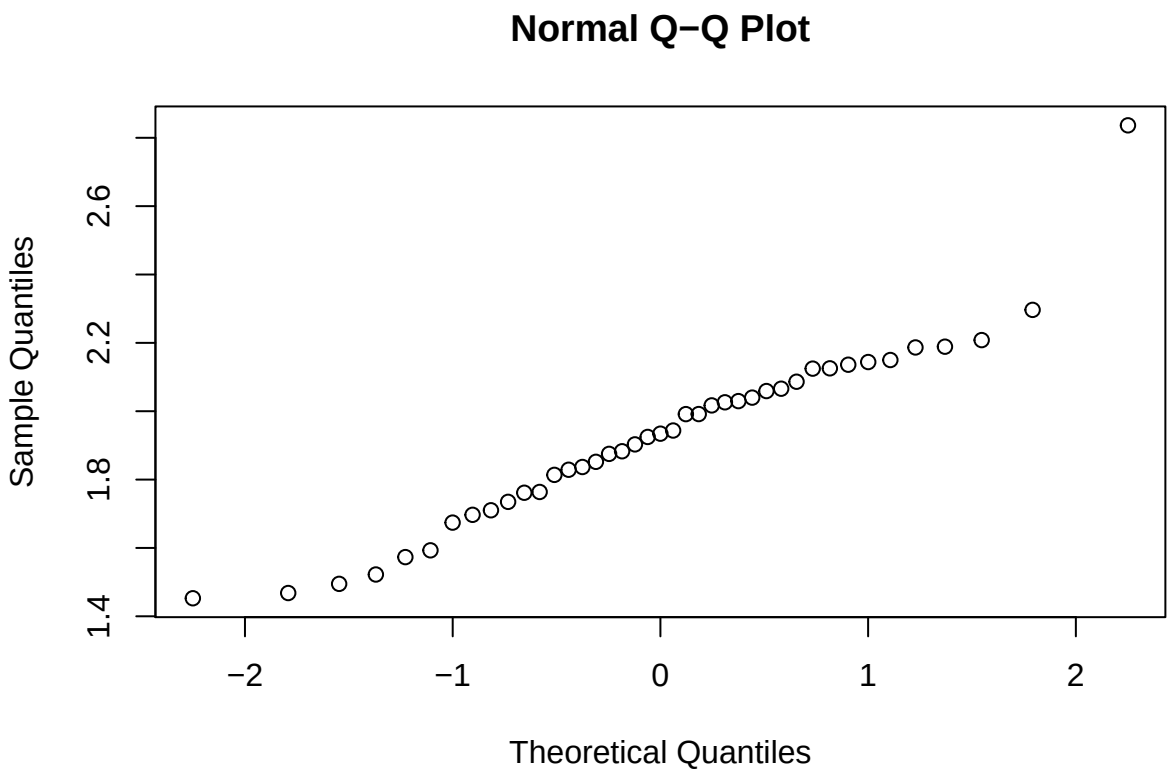
```
##
##  Shapiro-Wilk normality test
##
## data:  cn_kbs$carbon
## W = 0.98512, p-value = 0.5658
```

Data exploration: UMBS Cest

```r
hist(cn_kbs$nitrogen[cn_umbs$species == "Cest"])
```




```r
qqnorm(cn_kbs$nitrogen[cn_umbs$species == "Cest"])
```

