Supplementary Material 3: NEIGHBOURHOOD ANALYSIS to identify the most important growth-controlling variables for the two species at the tree neighborhood level, we analyzed the effect of admixing on tree growth while accounting for additional confounding factors

Julia Schwarz

# 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)

rm(list=ls(all=TRUE))  
data <- read.delim("../Data/lastyr.txt")  
str(data)

## 'data.frame': 153 obs. of 29 variables:  
## $ Tree : Factor w/ 153 levels "CoBu01","CoBu02",..: 1 2 3 4 5 6 7 8 9 10 ...  
## $ Site : Factor w/ 4 levels "Conventwald",..: 1 1 1 1 1 1 1 1 1 1 ...  
## $ Martonne : num 7.41 7.41 7.41 7.41 7.41 ...  
## $ Martonne\_new : num 6.76 6.76 6.76 6.76 6.76 6.76 6.76 6.76 6.76 6.76 ...  
## $ Soil : Factor w/ 2 levels "Braunerde","Rendzina": 1 1 1 1 1 1 1 1 1 1 ...  
## $ Soil.1 : int 1 1 1 1 1 1 1 1 1 1 ...  
## $ Species : Factor w/ 2 levels "Beech","Fir": 1 1 1 1 1 1 1 1 1 1 ...  
## $ Year : int 2016 2016 2016 2016 2016 2016 2016 2016 2016 2016 ...  
## $ DBH : num 71.3 60.9 63 52 59.9 52.9 57.3 51.5 56.3 46 ...  
## $ N\_nbors : int 6 4 6 4 4 6 7 6 5 5 ...  
## $ mean\_distance : num 8.53 6.8 7.03 4.95 7.15 ...  
## $ nrbydist : num 0.703 0.588 0.853 0.808 0.559 ...  
## $ meandistlarger: num 8.1 5.97 9.7 4.5 6.5 ...  
## $ nrlarger : int 3 3 2 3 2 3 3 3 4 5 ...  
## $ nrbydistlarger: num 0.37 0.503 0.206 0.667 0.308 ...  
## $ BAL : num 17.44 13.89 10.29 15.17 7.75 ...  
## $ Hegyi\_old : num 0.696 0.953 0.96 1.236 0.673 ...  
## $ Hegyi : num 0.602 0.787 0.909 0.996 0.543 ...  
## $ Beech\_prop : num 34.5 11.7 76.3 0 0 ...  
## $ Fir\_prop : num 65.5 88.3 23.7 100 100 ...  
## $ Other\_prop : num 0 0 0 0 0 0 0 0 0 0 ...  
## $ Admixed\_prop : num 65.5 88.3 23.7 100 100 ...  
## $ Mixture : Factor w/ 3 levels "1\_monospecific",..: 2 3 1 3 3 1 1 1 3 2 ...  
## $ mixed : Factor w/ 2 levels "less","more": 2 2 1 2 2 1 1 1 2 1 ...  
## $ BAI2016 : num 1485 2433 1187 527 512 ...  
## $ BAIsum3 : num 4838 6142 5043 3898 2944 ...  
## $ BAIsum5 : num 9630 11587 8513 6848 6630 ...  
## $ RelBAI2016 : num 0.895 1.467 0.715 0.318 0.309 ...  
## $ RW : num 0.702 1.358 0.639 0.349 0.291 ...

summary(data)

## Tree Site Martonne Martonne\_new   
## CoBu01 : 1 Conventwald:39 Min. :3.866 Min. :5.130   
## CoBu02 : 1 Croatia :41 1st Qu.:6.278 1st Qu.:5.130   
## CoBu03 : 1 Freiamt :33 Median :6.769 Median :6.760   
## CoBu04 : 1 Hexental :40 Mean :6.179 Mean :6.004   
## CoBu05 : 1 3rd Qu.:7.413 3rd Qu.:6.840   
## CoBu06 : 1 Max. :7.413 Max. :6.840   
## (Other):147   
## Soil Soil.1 Species Year DBH   
## Braunerde:112 Min. :1.000 Beech:73 Min. :2016 Min. :19.90   
## Rendzina : 41 1st Qu.:1.000 Fir :80 1st Qu.:2016 1st Qu.:38.60   
## Median :1.000 Median :2016 Median :49.40   
## Mean :1.268 Mean :2016 Mean :49.48   
## 3rd Qu.:2.000 3rd Qu.:2016 3rd Qu.:60.00   
## Max. :2.000 Max. :2016 Max. :88.70   
##   
## N\_nbors mean\_distance nrbydist meandistlarger   
## Min. : 2.000 Min. : 3.300 Min. :0.2920 Min. : 2.300   
## 1st Qu.: 5.000 1st Qu.: 5.200 1st Qu.:0.7660 1st Qu.: 5.276   
## Median : 6.000 Median : 6.211 Median :0.9627 Median : 6.617   
## Mean : 6.346 Mean : 6.339 Mean :1.0775 Mean : 6.727   
## 3rd Qu.: 7.000 3rd Qu.: 7.375 3rd Qu.:1.3032 3rd Qu.: 7.987   
## Max. :13.000 Max. :14.600 Max. :2.6190 Max. :13.300   
## NA's :35   
## nrlarger nrbydistlarger BAL Hegyi\_old   
## Min. :0.00 Min. :0.09901 Min. : 0.000 Min. :0.2333   
## 1st Qu.:1.00 1st Qu.:0.25647 1st Qu.: 2.043 1st Qu.:0.7256   
## Median :2.00 Median :0.40678 Median : 4.034 Median :0.9494   
## Mean :2.17 Mean :0.45518 Mean : 5.878 Mean :1.0800   
## 3rd Qu.:3.00 3rd Qu.:0.60728 3rd Qu.: 9.663 3rd Qu.:1.3272   
## Max. :8.00 Max. :1.47806 Max. :21.823 Max. :2.6195   
## NA's :35   
## Hegyi Beech\_prop Fir\_prop Other\_prop   
## Min. :0.2680 Min. : 0.00 Min. : 0.00 Min. : 0.000   
## 1st Qu.:0.7499 1st Qu.: 18.49 1st Qu.: 19.15 1st Qu.: 0.000   
## Median :0.9800 Median : 48.53 Median : 51.25 Median : 0.000   
## Mean :1.0878 Mean : 48.35 Mean : 48.30 Mean : 3.359   
## 3rd Qu.:1.3604 3rd Qu.: 76.30 3rd Qu.: 76.68 3rd Qu.: 0.000   
## Max. :2.8336 Max. :100.00 Max. :100.00 Max. :40.958   
##   
## Admixed\_prop Mixture mixed BAI2016   
## Min. : 0.00 1\_monospecific :61 less:86 Min. : 288.5   
## 1st Qu.: 18.49 2\_mixed :43 more:67 1st Qu.: 1448.6   
## Median : 47.13 3\_heterospecific:49 Median : 2346.6   
## Mean : 47.16 Mean : 2741.1   
## 3rd Qu.: 76.08 3rd Qu.: 3635.5   
## Max. :100.00 Max. :14123.1   
##   
## BAIsum3 BAIsum5 RelBAI2016 RW   
## Min. : 1033 Min. : 1867 Min. :0.1205 Min. :0.166   
## 1st Qu.: 4962 1st Qu.: 8513 1st Qu.:0.6909 1st Qu.:1.071   
## Median : 7711 Median :12555 Median :0.9713 Median :1.768   
## Mean : 8519 Mean :13887 Mean :1.1452 Mean :1.959   
## 3rd Qu.:10791 3rd Qu.:17659 3rd Qu.:1.4749 3rd Qu.:2.566   
## Max. :35774 Max. :51292 Max. :5.0029 Max. :6.455   
##

data$N\_nbors <- as.numeric(data$N\_nbors)  
data$nrlarger <- as.numeric(data$nrlarger)  
data$Year <- as.numeric(data$Year)  
data$meanBAI3 <-data$BAIsum3/3  
data$meanBAI5 <-data$BAIsum5/5  
str(data)

## 'data.frame': 153 obs. of 31 variables:  
## $ Tree : Factor w/ 153 levels "CoBu01","CoBu02",..: 1 2 3 4 5 6 7 8 9 10 ...  
## $ Site : Factor w/ 4 levels "Conventwald",..: 1 1 1 1 1 1 1 1 1 1 ...  
## $ Martonne : num 7.41 7.41 7.41 7.41 7.41 ...  
## $ Martonne\_new : num 6.76 6.76 6.76 6.76 6.76 6.76 6.76 6.76 6.76 6.76 ...  
## $ Soil : Factor w/ 2 levels "Braunerde","Rendzina": 1 1 1 1 1 1 1 1 1 1 ...  
## $ Soil.1 : int 1 1 1 1 1 1 1 1 1 1 ...  
## $ Species : Factor w/ 2 levels "Beech","Fir": 1 1 1 1 1 1 1 1 1 1 ...  
## $ Year : num 2016 2016 2016 2016 2016 ...  
## $ DBH : num 71.3 60.9 63 52 59.9 52.9 57.3 51.5 56.3 46 ...  
## $ N\_nbors : num 6 4 6 4 4 6 7 6 5 5 ...  
## $ mean\_distance : num 8.53 6.8 7.03 4.95 7.15 ...  
## $ nrbydist : num 0.703 0.588 0.853 0.808 0.559 ...  
## $ meandistlarger: num 8.1 5.97 9.7 4.5 6.5 ...  
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## $ BAL : num 17.44 13.89 10.29 15.17 7.75 ...  
## $ Hegyi\_old : num 0.696 0.953 0.96 1.236 0.673 ...  
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## $ Admixed\_prop : num 65.5 88.3 23.7 100 100 ...  
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## $ mixed : Factor w/ 2 levels "less","more": 2 2 1 2 2 1 1 1 2 1 ...  
## $ BAI2016 : num 1485 2433 1187 527 512 ...  
## $ BAIsum3 : num 4838 6142 5043 3898 2944 ...  
## $ BAIsum5 : num 9630 11587 8513 6848 6630 ...  
## $ RelBAI2016 : num 0.895 1.467 0.715 0.318 0.309 ...  
## $ RW : num 0.702 1.358 0.639 0.349 0.291 ...  
## $ meanBAI3 : num 1613 2047 1681 1299 981 ...  
## $ meanBAI5 : num 1926 2317 1703 1370 1326 ...

data$resp <- log(data$meanBAI3)  
data$back <- exp(data$resp)  
  
summary(data)

