

Co-infetion

R Markdown

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
library(ggplot2)
library(reshape2)
library(lme4)
library(nlme)
library(car)
library(emmeans)
library(cooccur)
library(gmp)
library(asnipe)
library(Rmisc)
library(multcomp)
bcfrt <- read.csv("D:/Macquarie/PhD/Data/bacteria.csv", header = T, stringsAsFactors = F)
bcfrt <- bcfrt[, -1]
bcprv <- read.csv("D:/Macquarie/PhD/Data/subset/lizard.infection.csv", header = T, stringsAsFactors = F)
bcprv <- bcprv[-c(25,26),]
bcprv <- melt(bcprv, id=c("sex_code", "site_code", "Sampling.point", "ind.count"))
colnames(bcprv) <- c("sex", "site", "frt", "sz", "strain", "lizard")
bcfrt$Sampling.point <- as.factor(bcfrt$Sampling.point)
bcprv$frt <- as.factor(bcprv$frt)
```

Variation of infection

Lizards were swabbed every fortnight during their active season. The presence or absence of each bacterial strain was recorded. In the dataset, site A represented the location of “church”, while site B represented the location of “PhD”.

```
frt_mod1 <- lmer(Sequence.Type.Richness~site_code+sex_code+Sampling.point+site_code*sex_code+(1|Lizard), data = bcfrt, REML = F)
Anova(frt_mod1)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
```

```
## Response: Sequence.Type.Richness
##               Chisq Df Pr(>Chisq)
## site_code      5.0293  1  0.02492 *
## sex_code        0.0292  1  0.86420
## Sampling.point 342.8885  5  < 2e-16 ***
## site_code:sex_code 1.5349  1  0.21538
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#interaction was removed since not significant
frt_mod2 <- lmer(Sequence.Type.Richness~site_code+Sampling.point+(1|Lizard)
ard)
, data = bcfrt, REML = F)
summary(frt_mod2)

## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula:
## Sequence.Type.Richness ~ site_code + Sampling.point + (1 | Lizard)
## Data: bcfrt
##
##      AIC      BIC    logLik deviance df.resid
## 2933.5   2970.8  -1457.8   2915.5     459
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7688 -0.6448  0.0667  0.6772  3.3616
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## Lizard   (Intercept) 2.787    1.670
## Residual                27.410    5.235
## Number of obs: 468, groups: Lizard, 87
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    16.1781    0.7642  21.169
## site_codeB       1.3343    0.6034   2.211
## Sampling.point2   1.1820    0.9121   1.296
## Sampling.point3   1.9679    0.8843   2.225
## Sampling.point4  -1.7904    0.8893  -2.013
## Sampling.point5   3.8022    0.8864   4.289
## Sampling.point6  12.0443    0.8945  13.465
##
## Correlation of Fixed Effects:
##              (Intr) st_cdB Smpl.2 Smpl.3 Smpl.4 Smpl.5
## site_codeB   -0.400
## SmpIng.pnt2  -0.654 -0.009
## SmpIng.pnt3  -0.679  0.001  0.568
## SmpIng.pnt4  -0.673 -0.005  0.565  0.585
```

```
## SmpIng.pnt5 -0.681  0.009  0.566  0.585  0.582
## SmpIng.pnt6 -0.674  0.006  0.562  0.581  0.578  0.580

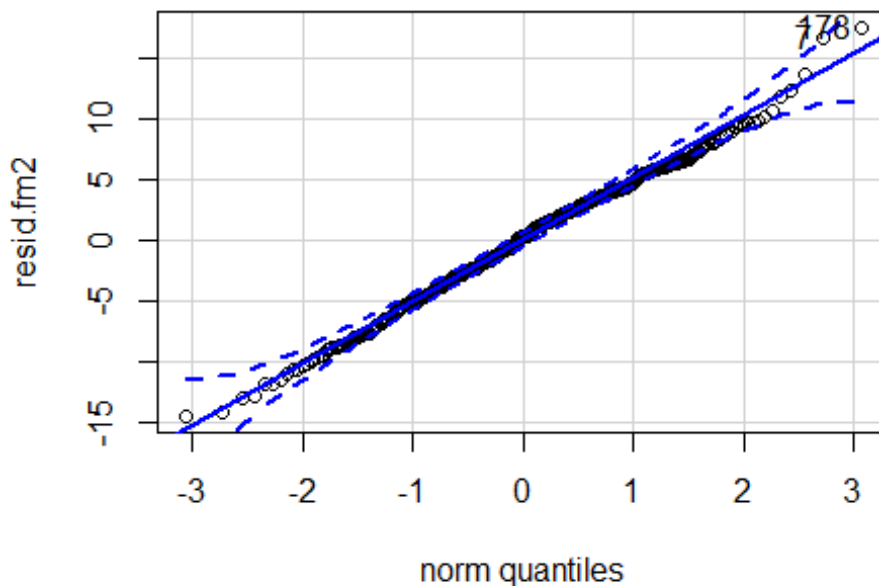
Anova(frt_mod2)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Sequence.Type.Richness
##              Chisq Df Pr(>Chisq)
## site_code      4.8902  1    0.02701 *
## Sampling.point 343.0674  5    < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

lsmeans(frt_mod2, ~site_code)

##   site_code  lsmean      SE    df lower.CL upper.CL
##   A          19.04579 0.4355147 89.54  18.1805 19.91108
##   B          20.38006 0.4303160 88.80  19.5250 21.23511
##
## Results are averaged over the levels of: Sampling.point
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95

#normality test
resid.fm2 <- resid(frt_mod2)
qqp(resid.fm2, "norm")
```



```
## [1] 178    7

shapiro.test(resid.fm2)

##
## Shapiro-Wilk normality test
##
## data:  resid.fm2
## W = 0.99547, p-value = 0.1924

#auto-correlation test
summary(lm(resid.fm2~bcfrt$Sampling.point))

##
## Call:
## lm(formula = resid.fm2 ~ bcfrt$Sampling.point)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.4959  -3.3758   0.3491   3.5457  17.5993
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -6.025e-14  6.522e-01      0      1
## bcfrt$Sampling.point2  5.613e-14  8.809e-01      0      1
## bcfrt$Sampling.point3  6.129e-14  8.548e-01      0      1
## bcfrt$Sampling.point4  6.440e-14  8.591e-01      0      1
## bcfrt$Sampling.point5  6.120e-14  8.569e-01      0      1
## bcfrt$Sampling.point6  6.121e-14  8.635e-01      0      1
##
## Residual standard error: 5.094 on 462 degrees of freedom
## Multiple R-squared:  1.718e-29, Adjusted R-squared:  -0.01082
## F-statistic: 1.587e-27 on 5 and 462 DF, p-value: 1

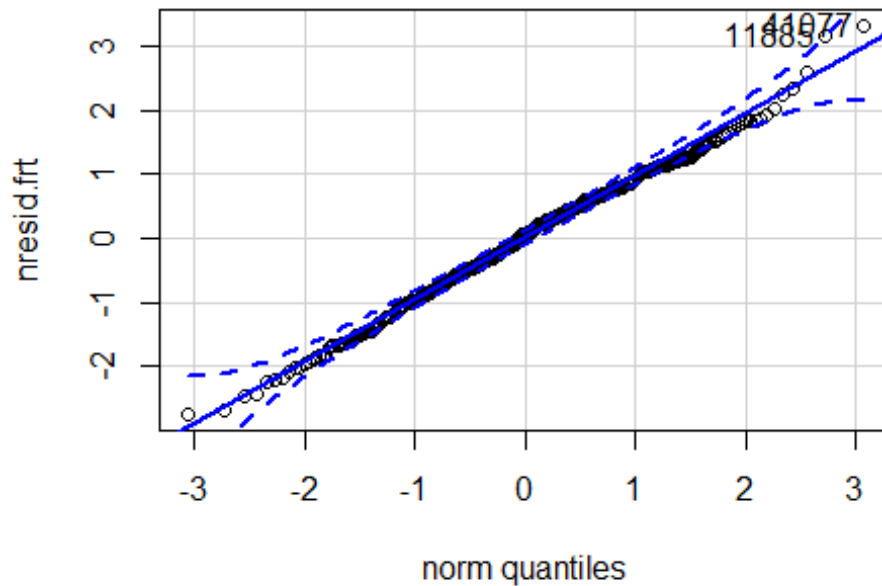
#homogeneity test
leveneTest(resid.fm2~as.character(bcfrt$Sampling.point))

