BIOVEG - Statistical analyses in R

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A PROTOCOL TO LEARN AND TEACH STATISTICS IN R WITH VEGETATION DATA

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RECOMMENDATIONS

1- Complete an introductory R course to understand the basic operations used in the software: e.g. how to import files, attach data, install packages and create objects and graphs.

2- It is important to have a basic understanding of the principles and functions of the statistical analysis you wish to perform.

3- If your analysis does not execute successfully using these syntaxes, it is useful to consult R forums (e.g. Stack Overflow and Stack Exchange - Cross Validated) check if there is something wrong, missing or if this is simply not the appropriate analysis for your data.

4- Be sure about your choice of analysis. Refer to existing literature to help decide which analysis is most appropriate for your data.

5- If possible, it is highly recommended to read the references at the end of this script, especially those which are highlighted.

6- Try not to be overwhelmed by the various methodologies of statistical analysis which might be used to investigate the data. Again, consult with existing literature to help decide which analyses are most suitable.

7- Remember that this script was not created by statisticians. The adaptable nature of the R means that there are often several ways to complete the same analysis. This script describes one way to perform typical statistical analysis of the kind of data commonly generated in biological research.

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```

Read test datasets

BIOVEG = your source (file) of data. Example:

setwd("C:/")

```r
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG)
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
## 5 Semidecidual p005 AREA1  Aspidosperma_australe        9    34.31
## 6 Semidecidual p006 AREA1 Aspidosperma_olivaceum        7    16.03
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
## 5         6.724      0.092        19               1250
24.4
## 6         7.536      0.020        23               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
## 5      2.35        1.02     -40       0 747923 7807727      747883
## 6      2.90        5.74       0     -10 747923 7807727      747923
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
## 5     7807727
## 6     7807717
```

```r
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed)
```

```
##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
```

```
23
## 5   s5        VOL ruderal.grass 2002        0.7        75
27
## 6   s6        VOL      woodland 2002        0.2         5
16
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
## 5            0.8            20     NONE        NONE  292.112
2
## 6            0.8            10     NONE        NONE  298.394
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
## 5          W   0.12      2.53     12.34
## 6         NW   0.16      2.62     10.77
```

NORMALITY TEST

One of the most commonly used tests in Botany is Shapiro-Wilk. This test verifies whether one specific variable from your data is normally (gaussian) distributed. If the p-value is below the critical level (e.g. below 0.05) the variable can be described as deviating significantly from the normal (gaussian) distribution.

```
# usage:
shapiro.test(BIOVEG$Basal.area)

##
##  Shapiro-Wilk normality test
##
## data:  BIOVEG$Basal.area
## W = 0.50624, p-value < 2.2e-16
```

DATA TRANSFORMATION

In some cases it is necessary to transform your data, either to achieve normality or to get a better fit for the residuals of your model. Here the mention some of the most commonly applied transformations, but there are many others (e.g. Box cox) and it's

always good to read about other possibilities to maximize the fit and robustness of your analysis.

plus:

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4) # reading only the first 4 rows
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```
Basal.plus <- BIOVEG$Basal.area + 5
plus<- cbind(BIOVEG$Basal.area, Basal.plus) # just to have a look at the
result
head(plus, 10) # reading only the first 10 rows of the outcome
```

```
##             Basal.plus
##  [1,] 0.058      5.058
##  [2,] 0.120      5.120
##  [3,] 0.090      5.090
##  [4,] 0.128      5.128
##  [5,] 0.092      5.092
##  [6,] 0.020      5.020
##  [7,] 0.143      5.143
##  [8,] 0.139      5.139
##  [9,] 0.721      5.721
## [10,] 0.107      5.107
```

log:

Mainly indicated to try to make right-skewed data normal and by default included in Poisson GLM (i.e. the default link function is log). But, many authors have suggested not to transform count (poisson) data. Read about it if possible.

Note: in case your data contain zeros or negative values, you have to add a constant to all values so that all of them are positive before you can take the logarithm.

```
Basal.log <- log(BIOVEG$Basal.area)
c1<- cbind(BIOVEG$Basal.area, Basal.log)
head(c1, 10) # reading only the first 10 rows of the outcome
```

```
##              Basal.log
##  [1,] 0.058 -2.8473123
##  [2,] 0.120 -2.1202635
##  [3,] 0.090 -2.4079456
##  [4,] 0.128 -2.0557250
##  [5,] 0.092 -2.3859667
##  [6,] 0.020 -3.9120230
##  [7,] 0.143 -1.9449106
##  [8,] 0.139 -1.9732813
##  [9,] 0.721 -0.3271161
## [10,] 0.107 -2.2349264
```

```
x <- rnorm(10, mean = 2, sd = 2) # example of a variable with values =< 0
log(x) # does not work
```

```
## Warning in log(x): NaNs produced
```

```
##  [1]        NaN  1.2659236  0.4878708  1.1354343        NaN  0.8612742
##  [7] -0.6677834        NaN  1.3378603  1.4309497
```

```
c2 <- abs(min(x)) + 0.1 # the constant you have to add to x to make all
values > 0
head(c2, 10) #... 10 rows of the outcome
```

```
## [1] 1.567473
```

```
x.log <- log(x + c2) # works
head (x.log, 10) # ...10 rows of the outcome
```

```
##  [1] -2.3025851  1.6319505  1.1619993  1.5432977  0.1195393  1.3695669
##  [7]  0.7325203 -0.1414484  1.6823823  1.7492247
```

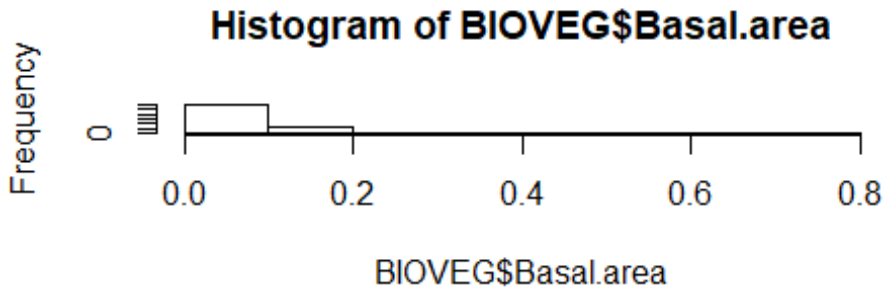
```
c3<- cbind(x, x.log)
head(c3, 10) # ... 10 rows of the outcome
```

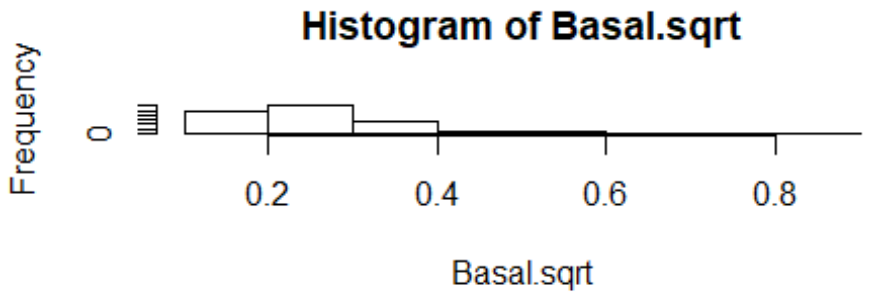
```
##                x      x.log
##  [1,] -1.4674729 -2.3025851
##  [2,]  3.5463668  1.6319505
##  [3,]  1.6288444  1.1619993
##  [4,]  3.1125251  1.5432977
```

```
##  [5,] -0.4404954  0.1195393
##  [6,]  2.3661737  1.3695669
##  [7,]  0.5128441  0.7325203
##  [8,] -0.6993730 -0.1414484
##  [9,]  3.8108808  1.6823823
## [10,]  4.1826696  1.7492247
```

square:

```
Basal.sqrt <- sqrt(BIOVEG$Basal.area)
par(mfrow=c(2,1)) # let's check the transformation using histograms
hist(BIOVEG$Basal.area)
hist(Basal.sqrt)
```





Inverse:

```
Basal.inv <- 1 / BIOVEG$Basal.area
head(Basal.inv, 10) # reading only the first 10 rows