## Tree Site Martonne Martonne\_new   
## CoBu01 : 1 Conventwald:39 Min. :3.866 Min. :5.130   
## CoBu02 : 1 Croatia :41 1st Qu.:6.278 1st Qu.:5.130   
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## Soil Soil.1 Species Year DBH   
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## N\_nbors mean\_distance nrbydist meandistlarger   
## Min. : 2.000 Min. : 3.300 Min. :0.2920 Min. : 2.300   
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## Median : 6.000 Median : 6.211 Median :0.9627 Median : 6.617   
## Mean : 6.346 Mean : 6.339 Mean :1.0775 Mean : 6.727   
## 3rd Qu.: 7.000 3rd Qu.: 7.375 3rd Qu.:1.3032 3rd Qu.: 7.987   
## Max. :13.000 Max. :14.600 Max. :2.6190 Max. :13.300   
## NA's :35   
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## Min. :0.00 Min. :0.09901 Min. : 0.000 Min. :0.2333   
## 1st Qu.:1.00 1st Qu.:0.25647 1st Qu.: 2.043 1st Qu.:0.7256   
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## Min. :0.2680 Min. : 0.00 Min. : 0.00 Min. : 0.000   
## 1st Qu.:0.7499 1st Qu.: 18.49 1st Qu.: 19.15 1st Qu.: 0.000   
## Median :0.9800 Median : 48.53 Median : 51.25 Median : 0.000   
## Mean :1.0878 Mean : 48.35 Mean : 48.30 Mean : 3.359   
## 3rd Qu.:1.3604 3rd Qu.: 76.30 3rd Qu.: 76.68 3rd Qu.: 0.000   
## Max. :2.8336 Max. :100.00 Max. :100.00 Max. :40.958   
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## Median : 47.13 3\_heterospecific:49 Median : 2346.6   
## Mean : 47.16 Mean : 2741.1   
## 3rd Qu.: 76.08 3rd Qu.: 3635.5   
## Max. :100.00 Max. :14123.1   
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## Median : 7711 Median :12555 Median :0.9713 Median :1.768   
## Mean : 8519 Mean :13887 Mean :1.1452 Mean :1.959   
## 3rd Qu.:10791 3rd Qu.:17659 3rd Qu.:1.4749 3rd Qu.:2.566   
## Max. :35774 Max. :51292 Max. :5.0029 Max. :6.455   
##   
## meanBAI3 meanBAI5 resp back   
## Min. : 344.4 Min. : 373.4 Min. :5.842 Min. : 344.4   
## 1st Qu.: 1653.9 1st Qu.: 1702.6 1st Qu.:7.411 1st Qu.: 1653.9   
## Median : 2570.4 Median : 2511.0 Median :7.852 Median : 2570.4   
## Mean : 2839.7 Mean : 2777.4 Mean :7.794 Mean : 2839.7   
## 3rd Qu.: 3597.1 3rd Qu.: 3531.8 3rd Qu.:8.188 3rd Qu.: 3597.1   
## Max. :11924.6 Max. :10258.4 Max. :9.386 Max. :11924.6   
##

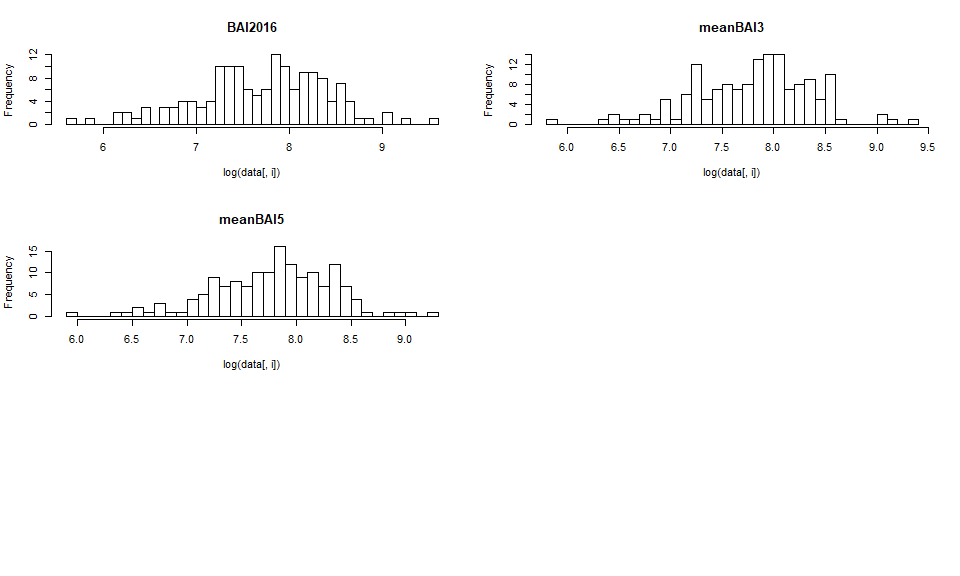
#Collinearity analysis: VIF : <https://hlplab.wordpress.com/2011/02/24/diagnosing-collinearity-in-lme4/>

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  
}

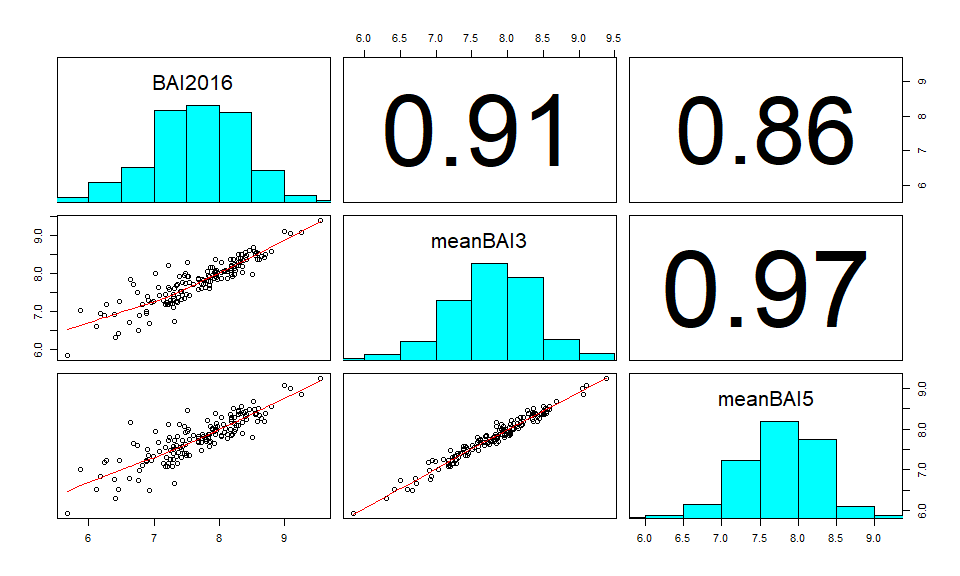
# Response variables: BAI or mean BAI of last 3 years (2014-16) or mean BAI of last 5 years (2011-16)

##pre-correlation analysis for the predictors

resp= c(which(names(data)=="BAI2016"), which(names(data)=="meanBAI3"), which(names(data)=="meanBAI5"))  
  
oldpar <- par(mfrow = c(3,2))  
  
for (i in resp){  
 hist(log(data[,i]), main = colnames(data)[i], breaks = 30)  
}  
par(oldpar)



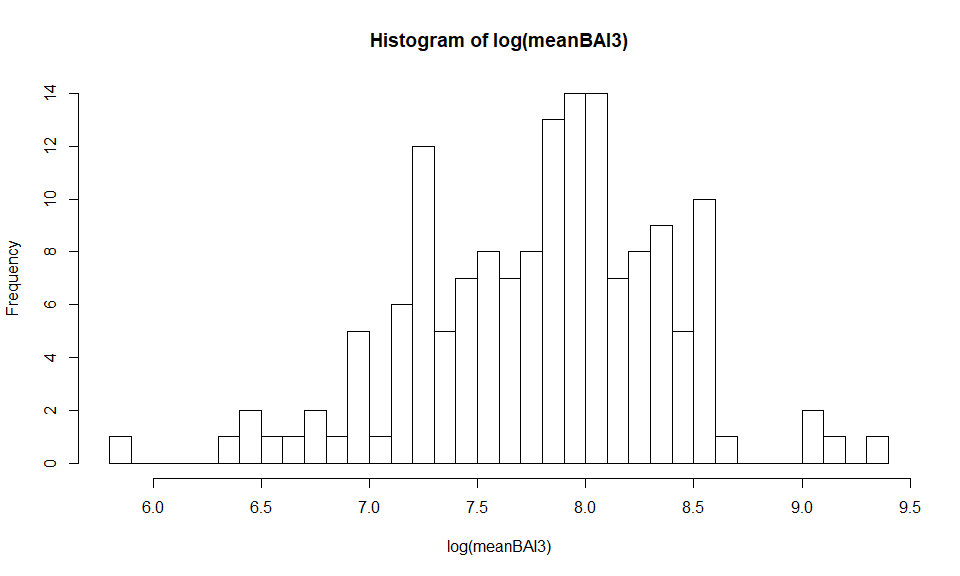
pairs(log(data[resp]), lower.panel = panel.smooth, diag.panel = panel.hist, upper.panel = panel.cor)



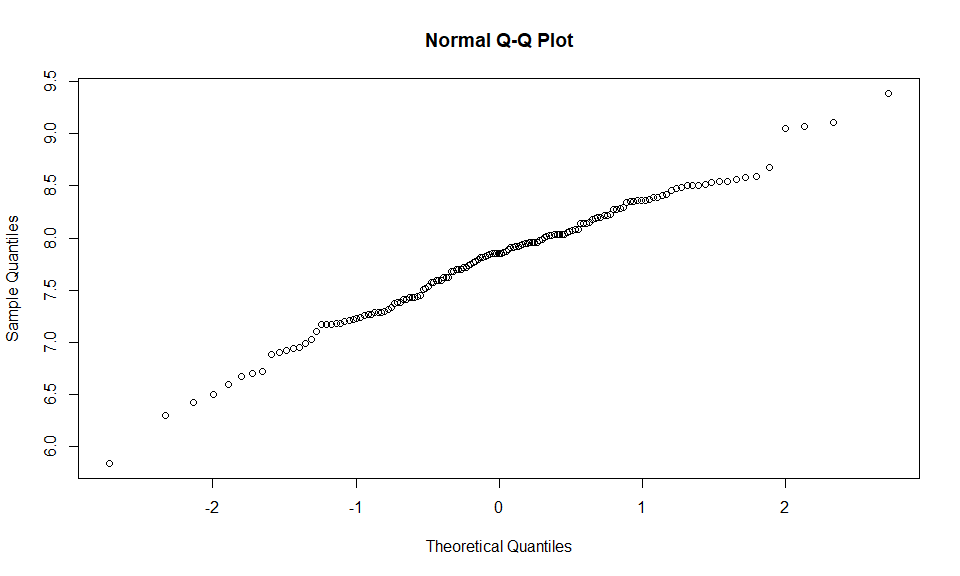
# we use only one as high correlation  
attach(data)

