

**Crop functional diversity drives multiple ecosystem functions during early agroforestry
succession**

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DATA AND R CODE

This detailed R code was generated by “rmarkdown” (Allaire *et al.*, 2018; Xie, Allaire and Golemund, 2018).

```
data<-read.table("mydataset2_123_treatments.txt", header = T )
data$Block<-as.factor(data$Block)
data$Cycle<-as.factor(data$Cycle)
data$Treatment<-as.factor(data$Treatment)

str(data)

## 'data.frame':  36 obs. of  16 variables:
## $ Block      : Factor w/ 6 levels "1","2","3","4",...: 1 1 1 2 2 2 3 3 3
## $ Treatment  : Factor w/ 3 levels "1","2","3": 3 1 2 3 1 2 3 1 2 3 ...
## $ Cycle      : Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## $ Productivity: num  5.32 3.11 4.84 6.29 1.79 ...
## $ LAI_weed   : num  1.661 0.747 0.934 1.341 1.314 ...
## $ LAI_crop   : num  3.24 1.96 2.88 3.81 2.69 ...
## $ FD_weed    : num  0.321 0.49 0.324 0.425 0.338 ...
## $ FR_weed    : num  0.321 0.388 0.306 0.403 0.312 ...
## $ FD_crop    : num  0.308 0.183 0.276 0.335 0.238 ...
## $ FR_crop    : num  0.428 0.451 0.477 0.448 0.524 ...
## $ COVER_WEED : num  0.429 0.447 0.351 0.307 0.495 ...
## $ COVER_CROP : num  0.341 0.23 0.311 0.427 0.222 ...
## $ SOLO_EXPOSTO: num  0.0846 0.0821 0.072 0.0776 0.1365 ...
## $ Weed_supp  : num  -0.0882 -0.2163 -0.0398 0.1208 -0.2731 ...
## $ Litter     : num  0.23 0.323 0.339 0.266 0.284 ...
## $ Soil_protec : num  0.77 0.677 0.661 0.734 0.716 ...

data

##   Block Treatment Cycle Productivity LAI_weed LAI_crop  FD_weed
## 1     1         3     1    5.320742 1.6611111 3.242000 0.3209819
## 2     1         1     1    3.106551 0.7465179 1.955875 0.4904121
## 3     1         2     1    4.842536 0.9340972 2.883500 0.3237987
## 4     2         3     1    6.285348 1.3405556 3.814000 0.4249353
## 5     2         1     1    1.794701 1.3135417 2.689500 0.3378650
## 6     2         2     1    4.974534 0.5523611 2.674250 0.4477675
## 7     3         3     1    6.537502 1.2362500 3.780500 0.3368097
## 8     3         1     1    2.899507 1.2415278 2.878125 0.4038419
## 9     3         2     1    3.584553 0.9056250 3.092250 0.4656119
## 10    4         3     1    4.792176 1.7286806 3.713500 0.4571516
## 11    4         1     1    3.809759 0.9075000 2.036181 0.3999565
## 12    4         2     1    3.732795 1.3618056 3.209625 0.3837403
## 13    5         3     1    5.139907 1.1706250 3.778250 0.3987745
```

## 14	5	1	1	2.680120	1.2722917	3.665375	0.3930073
## 15	5	2	1	2.242545	1.4054861	2.863875	0.4013299
## 16	6	3	1	4.864962	1.1202083	3.580000	0.2682189
## 17	6	1	1	3.307587	1.8375000	2.931250	0.3342842
## 18	6	2	1	2.615713	1.6893750	2.735375	0.3443990
## 19	1	3	2	2.151233	1.3037500	1.954375	0.3587296
## 20	1	1	2	1.809133	1.0481250	1.974375	0.2765687
## 21	1	2	2	3.068852	1.1893750	1.683750	0.2378234
## 22	2	3	2	2.978826	0.7818750	1.643125	0.3046088
## 23	2	1	2	2.931335	1.0656250	1.326250	0.3425952
## 24	2	2	2	3.830527	0.5956250	2.006250	0.2493723
## 25	3	3	2	2.232335	1.5887500	1.948125	0.2489992
## 26	3	1	2	2.300982	0.8068750	2.001250	0.2434812
## 27	3	2	2	4.102836	0.7062500	1.878125	0.2844270
## 28	4	3	2	1.932809	0.8212500	1.927500	0.2803398
## 29	4	1	2	2.035101	0.6975000	1.258125	0.2479659
## 30	4	2	2	3.644507	0.6193750	1.651250	0.2971503
## 31	5	3	2	3.487012	0.8800000	2.301875	0.2831478
## 32	5	1	2	2.252240	0.5431250	1.554375	0.2972682
## 33	5	2	2	3.780196	0.6750000	1.890625	0.2831828
## 34	6	3	2	2.618333	0.7462500	2.006875	0.2571256
## 35	6	1	2	1.036443	0.6287500	1.236250	0.2824760
## 36	6	2	2	2.761925	0.5537500	1.353750	0.3575865
##	FR_weed	FD_crop	FR_crop	COVER_WEED	COVER_CROP	SOLO_EXPOSTO	
## 1	0.3208430	0.3077077	0.4278491	0.4289050	0.3406873	0.08462856	
## 2	0.3877109	0.1831720	0.4505302	0.4466522	0.2303347	0.08209961	
## 3	0.3062050	0.2761078	0.4766354	0.3505570	0.3107442	0.07198649	
## 4	0.4034900	0.3353530	0.4477740	0.3065513	0.4273351	0.07762093	
## 5	0.3121833	0.2383060	0.5240863	0.4946225	0.2215520	0.13653881	
## 6	0.3362843	0.1688956	0.2743008	0.4142167	0.3025387	0.03724413	
## 7	0.3349208	0.3536935	0.4129074	0.3236091	0.3705967	0.07755083	
## 8	0.3020838	0.2019427	0.5056090	0.4566341	0.1901974	0.09629206	
## 9	0.3407024	0.2867532	0.4518139	0.2761656	0.4083921	0.06422914	
## 10	0.3668085	0.2859485	0.2852086	0.2869759	0.4420389	0.08340666	
## 11	0.3929043	0.1885511	0.4476421	0.4454192	0.2806958	0.04532808	
## 12	0.4088374	0.2925218	0.4895490	0.3845010	0.3881123	0.04855212	
## 13	0.3936564	0.2163054	0.4766048	0.2843878	0.5248660	0.07827816	
## 14	0.3149414	0.2522795	0.5006607	0.4190463	0.2453019	0.06790082	
## 15	0.3575032	0.2393310	0.4639042	0.5454449	0.2649439	0.05035910	
## 16	0.2622244	0.3808370	0.3493179	0.2630817	0.5355710	0.06501633	
## 17	0.3434541	0.2195807	0.5012616	0.4781984	0.2922134	0.04303469	
## 18	0.2992661	0.2816615	0.4846735	0.5653842	0.1750751	0.09222522	
## 19	0.5409809	0.3966740	0.3670638	0.3860899	0.4025676	0.05053971	
## 20	0.6203591	0.3004331	0.4244282	0.4727804	0.2730589	0.04744713	
## 21	0.5855163	0.3530704	0.4099039	0.3532224	0.4204177	0.03762543	
## 22	0.5244473	0.3641906	0.3985075	0.2459151	0.5281435	0.05774976	
## 23	0.5255310	0.1982136	0.2972684	0.4698294	0.2203147	0.02490324	
## 24	0.6052591	0.3067712	0.4043170	0.4044524	0.3152622	0.06715942	
## 25	0.6263773	0.3968759	0.3407985	0.3658152	0.4588451	0.03785163	
## 26	0.5974005	0.3392464	0.4278561	0.3681041	0.3401203	0.01984409	

## 27	0.5894200	0.3502847	0.4033417	0.2616204	0.4773178	0.01300574
## 28	0.5948501	0.3166228	0.3699246	0.2209508	0.5829211	0.03010191
## 29	0.5967959	0.3177542	0.4313092	0.3930518	0.3586288	0.03027933
## 30	0.5575954	0.2688902	0.4536118	0.4101062	0.3363241	0.03006471
## 31	0.5973226	0.3688064	0.3835545	0.3940218	0.3941593	0.08972046
## 32	0.5849646	0.3127510	0.4352639	0.4275392	0.3008833	0.03293778
## 33	0.6137468	0.3224322	0.4603361	0.5197013	0.2506697	0.05793557
## 34	0.5527304	0.2918010	0.3654330	0.1727483	0.5951014	0.03385355
## 35	0.5930849	0.2756243	0.4427438	0.3896564	0.3334489	0.05267263
## 36	0.5365736	0.3329754	0.3461957	0.5263602	0.3049851	0.03602717
##	Weed_supp	Litter	Soil_protec			
## 1	-0.088217674	0.2304077	0.7695923			
## 2	-0.216317465	0.3230131	0.6769869			
## 3	-0.039812766	0.3386988	0.6613012			
## 4	0.120783767	0.2661136	0.7338864			
## 5	-0.273070519	0.2838255	0.7161745			
## 6	-0.111678033	0.2832446	0.7167554			
## 7	0.046987551	0.3057942	0.6942058			
## 8	-0.266436772	0.3531685	0.6468315			
## 9	0.132226476	0.3154424	0.6845576			
## 10	0.155062925	0.2709852	0.7290148			
## 11	-0.164723396	0.2738851	0.7261149			
## 12	0.003611284	0.2273866	0.7726134			
## 13	0.240478260	0.1907462	0.8092538			
## 14	-0.173744351	0.3356518	0.6643482			
## 15	-0.280501050	0.1896112	0.8103888			
## 16	0.272489338	0.2013473	0.7986527			
## 17	-0.185985003	0.2295883	0.7704117			
## 18	-0.390309091	0.2595408	0.7404592			
## 19	0.016477678	0.2113424	0.7886576			
## 20	-0.199721460	0.2541606	0.7458394			
## 21	0.067195261	0.2263598	0.7736402			
## 22	0.282228434	0.2259414	0.7740586			
## 23	-0.249514663	0.3098559	0.6901441			
## 24	-0.089190225	0.2802854	0.7197146			
## 25	0.093029819	0.1753397	0.8246603			
## 26	-0.027983719	0.2917756	0.7082244			
## 27	0.215697391	0.2610617	0.7389383			
## 28	0.361970281	0.1961281	0.8038719			
## 29	-0.034422995	0.2483195	0.7516805			
## 30	-0.073782095	0.2535696	0.7464304			
## 31	0.000137496	0.2118188	0.7881812			
## 32	-0.126655927	0.2715774	0.7284226			
## 33	-0.269031587	0.2296290	0.7703710			
## 34	0.422353091	0.2321502	0.7678498			
## 35	-0.056207495	0.2768947	0.7231053			
## 36	-0.221375130	0.1686547	0.8313453			

Exploring data

data cycle 1

```
attach(data)
data1 <- data[ which(Cycle=='1'),]
detach(data)

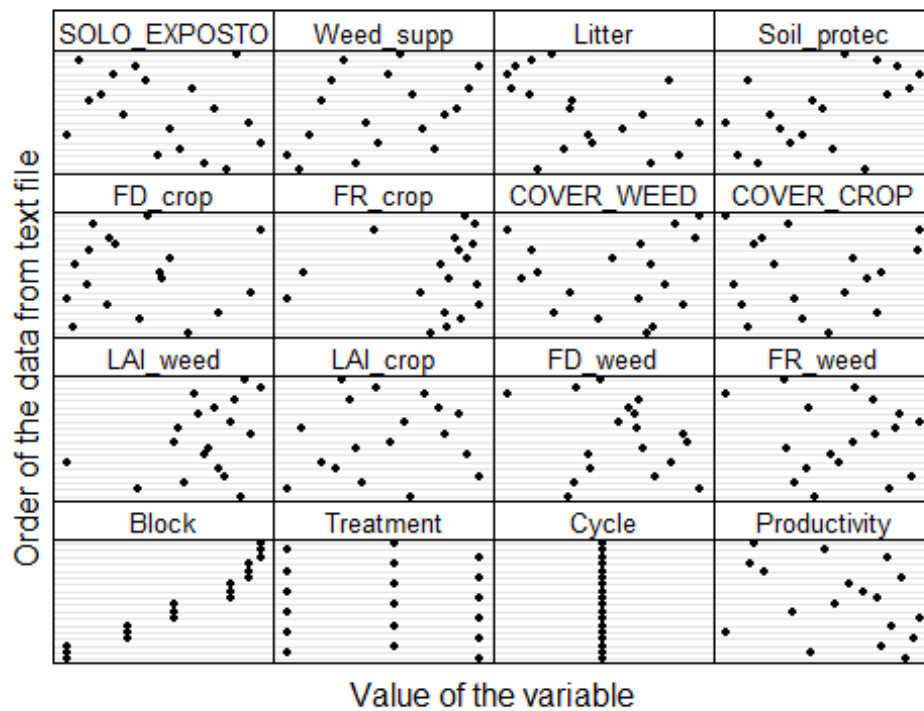
str(data1)

## 'data.frame':    18 obs. of  16 variables:
## $ Block          : Factor w/ 6 levels "1","2","3","4",...: 1 1 1 2 2 2 3 3 3
## 4 ...
## $ Treatment      : Factor w/ 3 levels "1","2","3": 3 1 2 3 1 2 3 1 2 3 ...
## $ Cycle          : Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## $ Productivity:  num  5.32 3.11 4.84 6.29 1.79 ...
## $ LAI_weed       : num  1.661 0.747 0.934 1.341 1.314 ...
## $ LAI_crop       : num  3.24 1.96 2.88 3.81 2.69 ...
## $ FD_weed        : num  0.321 0.49 0.324 0.425 0.338 ...
## $ FR_weed        : num  0.321 0.388 0.306 0.403 0.312 ...
## $ FD_crop        : num  0.308 0.183 0.276 0.335 0.238 ...
## $ FR_crop        : num  0.428 0.451 0.477 0.448 0.524 ...
## $ COVER_WEED     : num  0.429 0.447 0.351 0.307 0.495 ...
## $ COVER_CROP     : num  0.341 0.23 0.311 0.427 0.222 ...
## $ SOLO_EXPOSTO:  num  0.0846 0.0821 0.072 0.0776 0.1365 ...
## $ Weed_supp      : num  -0.0882 -0.2163 -0.0398 0.1208 -0.2731 ...
## $ Litter         : num  0.23 0.323 0.339 0.266 0.284 ...
## $ Soil_protec    : num  0.77 0.677 0.661 0.734 0.716 ...
```

Verifying outliers

```
library(lattice)
library(reshape)
library(ggplot2)

#Multi-panel Cleveland dotplot
#cycle 1
p1<-dotplot(as.matrix(data1), groups = FALSE,
            strip = strip.custom(bg = 'white',
            par.strip.text = list(cex = 0.8)),
            scales = list(x = list(relation = "free"),
            y = list(relation = "free"),
            draw = FALSE),
            col = 1, cex = 0.5, pch = 16,
            xlab = "Value of the variable",
            ylab = "Order of the data from text file")
p1
```



