LTER_metacom_hellenger_prelim.R

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```r
rm(list = ls())

# Check for and install required packages
for (package in c('tidyverse', 'PerformanceAnalytics', 'ggthemes', 'vegan',
                  'gridExtra', 'grid', 'viridis', 'lme4', 'lmerTest', 'car',
                  'ggpubr')) {
  if (!require(package, character.only = T, quietly = T)) {
    install.packages(package)
    library(package, character.only = T)
  }
}

theme_set(theme_classic())

# 1. IMPORT DATA SETS --------------------------------------------------------
-----
df <- read_csv("output/metacom_data_for_models_20190311.csv")

length(unique(df$l3_filename)) #33
```

```
## [1] 33
```

```r
colnames(df)
```

```
##  [1] "X1"                  "dataset_id"
##  [3] "l3_filename"         "site"
##  [5] "body.size"           "dispersal.habit"
##  [7] "trophic.group"       "biome"
##  [9] "organism_group"      "initial.year"
## [11] "study.length"        "n.years"
## [13] "n.plots"             "n.taxa"
## [15] "organism"            "lat"
## [17] "lon"                 "ndvi_temporal_sd"
## [19] "temp_temporal_sd"    "env_heterogeneity"
## [21] "dataset_google_id"   "start_year"
## [23] "end_year"            "n_years_observed"
## [25] "study_duration"      "organism_count_type"
## [27] "variability_type"    "standardization_method"
## [29] "metric"              "metric_value"
## [31] "messages"
```

```r
df <- df %>%
  select(-c(X1, dataset_id, l3_filename, start_year, end_year, n_years_observ
```

```
ed,
              study_duration, messages, dataset_google_id))

#combine micro and meso (only two micro, not enough to parse out), then chang
e
# terminology to large vs small body organisms.
# NOTE: For now considering molluscs active dispersers since they are "mobile
"
df <- df %>%
  mutate(body.size = replace(body.size, body.size == "micro", "meso")) %>%
  mutate(body.size = replace(body.size, body.size == "macro", "large")) %>%
  mutate(body.size = replace(body.size, body.size == "meso", "small")) %>%
  mutate(dispersal.habit = replace(dispersal.habit,
                                   dispersal.habit == "need to look at taxa",
"active"))

# Subset data by standardization type
q.0 <- filter(df, standardization_method == "q_order_0")
h   <- filter(df, standardization_method == "h")
hT  <- filter(df, standardization_method == "hT")

#subset data for wang & Loreau aggregate metric
agg <- filter(df, variability_type == "agg")


# Spread to wide format
q0.wide <- spread(q.0, metric, metric_value)
h.wide <- spread(h, metric, metric_value)
hT.wide <- spread(hT, metric, metric_value)
agg.wide <- spread(agg, metric, metric_value)

length(q0.wide$site)

## [1] 27

length(h.wide$site)

## [1] 27

length(hT.wide$site)

## [1] 27

length(agg.wide$site)

## [1] 27

# Visiualize correlations between continuous variables
var.h <- h.wide %>%
  na.omit()
```
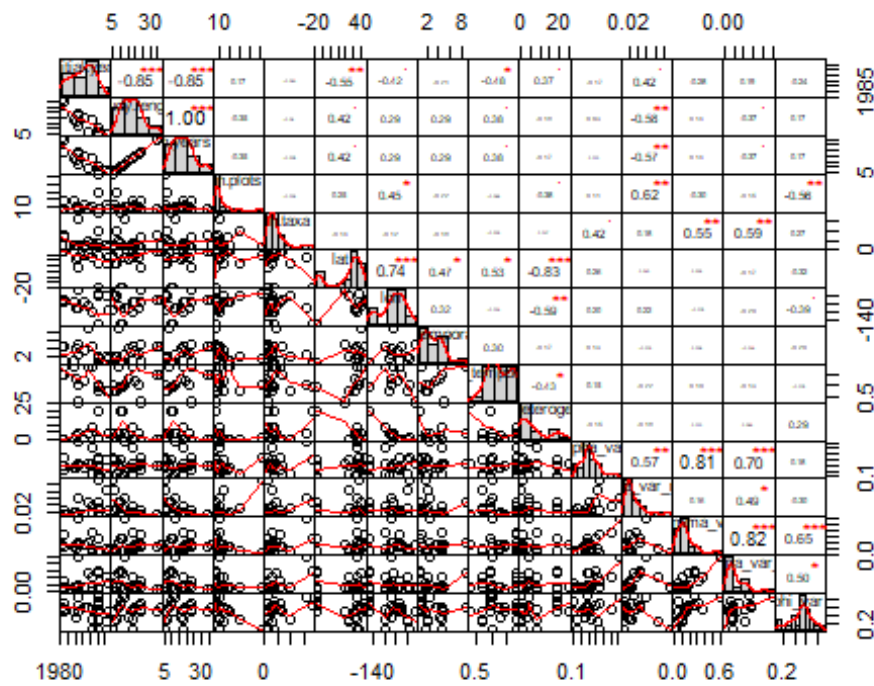
```
var.h %>% select_if(is.numeric) %>%
  chart.Correlation(., histogram = TRUE, pch = "+")
```
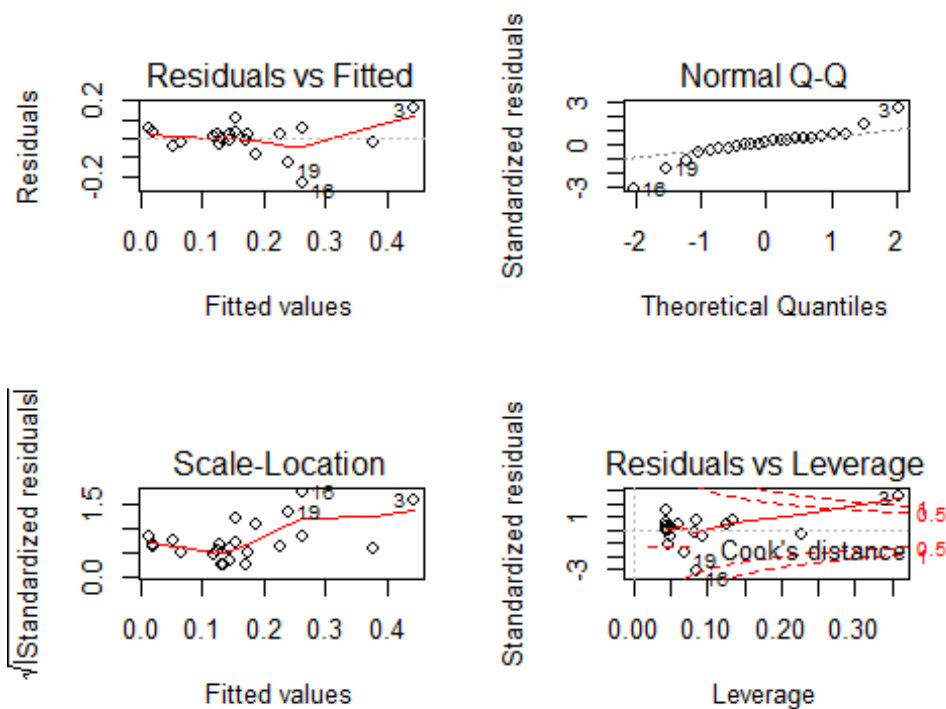
```
# initial models ------------------------------------------------------------
-----
# For now use hellenger transformed metrics of community turnover
# (based on relative abundances) until we know which data sets have measures
of abundance

# Relative importance of local and spatial variability for regional variabili
ty
lm_gamma_alpha <- lm(gamma_var ~ alpha_var,
                     data = h.wide)
par(mfrow = c(2,2))
plot(lm_gamma_alpha)
```
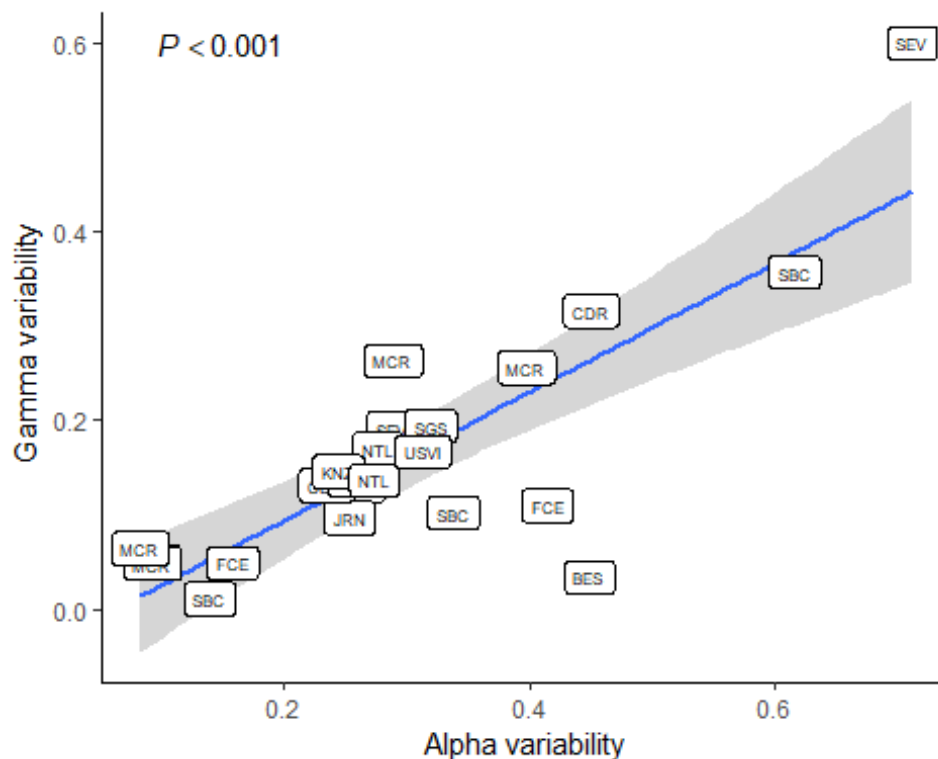


```
summary(lm_gamma_alpha)

