Supplementary Material 2: Temporal analysis to test for the overall effect of mixing on growth complementarity of the two species over time (testing H1)

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# load libraries

rm(list=ls(all=TRUE))  
set.seed(1234)  
  
library(lme4)  
library(lmerTest)  
library(effects)  
library(tidyr)  
library(sciplot)  
library(RColorBrewer)  
library(psych)  
library(MuMIn)  
 library(dplyr)  
 library(stringr)  
 library(ggplot2)  
 library(qpcR)  
  
 library(effects)  
 library(nlme)   
 library(geoR)  
 library(AICcmodavg)  
 library(piecewiseSEM)  
 library(emmeans)  
 library(inlabru)  
 library(gridExtra)  
 library(ggsci)  
library(car)  
library(MASS)  
library(rcompanion)  
library(flexsurv)   
library(ggpubr)

#Collinearity analysis: VIF : <https://hlplab.wordpress.com/2011/02/24/diagnosing-collinearity-in-lme4/>

vif.mer <- function (fit) {  
 ## adapted from rms::vif  
   
 v <- vcov(fit)  
 nam <- names(fixef(fit))  
   
 ## exclude intercepts  
 ns <- sum(1 \* (nam == "Intercept" | nam == "(Intercept)"))  
 if (ns > 0) {  
 v <- v[-(1:ns), -(1:ns), drop = FALSE]  
 nam <- nam[-(1:ns)]  
 }  
   
 d <- diag(v)^0.5  
 v <- diag(solve(v/(d %o% d)))  
 names(v) <- nam  
 v  
}

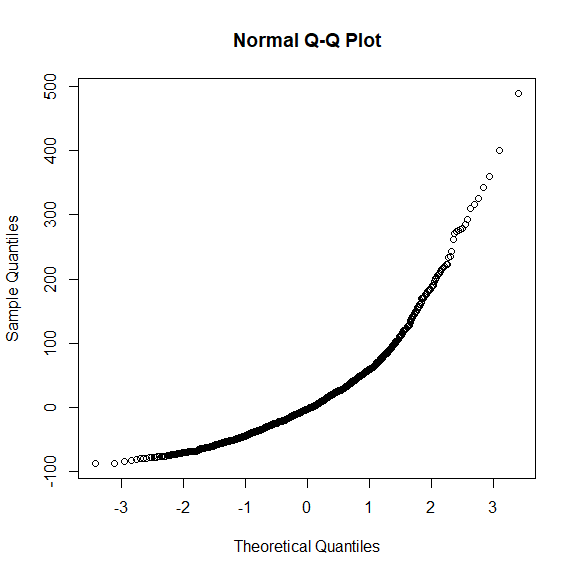
# LMMs with only Year and Species plus their interaction as fixed effects.

##To reduce the temporal autocorrelation of samples from subsequent years or periods we used the first order auto-regressive covariance structure (AR1) which introduces smaller correlations with increasing time difference between sampling dates (Zuur et al., 2009; Pinheiro et al., 2018).

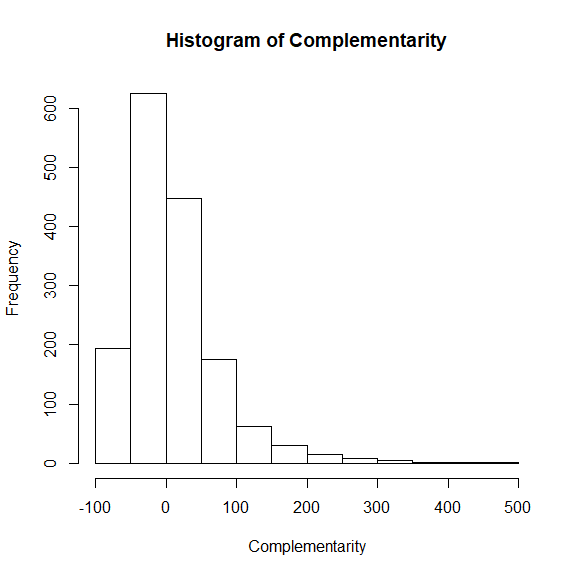
comp <- read.delim("../Data/comp\_bai.txt")  
attach(comp)  
summary(comp)

