

## TEST\_BB\_OLS

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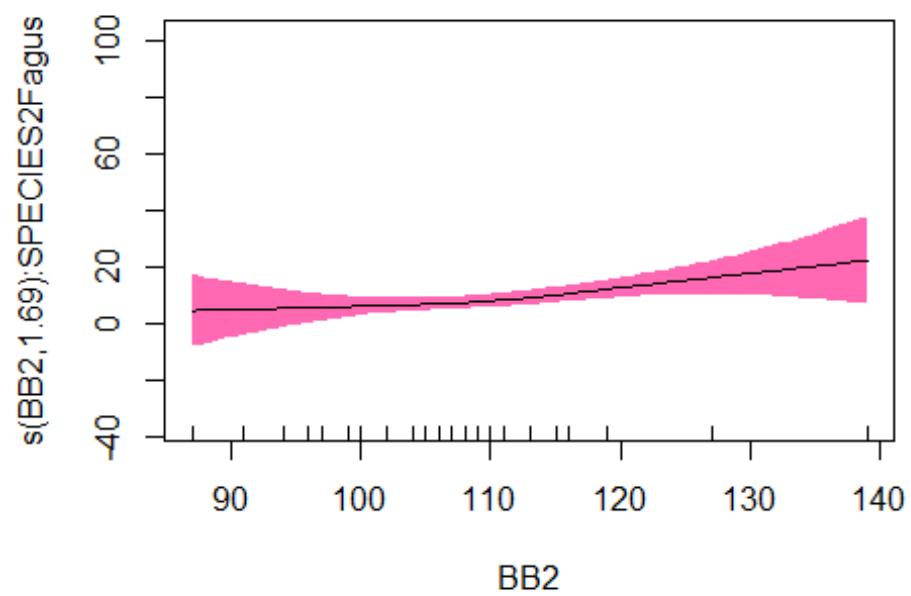
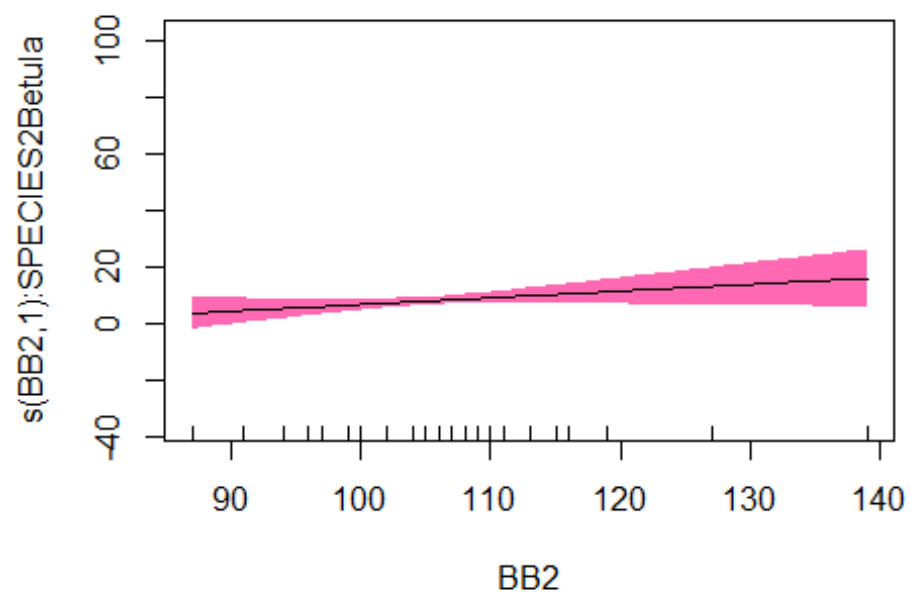
```
#####  
#####  
data <-  
read.csv("C:/Users/BMarien/Desktop/laptop/Own_work/Droughts_do_not_advance_the_onset_of_autumn_leaf_senescence_in_temperate_deciduous_forest_trees/Data/Data_used_in_article/BB_vs_CCI_breakpoints.csv", sep=";")  
names(data)  
  
## [1] "ID"      "Site"    "Species" "Number"  "Year"    "BB"      "SE_BB"  
## [8] "OLS"     "SE_OLS"  
  
ID2 <- as.factor(as.character(data[,1]))  
SITE2 <- as.factor(as.character(data[,2]))  
SPECIES2 <- as.factor(as.character(data[,3]))  
NUMBER2 <- as.factor(as.character(data[,4]))  
YEAR2 <- as.numeric(as.character(data[,5]))  
BB2 <- as.numeric(as.character(data[,6]))  
OLS2 <- as.numeric(as.character(data[,7]))  
  
##  
data3 <- data.frame(ID2, SITE2, SPECIES2, NUMBER2, YEAR2, BB2, OLS2)  
  
##  
data4 <- na.omit(data3)  
  
library(mgcv)  
  
## Loading required package: nlme  
  
## This is mgcv 1.8-31. For overview type 'help("mgcv-package")'.  
  
m1 <- gamm(OLS2 ~ s(BB2, bs = 'tp', by = SPECIES2),  
          random = list(NUMBER2=~1),  
          family = gaussian(),  
          method = "REML",  
          data = data4)  
  
## Get the summary results  
summary(m1$gam)  
  
##  
## Family: gaussian  
## Link function: identity
```