##
## Call:
## lm(formula = gamma_var ~ alpha_var, data = h.wide)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.23037 -0.01840  0.01394  0.02872  0.15724
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.04380    0.03643  -1.202    0.243
## alpha_var    0.68516    0.10758   6.369 2.58e-06 ***
```
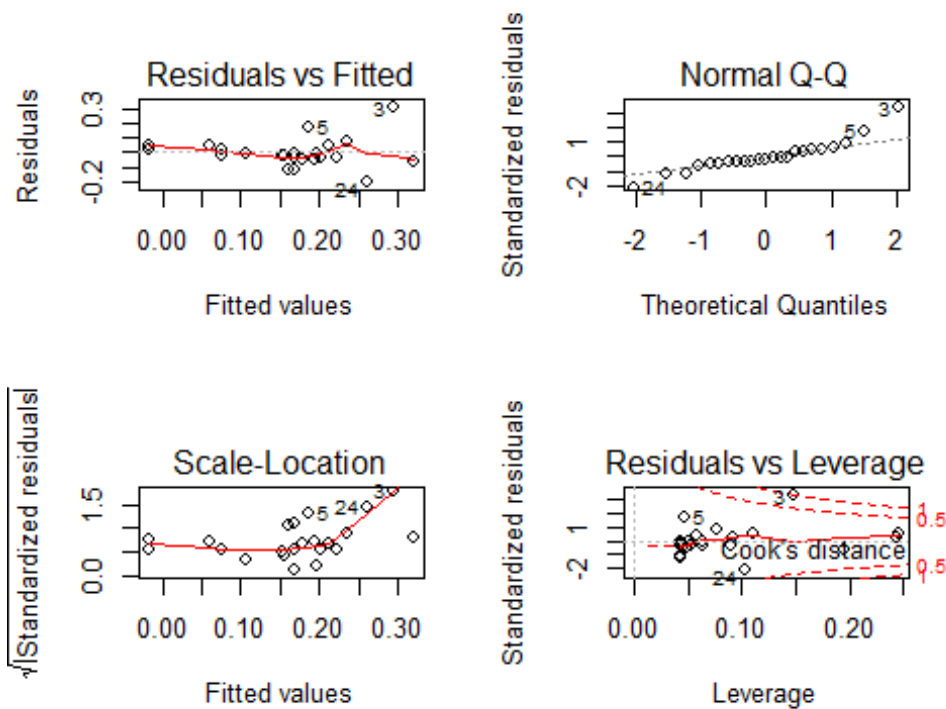
4

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07824 on 21 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.6589, Adjusted R-squared:  0.6427
## F-statistic: 40.57 on 1 and 21 DF,  p-value: 2.584e-06
```

```r
(alpha_vs_gamma_var <- ggplot(aes(x = alpha_var, y = gamma_var, label = site)
,
                              data = h.wide) +
    stat_smooth(method = "lm", se = T, size = 1) +
    geom_point(size = 2, alpha = 0.7) +
    geom_label(size = 2) +
    xlab("Alpha variability") +
    ylab(expression(paste("Gamma variability"))) +
    annotate("text", x = 0.15, y = 0.6, label = "italic(P) < 0.001", parse =
TRUE)
)
```



```r
lm_gamma_phi <- lm(gamma_var ~ phi_var, data = h.wide)
par(mfrow = c(2,2))
plot(lm_gamma_phi)
```

5

```r
summary(lm_gamma_phi)

##
## Call:
## lm(formula = gamma_var ~ phi_var, data = h.wide)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.19757 -0.03887 -0.01771  0.03534  0.30713
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.04682    0.05725  -0.818 0.422651
## phi_var      0.40315    0.10190   3.956 0.000721 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1014 on 21 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.427,  Adjusted R-squared:  0.3998
## F-statistic: 15.65 on 1 and 21 DF,  p-value: 0.0007212

(phi_vs_gamma_var <- ggplot(aes(x = phi_var, y = gamma_var, label = site),
                            data = h.wide) +
    stat_smooth(method = "lm", se = T, size = 1) +
    #geom_point(size = 2, alpha = 0.6) +
    geom_label(size = 2) +
```
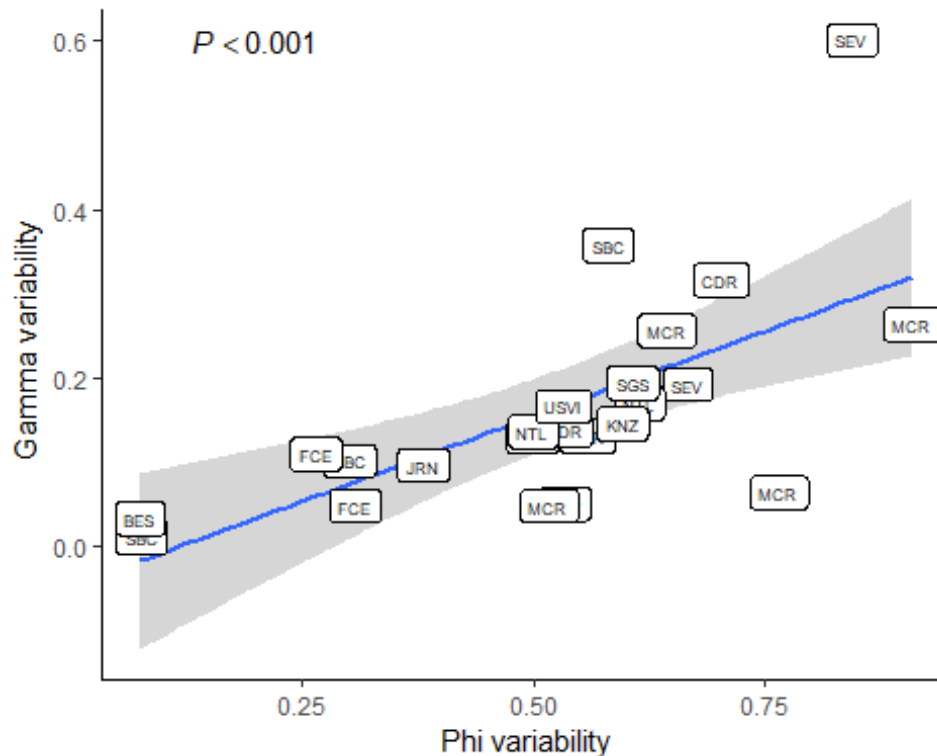
```
    xlab("Phi variability") +
    ylab(expression(paste("Gamma variability"))) +
    annotate("text", x = 0.2, y = 0.6, label = "italic(P) < 0.001", parse = T
RUE)
)
```

Warning: Removed 4 rows containing non-finite values (stat_smooth).

Warning: Removed 4 rows containing missing values (geom_label).


```
jpeg(file = "metacommunity_components_h.jpeg", width = 6.75, height = 3.25, u
nits = 'in', res = 1000)
ggarrange(alpha_vs_gamma_var, phi_vs_gamma_var,
          ncol = 2, nrow = 1)

dev.off()
```

png
2

```
# How do variability component differ with metacommunity features
# visualize differences for metacommunity factors, by biome.

# Currently only 2 data sets each for freshwater and marine small body organi
sms.
# collaps marine and freshwater into single "aquatic" biome to increase sampl
e
# size for analysis

h.wide$biome2 <- "terrestrial"
h.wide[h.wide$biome == "freshwater" | h.wide$biome == "marine", ]$biome2 <- "
aquatic"


(phi_size_biome <- ggplot(h.wide, aes(x = body.size, y = phi_var,
                                      colour = body.size, group = body.size))
+
    geom_boxplot() +
    facet_grid(. ~ biome2) +
    geom_jitter(shape = 16, position = position_jitter(0.2)) +
    theme_bw()+
    theme(legend.position = "none") +
    ggsave("body.size_by_biome_phi.jpeg"))
## Saving 5 x 4 in image
```
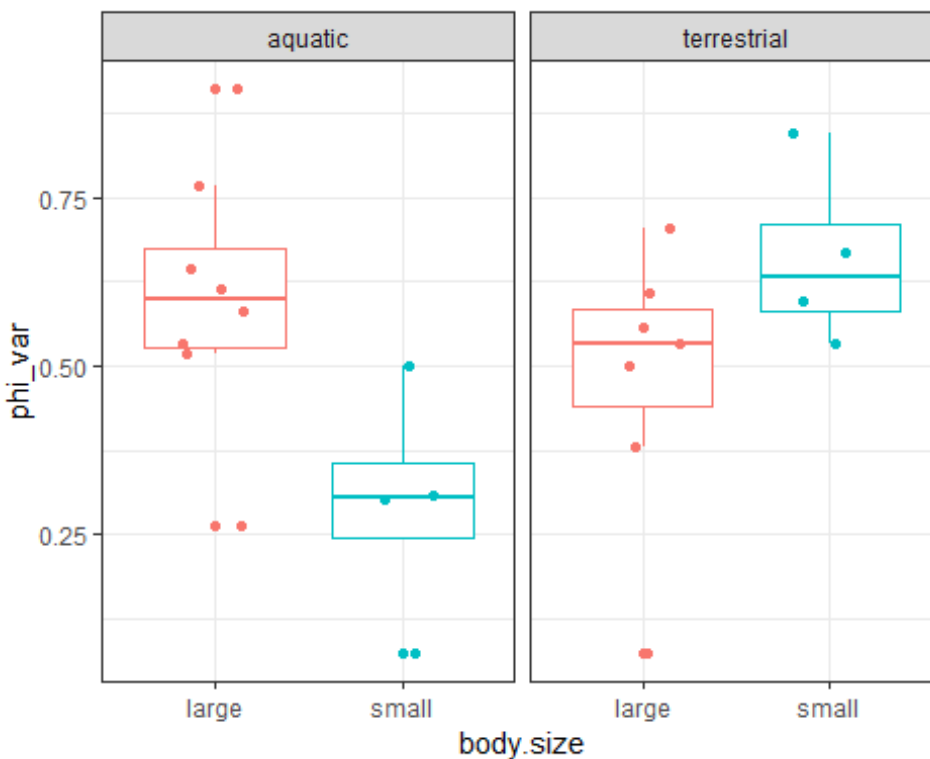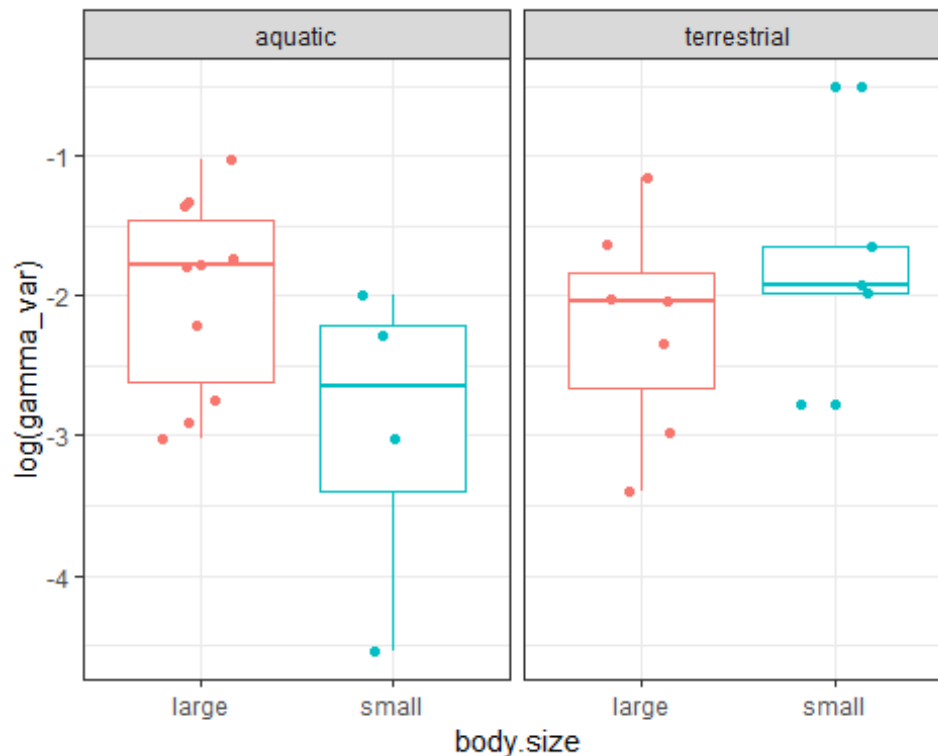
```
(gam_size_biome <- ggplot(h.wide, aes(x = body.size, y = log(gamma_var),
                                        colour = body.size, group = body.size))
+
    geom_boxplot() +
    facet_grid(. ~ biome2) +
    geom_jitter(shape = 16, position = position_jitter(0.2)) +
    theme_bw()+
    theme(legend.position = "none") +
    ggsave("body.size_by_biome_gamma.jpeg"))
```