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

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group  5  3.4589 0.004436 **
##      462
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#normalized residuals-----
frt_lme <- lme(Sequence.Type.Richness~site_code+Sampling.point,
              data = bcfrt, method = "REML", random = ~1|Lizard)
```

```
nresid.frt <- residuals(frt_lme, type = "normalized")
qqp(nresid.frt, "norm")
```

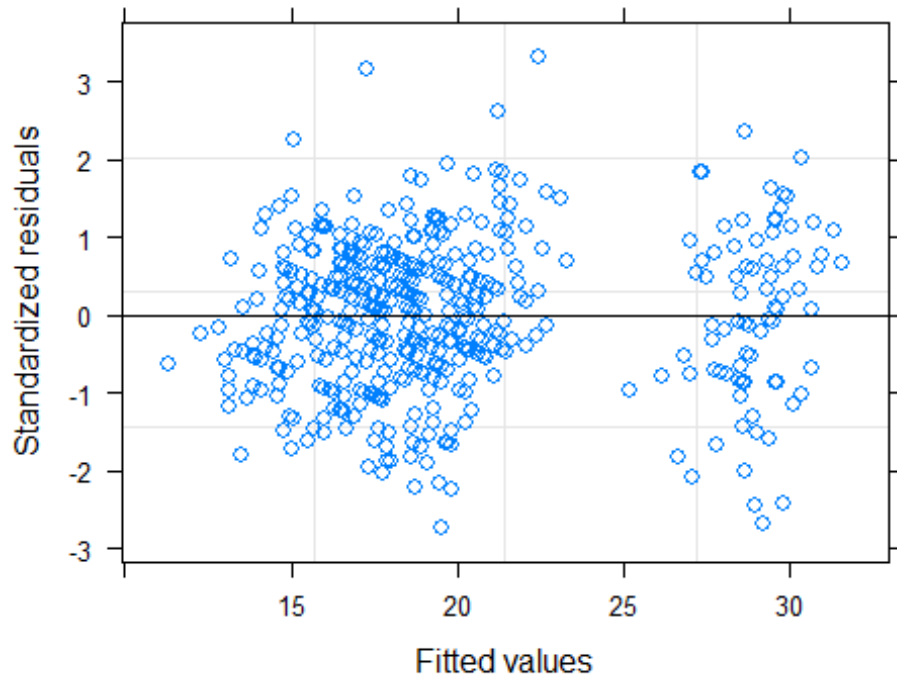


```
## 41077 11885
## 178 7

shapiro.test(nresid.frt)

##
## Shapiro-Wilk normality test
##
## data: nresid.frt
## W = 0.99548, p-value = 0.1942

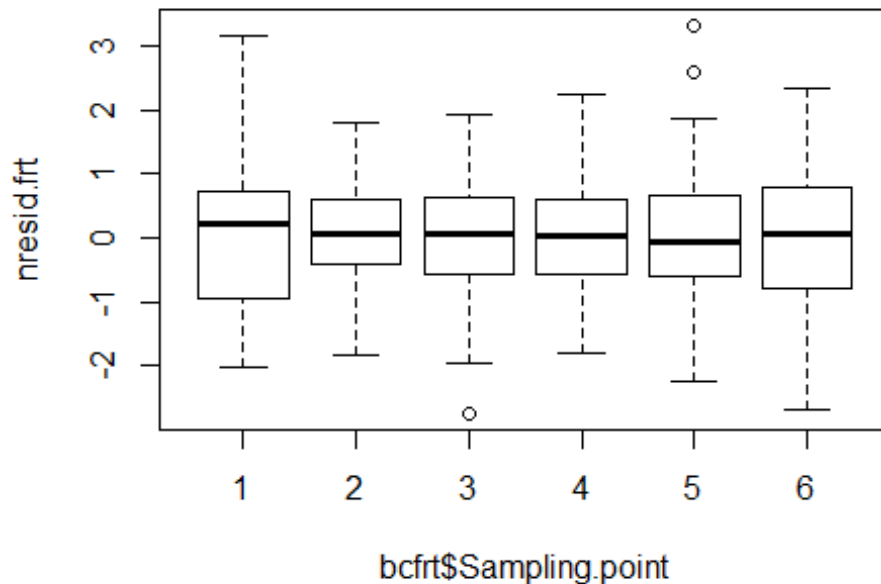
#homogeneity test
plot(frt_lme)
```



```
bartlett.test(nresid.frt~bcfrt$Sampling.point)

##
## Bartlett test of homogeneity of variances
##
## data:  nresid.frt by bcfrt$Sampling.point
## Bartlett's K-squared = 17.431, df = 5, p-value = 0.00375

#autocorrelation test
plot(nresid.frt~bcfrt$Sampling.point)
```



```
summary(lm(nresid.frt~bcfrt$Sampling.point))

##
## Call:
## lm(formula = nresid.frt ~ bcfrt$Sampling.point)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7509 -0.6379  0.0615  0.6660  3.3302
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.302e-15  1.236e-01      0      1
## bcfrt$Sampling.point2 -1.478e-15  1.669e-01      0      1
## bcfrt$Sampling.point3 -6.724e-16  1.620e-01      0      1
## bcfrt$Sampling.point4  2.284e-15  1.628e-01      0      1
## bcfrt$Sampling.point5 -1.796e-15  1.624e-01      0      1
## bcfrt$Sampling.point6 -1.487e-15  1.636e-01      0      1
##
## Residual standard error: 0.9653 on 462 degrees of freedom
## Multiple R-squared:  2.498e-30, Adjusted R-squared:  -0.01082
## F-statistic: 2.308e-28 on 5 and 462 DF, p-value: 1
```

The model violated the assumption of homogeneity. Thus, we added varIdent to allow the model to have different variances.

```

frt_lme2 <- lme(data = bcfrt, Sequence.Type.Richness~site_code+Sampling.
point, random = ~1|Lizard,
               method = "REML")
frt_lme2 <- update(frt_lme2, weights=varIdent(form = ~1|Sampling.point))
summary(frt_lme2)

## Linear mixed-effects model fit by REML
## Data: bcfrt
##      AIC      BIC    logLik
## 2919.389 2977.257 -1445.695
##
## Random effects:
## Formula: ~1 | Lizard
##      (Intercept) Residual
## StdDev:      1.636341  5.52575
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sampling.point
## Parameter estimates:
##      1      2      3      4      5      6
## 1.0000000 0.7414994 0.9008105 0.8103344 1.0827113 1.1372130
## Fixed effects: Sequence.Type.Richness ~ site_code + Sampling.point
##      Value Std.Error DF  t-value p-value
## (Intercept) 16.135104 0.7923441 376 20.363759 0.0000
## site_codeB  1.389346 0.5853600  85  2.373489 0.0199
## Sampling.point2 1.180627 0.8596408 376  1.373396 0.1704
## Sampling.point3 1.984595 0.8954136 376  2.216401 0.0273
## Sampling.point4 -1.780642 0.8676542 376 -2.052248 0.0408
## Sampling.point5  3.816339 0.9675395 376  3.944376 0.0001
## Sampling.point6 12.062481 0.9998168 376 12.064691 0.0000
## Correlation:
##      (Intr) st_cdB Smpl.2 Smpl.3 Smpl.4 Smpl.5
## site_codeB -0.374
## Sampling.point2 -0.743 -0.009
## Sampling.point3 -0.718  0.000  0.661
## Sampling.point4 -0.739 -0.005  0.683  0.657
## Sampling.point5 -0.667  0.007  0.611  0.588  0.607
## Sampling.point6 -0.646  0.005  0.592  0.570  0.588  0.528
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -2.83722406 -0.65729468  0.06708126  0.68183241  3.11135670
##
## Number of Observations: 468
## Number of Groups: 87