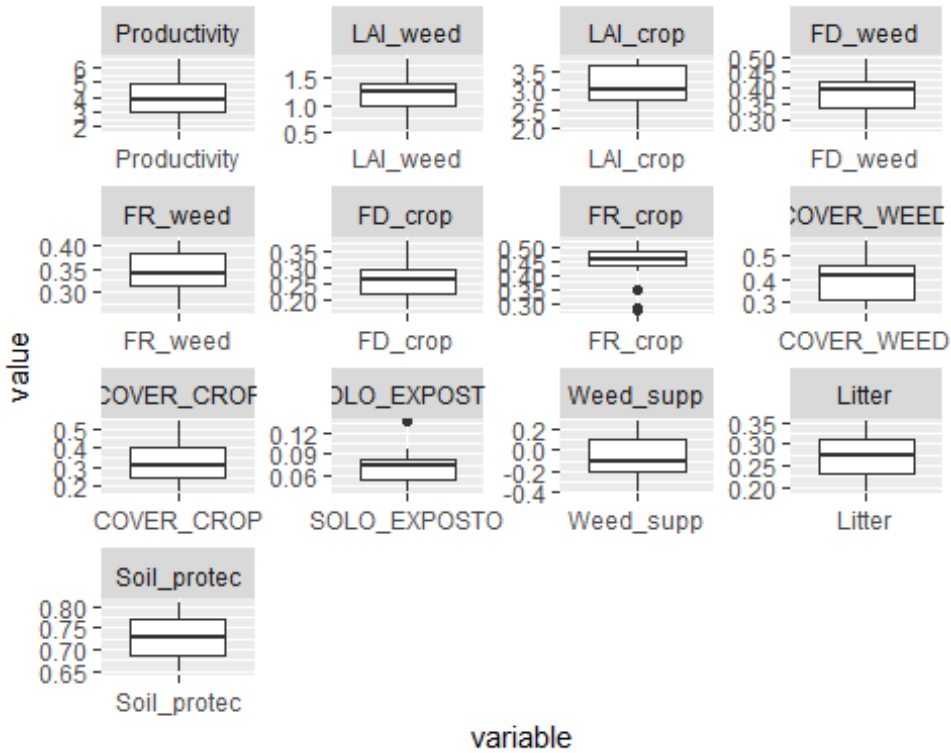
```

#Multi-panel boxplot
m1 <- melt(as.data.frame(data1))

## Using Block, Treatment, Cycle as id variables

p2=ggplot(m1,aes(x = variable, y = value)) + facet_wrap(~variable, scales="free") + geom_boxplot()
p2

```



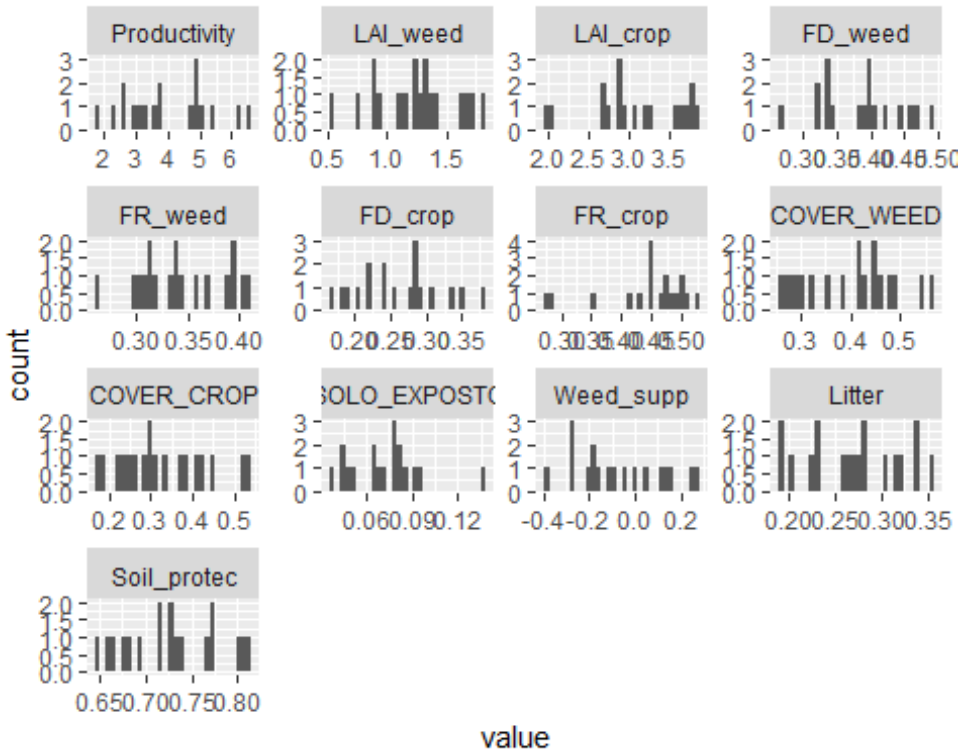
Histograms

```
m2 <- melt(as.data.frame(data1))

## Using Block, Treatment, Cycle as id variables

p3<-ggplot(m2, aes(value))+ facet_wrap(~variable, scales="free") + geom_histogram()
p3

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



data cycle 2

```
attach(data)
data2 <- data[ which(Cycle=='2'),]
detach(data)
```

```
str(data2)
```

```
## 'data.frame':  18 obs. of  16 variables:
## $ Block      : Factor w/ 6 levels "1","2","3","4",...: 1 1 1 2 2 2 3 3 3
## $ Treatment  : Factor w/ 3 levels "1","2","3": 3 1 2 3 1 2 3 1 2 3 ...
## $ Cycle      : Factor w/ 2 levels "1","2": 2 2 2 2 2 2 2 2 2 2 ...
## $ Productivity: num  2.15 1.81 3.07 2.98 2.93 ...
## $ LAI_weed   : num  1.304 1.048 1.189 0.782 1.066 ...
## $ LAI_crop   : num  1.95 1.97 1.68 1.64 1.33 ...
## $ FD_weed    : num  0.359 0.277 0.238 0.305 0.343 ...
## $ FR_weed    : num  0.541 0.62 0.586 0.524 0.526 ...
## $ FD_crop    : num  0.397 0.3 0.353 0.364 0.198 ...
## $ FR_crop    : num  0.367 0.424 0.41 0.399 0.297 ...
## $ COVER_WEED : num  0.386 0.473 0.353 0.246 0.47 ...
## $ COVER_CROP : num  0.403 0.273 0.42 0.528 0.22 ...
## $ SOLO_EXPOSTO: num  0.0505 0.0474 0.0376 0.0577 0.0249 ...
## $ Weed_supp  : num  0.0165 -0.1997 0.0672 0.2822 -0.2495 ...
## $ Litter     : num  0.211 0.254 0.226 0.226 0.31 ...
## $ Soil_protec : num  0.789 0.746 0.774 0.774 0.69 ...
```


Verifying outliers

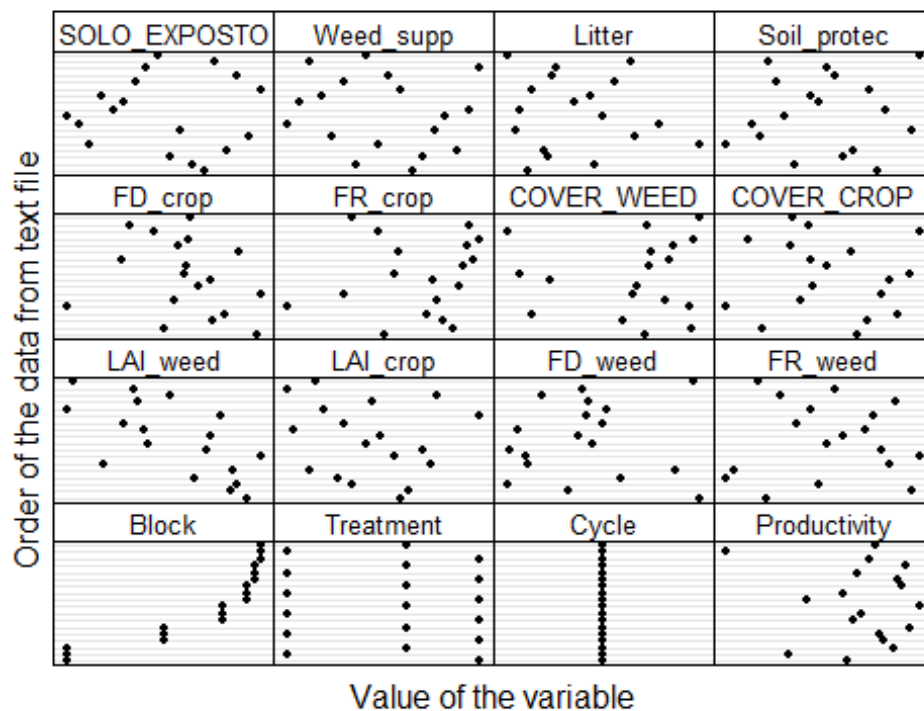
```
library(lattice)
library(reshape)
library(ggplot2)
```

```
#Multi-panel Cleveland dotplot
```

```
#cycle 1
```

```
p1<-dotplot(as.matrix(data2), groups = FALSE,
  strip = strip.custom(bg = 'white',
  par.strip.text = list(cex = 0.8)),
  scales = list(x = list(relation = "free"),
  y = list(relation = "free"),
  draw = FALSE),
  col = 1, cex = 0.5, pch = 16,
  xlab = "Value of the variable",
  ylab = "Order of the data from text file")
```

p1



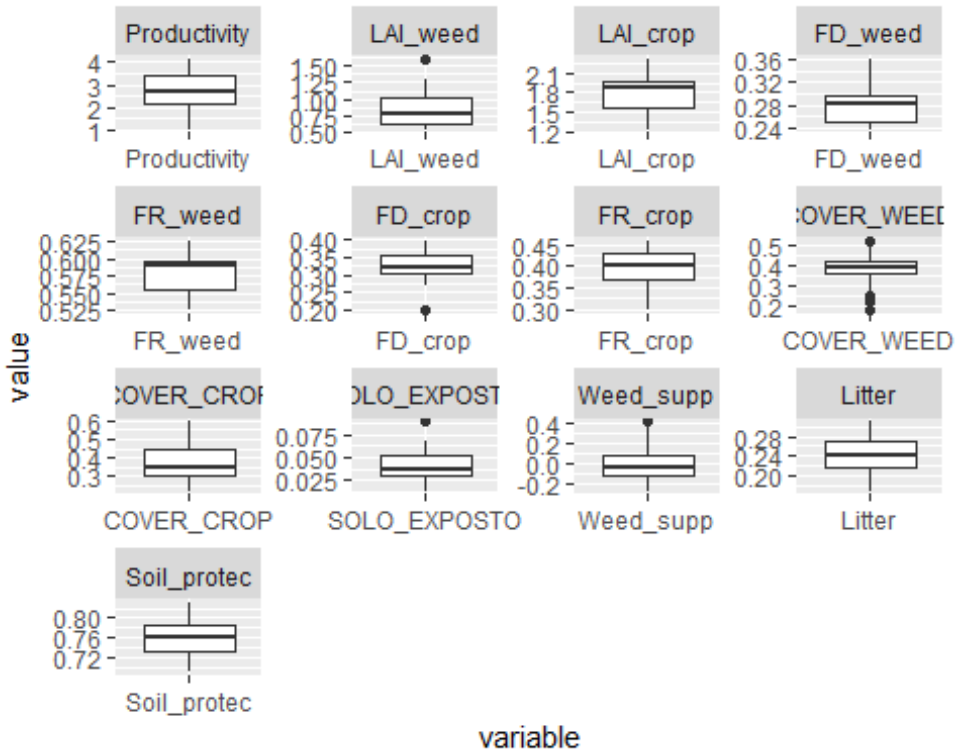
```
#Multi-panel boxplot
```

```
m1 <- melt(as.data.frame(data2))
```

```
## Using Block, Treatment, Cycle as id variables
```

```
p2=ggplot(m1,aes(x = variable, y = value)) + facet_wrap(~variable, scales="free") + geom_boxplot()
```

p2



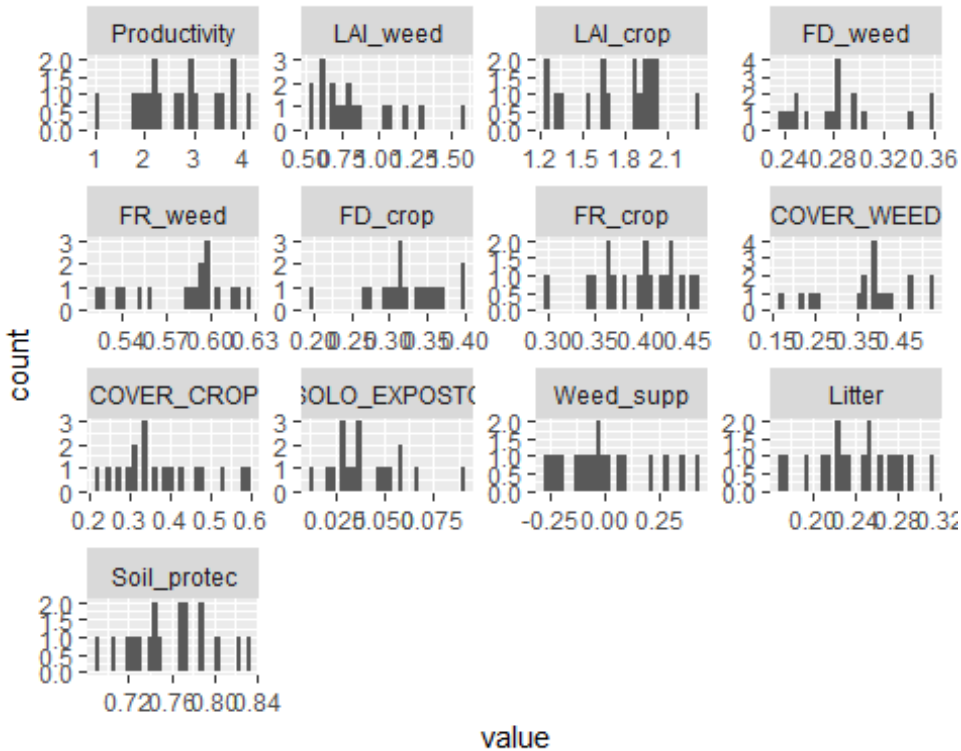
Histograms

```
m2 <- melt(as.data.frame(data2))

## Using Block, Treatment, Cycle as id variables

p3<-ggplot(m2, aes(value))+ facet_wrap(~variable, scales="free") + geom_histogram()
p3

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



Fitting SEM

```
library(piecewiseSEM)
```

```
##
## This is piecewiseSEM version 2.0.2
##
## If you have used the package before, it is strongly recommended you read
## Section 3 of the vignette('piecewiseSEM') to familiarize yourself with the new
## syntax
##
## Questions or bugs can be addressed to <jlefcheck@bigelow.org>
```

```
vignette("piecewiseSEM")
```

```
## starting httpd help server ...
```

```
## done
```

```
library(nlme)
```

```
str(data)
```