Saving 5 x 4 in image


```
(alpha_size_biome <- ggplot(h.wide, aes(x = body.size, y = log(alpha_var),
                                          colour = body.size, group = body.size
)) +
    geom_boxplot() +
    facet_grid(. ~ biome2) +
    geom_jitter(shape = 16, position = position_jitter(0.2)) +
    theme_bw() +
    theme(legend.position = "none") +
    ggsave("body.size_by_biome_alpha.jpeg"))
```

Saving 5 x 4 in image
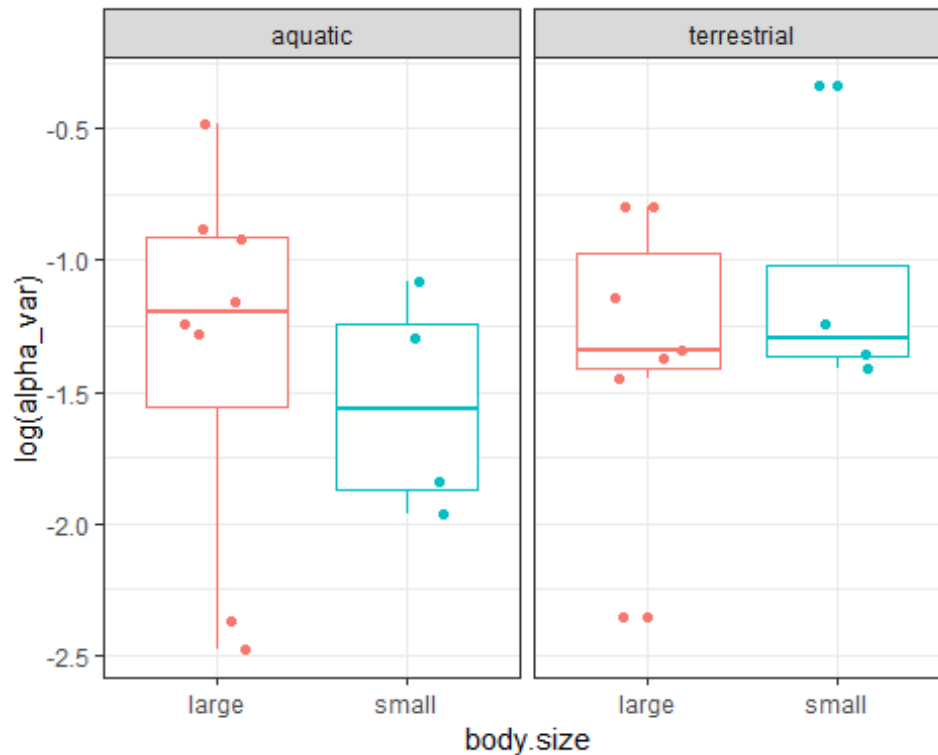
```
jpeg(file = "bodysize_biome_h.jpeg", width = 6.5, height = 5, units = 'in', r
es = 1000)
ggarrange(gam_size_biome, alpha_size_biome, phi_size_biome,
          ncol = 2, nrow = 2, common.legend = F)

dev.off()

## png
##    2

# Test above patterns with mixed model. Random effect for organism type neste
d within sites
lmer.model1 <- lmer(phi_var ~ log(n.plots) + biome2 * body.size + (1 | site/o
rganism_group),
                    data = h.wide)
summary(lmer.model1)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## phi_var ~ log(n.plots) + biome2 * body.size + (1 | site/organism_group)
##    Data: h.wide
##
## REML criterion at convergence: -8.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```
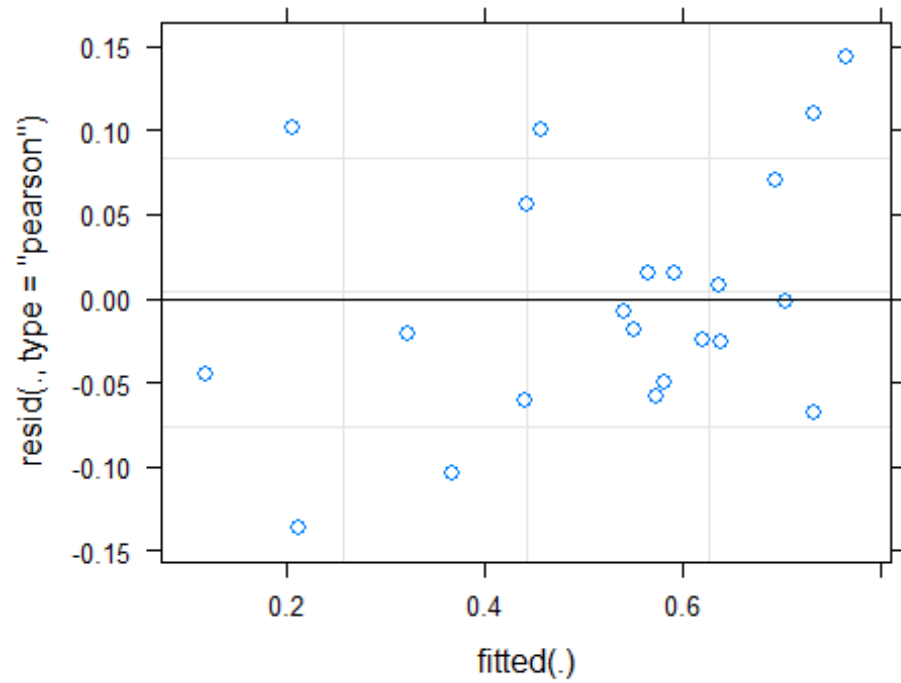
```
## -1.2658 -0.4509 -0.1218  0.4257  1.3345
##
## Random effects:
##  Groups               Name        Variance Std.Dev.
##  organism_group:site (Intercept) 0.01102  0.1050
##  site                (Intercept) 0.00000  0.0000
##  Residual                        0.01168  0.1081
## Number of obs: 22, groups:  organism_group:site, 20; site, 12
##
## Fixed effects:
##                                   Estimate Std. Error       df t value
## (Intercept)                        0.97431    0.12232 15.41856   7.965
## log(n.plots)                      -0.19256    0.05719 14.12636  -3.367
## biome2terrestrial                 -0.05180    0.08871 15.29871  -0.584
## body.sizesmall                    -0.20947    0.09676 16.48976  -2.165
## biome2terrestrial:body.sizesmall  0.42388    0.14124 14.44925   3.001
##                                   Pr(>|t|)
## (Intercept)                       7.55e-07 ***
## log(n.plots)                       0.00455 **
## biome2terrestrial                  0.56776
## body.sizesmall                     0.04539 *
## biome2terrestrial:body.sizesmall   0.00926 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) lg(n.) bm2trr bdy.sz
## log(n.plts) -0.900
## bim2trrstrl  0.023 -0.316
## body.szsmll  0.031 -0.301  0.426
## bm2trrstr:.  0.036  0.143 -0.610 -0.666

anova(lmer.model1)