##  [1] 17.241379  8.333333 11.111111  7.812500 10.869565 50.000000
6.993007
##  [8]  7.194245  1.386963  9.345794
```

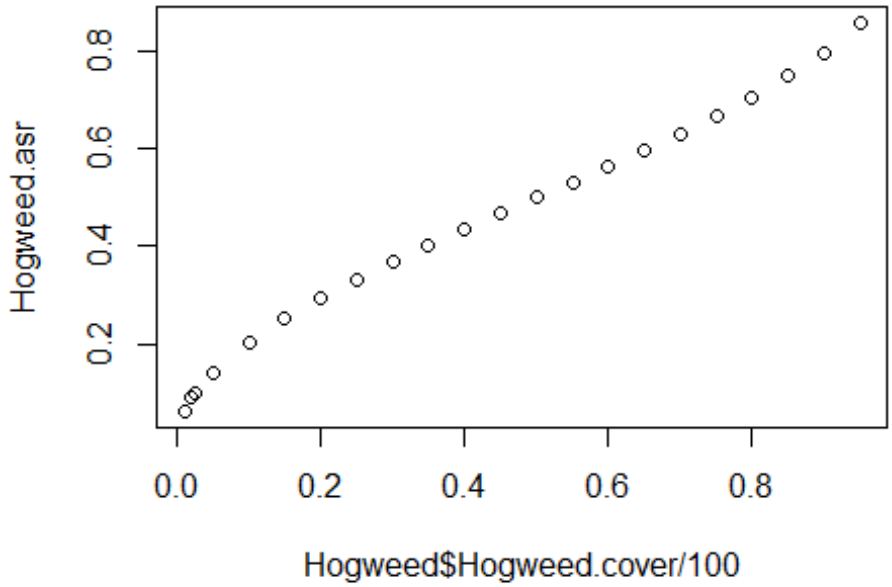
Arcsine square root:

Can be used for data that range between zero and 1. Often indicated for binomial data (proportions/ percentages), but it is preferable to use a model with binomial distribution rather than an arcsine square root transformation in this case.

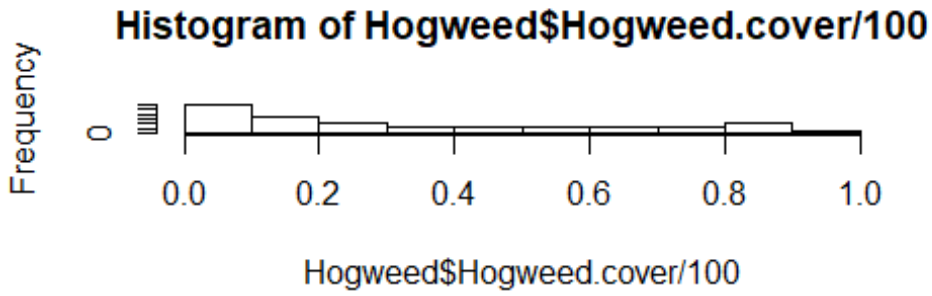
```r
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed, 4) # reading only the first 4 rows of data
```

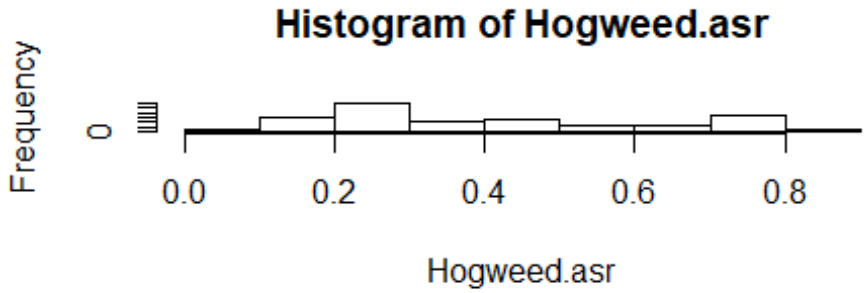
```
##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
```

```r
Hogweed.asr <- asin(sqrt(Hogweed$Hogweed.cover/100))*2/pi
plot(Hogweed$Hogweed.cover/100, Hogweed.asr)
```




```
par(mfrow=c(2,1))
hist(Hogweed$Hogweed.cover/100)
hist(Hogweed.asr)
```





ONE SAMPLE TEST

Indication: to test one sample mean against zero to verify whether there is a significant difference.

Parametric

T-TEST - One sample

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4) # reading only the first 4 rows
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```
# Usage:

t.test(BIOVEG$Basal.area, mu=0) # test against zero
```

```
##
##  One Sample t-test
##
## data:  BIOVEG$Basal.area
## t = 9.3933, df = 149, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.06618719 0.10145281
```

```
## sample estimates:
## mean of x
##   0.08382
```

Nonparametric

Wilcoxon Signed Rank Test

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4) # reading only the first 4 rows
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```
# Usage:

wilcox.test(BIOVEG$Basal.area, mu=0)
```

```
##
##  Wilcoxon signed rank test with continuity correction
##
## data:  BIOVEG$Basal.area
## V = 11325, p-value < 2.2e-16
## alternative hypothesis: true location is not equal to 0
```

TWO SAMPLE TEST

Indication: to compare two independent samples.

Independent Two samples

Parametric: T-TEST - Two sample:

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4) # reading only the first 4 rows
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```
# Testing whether vegetation type differ in tree basal area average

# usage:

t.test(BIOVEG$Basal.area[BIOVEG$type=="Aluvial"],

BIOVEG$Basal.area[BIOVEG$type=="Ombrofila"],alternative="two.sided")
```

```
##
##  Welch Two Sample t-test
##
## data:  BIOVEG$Basal.area[BIOVEG$type == "Aluvial"] and
BIOVEG$Basal.area[BIOVEG$type == "Ombrofila"]
## t = -0.9419, df = 61.174, p-value = 0.3499
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
##  -0.04934092  0.01774092
## sample estimates:
## mean of x mean of y
##    0.0599    0.0757

# Testing whether a vegetation type has significantly less tree basal
# than the other

t.test(BIOVEG$Basal.area[BIOVEG$type=="Aluvial"],
       BIOVEG$Basal.area[BIOVEG$type=="Ombrofila"], alternative="less",
       var.equal=TRUE)

##
##  Two Sample t-test
##
## data:  BIOVEG$Basal.area[BIOVEG$type == "Aluvial"] and
BIOVEG$Basal.area[BIOVEG$type == "Ombrofila"]
## t = -0.9419, df = 98, p-value = 0.1743
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf 0.01205505
## sample estimates:
## mean of x mean of y
##    0.0599    0.0757
```

Dependent samples

Indication: to compare two dependent samples.

Parametric: PAIRED T-TEST

```
t.test(BIOVEG$Basal.area[BIOVEG$type=="Aluvial"],
       BIOVEG$Basal.area[BIOVEG$type=="Ombrofila"],paired = TRUE)

##
##  Paired t-test
##
## data:  BIOVEG$Basal.area[BIOVEG$type == "Aluvial"] and
BIOVEG$Basal.area[BIOVEG$type == "Ombrofila"]
## t = -0.92713, df = 49, p-value = 0.3584
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.05004692  0.01844692
## sample estimates:
## mean of the differences
##                 -0.0158
```

Independent Two samples

Nonparametric: Wilcoxon Rank-Sum Test (or Mann-Whitney U-test)

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4)
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

Where y is numeric and A is a binary factor (presence or absence, 0 or 1, or similar) we can use the formula notation in wilcox.test

```
BIOVEG$Aluvial <- ifelse(BIOVEG$type=="Aluvial", 1, 0) # create binary
factor
wilcox.test(BIOVEG$Basal.area ~ BIOVEG$Aluvial)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  BIOVEG$Basal.area by BIOVEG$Aluvial
## W = 2754, p-value = 0.3121
## alternative hypothesis: true location shift is not equal to 0
```

independent 2-group Mann-Whitney U Test; here we specify the two groups to be compared using indexing (square brackets)

```
wilcox.test(BIOVEG$Basal.area[BIOVEG$type=="Aluvial"],
            BIOVEG$Basal.area[BIOVEG$type=="Ombrofila"], paired=FALSE)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  BIOVEG$Basal.area[BIOVEG$type == "Aluvial"] and
BIOVEG$Basal.area[BIOVEG$type == "Ombrofila"]
## W = 1385.5, p-value = 0.3519
## alternative hypothesis: true location shift is not equal to 0
```

Dependent (i.e. Paired) Two-Sample

Nonparametric: Wilcoxon Rank-Sum Test

Indication: the same function as the Wilcoxon test and two sample T-test, but addressing paired samples. This applies to data which has been collected on the same plots, for example, either on the same date or at different dates (e.g. comparison between basal area in 2010 and 2014. The basal area of 2014 in general is dependent on how much was accumulated in 2010).

Another test dataset describes the soil nutrient content of a number of different plots. The quantities of each nutrient (N, P, K) were derived from a single soil sample per plot.

```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed, 4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
```

When you have dependent samples, in “paired” insert TRUE. For independent samples insert FALSE.

```
# Usage:

wilcox.test(Hogweed$P_mg_100g, Hogweed$K_mg_100g, paired=TRUE)

##
##  Wilcoxon signed rank test with continuity correction
##
## data:  Hogweed$P_mg_100g and Hogweed$K_mg_100g
## V = 891, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

ANALYSIS OF VARIANCE

Indication: tests for differences between the means of more than two groups e.g. Diameter in treatment1, Diameter in treatment2, Diameter in treatment3).

Note: All Analyses below relate to variance, one-sample and two-sample. The majority of this analysis can be completed using the basic pre-loaded built-in “stats” package. To perform Dunn’s test (Post hoc), which follows Kruskal-Wallis,the “dunn.test” package must be installed.

Parametric tests: One-Way Anova

Note 2: transformations of the dependent variable, e.g. log, can be specified in the syntax of ANOVA and other functions directly.

```
# usage:

BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4)

##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
```

```
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```
aov(log(Diameter) ~ type, data=BIOVEG)
```

```
## Call:
##    aov(formula = log(Diameter) ~ type, data = BIOVEG)
##
## Terms:
##                       type Residuals
## Sum of Squares   1.590824 22.039904
## Deg. of Freedom         2       147
##
## Residual standard error: 0.3872097
## Estimated effects may be unbalanced
```

```
results <- aov(log(Diameter) ~ type, data=BIOVEG)
summary(results)
```

```
##              Df Sum Sq Mean Sq F value  Pr(>F)
## type          2  1.591  0.7954   5.305 0.00596 **
## Residuals   147 22.040  0.1499
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

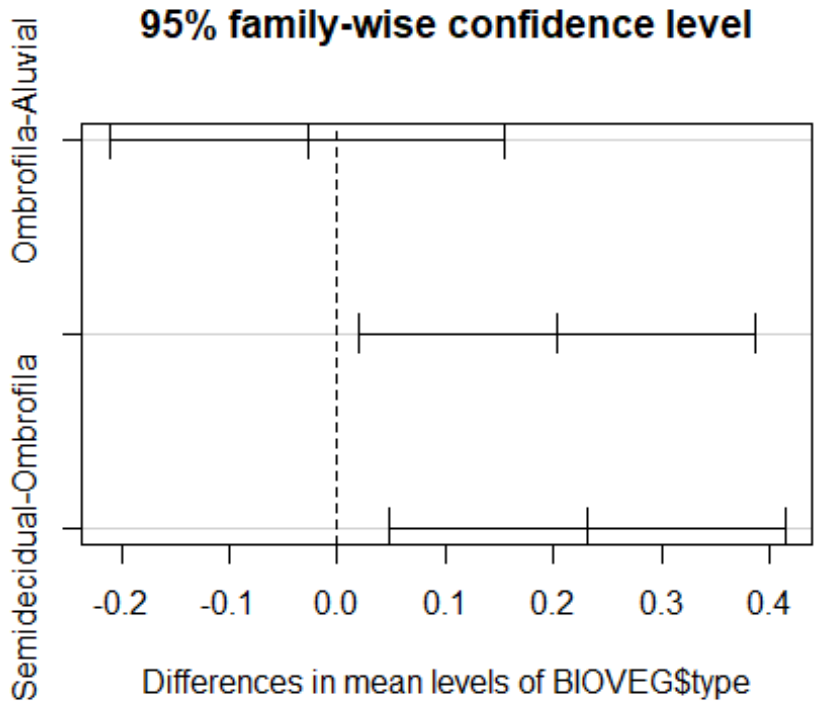
Tukey test (post hoc)