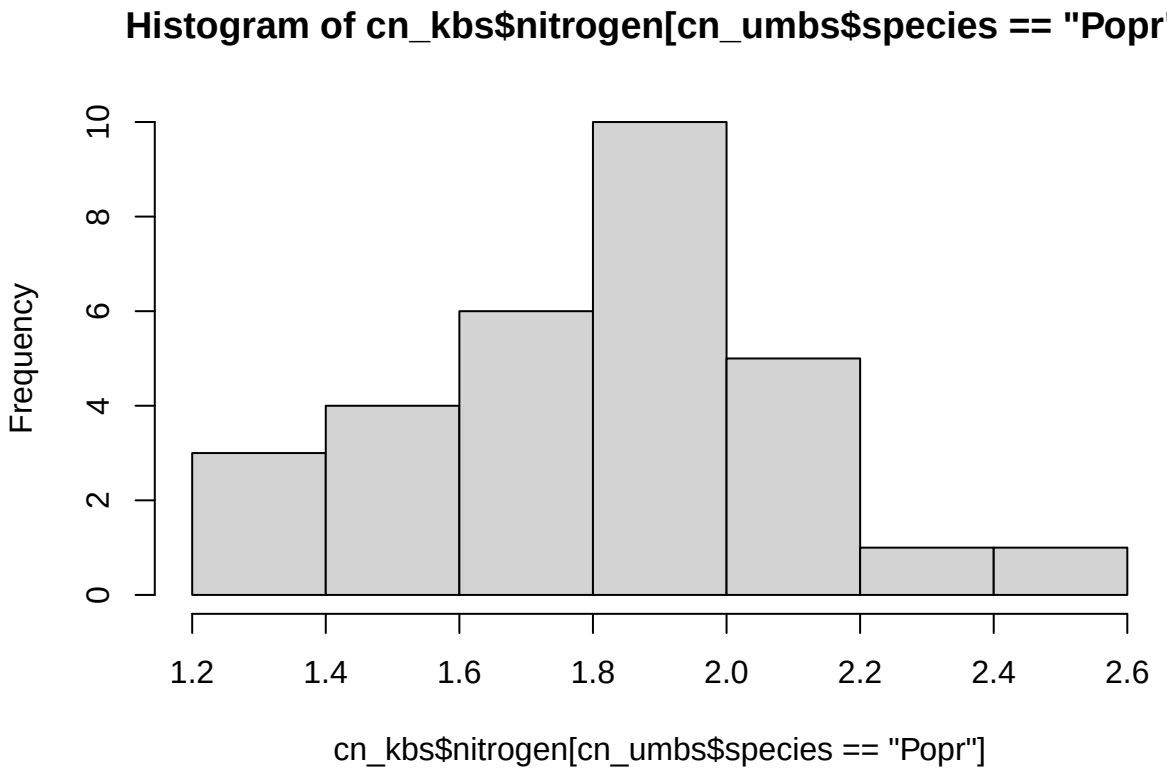



```
shapiro.test(cn_kbs$nitrogen[cn_umbs$species == "Cest"])
```

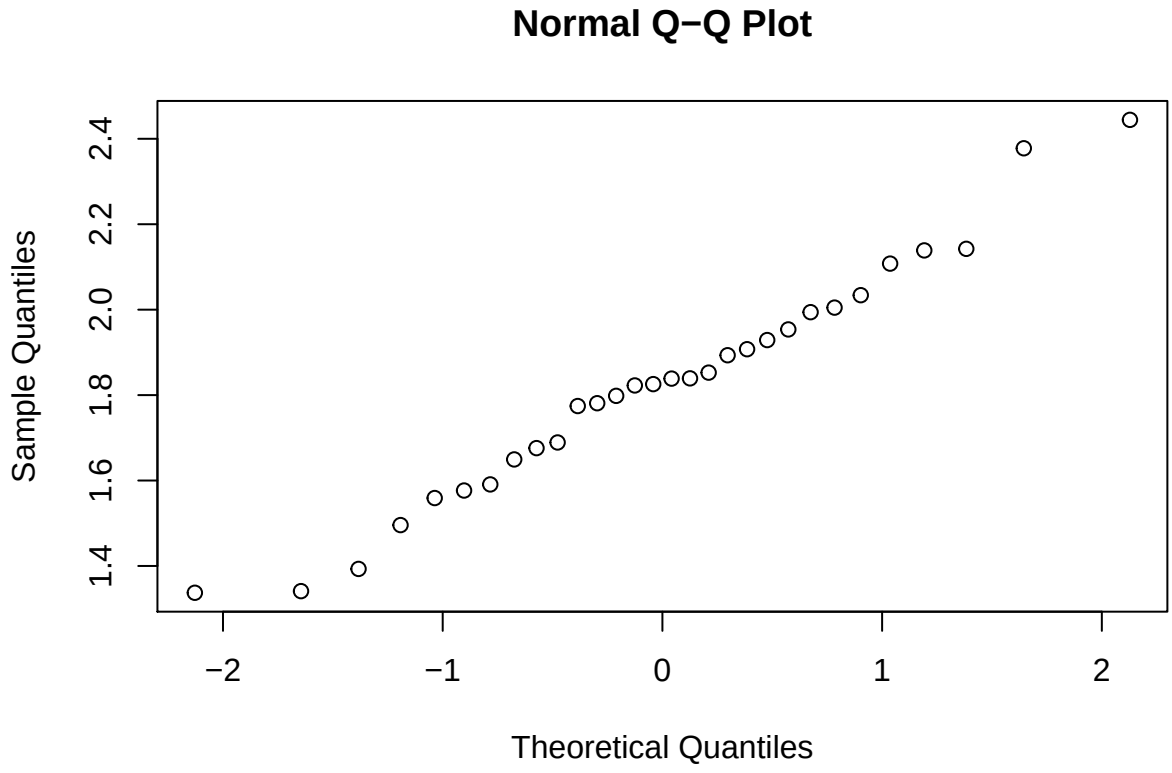
```
##
##  Shapiro-Wilk normality test
##
## data:  cn_kbs$nitrogen[cn_umbs$species == "Cest"]
## W = 0.94488, p-value = 0.04634
```