## The following object is masked \_by\_ .GlobalEnv:  
##   
## resp

hist(log(meanBAI3), breaks = 40) #looks good

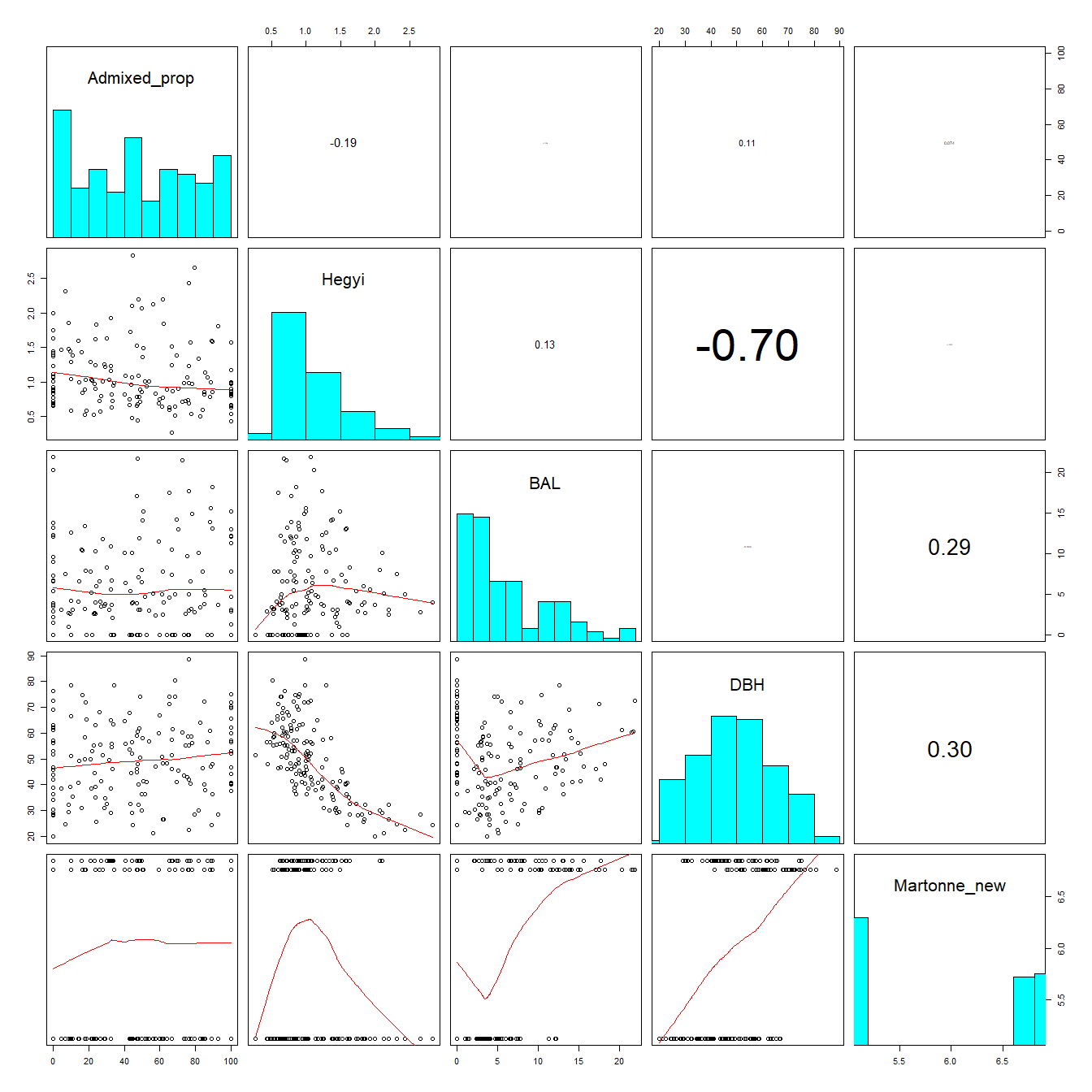


qqnorm(log(meanBAI3))# yes



# Before modelling we have to reduce collinearity among predictors by doing precorrelation anaylos

finalPred2016 = resp= c(which(names(data)=="Admixed\_prop"),   
 which(names(data)=="Hegyi"),  
 which(names(data)=="BAL"),  
 which(names(data)=="DBH"),  
 which(names(data)=="Martonne\_new"))  
   
  
pairs(data[,finalPred2016], lower.panel = panel.smooth, diag.panel = panel.hist, upper.panel = panel.cor)



# looks fine

#Random effect structure selection: For comparing random structures via AIC keep fixed effects constant and use REML!!! AIC is a good option to use, see also Zuur et al.2009, We should use full model with as many interactions as possible.

lme\_r1 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site , data=data)  
   
  
lme\_r2 <- lme(log(meanBAI3)~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site/Tree , data=data, )  
  
lme\_r3 <- lme(log(meanBAI3) ~scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Species/Site/Tree , data=data)  
  
lme\_r4 <- lme(log(meanBAI3) ~scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Species/Site , data=data)  
  
  
aictab(mget(str\_subset(ls(), "lme\_r")))# sites!!!

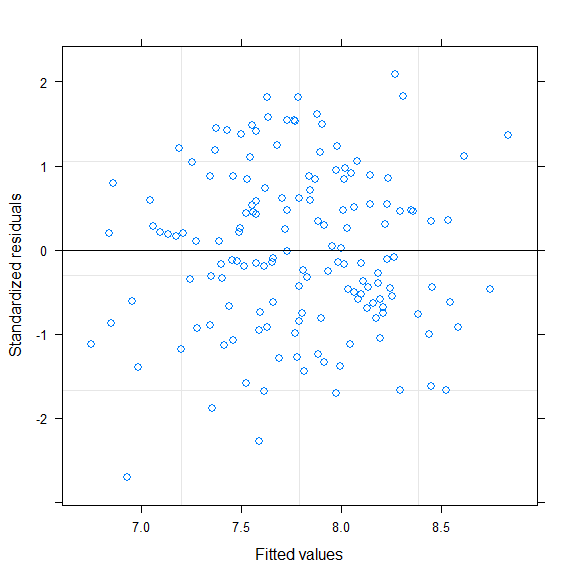
## Warning in aictab.AIClme(mget(str\_subset(ls(), "lme\_r"))):   
## Model selection for fixed effects is only appropriate with method=ML:  
## REML (default) should only be used to select random effects for a constant set of fixed effects

##   
## Model selection based on AICc:  
##   
## K AICc Delta\_AICc AICcWt Cum.Wt Res.LL  
## lme\_r1 14 234.44 0.00 0.77 0.77 -101.70  
## lme\_r2 15 236.90 2.46 0.22 0.99 -101.70  
## lme\_r4 15 244.61 10.17 0.00 1.00 -105.55  
## lme\_r3 16 247.11 12.67 0.00 1.00 -105.55

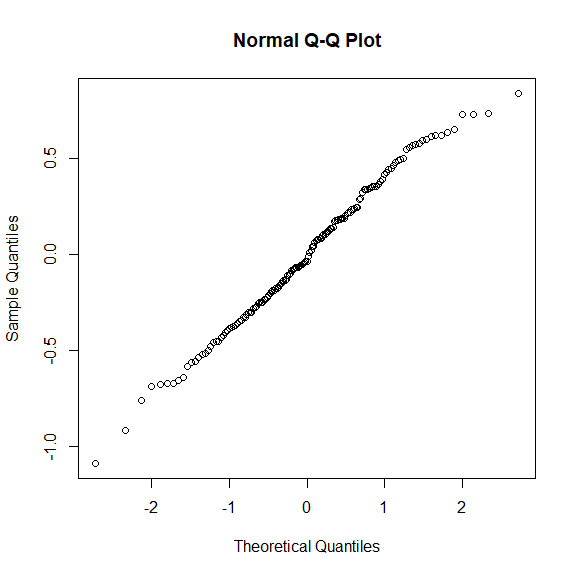
summary(lme\_r1)

## Linear mixed-effects model fit by REML  
## Data: data   
## AIC BIC logLik  
## 231.3934 272.676 -101.6967  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.3442674 0.4038346  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi) + scale(Admixed\_prop) \* scale(BAL) + scale(Admixed\_prop) \* scale(Martonne\_new)   
## Value Std.Error DF t-value  
## (Intercept) 7.730547 0.18163474 139 42.56095  
## scale(Admixed\_prop) 0.026890 0.05704710 139 0.47137  
## scale(Hegyi) -0.155606 0.05965785 139 -2.60831  
## scale(BAL) -0.065318 0.05169171 139 -1.26361  
## scale(DBH) 0.351012 0.07206333 139 4.87088  
## scale(Martonne\_new) -0.291207 0.18066306 2 -1.61188  
## SpeciesFir 0.159464 0.08940888 139 1.78354  
## scale(Admixed\_prop):SpeciesFir 0.070199 0.08949689 139 0.78437  
## scale(Admixed\_prop):scale(DBH) 0.137776 0.06512736 139 2.11549  
## scale(Admixed\_prop):scale(Hegyi) 0.198990 0.06157935 139 3.23144  
## scale(Admixed\_prop):scale(BAL) 0.068966 0.04095012 139 1.68414  
## scale(Admixed\_prop):scale(Martonne\_new) 0.002508 0.04394349 139 0.05707  
## p-value  
## (Intercept) 0.0000  
## scale(Admixed\_prop) 0.6381  
## scale(Hegyi) 0.0101  
## scale(BAL) 0.2085  
## scale(DBH) 0.0000  
## scale(Martonne\_new) 0.2483  
## SpeciesFir 0.0767  
## scale(Admixed\_prop):SpeciesFir 0.4342  
## scale(Admixed\_prop):scale(DBH) 0.0362  
## scale(Admixed\_prop):scale(Hegyi) 0.0015  
## scale(Admixed\_prop):scale(BAL) 0.0944  
## scale(Admixed\_prop):scale(Martonne\_new) 0.9546  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH)  
## scale(Admixed\_prop) 0.039   
## scale(Hegyi) 0.056 -0.063   
## scale(BAL) -0.087 -0.261 -0.137   
## scale(DBH) 0.099 -0.171 0.557 0.217   
## scale(Martonne\_new) 0.035 0.031 -0.008 -0.170 -0.172  
## SpeciesFir -0.257 -0.135 -0.267 0.353 -0.381  
## scale(Admixed\_prop):SpeciesFir -0.043 -0.810 0.097 0.320 0.188  
## scale(Admixed\_prop):scale(DBH) -0.038 0.296 -0.123 0.271 -0.006  
## scale(Admixed\_prop):scale(Hegyi) -0.019 0.221 -0.229 0.237 -0.062  
## scale(Admixed\_prop):scale(BAL) -0.076 -0.371 0.113 0.112 0.157  
## scale(Admixed\_prop):scale(Martonne\_new) 0.006 -0.099 -0.064 -0.112 -0.153  
## sc(M\_) SpcsFr s(A\_):S s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir 0.018   
## scale(Admixed\_prop):SpeciesFir -0.044 0.151   
## scale(Admixed\_prop):scale(DBH) -0.064 0.176 -0.374   
## scale(Admixed\_prop):scale(Hegyi) -0.064 0.170 -0.236 0.763   
## scale(Admixed\_prop):scale(BAL) -0.015 0.298 0.410 -0.042   
## scale(Admixed\_prop):scale(Martonne\_new) 0.045 -0.063 0.175 -0.544   
## s(A\_):(H s(A\_):(B  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi)   
## scale(Admixed\_prop):scale(BAL) -0.043   
## scale(Admixed\_prop):scale(Martonne\_new) -0.308 -0.257   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.69742406 -0.67795313 -0.08993041 0.71315404 2.08442327   
##   
## Number of Observations: 153  
## Number of Groups: 4