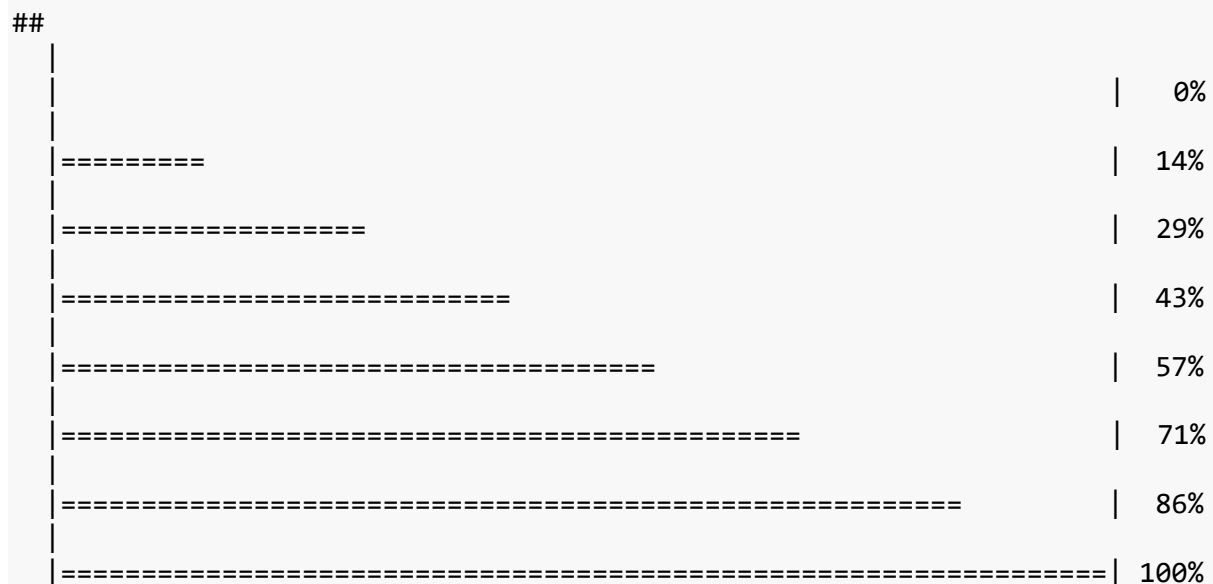
```
## 'data.frame': 36 obs. of 16 variables:
## $ Block : Factor w/ 6 levels "1","2","3","4",...: 1 1 1 2 2 2 3 3 3
## 4 ...
## $ Treatment : Factor w/ 3 levels "1","2","3": 3 1 2 3 1 2 3 1 2 3 ...
```

```
## $ Cycle      : Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## $ Productivity: num  5.32 3.11 4.84 6.29 1.79 ...
## $ LAI_weed   : num  1.661 0.747 0.934 1.341 1.314 ...
## $ LAI_crop   : num  3.24 1.96 2.88 3.81 2.69 ...
## $ FD_weed    : num  0.321 0.49 0.324 0.425 0.338 ...
## $ FR_weed    : num  0.321 0.388 0.306 0.403 0.312 ...
## $ FD_crop    : num  0.308 0.183 0.276 0.335 0.238 ...
## $ FR_crop    : num  0.428 0.451 0.477 0.448 0.524 ...
## $ COVER_WEED : num  0.429 0.447 0.351 0.307 0.495 ...
## $ COVER_CROP : num  0.341 0.23 0.311 0.427 0.222 ...
## $ SOLO_EXPOSTO: num  0.0846 0.0821 0.072 0.0776 0.1365 ...
## $ Weed_supp  : num  -0.0882 -0.2163 -0.0398 0.1208 -0.2731 ...
## $ Litter     : num  0.23 0.323 0.339 0.266 0.284 ...
## $ Soil_protec : num  0.77 0.677 0.661 0.734 0.716 ...
```

#model1

```
sem1 <- psem(
  lme(FD_weed ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(LAI_crop ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(COVER_CROP ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(COVER_WEED ~ FD_weed, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  COVER_CROP %~~% COVER_WEED,
  lme(Productivity ~ LAI_crop + COVER_WEED + COVER_CROP, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data))
```

```
summary(sem1, conditional = T)
```



```

##
## Structural Equation Model of sem1
##
## Call:
##   FD_weed ~ FD_crop
##   LAI_crop ~ FD_crop
##   COVER_CROP ~ FD_crop
##   COVER_WEED ~ FD_weed
##   COVER_CROP ~~ COVER_WEED
##   Productivity ~ LAI_crop + COVER_WEED + COVER_CROP
##
##      AIC      BIC
## 68.229  110.984
##
## ---
## Tests of directed separation:
##
##                                     Independ.C
laim
##                                     COVER_WEED ~ FD_crop + FD_w
eed
##                                     Productivity ~ FD_crop + LAI_crop + COVER_CROP + COVER_W
EED
##                                     LAI_crop ~ FD_weed + FD_c
rop
##                                     COVER_CROP ~ FD_weed + FD_c
rop
##   Productivity ~ FD_weed + FD_crop + LAI_crop + COVER_CROP + COVER_W
EED
##                                     COVER_CROP ~ LAI_crop + FD_c
rop
##                                     COVER_WEED ~ LAI_crop + FD_crop + FD_w
eed
##
## Estimate Std.Error DF Crit.Value P.Value
## -0.6794  0.3039 22 -2.2356 0.0358 *
##  0.8469  3.3865 20  0.2501 0.8051
##  0.3787  1.5810 22  0.2395 0.8129
##  0.0901  0.2853 22  0.3159 0.7551
##  1.5895  3.5960 19  0.4420 0.6635
##  0.0206  0.0199 22  1.0351 0.3119
## -0.0281  0.0224 21 -1.2588 0.2219
##
## Global goodness-of-fit:
##
## Fisher's C = 14.229 with P-value = 0.433 and on 14 degrees of freedom
##
## ---
## Coefficients:
##
##      Response      Predictor Estimate Std.Error DF Crit.Value P.Value

```

```

##          FD_weed          FD_crop -0.5026    0.1541 23    -3.2610  0.0034
##          LAI_crop          FD_crop  4.8921    1.2902 23     3.7918  0.0009
##          COVER_CROP        FD_crop  0.9299    0.2584 23     3.5980  0.0015
##          COVER_WEED        FD_weed  0.1892    0.2298 23     0.8233  0.4188
##          ~~COVER_CROP    ~~COVER_WEED -0.8443          NA 36    -9.0516  0.0000
##          Productivity    LAI_crop  0.9967    0.2131 21     4.6778  0.0001
##          Productivity    COVER_WEED -3.6269    4.1888 21    -0.8659  0.3964
##          Productivity    COVER_CROP -1.0833    3.5847 21    -0.3022  0.7655
##          Std.Estimate
##          -0.4436 **
##           0.3747 ***
##           0.5251 **
##           0.1398
##          -0.8443 ***
##           0.6212 ***
##          -0.2654
##          -0.0916
##
##          Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
##          Individual R-squared:
##
##          Response method Marginal Conditional
##          FD_weed      none      0.22      0.44
##          LAI_crop      none      0.10      0.85
##          COVER_CROP    none      0.27      0.27
##          COVER_WEED    none      0.02      0.02
##          Productivity  none      0.45      0.45

```

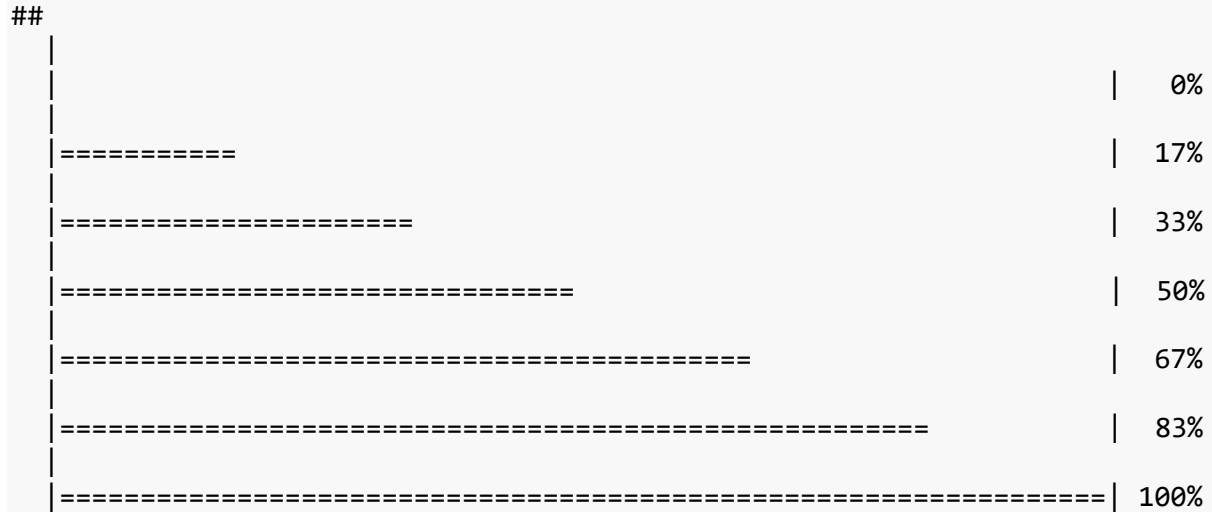
Adding missing paths

```

#model2
sem2 <- psem(
  lme(FD_weed ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(LAI_crop ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(COVER_CROP ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(COVER_WEED ~ FD_weed + FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  COVER_CROP %~~% COVER_WEED,
  lme(Productivity ~ LAI_crop + COVER_WEED + COVER_CROP, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data))

summary(sem2, conditional = T)

```



```
##
## Structural Equation Model of sem2
##
## Call:
##   FD_weed ~ FD_crop
##   LAI_crop ~ FD_crop
##   COVER_CROP ~ FD_crop
##   COVER_WEED ~ FD_weed + FD_crop
##   COVER_CROP ~~ COVER_WEED
##   Productivity ~ LAI_crop + COVER_WEED + COVER_CROP
##
##      AIC      BIC
## 63.572 107.911
##
## ---
## Tests of directed separation:
##
##                                     Independ.C
laim
##           Productivity ~ FD_crop + LAI_crop + COVER_CROP + COVER_W
EED
##                                     LAI_crop ~ FD_weed + FD_c
rop
##                                     COVER_CROP ~ FD_weed + FD_c
rop
##   Productivity ~ FD_weed + FD_crop + LAI_crop + COVER_CROP + COVER_W
EED
##                                     COVER_CROP ~ LAI_crop + FD_c
rop
##                                     COVER_WEED ~ LAI_crop + FD_crop + FD_w
eed
##   Estimate Std.Error DF Crit.Value P.Value
##     0.8469   3.3865 20     0.2501 0.8051
##     0.3787   1.5810 22     0.2395 0.8129
```

```

##      0.0901    0.2853 22      0.3159  0.7551
##      1.5895    3.5960 19      0.4420  0.6635
##      0.0206    0.0199 22      1.0351  0.3119
##     -0.0281    0.0224 21     -1.2588  0.2219
##
## Global goodness-of-fit:
##
## Fisher's C = 7.572 with P-value = 0.818 and on 12 degrees of freedom
##
## ---
## Coefficients:
##
##      Response      Predictor Estimate Std.Error DF Crit.Value P.Value
##      FD_weed      FD_crop   -0.5026   0.1541 23    -3.2610  0.0034
##      LAI_crop      FD_crop    4.8921   1.2902 23     3.7918  0.0009
##      COVER_CROP    FD_crop    0.9299   0.2584 23     3.5980  0.0015
##      COVER_WEED    FD_weed   -0.1622   0.2682 22    -0.6048  0.5515
##      COVER_WEED    FD_crop   -0.6794   0.3039 22    -2.2356  0.0358
##      ~~COVER_CROP  ~~COVER_WEED -0.8935      NA 36   -11.4286  0.0000
##      Productivity  LAI_crop    0.9967   0.2131 21     4.6778  0.0001
##      Productivity  COVER_WEED -3.6269   4.1888 21    -0.8659  0.3964
##      Productivity  COVER_CROP -1.0833   3.5847 21    -0.3022  0.7655
##      Std.Estimate
##      -0.4436 **
##      0.3747 ***
##      0.5251 **
##      -0.1199
##      -0.4432 *
##      -0.8935 ***
##      0.6212 ***
##      -0.2654
##      -0.0916
##
##      Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
##
## Individual R-squared:
##
##      Response method Marginal Conditional
##      FD_weed      none      0.22      0.44
##      LAI_crop      none      0.10      0.85
##      COVER_CROP    none      0.27      0.27
##      COVER_WEED    none      0.14      0.14
##      Productivity  none      0.45      0.45

```

#Sequentially eliminated non-significant paths with Lowest ratio $\hat{\beta}^2/SE\hat{\beta}^2$ from model list

##(where $\hat{\beta}^2$ = raw parameter estimate and $SE\hat{\beta}^2$ = its corresponding standard error)

```

coef<-coef(sem2)
criterio<-{coef_no_sig<-coef[coef$P.Value>0.05,]}

```



```
coef_padrao<-with(coef_no_sig, ((Estimate/Std.Error)^2))
coef_no_sig$estimate_std<-coef_padrao
coef_no_sig
coef_no_sig[order(coef_no_sig$estimate_std, decreasing=FALSE),] }
criterio
```

```
##      Response Predictor Estimate Std.Error DF Crit.Value P.Value
## 9 Productivity COVER_CROP -1.0833 3.5847 21 -0.3022 0.7655
## 4 COVER_WEED FD_weed -0.1622 0.2682 22 -0.6048 0.5515
## 8 Productivity COVER_WEED -3.6269 4.1888 21 -0.8659 0.3964
## Std.Estimate estimate_std
## 9 -0.0916 0.09132546
## 4 -0.1199 0.36574985
## 8 -0.2654 0.74970760
```

```
#model3
```

```
sem3 <- psem(
  lme(FD_weed ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(LAI_crop ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(COVER_CROP ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  lme(COVER_WEED ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data),
  COVER_CROP %~~% COVER_WEED,
  lme(Productivity ~ LAI_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data))
```

```
summary(sem3, conditional = T)
```

```
##
|
|
|=====| 11%
|=====| 22%
|=====| 33%
|=====| 44%
|=====| 56%
|=====| 67%
|=====| 78%
```

```

===== | 89%
===== | 100%

##
## Structural Equation Model of sem3
##
## Call:
##   FD_weed ~ FD_crop
##   LAI_crop ~ FD_crop
##   COVER_CROP ~ FD_crop
##   COVER_WEED ~ FD_crop
##   COVER_CROP ~~ COVER_WEED
##   Productivity ~ LAI_crop
##
##      AIC      BIC
## 64.984  104.572
##
## ---
## Tests of directed separation:
##
##                                Independ.Claim Estimate Std.Error D
F
##          Productivity ~ FD_crop + LAI_crop      1.7486    2.7471 2
2
##          LAI_crop ~ FD_weed + FD_crop           0.3787    1.5810 2
2
##          COVER_CROP ~ FD_weed + FD_crop          0.0901    0.2853 2
2
##          COVER_WEED ~ FD_weed + FD_crop         -0.1622    0.2682 2
2
##          Productivity ~ FD_weed + FD_crop + LAI_crop 1.5282    3.5669 2
1
##          COVER_CROP ~ LAI_crop + FD_crop          0.0206    0.0199 2
2
##          COVER_WEED ~ LAI_crop + FD_crop         -0.0262    0.0186 2
2
##          Productivity ~ COVER_CROP + FD_crop + LAI_crop 1.6870    1.8422 2
1
##          Productivity ~ COVER_WEED + FD_crop + LAI_crop -2.4114    1.9576 2
1
##          Crit.Value P.Value
##            0.6365 0.5310
##            0.2395 0.8129
##            0.3159 0.7551
##           -0.6048 0.5515
##            0.4284 0.6727
##            1.0351 0.3119
##           -1.4103 0.1724
##            0.9157 0.3702