## Type III Analysis of Variance Table with Satterthwaite's method
##                    Sum Sq  Mean Sq NumDF  DenDF F value    Pr(>F)
## log(n.plots)     0.132443 0.132443     1 14.126 11.3381 0.004553 **
## biome2           0.057520 0.057520     1 14.420  4.9242 0.042996 *
## body.size        0.000014 0.000014     1 14.660  0.0012 0.973232
## biome2:body.size 0.105204 0.105204     1 14.449  9.0063 0.009260 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#checking assumptions
plot(lmer.model1)
```
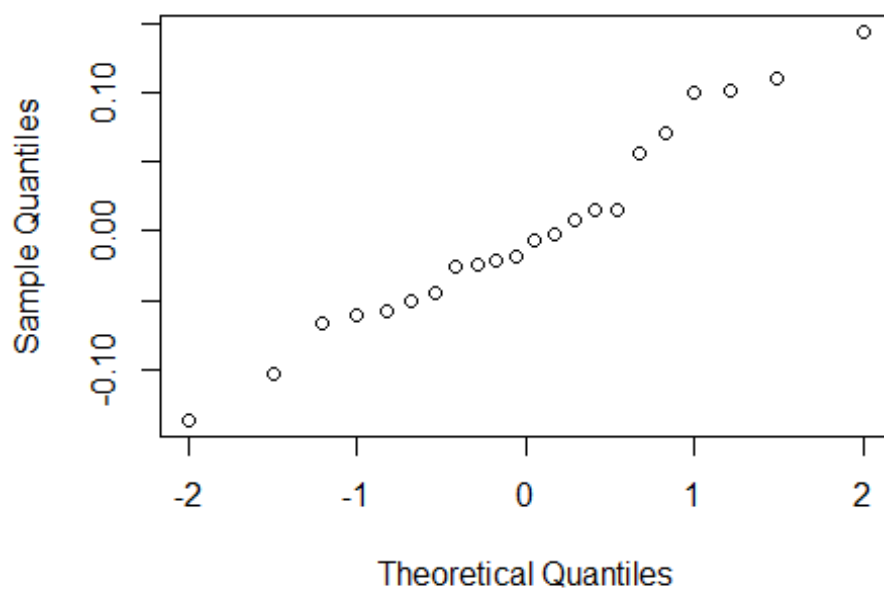
```
qqnorm(resid(lmer.model1))
```

Normal Q-Q Plot
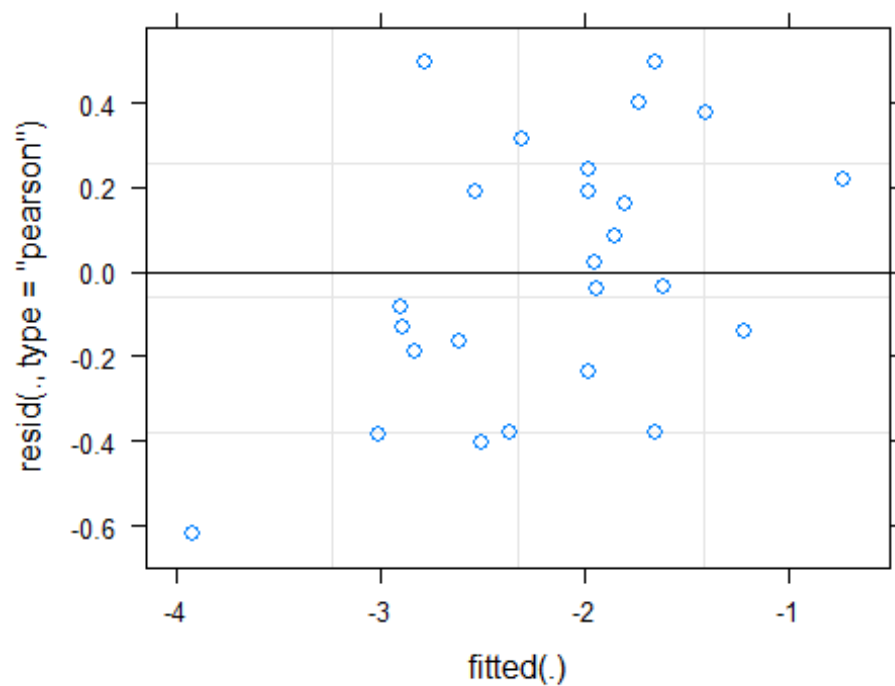
```
lmer.model2 <- lmer(log(gamma_var) ~ log(n.taxa) + biome2 * body.size + (1 |
site/organism_group),
                    data = h.wide)
summary(lmer.model2)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## log(gamma_var) ~ log(n.taxa) + biome2 * body.size + (1 | site/organism_gro
up)
##    Data: h.wide
##
## REML criterion at convergence: 53
##
## Scaled residuals:
##      Min      1Q  Median      3Q     Max
## -1.29130 -0.38779 -0.07429  0.45682  1.03504
##
## Random effects:
##  Groups               Name          Variance  Std.Dev.
##  organism_group:site (Intercept) 3.137e-01 5.601e-01
##  site                (Intercept) 4.567e-17 6.758e-09
##  Residual                        2.314e-01 4.811e-01
## Number of obs: 25, groups:  organism_group:site, 22; site, 13
##
## Fixed effects:
##                                   Estimate Std. Error      df t value
## (Intercept)                        -3.9968     0.7461 19.6640  -5.357
## log(n.taxa)                         0.5001     0.1761 19.1906   2.840
## biome2terrestrial                  -0.2363     0.4050 14.8856  -0.583
## body.sizesmall                     -1.2137     0.4502 17.2632  -2.696
## biome2terrestrial:body.sizesmall    1.5898     0.6553 15.5685   2.426
##                                   Pr(>|t|)
## (Intercept)                       3.22e-05 ***
## log(n.taxa)                         0.0104 *
## biome2terrestrial                   0.5684
## body.sizesmall                      0.0152 *
## biome2terrestrial:body.sizesmall    0.0278 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) lg(n.) bm2trr bdy.sz
## log(n.taxa) -0.946
## bim2trrstrl -0.292  0.103
## body.szsmll  0.008 -0.193  0.303
## bm2trrstr:.  0.038  0.087 -0.602 -0.678

anova(lmer.model2)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## log(n.taxa)      1.86725 1.86725     1 19.191  8.0684 0.01039 *
## biome2           0.64763 0.64763     1 15.213  2.7984 0.11479
## body.size        0.36907 0.36907     1 15.821  1.5948 0.22494
## biome2:body.size 1.36188 1.36188     1 15.569  5.8847 0.02784 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#checking assumptions
par(mfrow = c(1,1))
plot(lmer.model2)
```



```
qqnorm(resid(lmer.model2))
```

Normal Q-Q Plot
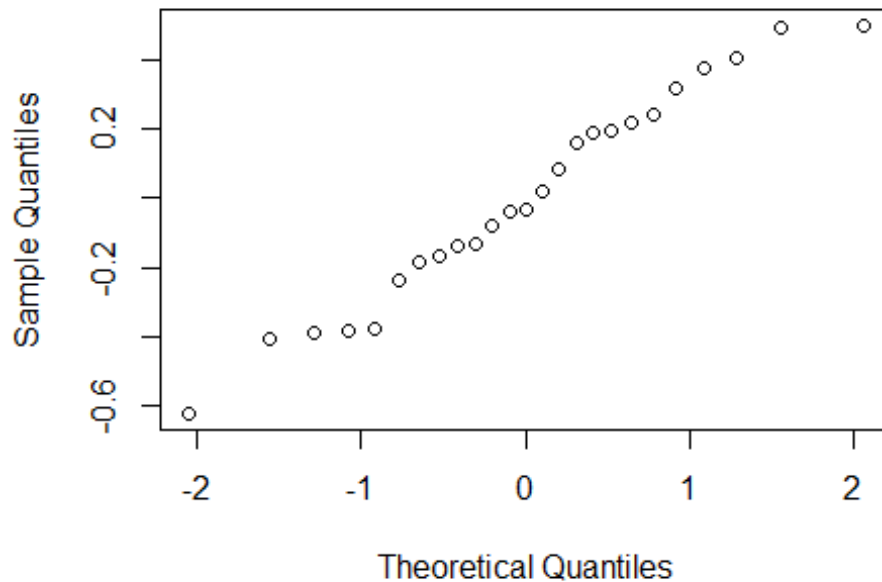

```r
lmer.model3 <- lmer(log(alpha_var) ~ log(n.taxa) + biome2 * body.size + (1 |
site/organism_group),
                    data = h.wide)
summary(lmer.model3)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## log(alpha_var) ~ log(n.taxa) + biome2 * body.size + (1 | site/organism_gro
up)
##    Data: h.wide
##
## REML criterion at convergence: 37.4
##
## Scaled residuals:
##     Min      1Q   Median      3Q      Max
## -1.79127 -0.57161 -0.01902  0.61421  1.12608
##
## Random effects:
##  Groups              Name         Variance Std.Dev.
##  organism_group:site (Intercept) 0.07144  0.2673
##  site                (Intercept) 0.04508  0.2123
##  Residual                        0.20400  0.4517
## Number of obs: 22, groups:  organism_group:site, 20; site, 12
##
## Fixed effects:
##                                        Estimate Std. Error       df t value
```

```
## (Intercept)                         -2.481270   0.595517 16.080219  -4.167
## log(n.taxa)                          0.300563   0.139036 14.695796   2.162
## biome2terrestrial                    0.002847   0.325336  9.237460   0.009
## body.sizesmall                      -0.492473   0.351209 14.815192  -1.402
## biome2terrestrial:body.sizesmall  0.557770   0.511233  9.624091   1.091
##                                    Pr(>|t|)
## (Intercept)                        0.000721 ***
## log(n.taxa)                        0.047566 *
## biome2terrestrial                  0.993205
## body.sizesmall                     0.181454
## biome2terrestrial:body.sizesmall 0.301821
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) lg(n.) bm2trr bdy.sz
## log(n.taxa) -0.931
## bim2trrstrl -0.307  0.069
## body.szsmll  0.003 -0.211  0.339
## bm2trrstr:.  0.096  0.040 -0.570 -0.665
```