Indication: to identify when there is a significant difference between categories previously shown as overall result by parametric ANOVA.

```
# Usage:

a1 <- aov(log(BIOVEG$Diameter) ~ BIOVEG$type)
posthoc <- TukeyHSD(x=a1, 'BIOVEG$type', conf.level=0.95)
print(posthoc)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = log(BIOVEG$Diameter) ~ BIOVEG$type)
##
## $`BIOVEG$type`
##                               diff         lwr       upr     p adj
## Ombrofila-Aluvial      -0.0280405 -0.21139925 0.1553182 0.9303204
```

```
## Semidecidual-Aluvial    0.2030858  0.01972702 0.3864445 0.0259703
## Semidecidual-Ombrofila  0.2311263  0.04776753 0.4144850 0.0092752

plot(posthoc)
```



Non-Parametric tests: Kruskal-Wallis

Indication: use following a significant result in the Kruskal-Wallace test (a non-parametric analysis, the underlying distribution is not assumed in advance).

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4)

##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
```

```
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727

#Usage:

r4<- kruskal.test(BIOVEG$Basal.area ~ BIOVEG$type)
r4

##
##  Kruskal-Wallis rank sum test
##
## data:  BIOVEG$Basal.area by BIOVEG$type
## Kruskal-Wallis chi-squared = 10.899, df = 2, p-value = 0.004299
```

Dunn's Test (post hoc)

It performs the same function as a TukeyHSD test following ANOVA, but here is following Kruskal-Wallis.

install.packages("dunn.test")

```
# Usage:

library(dunn.test)

dunn.test(BIOVEG$Basal.area, g=BIOVEG$type, kw=TRUE, label=TRUE,
wrap=TRUE,
          table=TRUE, list=FALSE, rmc=FALSE, alpha=0.05)

##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 10.8989, df = 2, p-value = 0
##
##
##                             Comparison of x by group
##                                  (No adjustment)
## Col Mean-|
## Row Mean |    Aluvial   Ombrofil
## ---------+----------------------
## Ombrofil |   0.694041
##          |     0.2438
##          |
```

```
## Semideci |  -2.448136  -3.142178
##          |    0.0072*    0.0008*
##
## alpha = 0.05
## Reject Ho if p <= alpha/2

# when the command line extends beyond more than one row in the text, be
sure  to select all rows to run the complete command.
```

Independence test - Chi-squared

The Chi-squared test is one of the most commonly used tests in biology and biomedicine because it can test if one variable is dependent or not on a certain category. In the example below we use the phenology stages of a species and the abundance of individuals counted at each stage over 4 months (Feb, Mar, Apr, May). Our aim is to check if the abundances at each stage are dependent on the months. In case Chi-squared is significant and, thus, shows dependence, you need to split the table into two in a 2 x 2 format and run the test again. This post-hoc test is called: Partition of Chi-squared. Further Information about this test is widely available online.

install and load the MASS package:

```
# install.packages("MASS")
library(MASS)
```

To build a contingency from columns of a data table you can use. For example:

```
# tbl <- table(Data$flowering, Data$fruits, Data$Month)
```

Here, we will just create a contingency table "manually":

```
tbl <- rbind(c(7,1,3,9), c(8,5,2,0))
colnames(tbl) <- c("Feb", "Mar", "Apr", "May")
rownames(tbl) <- c("Flowering", "Fruits")
tbl

##           Feb Mar Apr May
## Flowering   7   1   3   9
## Fruits      8   5   2   0

# Usage:

chisq.test(tbl) # normal p-value of Chi-squared test

## Warning in chisq.test(tbl): Chi-squared approximation may be incorrect

##
##  Pearson's Chi-squared test
##
```

```
## data:  tbl
## X-squared = 11.453, df = 3, p-value = 0.009513
```

```
chisq.test(tbl, simulate.p.value=TRUE) # simulated p-value (Monte Carlo test)
```

```
##
##  Pearson's Chi-squared test with simulated p-value (based on 2000
##  replicates)
##
## data:  tbl
## X-squared = 11.453, df = NA, p-value = 0.004498
```

The outcome showed a message about the robustness of the Chi-squared appproximation. Thus, first of all be sure about the quality of the dataset you are using for such analyses.

```
# "Posthoc" test comparing only two month

tbl.1 <- tbl[,c("Mar", "Apr")]
tbl.1
```

```
##           Mar Apr
## Flowering   1   3
## Fruits      5   2
```

```
chisq.test(tbl.1)
```

```
## Warning in chisq.test(tbl.1): Chi-squared approximation may be
incorrect

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tbl.1
## X-squared = 0.73661, df = 1, p-value = 0.3907
```

CORRELATION ANALYSIS

Pearson's correlation test

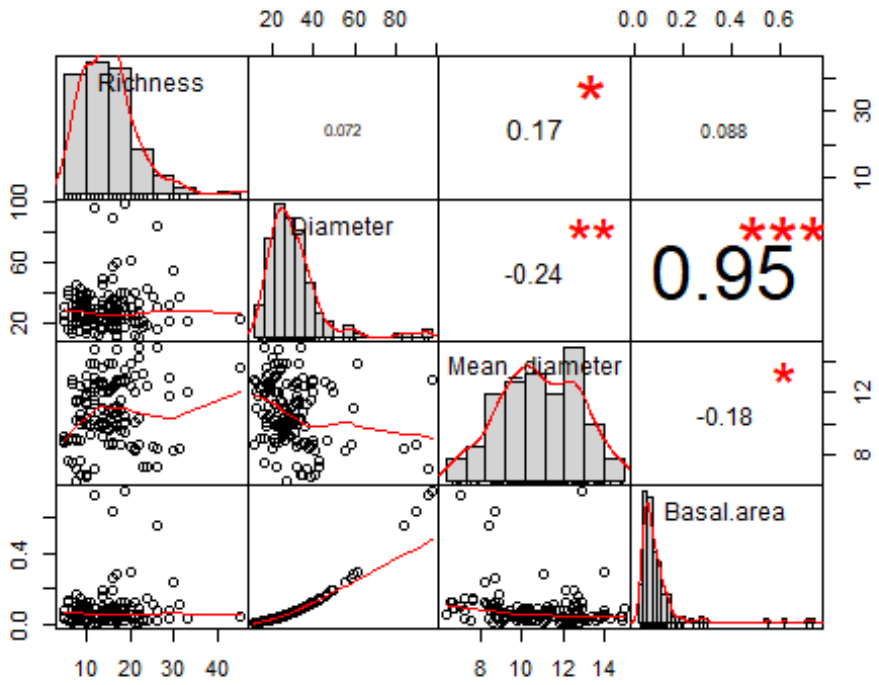
use PerformanceAnalytics package

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4)
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
```

```
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```r
# Usage:

# install.packages("PerformanceAnalytics")
library(PerformanceAnalytics)
chart.Correlation(BIOVEG[,c(5, 6, 7, 8)])
```



```
correlacao<- cor(BIOVEG[,c(5, 6, 7, 8)])
round(correlacao, digits=2)

##               Richness Diameter Mean_diameter Basal.area
## Richness          1.00     0.07          0.17       0.09
## Diameter          0.07     1.00         -0.24       0.95
## Mean_diameter     0.17    -0.24          1.00      -0.18
## Basal.area        0.09     0.95         -0.18       1.00
```

Correlation test between just two variables:

```
## use the default R function "cor.test"

cor.test(BIOVEG$Richness, BIOVEG$Basal.area)

##
##  Pearson's product-moment correlation
##
## data:  BIOVEG$Richness and BIOVEG$Basal.area
## t = 1.0703, df = 148, p-value = 0.2862
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.07365322  0.24447057
## sample estimates:
##       cor
## 0.08764283
```

The number between parentheses are the column numbers of your data file (e.g. Excel file). This is how you select the variables whose correlation you want to check.

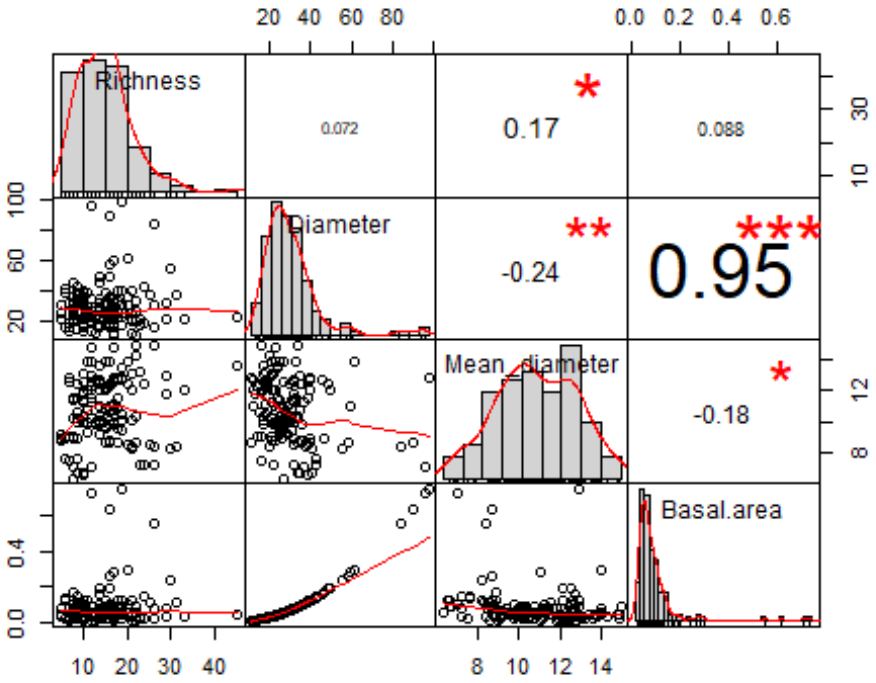
REMEMBER: correlation just shows you if one data value increases/ decreases with the other, but it does not say that they are dependent on each other. To check dependence between variables you need to test their relation and for that there are regression models. However, even regression models do not prove that there is a causal relationships between the variables. Correlation and regression cannot discern between real causal effects and spurious correlations (that are caused by a third variable/ other variables).