#Checking residuals  
plot(lme\_r1)



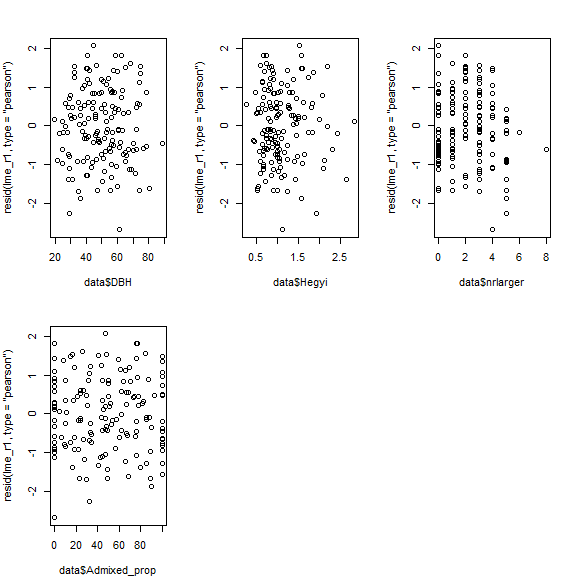
# that looks quite good   
qqnorm(resid(lme\_r1))# good



shapiro.test(resid(lme\_r1))# good

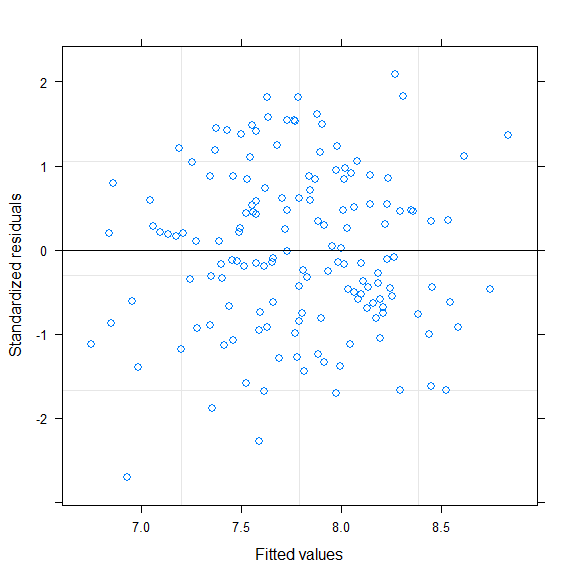
##   
## Shapiro-Wilk normality test  
##   
## data: resid(lme\_r1)  
## W = 0.99093, p-value = 0.4361

op <- par(mfrow = c(2, 3), mar = c(4, 4, 3, 2))  
plot(data$DBH,resid(lme\_r1,type="pearson")) #ok  
plot(data$Hegyi,resid(lme\_r1,type="pearson")) #quite ok   
plot(data$nrlarger,resid(lme\_r1,type="pearson")) # naja  
plot(data$Admixed\_prop,resid(lme\_r1,type="pearson")) # naja

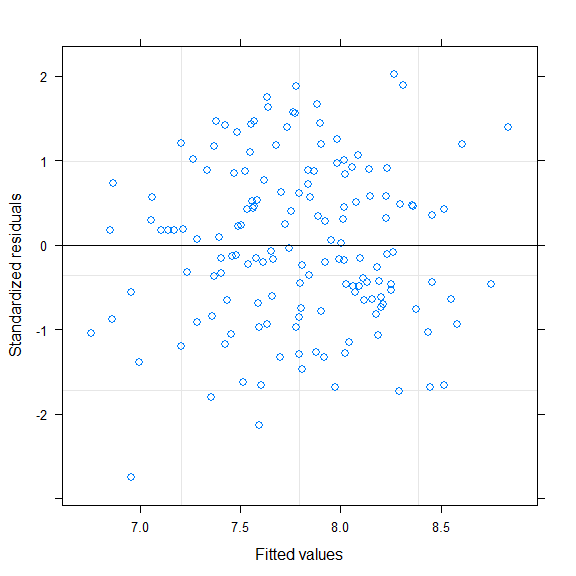


#Variance structure selection with lme: We tested different methods of incorporating heterogeneity into the model (variance structures). AR not needed as no repeated measureas (Pinheiro and Bates, 2000; Zuur et al., 2009). To address heteroscedasticity of the predictor variables we tested either a constant variance structure per group (varIdent) an exponential (varExp) or power (varPower) variance function for continuous predictor variables (Pinheiro et al., 2018).

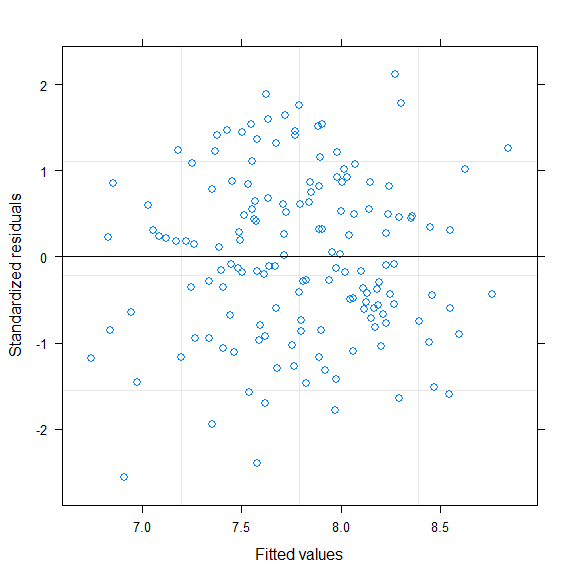
lme\_r1 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site , data=data)  
   
lme\_v1 <- lme\_r1  
  
  
plot(lme\_v1)



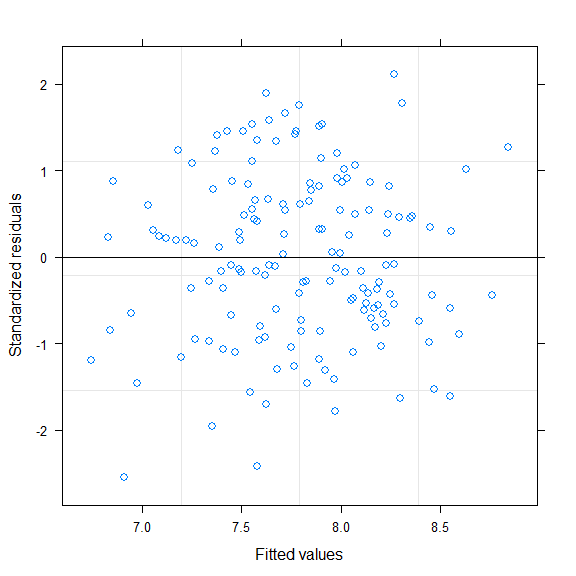
lme\_v2 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site  
 ,weights = varExp( form = ~ Hegyi)  
 , data=data)  
plot(lme\_v2)



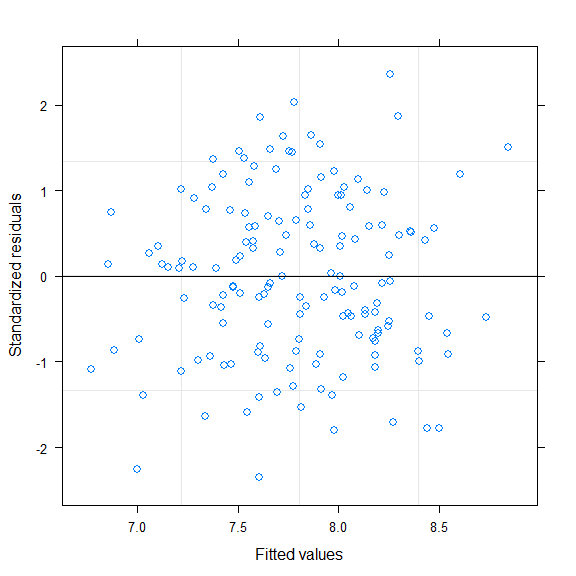
lme\_v4 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site  
 ,weights = varExp( form = ~ DBH)  
 , data=data)  
plot(lme\_v4)



lme\_v5 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site  
 ,weights = varPower( form = ~ DBH)  
 ,data=data)  
  
plot(lme\_v5)



lme\_v8 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site  
 ,weights = varExp( form = ~ BAL)  
 ,data=data, na.action=na.exclude)  
  
plot(lme\_v8)



aictab(mget(str\_subset(ls(), "lme\_v")))# aictab: no adjustement of varaince structure needed

