LMM_fisheries

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```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 4.0.5

## Loading required package: Matrix
```

```
library(broom.mixed)
library(knitr)
library(patchwork)
library(nlme)
```

```
##
## Attaching package: 'nlme'

## The following object is masked from 'package:lme4':
##
##     lmList

## The following object is masked from 'package:dplyr':
##
##     collapse
```

```
library(mgcv)
```

```
## This is mgcv 1.8-33. For overview type 'help("mgcv-package")'.
```

```
library(car)
```

```
## Loading required package: carData
```

```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

1. Input Data; Basic Data Processing

```
x<-read.csv("fullSetWithMask.csv",as.is=TRUE,
            na.strings=c("NA",".","","  "))
dim(x) ## Check the dimension (number of rows and columns) of the data matrix.
```

```
## [1] 193439     10
```

```
head(x)
```

```
##   X     uniqueid year month     cpue  logcpue taxa_grouped_weight
## 1 1 00000-BCSCAM 2009     7 24.61905 3.203520          Lutjanidae
## 2 2 00000-BCSCAM 2013     8 19.33333 2.961831          Lutjanidae
## 3 3 00000-BCSCAM 2012     2 32.76190 3.489266          Lutjanidae
## 4 4 00000-BCSCAM 2010     3 10.28571 2.330756          Carangidae
## 5 5 00000-BCSCAM 2013    10  9.52381 2.253795          Carangidae
## 6 6 00000-BCSCAM 2008     8 33.33333 3.506558          Lutjanidae
##                                                                    agremiacion_fed
## 1 Federacion de Sociedades Cooperativas Pesqueras Zona Centro de Baja California Sur
## 2 Federacion de Sociedades Cooperativas Pesqueras Zona Centro de Baja California Sur
## 3 Federacion de Sociedades Cooperativas Pesqueras Zona Centro de Baja California Sur
## 4 Federacion de Sociedades Cooperativas Pesqueras Zona Centro de Baja California Sur
## 5 Federacion de Sociedades Cooperativas Pesqueras Zona Centro de Baja California Sur
## 6 Federacion de Sociedades Cooperativas Pesqueras Zona Centro de Baja California Sur
##   rr coop_edad_10
## 1  3          1.4
## 2  3          1.4
## 3  3          1.4
## 4  3          1.4
## 5  3          1.4
## 6  3          1.4
```

```
## Drop Column of Row Numbers:
x<-x[,-1]
## Rename a Few Variables:
colnames(x)[colnames(x)=="taxa_grouped_weight"]<-"taxa"
colnames(x)[colnames(x)=="agremiacion_fed"]<-"fed"
colnames(x)[colnames(x)=="coop_edad_10"]<-"age"
colnames(x)[colnames(x)=="rr"]<-"region"
x$uniqueid<-as.factor(x$uniqueid)
x$fed<-as.factor(x$fed)
x$taxa<-as.factor(x$taxa)
x$region<-as.factor(x$region)
x$yearFactor<-as.factor(x$year)
x$monthFactor<-as.factor(x$month)
```

2. Basic Summaries

```
table(x$taxa,useNA="always")
```

```
##
##     Carangidae  Centropomidae      Cichlidae      Clupeidae Elasmobranchii
##          13299          11935          11541            291          12759
##      Gerreidae     Haliotidae     Lutjanidae      Mugilidae    Octopodidae
##           8294           3586          16117           5183           4555
## Ommastrephidae      Ostreidae          OTRAS    Palinuridae     Pectinidae
##            472           2568          38234           6234            860
##      Penaeidae     Portunidae     Sciaenidae     Scombridae     Serranidae
##          18103           6642          12300           3704          16002
##  Stichopodidae           <NA>
##            760              0
```

```
table(x$region,useNA="always")
```

```
##
##     1     2     3     4     5     6  <NA>
##  4450 10633 62428 50213 22450 43265     0
```

```
length(unique(x$uniqueid))
```

```
## [1] 182
```

```
length(unique(x$fed))
```

```
## [1] 54
```

```
table(x$year)
```

```
##
##  2008  2009  2010  2011  2012  2013  2014  2015  2016
## 19573 20485 20413 19346 21198 20111 20515 24172 27626
```

```
summary(x$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.100   1.800   2.900   3.706   5.900   8.500
```

```
summary(x$age[x$uniqueid=="00000-BCSCAM"])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     1.4     1.4     1.4     1.4     1.4     1.4
```

```
x$age2<-((10*x$age) + (x$year - 2016))
summary(x$age2)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   -6.00   15.00   27.00   33.29   53.00   85.00
```

```
table(x$age2<0)
```

```
##
##  FALSE   TRUE
## 192186   1253
```

```
tbl<-table(as.character(x$uniqueid)[x$age2<0]); tbl
```

```
##
## 00549-TAB 00685-BCS 00747-YUC 00748-YUC
##       109       226       212       706
```

```
table(x$age2[x$uniqueid %in% names(tbl)],
      as.character(x$uniqueid[x$uniqueid %in% names(tbl)]),
      useNA="always")
```

```
##
##        00549-TAB 00685-BCS 00747-YUC 00748-YUC <NA>
##   -6           0         0         3         0    0
##   -5          35         0        35         0    0
##   -4          32         0        68         0    0
##   -3          23         0        28         0    0
##   -2          17       130        35       420    0
##   -1           2        96        43       286    0
##   0            0       102        31       180    0
##   1            0       127        24       440    0
##   2            0       194        53       455    0
##   3          136       200         0       265    0
##   4            0        89         0       438    0
##   5            0       145         0       401    0
##   6            0        51         0       454    0
##   <NA>         0         0         0         0    0
```

```
## Naive Age Fix (the years associated w/ these samples may be incorrect):
x$age[(x$uniqueid=="00549-TAB")&(x$age2<0)]<-(x$age[(x$uniqueid=="00549-TAB")&(x$age2<0)] + 0.5)
x$age[(x$uniqueid=="00685-BCS")&(x$age2<0)]<-(x$age[(x$uniqueid=="00685-BCS")&(x$age2<0)] + 0.2)
x$age[(x$uniqueid=="00747-YUC")&(x$age2<0)]<-(x$age[(x$uniqueid=="00747-YUC")&(x$age2<0)] + 0.6)
x$age[(x$uniqueid=="00748-YUC")&(x$age2<0)]<-(x$age[(x$uniqueid=="00748-YUC")&(x$age2<0)] + 0.2)
x$age2<-((10*x$age) + (x$year - 2016))
summary(x$age2)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.00   15.00   27.00   33.31   53.00   85.00
```

2.2 Taxa by coop

```
tbl<-table(x$uniqueid,x$taxa)
dim(tbl)
```

```
## [1] 182  21
```

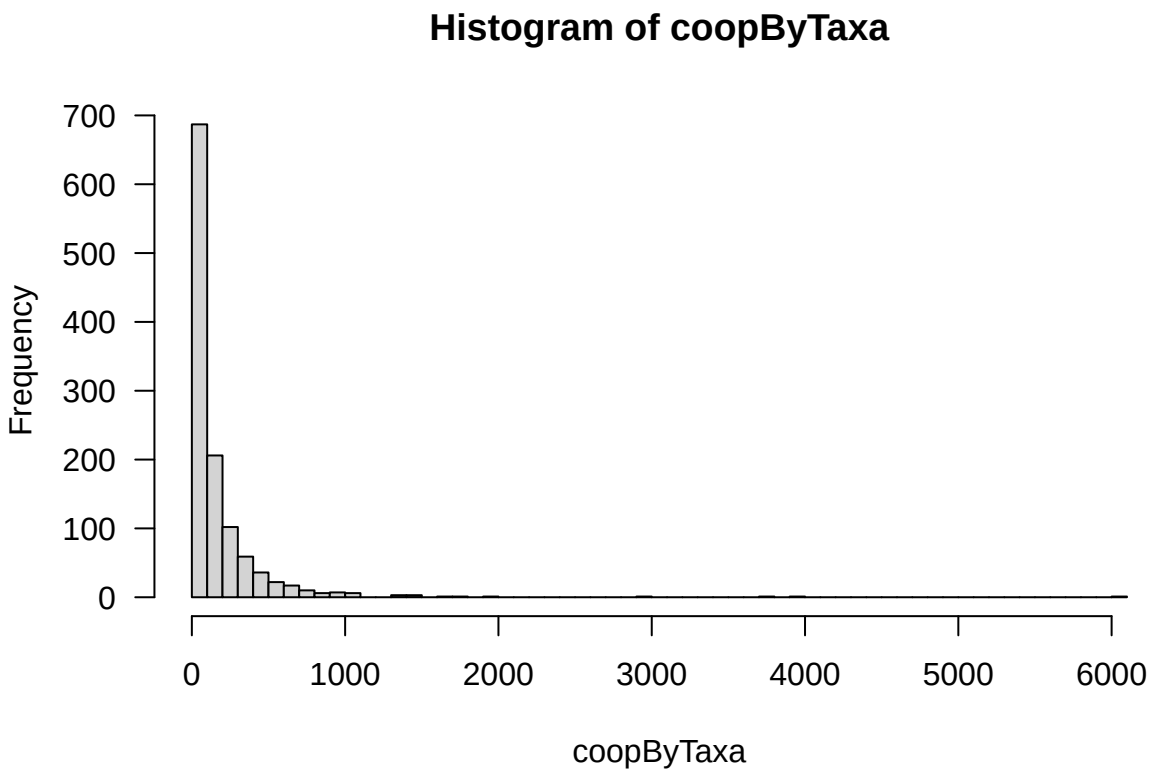
```
summary(coopByTaxa<-as.numeric(tbl))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.00    0.00    0.00   50.61   12.00 6074.00
```

```
table(coopByTaxa==0)
```

```
##
## FALSE  TRUE
##  1171  2651
```

```
coopByTaxa<-coopByTaxa[coopByTaxa>0]
hist(coopByTaxa,nclass=50,las=1)
```



3. Client's LME model

Note, from the nlme::ACF documentation: "This method function calculates the empirical autocorrelation function for the within-group residuals from an lme fit. The autocorrelation values are calculated using pairs of residuals within the innermost group level. The autocorrelation function is useful for investigating serial correlation models for equally spaced data."

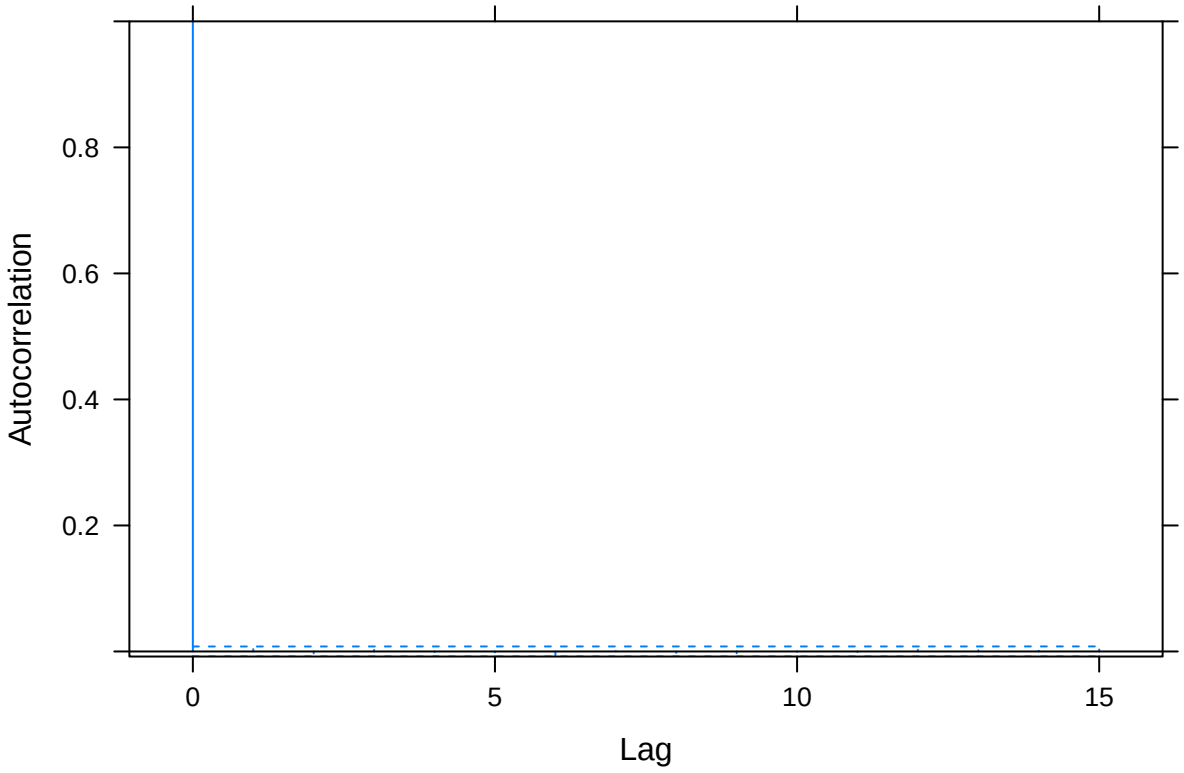
3.1 Full data set

```
keep<-(!is.na(x$logcpue))
lme.out<-nlme::lme(logcpue ~ age + yearFactor + monthFactor + region + taxa,
                   random = ~ 1|fed/uniqueid, data=x,subset=keep)
summary(lme.out)$tTable
```