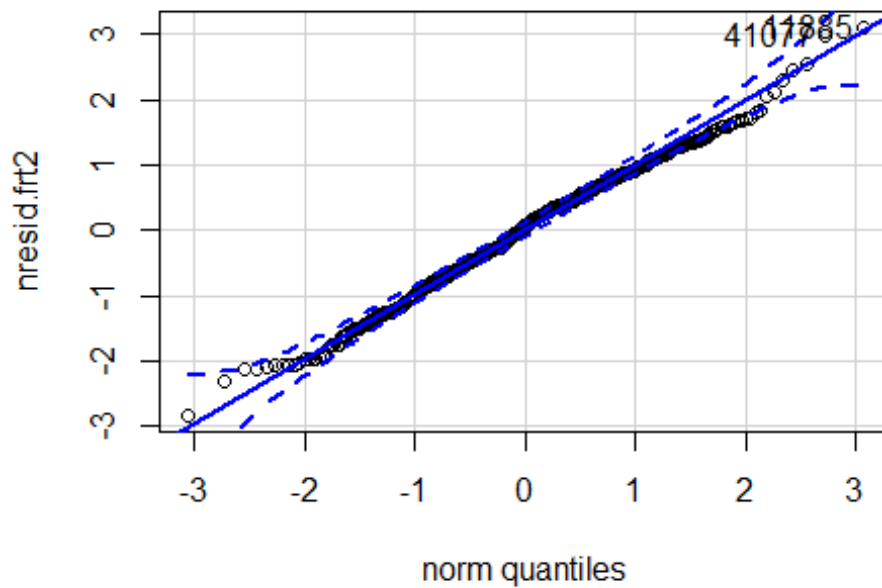
hoc.frt <- summary(glht(frt_lme2, linfct = mcp("Sampling.point" = "Tukey
y")), test = adjusted("holm"))
hoc.frt

```



```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
## Fit: lme.formula(fixed = Sequence.Type.Richness ~ site_code + Sampling.point,
## data = bcfrr, random = ~1 | Lizard, weights = varIdent(form = ~1
|
## Sampling.point), method = "REML")
##
## Linear Hypotheses:
## Estimate Std. Error z value Pr(>|z|)
## 2 - 1 == 0 1.1806 0.8596 1.373 0.339259
## 3 - 1 == 0 1.9846 0.8954 2.216 0.133320
## 4 - 1 == 0 -1.7806 0.8677 -2.052 0.133320
## 5 - 1 == 0 3.8163 0.9675 3.944 0.000560 ***
## 6 - 1 == 0 12.0625 0.9998 12.065 < 2e-16 ***
## 3 - 2 == 0 0.8040 0.7231 1.112 0.339259
## 4 - 2 == 0 -2.9613 0.6882 -4.303 0.000135 ***
## 5 - 2 == 0 2.6357 0.8112 3.249 0.006943 **
## 6 - 2 == 0 10.8819 0.8488 12.821 < 2e-16 ***
## 4 - 3 == 0 -3.7652 0.7305 -5.155 2.29e-06 ***
## 5 - 3 == 0 1.8317 0.8479 2.160 0.133320
## 6 - 3 == 0 10.0779 0.8838 11.403 < 2e-16 ***
## 5 - 4 == 0 5.5970 0.8183 6.839 7.95e-11 ***
## 6 - 4 == 0 13.8431 0.8555 16.182 < 2e-16 ***
## 6 - 5 == 0 8.2461 0.9565 8.621 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- holm method)

nresid.frt2 <- residuals(frt_lme2, type = "normalized")
qqp(nresid.frt2,"norm")
```

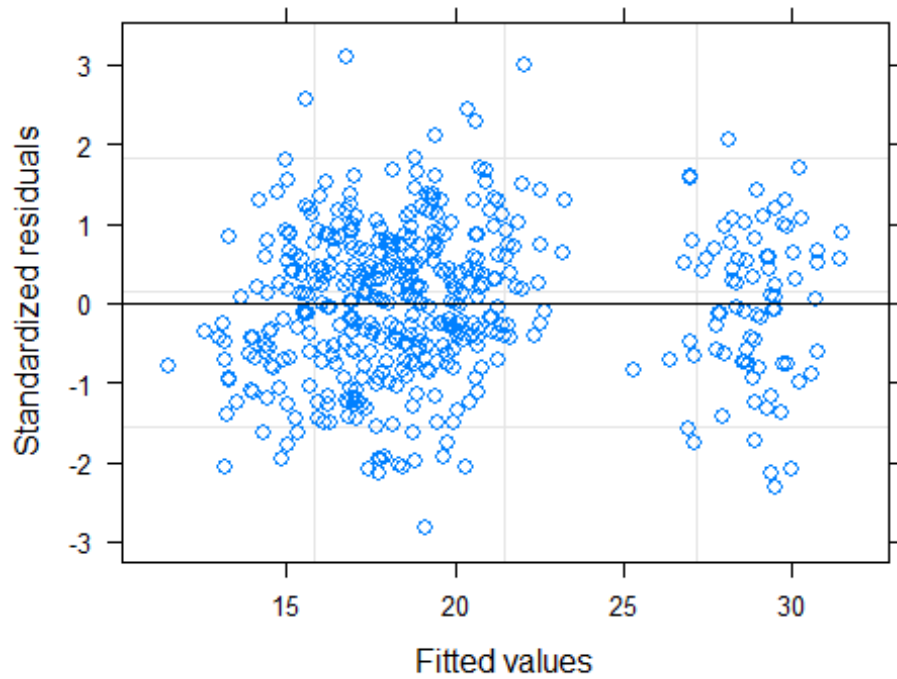


```
## 11885 41077
##      7   178

shapiro.test(nresid.frt2)

##
##  Shapiro-Wilk normality test
##
## data:  nresid.frt2
## W = 0.99461, p-value = 0.09961

#homogeneity plot
plot(frt_lme2)
```



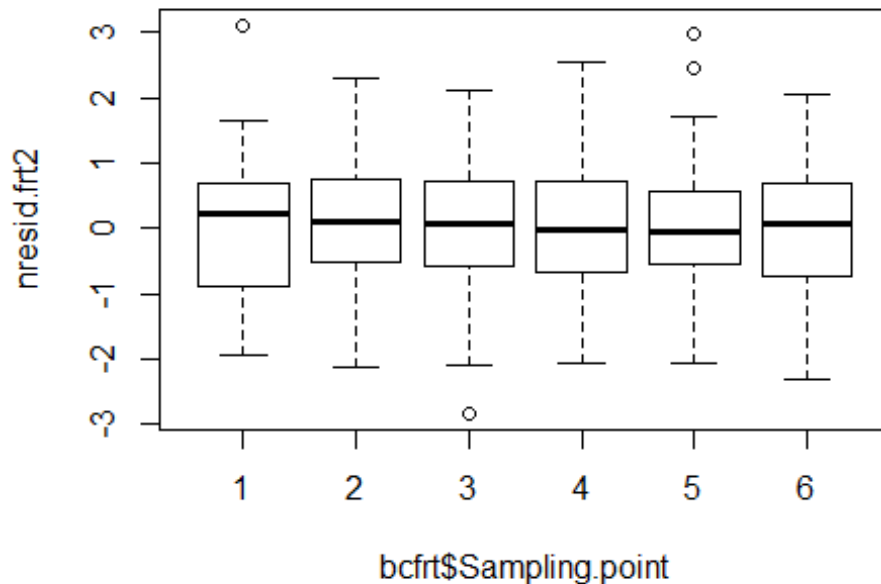
```
bartlett.test(nresid.frt2~bcfrt$Sampling.point)
```


Bartlett test of homogeneity of variances

data: nresid.frt2 by bcfrt\$Sampling.point
Bartlett's K-squared = 0.11617, df = 5, p-value = 0.9998

#autocorrelation test