## Tree Site Species Year mix   
## CoBu01 : 17 Conventwald:408 Beech:731 Min. :2000 mixed:1564   
## CoBu02 : 17 Croatia :459 Fir :833 1st Qu.:2004   
## CoBu04 : 17 Freiamt :272 Median :2008   
## CoBu05 : 17 Hexental :425 Mean :2008   
## CoBu09 : 17 3rd Qu.:2012   
## CoBu10 : 17 Max. :2016   
## (Other):1462   
## RingWidth BAI mean.BAI.conspecific Complementarity   
## Min. :0.2885 Min. : 313.7 Min. :1275 Min. :-87.278   
## 1st Qu.:1.3529 1st Qu.: 1656.5 1st Qu.:2144 1st Qu.:-31.660   
## Median :2.0208 Median : 2554.8 Median :2562 Median : -3.229   
## Mean :2.2310 Mean : 2905.8 Mean :2706 Mean : 10.169   
## 3rd Qu.:2.8960 3rd Qu.: 3784.3 3rd Qu.:2978 3rd Qu.: 34.830   
## Max. :8.5395 Max. :14534.2 Max. :5768 Max. :489.359   
##

qqnorm(Complementarity)



hist(Complementarity)



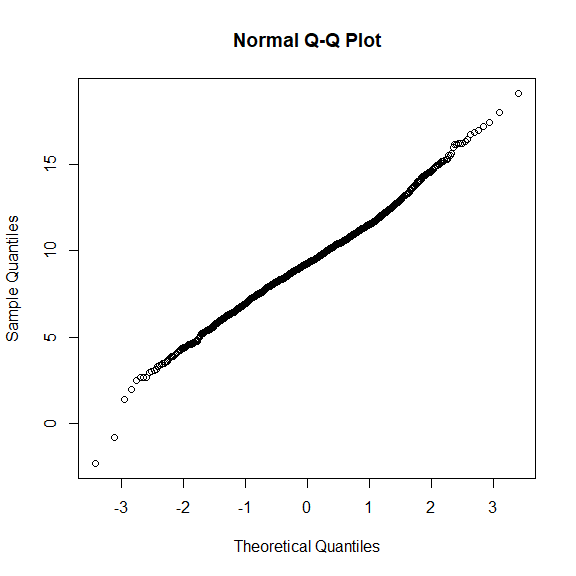
#normal transformations failed, final Boxcox  
comp$compl <- comp$Complementarity+87.3 # box-cox works only with non-zero values  
summary(comp)

## Tree Site Species Year mix   
## CoBu01 : 17 Conventwald:408 Beech:731 Min. :2000 mixed:1564   
## CoBu02 : 17 Croatia :459 Fir :833 1st Qu.:2004   
## CoBu04 : 17 Freiamt :272 Median :2008   
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## Max. :8.5395 Max. :14534.2 Max. :5768 Max. :489.359   
##   
## compl   
## Min. : 0.0217   
## 1st Qu.: 55.6400   
## Median : 84.0707   
## Mean : 97.4688   
## 3rd Qu.:122.1299   
## Max. :576.6588   
##

ccomp <-boxcoxfit(comp$compl)   
ccomp

## Fitted parameters:  
## lambda beta sigmasq   
## 0.2997571 9.2909251 6.0352179   
##   
## Convergence code returned by optim: 0

comp$complbox <- ((comp$compl)^ccomp$lambda-1)/ccomp$lambda  
qqnorm(comp$complbox)# goodish



summary(comp)

## Tree Site Species Year mix   
## CoBu01 : 17 Conventwald:408 Beech:731 Min. :2000 mixed:1564   
## CoBu02 : 17 Croatia :459 Fir :833 1st Qu.:2004   
## CoBu04 : 17 Freiamt :272 Median :2008   
## CoBu05 : 17 Hexental :425 Mean :2008   
## CoBu09 : 17 3rd Qu.:2012   
## CoBu10 : 17 Max. :2016   
## (Other):1462   
## RingWidth BAI mean.BAI.conspecific Complementarity   
## Min. :0.2885 Min. : 313.7 Min. :1275 Min. :-87.278   
## 1st Qu.:1.3529 1st Qu.: 1656.5 1st Qu.:2144 1st Qu.:-31.660   
## Median :2.0208 Median : 2554.8 Median :2562 Median : -3.229   
## Mean :2.2310 Mean : 2905.8 Mean :2706 Mean : 10.169   
## 3rd Qu.:2.8960 3rd Qu.: 3784.3 3rd Qu.:2978 3rd Qu.: 34.830   
## Max. :8.5395 Max. :14534.2 Max. :5768 Max. :489.359   
##   
## compl complbox   
## Min. : 0.0217 Min. :-2.277   
## 1st Qu.: 55.6400 1st Qu.: 7.792   
## Median : 84.0707 Median : 9.258   
## Mean : 97.4688 Mean : 9.291   
## 3rd Qu.:122.1299 3rd Qu.:10.749   
## Max. :576.6588 Max. :19.094   
##