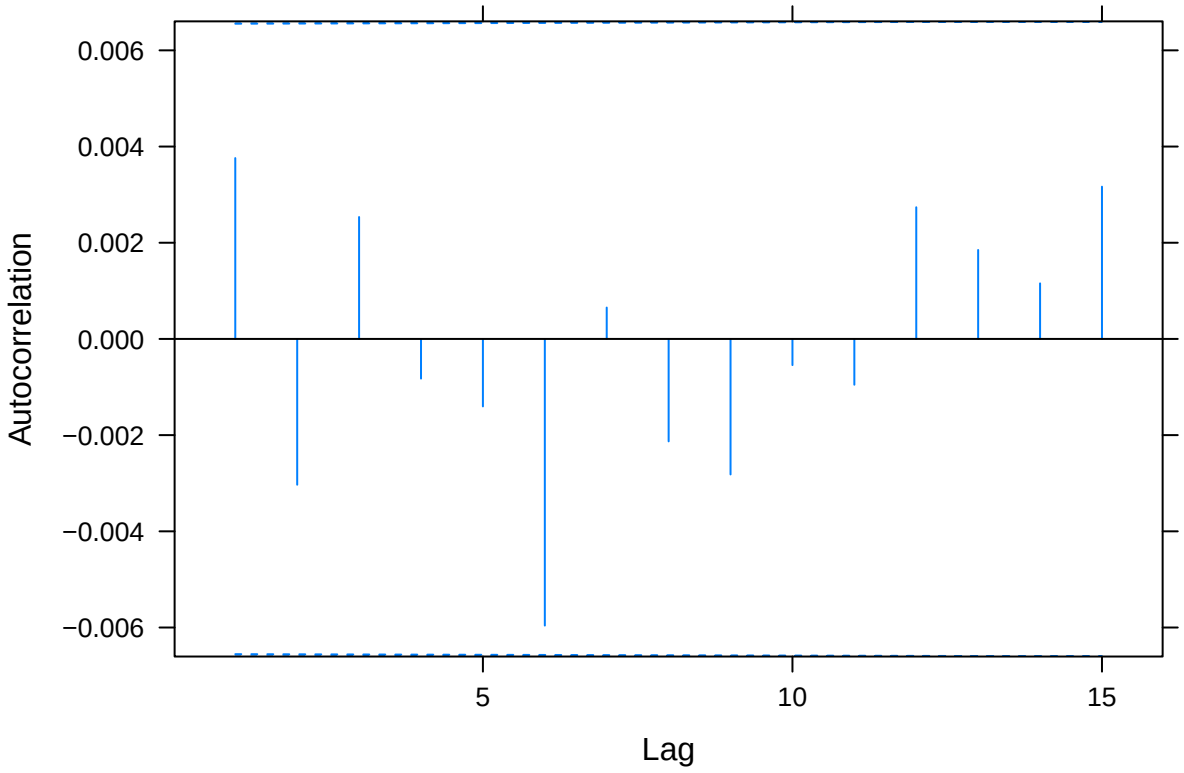
```
##                         Value  Std.Error     DF      t-value       p-value
## (Intercept)         1.403663443 0.41978772 183217   3.34374582  8.267199e-04
## age                -0.195871810 0.05006573 183217  -3.91229336  9.145672e-05
## yearFactor2009      0.027262125 0.01630194 183217   1.67232427  9.446210e-02
## yearFactor2010     -0.109544495 0.01649317 183217  -6.64180891  3.107173e-11
## yearFactor2011      0.023352258 0.01669296 183217   1.39892864  1.618361e-01
## yearFactor2012     -0.073363190 0.01635476 183217  -4.48573939  7.270559e-06
## yearFactor2013     -0.009533991 0.01666463 183217  -0.57210948  5.672485e-01
## yearFactor2014      0.016596349 0.01664188 183217   0.99726401  3.186377e-01
```

```
## yearFactor2015      0.005374221 0.01612237 183217   0.33333944  7.388785e-01
## yearFactor2016      0.056012774 0.01570492 183217   3.56657478  3.617698e-04
## monthFactor2        0.035024597 0.01879784 183217   1.86322403  6.243235e-02
## monthFactor3        0.128733929 0.01928850 183217   6.67412803  2.494106e-11
## monthFactor4        0.108429593 0.01939200 183217   5.59145938  2.254885e-08
## monthFactor5        0.153125799 0.01900357 183217   8.05773959  7.818014e-16
## monthFactor6        0.177137033 0.01885260 183217   9.39589312  5.735454e-21
## monthFactor7        0.234956217 0.01801286 183217  13.04380656  7.173641e-39
## monthFactor8        0.190238515 0.01790645 183217  10.62402447  2.345190e-26
## monthFactor9        0.261755659 0.01857591 183217  14.09113312  4.546237e-45
## monthFactor10       0.212403148 0.01807485 183217  11.75130642  7.139438e-32
## monthFactor11       0.167565715 0.01839680 183217   9.10841468  8.440205e-20
## monthFactor12       0.132478801 0.01870975 183217   7.08073436  1.439046e-12
## region2             0.539233765 0.61064720    124   0.88305287  3.789165e-01
## region3             2.078880747 0.46305246     52   4.48951448  3.990735e-05
## region4             1.779437804 0.43295413    124   4.10999157  7.140397e-05
## region5            -0.009984212 0.50885880    124  -0.01962079  9.843774e-01
## region6             0.679820678 0.43890199    124   1.54891226  1.239513e-01
## taxaCentropomidae  -0.965678518 0.02264463 183217 -42.64491975  0.000000e+00
## taxaCichlidae      -0.239872411 0.03169818 183217  -7.56738736  3.825719e-14
## taxaClupeidae       2.519489134 0.09733478 183217  25.88477781 1.824149e-147
## taxaElasmobranchii -0.035590802 0.02147244 183217  -1.65751100  9.741792e-02
## taxaGerreidae      -0.748917162 0.02405025 183217 -31.13968742 2.518876e-212
## taxaHaliotidae      1.314033166 0.03325820 183217  39.51005498  0.000000e+00
## taxaLutjanidae     -0.426832776 0.01958706 183217 -21.79156898 3.797143e-105
## taxaMugilidae       0.003277102 0.02865295 183217   0.11437223  9.089429e-01
## taxaOctopodidae     1.240885722 0.03009656 183217  41.23015203  0.000000e+00
## taxaOmmastrephidae  2.599530248 0.08024495 183217  32.39493979 1.449267e-229
## taxaOstreidae       1.952268769 0.03814656 183217  51.17811472  0.000000e+00
## taxaOTRAS          -0.558432769 0.01741086 183217 -32.07382565 4.319535e-225
## taxaPalinuridae     0.663597312 0.02706263 183217  24.52080346 1.452410e-132
## taxaPectinidae      3.039571059 0.06591888 183217  46.11077891  0.000000e+00
## taxaPenaeidae       0.095062030 0.02406377 183217   3.95042196  7.804271e-05
## taxaPortunidae      0.907555138 0.03057724 183217  29.68074025 3.920776e-193
## taxaSciaenidae     -0.170047445 0.02124898 183217  -8.00261698  1.225070e-15
## taxaScombridae      0.047579863 0.03057967 183217   1.55593096  1.197262e-01
## taxaSerranidae      0.556641242 0.02009494 183217  27.70057070 1.534479e-168
## taxaStichopodidae   3.192020724 0.06563502 183217  48.63288706  0.000000e+00
```

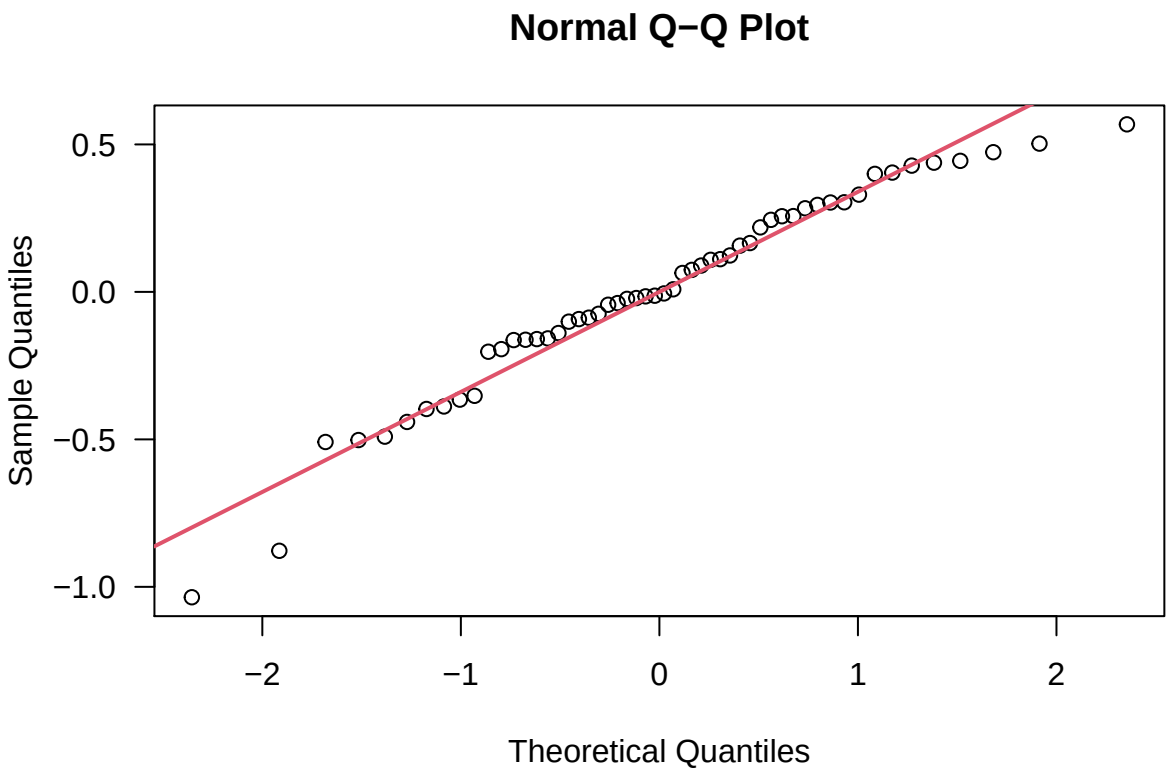
```
acf.lme<-nlme::ACF(lme.out,maxLag=15)
plot(acf.lme,alpha=0.01/15)
```



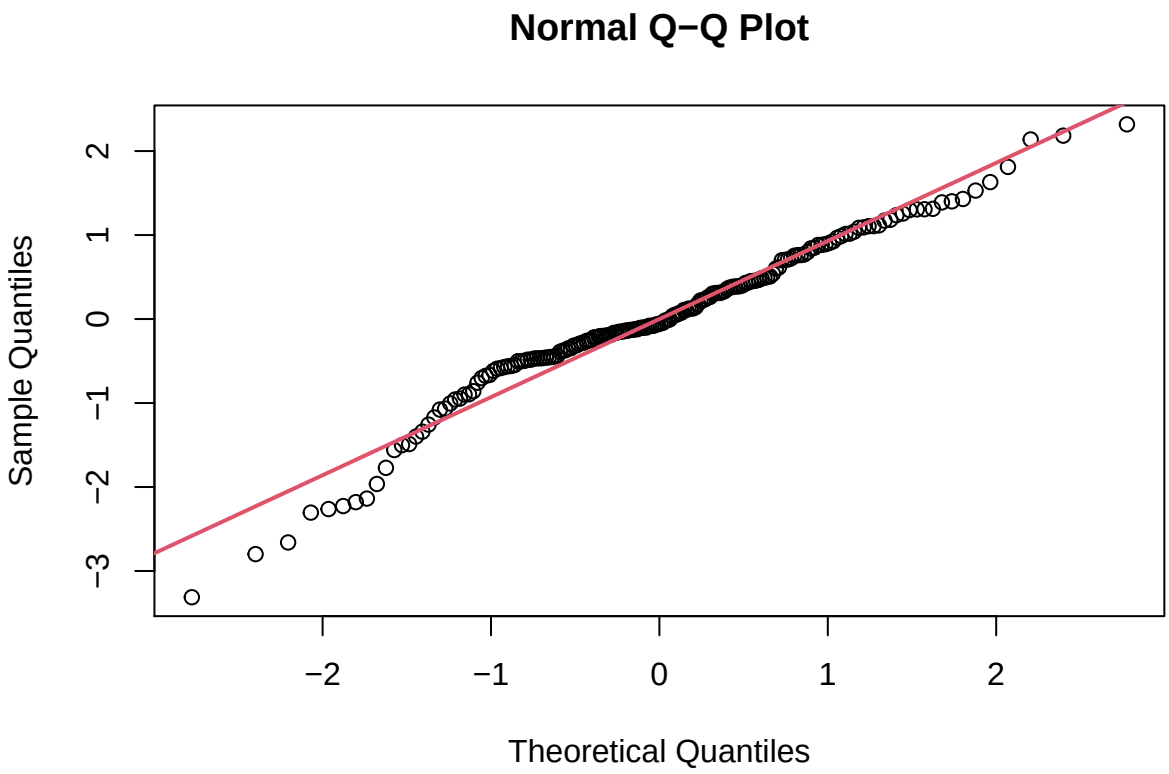

```
acf.lme<-acf.lme[-1,]
plot(acf.lme,alpha=0.005)
```




```
qqnorm(fedn.re<-unlist(nlme::ranef(lme.out)$fed),las=1)
abline(a=0,b=sd(fedn.re),lwd=2,col=2)
```




```
qqnorm(uid.re<-unlist(nlme::ranef(lme.out)$uniqueid))
abline(a=0,b=sd(uid.re),lwd=2,col=2)
```