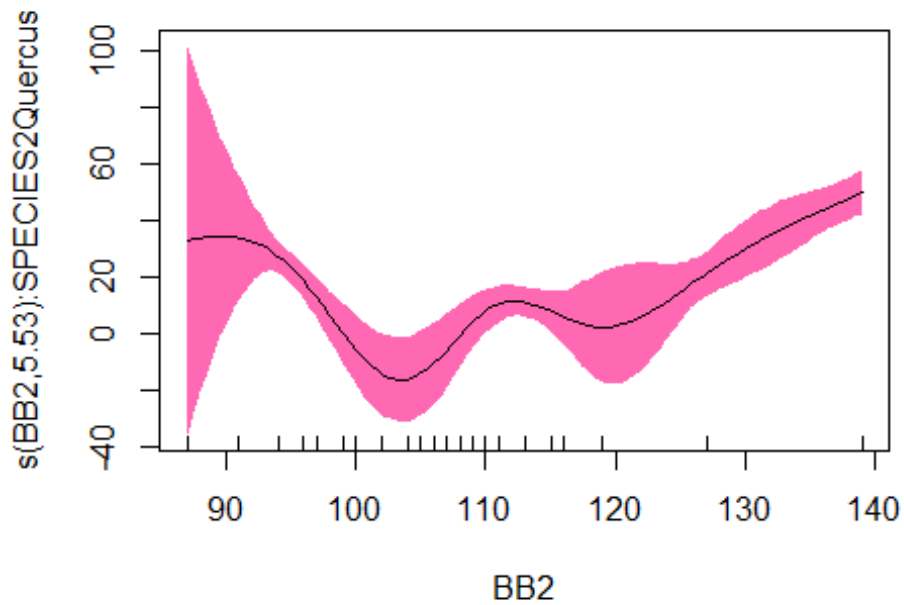
```

##
## Formula:
## OLS2 ~ s(BB2, bs = "tp", by = SPECIES2)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   8.486      1.236   6.863 5.64e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##             edf Ref.df      F p-value
## s(BB2):SPECIES2Betula  1.000  1.000  2.592  0.121
## s(BB2):SPECIES2Fagus   1.690  1.690  4.747  0.079 .
## s(BB2):SPECIES2Quercus 5.531  5.531 23.976 1.35e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) = 0.842
##   Scale est. = 15.721    n = 32

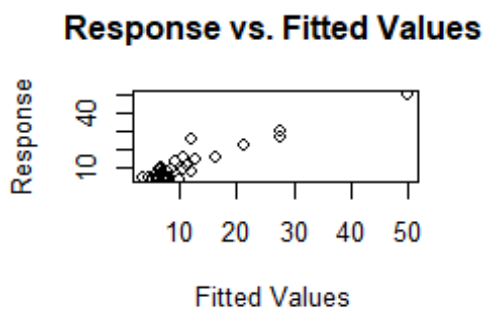
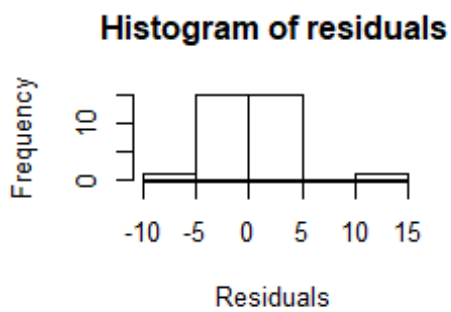
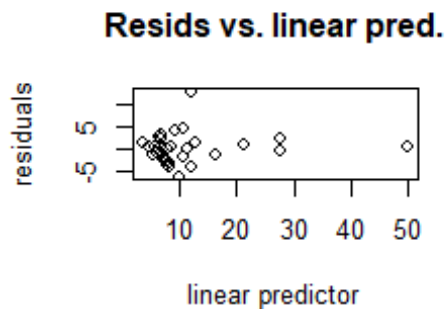
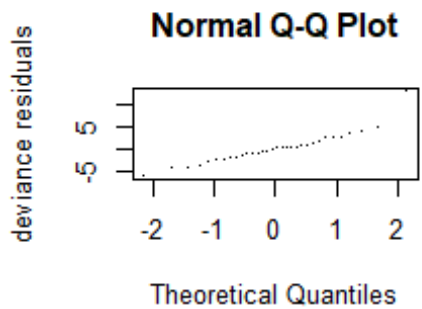
## Get a quick & dirty plot
plot(m1$gam, rug = TRUE, all.terms = TRUE, #pages = 1,
      seWithMean = TRUE, shade = TRUE, shade.col = "hotpink", # SE of partial
      effect + SE of model intercept, reflect overall uncertainty better than CI
      shift = coef(m1$gam)[1]) #Shift scale to include intercept

```





```
## Check the assumptions of normality & homogeneity quick & dirty
par(mfrow = c(2,2))
gam.check(m1$gam)
```



```
##  
## 'gamm' based fit - care required with interpretation.  
## Checks based on working residuals may be misleading.  
## Basis dimension (k) checking results. Low p-value (k-index<1) may  
## indicate that k is too low, especially if edf is close to k'.  
##  
##           k'  edf k-index p-value  
## s(BB2):SPECIES2Betula 9.00 1.00  1.08  0.58  
## s(BB2):SPECIES2Fagus  9.00 1.69  1.08  0.61  
## s(BB2):SPECIES2Quercus 9.00 5.53  1.08  0.61
```