# testing for random structure: Site or trees nested in sites  
  
fitr1 <- lme(complbox ~ scale(Year) + Species + scale(Year)\* Species   
 ,random= ~1|Site/Tree , data=comp, correlation = corAR1())  
  
fitr2 <- lme(complbox ~ scale(Year) + Species + scale(Year)\* Species   
 ,random= ~1|Site , data=comp, correlation = corAR1())  
  
  
aictab(mget(str\_subset(ls(), "fitr")))# trees nested sites!!

## Warning in aictab.AIClme(mget(str\_subset(ls(), "fitr"))):   
## Model selection for fixed effects is only appropriate with method=ML:  
## REML (default) should only be used to select random effects for a constant set of fixed effects

##   
## Model selection based on AICc:  
##   
## K AICc Delta\_AICc AICcWt Cum.Wt Res.LL  
## fitr1 8 5506.41 0.00 1 1 -2745.16  
## fitr2 7 6287.74 781.33 0 1 -3136.83

fit <- lme(complbox ~ scale(Year) + Species + scale(Year)\* Species   
 ,random= ~1|Site/Tree , data=comp, correlation = corAR1())  
summary(fit)

## Linear mixed-effects model fit by REML  
## Data: comp   
## AIC BIC logLik  
## 5506.318 5549.137 -2745.159  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept)  
## StdDev: 0.0007343646  
##   
## Formula: ~1 | Tree %in% Site  
## (Intercept) Residual  
## StdDev: 2.022308 1.371228  
##   
## Correlation Structure: AR(1)  
## Formula: ~1 | Site/Tree   
## Parameter estimate(s):  
## Phi   
## 0.367328   
## Fixed effects: complbox ~ scale(Year) + Species + scale(Year) \* Species   
## Value Std.Error DF t-value p-value  
## (Intercept) 8.898965 0.3167395 1470 28.095530 0.0000  
## scale(Year) 0.148115 0.0500413 1470 2.959843 0.0031  
## SpeciesFir 0.753101 0.4340087 87 1.735221 0.0862  
## scale(Year):SpeciesFir -0.044233 0.0686517 1470 -0.644311 0.5195  
## Correlation:   
## (Intr) scl(Y) SpcsFr  
## scale(Year) -0.010   
## SpeciesFir -0.730 0.007   
## scale(Year):SpeciesFir 0.007 -0.729 -0.010  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -4.88487834 -0.53499688 -0.01029198 0.53510507 5.15221565   
##   
## Number of Observations: 1564  
## Number of Groups:   
## Site Tree %in% Site   
## 4 92

max(vif.mer(fit))

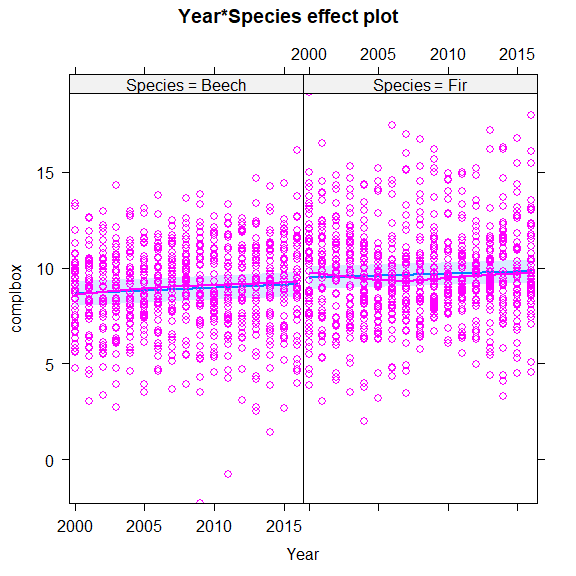
## [1] 2.133753

r.squaredGLMM(fit)