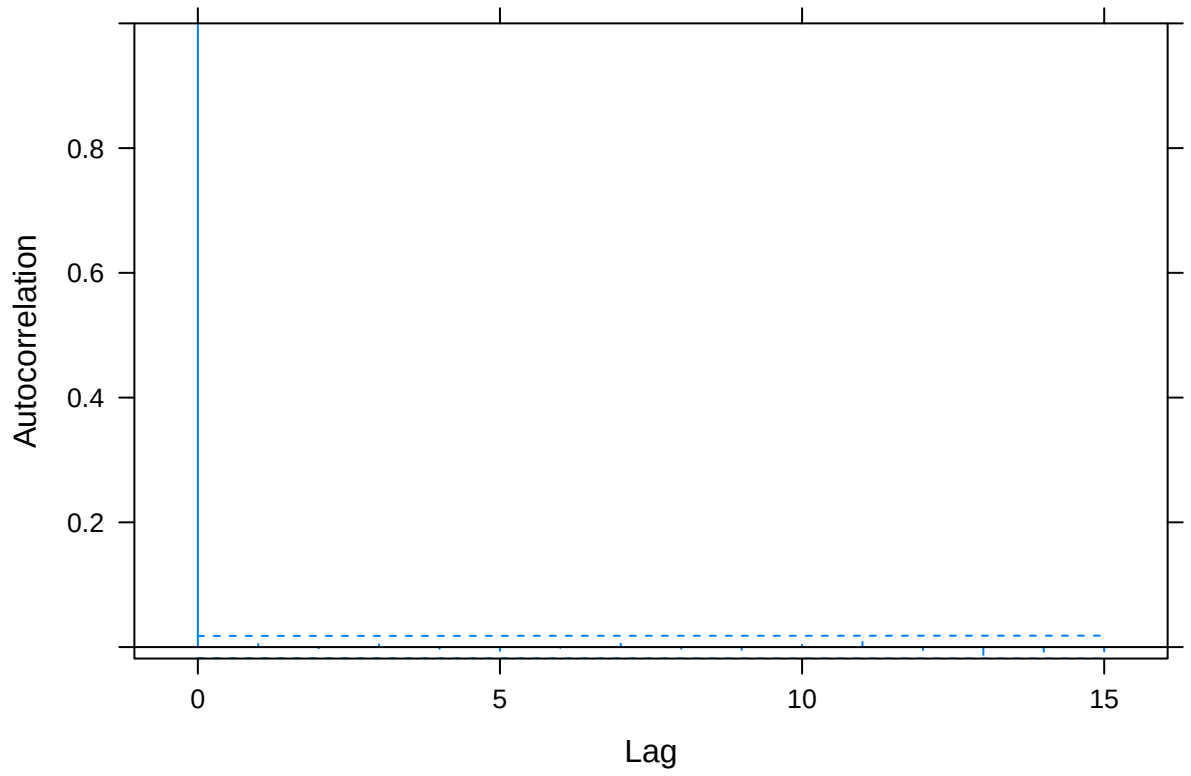
3.2 Single taxa model

```
keep<-((x$taxa=="OTRAS")&(!is.na(x$logcpue)))
otras.out<-nlme::lme(logcpue ~ age + yearFactor + monthFactor + region,
                     random = ~ 1|fed/uniqueid, data=x,subset=keep)
summary(otras.out)$tTable
```

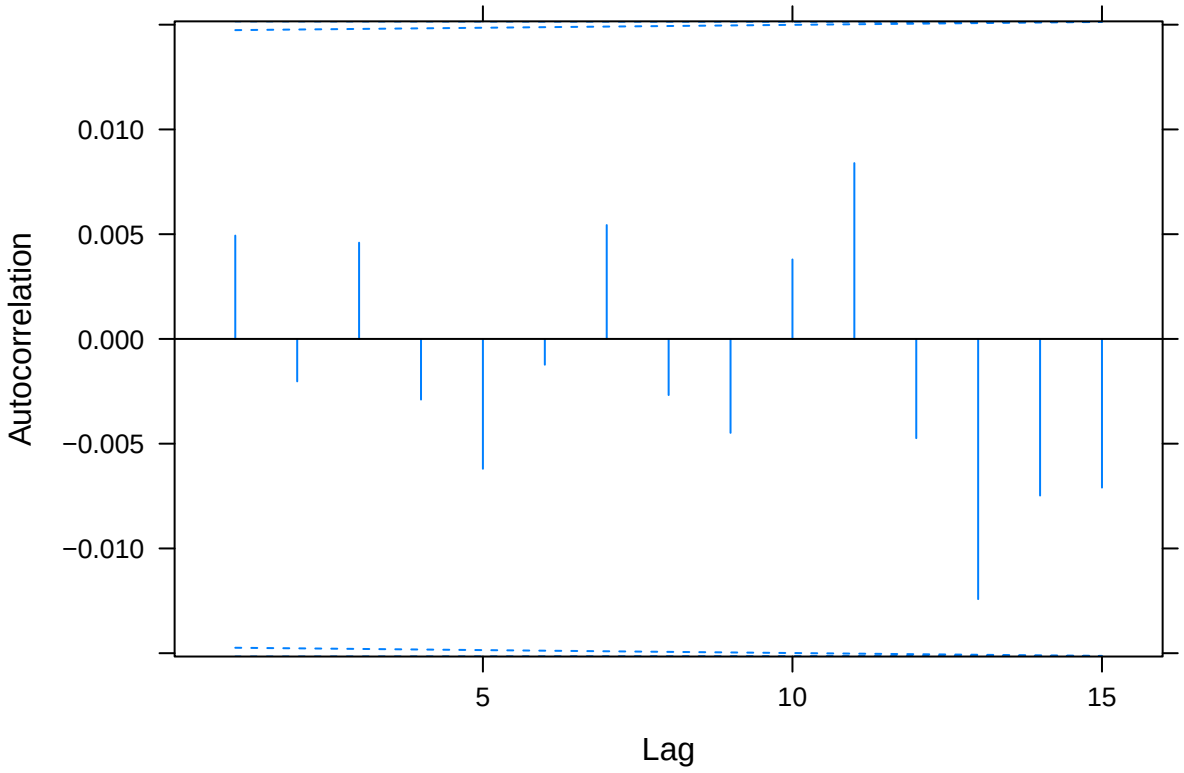
```
##                      Value  Std.Error    DF     t-value      p-value
## (Intercept)     1.08138634 0.84421113 36105  1.28094300 2.002219e-01
## age            -0.28365849 0.08467958 36105 -3.34978610 8.095677e-04
## yearFactor2009  0.04673876 0.03509398 36105  1.33181716 1.829287e-01
## yearFactor2010 -0.09705218 0.03579162 36105 -2.71158925 6.699319e-03
## yearFactor2011  0.13060751 0.03577393 36105  3.65091294 2.616786e-04
## yearFactor2012  0.15795034 0.03464800 36105  4.55871433 5.163641e-06
## yearFactor2013  0.08099962 0.03501745 36105  2.31312171 2.072154e-02
## yearFactor2014  0.09254657 0.03552113 36105  2.60539506 9.180602e-03
## yearFactor2015  0.19715933 0.03424718 36105  5.75695037 8.633969e-09
## yearFactor2016  0.24684516 0.03310370 36105  7.45672392 9.068682e-14
## monthFactor2    0.04320187 0.03999201 36105  1.08026257 2.800325e-01
## monthFactor3    0.03424256 0.03893670 36105  0.87944178 3.791676e-01
## monthFactor4   -0.02316908 0.03917392 36105 -0.59144151 5.542283e-01
## monthFactor5    0.08849087 0.03770718 36105  2.34679076 1.894126e-02
## monthFactor6    0.20005985 0.03774298 36105  5.30058458 1.161094e-07
## monthFactor7    0.13976807 0.03740019 36105  3.73709550 1.864450e-04
```

```
## monthFactor8   -0.04185668 0.03853893 36105 -1.08608830 2.774472e-01
## monthFactor9   -0.15388514 0.04165876 36105 -3.69394395 2.211281e-04
## monthFactor10  -0.04671011 0.04076475 36105 -1.14584556 2.518667e-01
## monthFactor11  -0.00108303 0.04102094 36105 -0.02640188 9.789369e-01
## monthFactor12   0.02164900 0.04099621 36105  0.52807330 5.974517e-01
## region2         0.50800884 1.03291245    87  0.49182178 6.240840e-01
## region3         2.51046462 0.88150159    46  2.84794111 6.557393e-03
## region4         2.13323557 0.87085476    87  2.44958822 1.630636e-02
## region5         0.29610271 0.93507039    87  0.31666355 7.522575e-01
## region6         0.50720661 0.85832077    87  0.59092897 5.561001e-01
```

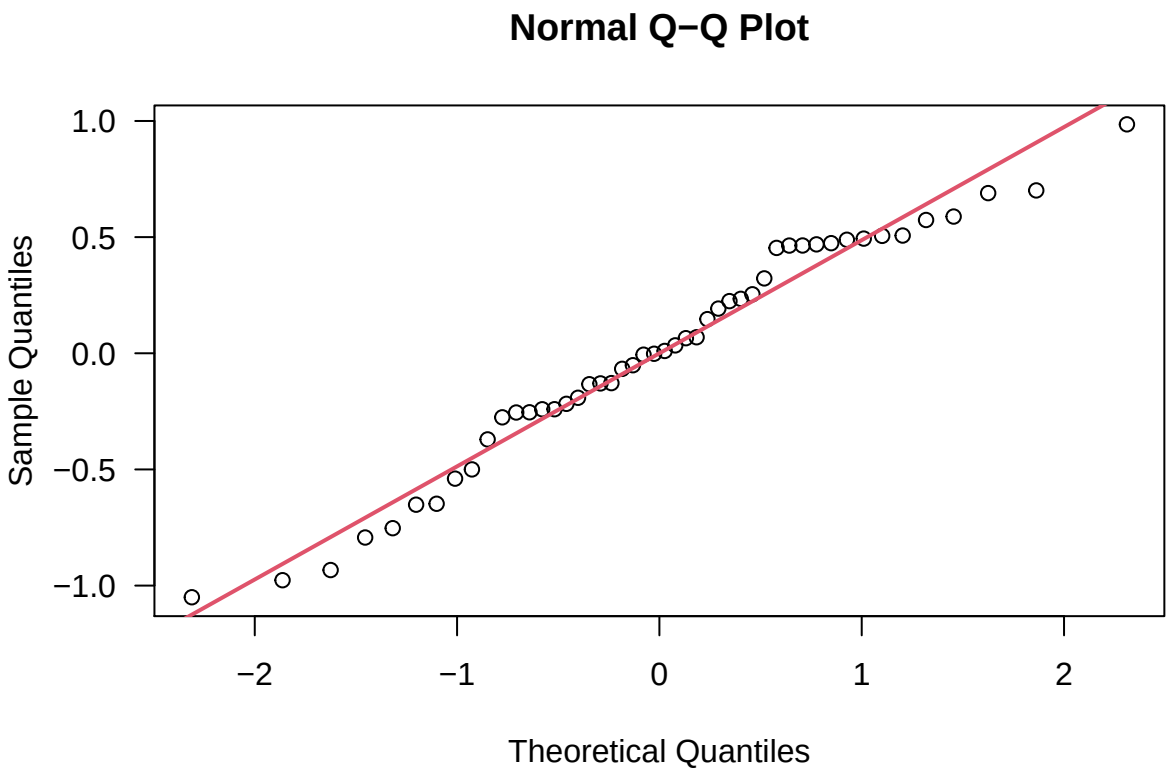
```
acf.otras<-nlme::ACF(otras.out,maxLag=15)
plot(acf.otras,alpha=0.01/15)
```