Spearman's correlation test

There is a perpetual discussion among statisticians about whetherPearson analysis assumes strictly normality, but a large majority of high impact literature continues to use it, even in non-normal cases. Some researchers recommend Spearman, but, for a number of reasons, its application is more limited than Pearson. Please read about this subject further if it applies to your analysis.

If you want to use Spearman rank correlation just use the 'method' argument:

```
chart.Correlation(BIOVEG[,c(5, 6, 7, 8)], method="spearman")
```




```
correlacao<- cor(BIOVEG[,c(5, 6, 7, 8)], method="spearman")
round(correlacao, digits=2)

##                Richness Diameter Mean_diameter Basal.area
## Richness           1.00     0.00          0.16       0.00
## Diameter           0.00     1.00         -0.29       1.00
## Mean_diameter      0.16    -0.29          1.00      -0.29
## Basal.area         0.00     1.00         -0.29       1.00
```

Correlation test between just two variables:

```
## use the default R function "cor.test"

cor.test(BIOVEG$Richness, BIOVEG$Basal.area, method="spearman")

## Warning in cor.test.default(BIOVEG$Richness, BIOVEG$Basal.area, method
=
## "spearman"): Cannot compute exact p-value with ties

##
##  Spearman's rank correlation rho
##
## data:  BIOVEG$Richness and BIOVEG$Basal.area
## S = 563580, p-value = 0.981
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##         rho
## -0.00196546
```

Sometimes Spearman ranking is not able to precisely compute p-values. Thus, an option is also test Pearson and provide the results of both.

VIF - Variance Inflation Factor

Among the most robust approaches used nowadays, the variance inflation factor (VIF) is the quotient of the variance in a model with multiple terms (predictors) by the variance of a model with one term alone. This is a great method to quantify the severity of multicollinearity in an ordinary least squares regression analysis (e.g. LM, LME, GLS, etc). VIF provides an index that returns an outcome measuring how much the variance (the square of the estimate's standard deviation) of an estimated model coefficient is increased because of collinearity.

In Ecology, an usual threshold to consider collinearity among predictors acceptable is VIF < 0.5

For further details and information on the statistical backbone and potential of VIF, please read the great revision and simulations of Dormann et al. 2013 and Zurr et al.2010.

Dormann et al. Collinearity: A review of methods to deal with it and a simulation study evaluating their performance. Ecography, 36(1): 27-46, 2013.

Zuur AF, Ieno EN & Elphick CS. A protocol for data exploration to avoid common statistical problems. Methods in Ecology and Evolution 1: 3-14, 2010.

We use the function vif of the package car to calculate the variance inflation factor:

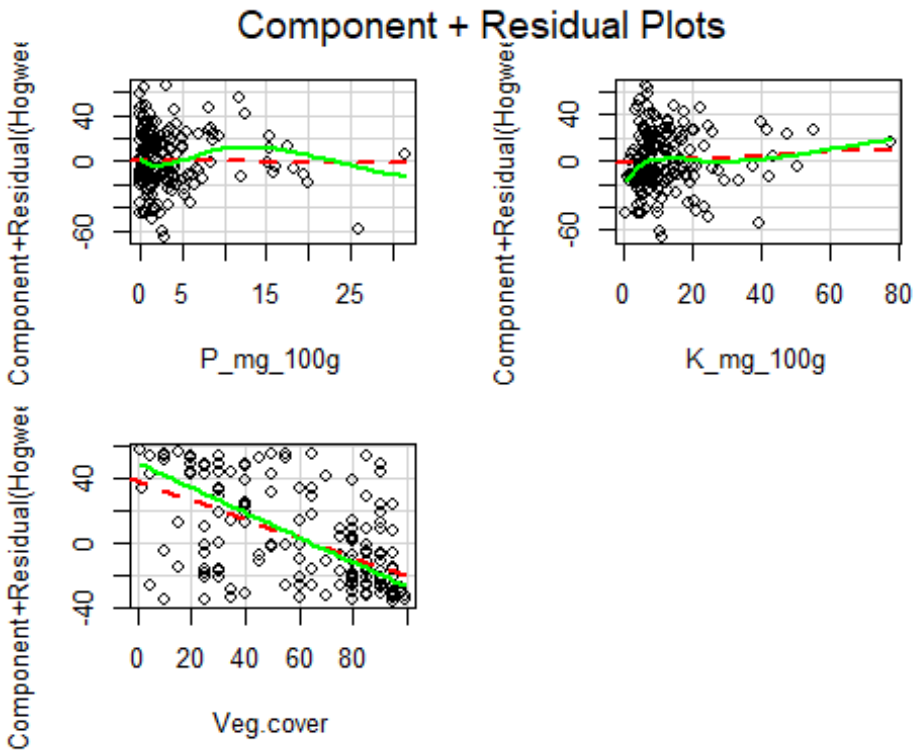
```
# install.packages("car")
library(car)


BIODIV.vif<- lm(Species.richness ~ P_mg_100g + Hogweed.cover + N_perc +
                  Habitat.type, data=Hogweed)

vif(BIODIV.vif)

##                    GVIF Df GVIF^(1/(2*Df))
## P_mg_100g      1.093411  1        1.045663
## Hogweed.cover 1.293545  1        1.137341
## N_perc         1.122377  1        1.059423
## Habitat.type   1.434640  4        1.046147
```

The outcome shows that all predictors have VIF < 5, thus they can be kept together in the same model.

Diagnostic for linearity

To check for linear relationships among dependent (Y) and predictor variables (X) we can use the function "crPlots" of the package "car". This function returns a graph that bases the diagnostic on the residuals of the model. The more closely the two lines (solid and dashed) fit each other, the more linear is the relationship among Y and X.

```
library(car) # graphical diagnostic for linearity

Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34

DBH<- glm(Hogweed.cover ~ P_mg_100g + K_mg_100g + Veg.cover,
data=Hogweed,
                                                    family="gaussian")

crPlots(DBH, col.lines=c("red", "green"))
```



In the diagnostic we can see that the predictor "Veg.cover" shows the best, and an acceptable, fit for linearity. This is indicated by the close fit between the red line (best fit) and green line. Conversely, the linearity of "P_mg_100g" and "K_mg_100g" deviates considerably.

REGRESSION

Indication: Regression analysis is a statistical approach for estimating the relationships between a dependent variable (axis Y and commonly called the outcome variable') and one or more independent variables (predictors).There are linear and nonlinear regression models, although the linear ones are the most common form of used regression analysis.

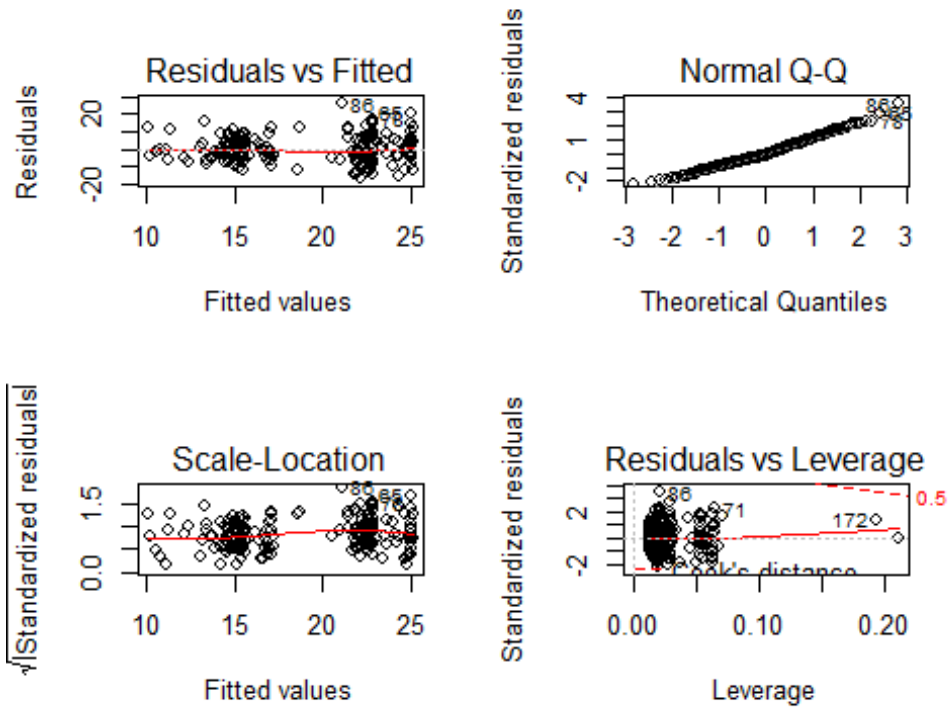
LM (Linear Model)

This is the most famous type of regression of analysis and relies in the assumptions of the Ordinary least squares: normal distribution, homoscedasticity, linearity between, predictors and dependent variable, weak multicollinearity among predictors, independence of errors and residuals not correlated.