```
plot(nresid.frt2~bcfrt$Sampling.point)
```



```
summary(lm(nresid.frt2~bcfrt$Sampling.point))
```

```
##
## Call:
## lm(formula = nresid.frt2 ~ bcfrt$Sampling.point)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.83722 -0.65729  0.06708  0.68183  3.11136
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.022e-15  1.236e-01      0      1
## bcfrt$Sampling.point2 -6.828e-16  1.669e-01      0      1
## bcfrt$Sampling.point3 -1.701e-15  1.620e-01      0      1
## bcfrt$Sampling.point4 -2.177e-15  1.628e-01      0      1
## bcfrt$Sampling.point5  7.074e-16  1.624e-01      0      1
## bcfrt$Sampling.point6 -2.296e-15  1.636e-01      0      1
##
## Residual standard error: 0.9653 on 462 degrees of freedom
## Multiple R-squared:  1.315e-30, Adjusted R-squared:  -0.01082
## F-statistic: 1.216e-28 on 5 and 462 DF, p-value: 1
```

#number of infeceted lizards

```
il <- c(438,459,445,352,363,397,394,304,197,231,217,142,119,87,162,42,1
27,128,205,92,217,133,93,77,90,103,113,78,49,58,56,102,40,235,46,136,10
7,192,24,54,61,130,69,108,26,36,48,58,60,123,27,58,43,24,15,60,61,9,8,1
```

```

18,24,19,56,126,80,9,10,25,12,26,27,40,9,47,17,38,7,31,11,26,26,12,17,2
9,10,28,15,10,19,19,9,14,20,19,21,19,14,9,16,9,13,15,10,8,3,10,15,14,6,
2,8,6,14,4,3,4,6,10,9,5,6,3,3,8,7,2,7,1,3,3,0,3,5,0,2,5,1,3,5,1,4,2,1,3,
2,1,0,13,2,0,0,0,1,1,0,0
)
quantile(il)

##      0%   25%   50%   75%  100%
##      0     6    19    63   459

#remove strains infecting lizards less than the median. I assumed that
they were less common strains.
bcprv.s <- subset(bcprv, !strain %in% c("S094","S110","S156","S055","S1
16","S165","S192","S135","S145","S202","S243","S161","S714","S080","S10
9","S102","S075","S114","S120","S167","S190","S281","S059","S071","S089
","S134","S146","S160","S284","S060","S171","S238","S372","S099","S379",
"S427","S212","S241","S269","S323","S303","S537","S561","S617","S252","
S267","S667","S178","S266","S350","S363","S467","S484","S521","S583","S
693","S225","S382","S554","S681","S694","S725","S458","S579","S661","S6
87","S705","S747","S749","S505","S539","S709","S731","S735","S745","S76
2","S772"
))
bcprv.s$frt <- as.factor(bcprv.s$frt)
prv_mod <- lme(lizard~sex+site+frt+sz+sex*site, random = ~1|strain,
              data = bcprv.s, method = "REML")
#normality assumption was violated
prv_mod2 <- lme(sqrt(lizard)~sex+site+frt+sz+sex*site, random = ~1|stra
in,
              data = bcprv.s, method = "REML")
summary(prv_mod2)

## Linear mixed-effects model fit by REML
## Data: bcprv.s
##      AIC      BIC    logLik
## 4487.346 4553.852 -2231.673
##
## Random effects:
## Formula: ~1 | strain
##      (Intercept) Residual
## StdDev:    1.024952 0.717297
##
## Fixed effects: sqrt(lizard) ~ sex + site + frt + sz + sex * site
##      Value Std.Error DF t-value p-value
## (Intercept) 0.0715367 0.25912136 1808 0.276074 0.7825
## sexM        0.0278143 0.05007578 1808 0.555445 0.5787
## siteB       0.2440937 0.06447020 1808 3.786148 0.0002
## frt2        0.0579985 0.07660794 1808 0.757082 0.4491
## frt3        0.0800063 0.11027268 1808 0.725531 0.4682
## frt4       -0.1394117 0.10362411 1808 -1.345359 0.1787
## frt5        0.1925490 0.10692779 1808 1.800738 0.0719

```

```

## frt6          0.6140035 0.09715713 1808  6.319696  0.0000
## sz            0.0746098 0.01572652 1808  4.744206  0.0000
## sexM:siteB    -0.3037423 0.12383072 1808 -2.452884  0.0143
## Correlation:
##              (Intr) sexM   siteB  frt2   frt3   frt4   frt5   frt6   s
z
## sexM          0.237

## siteB         -0.670  0.083

## frt2          0.502  0.244 -0.461

## frt3          0.692  0.314 -0.591  0.764

## frt4          0.670  0.306 -0.577  0.762  0.857

## frt5          0.681  0.310 -0.584  0.763  0.862  0.853

## frt6          0.643  0.297 -0.559  0.759  0.845  0.837  0.841

## sz           -0.875 -0.366  0.691 -0.667 -0.856 -0.835 -0.846 -0.809

## sexM:siteB    0.775 -0.040 -0.857  0.565  0.724  0.707  0.716  0.685 -
0.847
##
## Standardized Within-Group Residuals:
##              Min           Q1           Med           Q3           Max
## -3.56147181 -0.62186533  0.03643577  0.65584321  3.26083938
##
## Number of Observations: 1896
## Number of Groups: 79

prv_mod2 <- update(prv_mod2, weights=varIdent(form = ~1|frt))
#remove sex and interaction since not significant
prv_mod3 <- lme(sqrt(lizard)~site+frt+sz, random = ~1|strain,
               data = bcprv.s, method = "REML", weights=varIdent(form
= ~1|frt))
summary(prv_mod3)

## Linear mixed-effects model fit by REML
## Data: bcprv.s
##      AIC      BIC    logLik
## 4463.154 4546.303 -2216.577
##
## Random effects:
## Formula: ~1 | strain
##      (Intercept) Residual
## StdDev:      1.035347 0.8482748
##
## Variance function:

```

```

## Structure: Different standard deviations per stratum
## Formula: ~1 | frt
## Parameter estimates:
##      1      2      3      4      5      6
## 1.000000 0.850870 0.806024 0.740443 0.771076 0.890213
## Fixed effects: sqrt(lizard) ~ site + frt + sz
##      Value Std.Error DF   t-value p-value
## (Intercept) 0.5300887 0.1501154 1810  3.531208  0.0004
## siteB      0.1165964 0.0324944 1810  3.588198  0.0003
## frt2       0.1553561 0.0650204 1810  2.389342  0.0170
## frt3       0.2597434 0.0691782 1810  3.754698  0.0002
## frt4       0.0253473 0.0662594 1810  0.382547  0.7021
## frt5       0.3647970 0.0676472 1810  5.392637  0.0000
## frt6       0.7637844 0.0692557 1810 11.028459  0.0000
## sz         0.0446537 0.0053466 1810  8.351711  0.0000
## Correlation:
##      (Intr) siteB frt2 frt3 frt4 frt5 frt6
## siteB -0.062
## frt2  -0.091  0.023
## frt3   0.028  0.039  0.630
## frt4   0.008  0.037  0.647  0.703
## frt5   0.018  0.038  0.639  0.697  0.710
## frt6  -0.013  0.033  0.609  0.654  0.668  0.661
## sz    -0.534 -0.084 -0.267 -0.464 -0.444 -0.454 -0.386
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.2654812 -0.6364545  0.0197759  0.6615137  2.8120615
##
## Number of Observations: 1896
## Number of Groups: 79

hoc.prv <- summary(glht(prv_mod3, linfct = mcp("frt" = "Tukey")), test
= adjusted("holm"))
hoc.prv