```

```

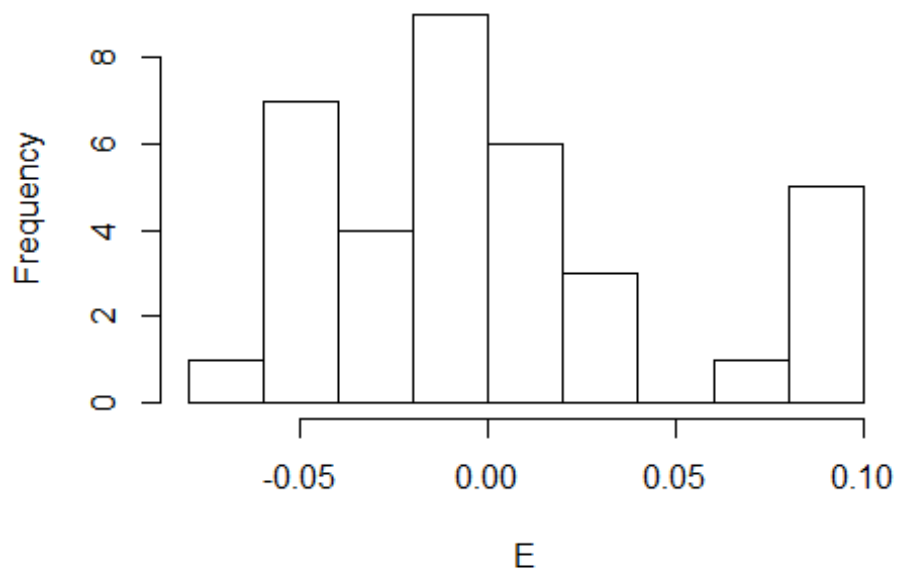
##      -1.2318  0.2316
##
## Global goodness-of-fit:
##
## Fisher's C = 14.984 with P-value = 0.663 and on 18 degrees of freedom
##
## ---
## Coefficients:
##
##      Response      Predictor Estimate Std.Error DF Crit.Value P.Value
##      FD_weed      FD_crop   -0.5026   0.1541 23    -3.2610  0.0034
##      LAI_crop      FD_crop    4.8921   1.2902 23     3.7918  0.0009
##      COVER_CROP    FD_crop    0.9299   0.2584 23     3.5980  0.0015
##      COVER_WEED    FD_crop   -0.5717   0.2440 23    -2.3435  0.0281
##      ~~COVER_CROP  ~~COVER_WEED -0.8943      NA 36   -11.4821  0.0000
##      Productivity  LAI_crop    1.0579   0.2069 23     5.1134  0.0000
## Std.Estimate
##      -0.4436 **
##      0.3747 ***
##      0.5251 **
##      -0.3729 *
##      -0.8943 ***
##      0.6593 ***
##
## Signif. codes:  0 '****' 0.001 '***' 0.01 '**' 0.05
##
## Individual R-squared:
##
##      Response method Marginal Conditional
##      FD_weed      none      0.22      0.44
##      LAI_crop      none      0.10      0.85
##      COVER_CROP    none      0.27      0.27
##      COVER_WEED    none      0.14      0.14
##      Productivity  none      0.43      0.43

m1<-lme(FD_weed ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action
=na.omit, data=data)
m2<-lme(LAI_crop ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.actio
n=na.omit, data=data)
m3<-lme(COVER_CROP ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.act
ion=na.omit, data=data)
m4<-lme(COVER_WEED ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.act
ion=na.omit, data=data)
m5<-lme(Productivity ~ LAI_crop, random =~1 | Block/Cycle, method="REML", na.
action=na.omit, data=data)

mm<-m1
E=resid(mm)
hist(E)

```

Histogram of E

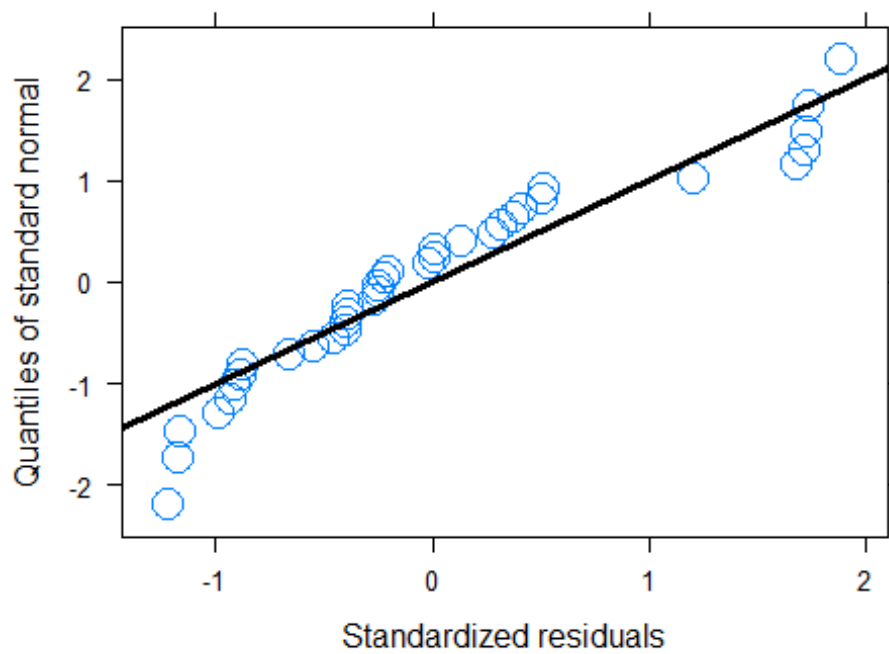


```
qqnorm(mm, ~ resid(., type="normalized"),  
        abline=c(0,1), main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```

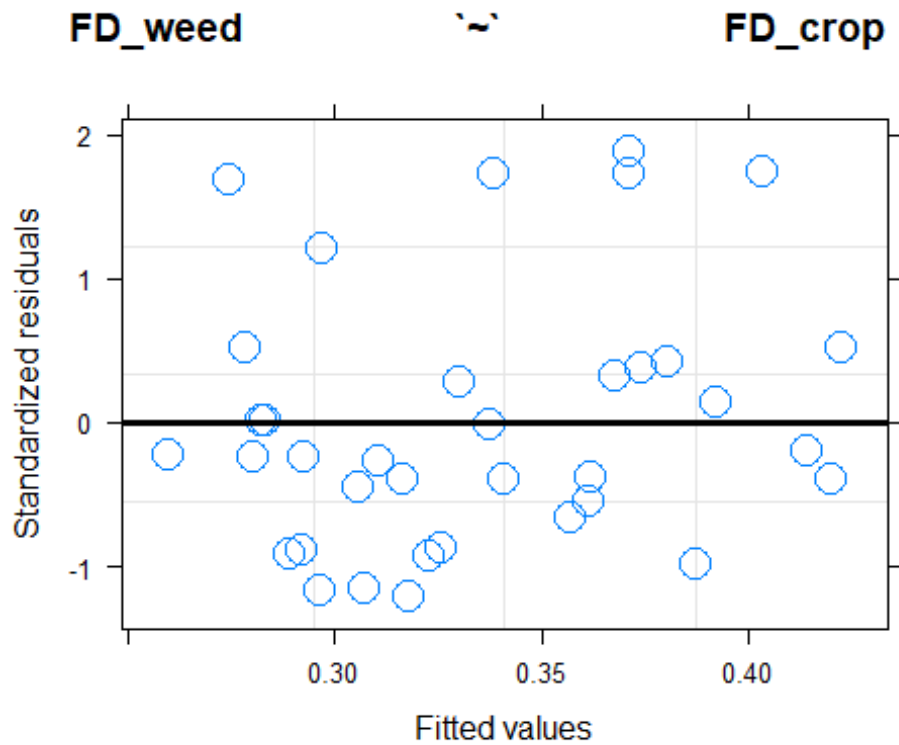
FD_weed

~

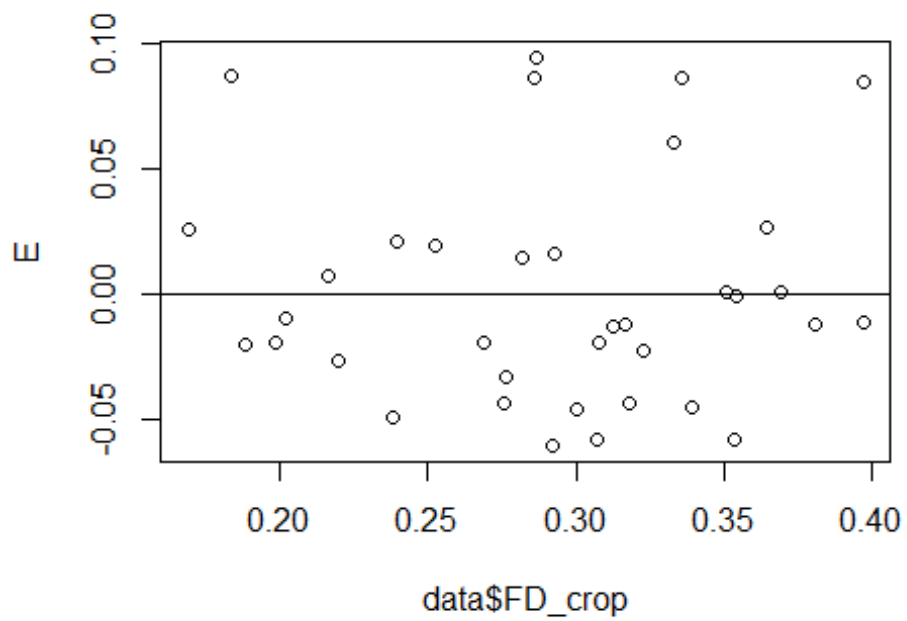
FD_crop



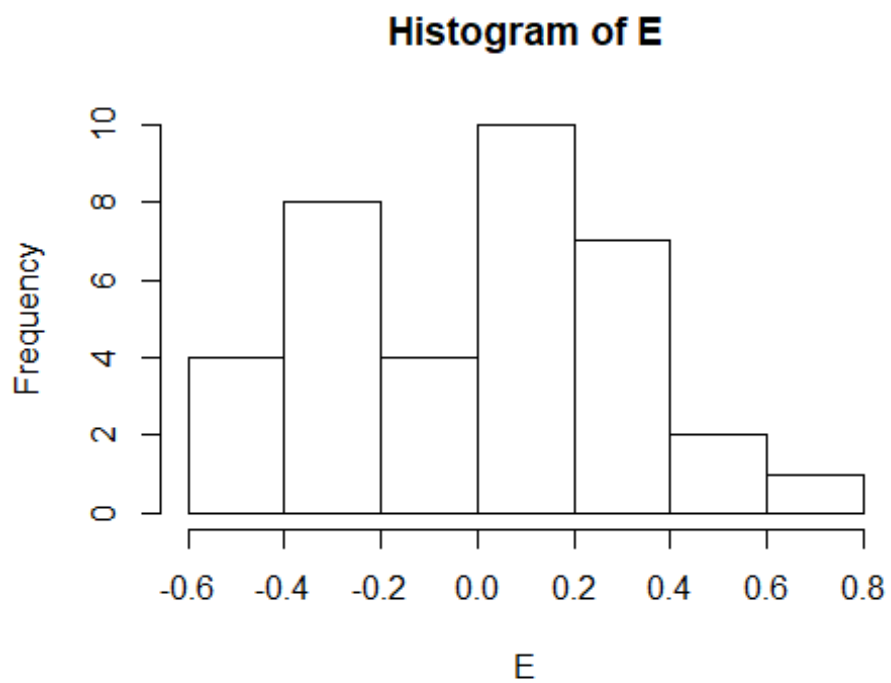
```
## HOMOGENEITY
plot(mm, main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```



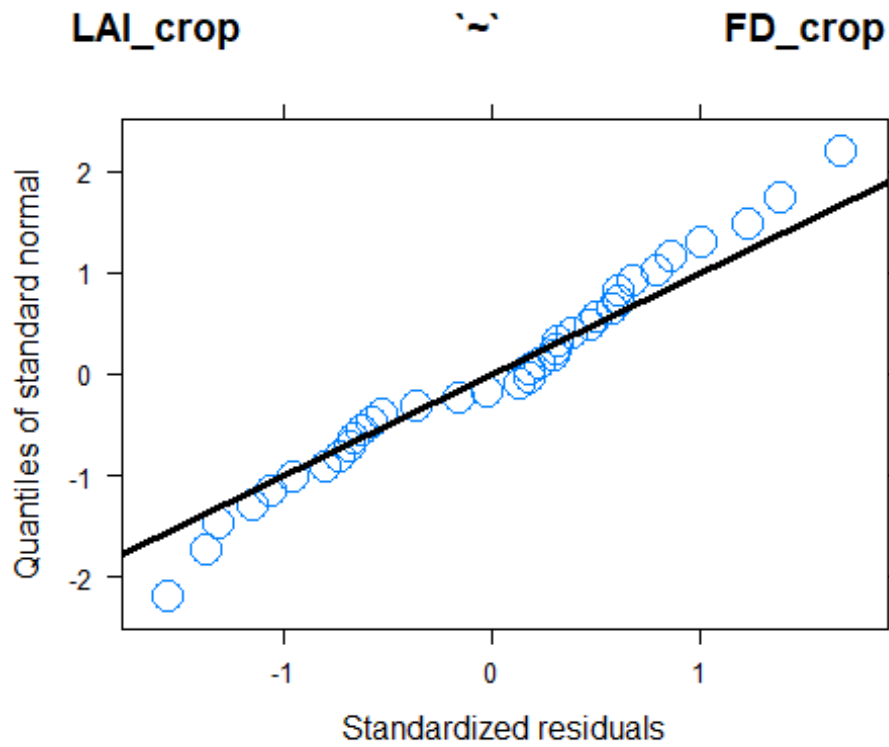
```
#You should also plot the residuals against each explanatory variable.
plot(E~data$FD_crop)
  abline(h=0)
```