```r
anova(lmer.model3)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF   DenDF F value  Pr(>F)
## log(n.taxa)     0.95335 0.95335     1 14.6958  4.6732 0.04757 *
## biome2          0.21180 0.21180     1  7.1563  1.0382 0.34144
## body.size       0.13424 0.13424     1  9.6787  0.6580 0.43675
## biome2:body.size 0.24283 0.24283     1  9.6241  1.1903 0.30182
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
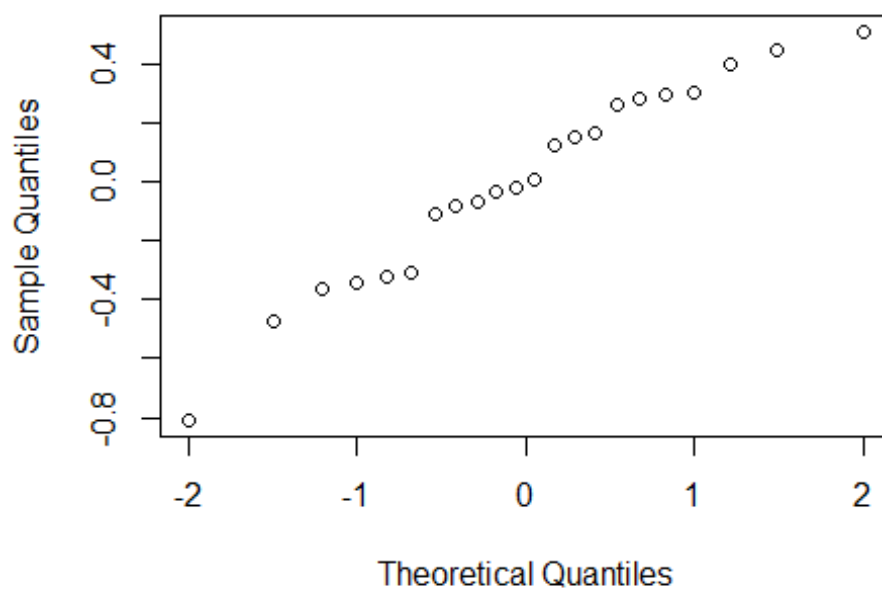
```r
#checking assumptions
par(mfrow = c(1,1))
plot(lmer.model3)
```
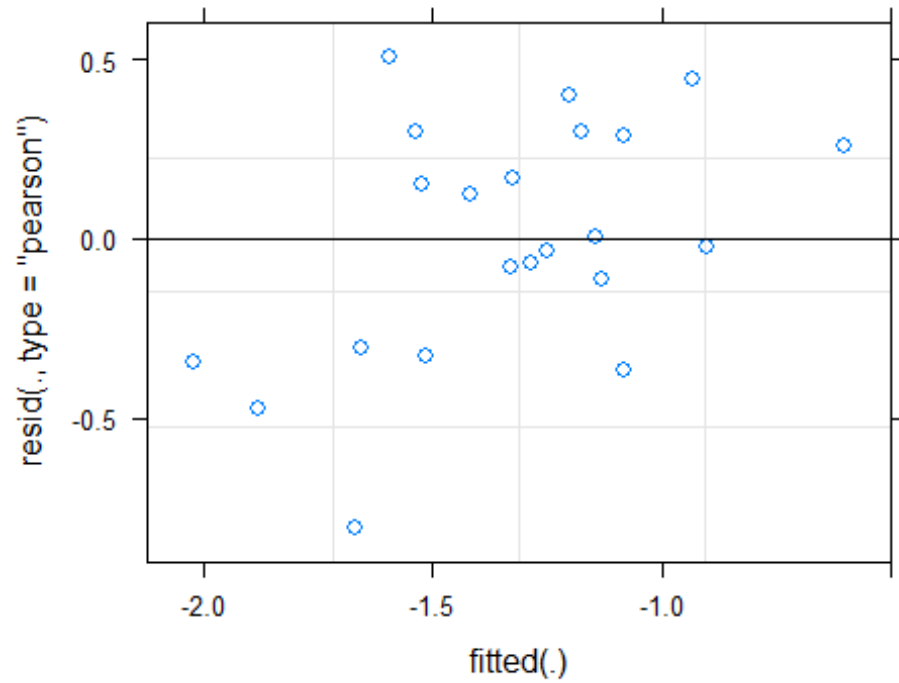
```
qqnorm(resid(lmer.model3))
```

Normal Q-Q Plot

```r
# metacommunity variability has important covariates to account for in models
summary(lmer(log(gamma_var) ~ log(n.taxa) + (1 | site/organism_group), data =
h.wide))
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: log(gamma_var) ~ log(n.taxa) + (1 | site/organism_group)
##    Data: h.wide
##
## REML criterion at convergence: 61.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.70131 -0.38053  0.07433  0.31362  1.03158
##
## Random effects:
##  Groups              Name        Variance Std.Dev.
##  organism_group:site (Intercept) 0.4528   0.6729
##  site                (Intercept) 0.0000   0.0000
##  Residual                        0.2384   0.4883
## Number of obs: 25, groups:  organism_group:site, 22; site, 13
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  -3.8387     0.7747 20.1471  -4.955 7.47e-05 ***
## log(n.taxa)   0.4000     0.1876 19.9836   2.132   0.0456 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## log(n.taxa) -0.974
```

```r
summary(lmer(log(alpha_var) ~ log(n.taxa) + (1 | site/organism_group), data =
h.wide))
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: log(alpha_var) ~ log(n.taxa) + (1 | site/organism_group)
##    Data: h.wide
##
## REML criterion at convergence: 38
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2020 -0.5012  0.1632  0.6323  1.5505
##
## Random effects:
##  Groups              Name        Variance  Std.Dev.
##  organism_group:site (Intercept) 4.664e-14 2.160e-07
```

```
## site              (Intercept) 0.000e+00 0.000e+00
## Residual                      2.915e-01 5.399e-01
## Number of obs: 22, groups:  organism_group:site, 20; site, 12
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  -2.3827     0.5629 20.0000  -4.233 0.000408 ***
## log(n.taxa)   0.2550     0.1334 20.0000   1.911 0.070424 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## log(n.taxa) -0.979
```

```r
summary(lmer(phi_var ~ log(n.plots) + (1 | site/organism_group), data = h.wide))
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: phi_var ~ log(n.plots) + (1 | site/organism_group)
##    Data: h.wide
##
## REML criterion at convergence: -8.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.40346 -0.41552 -0.07137  0.41946  1.33867
##
## Random effects:
##  Groups              Name        Variance Std.Dev.
##  organism_group:site (Intercept) 0.014691 0.12121
##  site                (Intercept) 0.008012 0.08951
##  Residual                        0.010389 0.10193
## Number of obs: 22, groups:  organism_group:site, 20; site, 12
##
## Fixed effects:
##              Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)   0.90509    0.14675 12.80436   6.168 3.62e-05 ***
## log(n.plots) -0.17575    0.06104 12.40356  -2.879   0.0134 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## log(n.plts) -0.952
```

```r
# Effects of temporal variability in NDVI
# dispersal habit by ndvi variability interaction
lmer.model2 <- lmer(phi_var ~ log(n.plots) + dispersal.habit * log(ndvi_tempo
```

```
ral_sd) +
                    (1 | site/organism_group),
                data = h.wide)
summary(lmer.model2)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## phi_var ~ log(n.plots) + dispersal.habit * log(ndvi_temporal_sd) +
##     (1 | site/organism_group)
##     Data: h.wide
##
## REML criterion at convergence: -3.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.19601 -0.44144 -0.04676  0.41667  1.38325
##
## Random effects:
##  Groups              Name        Variance Std.Dev.
##  organism_group:site (Intercept) 0.010126 0.10063
##  site                (Intercept) 0.009746 0.09872
##  Residual                        0.010237 0.10118
## Number of obs: 22, groups:  organism_group:site, 20; site, 12
##
## Fixed effects:
##                                                Estimate Std. Error
## (Intercept)                                    0.908210   0.168043
## log(n.plots)                                  -0.177629   0.060056
## dispersal.habitpassive                         0.128053   0.090297
## log(ndvi_temporal_sd)                          0.007719   0.072701
## dispersal.habitpassive:log(ndvi_temporal_sd) -0.156435   0.082159
##                                                      df t value Pr(>|t|)
## (Intercept)                                    8.896292   5.405 0.000448
## log(n.plots)                                  10.313371  -2.958 0.013898
## dispersal.habitpassive                         6.091898   1.418 0.205218
## log(ndvi_temporal_sd)                          7.866310   0.106 0.918098
## dispersal.habitpassive:log(ndvi_temporal_sd) 10.751305  -1.904 0.083995
##
## (Intercept)                                  ***
## log(n.plots)                                 *
## dispersal.habitpassive
## log(ndvi_temporal_sd)
## dispersal.habitpassive:log(ndvi_temporal_sd) .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) lg(n.) dsprs. lg(__)
## log(n.plts) -0.885
```

```
## dsprsl.hbtp -0.331  0.118
## lg(ndv_tm_) -0.468  0.129  0.372
## dsprs.:(__)  0.234 -0.045 -0.602 -0.617
```

anova(lmer.model2)