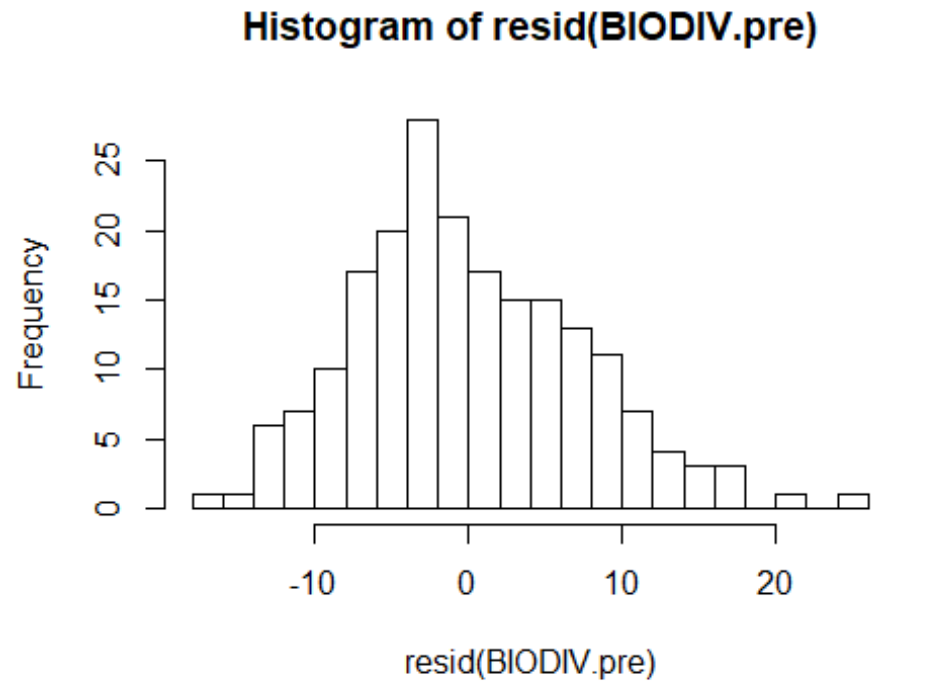
```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)
```

```
##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34

# install.packages("car")
library(car) # Anova function

# Usage:
# Model:

BIODIV.pre<- lm(Species.richness ~ P_mg_100g + Habitat.type,
data=Hogweed)

summary(BIODIV.pre)

##
## Call:
## lm(formula = Species.richness ~ P_mg_100g + Habitat.type, data =
Hogweed)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -16.117  -5.058  -1.152   4.912  25.871
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               25.1319     1.2887  19.503  < 2e-16 ***
## P_mg_100g                 -0.2768     0.1170  -2.366 0.018946 *
```

```
## Habitat.typeruderal.grass  -2.2314     1.6361  -1.364 0.174184
## Habitat.typetall.herbs     -9.4813     1.5449  -6.137  4.6e-09 ***
## Habitat.typewasteland      -2.2797     2.2731  -1.003 0.317153
## Habitat.typewoodland       -7.8197     2.1460  -3.644 0.000344 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.564 on 195 degrees of freedom
## Multiple R-squared:  0.2505, Adjusted R-squared:  0.2313
## F-statistic: 13.04 on 5 and 195 DF,  p-value: 5.965e-11

# Anova of the model using the package car:
Anova(BIODIV.pre)

## Anova Table (Type II tests)
##
## Response: Species.richness
##               Sum Sq  Df F value    Pr(>F)
## P_mg_100g      320.4   1  5.5995   0.01895 *
## Habitat.type  3060.2   4 13.3714 1.199e-09 ***
## Residuals    11156.9 195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Anova of the model using the built-in R function:
BIODIV.lm.aov <- anova(BIODIV.pre, test="F")
BIODIV.lm.aov

## Analysis of Variance Table
##
## Response: Species.richness
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## P_mg_100g      1   668.9  668.94  11.692 0.0007644 ***
## Habitat.type   4  3060.2  765.04  13.371 1.199e-09 ***
## Residuals    195 11156.9   57.21
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Residuals
x11(width=12, height=12)
par(mfrow=c(2,2))
plot(BIODIV.pre)
```

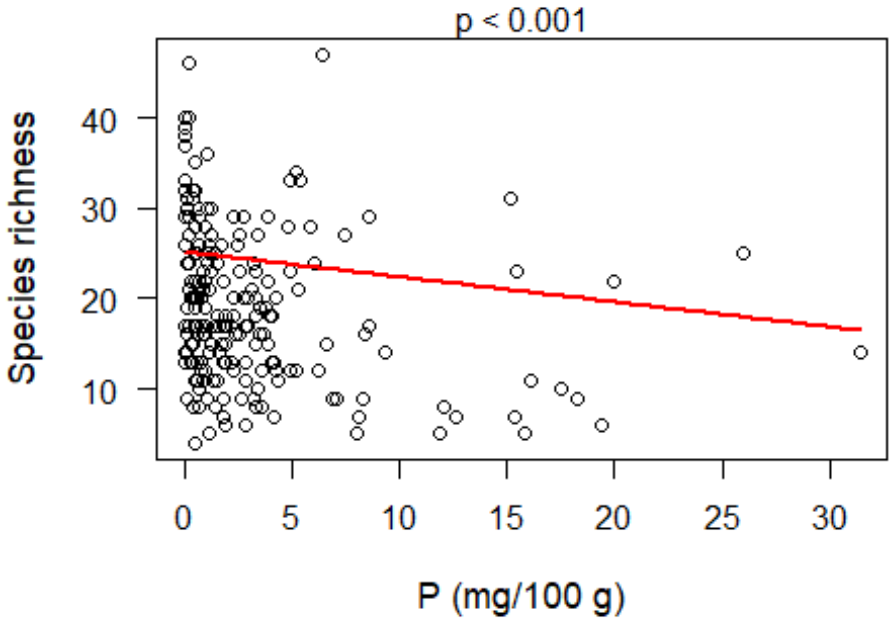



```
hist(resid(BIODIV.pre),breaks=20)
```




```
# Scatterplot graph:
```

```
b.0.BIODIV<- BIODIV.pre$coefficients[1]
b.1.BIODIV<- BIODIV.pre$coefficients[2]
plot(Hogweed$Species.richness ~ Hogweed$P_mg_100g, las=1,
     ylab="Species richness", xlab="P (mg/100 g)", cex.lab=1.1)
curve(b.0.BIODIV + b.1.BIODIV*x, add=TRUE, col="red", lwd=2)
mtext(ifelse(BIODIV.lm.aov[1,5]<0.001, "p < 0.001",
      paste("p = ", round(BIODIV.lm.aov[1,5],3))))
```



To construct the curve (or line) in this LM example, the dependent variable, Species richness, is on the y axis and the metric predictor variable, phosphorous, is on the x axis. The regression line is calculated using the intercept (b.0.BIODIV) plus the estimate of phosphorous (b.1.BIODIV) multiplied by x. The insertion of the P-value of ANOVA is placed according to the location of values in the ANOVA output. That is, the "P_mg_100g" is being tested in relation to "Species.richness" and it's located in the first row of the ANOVA output and its P-value on the 5th column in this row. Thus: BIODIV.lm.aov[1,5]. If you have done any data transformation before (log, square …) you must include it in the syntax of the scatterplot, e.g. log(Hogweed$Species.richness). If the variable include zeros, add a constant, e.g. +1, before taking the log.

GLM (Generalized Linear Models)

Note: in GLM you must specify the distribution family of the dependent variable. Thus:

- Gaussian (normal) distribution: Continuous data (e.g. body weight, basal area, height). If the residuals don't satisfactorily fit the Gaussian distribution, you can try Gamma distribution. BUT, first of all read about both kinds of distribution before you decide which to use . Gamma doesn't accept negative values.

- Poisson: count data (e.g. species richnees). First check if the Poisson model shows overdispersion. If it does, try "quasipoisson" distribution.

- Binomial: this distribution is often used to model the number of successes
(1) or failure (0), but also presence (1) or absence (0), in a sample. Furthermore, data regarding percentage or proportion in a sample.
- Negative BinomiaL: count data in case of overdispersion in "poisson" or "quasipoisson".

A Poisson or Binomial distribution model might be likely to show under- or overdispersion, indicating that your model fit is not satisfactory. After running the "summary", check for evidence of overdispersion. You do this by checking residuals and degrees of freedom: residual deviance/degrees of freedom << 1 (e.g. < 0.7) indicate underdispersion, while residual deviance/degrees of freedom >> 1 (e.g. > 1.3) indicate overdispersion. In such cases, you need to use "quasipoisson" or "quasibinomial" distributions instead. The model will then estimate a dispersion parameter that adjusts the variation in the data to the fixed variation of the Poisson or Binomial distribution. If you are analyzing count data (integers), you can also use the Negative Binomial distribution instead of "quasipoisson". To use Negative Binomial distribution, you use the function "glm.nb", which is the function for negative binomial glm from the package MASS.