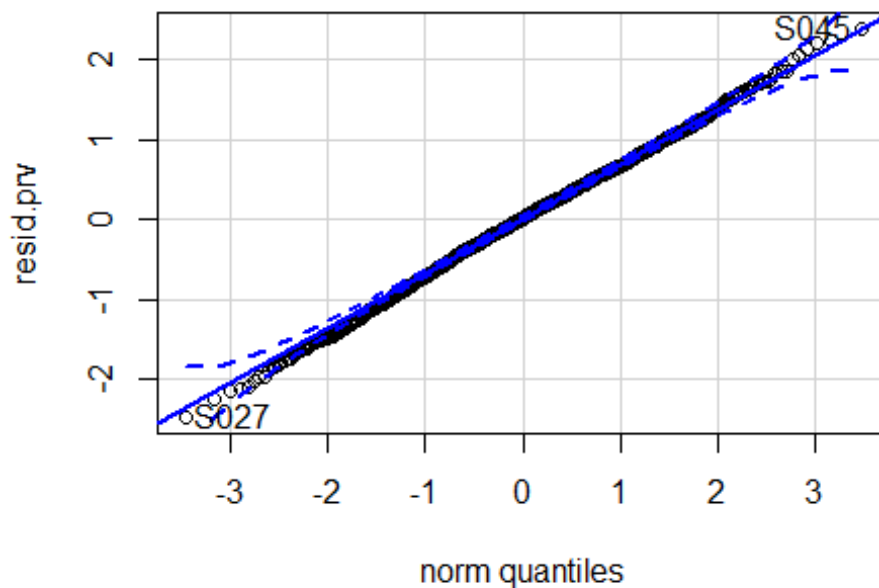
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = sqrt(lizard) ~ site + frt + sz, data = bcpr
v.s,
## random = ~1 | strain, weights = varIdent(form = ~1 | frt),
## method = "REML")
##
## Linear Hypotheses:
##      Estimate Std. Error z value Pr(>|z|)
## 2 - 1 == 0  0.15536    0.06502  2.389  0.08439 .

```

```
## 3 - 1 == 0 0.25974 0.06918 3.755 0.00121 **
## 4 - 1 == 0 0.02535 0.06626 0.383 0.70206
## 5 - 1 == 0 0.36480 0.06765 5.393 6.25e-07 ***
## 6 - 1 == 0 0.76378 0.06926 11.028 < 2e-16 ***
## 3 - 2 == 0 0.10439 0.05783 1.805 0.14548
## 4 - 2 == 0 -0.13001 0.05515 -2.357 0.08439 .
## 5 - 2 == 0 0.20944 0.05640 3.713 0.00123 **
## 6 - 2 == 0 0.60843 0.05950 10.225 < 2e-16 ***
## 4 - 3 == 0 -0.23440 0.05230 -4.482 5.92e-05 ***
## 5 - 3 == 0 0.10505 0.05325 1.973 0.14548
## 6 - 3 == 0 0.50404 0.05755 8.758 < 2e-16 ***
## 5 - 4 == 0 0.33945 0.05103 6.652 2.89e-10 ***
## 6 - 4 == 0 0.73844 0.05532 13.349 < 2e-16 ***
## 6 - 5 == 0 0.39899 0.05634 7.081 1.57e-11 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- holm method)
```

What's the difference between auto-correlation test and leveneTest here

```
#residuals----
#normality test
resid.prv <- resid(prv_mod3)
qqp(resid.prv, "norm")
```




```
## S027 S045
## 630 1069

shapiro.test(resid.prv)

##
## Shapiro-Wilk normality test
##
## data: resid.prv
## W = 0.99871, p-value = 0.1682

#auto-correlation test
summary(lm(resid.prv~bcprv.s$frt))

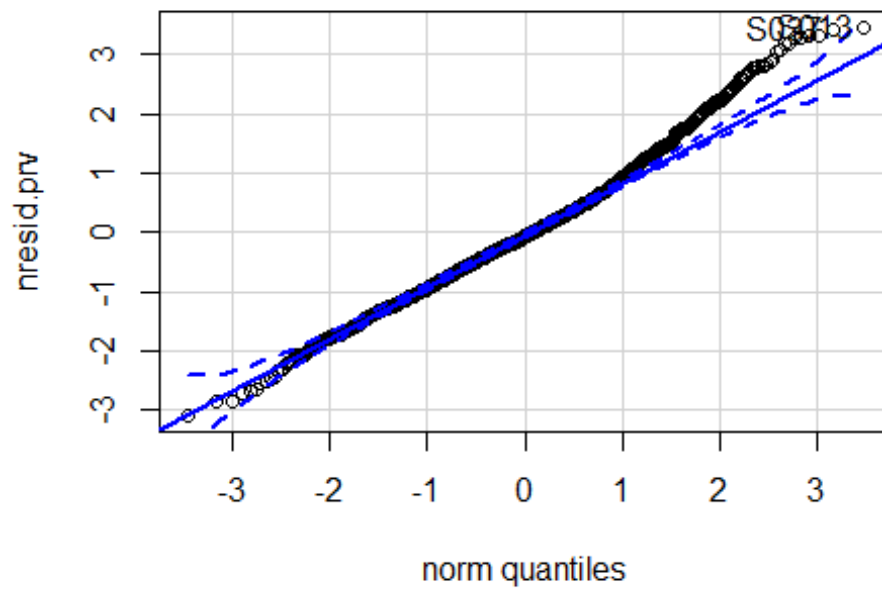
##
## Call:
## lm(formula = resid.prv ~ bcprv.s$frt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.46592 -0.44772  0.01404  0.47341  2.38540
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  9.641e-16  3.962e-02      0      1
## bcprv.s$frt2 -2.968e-15  5.604e-02      0      1
## bcprv.s$frt3 -2.984e-15  5.604e-02      0      1
## bcprv.s$frt4 -9.275e-16  5.604e-02      0      1
## bcprv.s$frt5 -1.675e-16  5.604e-02      0      1
## bcprv.s$frt6  2.923e-15  5.604e-02      0      1
##
## Residual standard error: 0.7044 on 1890 degrees of freedom
## Multiple R-squared:  7.764e-30, Adjusted R-squared:  -0.002646
## F-statistic: 2.935e-27 on 5 and 1890 DF,  p-value: 1

#homogeneity test
leveneTest(resid.prv~as.character(bcprv.s$frt))

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

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group  5   6.146 1.172e-05 ***
##      1890
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#normalized residuals mod----
nresid.prv <- residuals(prv_mod, type = "normalized")
qqp(nresid.prv,"norm")
```



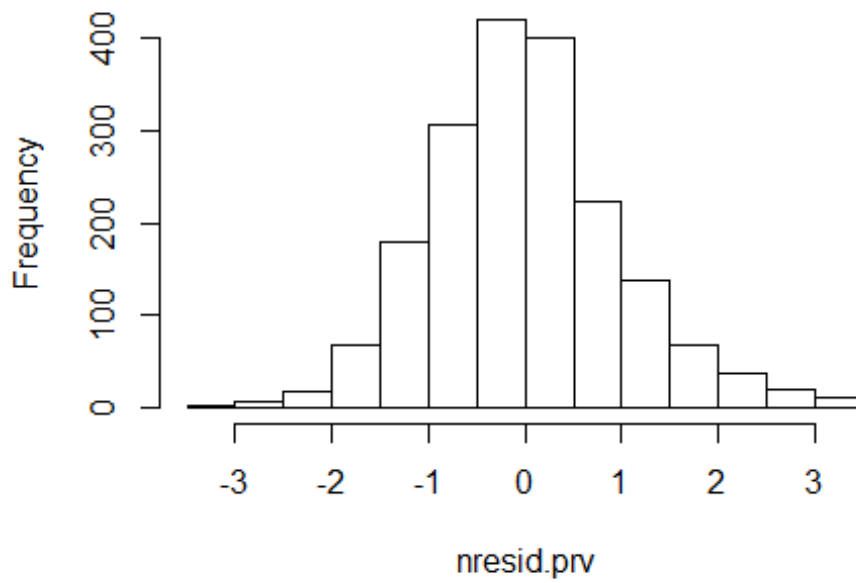
```
## S013 S037
## 303 868

shapiro.test(nresid.prv)