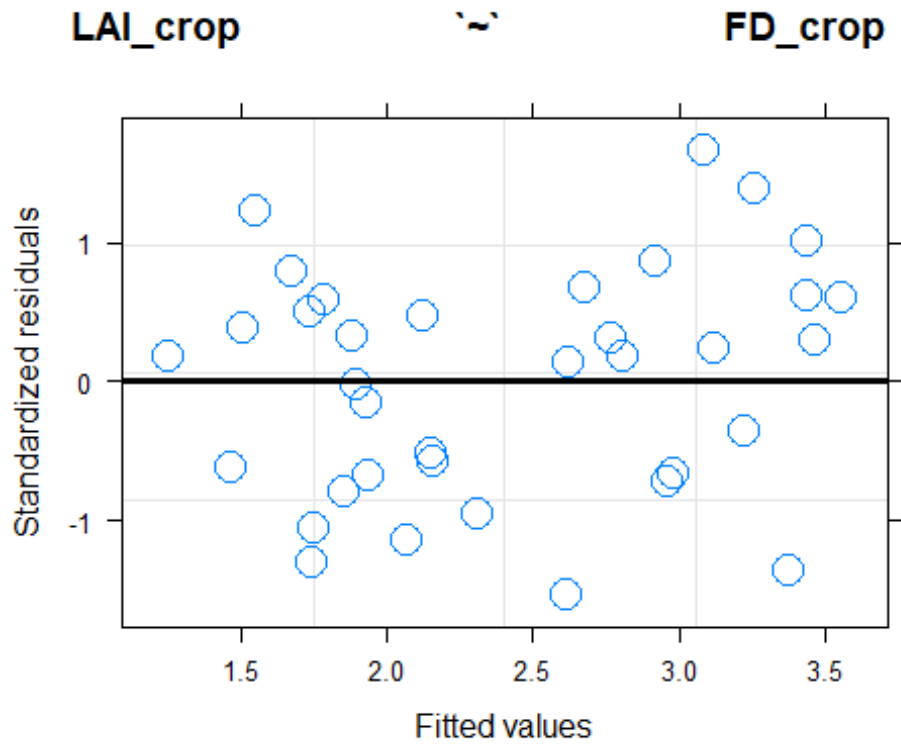
```
mm<-m2  
E=resid(mm)  
hist(E)
```



```
qqnorm(mm, ~ resid(., type="normalized"),  
        abline=c(0,1), main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```

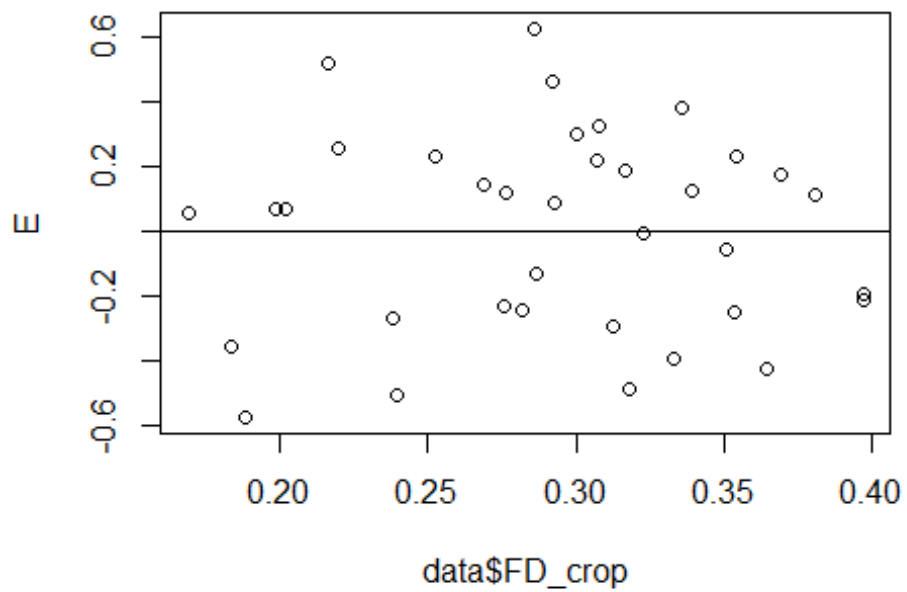


```
## HOMOGENEITY  
plot(mm, main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```

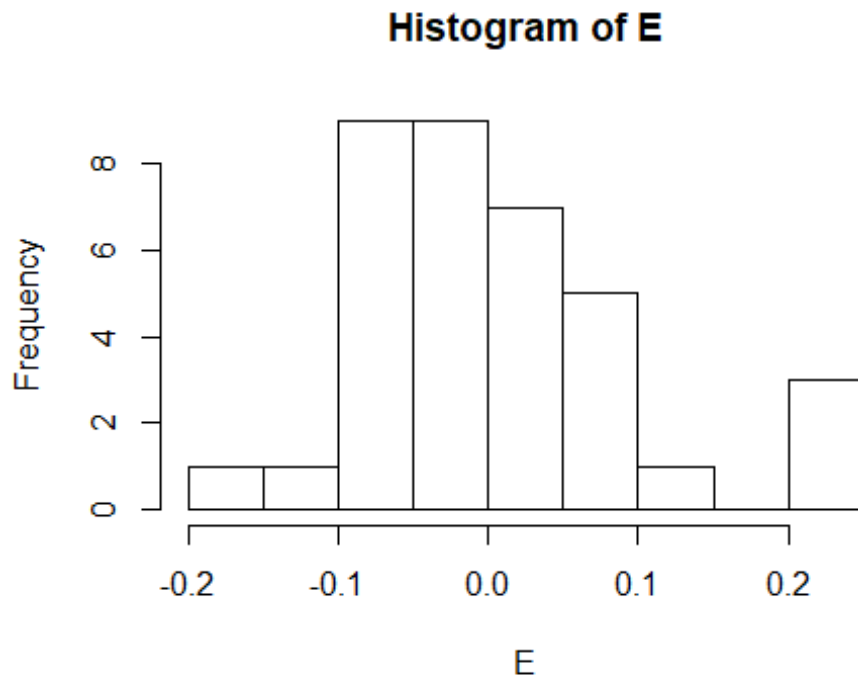


#You should also plot the residuals against each explanatory variable.


```
plot(E~data$FD_crop)
abline(h=0)
```

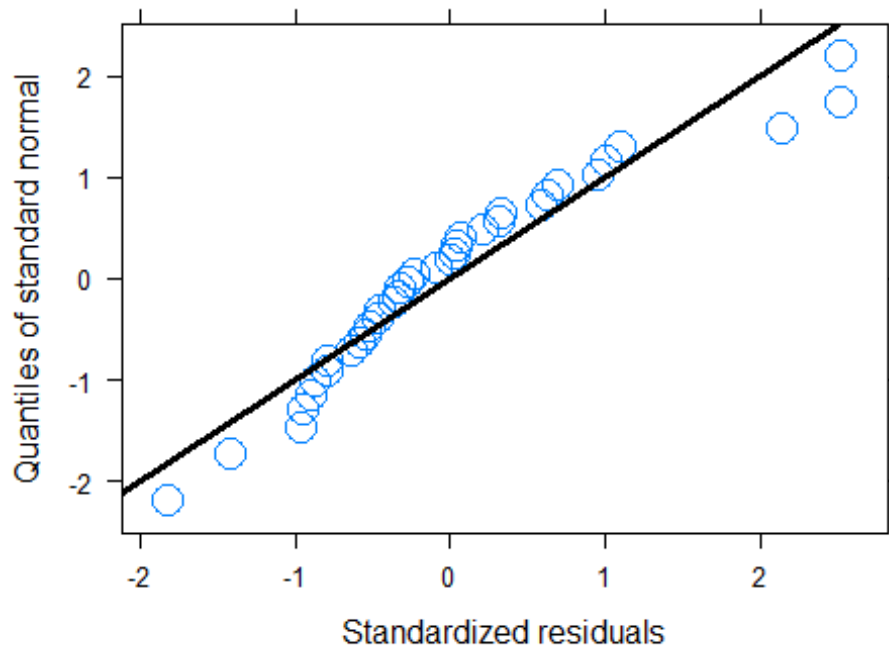



```
mm <- m3
E = resid(mm)
hist(E)
```




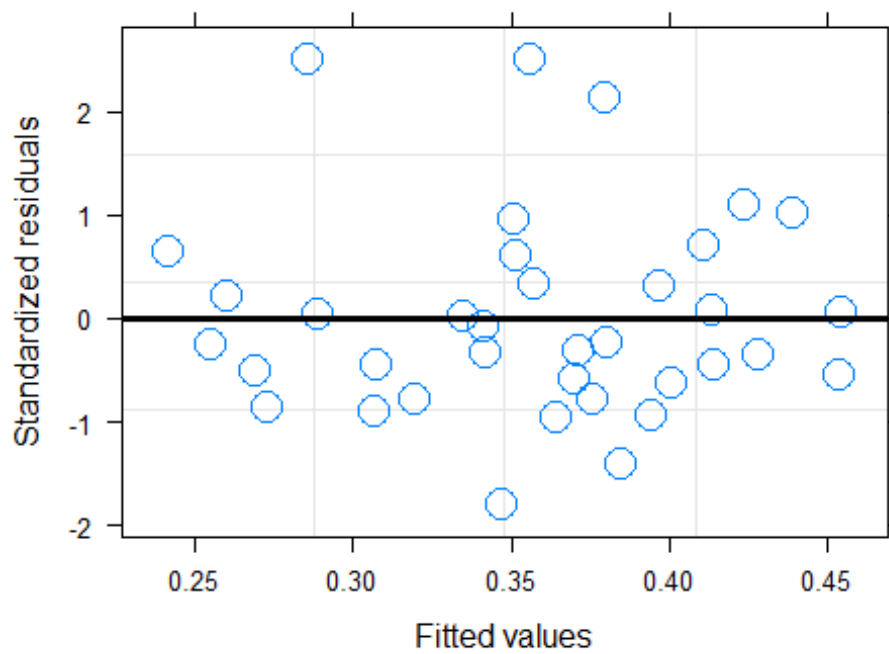
```
qqnorm(mm, ~ resid(., type="normalized"),
        abline=c(0,1), main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```

COVER_CROP  **FD_crop**

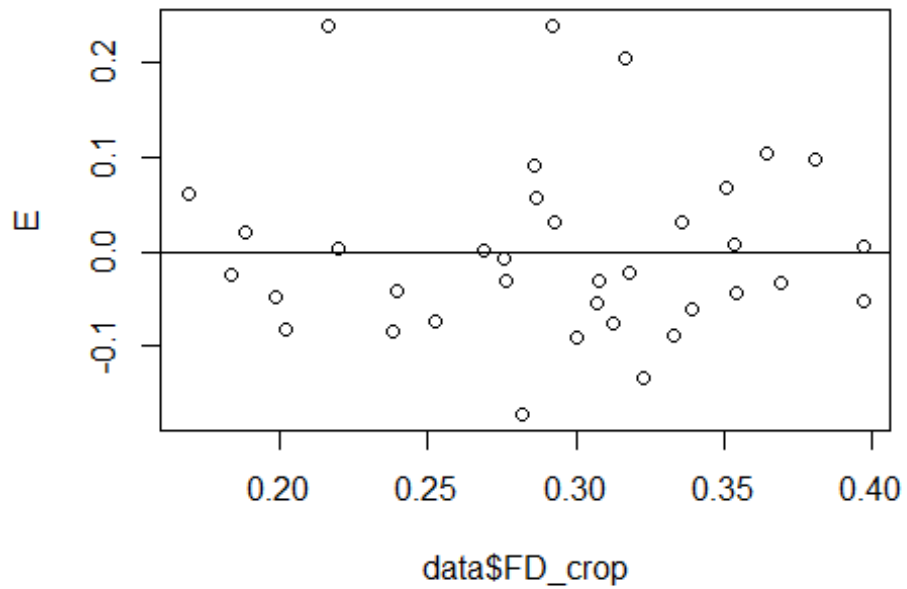


```
## HOMOGENEITY  
plot(mm, main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```

COVER_CROP  **FD_crop**

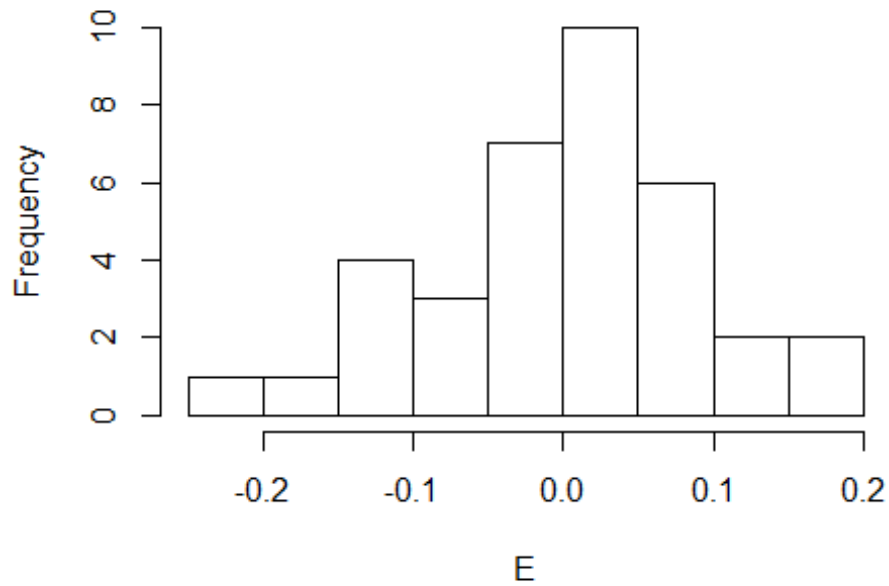


```
#You should also plot the residuals against each explanatory variable.  
plot(E~data$FD_crop)  
abline(h=0)
```



```
mm<-m4  
E=resid(mm)  
hist(E)
```