To use Negative Binomial distribution, you just insert like this example: "glm.nb" is the function for negative binomial glm from the package MASS.

```
# install.packages(MASS)
library(MASS) # For Negative Binomial GLM

Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
```

```
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34

riqueza.glm<- glm.nb(Species.richness ~ P_mg_100g + Land.use,
data=Hogweed)
summary(riqueza.glm)

##
## Call:
## glm.nb(formula = Species.richness ~ P_mg_100g + Land.use, data =
Hogweed,
##     init.theta = 7.646689121, link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.5831  -0.8338  -0.1544   0.5509   2.9755
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           3.258909   0.085480  38.125  < 2e-16 ***
## P_mg_100g            -0.018549   0.006899  -2.689 0.007176 **
## Land.useMAINTENANCE -0.182235   0.111953  -1.628 0.103570
## Land.useNONE         -0.322205   0.092300  -3.491 0.000482 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(7.6467) family taken to be
1)
##
##     Null deviance: 230.83  on 200  degrees of freedom
## Residual deviance: 206.28  on 197  degrees of freedom
## AIC: 1402.9
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  7.65
##           Std. Err.:  1.08
##
##  2 x log-likelihood:  -1392.889
```

```r
Anova(riqueza.glm)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Species.richness
##           LR Chisq Df Pr(>Chisq)
## P_mg_100g    7.676  1   0.005596 **
## Land.use    13.723  2   0.001047 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

GLM - Poisson:

```r
riqueza.glm<- glm(Species.richness ~ P_mg_100g + Land.use, data=Hogweed,
                  family="poisson")
summary(riqueza.glm)
```

```
##
## Call:
## glm(formula = Species.richness ~ P_mg_100g + Land.use, family =
"poisson",
##     data = Hogweed)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.1479  -1.5324  -0.3102   1.0464   6.0723
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           3.263022   0.041535  78.562  < 2e-16 ***
## P_mg_100g            -0.020470   0.004104  -4.988 6.11e-07 ***
## Land.useMAINTENANCE -0.181567   0.055790  -3.254  0.00114 **
## Land.useNONE         -0.320027   0.045601  -7.018 2.25e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 775.16  on 200  degrees of freedom
## Residual deviance: 686.47  on 197  degrees of freedom
## AIC: 1636.8
##
## Number of Fisher Scoring iterations: 4
```

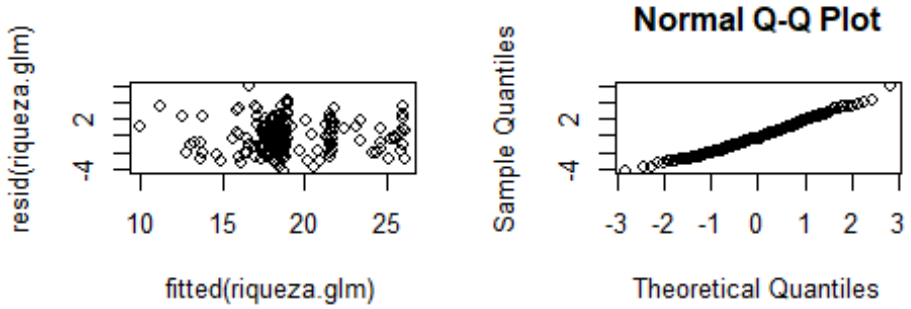
```r
library(car)
riqueza.aov <- Anova(riqueza.glm)
riqueza.aov
```

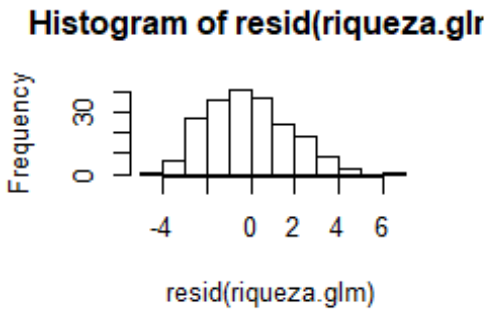
```
## Analysis of Deviance Table (Type II tests)
##
## Response: Species.richness
```

```
##           LR Chisq Df Pr(>Chisq)
## P_mg_100g   27.195  1  1.839e-07 ***
## Land.use    49.816  2  1.523e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

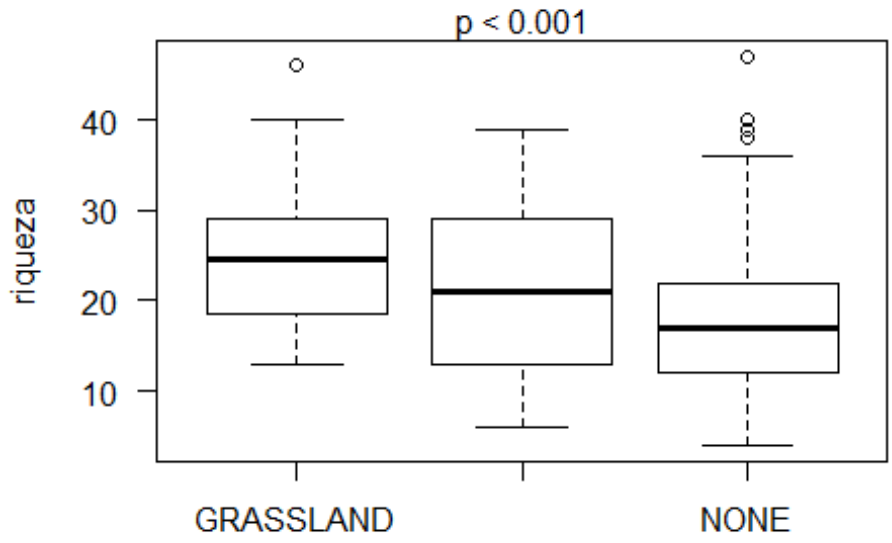
Checking the residuals and see if it does fit good to the model

```
# residuals

par(mfrow=c(2,2))
plot(fitted(riqueza.glm), resid(riqueza.glm))
qqnorm(resid(riqueza.glm))
hist(resid(riqueza.glm))
```

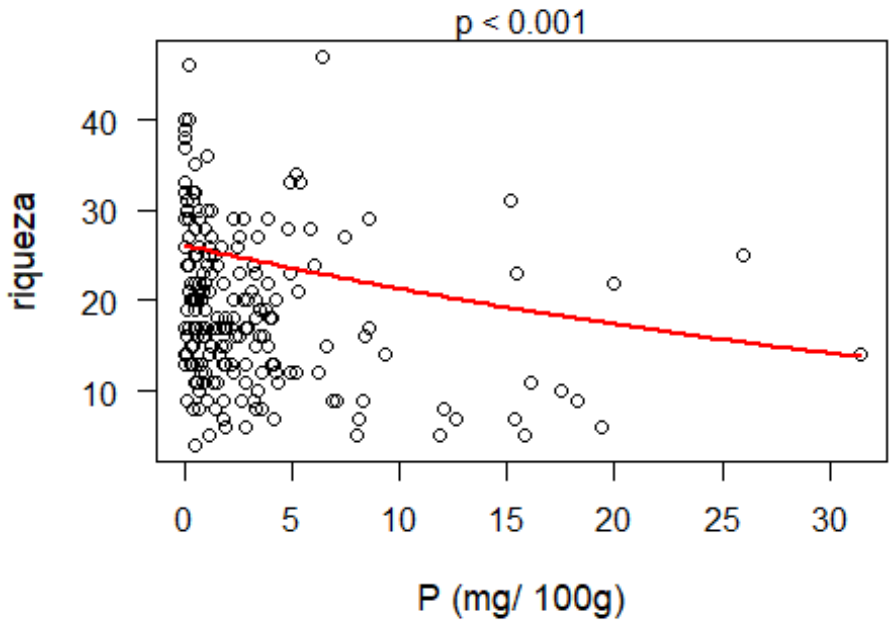





```
# Boxplot

par(mfrow=c(1,1))
boxplot(Hogweed$Species.richness ~ Hogweed$Land.use, las=1,
ylab="riqueza")
mtext(ifelse(riqueza.aov[2,3]<0.001, "p < 0.001",
paste("p = ", round(riqueza.aov[2,3],3))))
```




```r
# Scatterplot graph:

b.0.riqueza<- riqueza.glm$coefficients[1]
b.1.riqueza<- riqueza.glm$coefficients[2]
plot(Hogweed$Species.richness ~ Hogweed$P_mg_100g, las=1, ylab="riqueza",
     xlab="P (mg/ 100g)", cex.lab=1.1)
curve(exp(b.0.riqueza + b.1.riqueza*x), add=TRUE, col="red", lwd=2)
mtext(ifelse(riqueza.aov[1,3]<0.001, "p < 0.001",
      paste("p = ", round(riqueza.aov[1,3],3))))
```



Note 3.: the graph construction follows the principles described with LM previously. If you have used a transformation or a link function (other than "=") in the model, you can include it in the scatterplot syntax, e.g.log (Species.richness). But if you want to plot the original values of the dependent variable, you can do that, too, you just need to back-transform the model predictions to the original scale. In this case you need to transform from the log-scale (used in the Poisson model) to the untransformed species richness used in the scatterplot. That's why we need the "exp" function in the example above.

GLMM (Generalized Linear Mixed Models)

Note 1: Like GLM, the GLMM also require to specify the distribution family (e.g. Poisson), but they don't accept "quasipoisson" or "quasibinomial". If poisson doesn't fit the data because of overdispersion, try negative binomial distribution as explained in GLM section. The syntax is the same: just insert the argument "nb". Example: basalarea1<- glmer.nb(…, Do not write family name).

GLMM indication: when you have pseudoreplicates. It's very common in ecological field research to use subplots within each site and these subplots cannot be considered as real replicates. So, a mixed model is appropriate to treat this situation. The definition of what variable is a fixed effect (e.g. in the example below it is "Hogweed.cover" (cover of giant hogweed) and "Habitat.type") and what is random effect (e.g. in the example below "Study.area") depends on your research questions and study design. Usually, design factors, such as "block" or "study area" will be

random effects, and the variables that you are really interested in (treatments, soil parameters etc.) will be fixed effects. BUT, read about random and fixed effects before constructing your model.