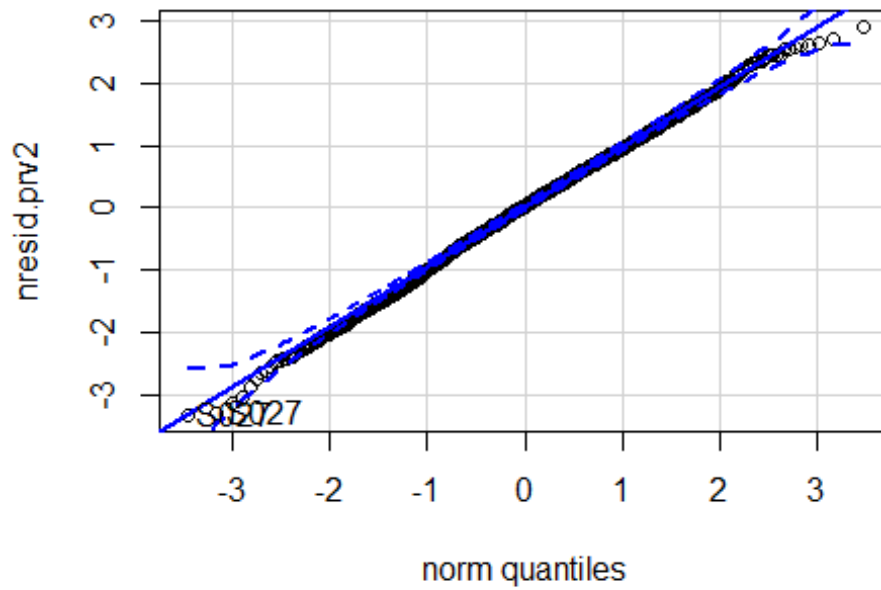
##
## Shapiro-Wilk normality test
##
## data: nresid.prv
## W = 0.98805, p-value = 1.94e-11

hist(nresid.prv)
```

Histogram of nresid.prv



```
#normalized residuals mod2----  
nresid.prv2 <- residuals(prv_mod2, type = "normalized")  
qqp(nresid.prv2,"norm")
```

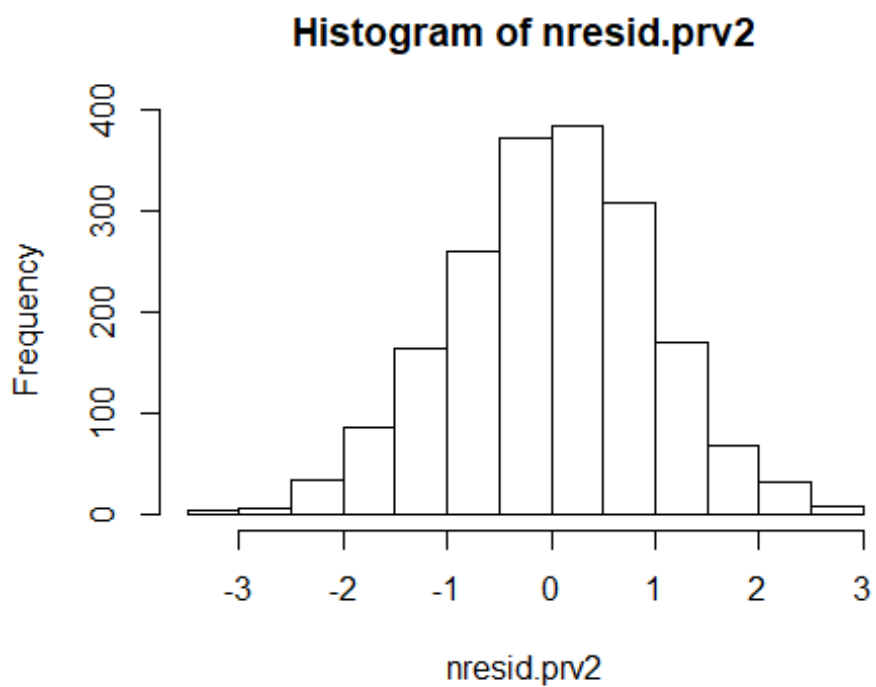


```
## S027 S027
## 630 629

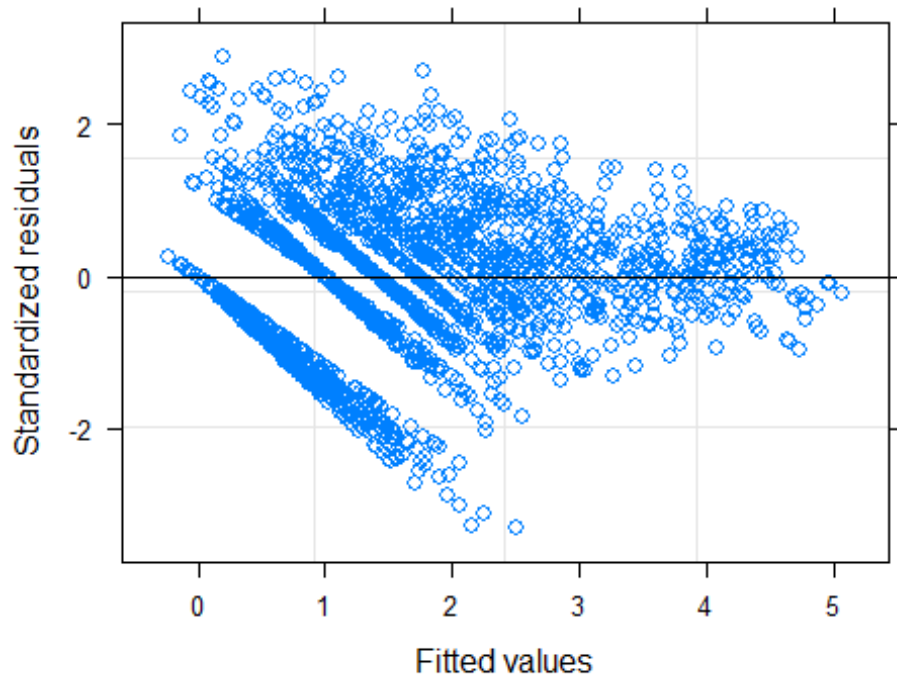
shapiro.test(nresid.prv2)

##
## Shapiro-Wilk normality test
##
## data:  nresid.prv2
## W = 0.99832, p-value = 0.05228

hist(nresid.prv2)
```



```
#homogeneity test
plot(prv_mod2)
```



```
bartlett.test(nresid.prv2~bcprv.s$frt)
```

```
##
```

```
## Bartlett test of homogeneity of variances
```

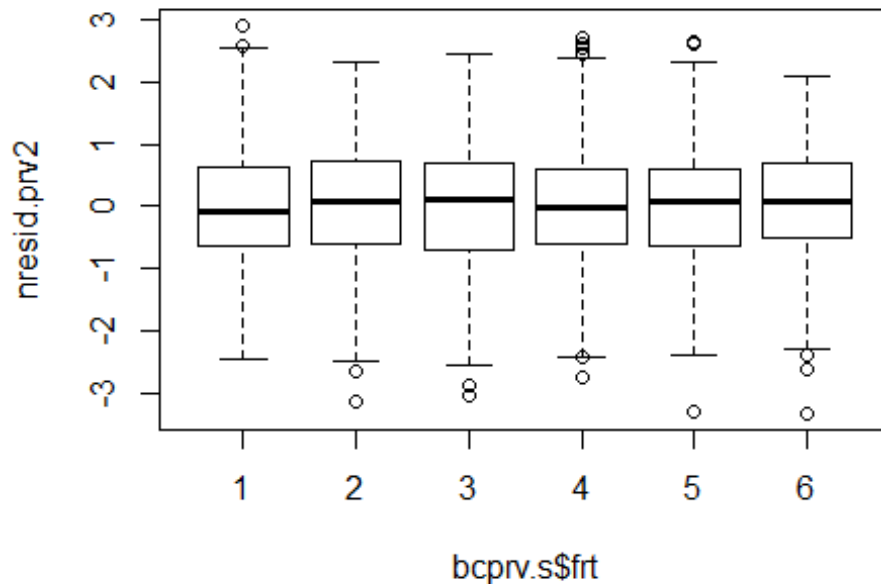
```
##
```