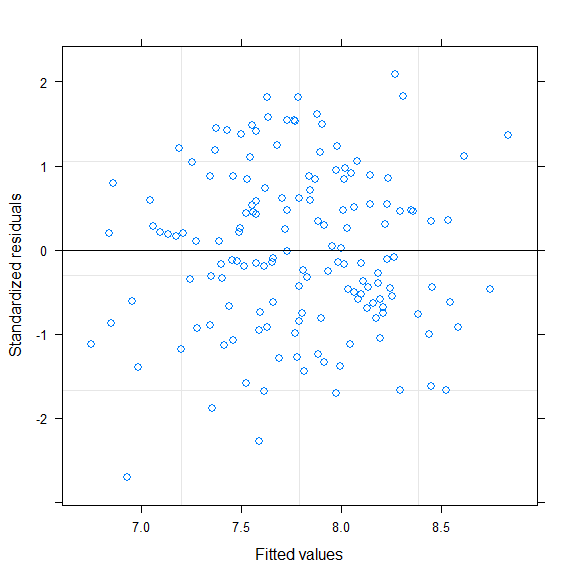
## Warning in aictab.AIClme(mget(str\_subset(ls(), "lme\_v"))):   
## Model selection for fixed effects is only appropriate with method=ML:  
## REML (default) should only be used to select random effects for a constant set of fixed effects

##   
## Model selection based on AICc:  
##   
## K AICc Delta\_AICc AICcWt Cum.Wt Res.LL  
## lme\_v1 14 234.44 0.00 0.33 0.33 -101.70  
## lme\_v8 15 234.57 0.13 0.31 0.64 -100.53  
## lme\_v5 15 236.33 1.89 0.13 0.76 -101.41  
## lme\_v4 15 236.42 1.98 0.12 0.89 -101.46  
## lme\_v2 15 236.54 2.10 0.11 1.00 -101.52

summary(lme\_v1)# same as lme\_r1

## Linear mixed-effects model fit by REML  
## Data: data   
## AIC BIC logLik  
## 231.3934 272.676 -101.6967  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.3442674 0.4038346  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi) + scale(Admixed\_prop) \* scale(BAL) + scale(Admixed\_prop) \* scale(Martonne\_new)   
## Value Std.Error DF t-value  
## (Intercept) 7.730547 0.18163474 139 42.56095  
## scale(Admixed\_prop) 0.026890 0.05704710 139 0.47137  
## scale(Hegyi) -0.155606 0.05965785 139 -2.60831  
## scale(BAL) -0.065318 0.05169171 139 -1.26361  
## scale(DBH) 0.351012 0.07206333 139 4.87088  
## scale(Martonne\_new) -0.291207 0.18066306 2 -1.61188  
## SpeciesFir 0.159464 0.08940888 139 1.78354  
## scale(Admixed\_prop):SpeciesFir 0.070199 0.08949689 139 0.78437  
## scale(Admixed\_prop):scale(DBH) 0.137776 0.06512736 139 2.11549  
## scale(Admixed\_prop):scale(Hegyi) 0.198990 0.06157935 139 3.23144  
## scale(Admixed\_prop):scale(BAL) 0.068966 0.04095012 139 1.68414  
## scale(Admixed\_prop):scale(Martonne\_new) 0.002508 0.04394349 139 0.05707  
## p-value  
## (Intercept) 0.0000  
## scale(Admixed\_prop) 0.6381  
## scale(Hegyi) 0.0101  
## scale(BAL) 0.2085  
## scale(DBH) 0.0000  
## scale(Martonne\_new) 0.2483  
## SpeciesFir 0.0767  
## scale(Admixed\_prop):SpeciesFir 0.4342  
## scale(Admixed\_prop):scale(DBH) 0.0362  
## scale(Admixed\_prop):scale(Hegyi) 0.0015  
## scale(Admixed\_prop):scale(BAL) 0.0944  
## scale(Admixed\_prop):scale(Martonne\_new) 0.9546  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH)  
## scale(Admixed\_prop) 0.039   
## scale(Hegyi) 0.056 -0.063   
## scale(BAL) -0.087 -0.261 -0.137   
## scale(DBH) 0.099 -0.171 0.557 0.217   
## scale(Martonne\_new) 0.035 0.031 -0.008 -0.170 -0.172  
## SpeciesFir -0.257 -0.135 -0.267 0.353 -0.381  
## scale(Admixed\_prop):SpeciesFir -0.043 -0.810 0.097 0.320 0.188  
## scale(Admixed\_prop):scale(DBH) -0.038 0.296 -0.123 0.271 -0.006  
## scale(Admixed\_prop):scale(Hegyi) -0.019 0.221 -0.229 0.237 -0.062  
## scale(Admixed\_prop):scale(BAL) -0.076 -0.371 0.113 0.112 0.157  
## scale(Admixed\_prop):scale(Martonne\_new) 0.006 -0.099 -0.064 -0.112 -0.153  
## sc(M\_) SpcsFr s(A\_):S s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir 0.018   
## scale(Admixed\_prop):SpeciesFir -0.044 0.151   
## scale(Admixed\_prop):scale(DBH) -0.064 0.176 -0.374   
## scale(Admixed\_prop):scale(Hegyi) -0.064 0.170 -0.236 0.763   
## scale(Admixed\_prop):scale(BAL) -0.015 0.298 0.410 -0.042   
## scale(Admixed\_prop):scale(Martonne\_new) 0.045 -0.063 0.175 -0.544   
## s(A\_):(H s(A\_):(B  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi)   
## scale(Admixed\_prop):scale(BAL) -0.043   
## scale(Admixed\_prop):scale(Martonne\_new) -0.308 -0.257   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.69742406 -0.67795313 -0.08993041 0.71315404 2.08442327   
##   
## Number of Observations: 153  
## Number of Groups: 4

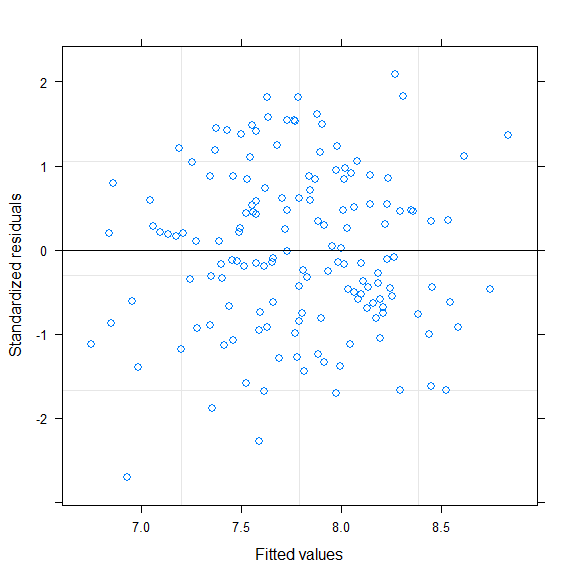
plot(lme\_v1)



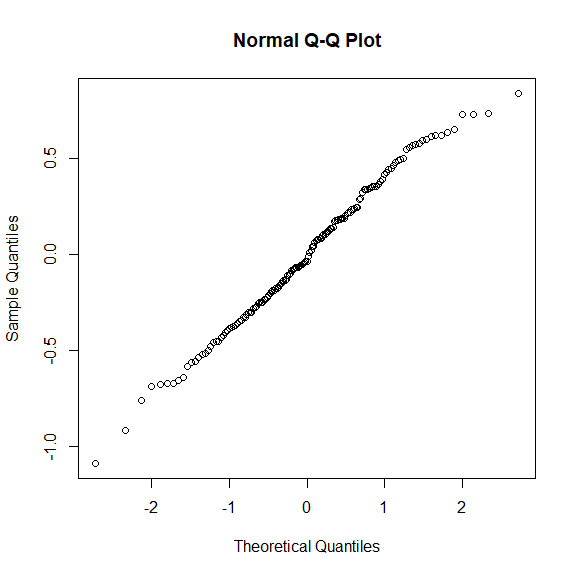
# Final random structure  
lme\_rv <- lme\_v1  
summary(lme\_rv)

## Linear mixed-effects model fit by REML  
## Data: data   
## AIC BIC logLik  
## 231.3934 272.676 -101.6967  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.3442674 0.4038346  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi) + scale(Admixed\_prop) \* scale(BAL) + scale(Admixed\_prop) \* scale(Martonne\_new)   
## Value Std.Error DF t-value  
## (Intercept) 7.730547 0.18163474 139 42.56095  
## scale(Admixed\_prop) 0.026890 0.05704710 139 0.47137  
## scale(Hegyi) -0.155606 0.05965785 139 -2.60831  
## scale(BAL) -0.065318 0.05169171 139 -1.26361  
## scale(DBH) 0.351012 0.07206333 139 4.87088  
## scale(Martonne\_new) -0.291207 0.18066306 2 -1.61188  
## SpeciesFir 0.159464 0.08940888 139 1.78354  
## scale(Admixed\_prop):SpeciesFir 0.070199 0.08949689 139 0.78437  
## scale(Admixed\_prop):scale(DBH) 0.137776 0.06512736 139 2.11549  
## scale(Admixed\_prop):scale(Hegyi) 0.198990 0.06157935 139 3.23144  
## scale(Admixed\_prop):scale(BAL) 0.068966 0.04095012 139 1.68414  
## scale(Admixed\_prop):scale(Martonne\_new) 0.002508 0.04394349 139 0.05707  
## p-value  
## (Intercept) 0.0000  
## scale(Admixed\_prop) 0.6381  
## scale(Hegyi) 0.0101  
## scale(BAL) 0.2085  
## scale(DBH) 0.0000  
## scale(Martonne\_new) 0.2483  
## SpeciesFir 0.0767  
## scale(Admixed\_prop):SpeciesFir 0.4342  
## scale(Admixed\_prop):scale(DBH) 0.0362  
## scale(Admixed\_prop):scale(Hegyi) 0.0015  
## scale(Admixed\_prop):scale(BAL) 0.0944  
## scale(Admixed\_prop):scale(Martonne\_new) 0.9546  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH)  
## scale(Admixed\_prop) 0.039   
## scale(Hegyi) 0.056 -0.063   
## scale(BAL) -0.087 -0.261 -0.137   
## scale(DBH) 0.099 -0.171 0.557 0.217   
## scale(Martonne\_new) 0.035 0.031 -0.008 -0.170 -0.172  
## SpeciesFir -0.257 -0.135 -0.267 0.353 -0.381  
## scale(Admixed\_prop):SpeciesFir -0.043 -0.810 0.097 0.320 0.188  
## scale(Admixed\_prop):scale(DBH) -0.038 0.296 -0.123 0.271 -0.006  
## scale(Admixed\_prop):scale(Hegyi) -0.019 0.221 -0.229 0.237 -0.062  
## scale(Admixed\_prop):scale(BAL) -0.076 -0.371 0.113 0.112 0.157  
## scale(Admixed\_prop):scale(Martonne\_new) 0.006 -0.099 -0.064 -0.112 -0.153  
## sc(M\_) SpcsFr s(A\_):S s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir 0.018   
## scale(Admixed\_prop):SpeciesFir -0.044 0.151   
## scale(Admixed\_prop):scale(DBH) -0.064 0.176 -0.374   
## scale(Admixed\_prop):scale(Hegyi) -0.064 0.170 -0.236 0.763   
## scale(Admixed\_prop):scale(BAL) -0.015 0.298 0.410 -0.042   
## scale(Admixed\_prop):scale(Martonne\_new) 0.045 -0.063 0.175 -0.544   
## s(A\_):(H s(A\_):(B  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi)   
## scale(Admixed\_prop):scale(BAL) -0.043   
## scale(Admixed\_prop):scale(Martonne\_new) -0.308 -0.257   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.69742406 -0.67795313 -0.08993041 0.71315404 2.08442327   
##   
## Number of Observations: 153  
## Number of Groups: 4