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                      Sum Sq  Mean Sq NumDF    DenDF
## log(n.plots)                        0.089554 0.089554     1 10.3134
## dispersal.habit                     0.020587 0.020587     1  6.0919
## log(ndvi_temporal_sd)               0.015488 0.015488     1  3.9426
## dispersal.habit:log(ndvi_temporal_sd) 0.037112 0.037112     1 10.7513
##                                      F value  Pr(>F)
## log(n.plots)                          8.7483 0.01390 *
## dispersal.habit                       2.0111 0.20522
## log(ndvi_temporal_sd)                 1.5129 0.28699
## dispersal.habit:log(ndvi_temporal_sd) 3.6254 0.08399 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
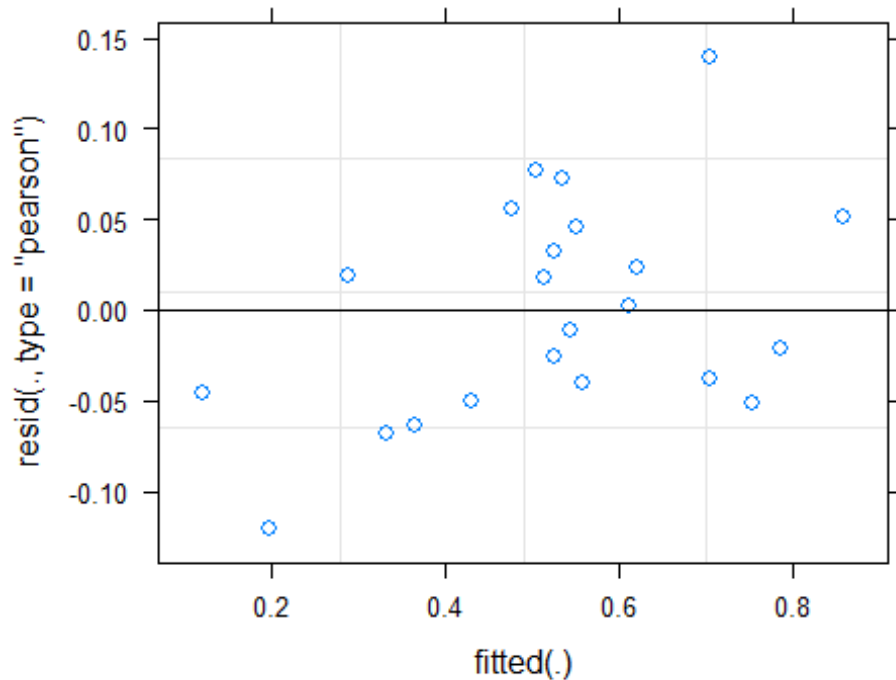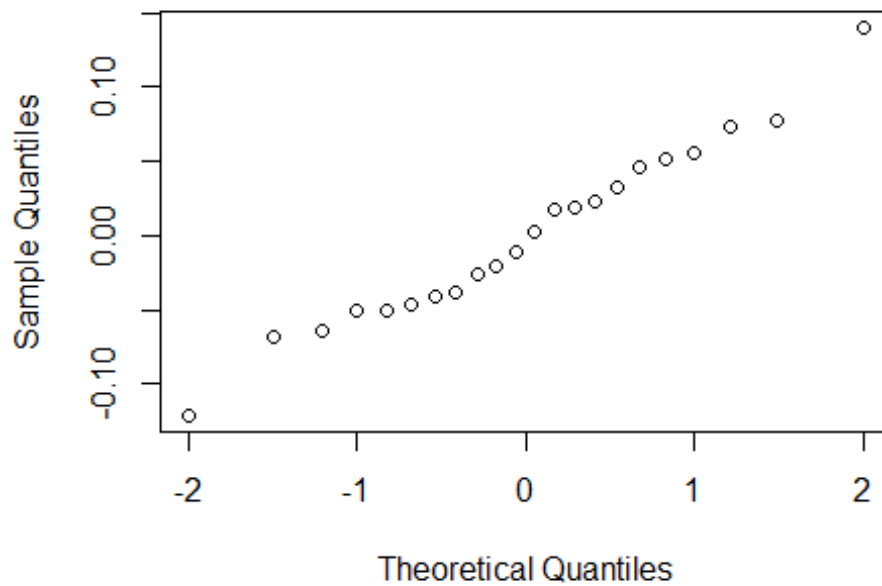
#checking assumptions
par(mfrow = **c**(1,1))
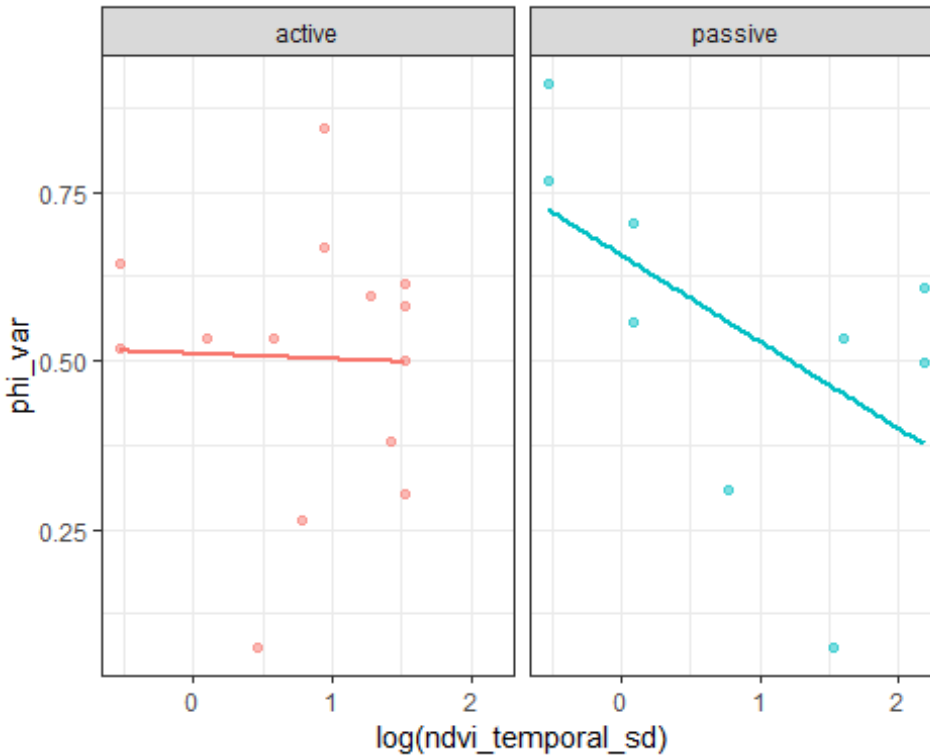**plot**(lmer.model2)

qqnorm(**resid**(lmer.model2))