Histogram of E

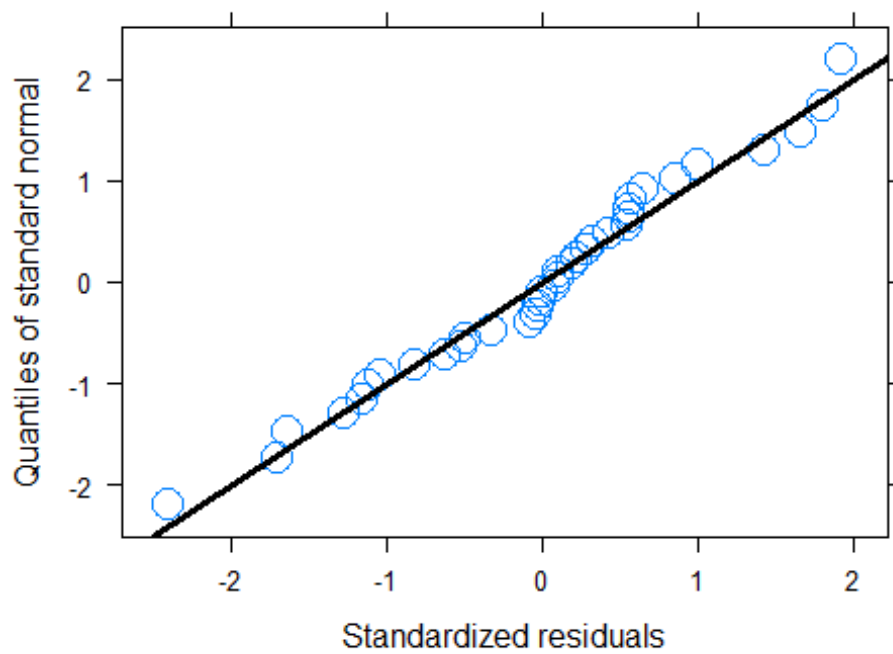


```
qqnorm(mm, ~ resid(., type="normalized"),  
        abline=c(0,1), main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```

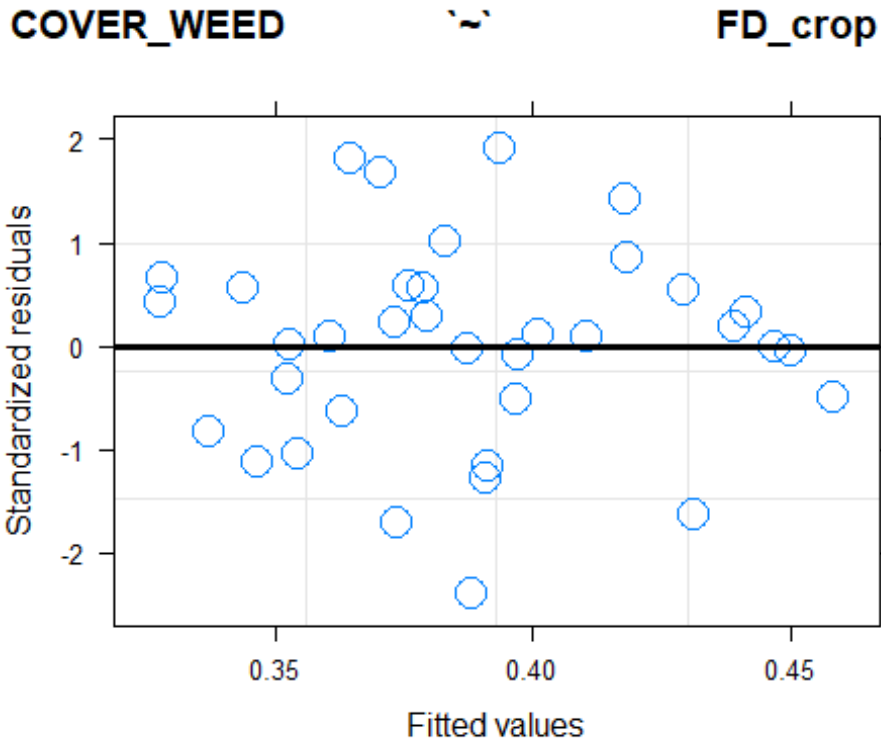
COVER_WEED

~

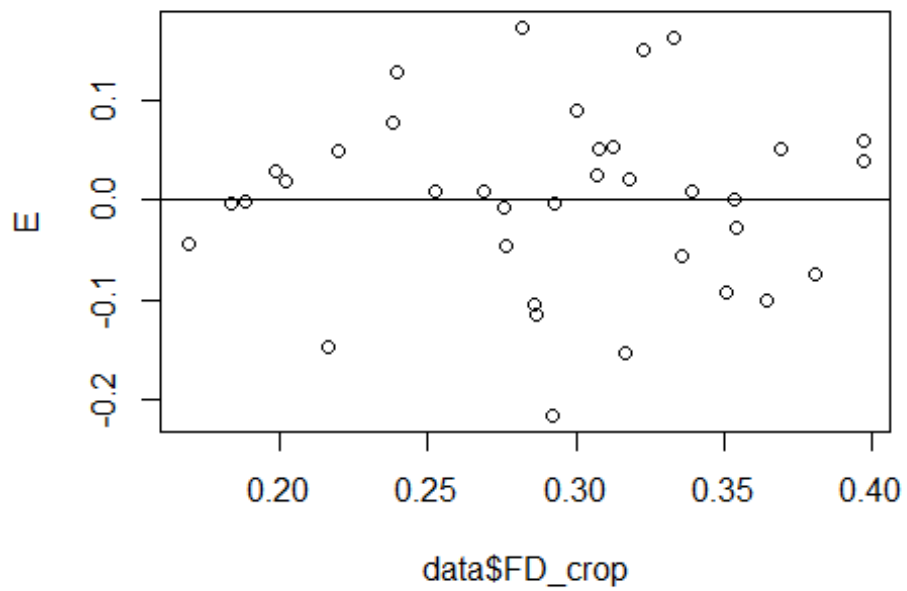
FD_crop



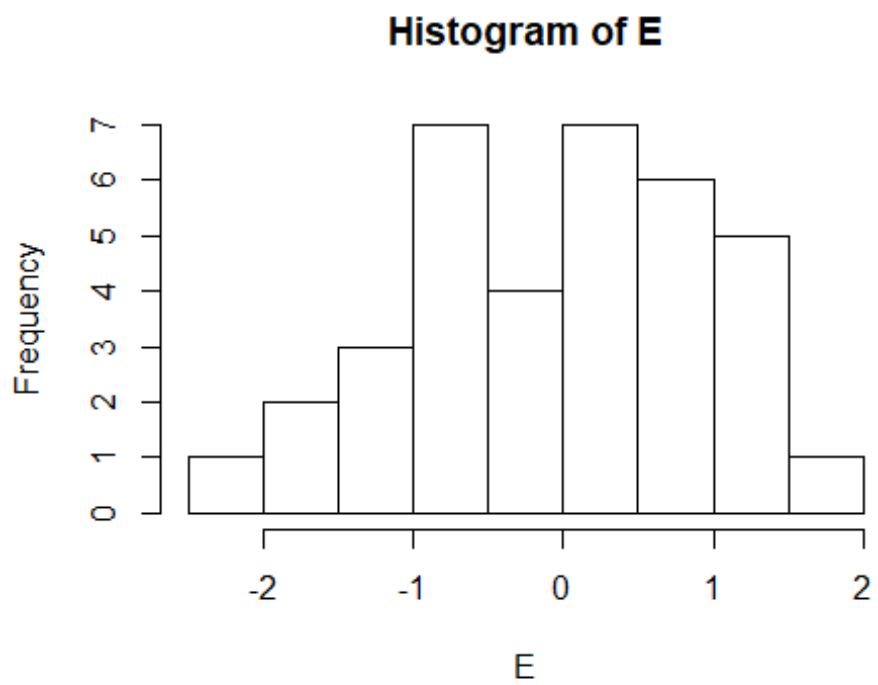
```
## HOMOGENEITY
plot(mm, main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```



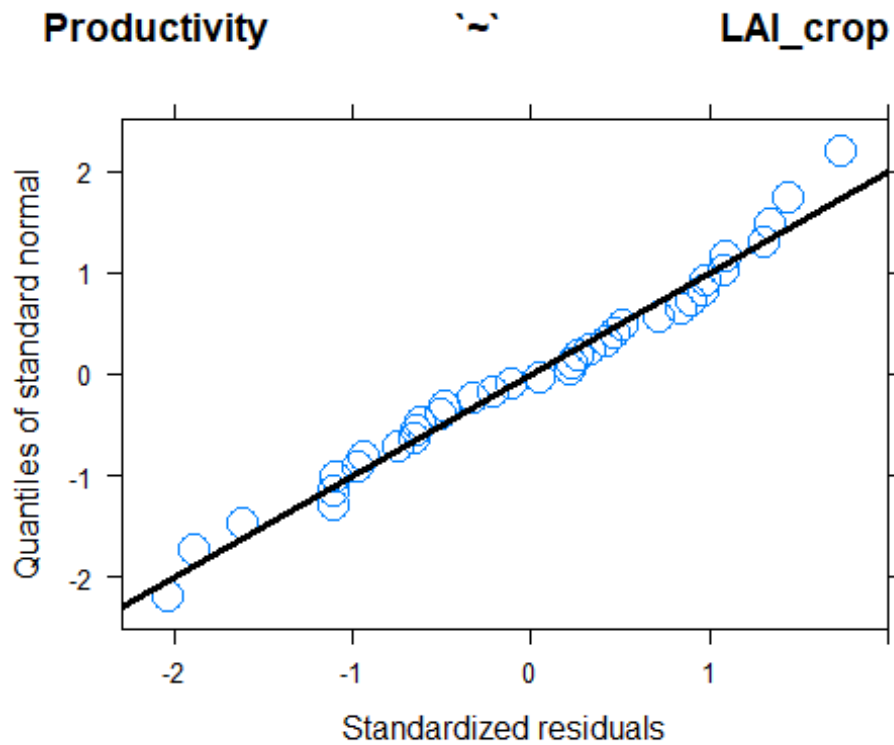
```
#You should also plot the residuals against each explanatory variable.
plot(E~data$FD_crop)
abline(h=0)
```



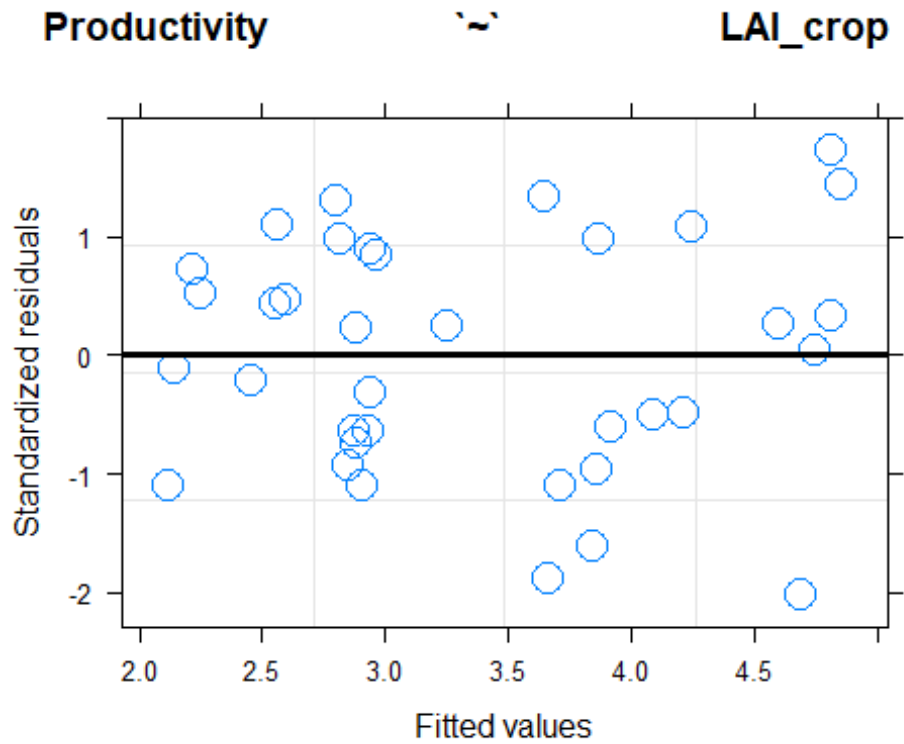
```
mm<-m5  
E=resid(mm)  
hist(E)
```



```
qqnorm(mm, ~ resid(., type="normalized"),  
        abline=c(0,1), main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```

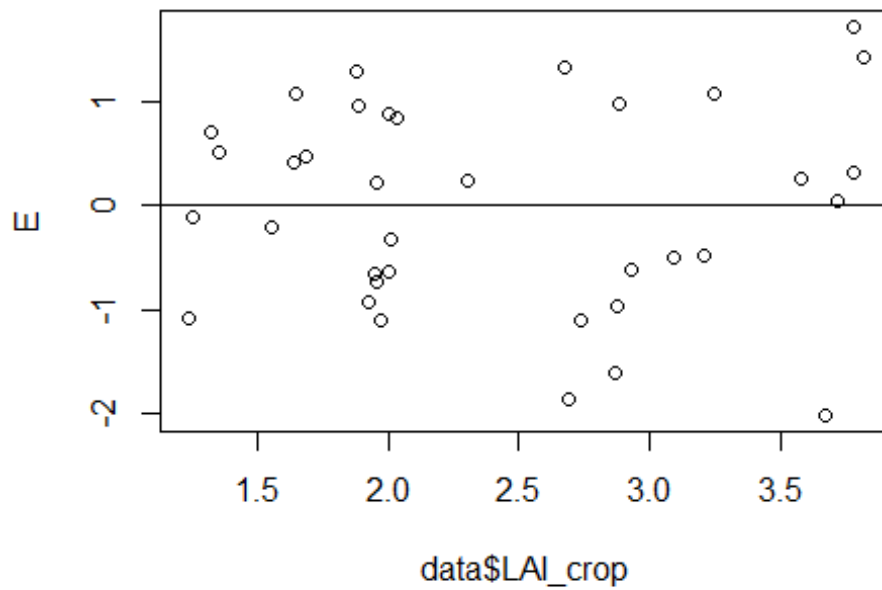


```
## HOMOGENEITY  
plot(mm, main=paste(formula(mm)[c(2,1,3)]), cex=2, lwd=3)
```



#You should also plot the residuals against each explanatory variable.

```
plot(E~data$LAI_crop)
abline(h=0)
```



Plotting models

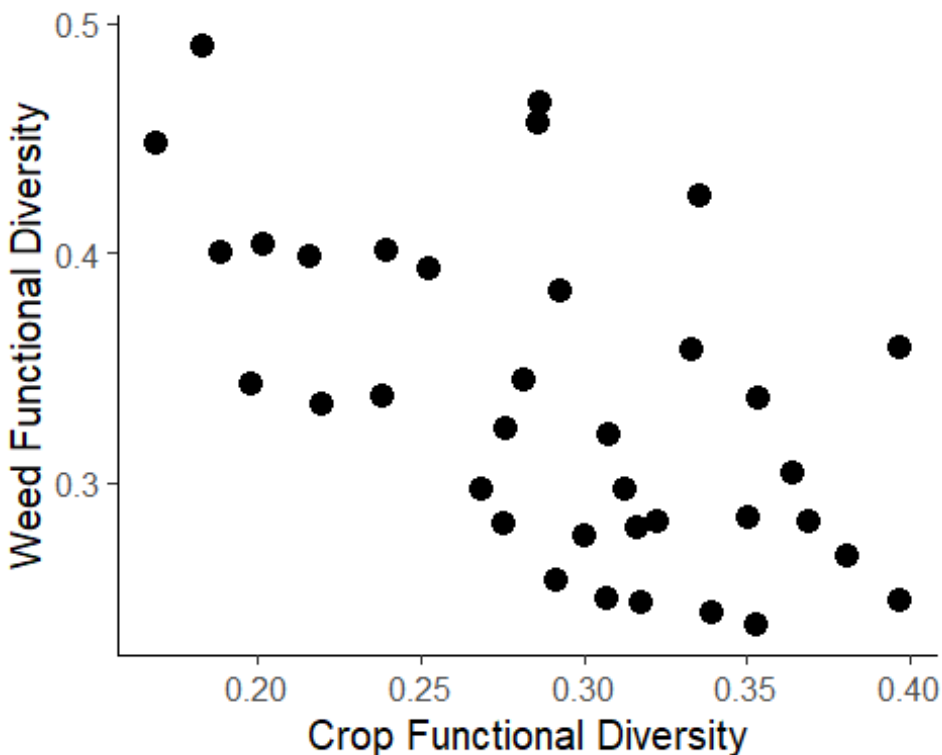
Model 1

```
library(ggplot2)
m1<-lme(FD_weed ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action
=na.omit, data=data)