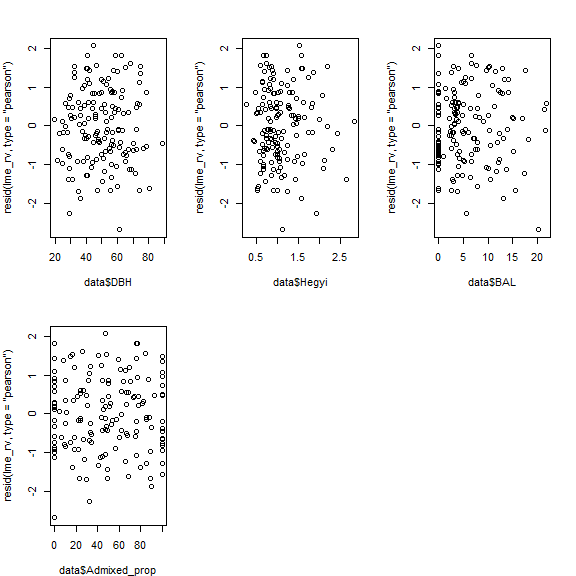
# model check:  
plot(lme\_rv) #looks good



qqnorm(resid(lme\_rv))



##checking predictors  
  
op <- par(mfrow = c(2, 3), mar = c(4, 4, 3, 2))  
plot(data$DBH,resid(lme\_rv,type="pearson"))   
plot(data$Hegyi,resid(lme\_rv,type="pearson"))   
plot(data$BAL,resid(lme\_rv,type="pearson"))   
plot(data$Admixed\_prop,resid(lme\_rv,type="pearson"))  
  
  
# seems all ok  
par(op)



#Fixed effects selection based on likelihood ratio tests using anova()

#best full model  
lme\_v1 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site , data=data, method="ML")  
   
lme\_f0 <-lme\_v1  
 summary(lme\_f0)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 184.8334 227.2595 -78.41669  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.2175692 0.3907217  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi) + scale(Admixed\_prop) \* scale(BAL) + scale(Admixed\_prop) \* scale(Martonne\_new)   
## Value Std.Error DF t-value  
## (Intercept) 7.726272 0.12731863 139 60.68454  
## scale(Admixed\_prop) 0.028656 0.05747569 139 0.49858  
## scale(Hegyi) -0.147207 0.05959186 139 -2.47025  
## scale(BAL) -0.075688 0.05160712 139 -1.46662  
## scale(DBH) 0.335678 0.07176328 139 4.67758  
## scale(Martonne\_new) -0.276611 0.12530337 2 -2.20753  
## SpeciesFir 0.164986 0.09001963 139 1.83278  
## scale(Admixed\_prop):SpeciesFir 0.066430 0.09016113 139 0.73680  
## scale(Admixed\_prop):scale(DBH) 0.135478 0.06561878 139 2.06462  
## scale(Admixed\_prop):scale(Hegyi) 0.195753 0.06198898 139 3.15787  
## scale(Admixed\_prop):scale(BAL) 0.069736 0.04125395 139 1.69041  
## scale(Admixed\_prop):scale(Martonne\_new) 0.004532 0.04426474 139 0.10239  
## p-value  
## (Intercept) 0.0000  
## scale(Admixed\_prop) 0.6189  
## scale(Hegyi) 0.0147  
## scale(BAL) 0.1447  
## scale(DBH) 0.0000  
## scale(Martonne\_new) 0.1580  
## SpeciesFir 0.0690  
## scale(Admixed\_prop):SpeciesFir 0.4625  
## scale(Admixed\_prop):scale(DBH) 0.0408  
## scale(Admixed\_prop):scale(Hegyi) 0.0019  
## scale(Admixed\_prop):scale(BAL) 0.0932  
## scale(Admixed\_prop):scale(Martonne\_new) 0.9186  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH)  
## scale(Admixed\_prop) 0.057   
## scale(Hegyi) 0.083 -0.064   
## scale(BAL) -0.130 -0.260 -0.129   
## scale(DBH) 0.141 -0.169 0.577 0.201   
## scale(Martonne\_new) 0.024 0.043 -0.019 -0.239 -0.241  
## SpeciesFir -0.369 -0.136 -0.272 0.363 -0.379  
## scale(Admixed\_prop):SpeciesFir -0.062 -0.810 0.099 0.319 0.186  
## scale(Admixed\_prop):scale(DBH) -0.055 0.297 -0.121 0.271 -0.009  
## scale(Admixed\_prop):scale(Hegyi) -0.028 0.221 -0.224 0.236 -0.066  
## scale(Admixed\_prop):scale(BAL) -0.109 -0.372 0.115 0.115 0.162  
## scale(Admixed\_prop):scale(Martonne\_new) 0.009 -0.100 -0.069 -0.109 -0.152  
## sc(M\_) SpcsFr s(A\_):S s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir 0.023   
## scale(Admixed\_prop):SpeciesFir -0.061 0.152   
## scale(Admixed\_prop):scale(DBH) -0.091 0.177 -0.375   
## scale(Admixed\_prop):scale(Hegyi) -0.090 0.172 -0.237 0.763   
## scale(Admixed\_prop):scale(BAL) -0.024 0.297 0.411 -0.042   
## scale(Admixed\_prop):scale(Martonne\_new) 0.063 -0.065 0.176 -0.543   
## s(A\_):(H s(A\_):(B  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi)   
## scale(Admixed\_prop):scale(BAL) -0.044   
## scale(Admixed\_prop):scale(Martonne\_new) -0.307 -0.257   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.78269666 -0.69489230 -0.07780347 0.69787944 2.20653033   
##   
## Number of Observations: 153  
## Number of Groups: 4

max(vif.mer(lme\_f0))# 3.9 too high

## [1] 3.933407

#drop term with highest P-value: species\* admixed\_prop  
lme\_f1 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)+scale(Admixed\_prop)\*scale(Martonne\_new)  
 ,random= ~1|Site , data=data, method="ML")  
summary(lme\_f1)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 183.4185 222.8142 -78.70924  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.2128957 0.3916976  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi) + scale(Admixed\_prop) \* scale(BAL) + scale(Admixed\_prop) \* scale(Martonne\_new)   
## Value Std.Error DF t-value  
## (Intercept) 7.731728 0.12452619 140 62.08917  
## scale(Admixed\_prop) 0.062954 0.03365228 140 1.87073  
## scale(Hegyi) -0.150921 0.05919255 140 -2.54966  
## scale(BAL) -0.088556 0.04882058 140 -1.81391  
## scale(DBH) 0.324753 0.07037946 140 4.61432  
## scale(Martonne\_new) -0.269893 0.12244779 2 -2.20415  
## SpeciesFir 0.155355 0.08887078 140 1.74810  
## scale(Admixed\_prop):scale(DBH) 0.153335 0.06077661 140 2.52293  
## scale(Admixed\_prop):scale(Hegyi) 0.206282 0.06015586 140 3.42913  
## scale(Admixed\_prop):scale(BAL) 0.057359 0.03756915 140 1.52675  
## scale(Admixed\_prop):scale(Martonne\_new) -0.001024 0.04352786 140 -0.02353  
## p-value  
## (Intercept) 0.0000  
## scale(Admixed\_prop) 0.0635  
## scale(Hegyi) 0.0119  
## scale(BAL) 0.0718  
## scale(DBH) 0.0000  
## scale(Martonne\_new) 0.1583  
## SpeciesFir 0.0826  
## scale(Admixed\_prop):scale(DBH) 0.0128  
## scale(Admixed\_prop):scale(Hegyi) 0.0008  
## scale(Admixed\_prop):scale(BAL) 0.1291  
## scale(Admixed\_prop):scale(Martonne\_new) 0.9813  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH)  
## scale(Admixed\_prop) 0.012   
## scale(Hegyi) 0.092 0.028   
## scale(BAL) -0.119 -0.003 -0.170   
## scale(DBH) 0.158 -0.032 0.573 0.151   
## scale(Martonne\_new) 0.020 -0.011 -0.014 -0.236 -0.238  
## SpeciesFir -0.372 -0.022 -0.293 0.337 -0.419  
## scale(Admixed\_prop):scale(DBH) -0.087 -0.012 -0.090 0.445 0.066  
## scale(Admixed\_prop):scale(Hegyi) -0.045 0.052 -0.207 0.338 -0.024  
## scale(Admixed\_prop):scale(BAL) -0.093 -0.073 0.082 -0.018 0.096  
## scale(Admixed\_prop):scale(Martonne\_new) 0.021 0.074 -0.089 -0.177 -0.190  
## sc(M\_) SpcsFr s(A\_):(D s(A\_):(H  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir 0.033   
## scale(Admixed\_prop):scale(DBH) -0.125 0.255   
## scale(Admixed\_prop):scale(Hegyi) -0.110 0.216 0.748   
## scale(Admixed\_prop):scale(BAL) 0.001 0.261 0.132 0.061   
## scale(Admixed\_prop):scale(Martonne\_new) 0.077 -0.094 -0.523 -0.277   
## s(A\_):(B  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi)   
## scale(Admixed\_prop):scale(BAL)   
## scale(Admixed\_prop):scale(Martonne\_new) -0.367   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.88578571 -0.68003191 -0.01993937 0.62699635 2.20584845   
##   
## Number of Observations: 153  
## Number of Groups: 4

anova(lme\_f0,lme\_f1) #decreases AIC although not sig better as null

## Model df AIC BIC logLik Test L.Ratio p-value  
## lme\_f0 1 14 184.8334 227.2595 -78.41669   
## lme\_f1 2 13 183.4185 222.8142 -78.70924 1 vs 2 0.5851089 0.4443