```
## data: nresid.prv2 by bcprv.s$frt
```

```
## Bartlett's K-squared = 0.060273, df = 5, p-value = 1
```

```
#autocorrelation test
```

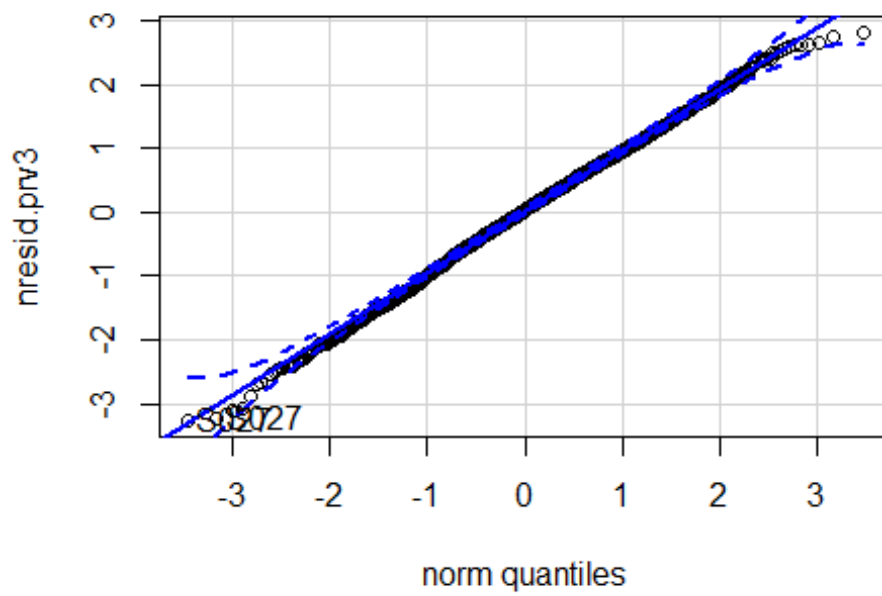
```
plot(nresid.prv2~bcprv.s$frt)
```



```
summary(lm(nresid.prv2~bcprv.s$frt))

##
## Call:
## lm(formula = nresid.prv2 ~ bcprv.s$frt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3169 -0.6252  0.0334  0.6672  2.8982
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.806e-15  5.504e-02      0      1
## bcprv.s$frt2  1.003e-15  7.784e-02      0      1
## bcprv.s$frt3  1.970e-15  7.784e-02      0      1
## bcprv.s$frt4  4.049e-15  7.784e-02      0      1
## bcprv.s$frt5  2.425e-15  7.784e-02      0      1
## bcprv.s$frt6  2.853e-15  7.784e-02      0      1
##
## Residual standard error: 0.9785 on 1890 degrees of freedom
## Multiple R-squared:  1.599e-30, Adjusted R-squared:  -0.002646
## F-statistic: 6.044e-28 on 5 and 1890 DF,  p-value: 1

#normalized residuals mod3----
nresid.prv3 <- residuals(prv_mod3, type = "normalized")
qqp(nresid.prv3,"norm")
```

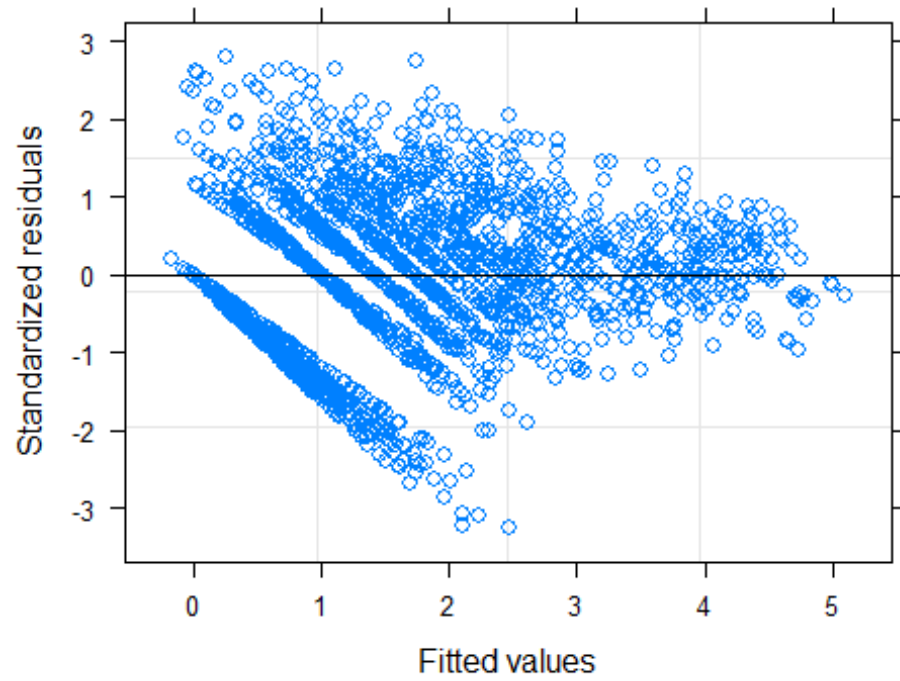


```
## S027 S027
## 630 629

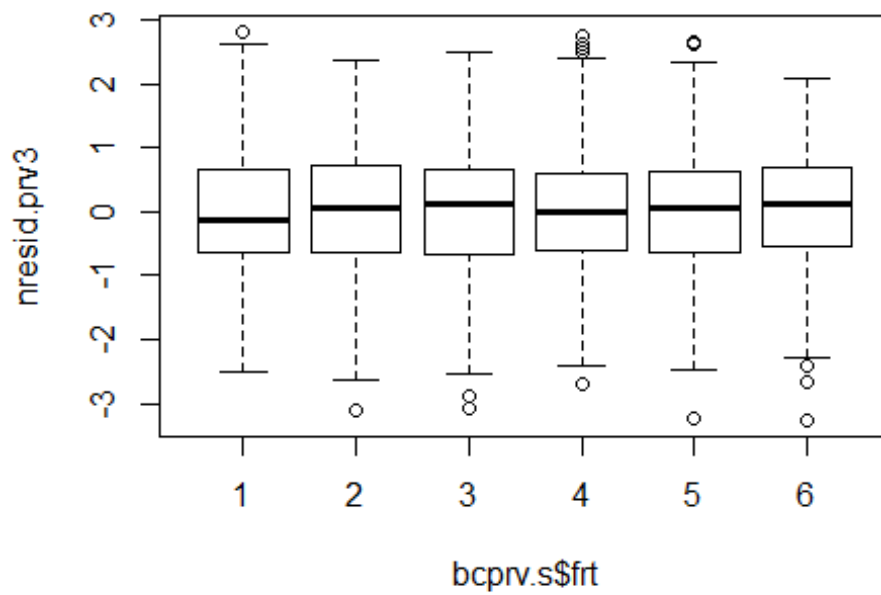
shapiro.test(nresid.prv3)