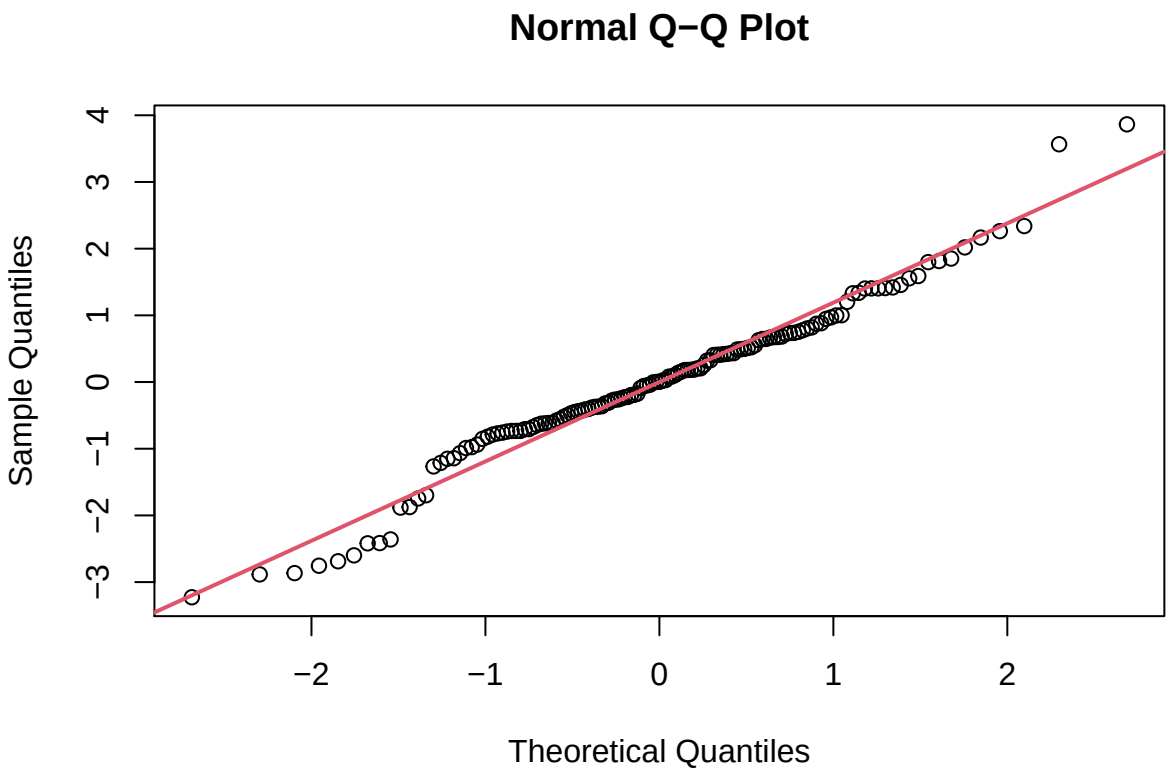

```
acf.otras<-acf.otras[-1,]
plot(acf.otras,alpha=0.005)
```




```
qqnorm(fedn.re<-unlist(nlme::ranef(otras.out)$fed),las=1)
abline(a=0,b=sd(fedn.re),lwd=2,col=2)
```




```
qqnorm(uid.re<-unlist(nlme::ranef(otras.out)$uniqueid))
abline(a=0,b=sd(uid.re),lwd=2,col=2)
```



4. Your mgcv Models

EDA

```
response_summary <- x %>%
    summarise(mean = mean(logcpue, na.rm=TRUE),
              median = median(logcpue, na.rm=TRUE),
              variance = var(logcpue, na.rm=TRUE),
              IQR = IQR(logcpue, na.rm=TRUE),
              sd = sd(logcpue, na.rm=TRUE),
              min = min(logcpue, na.rm=TRUE),
              max = max(logcpue, na.rm=TRUE))
knitr::kable(response_summary, caption = "Summary Statistics for \n the logcpue")
```

Table 1: Summary Statistics for the logcpue

mean	median	variance	IQR	sd	min	max
1.740824	1.966113	4.71467	2.888958	2.171329	-7.863267	10.04138

```
ggplot(data = x, aes(x = logcpue)) +
  geom_histogram(fill = "darkgreen", color = "black") +
  labs(x = "logcpue", y = "Count",
```

```
       title = "Distribution of logcpue",
       caption = "Figure 1") +
  theme_bw()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 10000 rows containing non-finite values (stat_bin).
```

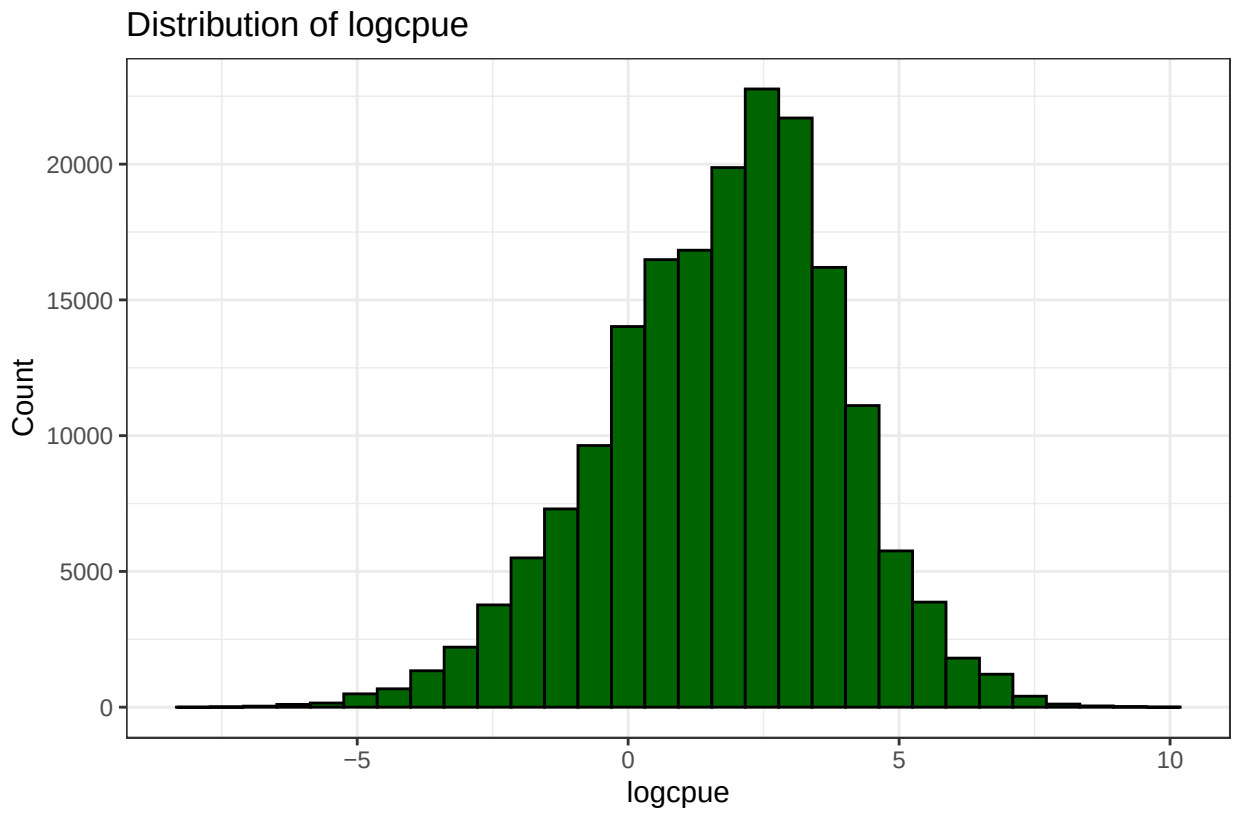


Figure 1

In this dataset, the response variable is `logcpue`, which represents catch per unit of effort, measured during different time points (Figure 1, Table 1). The distribution of this variable is unimodal and slightly skewed to the left. The center, defined by median, is 1.97. The spread, defined by the interquartile range (IQR), is 2.89. There are no evident outliers based on the histogram shown in Figure 1. To better capture the distribution of logcpue for individual cooperation, a random sample of 30 cooperation were selected, and their logcpue measured at different time points were plotted (Figure 2). Indeed, cooperation exhibit different patterns for the distribution of logcpue. Some shows a bimodel distribution, while some shows a unimodel distribution, This suggests that the distribution of logcpue differs based on cooperations, so we decided to include it as an individual level in our LMM model.

```
set.seed(031622)
# get sample of 30 cooperations

sample_org <- x %>%
  distinct(uniqueid) %>%
  sample_n(30) %>% pull()
# get data for those cooperation
```

```
sample_data <- x %>%
  filter(uniqueid %in% sample_org)
# make a histogram of the response for each lemur
ggplot(data = sample_data, aes(x = logcpue)) +
  geom_histogram(fill = "darkgreen", color = "black") +
  facet_wrap(~ uniqueid, scales = "free") +
  labs(x = "logcpue",
       title = "Distribution of logcpue by randomly sampled 30 cooperation",
       caption = "Figure 2") +
  theme_bw()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 1821 rows containing non-finite values (stat_bin).
```

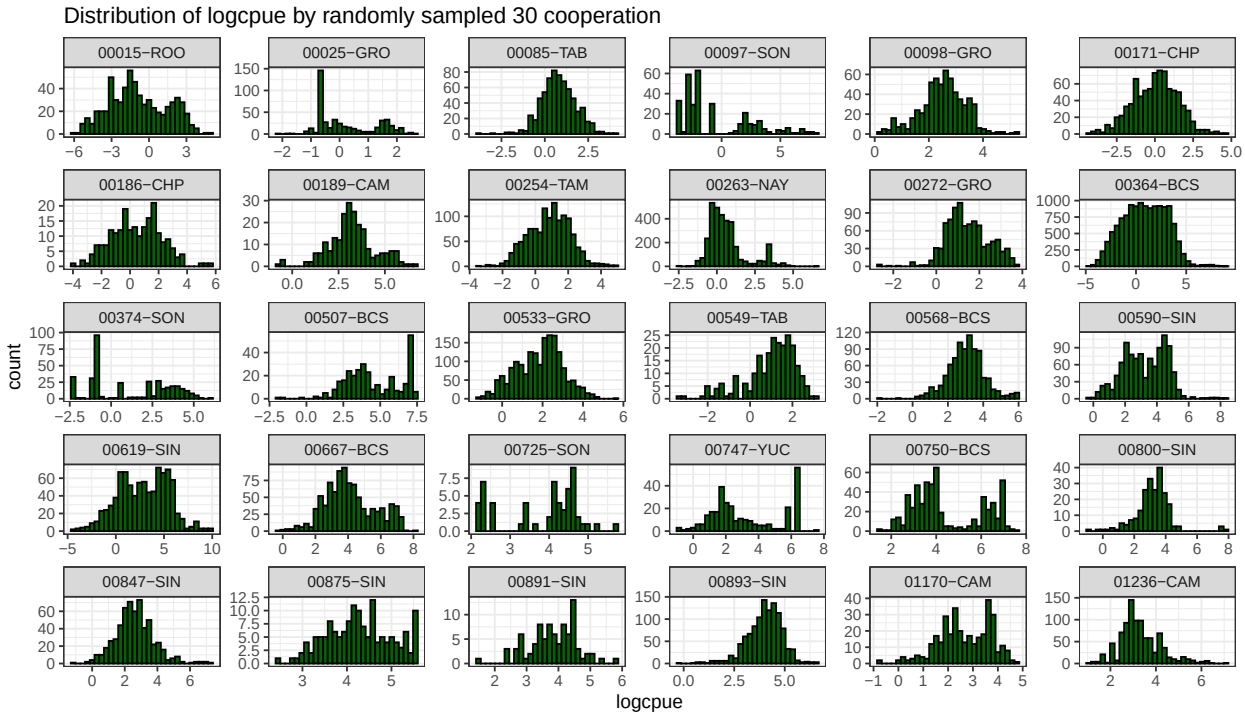


Figure 2

Other variables in the data that are of interests include year and month of each fishing event, region, taxa, and age of the federations. Figure 3 shows the relationships between year and logcpue for 30 randomly selected cooperations. Figure 4 shows the relationships between month and logcpue for 30 randomly selected cooperations. While some cooperations have a constant logcpue value across years or months, some cooperations have varying logcpue based on the year or month the fishery takes place, indicating that the effects of year or month on logcpue varies based on cooperations.

```
ggplot(data = sample_data, aes(x = yearFactor, y = logcpue)) +
  geom_boxplot(fill = "darkgreen", color = "black") +
  facet_wrap(~ uniqueid, scales = "free") +
  labs(x = "Year",
       y = "logcpue",
       title = "logcpue vs year",
```

```
       caption = "Figure 3") +
  theme_bw()
```

```
## Warning: Removed 1821 rows containing non-finite values (stat_boxplot).
```