Data exploration: UMBS Popr

```
hist(cn_kbs$nitrogen[cn_umbs$species == "Popr"])
```




```
qqnorm(cn_kbs$nitrogen[cn_umbs$species == "Popr"])
```




```
shapiro.test(cn_kbs$nitrogen[cn_umbs$species == "Popr"])
```

```
##
```

```
##  Shapiro-Wilk normality test
##
## data:  cn_kbs$nitrogen[cn_umbs$species == "Popr"]
## W = 0.97752, p-value = 0.7566
```

Model comparison: KBS Soca

```
# carbon
m1a <- lm(carbon ~ state, data = cn_kbs)
m1b <- lm(carbon ~ state + insecticide, data = cn_kbs)
m1c <- lmer(carbon ~ state + (1 | plot), data = cn_kbs)
m1d <- lmer(carbon ~ state + insecticide + (1 | plot), data = cn_kbs)
AICctab(m1a, m1b, m1c, m1d, weights = T)  # m1a better fit
```

```
##     dAICc df weight
## m1a 0.0   3  0.7098
## m1b 2.2   4  0.2332
## m1c 5.4   4  0.0473
## m1d 8.6   5  0.0097
```

```
summary(m1a)
```

```
##
## Call:
## lm(formula = carbon ~ state, data = cn_kbs)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.26732 -0.72064  0.04298  0.55648  2.24858
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  47.7409     0.1673  285.28   <2e-16 ***
## statewarmed   0.4125     0.2383    1.73    0.088 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.004 on 69 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.04159,    Adjusted R-squared:  0.0277
## F-statistic: 2.995 on 1 and 69 DF,  p-value: 0.08802
```

```
# nitrogen
m2a <- lm(nitrogen ~ state, data = cn_kbs)
m2b <- lm(nitrogen ~ state + insecticide, data = cn_kbs)
m2c <- lmer(nitrogen ~ state + (1 | plot), data = cn_kbs)
m2d <- lmer(nitrogen ~ state + insecticide + (1 | plot), data = cn_kbs)
AICctab(m2a, m2b, m2c, m2d, weights = T)  # m2b slightly better fit, but going with m2a as its the simp
```

```
##     dAICc df weight
## m2b 0.0   4  0.5138
## m2a 0.2   3  0.4574
## m2c 6.0   4  0.0251
## m2d 9.9   5  0.0037
```

```
summary(m2a)
```

```
##
## Call:
## lm(formula = nitrogen ~ state, data = cn_kbs)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.47449 -0.17566 -0.02393  0.16347  1.02461
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.95273    0.04392  44.458   <2e-16 ***
## statewarmed -0.14094    0.06256  -2.253   0.0274 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2635 on 69 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.06852,    Adjusted R-squared:  0.05502
## F-statistic: 5.076 on 1 and 69 DF,  p-value: 0.02745
```