#drop next term: martonne \* admix interaction  
lme\_f2 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)  
 ,random= ~1|Site   
 ,data=data, method="ML")  
summary(lme\_f2)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 181.4191 217.7843 -78.70954  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.2127117 0.3917067  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi) + scale(Admixed\_prop) \* scale(BAL)   
## Value Std.Error DF t-value p-value  
## (Intercept) 7.731776 0.12397931 141 62.36344 0.0000  
## scale(Admixed\_prop) 0.063012 0.03344283 141 1.88418 0.0616  
## scale(Hegyi) -0.151019 0.05875295 141 -2.57041 0.0112  
## scale(BAL) -0.088785 0.04788180 141 -1.85426 0.0658  
## scale(DBH) 0.324399 0.06885198 141 4.71154 0.0000  
## scale(Martonne\_new) -0.269633 0.12157197 2 -2.21789 0.1568  
## SpeciesFir 0.155177 0.08816942 141 1.75998 0.0806  
## scale(Admixed\_prop):scale(DBH) 0.152583 0.05161713 141 2.95604 0.0037  
## scale(Admixed\_prop):scale(Hegyi) 0.205882 0.05760251 141 3.57418 0.0005  
## scale(Admixed\_prop):scale(BAL) 0.057041 0.03482466 141 1.63794 0.1037  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH) sc(M\_)  
## scale(Admixed\_prop) 0.011   
## scale(Hegyi) 0.094 0.035   
## scale(BAL) -0.117 0.010 -0.189   
## scale(DBH) 0.165 -0.019 0.569 0.121   
## scale(Martonne\_new) 0.018 -0.017 -0.007 -0.227 -0.229   
## SpeciesFir -0.372 -0.015 -0.303 0.327 -0.447 0.040  
## scale(Admixed\_prop):scale(DBH) -0.089 0.031 -0.161 0.420 -0.040 -0.100  
## scale(Admixed\_prop):scale(Hegyi) -0.041 0.075 -0.242 0.306 -0.081 -0.093  
## scale(Admixed\_prop):scale(BAL) -0.092 -0.049 0.053 -0.091 0.029 0.032  
## SpcsFr s(A\_):(D s(A\_):(H  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH) 0.243   
## scale(Admixed\_prop):scale(Hegyi) 0.199 0.737   
## scale(Admixed\_prop):scale(BAL) 0.244 -0.076 -0.046   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.88580430 -0.68286539 -0.02037989 0.62857664 2.20675445   
##   
## Number of Observations: 153  
## Number of Groups: 4

anova(lme\_f0,lme\_f2,lme\_f1)# decreases AIC although not sig better as null

## Model df AIC BIC logLik Test L.Ratio p-value  
## lme\_f0 1 14 184.8334 227.2595 -78.41669   
## lme\_f2 2 12 181.4191 217.7843 -78.70954 1 vs 2 0.5857019 0.7461  
## lme\_f1 3 13 183.4185 222.8142 -78.70924 2 vs 3 0.0005930 0.9806

#drop next term: martonne  
lme\_f3 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH)+ Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) +scale(Admixed\_prop)\*scale(BAL)  
 ,random= ~1|Site   
 ,data=data, method="ML")  
  
summary(lme\_f3)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 182.9862 216.321 -80.49311  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.3488999 0.3914701  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi) + scale(Admixed\_prop) \* scale(BAL)   
## Value Std.Error DF t-value p-value  
## (Intercept) 7.746729 0.18865843 141 41.06219 0.0000  
## scale(Admixed\_prop) 0.062798 0.03331020 141 1.88524 0.0615  
## scale(Hegyi) -0.161085 0.05916867 141 -2.72247 0.0073  
## scale(BAL) -0.089524 0.04760040 141 -1.88073 0.0621  
## scale(DBH) 0.324052 0.06863147 141 4.72163 0.0000  
## SpeciesFir 0.151640 0.08791636 141 1.72482 0.0868  
## scale(Admixed\_prop):scale(DBH) 0.149264 0.05130824 141 2.90916 0.0042  
## scale(Admixed\_prop):scale(Hegyi) 0.203849 0.05732958 141 3.55574 0.0005  
## scale(Admixed\_prop):scale(BAL) 0.055758 0.03472980 141 1.60548 0.1106  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH) SpcsFr  
## scale(Admixed\_prop) 0.007   
## scale(Hegyi) 0.059 0.032   
## scale(BAL) -0.069 0.009 -0.199   
## scale(DBH) 0.116 -0.021 0.553 0.120   
## SpeciesFir -0.245 -0.015 -0.296 0.323 -0.451   
## scale(Admixed\_prop):scale(DBH) -0.056 0.031 -0.162 0.414 -0.047 0.244  
## scale(Admixed\_prop):scale(Hegyi) -0.024 0.075 -0.247 0.301 -0.087 0.199  
## scale(Admixed\_prop):scale(BAL) -0.062 -0.048 0.054 -0.095 0.023 0.246  
## s(A\_):(D s(A\_):(H  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi) 0.736   
## scale(Admixed\_prop):scale(BAL) -0.075 -0.045   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.88369701 -0.68037467 -0.03314333 0.60071907 2.19271023   
##   
## Number of Observations: 153  
## Number of Groups: 4

anova(lme\_f0,lme\_f2,lme\_f3, lme\_f1)# NO keep Martonne: increases AIC and model worse at p=0.05

## Model df AIC BIC logLik Test L.Ratio p-value  
## lme\_f0 1 14 184.8334 227.2595 -78.41669   
## lme\_f2 2 12 181.4191 217.7843 -78.70954 1 vs 2 0.585702 0.7461  
## lme\_f3 3 11 182.9862 216.3210 -80.49311 2 vs 3 3.567135 0.0589  
## lme\_f1 4 13 183.4185 222.8142 -78.70924 3 vs 4 3.567728 0.1680

#alternative drop BAL \* admix prop  
lme\_f4 <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) ,random= ~1|Site   
 ,data=data, method="ML")  
summary(lme\_f4)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 182.2465 215.5814 -80.12327  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.2267826 0.3948078  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(BAL) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi)   
## Value Std.Error DF t-value p-value  
## (Intercept) 7.751179 0.12973612 142 59.74573 0.0000  
## scale(Admixed\_prop) 0.065727 0.03355107 142 1.95902 0.0521  
## scale(Hegyi) -0.157669 0.05902966 142 -2.67101 0.0084  
## scale(BAL) -0.080052 0.04796318 142 -1.66903 0.0973  
## scale(DBH) 0.323730 0.06926729 142 4.67363 0.0000  
## scale(Martonne\_new) -0.278434 0.12794409 2 -2.17621 0.1615  
## SpeciesFir 0.118973 0.08589052 142 1.38517 0.1682  
## scale(Admixed\_prop):scale(DBH) 0.159210 0.05169823 142 3.07960 0.0025  
## scale(Admixed\_prop):scale(Hegyi) 0.210693 0.05780654 142 3.64479 0.0004  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(BAL) s(DBH) sc(M\_)  
## scale(Admixed\_prop) 0.006   
## scale(Hegyi) 0.095 0.037   
## scale(BAL) -0.121 0.006 -0.186   
## scale(DBH) 0.161 -0.017 0.565 0.127   
## scale(Martonne\_new) 0.023 -0.015 -0.007 -0.216 -0.220   
## SpeciesFir -0.346 -0.004 -0.326 0.360 -0.469 0.032  
## scale(Admixed\_prop):scale(DBH) -0.092 0.028 -0.158 0.415 -0.037 -0.094  
## scale(Admixed\_prop):scale(Hegyi) -0.043 0.073 -0.241 0.303 -0.079 -0.088  
## SpcsFr s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(BAL)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH) 0.270   
## scale(Admixed\_prop):scale(Hegyi) 0.217 0.736   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -3.31816496 -0.66945150 0.02929204 0.68065863 2.22363959   
##   
## Number of Observations: 153  
## Number of Groups: 4

anova(lme\_f0, lme\_f2,lme\_f4, lme\_f1) # increases AIC but gets not worse

## Model df AIC BIC logLik Test L.Ratio p-value  
## lme\_f0 1 14 184.8334 227.2595 -78.41669   
## lme\_f2 2 12 181.4191 217.7843 -78.70954 1 vs 2 0.5857019 0.7461  
## lme\_f4 3 11 182.2465 215.5814 -80.12327 2 vs 3 2.8274599 0.0927  
## lme\_f1 4 13 183.4185 222.8142 -78.70924 3 vs 4 2.8280528 0.2432

# drop also BAL?  
lme\_f5<- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) ,random= ~1|Site   
 ,data=data, method="ML")  
  
summary(lme\_f5)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 183.0242 213.3286 -81.5121  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.2664943 0.3968891  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi)   
## Value Std.Error DF t-value p-value  
## (Intercept) 7.728450 0.14727556 143 52.47612 0.0000  
## scale(Admixed\_prop) 0.066110 0.03361336 143 1.96678 0.0511  
## scale(Hegyi) -0.179064 0.05830838 143 -3.07099 0.0026  
## scale(DBH) 0.344735 0.06909773 143 4.98909 0.0000  
## scale(Martonne\_new) -0.328658 0.14397386 2 -2.28276 0.1499  
## SpeciesFir 0.165126 0.08043494 143 2.05291 0.0419  
## scale(Admixed\_prop):scale(DBH) 0.193742 0.04712556 143 4.11119 0.0001  
## scale(Admixed\_prop):scale(Hegyi) 0.239610 0.05520843 143 4.34011 0.0000  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(DBH) sc(M\_) SpcsFr  
## scale(Admixed\_prop) 0.006   
## scale(Hegyi) 0.064 0.038   
## scale(DBH) 0.158 -0.018 0.598   
## scale(Martonne\_new) 0.008 -0.012 -0.041 -0.175   
## SpeciesFir -0.287 -0.006 -0.279 -0.558 0.106   
## scale(Admixed\_prop):scale(DBH) -0.041 0.028 -0.089 -0.102 -0.003 0.143  
## scale(Admixed\_prop):scale(Hegyi) -0.006 0.075 -0.198 -0.126 -0.021 0.122  
## s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi) 0.704   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -3.60047272 -0.65519119 -0.02144695 0.69156824 2.20235398   
##   
## Number of Observations: 153  
## Number of Groups: 4

anova(lme\_f0, lme\_f2,lme\_f5, lme\_f1)# increases AIC but not worse sig

## Model df AIC BIC logLik Test L.Ratio p-value  
## lme\_f0 1 14 184.8334 227.2595 -78.41669   
## lme\_f2 2 12 181.4191 217.7843 -78.70954 1 vs 2 0.585702 0.7461  
## lme\_f5 3 10 183.0242 213.3286 -81.51210 2 vs 3 5.605123 0.0607  
## lme\_f1 4 13 183.4185 222.8142 -78.70924 3 vs 4 5.605716 0.1325

anova(lme\_f2,lme\_f5)