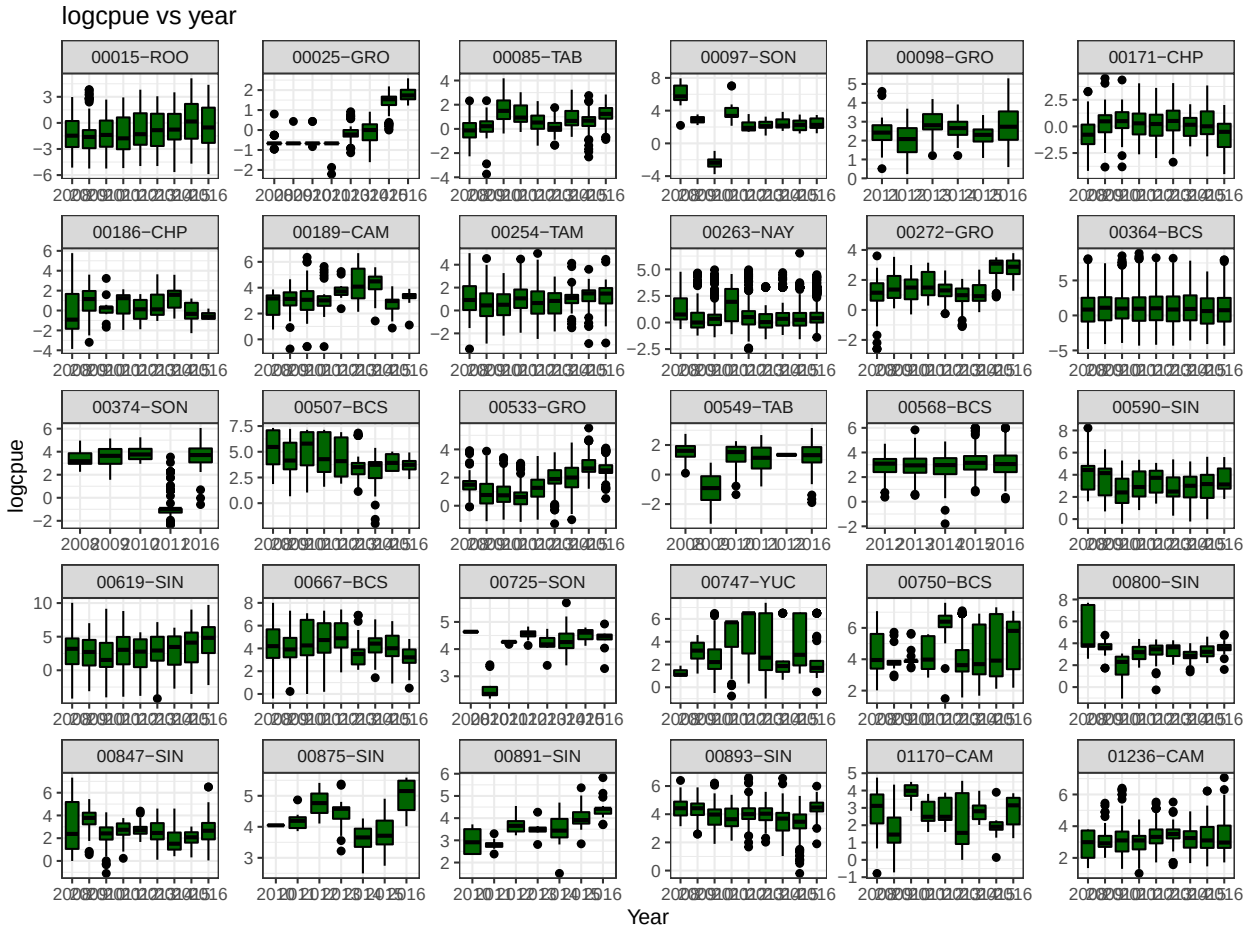


Figure 3

```
ggplot(data = sample_data, aes(x = monthFactor, y = logcpue)) +
  geom_boxplot(fill = "darkgreen", color = "black") +
  facet_wrap(~ uniqueid, scales = "free") +
  labs(x = "Month",
       y = "logcpue",
       title = "logcpue vs month",
       caption = "Figure 4") +
  theme_bw()
```

```
## Warning: Removed 1821 rows containing non-finite values (stat_boxplot).
```

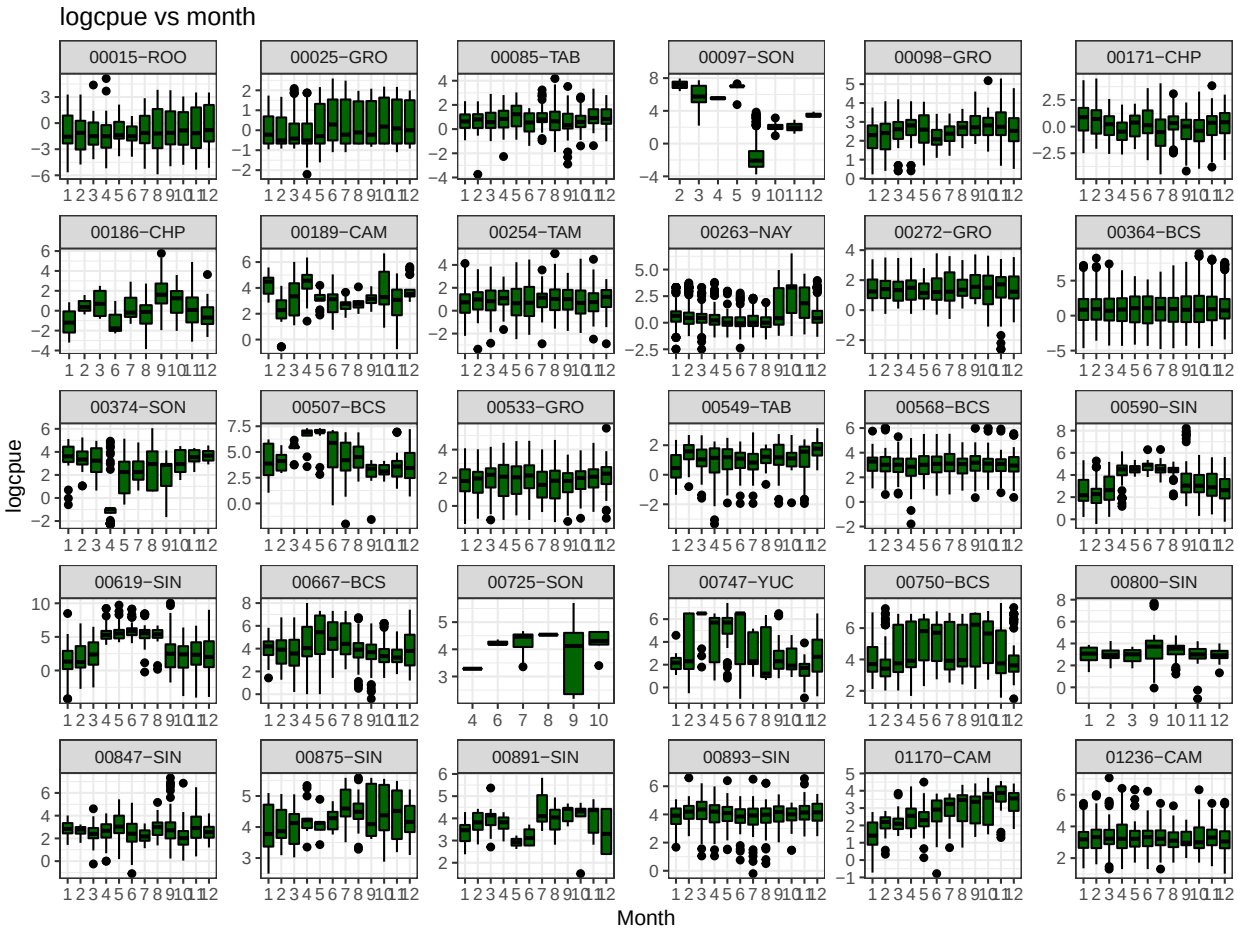


Figure 4

For simplicity purposes, we decided to combine year and month to make a new continuous variable that incorporated both year and month.

```
x$yearMonth <- ((x$year - min(x$year)) *12 + x$month)
```

In addition to year and month, region and taxa also play an important role in explaining logcpue. In particular, logcpue differs based on the region where the fisheries take place and on the taxa of the fish caught (Figure 5,6). Therefore, these two variables are worth including in the final models.

```
ggplot(data = x, aes(x = region, y = logcpue)) +
  geom_boxplot(fill = "darkgreen", color = "black") +
  labs(x = "Region",
       y = "logcpue",
       title = "logcpue vs. region",
       caption = "Figure 5") +
  theme_bw()
```

```
## Warning: Removed 10000 rows containing non-finite values (stat_boxplot).
```

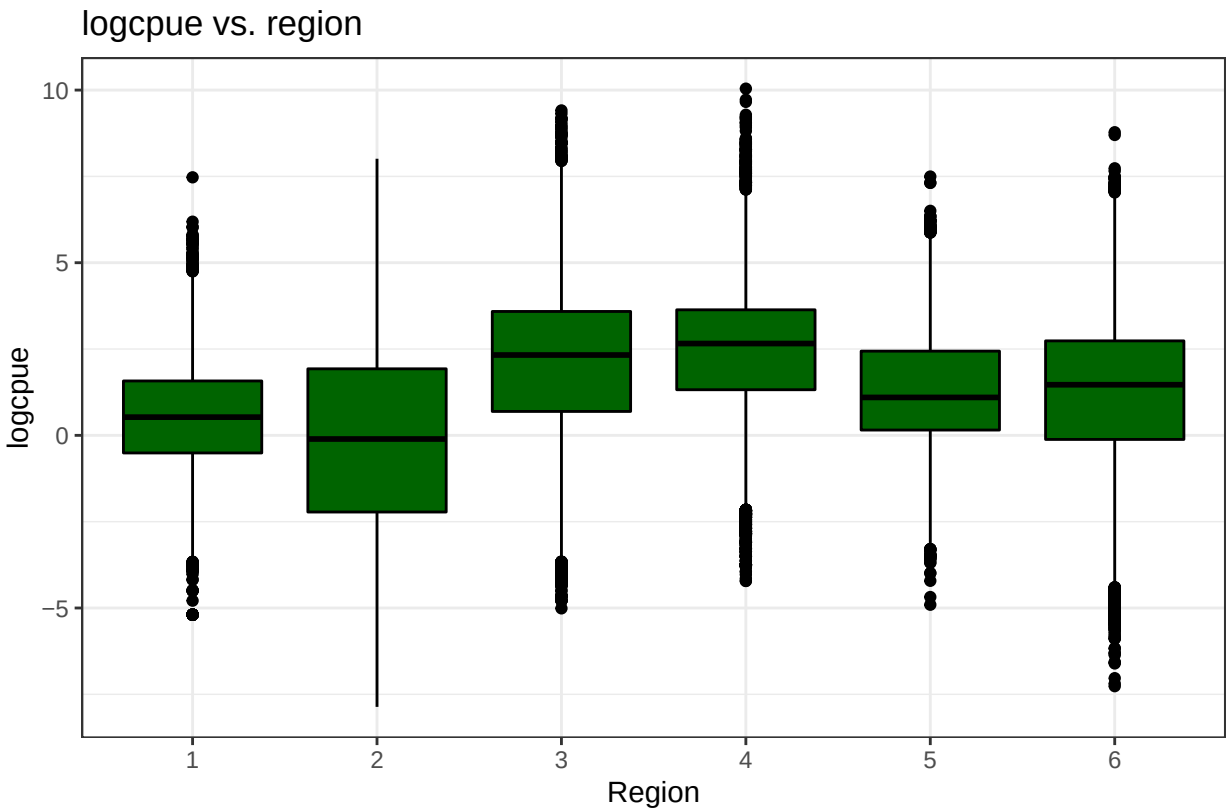


Figure 5

```
ggplot(data = x, aes(x = taxa, y = logcpue)) +
  geom_boxplot(fill = "darkgreen", color = "black") +
  labs(x = "Taxa",
       y = "logcpue",
       title = "logcpue vs. taxa",
       caption = "Figure 6") +
  theme_bw()
```

```
## Warning: Removed 10000 rows containing non-finite values (stat_boxplot).
```