When the command line doesn't end in the same row, but continues in the next one (like the first command of the GLMM example below), select and press the command of both two lines together. We broke some command lines here to fit in the R script style.

```
### GLMM usage:

Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34

library(lme4) # glmer

## Loading required package: Matrix

library(car) # Anova

Richness <- glmer(Species.richness ~ scale(Hogweed.cover) + Habitat.type
+
                  (1|Study.area), data=Hogweed, family="poisson")
# Here, the metric predictor variable (Hogweed.cover) was scaled to avoid
# problems in the calculation of the model
```

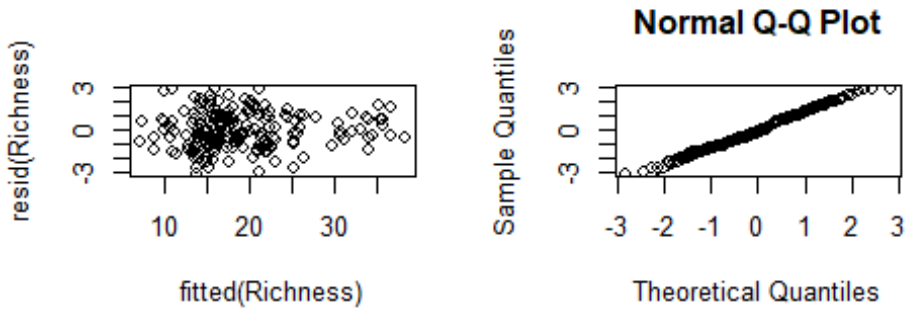
```r
summary(Richness)
```

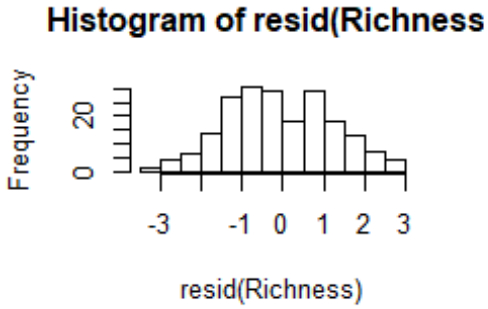
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Species.richness ~ scale(Hogweed.cover) + Habitat.type + (1 |
##     Study.area)
##    Data: Hogweed
##
##      AIC      BIC   logLik deviance df.resid
##   1352.4   1375.5   -669.2   1338.4      194
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.6389 -0.9970 -0.1876  0.9007  3.3432
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  Study.area (Intercept) 0.08313  0.2883
## Number of obs: 201, groups:  Study.area, 20
##
## Fixed effects:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 3.17346    0.07660  41.429  < 2e-16 ***
## scale(Hogweed.cover)       -0.07988    0.02052  -3.892 9.94e-05 ***
## Habitat.typeruderal.grass -0.13191    0.05530  -2.385   0.0171 *
## Habitat.typetall.herbs     -0.41489    0.05828  -7.118 1.09e-12 ***
## Habitat.typewasteland      -0.18083    0.07605  -2.378   0.0174 *
## Habitat.typewoodland       -0.50020    0.07356  -6.800 1.05e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) sc(H.) Hbtt.typr. Hbtt.typt. Hbtt.typws
## scl(Hgwd.c)  0.183
## Hbtt.typrd. -0.424 -0.342
## Hbtt.typtl. -0.415 -0.394  0.567
## Hbtt.typwst -0.279  0.057  0.416      0.316
## Hbtt.typwdl -0.281 -0.042  0.354      0.412      0.269
```

```r
Richness.aov <- Anova(Richness, Type="II")
Richness.aov
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Species.richness
##                         Chisq Df Pr(>Chisq)
## scale(Hogweed.cover) 15.149  1  9.937e-05 ***
## Habitat.type         76.133  4  1.147e-15 ***
```

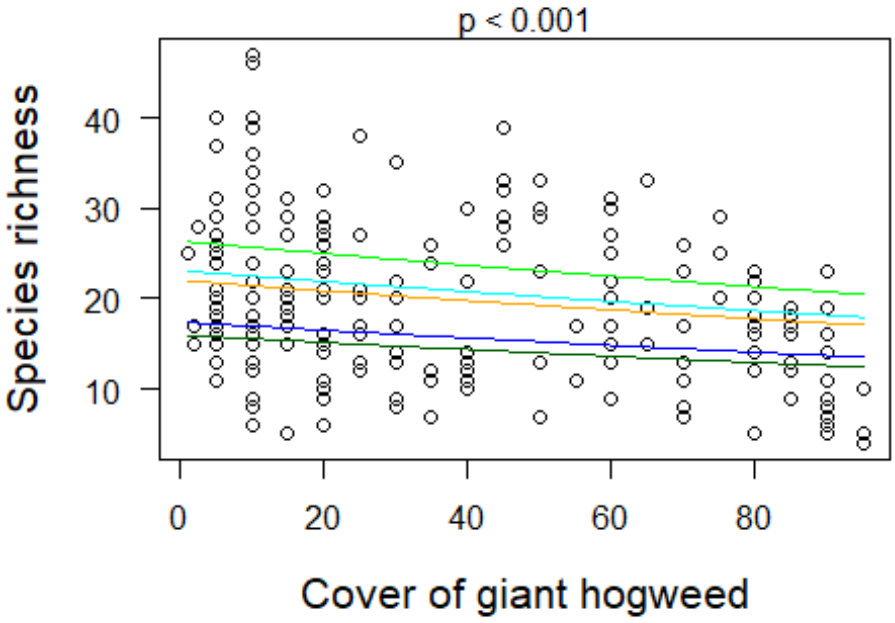
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Residuals

par(mfrow=c(2,2))
plot(fitted(Richness), resid(Richness))
qqnorm(resid(Richness))
qqline(resid(Richness))
hist(resid(Richness))
```






```
### Scatterplots ###

# With the syntax below you can construct graphs of the relation of the
depenent
# variable with a metric predictor variable. This can be done for all
levels of
# the categorical predictor variable (here: Habitat.type). To construct
the graph
# you can just select and run all of the command lines below.

b0<- coef(summary(Richness))[1,1] # intercept (habitat "agricultural
grassland")
b1<- coef(summary(Richness))[2,1] # estimate of hogweed cover
b2<- coef(summary(Richness))[3,1] # estimate of habitat "ruderal
grassland"
b3<- coef(summary(Richness))[4,1] # estimate of habitat "tall herbs"
```

```r
b4<- coef(summary(Richness))[5,1] # estimate of habitat "wasteland"
b5<- coef(summary(Richness))[6,1] # estimate of habitat "woodland"

x11(width=14, height=12)

plot(Hogweed$Species.richness ~ Hogweed$Hogweed.cover, las=1,
     ylab="Species richness", xlab="Cover of giant hogweed", cex.lab=1.3)


# The model that we apply here used poisson distribution which, by
default,
# includes a log-link (i.e. log transformation of the dependent
variable).
# Thus, we need to use exp() to back-transform the values predicted by
the model,
# to the original values of species richness.


mean <- mean(Hogweed$Hogweed.cover)
sd <- sd(Hogweed$Hogweed.cover)

curve(exp(b0 + b1*(x-mean)/sd), add=TRUE, col="green") # curve for
agricultural grassland
curve(exp(b0 + b2 + + b1*(x-mean)/sd), add=TRUE, col="cyan") # curve for
ruderal grassland
curve(exp(b0 + b3 + + b1*(x-mean)/sd), add=TRUE, col="blue") # curve for
tall-herb stands
curve(exp(b0 + b4 + + b1*(x-mean)/sd), add=TRUE, col="orange") # curve
for wasteland
curve(exp(b0 + b5 + + b1*(x-mean)/sd), add=TRUE, col="darkgreen") # curve
for woodland
mtext(ifelse(Richness.aov[1,3]<0.001, "p < 0.001",
      paste("p = ", round(Richness.aov[1,3],3))))
```



Note 2: the graph construction follows the principles previously described for LM. For further details type the following into your internet search engine: “how construct scatterplots for Mixed models - GLMM? If you have transformed your data, include it in the scatterplot syntax, e.g. log(Data.h3$area basal+1), OR back-transform the predicted values to the original scale (as in the previous example).

GLMM-PQL (Fit GLMM using Penalized Quasi-Likelihood - PQL)

This type of GLMM is used when you need to compute a mixed model for a non-normal dispersion (e.g. poisson, binomial) , it is necessary to use a generalized mixed model that allows the inclusion of correlation structures to account for spatial or temporal effects in the random effects and residuals of the model. The usual functions lmer and glmer of the package lme4 do not allow you to include such correlation structures. Thus, you can adjust Partial Quasi-likelihoods for glmm with the function glmmPQL of the package MASS. The most used spatial and temporal correlation structures for a wide range of situations are, respectively, corExp (exponential spatial correlation structure) and corAR1 (correlation structure of first order for time series) of the package nlme.

The glmmPQL approximates a quasi-likelihood by iterative fitting of (re)weighted linear mixed effects (lme) models based on the fit of Glm. Thus, it estimates the fixed effects parameters by fitting a Glm with its incorporated correlation (variance-covariance) structure. This constructs an Lme model and refits it to re-estimate the variance-covariance structure, utilizing the variance structure from the previous Glm.

The iterations continue until the fit improvement is below a threshold or a defined number of iterations has occurred. Therefore, this approach accommodates heterogeneity and spatial/temporal autocorrelation in the model. However, it worth being aware of the fit of PQL generalization for Poisson models, since it commonly performs poorly. If your performance with glmmPQL is poor using the Poisson model, take a look at glmmTMB and glmmADMB packages and functions.For more information on usage of glmmPQL, other models and correlation structures to account for spatial and temporal autocorrelation of residuals, read Dormann et al. (2007).