Model comparison: UMBS Cest

```
# carbon
m3a <- lm(carbon ~ state, data = cn_cest_umbs)
m3b <- lm(carbon ~ state + insecticide, data = cn_cest_umbs)
m3c <- lmer(carbon ~ state + (1 | plot), data = cn_cest_umbs)
m3d <- lmer(carbon ~ state + insecticide + (1 | plot), data = cn_cest_umbs)
AICctab(m3a, m3b, m3c, m3d, weights = T)  # m3a better fit
```

```
##     dAICc df weight
## m3a 0.0   3  0.48
## m3c 1.4   4  0.23
## m3b 2.1   4  0.17
## m3d 2.7   5  0.12
```

```
summary(m3a)
```

```
##
## Call:
## lm(formula = carbon ~ state, data = cn_cest_umbs)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.9371  -1.1730   0.0917   1.1498   5.1632
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  46.1235     0.4067 113.408   <2e-16 ***
## statewarmed   0.5035     0.5710   0.882    0.381
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.371 on 67 degrees of freedom
## Multiple R-squared:  0.01147,    Adjusted R-squared:  -0.003283
## F-statistic: 0.7775 on 1 and 67 DF,  p-value: 0.3811
```

```
# nitrogen
m4a <- lm(nitrogen ~ state, data = cn_cest_umbs)
```

```
m4b <- lm(nitrogen ~ state + insecticide, data = cn_cest_umbs)
m4c <- lmer(nitrogen ~ state + (1 | plot), data = cn_cest_umbs)
m4d <- lmer(nitrogen ~ state + insecticide + (1 | plot), data = cn_cest_umbs)
AICctab(m4a, m4b, m4c, m4d, weights = T)  # m4a better fit
```

```
##     dAICc df weight
## m4a  0.0  3  0.7383
## m4b  2.1  4  0.2528
## m4c  9.0  4  0.0082
## m4d 14.1  5  <0.001
```

```
summary(m4a)
```

```
##
## Call:
## lm(formula = nitrogen ~ state, data = cn_cest_umbs)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5740 -0.1970 -0.1005  0.1940  1.4726
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.69764    0.05935  28.605   <2e-16 ***
## statewarmed  0.18473    0.08333   2.217     0.03 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.346 on 67 degrees of freedom
## Multiple R-squared:  0.06834,    Adjusted R-squared:  0.05444
## F-statistic: 4.915 on 1 and 67 DF,  p-value: 0.03003
```

Model comparison: UMBS Popr

```
# carbon
m5a <- lm(carbon ~ state, data = cn_popr_umbs)
m5b <- lm(carbon ~ state + insecticide, data = cn_popr_umbs)
m5c <- lmer(carbon ~ state + (1 | plot), data = cn_popr_umbs)
m5d <- lmer(carbon ~ state + insecticide + (1 | plot), data = cn_popr_umbs)
AICctab(m5a, m5b, m5c, m5d, weights = T)  # m5a better fit
```

```
##     dAICc df weight
## m5a  0.0  3  0.7260
## m5b  2.2  4  0.2365
## m5c  6.2  4  0.0328
## m5d 10.1  5  0.0047
```

```
summary(m5a)
```

```
##
## Call:
## lm(formula = carbon ~ state, data = cn_popr_umbs)
##
## Residuals:
```

```
##     Min      1Q  Median      3Q     Max
## -1.9645 -0.2155  0.0791  0.3955  1.5634
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  43.7693     0.1105 395.993   <2e-16 ***
## statewarmed   0.1915     0.1620   1.182    0.242
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6154 on 56 degrees of freedom
## Multiple R-squared:  0.02435,    Adjusted R-squared:  0.006928
## F-statistic: 1.398 on 1 and 56 DF,  p-value: 0.2421
```

```
# nitrogen
m6a <- lm(nitrogen ~ state, data = cn_popr_umbs)
m6b <- lm(nitrogen ~ state + insecticide, data = cn_popr_umbs)
m6c <- lmer(nitrogen ~ state + (1 | plot), data = cn_popr_umbs)
m6d <- lmer(nitrogen ~ state + insecticide + (1 | plot), data = cn_popr_umbs)
AICctab(m6a, m6b, m6c, m6d, weights = T)  # m6a better fit
```

```
##     dAICc df weight
## m6a  0.0  3  0.7542
## m6b  2.3  4  0.2376
## m6c  9.1  4  0.0079
## m6d 15.4  5  <0.001
```

```
summary(m6a)
```

```
##
## Call:
## lm(formula = nitrogen ~ state, data = cn_popr_umbs)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.36742 -0.11669 -0.00407  0.07251  0.52918
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.19002    0.03227   36.88  < 2e-16 ***
## statewarmed -0.22326    0.04730   -4.72 1.62e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1797 on 56 degrees of freedom
## Multiple R-squared:  0.2846, Adjusted R-squared:  0.2719
## F-statistic: 22.28 on 1 and 56 DF,  p-value: 1.615e-05
```