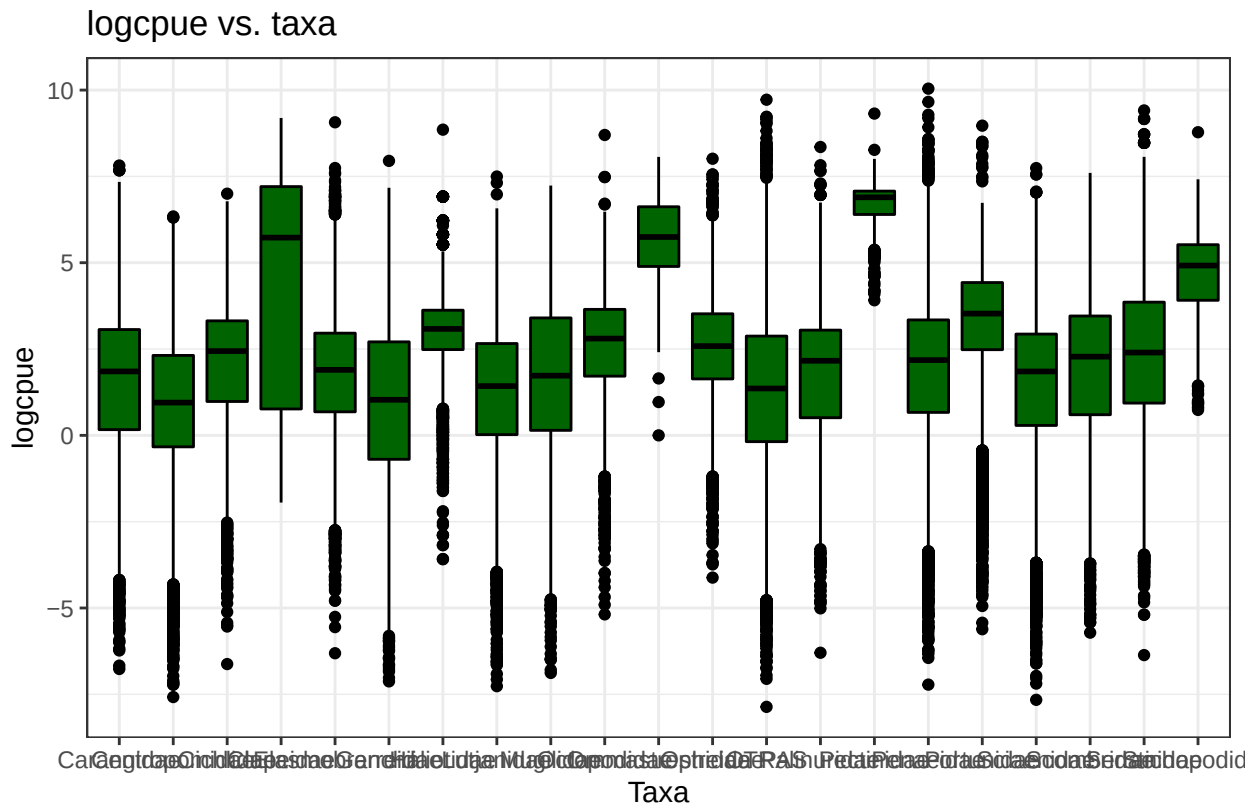


Figure 6

Methods

Both models using mgcv and lme are included in this section.

Since catch per unit of efforts (cpue) were measured at different time points for each cooperation and that cooperations from the same federations tend to have similar distribution of logcpue, a multilevel model analysis was used to model the distribution of logcpue. The multilevel analysis was done at three levels. The first level included time points when cpue were collected; the second level included individual cooperations (`uniqueid`); and the third level included federations (`fed`). To test whether a multilevel model is necessary to capture the distribution of logcpue, an unconditional means model in which there are no predictors at any level was first fitted, and intraclass correlation was calculated to estimate the relative variability between cooperations and between federations. Indeed, the intraclass correlation for cooperations is about 0.22 and for federations is about 0.26, which means that the average correlation between any two responses from the same cooperations or from the same federations is about 0.22 and 0.26 respectively. This suggests that about 48% of the variability in the logcpue is explained by cooperation to cooperation variability and federation to federation variability. Knowing cooperation and federation, therefore, can explain almost half of the variability in the data, providing evidence that the multilevel model structure is useful in this setting.

```
unconditional_means_mgcv <- bam(logcpue ~ 1 + s(fed, bs = "re") + s(uniqueid, bs = "re"),
           data = x, na.action = na.omit)
summary(unconditional_means_mgcv)
```

```
##
## Family: gaussian
## Link function: identity
```

```
##
## Formula:
## logcpue ~ 1 + s(fed, bs = "re") + s(uniqueid, bs = "re")
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.2669     0.1898   11.94   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##               edf Ref.df      F p-value
## s(fed)       38.5     53 710455 0.00906 **
## s(uniqueid) 140.5    181 238192 0.00028 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.396   Deviance explained = 39.7%
## fREML = 3.5679e+05  Scale est. = 2.8475    n = 183439
```

```
unconditional_means <- lme(logcpue ~ 1,
                           list(fed = ~1, uniqueid = ~1),
                            data = x, na.action = na.omit)
summary(unconditional_means)
```

```
## Linear mixed-effects model fit by REML
##  Data: x
##        AIC    BIC    logLik
##   713580.5 713621 -356786.2
##
## Random effects:
##  Formula: ~1 | fed
##         (Intercept)
## StdDev:    1.189196
##
##  Formula: ~1 | uniqueid %in% fed
##         (Intercept) Residual
## StdDev:    1.093864 1.687456
##
## Fixed effects: logcpue ~ 1
##                Value Std.Error     DF  t-value p-value
## (Intercept) 2.266913  0.189815 183257 11.94275       0
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -4.25341107 -0.59958742 -0.01052429  0.60605097  5.54494371
##
## Number of Observations: 183439
## Number of Groups:
##               fed uniqueid %in% fed
##                54                182
```

Next, to understand the effect of time before adding other Level One covariates, the model that only includes year and month as Level One predictors was fitted. The Pseudo R^2 estimating the change in within-

cooperation variance between the unconditional means and the Model with Time is about 0.42. Therefore, understanding changes of time (i.e. years) accounts for 42% variability in logcpue.

```
model_time <- lme(logcpue ~ yearMonth, random = list(fed = ~yearMonth + 1, uniqueid = ~yearMonth + 1),
                  data = x, na.action = na.omit)
summary(model_time)
```

```
## Linear mixed-effects model fit by REML
##  Data: x
##        AIC      BIC    logLik
##   704386.3 704477.4 -352184.2
##
## Random effects:
##  Formula: ~yearMonth + 1 | fed
##  Structure: General positive-definite, Log-Cholesky parametrization
##             StdDev      Corr
## (Intercept) 1.466296838 (Intr)
## yearMonth   0.008859054 -0.69
##
##  Formula: ~yearMonth + 1 | uniqueid %in% fed
##  Structure: General positive-definite, Log-Cholesky parametrization
##             StdDev     Corr
## (Intercept) 1.27828351 (Intr)
## yearMonth   0.01280207 -0.537
## Residual    1.64283974
##
## Fixed effects: logcpue ~ yearMonth
##                 Value  Std.Error     DF  t-value p-value
## (Intercept) 2.2279527 0.23275696 183256 9.572013  0.0000
## yearMonth   0.0004842 0.00166952 183256 0.290035  0.7718
##  Correlation:
##           (Intr)
## yearMonth -0.632
##
## Standardized Within-Group Residuals:
##          Min           Q1          Med           Q3          Max
## -4.432812192 -0.578993635 -0.006224082  0.588661168  5.862754093
##
## Number of Observations: 183439
## Number of Groups:
##               fed uniqueid %in% fed
##                54                182
```

```
# Pseudo R^2
sigm_moda <- 1.687456^2
sigm_madb <- 1.64283974
r <- (sigm_moda - sigm_madb)/sigm_moda
r
```

```
## [1] 0.4230605
```

Based on the EDA and model with only time as level one predictors, we decided to include `yearMonth`, `region`, and `taxa` as our level one predictors. `age2` was included as level three (federation) predictor since

we hypothesized that the age of federation would impact the efficiency of catching fish (logcpue) of its subsidiary cooperation. Therefore, two models were fitted. One that includes interactions between age of federations and region and between age of federations and taxa, and one that does not include any interactions. AIC and BIC of both models were compared. Since both AIC and BIC are lower for model with additional interaction effects, providing evidence that model with interactions is a better model. One thing to note is that no random slopes were included in level two or three in both model because adding them make the model too complex and too computational heavy.

The interaction between age2 and yearMonth was not considered because we believe that the age of federation does not impact the effects of year and month of fishing on logcpue.

```
model_no_int_mgcv <- bam(logcpue ~ yearMonth + region + taxa + age2
                         + s(fed, bs = "re") + s(uniqueid, bs = "re"),
                         data = x, na.action = na.omit)
```

```
model_no_int <- lme(logcpue ~ yearMonth + region + taxa + age2,
                    list(fed = ~1, uniqueid = ~1),
                    data = x, na.action = na.omit)
```

```
model_int_mgcv <- bam(logcpue ~ yearMonth + region + taxa + age2
                         + age2:region + age2:taxa +
                         + s(fed, bs = "re") + s(uniqueid, bs = "re"),
           data = x, na.action = na.omit)
```

```
model_int <- lme(logcpue ~ yearMonth + region + taxa + age2
                 + age2:region + age2:taxa,
                 list(fed = ~1, uniqueid = ~1),
                 data = x, na.action = na.omit)
```

```
glance(model_int_mgcv) %>%
  select(AIC, BIC) %>%
  kable(digits = 0, caption = "AIC and BIC for Model without Interaction")
```

Table 2: AIC and BIC for Model without Interaction

AIC	BIC
679974	682277

```
glance(model_no_int_mgcv) %>%
  select(AIC, BIC) %>%
  kable(digits = 0, caption = "AIC and BIC for Model with Interactions")
```

Table 3: AIC and BIC for Model with Interactions

AIC	BIC
688412	690458

Moreover, we have also tried adding different interactions in the model, such as interactions effects betwen yearMonth and region and between yearMonth and taxa as shown below. However, the model selection criterion by AIC and BIC is higher that than that for the previous model. Therefore, model with interactions between age2 and region and between age2 and taxa is our final model.

```
model_int2_mgcv <- bam(logcpue ~ yearMonth + region + taxa + age2
                         + yearMonth:region + yearMonth:taxa +
                         + s(fed, bs = "re") + s(uniqueid, bs = "re"),
          data = x, na.action = na.omit)
```

```
model_int2<- lme(logcpue ~ yearMonth + region + taxa + age2 + yearMonth:region + yearMonth:taxa,
                     list(fed = ~1, uniqueid = ~1),
                            data = x, na.action = na.omit)
```

```
glance(model_int2_mgcv) %>%
  select(AIC, BIC) %>%
  kable(digits = 0, caption = "AIC and BIC for Model with New Interactions")
```

Table 4: AIC and BIC for Model with New Interactions

AIC	BIC
684999	687297

Final Model

Level 1 Model: Time

$$Logcpue_{ijk} = a_{ij} + b_{ij}yearMonth_{ijk} + c_{ij}region_{ijk} + d_{ij}taxa_{ijk} + \epsilon_{ijk}, \epsilon_{ijk} \sim N(0, \sigma^2)$$

Level 2 Model: Cooperations

$$a_{ij} = a_i + u_{ij}$$

$$b_{ij} = b_i$$

$$c_{ij} = c_i$$

$$d_{ij} = d_i$$

Level 3 Model: Federations

$$a_i = \alpha_0 + \alpha_1 age_i + \tilde{u}_i$$

$$b_i = \beta_0$$

$$c_i = \gamma_0 + \gamma_1 age_i$$

$$d_i = \delta_0 + \delta_1 age_i$$

Composite model

$$Logcpue_{ijk} = a_i + u_{ij} + b_i yearMonth_{ijk} + c_i region_{ijk} + d_i taxa_{ijk} + \epsilon_{ijk}, \epsilon_{ijk} \sim N(0, \sigma^2)$$

$$= \alpha_0 + \alpha_1 age_i + \tilde{u}_i + u_{ij} + \beta_0 yearMonth_{ijk} + \gamma_0 region_{ijk} + \gamma_1 age_i region_{ijk} + \delta_0 taxa_{ijk} + \delta_1 age_i taxa_{ijk} + \epsilon_{ijk}$$

$$\epsilon_{ijk} \sim N(0, \sigma^2)$$

$$= \alpha_0 + \alpha_1 age_i + \beta_0 yearMonth_{ijk} + \gamma_0 region_{ijk} + \gamma_1 age_i region_{ijk} + \delta_0 taxa_{ijk} + \delta_1 age_i taxa_{ijk}$$

$$+ [\tilde{u}_i + u_{ij} + \epsilon_{ijk}]$$

$$\epsilon_{ijk} \sim N(0, \sigma^2), u_{ij} \sim N(0, \sigma_u^2), \tilde{u}_i \sim N(0, \sigma_{\tilde{u}}^2)$$