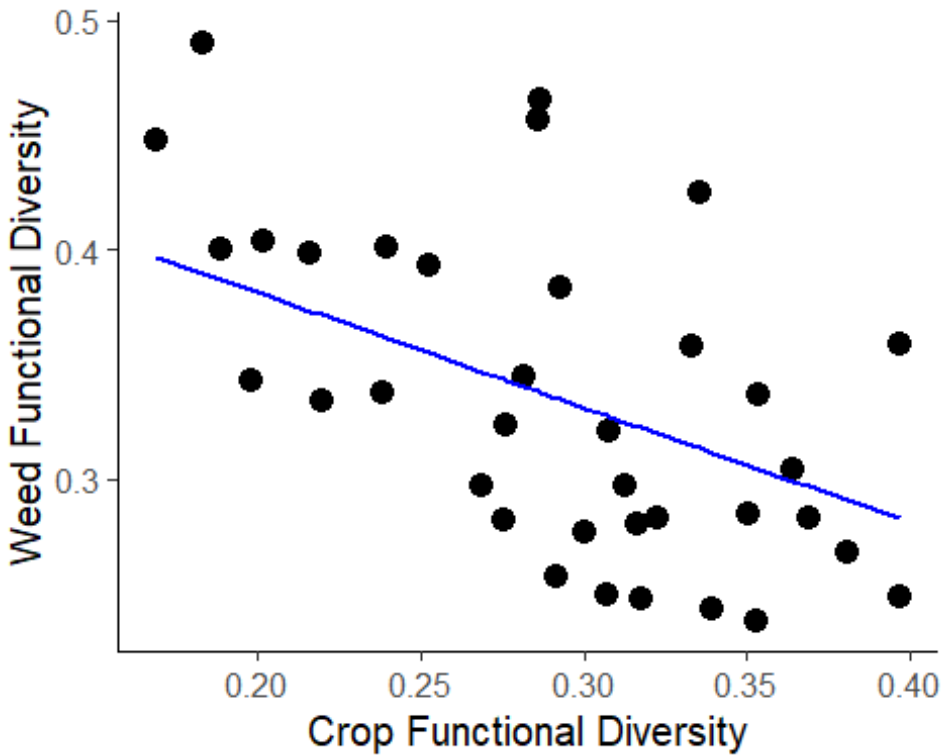
model<-m1
F0<-predict(model, level=0)

preditora <-data$FD_crop           #replace the covariate here
label_preditora<-"Crop Functional Diversity"   #change the name of the covariate here
Y=data$FD_weed; legendaY="Weed Functional Diversity"

g1=ggplot(data=data, aes(x = preditora, y = Y)) +
  geom_point(size=4) +
  theme_classic(base_size = 15)+
  ylab(legendaY) + xlab(label_preditora)
g1
```



```
g1 + geom_line(aes(x=preditora, y=F0), col="blue", size=1)
```



```
ggsave("MODEL01.png", width=5.5, height=6, dpi=400) # controlar a resolu??o
```

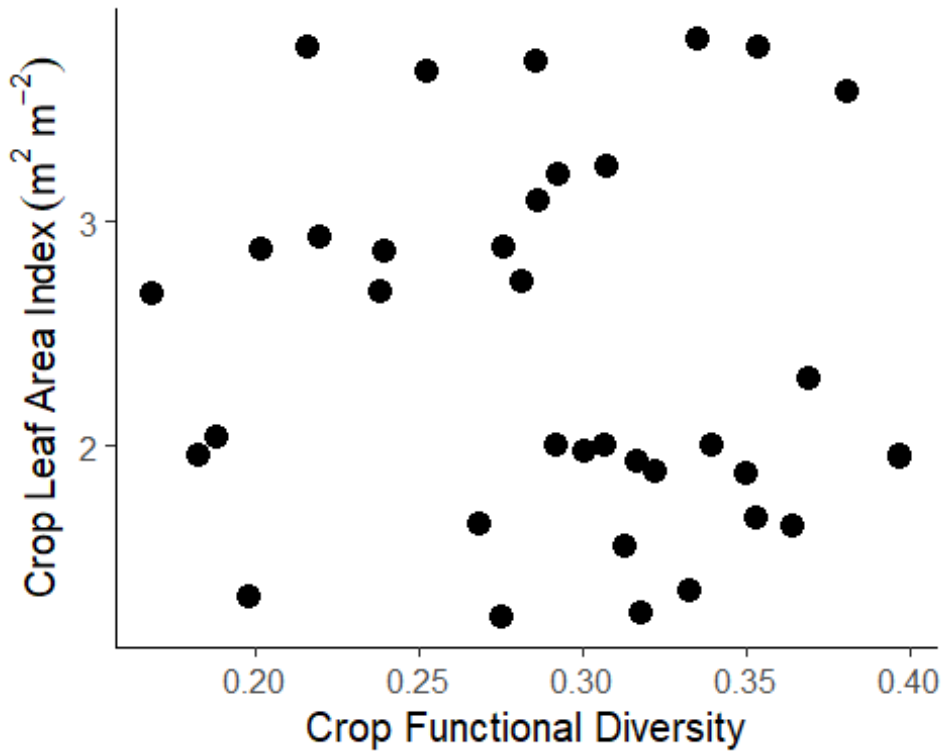
Model2

```
m2<-lme(LAI_crop ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.actio
n=na.omit, data=data)
```

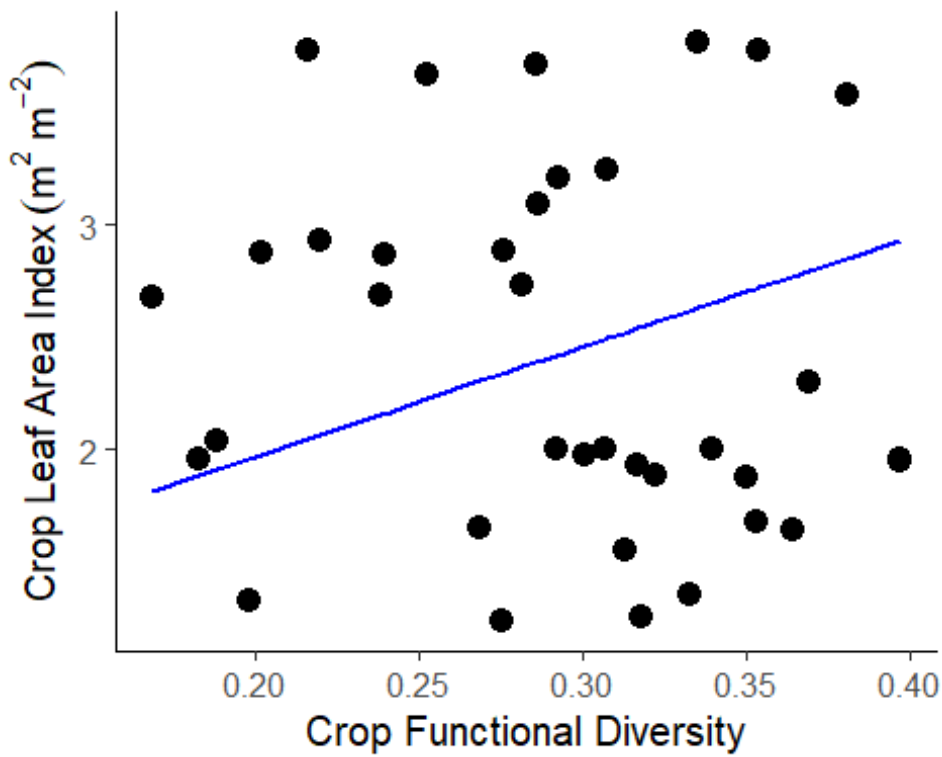
```
model<-m2
F0<-predict(model, level=0)
```

```
preditora <-data$FD_crop          #replace the covariate here
label_preditora<-"Crop Functional Diversity" #change the name of the cova
riate here
Y=data$LAI_crop; legendaY=expression(Crop~Leaf~Area~Index~(m^{2}~m^{-2}))
```

```
g2=ggplot(data=data, aes(x = preditora, y = Y)) +
  geom_point(size=4) +
  theme_classic(base_size = 15)+
  ylab(legendaY) + xlab(label_preditora)
g2
```



```
g2 + geom_line(aes(x=predictora, y=F0), col="blue", size=1)
```



```
ggsave("MODEL02.png", width=5.5, height=6, dpi=400) # controlar a resolu??o
```

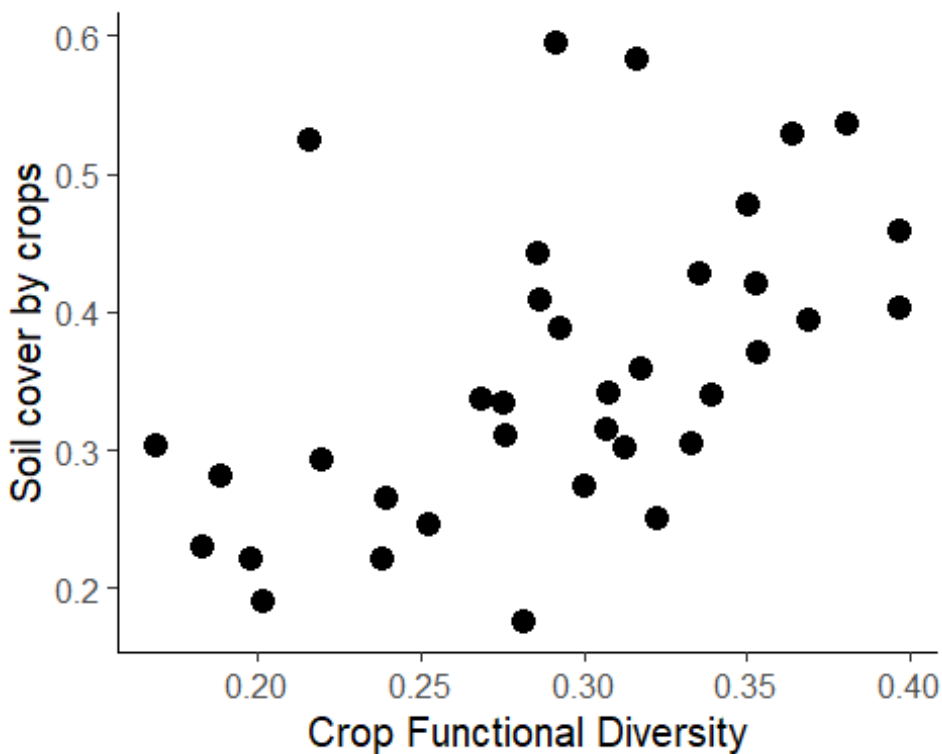
Model 3

```
m3<-lme(COVER_CROP ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.action=na.omit, data=data)
```

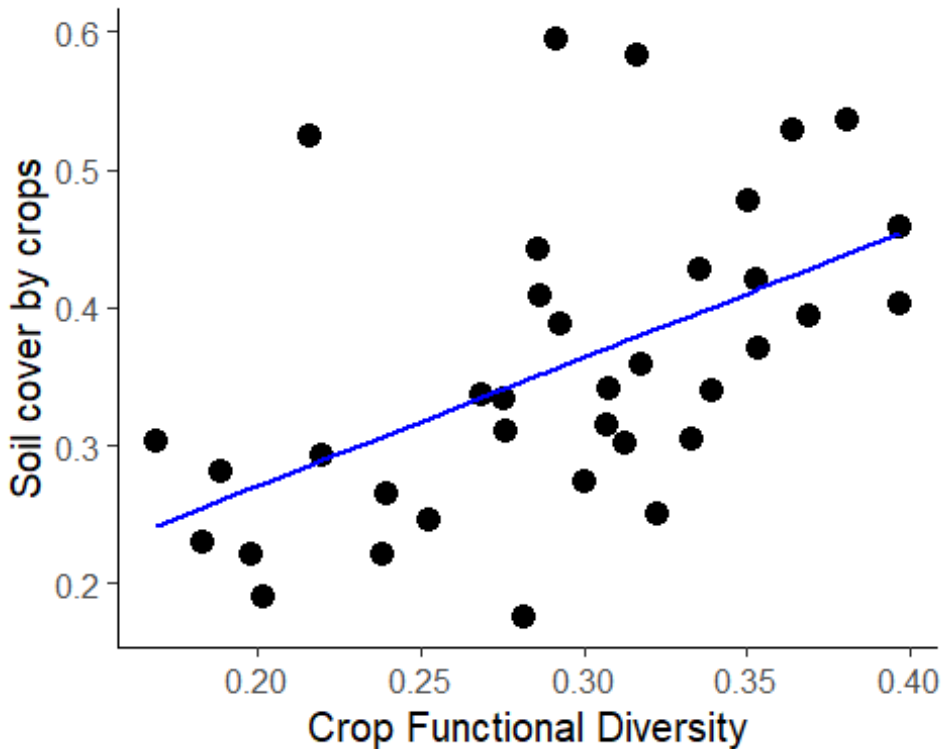
```
model<-m3  
F0<-predict(model, level=0)
```

```
predictora <-data$FD_crop           #replace the covariate here  
label_predictora<-"Crop Functional Diversity" #change the name of the covariate here  
Y=data$COVER_CROP; legendaY="Soil cover by crops"
```

```
g3=ggplot(data=data, aes(x = predictora, y = Y)) +  
  geom_point(size=4) +  
  theme_classic(base_size = 15)+  
  ylab(legendaY) + xlab(label_predictora)  
g3
```



```
g3 + geom_line(aes(x=predictora, y=F0), col="blue", size=1)
```



```
ggsave("MODEL03.png", width=5.5, height=6, dpi=400) # controlar a resolu??o
```

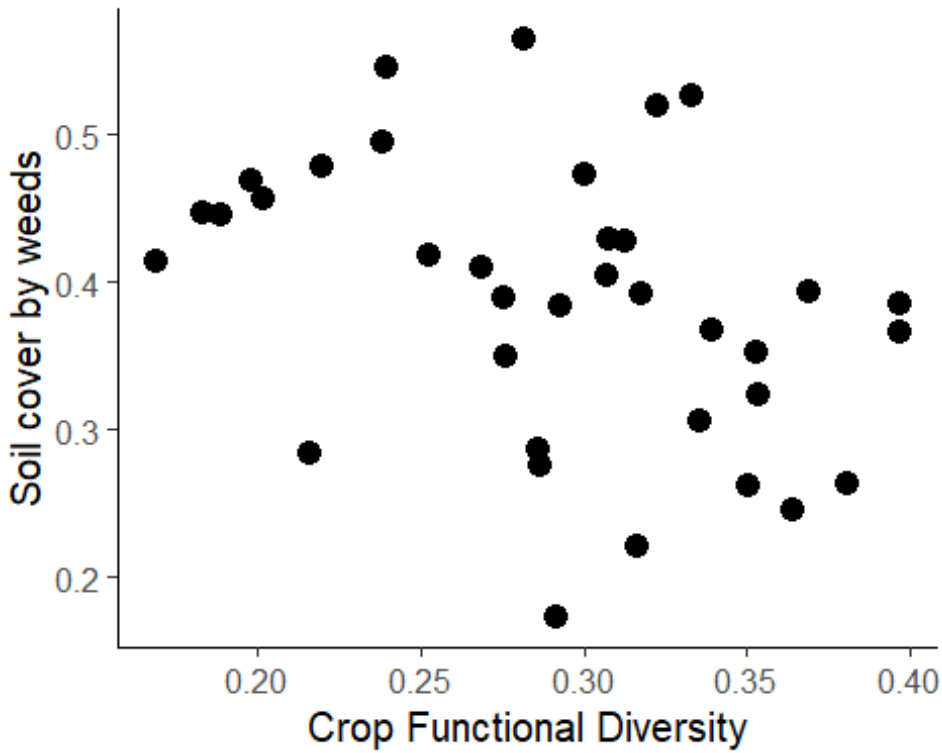
Model 4