##
## Shapiro-Wilk normality test
##
## data: nresid.prv3
## W = 0.99829, p-value = 0.04783

#homogeneity test
plot(prv_mod3)
```

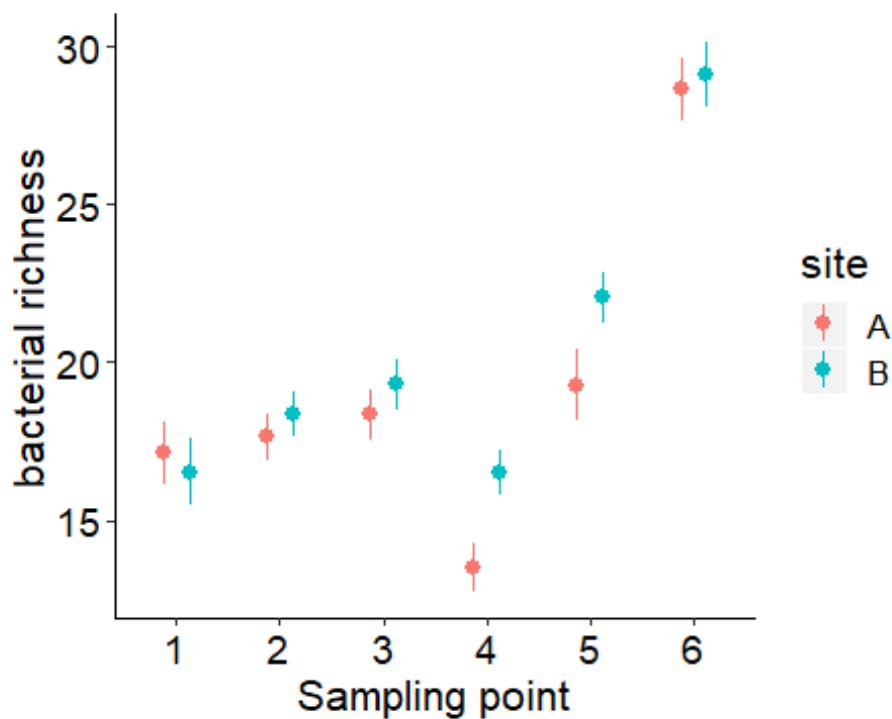


```
#autocorrelation test
plot(nresid.prv3~bcprv.s$frit)
```



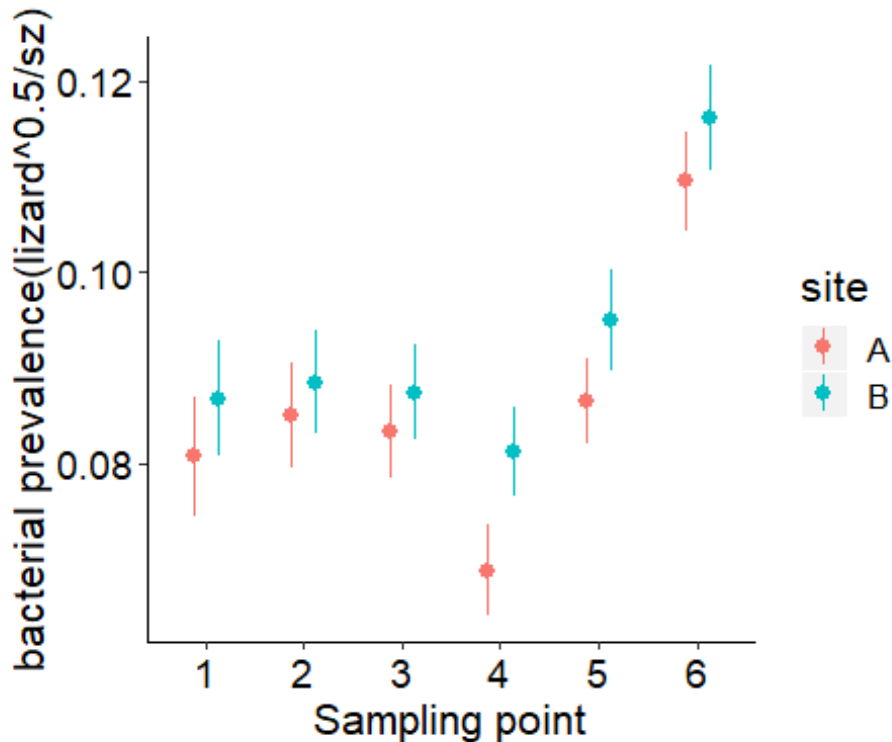

```
summary(lmer(nresid.prv3~frt+(1|strain),REML = F,data=bcprv.s))

## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: nresid.prv3 ~ frt + (1 | strain)
## Data: bcprv.s
##
##      AIC      BIC   logLik deviance df.resid
##  5310.2   5354.5  -2647.1   5294.2    1888
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3408 -0.6511  0.0202  0.6768  2.8769
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## strain   (Intercept)  0.0000    0.0000
## Residual                    0.9554    0.9775
## Number of obs: 1896, groups: strain, 79
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  1.175e-15  5.499e-02      0
## frt2         -3.840e-15  7.776e-02      0
## frt3         -4.108e-15  7.776e-02      0
## frt4         -1.137e-15  7.776e-02      0
## frt5         -1.657e-16  7.776e-02      0
## frt6          4.093e-15  7.776e-02      0
##
## Correlation of Fixed Effects:
##      (Intr) frt2   frt3   frt4   frt5
## frt2 -0.707
## frt3 -0.707  0.500
## frt4 -0.707  0.500  0.500
## frt5 -0.707  0.500  0.500  0.500
## frt6 -0.707  0.500  0.500  0.500  0.500
```



```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
## Fit: lme.formula(fixed = Sequence.Type.Richness ~ site_code + Sampling.point,
## data = bcfrr, random = ~1 | Lizard, weights = varIdent(form = ~1
## |
## Sampling.point), method = "REML")
##
## Linear Hypotheses:
## Estimate Std. Error z value Pr(>|z|)
## 2 - 1 == 0 1.1806 0.8596 1.373 0.339259
## 3 - 1 == 0 1.9846 0.8954 2.216 0.133320
## 4 - 1 == 0 -1.7806 0.8677 -2.052 0.133320
## 5 - 1 == 0 3.8163 0.9675 3.944 0.000560 ***
## 6 - 1 == 0 12.0625 0.9998 12.065 < 2e-16 ***
## 3 - 2 == 0 0.8040 0.7231 1.112 0.339259
## 4 - 2 == 0 -2.9613 0.6882 -4.303 0.000135 ***
## 5 - 2 == 0 2.6357 0.8112 3.249 0.006943 **
## 6 - 2 == 0 10.8819 0.8488 12.821 < 2e-16 ***
## 4 - 3 == 0 -3.7652 0.7305 -5.155 2.29e-06 ***
## 5 - 3 == 0 1.8317 0.8479 2.160 0.133320
## 6 - 3 == 0 10.0779 0.8838 11.403 < 2e-16 ***
## 5 - 4 == 0 5.5970 0.8183 6.839 7.95e-11 ***
```

```
## 6 - 4 == 0 13.8431 0.8555 16.182 < 2e-16 ***
## 6 - 5 == 0 8.2461 0.9565 8.621 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- holm method)
```



```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = sqrt(lizard) ~ site + frt + sz, data = bcpr
v.s,
## random = ~1 | strain, weights = varIdent(form = ~1 | frt),
## method = "REML")
##
## Linear Hypotheses:
## Estimate Std. Error z value Pr(>|z|)
## 2 - 1 == 0 0.15536 0.06502 2.389 0.08439 .
## 3 - 1 == 0 0.25974 0.06918 3.755 0.00121 **
## 4 - 1 == 0 0.02535 0.06626 0.383 0.70206
## 5 - 1 == 0 0.36480 0.06765 5.393 6.25e-07 ***
## 6 - 1 == 0 0.76378 0.06926 11.028 < 2e-16 ***
## 3 - 2 == 0 0.10439 0.05783 1.805 0.14548
## 4 - 2 == 0 -0.13001 0.05515 -2.357 0.08439 .
## 5 - 2 == 0 0.20944 0.05640 3.713 0.00123 **
```

```
## 6 - 2 == 0 0.60843 0.05950 10.225 < 2e-16 ***
## 4 - 3 == 0 -0.23440 0.05230 -4.482 5.92e-05 ***
## 5 - 3 == 0 0.10505 0.05325 1.973 0.14548
## 6 - 3 == 0 0.50404 0.05755 8.758 < 2e-16 ***
## 5 - 4 == 0 0.33945 0.05103 6.652 2.89e-10 ***
## 6 - 4 == 0 0.73844 0.05532 13.349 < 2e-16 ***
## 6 - 5 == 0 0.39899 0.05634 7.081 1.57e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- holm method)
```