Model Diagnostics

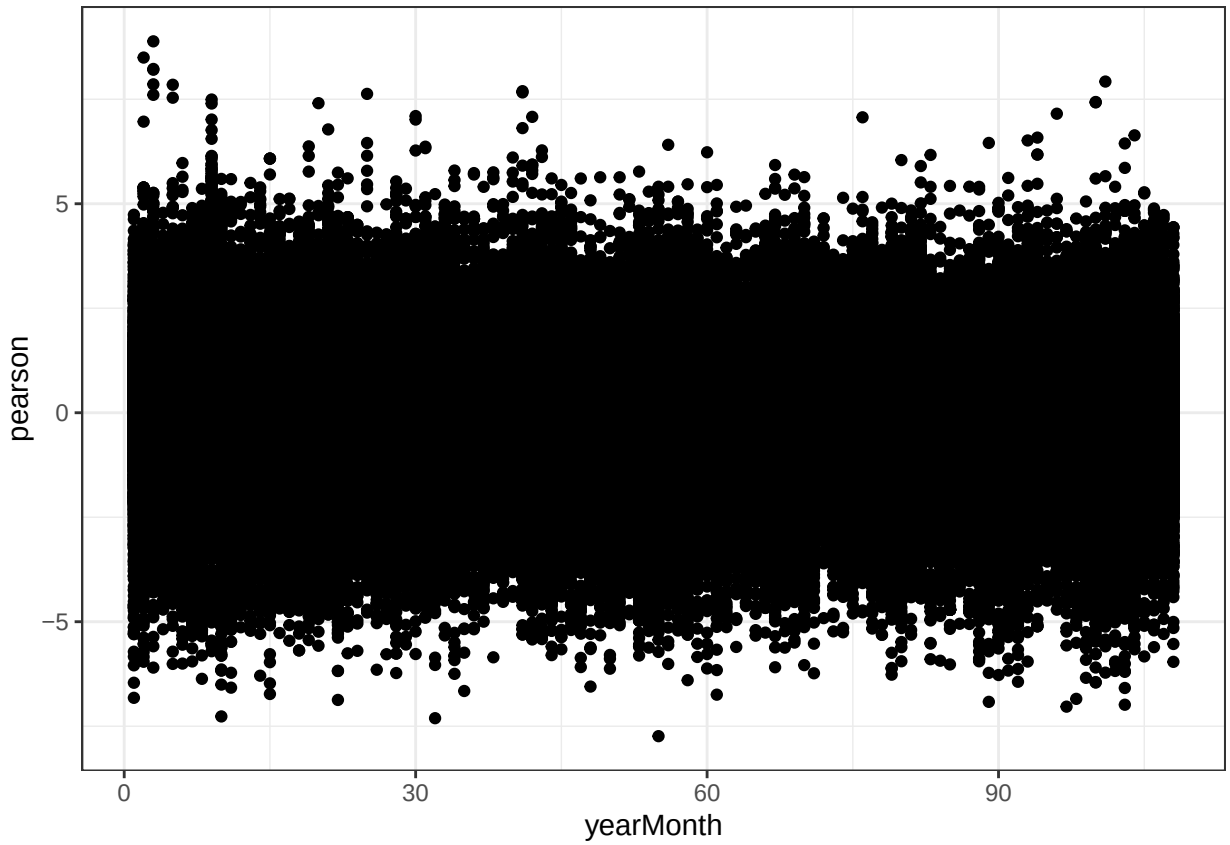
```
anova(model_int_mgcv)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## logcpue ~ yearMonth + region + taxa + age2 + age2:region + age2:taxa +
##     +s(fed, bs = "re") + s(uniqueid, bs = "re")
##
## Parametric Terms:
##             df       F p-value
## yearMonth    1 103.026  <2e-16
## region       5  34.050  <2e-16
## taxa        20 252.349  <2e-16
## age2         1   1.535   0.215
## region:age2  5 341.288  <2e-16
## taxa:age2   20 346.760  <2e-16
##
## Approximate significance of smooth terms:
##                edf Ref.df     F  p-value
## s(fed)       20.21  51.00 38482    0.359
## s(uniqueid) 153.25 176.00  8781 4.38e-05
```

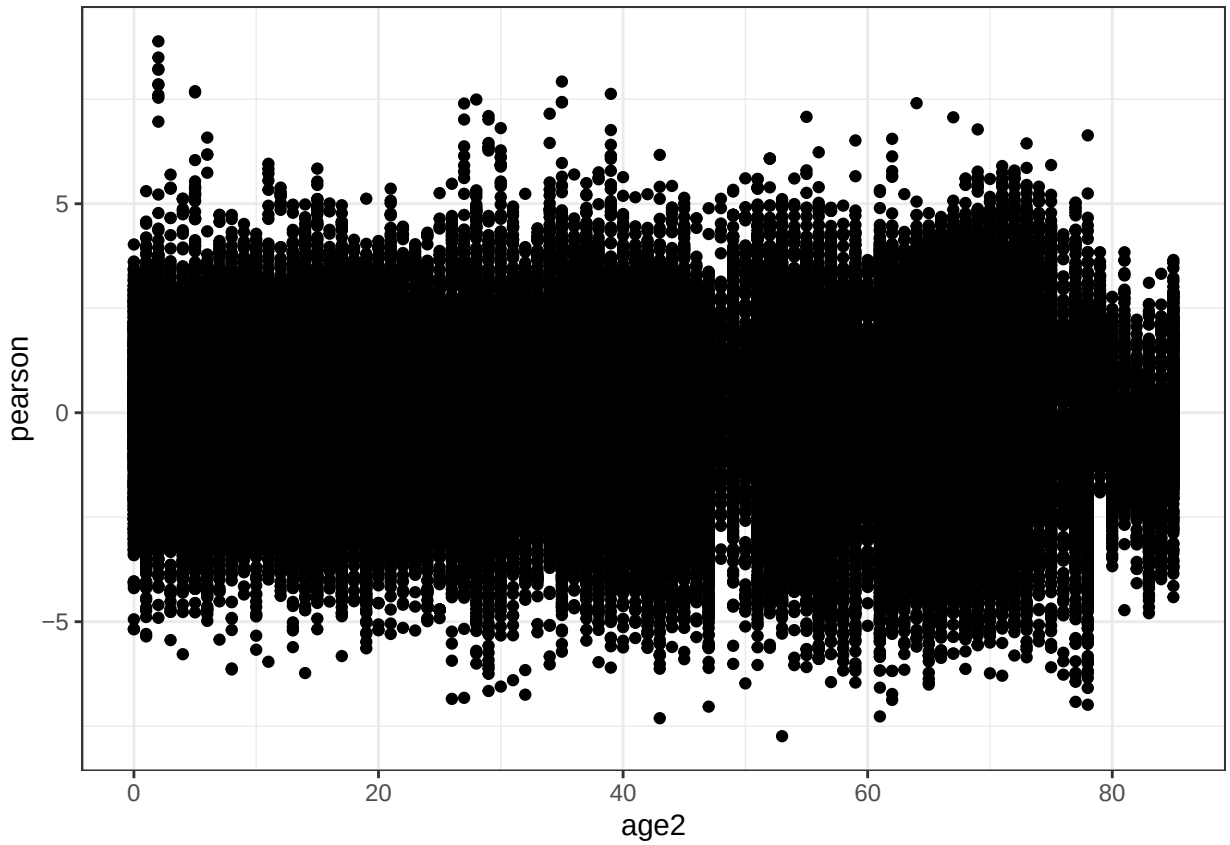
Linearity

```
x_na <- na.omit(x)
```

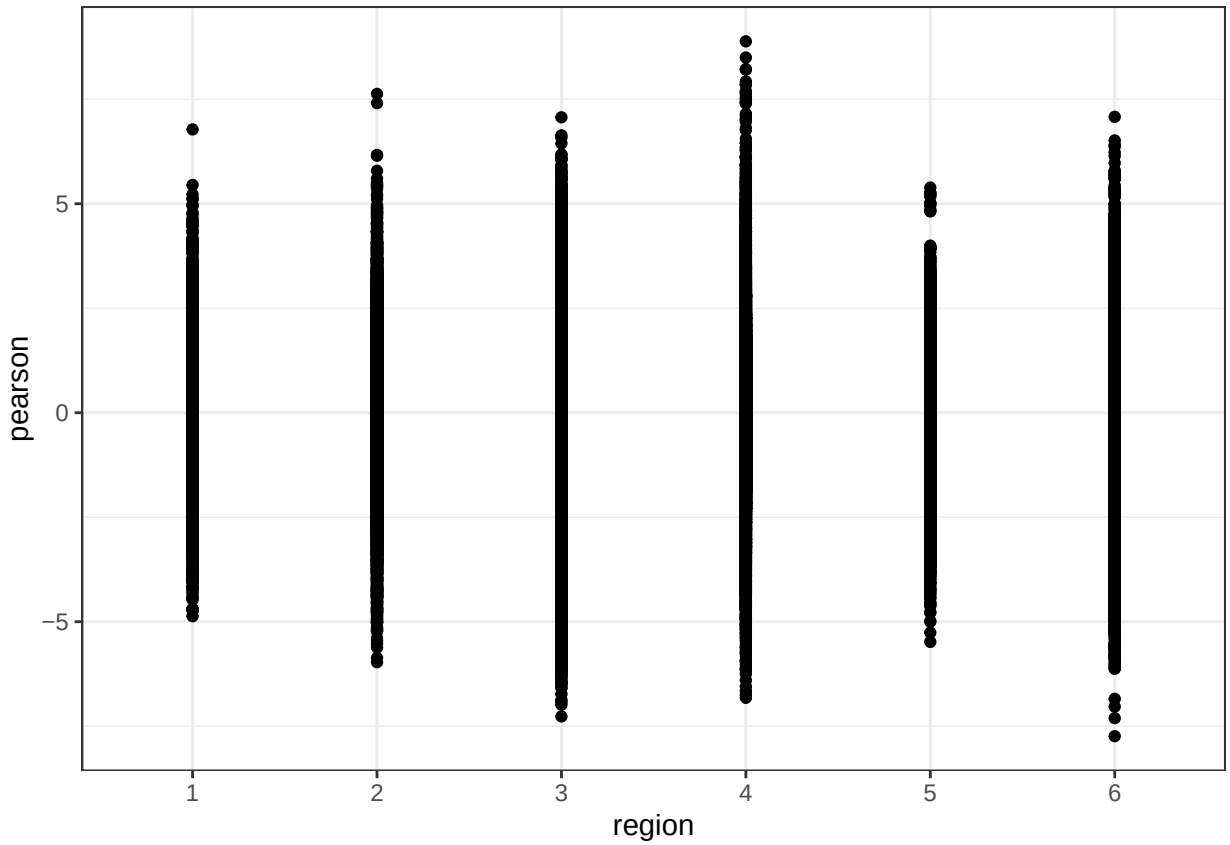
```
ggplot(data.frame(yearMonth=x_na$yearMonth,pearson=residuals(model_int_mgcv,type="pearson")),
      aes(x=yearMonth,y=pearson)) +
    geom_point() +
    theme_bw()
```