Normal Q-Q Plot


```
ggplot(h.wide, aes(x = log(ndvi_temporal_sd), y = phi_var,
                   colour = dispersal.habit, group = dispersal.habit)) +
  geom_point(alpha = 0.5) +
  geom_smooth(method = "lm", se = F) +
  facet_grid(. ~ dispersal.habit) +
  theme_bw() +
  theme(legend.position = "none") +
  ggsave("phi_disp_ndvi.jpeg")
```

```
## Saving 5 x 4 in image
```

```
lmer.model2 <- lmer(phi_var ~ log(n.plots) + body.size * log(ndvi_temporal_sd
) +
                    (1 | site/organism_group),
                data = h.wide)
summary(lmer.model2)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: phi_var ~ log(n.plots) + body.size * log(ndvi_temporal_sd) +
##      (1 | site/organism_group)
##     Data: h.wide
##
## REML criterion at convergence: -5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4051 -0.4161 -0.1348  0.3607  1.4034
##
## Random effects:
##  Groups              Name        Variance Std.Dev.
##  organism_group:site (Intercept) 0.01205  0.1098
##  site                (Intercept) 0.00000  0.0000
##  Residual                        0.01368  0.1169
## Number of obs: 22, groups:  organism_group:site, 20; site, 12
##
## Fixed effects:
##                                         Estimate Std. Error      df t value
```

```
## (Intercept)                                  1.09529    0.13980 15.55906    7.835
## log(n.plots)                                 -0.24096    0.06111 14.76091   -3.943
## body.sizesmall                                0.31410    0.16929 16.38884    1.855
## log(ndvi_temporal_sd)                         -0.06375    0.04757 16.25267   -1.340
## body.sizesmall:log(ndvi_temporal_sd) -0.26034    0.13742 16.58914   -1.894
##                                              Pr(>|t|)
## (Intercept)                                  8.74e-07 ***
## log(n.plots)                                  0.00134 **
## body.sizesmall                                0.08162 .
## log(ndvi_temporal_sd)                         0.19865
## body.sizesmall:log(ndvi_temporal_sd)  0.07573 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) lg(n.) bdy.sz lg(__)
## log(n.plts) -0.926
## body.szsmll  0.258 -0.405
## lg(ndv_tm_) -0.203 -0.005  0.174
## bdy.sz:(__) -0.211  0.305 -0.880 -0.348
```

```r
anova(lmer.model2)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                  Sum Sq  Mean Sq NumDF   DenDF F value
## log(n.plots)                    0.212650 0.212650     1 14.761 15.5485
## body.size                       0.047080 0.047080     1 16.389  3.4424
## log(ndvi_temporal_sd)           0.109186 0.109186     1 16.604  7.9834
## body.size:log(ndvi_temporal_sd) 0.049085 0.049085     1 16.589  3.5890
##                                   Pr(>F)
## log(n.plots)                    0.001339 **
## body.size                       0.081621 .
## log(ndvi_temporal_sd)           0.011859 *
## body.size:log(ndvi_temporal_sd) 0.075733 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
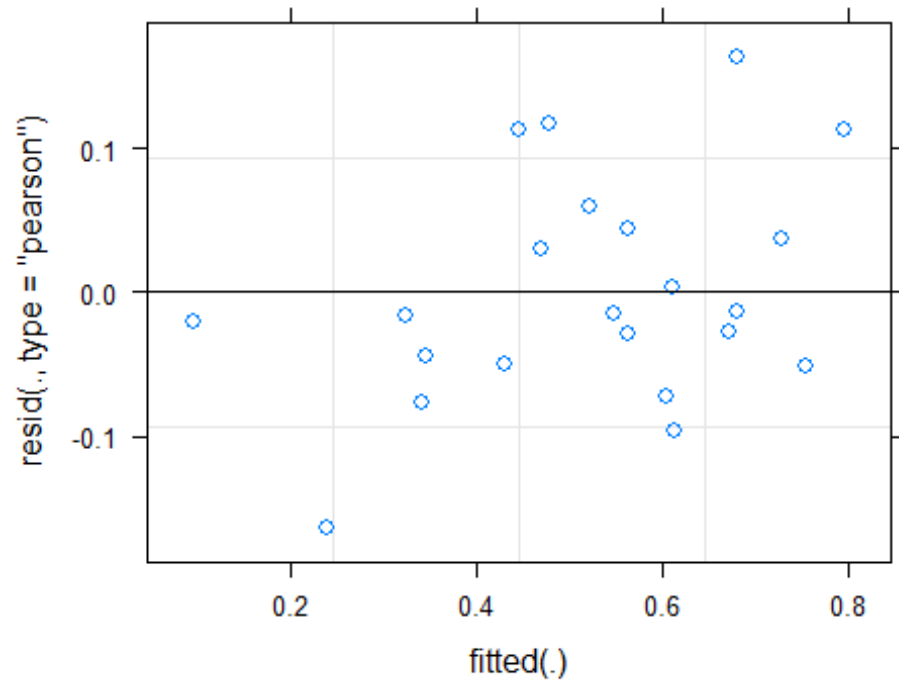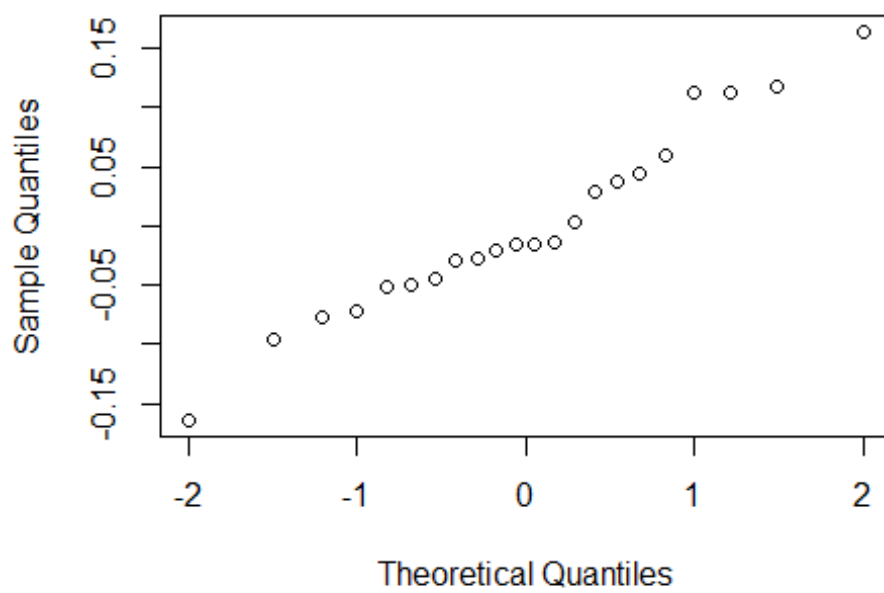
```r
#checking assumptions
par(mfrow = c(1,1))
plot(lmer.model2)
```
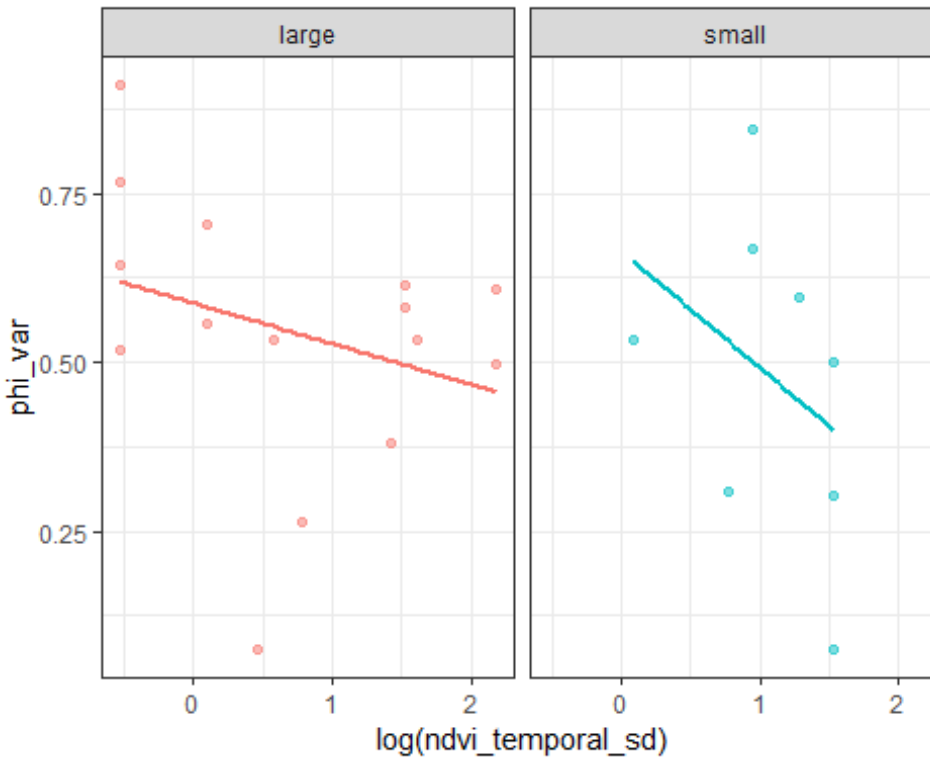
```
qqnorm(resid(lmer.model2))
```

Normal Q-Q Plot

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```r
ggplot(h.wide, aes(x = log(ndvi_temporal_sd), y = phi_var,
                   colour = body.size, group = body.size)) +
  geom_point(alpha = 0.5) +
  geom_smooth(method = "lm", se = F) +
  facet_grid(. ~ body.size) +
  theme_bw() +
  theme(legend.position = "none") +
  ggsave("phi_body_ndvi.jpeg")
```

```
## Saving 5 x 4 in image
```



```r
lmer.model2 <- lmer(phi_var ~ log(n.plots) + body.size * log(temp_temporal_sd
) +
                    (1 | site/organism_group),
                  data = h.wide)
summary(lmer.model2)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: phi_var ~ log(n.plots) + body.size * log(temp_temporal_sd) +
##     (1 | site/organism_group)
##    Data: h.wide
##
## REML criterion at convergence: -4.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

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```
## -1.3812 -0.3514 -0.1300  0.4732  1.3105
##
## Random effects:
##  Groups              Name         Variance Std.Dev.
##  organism_group:site (Intercept) 0.007905 0.08891
##  site                (Intercept) 0.009504 0.09749
##  Residual                        0.014136 0.11889
## Number of obs: 22, groups:  organism_group:site, 20; site, 12
##
## Fixed effects:
##                                   Estimate Std. Error       df t value
## (Intercept)                        0.96564    0.15317 12.37209   6.304
## log(n.plots)                      -0.20452    0.06672 11.39087  -3.065
## body.sizesmall                     0.10663    0.10081 14.39833   1.058
## log(temp_temporal_sd)              0.07046    0.09951 13.09089   0.708
## body.sizesmall:log(temp_temporal_sd) -0.42537    0.21079 13.31519  -2.018
##                                   Pr(>|t|)
## (Intercept)                       3.41e-05 ***
## log(n.plots)                        0.0104 *
## body.sizesmall                      0.3076
## log(temp_temporal_sd)               0.4913
## body.sizesmall:log(temp_temporal_sd)  0.0642 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) lg(n.) bdy.sz lg(__)
## log(n.plts) -0.939
## body.szsmll  0.178 -0.347
## lg(tmp_tm_) -0.001 -0.029  0.037
## bdy.sz:(__) -0.165  0.203 -0.584 -0.324

anova(lmer.model2)

## Type III Analysis of Variance Table with Satterthwaite's method
##                               Sum Sq   Mean Sq NumDF  DenDF F value
## log(n.plots)                 0.132821 0.132821     1 11.391  9.3960
## body.size                    0.015815 0.015815     1 14.398  1.1188
## log(temp_temporal_sd)        0.020110 0.020110     1 12.902  1.4226
## body.size:log(temp_temporal_sd) 0.057563 0.057563     1 13.315  4.0721
##                               Pr(>F)
## log(n.plots)                 0.01036 *
## body.size                    0.30761
## log(temp_temporal_sd)        0.25445
## body.size:log(temp_temporal_sd) 0.06421 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
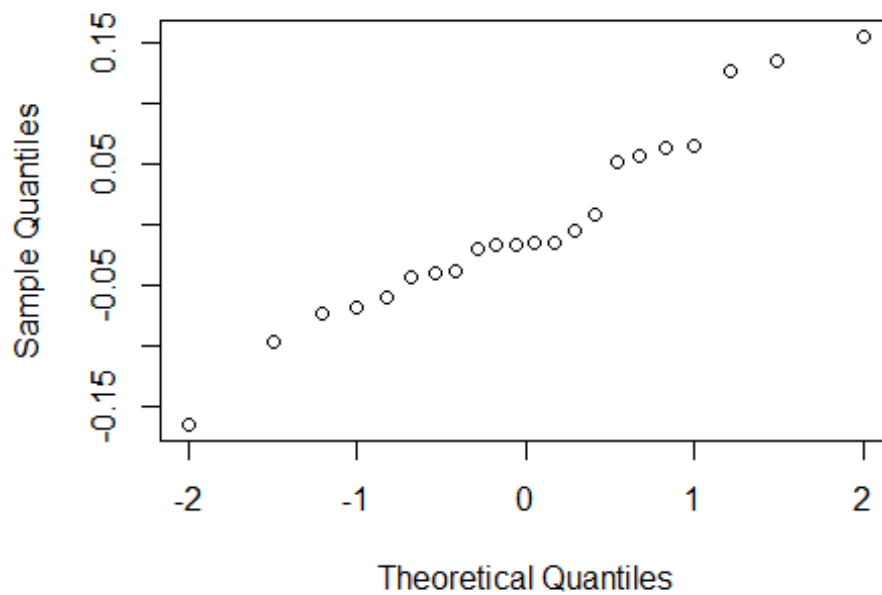
```
#checking assumptions
par(mfrow = c(1,1))
plot(lmer.model2)
```
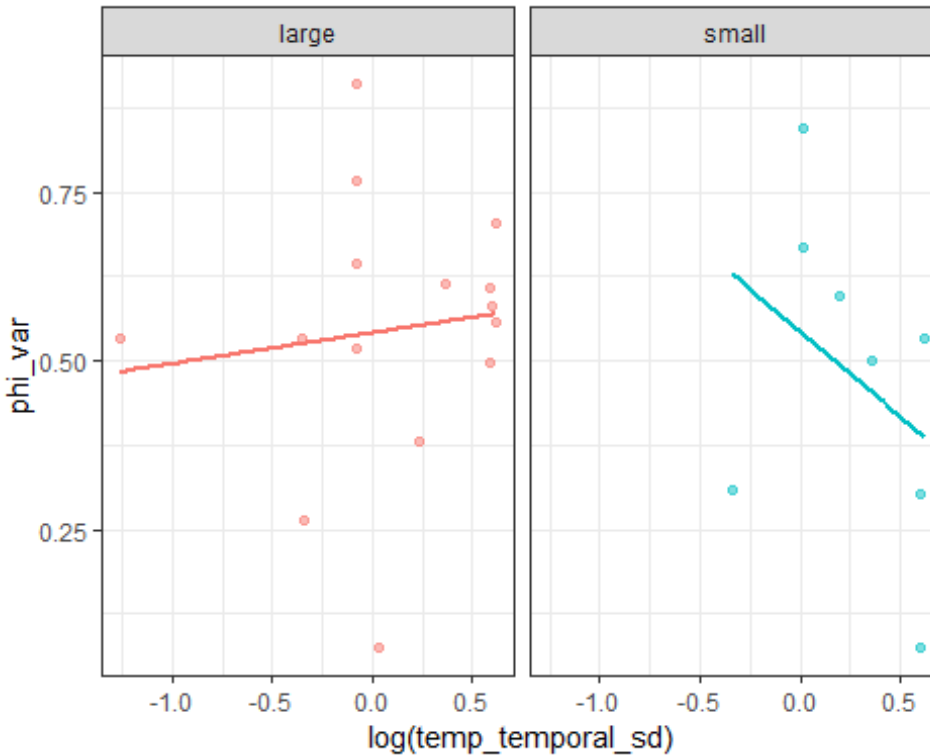