## Model df AIC BIC logLik Test L.Ratio p-value  
## lme\_f2 1 12 181.4191 217.7843 -78.70954   
## lme\_f5 2 10 183.0242 213.3286 -81.51210 1 vs 2 5.605123 0.0607

# check again if dropping last significant term martonne  
lme\_f6<- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(DBH) + Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) ,random= ~1|Site   
 ,data=data, method="ML")  
  
summary(lme\_f6)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 184.5486 211.8225 -83.27429  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.4273144 0.396735  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(DBH) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi)   
## Value Std.Error DF t-value p-value  
## (Intercept) 7.744986 0.22540068 143 34.36097 0.0000  
## scale(Admixed\_prop) 0.065842 0.03348843 143 1.96611 0.0512  
## scale(Hegyi) -0.187094 0.05844544 143 -3.20118 0.0017  
## scale(DBH) 0.344593 0.06887702 143 5.00302 0.0000  
## SpeciesFir 0.163458 0.08020853 143 2.03792 0.0434  
## scale(Admixed\_prop):scale(DBH) 0.191193 0.04697503 143 4.07011 0.0001  
## scale(Admixed\_prop):scale(Hegyi) 0.237969 0.05503089 143 4.32428 0.0000  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(DBH) SpcsFr  
## scale(Admixed\_prop) 0.004   
## scale(Hegyi) 0.041 0.035   
## scale(DBH) 0.108 -0.020 0.589   
## SpeciesFir -0.190 -0.005 -0.271 -0.559   
## scale(Admixed\_prop):scale(DBH) -0.027 0.028 -0.087 -0.106 0.146  
## scale(Admixed\_prop):scale(Hegyi) -0.004 0.076 -0.200 -0.129 0.123  
## s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(DBH)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi) 0.704   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -3.593445459 -0.660654453 0.001167001 0.719843657 2.192002393   
##   
## Number of Observations: 153  
## Number of Groups: 4

anova(lme\_f0, lme\_f2,lme\_f6, lme\_f5, lme\_f1)# gets sig worse, keep martonne

## Model df AIC BIC logLik Test L.Ratio p-value  
## lme\_f0 1 14 184.8334 227.2595 -78.41669   
## lme\_f2 2 12 181.4191 217.7843 -78.70954 1 vs 2 0.585702 0.7461  
## lme\_f6 3 9 184.5486 211.8225 -83.27429 2 vs 3 9.129507 0.0276  
## lme\_f5 4 10 183.0242 213.3286 -81.51210 3 vs 4 3.524383 0.0605  
## lme\_f1 5 13 183.4185 222.8142 -78.70924 4 vs 5 5.605716 0.1325

lme\_final <- lme\_f5  
summary(lme\_final)

## Linear mixed-effects model fit by maximum likelihood  
## Data: data   
## AIC BIC logLik  
## 183.0242 213.3286 -81.5121  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.2664943 0.3968891  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi)   
## Value Std.Error DF t-value p-value  
## (Intercept) 7.728450 0.14727556 143 52.47612 0.0000  
## scale(Admixed\_prop) 0.066110 0.03361336 143 1.96678 0.0511  
## scale(Hegyi) -0.179064 0.05830838 143 -3.07099 0.0026  
## scale(DBH) 0.344735 0.06909773 143 4.98909 0.0000  
## scale(Martonne\_new) -0.328658 0.14397386 2 -2.28276 0.1499  
## SpeciesFir 0.165126 0.08043494 143 2.05291 0.0419  
## scale(Admixed\_prop):scale(DBH) 0.193742 0.04712556 143 4.11119 0.0001  
## scale(Admixed\_prop):scale(Hegyi) 0.239610 0.05520843 143 4.34011 0.0000  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(DBH) sc(M\_) SpcsFr  
## scale(Admixed\_prop) 0.006   
## scale(Hegyi) 0.064 0.038   
## scale(DBH) 0.158 -0.018 0.598   
## scale(Martonne\_new) 0.008 -0.012 -0.041 -0.175   
## SpeciesFir -0.287 -0.006 -0.279 -0.558 0.106   
## scale(Admixed\_prop):scale(DBH) -0.041 0.028 -0.089 -0.102 -0.003 0.143  
## scale(Admixed\_prop):scale(Hegyi) -0.006 0.075 -0.198 -0.126 -0.021 0.122  
## s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi) 0.704   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -3.60047272 -0.65519119 -0.02144695 0.69156824 2.20235398   
##   
## Number of Observations: 153  
## Number of Groups: 4

max(vif.mer(lme\_final))

## [1] 2.167718

lme\_final <- lme(log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop)\*scale(DBH)+ scale(Admixed\_prop)\*scale(Hegyi) ,random= ~1|Site   
 ,data=data, method="REML")  
  
summary(lme\_final)

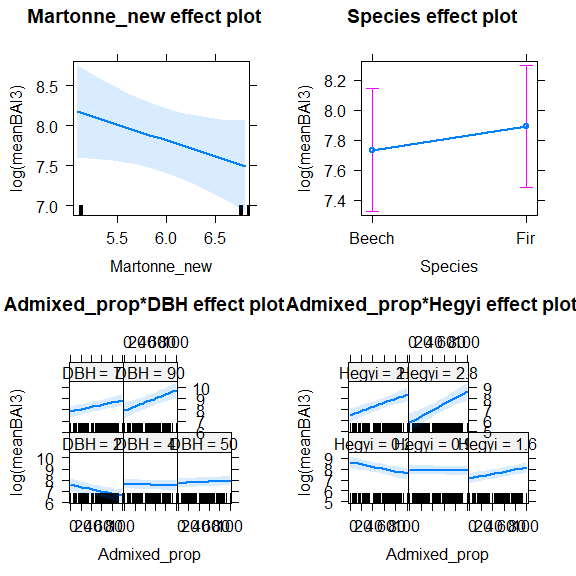
## Linear mixed-effects model fit by REML  
## Data: data   
## AIC BIC logLik  
## 212.0874 241.8548 -96.04371  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept) Residual  
## StdDev: 0.4000565 0.4047882  
##   
## Fixed effects: log(meanBAI3) ~ scale(Admixed\_prop) + scale(Hegyi) + scale(DBH) + scale(Martonne\_new) + Species + scale(Admixed\_prop) \* scale(DBH) + scale(Admixed\_prop) \* scale(Hegyi)   
## Value Std.Error DF t-value p-value  
## (Intercept) 7.734006 0.20733103 143 37.30270 0.0000  
## scale(Admixed\_prop) 0.066223 0.03337791 143 1.98405 0.0492  
## scale(Hegyi) -0.184152 0.05822242 143 -3.16290 0.0019  
## scale(DBH) 0.354954 0.06903446 143 5.14170 0.0000  
## scale(Martonne\_new) -0.335368 0.20523666 2 -1.63406 0.2439  
## SpeciesFir 0.156300 0.08010327 143 1.95123 0.0530  
## scale(Admixed\_prop):scale(DBH) 0.191599 0.04681564 143 4.09263 0.0001  
## scale(Admixed\_prop):scale(Hegyi) 0.239123 0.05484852 143 4.35971 0.0000  
## Correlation:   
## (Intr) sc(A\_) scl(H) s(DBH) sc(M\_) SpcsFr  
## scale(Admixed\_prop) 0.004   
## scale(Hegyi) 0.044 0.036   
## scale(DBH) 0.113 -0.019 0.589   
## scale(Martonne\_new) 0.027 -0.009 -0.027 -0.123   
## SpeciesFir -0.203 -0.006 -0.273 -0.562 0.076   
## scale(Admixed\_prop):scale(DBH) -0.030 0.028 -0.087 -0.105 -0.002 0.145  
## scale(Admixed\_prop):scale(Hegyi) -0.004 0.076 -0.199 -0.127 -0.014 0.122  
## s(A\_):(D  
## scale(Admixed\_prop)   
## scale(Hegyi)   
## scale(DBH)   
## scale(Martonne\_new)   
## SpeciesFir   
## scale(Admixed\_prop):scale(DBH)   
## scale(Admixed\_prop):scale(Hegyi) 0.704   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -3.4969022096 -0.6647776526 -0.0002223488 0.7210892616 2.1185847484   
##   
## Number of Observations: 153  
## Number of Groups: 4

r.squaredGLMM(lme\_final)

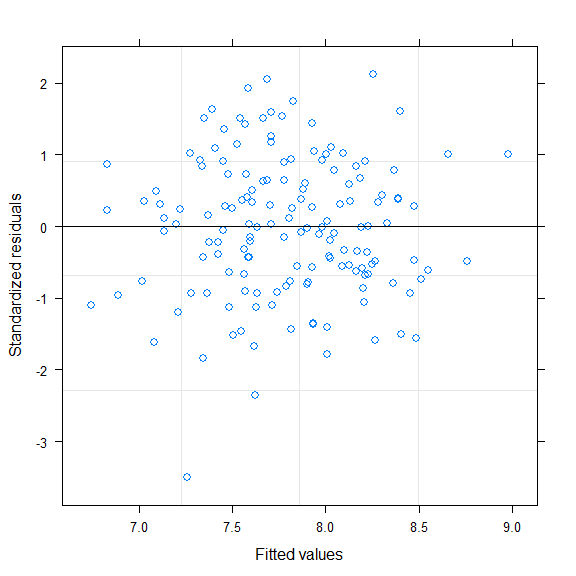
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help  
## page.

## R2m R2c  
## [1,] 0.4542337 0.7239084

plot(allEffects(lme\_final))



# model check:  
plot(lme\_final) #looks good



qqnorm(resid(lme\_final))



##checking predictors  
op <- par(mfrow = c(2, 3), mar = c(4, 4, 3, 2))  
plot(data$DBH,resid(lme\_final,type="pearson"))   
plot(data$Hegyi,resid(lme\_final,type="pearson"))   
plot(data$Martonne,resid(lme\_final,type="pearson"))   
plot(data$Admixed\_prop,resid(lme\_final,type="pearson"))  
# seems all ok  
par(op)