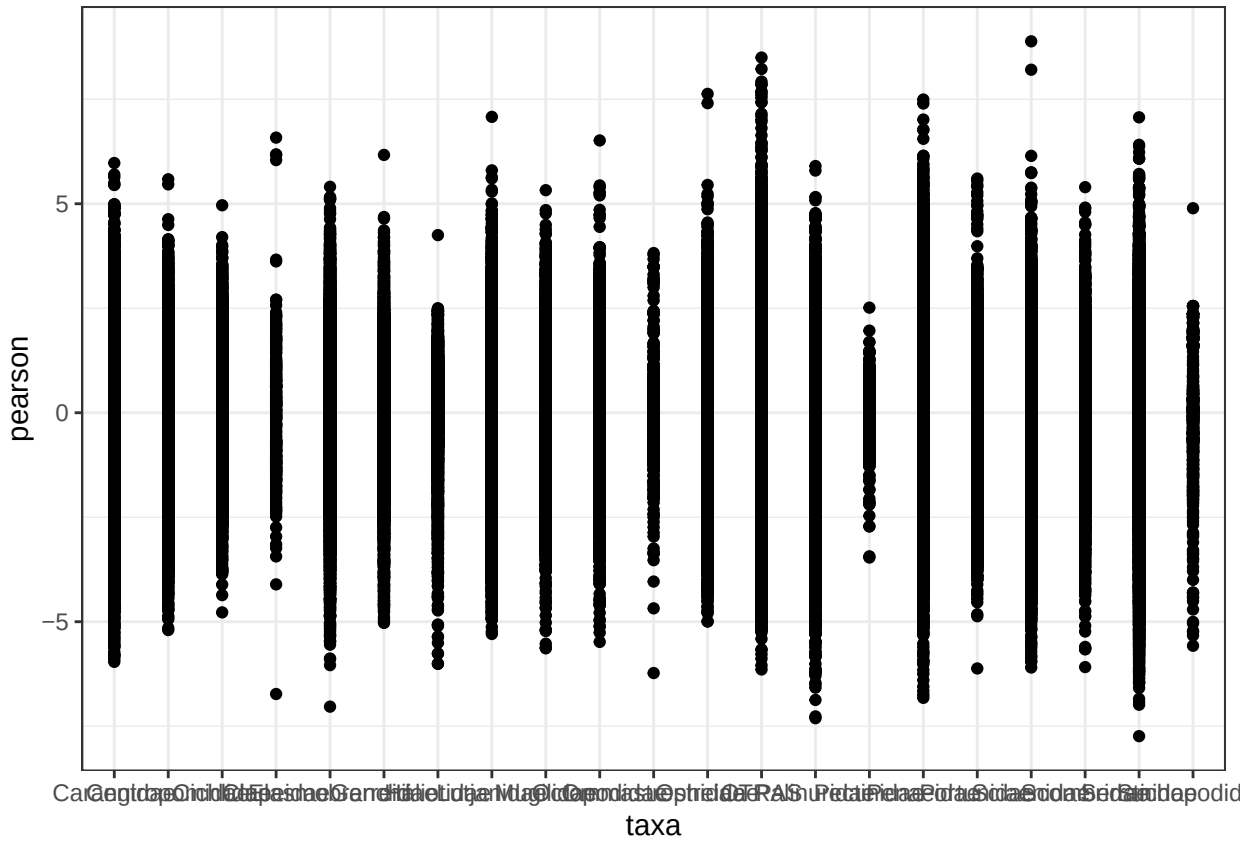

```
ggplot(data.frame(age2=x_na$age2,pearson=residuals(model_int_mgcv,type="pearson")),
       aes(x=age2,y=pearson)) +
    geom_point() +
    theme_bw()
```




```
ggplot(data.frame(region=x_na$region,pearson=residuals(model_int_mgcv,type="pearson")),
       aes(x=region,y=pearson)) +
    geom_point() +
    theme_bw()
```



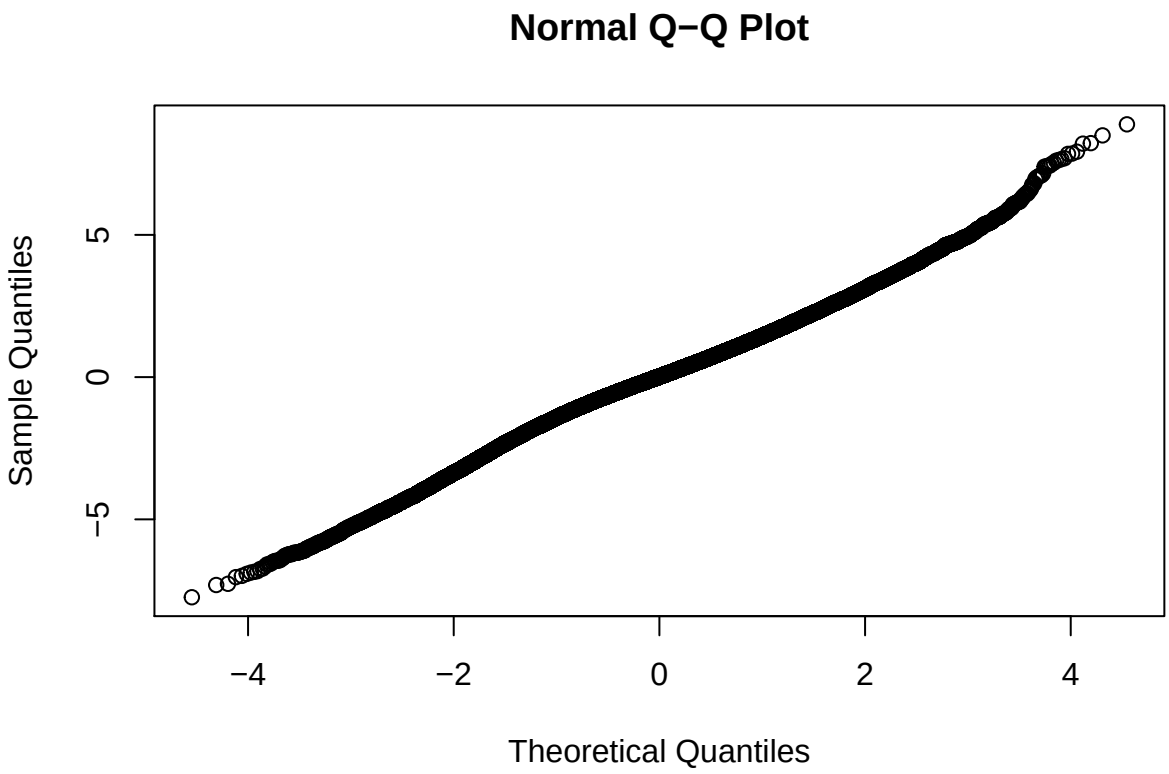

```
ggplot(data.frame(taxa=x_na$taxa,pearson=residuals(model_int_mgcv,type="pearson")),
       aes(x=taxa,y=pearson)) +
    geom_point() +
    theme_bw()
```



The residuals are randomly scattered, indicating that the data is linear and that there is a linear relationship between our predictors and the response.

Normality

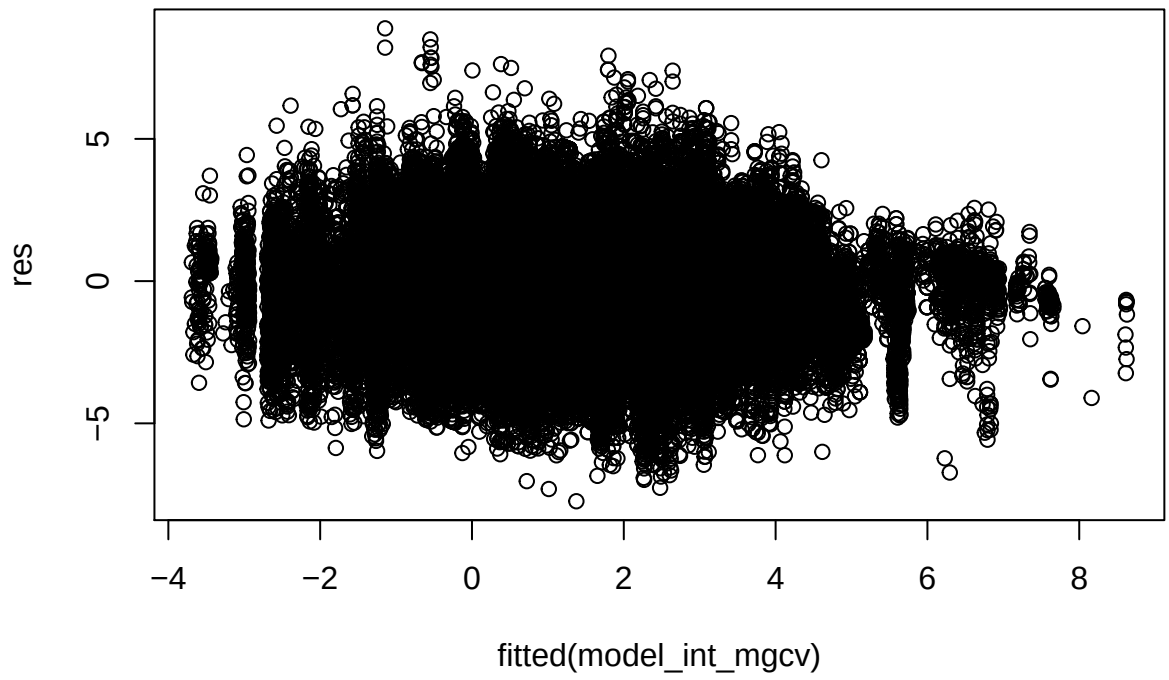
```
qqnorm(residuals(model_int_mgcv))
```



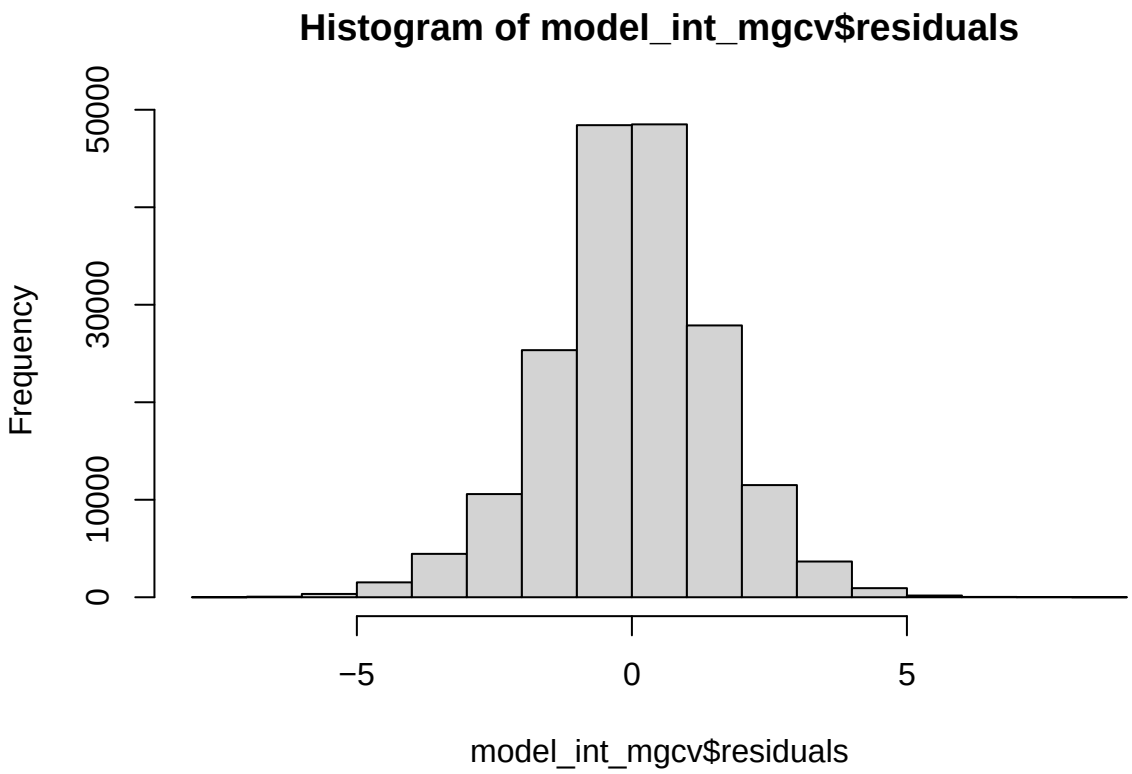
Points mostly fall along a straight diagonal line on the normal quantile plot, so we can safely assume that the data is normally distributed.

Constant Variance

```
res <- resid(model_int_mgcv)
plot(fitted(model_int_mgcv), res)
```




```
hist(model_int_mgcv$residuals)
```



The vertical spread of the residuals is not constant across the residual plot, suggesting that the constant variance condition is violated for linear mixed effects model. Therefore, some transformation should be done in the future to address this problem.

Colinearity

```
vif(model_int)
```

```
##                     GVIF Df GVIF^(1/(2*Df))
## yearMonth   1.603828e+01  1        4.004782
## region      1.574637e+00  5        1.046449
## taxa        2.949230e+13 20        2.171414
## age2        4.542232e+01  1        6.739608
## region:age2 5.155707e+01  5        1.483299
## taxa:age2   3.134794e+13 20        2.174729
```

The VIF value for `age2` is over 5, which is potentially concerning. Future model thus should take colinearity into consideration in modeling logcpue.

Prediction

```r
# generate prediction file
model <- model_int_mgcv
data <- x %>%
  filter(is.na(logcpue))
#################

df <- data %>%
  mutate(prediction = predict(model,data))%>%
  select(c('prediction'))
df <- cbind(index = rownames(df),df)
df$index <- as.numeric(as.character(df$index))
write.csv(df,'predictions.csv',row.names = FALSE) # format: index,prediction
```