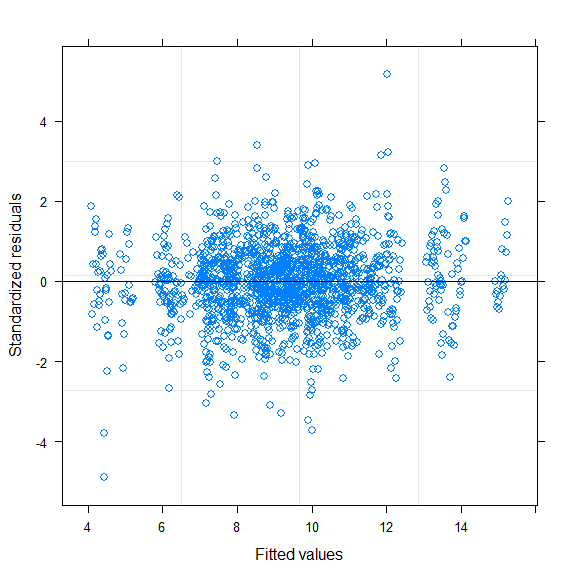
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help  
## page.

## R2m R2c  
## [1,] 0.02566862 0.6931319

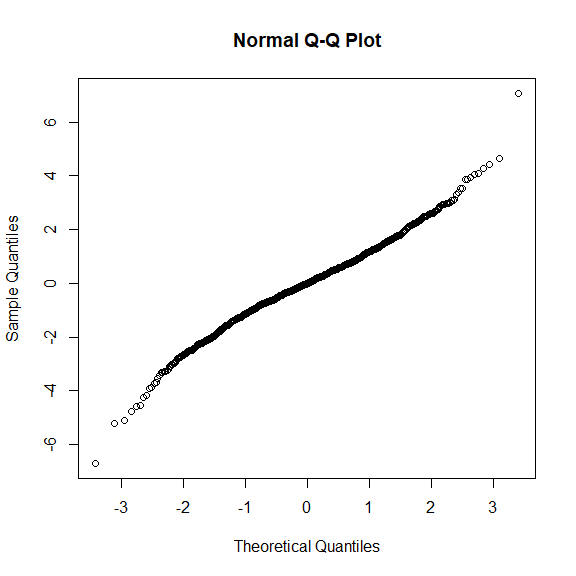
plot(allEffects(fit, partial.residuals=T))



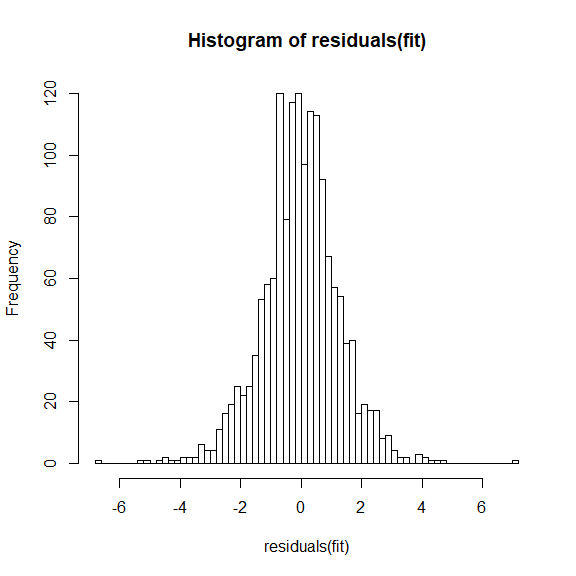
#Checking residuals  
plot(fit)



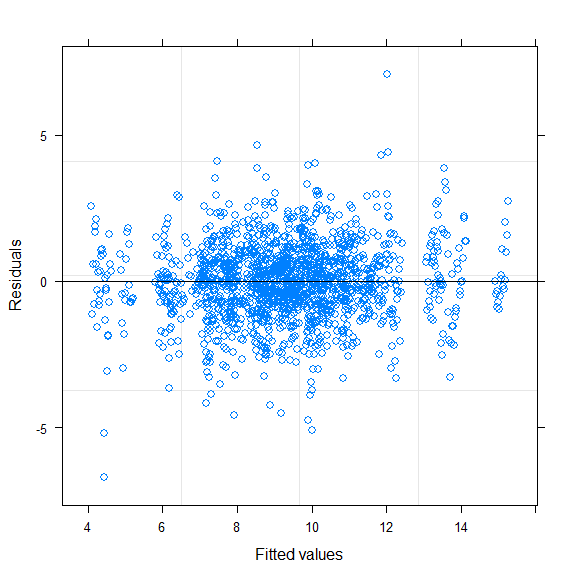
# that looks good   
qqnorm(residuals(fit))



hist(residuals(fit), breaks = 50)



plot(fit, resid(., scaled=TRUE) ~ fitted(.) , abline = 0)



plot(fit, resid(., scaled=TRUE) ~ Year , abline = 0)