```
m4<-lme(COVER_WEED ~ FD_crop, random =~1 | Block/Cycle, method="REML", na.act
ion=na.omit, data=data)
```

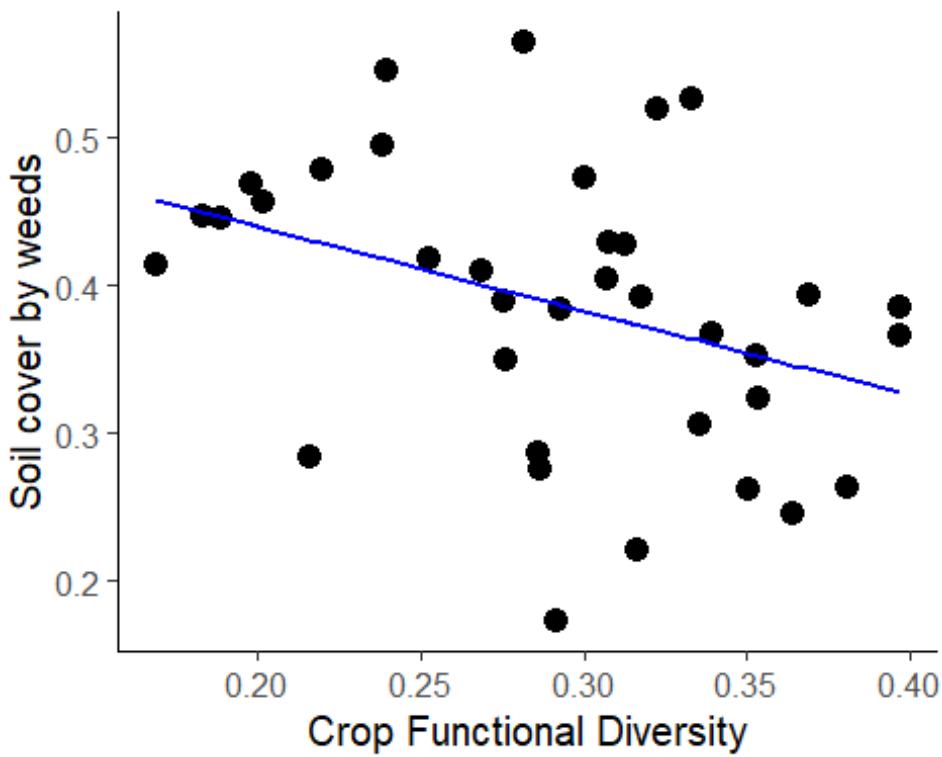
```
model<-m4
F0<-predict(model, level=0)
```

```
predictora <-data$FD_crop           #replace the covariate here
label_predictora<-"Crop Functional Diversity" #change the name of the cova
riate here
Y=data$COVER_WEED; legendaY="Soil cover by weeds"
```

```
g4=ggplot(data=data, aes(x = predictora, y = Y)) +
  geom_point(size=4) +
  theme_classic(base_size = 15)+
  ylab(legendaY) + xlab(label_predictora)
g4
```



```
g4 + geom_line(aes(x=predictora, y=F0), col="blue", size=1)
```



```
ggsave("MODELO4.png", width=5.5, height=6, dpi=400) # controlar a resolu??o
```

Model 5

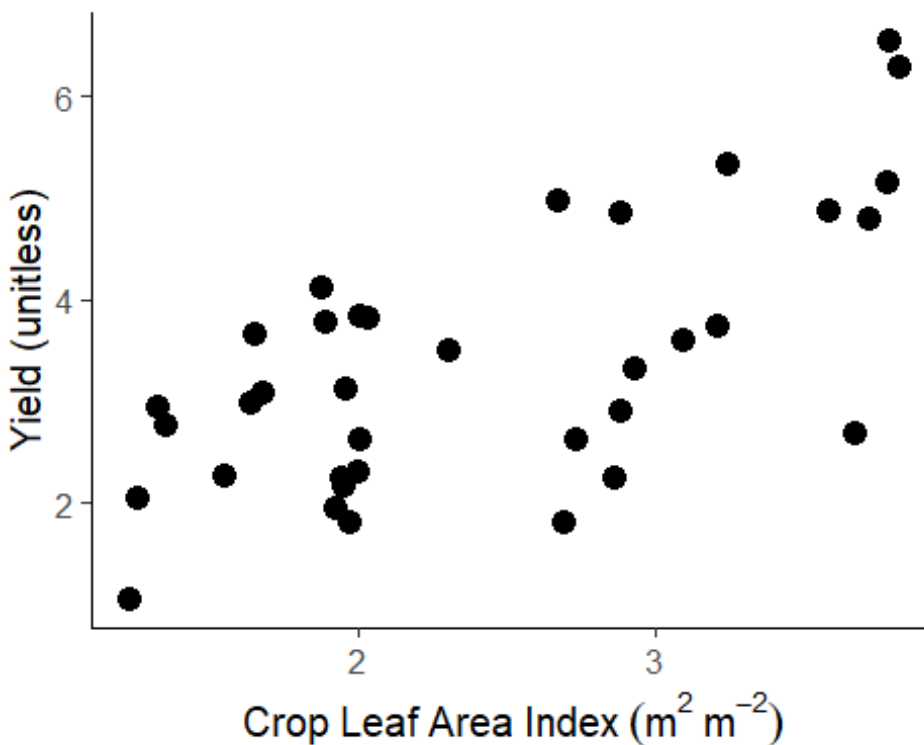
```
m5<-lme(Productivity ~ LAI_crop, random =~1 | Block/Cycle, method="REML", na.
action=na.omit, data=data)

model<-m5
F0<-predict(model, level=0)
expression(Concentration~mg~L^{-1})

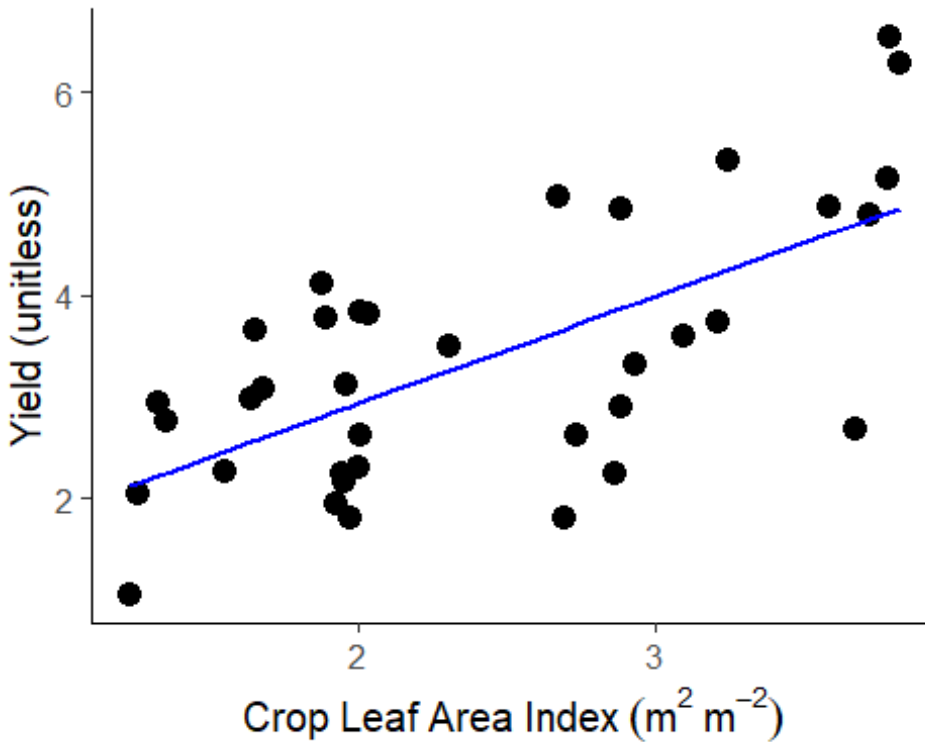
## expression(Concentration ~ mg ~ L^{
##     -1
## })

predictora <-data$LAI_crop           #replace the covariate here
label_predictora<-expression(Crop~Leaf~Area~Index~(m^{2}~m^{-2})) #change the
name of the covariate here
Y=data$Productivity; legendaY="Yield (unitless)"

g5=ggplot(data=data, aes(x = predictora, y = Y)) +
  geom_point(size=4) +
  theme_classic(base_size = 15)+
  ylab(legendaY) + xlab(label_predictora)
g5
```



```
g5 + geom_line(aes(x=predictora, y=F0), col="blue", size=1)
```

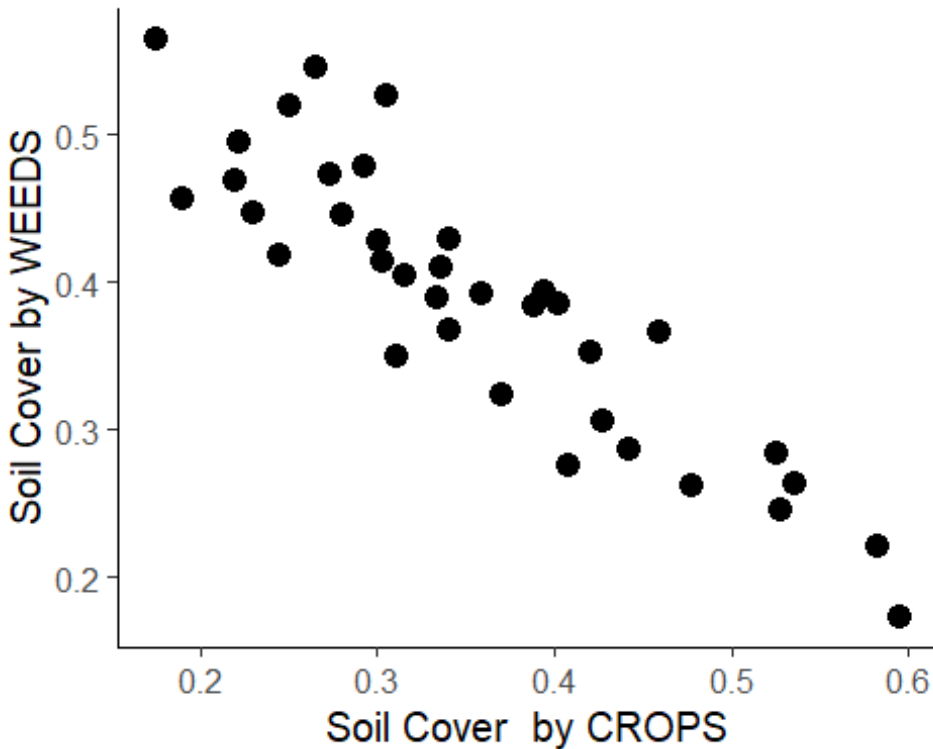


```
ggsave("MODEL05.png", width=5.5, height=6, dpi=400) # controlar a resolu??o
```

Plotting correlation

```
X <- data$COVER_CROP      #replace the covariate here
label_preditora <- "Soil Cover by CROPS" #change the name of the covariate here
Y = data$COVER_WEED; legendaY = "Soil Cover by WEEDS"

g6 = ggplot(data = data, aes(x = X, y = Y)) +
  geom_point(size = 4) +
  theme_classic(base_size = 15) +
  ylab(legendaY) + xlab(label_preditora)
g6
```

```
ggsave("MODEL06.png", width=5.5, height=6, dpi=400) # controlar a resolu??o
```

Plotting FD planned and FD observed

```
str(data)
```

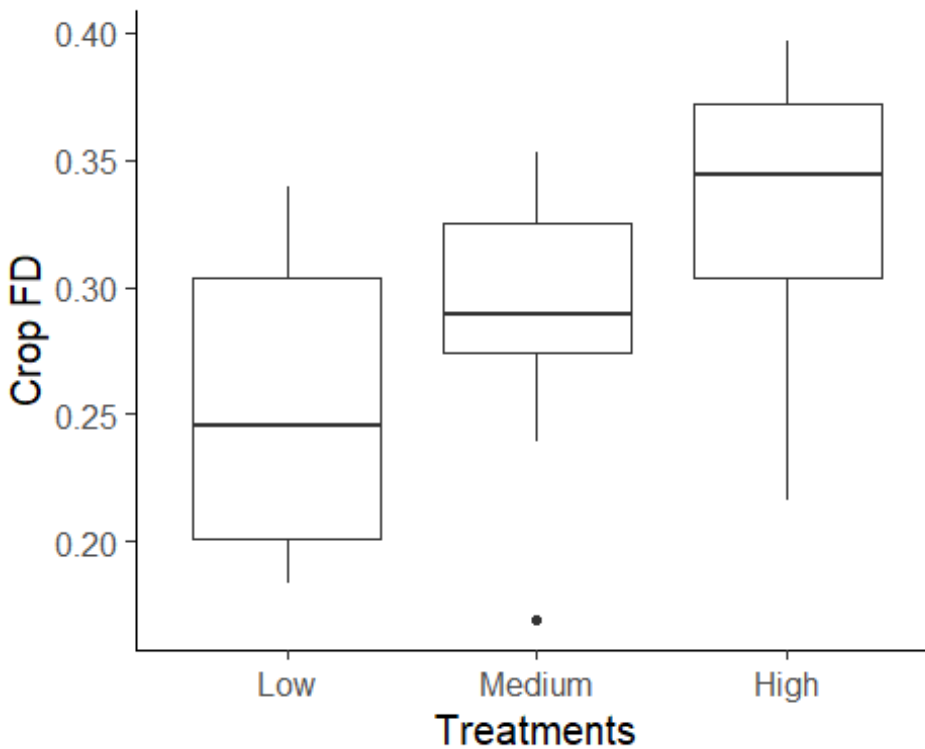
```
## 'data.frame':  36 obs. of  16 variables:
## $ Block      : Factor w/ 6 levels "1","2","3","4",...: 1 1 1 2 2 2 3 3 3
##             4 ...
## $ Treatment  : Factor w/ 3 levels "1","2","3": 3 1 2 3 1 2 3 1 2 3 ...
## $ Cycle      : Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## $ Productivity: num  5.32 3.11 4.84 6.29 1.79 ...
## $ LAI_weed   : num  1.661 0.747 0.934 1.341 1.314 ...
## $ LAI_crop   : num  3.24 1.96 2.88 3.81 2.69 ...
## $ FD_weed    : num  0.321 0.49 0.324 0.425 0.338 ...
## $ FR_weed    : num  0.321 0.388 0.306 0.403 0.312 ...
## $ FD_crop    : num  0.308 0.183 0.276 0.335 0.238 ...
## $ FR_crop    : num  0.428 0.451 0.477 0.448 0.524 ...
## $ COVER_WEED : num  0.429 0.447 0.351 0.307 0.495 ...
## $ COVER_CROP : num  0.341 0.23 0.311 0.427 0.222 ...
## $ SOLO_EXPOSTO: num  0.0846 0.0821 0.072 0.0776 0.1365 ...
## $ Weed_supp  : num  -0.0882 -0.2163 -0.0398 0.1208 -0.2731 ...
## $ Litter     : num  0.23 0.323 0.339 0.266 0.284 ...
## $ Soil_protec : num  0.77 0.677 0.661 0.734 0.716 ...
```

```

#treatments Label: "1"=Low; "2"=medium; "3"=high

X <-data$Treatment      #replace the covariate here
label_preditora<- "Treatments" #change the name of the covariate here
Y=data$FD_crop; legendaY="Crop FD"
g7=ggplot(data=data, aes(x = X, y = Y)) +
  geom_boxplot() +
  scale_x_discrete(labels=c("Low", "Medium", "High"))+
  theme_classic(base_size = 15)+
  ylab(legendaY) + xlab(label_preditora)
g7

```



```

ggsave("BOXPLOT_TREATMENTS.png", width=5.5, height=6, dpi=400) # controlar a
resolu??o

```

REFERENCES

Allaire, J. *et al.* (2018) 'rmarkdown: Dynamic Documents for R'. Available at: <https://rmarkdown.rstudio.com>.

Xie, Y., Allaire, J. J. and Golemund, G. (2018) *R Markdown: The Definitive Guide*. Chapman and Hall/CRC. Available at: <https://bookdown.org/yihui/rmarkdown>.