```
qqnorm(resid(lmer.model2))
```
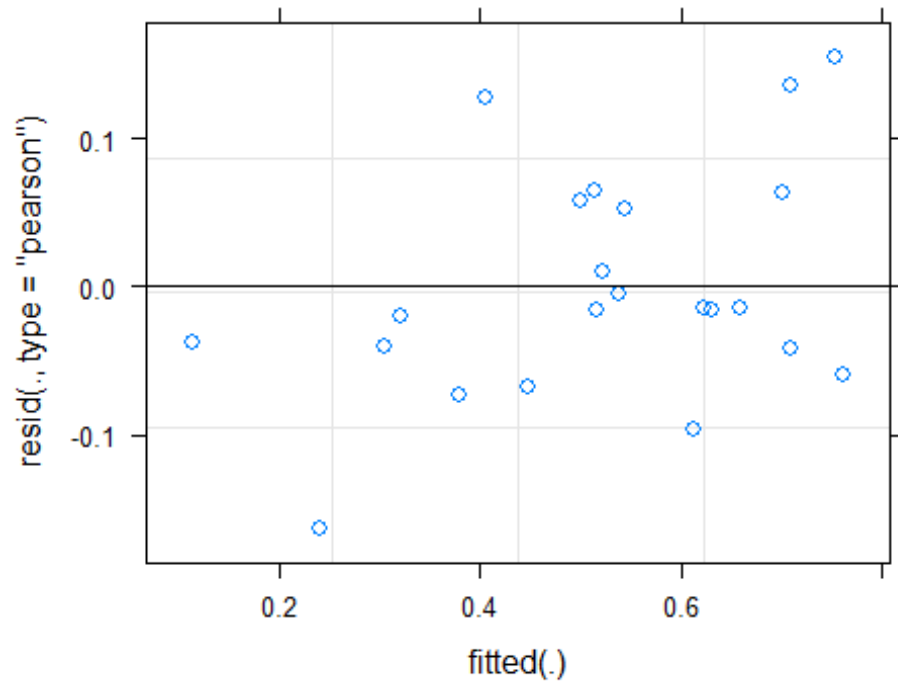
Normal Q-Q Plot


```
ggplot(h.wide, aes(x = log(temp_temporal_sd), y = phi_var,
                   colour = body.size, group = body.size)) +
  geom_point(alpha = 0.5) +
  geom_smooth(method = "lm", se = F) +
  facet_grid(. ~ body.size) +
  theme_bw() +
  theme(legend.position = "none") +
  ggsave("phi_body_temp.jpeg")

## Saving 5 x 4 in image
```

```
lmer.modelx <- lmer(phi_var ~ log(n.plots) + body.size * env_heterogeneity +
                    (1 | site/organism_group),
                  data = h.wide)
anova(lmer.modelx)

## Type III Analysis of Variance Table with Satterthwaite's method
##                                Sum Sq  Mean Sq NumDF    DenDF F value
## log(n.plots)                  0.086962 0.086962     1  9.9006  9.6350
## body.size                     0.019920 0.019920     1 13.6185  2.2071
## env_heterogeneity             0.033739 0.033739     1  8.9965  3.7381
## body.size:env_heterogeneity   0.058438 0.058438     1 13.2089  6.4747
##                                 Pr(>F)
## log(n.plots)                   0.01130 *
## body.size                      0.16016
## env_heterogeneity              0.08522 .
## body.size:env_heterogeneity    0.02420 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

ggplot(h.wide, aes(x = env_heterogeneity, y = phi_var,
                  colour = body.size, group = body.size)) +
  geom_point(alpha = 0.5) +
  geom_smooth(method = "lm", se = F) +
  facet_grid(. ~ body.size) +
  theme_bw() +
```
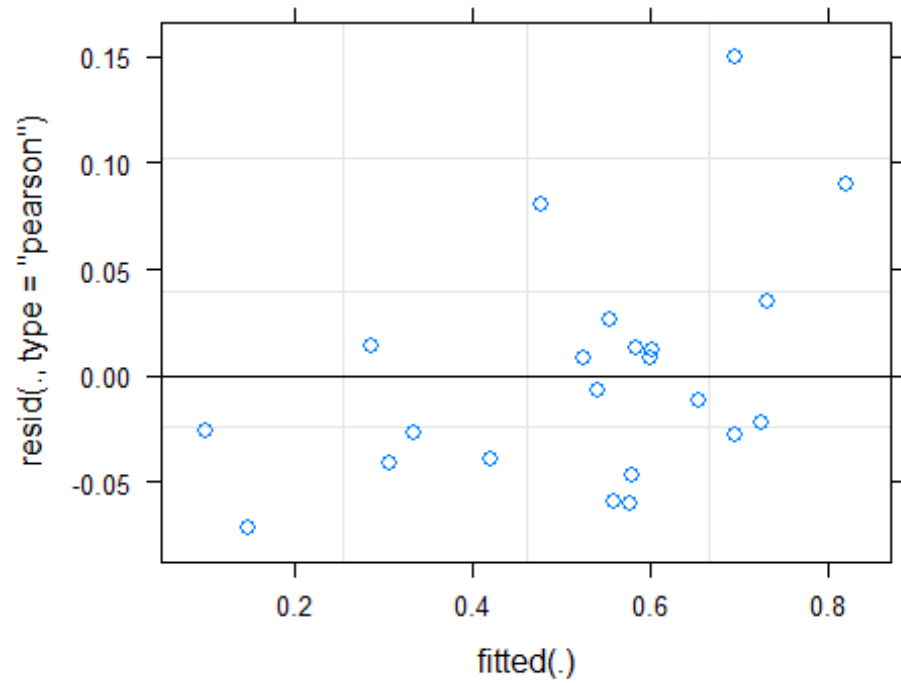
```
    theme(legend.position = "none") +
    ggsave("phi_body_envhet.jpeg")
```
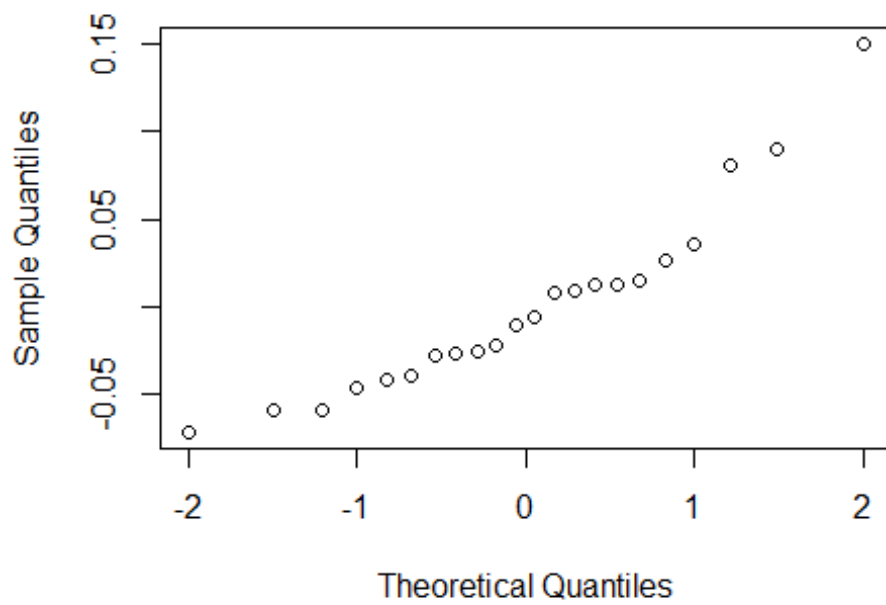
Saving 5 x 4 in image
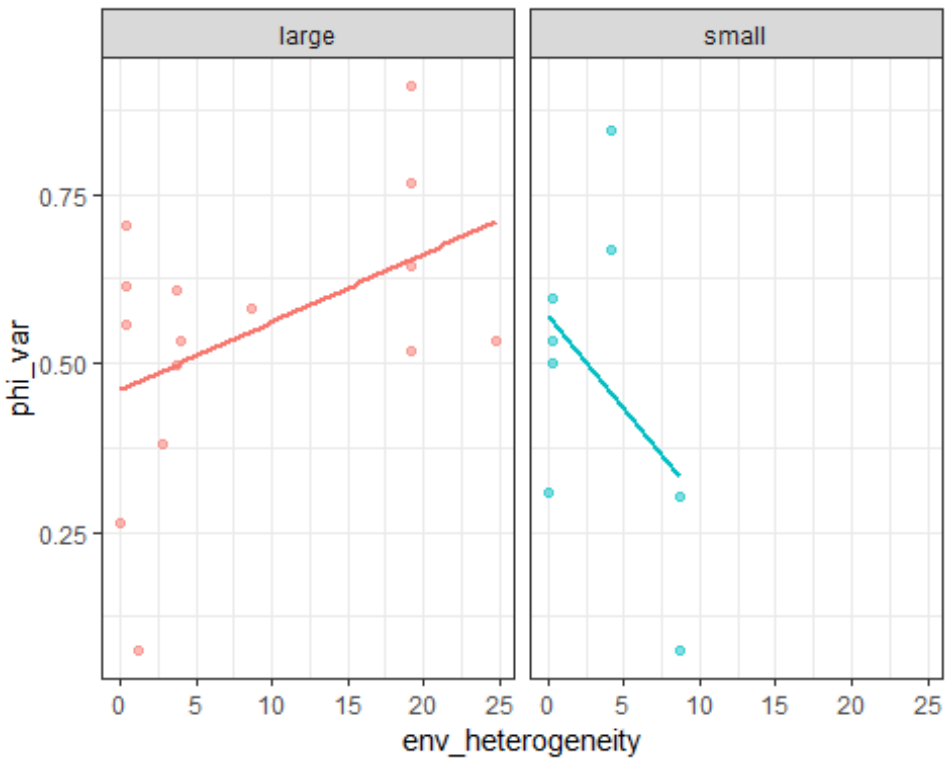

```
par(mfrow = c(1,1))
plot(lmer.modelx)
```

```
qqnorm(resid(lmer.modelx))
```

Normal Q-Q Plot

```
# neither gamma nor alpha var are related to interactions between dispersal h
abit or body size and ndvi, temp, or env heterogeneity.
```