GLMM - PQL: Temporal autocorrelation

Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".") head(Hogweed)

install.packages("MASS") install.packages("nlme") install.packages("lme4")

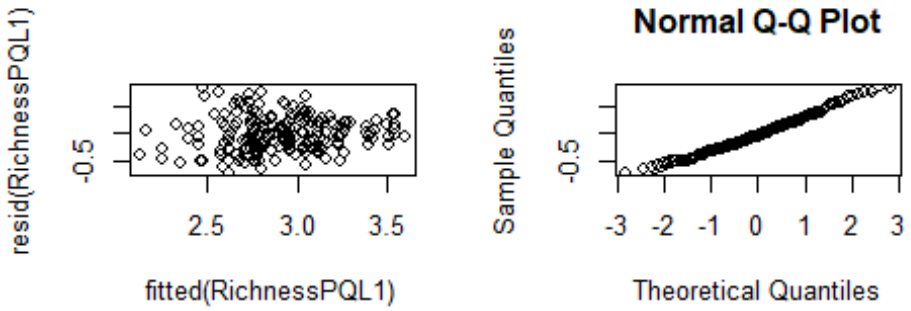
```
library(MASS) # PQL Estimation Of Generalized Linear Mixed Models
(glmmPQL)
library(nlme) # corAR1 (autocorrelation structure of order 1.
              # For temporal autocorrelation correction)
library(lme4) # glmer

RichnessPQL1 <- glmmPQL(Species.richness ~ scale(Hogweed.cover) +
                          Habitat.type, random=~1| Study.area,
data=Hogweed,
                        family="poisson", correlation=corAR1())

summary(RichnessPQL1)

## Linear mixed-effects model fit by maximum likelihood
##  Data: Hogweed
##    AIC BIC logLik
##     NA  NA     NA
##
## Random effects:
##  Formula: ~1 | Study.area
##         (Intercept) Residual
## StdDev:     0.25502 1.360019
##
## Correlation Structure: AR(1)
##  Formula: ~1 | Study.area
##  Parameter estimate(s):
##      Phi
## 0.212907
## Variance function:
##  Structure: fixed weights
##  Formula: ~invwt
## Fixed effects: Species.richness ~ scale(Hogweed.cover) + Habitat.type
##                                Value  Std.Error  DF  t-value p-value
```

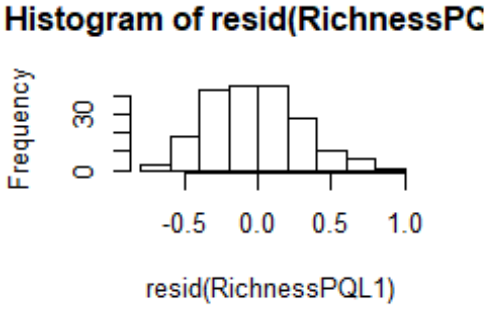
```
## (Intercept)                3.179347 0.08077289 176 39.36156  0.0000
## scale(Hogweed.cover)      -0.084974 0.02702220 176 -3.14458  0.0020
## Habitat.typeruderal.grass -0.113853 0.07240569 176 -1.57243  0.1176
## Habitat.typetall.herbs    -0.418886 0.07631617 176 -5.48882  0.0000
## Habitat.typewasteland     -0.154868 0.10070796 176 -1.53779  0.1259
## Habitat.typewoodland      -0.471932 0.09683872 176 -4.87338  0.0000
##  Correlation:
##                           (Intr) sc(H.) Hbtt.typr. Hbtt.typt.
Hbtt.typws
## scale(Hogweed.cover)       0.240
## Habitat.typeruderal.grass -0.523 -0.343
## Habitat.typetall.herbs    -0.507 -0.409  0.561
## Habitat.typewasteland     -0.337  0.055  0.408      0.299
## Habitat.typewoodland      -0.357 -0.072  0.368      0.440       0.260
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -1.9455147 -0.7636449 -0.1452796  0.6615598  2.3691106
##
## Number of Observations: 201
## Number of Groups: 20
```

```
class(RichnessPQL1)="lme"
anova(object=RichnessPQL1,test="Chisq")
```

```
##                      numDF denDF  F-value p-value
## (Intercept)              1   176 2142.125  <.0001
## scale(Hogweed.cover)     1   176   29.293  <.0001
## Habitat.type             4   176   10.733  <.0001
```

```
# Residuals

par(mfrow=c(2,2))
plot(fitted(RichnessPQL1), resid(RichnessPQL1))
qqnorm(resid(RichnessPQL1))
qqline(resid(RichnessPQL1))
hist(resid(RichnessPQL1))
```



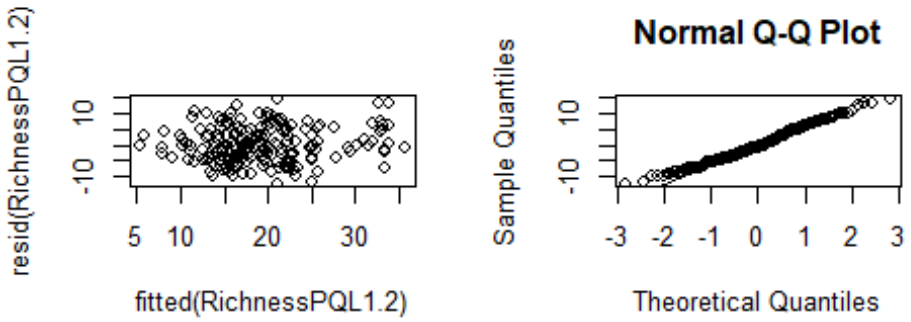


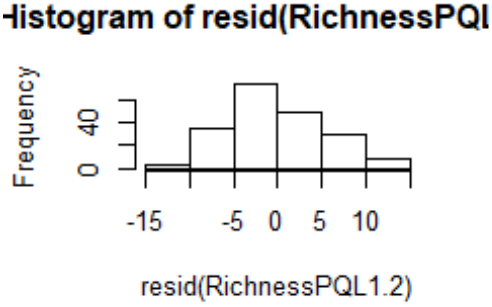
Note: Fitting a "lme" class for the glmmPQL is not recommended as the most appropriate way to acquire p-values from anova of the model above. Here we can compute a lme model for the same variables of the glmmPQL model and compare the outcomes of the anova of both models. Despite lme requiring data to conform to assumptions of normality, we can use this model for a dataset where Y is discrete (Poisson), once the residual fit is as close as possible to normal, which were already complied using the residuals of glmmPQL model.. Let's see.

```
RichnessPQL1.2 <- lme(Species.richness ~ scale(Hogweed.cover) +
                        Habitat.type, random=~1| Study.area,
                        data=Hogweed, correlation = corAR1())

summary(RichnessPQL1.2)
```

```
## Linear mixed-effects model fit by REML
##  Data: Hogweed
##        AIC      BIC    logLik
##   1316.934 1346.391 -649.4672
##
## Random effects:
##  Formula: ~1 | Study.area
##         (Intercept) Residual
## StdDev:    5.656911 5.910775
##
## Correlation Structure: AR(1)
##  Formula: ~1 | Study.area
```

```
##  Parameter estimate(s):
##       Phi
## 0.1828919
## Fixed effects: Species.richness ~ scale(Hogweed.cover) + Habitat.type
##                                 Value Std.Error  DF   t-value p-value
## (Intercept)                 24.741612 1.7117346 176 14.454117  0.0000
## scale(Hogweed.cover)        -1.420397 0.4884303 176 -2.908086  0.0041
## Habitat.typeruderal.grass -2.853129 1.4641553 176 -1.948652  0.0529
## Habitat.typetall.herbs      -7.851275 1.4603586 176 -5.376265  0.0000
## Habitat.typewasteland       -3.446089 2.0679085 176 -1.666461  0.0974
## Habitat.typewoodland        -9.293588 1.8178651 176 -5.112364  0.0000
##  Correlation:
##                             (Intr) sc(H.) Hbtt.typr. Hbtt.typt.
Hbtt.typws
## scale(Hogweed.cover)         0.200
## Habitat.typeruderal.grass -0.517 -0.332
## Habitat.typetall.herbs      -0.529 -0.417  0.618
## Habitat.typewasteland       -0.345  0.046  0.412       0.352
## Habitat.typewoodland        -0.398 -0.081  0.431       0.506       0.317
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -2.0616284 -0.7119363 -0.1222464  0.6971461  2.5063006
##
## Number of Observations: 201
## Number of Groups: 20

anova(RichnessPQL1.2)

##                       numDF denDF   F-value p-value
## (Intercept)               1   176 212.89541  <.0001
## scale(Hogweed.cover)      1   176  27.24646  <.0001
## Habitat.type              4   176  10.43767  <.0001

# Residuals

par(mfrow=c(2,2))
plot(fitted(RichnessPQL1.2), resid(RichnessPQL1.2))
qqnorm(resid(RichnessPQL1.2))
qqline(resid(RichnessPQL1.2))
hist(resid(RichnessPQL1.2))
```





Overall, we can see that both the lme and glmmPQL models in this example display well-fitting residuals and the anova outcomes of both provide very similar results.

Wald Test for GLMM-PQL

The recommended way to test hypotheses (H0/H1) for glmmPQL, is to compute the Wald between the Wald approach and a typical anova, is that Wald tests encompass marginal tests of parameters, i.e. as they show up in the summary of the model in Wald outcome versus nested model comparisons (either F or Chisq (likedlihood ratio)) in anova() function.

```
RichnessPQL1 <- glmmPQL(Species.richness ~ scale(Hogweed.cover) +
                          Habitat.type, random=~1| Study.area,
data=Hogweed,
                        family="poisson", correlation=corAR1())

## iteration 1

## iteration 2

## iteration 3

summary(RichnessPQL1)

## Linear mixed-effects model fit by maximum likelihood
##  Data: Hogweed
```

```
##   AIC BIC logLik
##    NA  NA     NA
##
## Random effects:
##  Formula: ~1 | Study.area
##         (Intercept) Residual
## StdDev:     0.25502 1.360019
##
## Correlation Structure: AR(1)
##  Formula: ~1 | Study.area
##  Parameter estimate(s):
##      Phi
## 0.212907
## Variance function:
##  Structure: fixed weights
##  Formula: ~invwt
## Fixed effects: Species.richness ~ scale(Hogweed.cover) + Habitat.type
##                                Value  Std.Error  DF  t-value p-value
## (Intercept)                 3.179347 0.08077289 176 39.36156  0.0000
## scale(Hogweed.cover)       -0.084974 0.02702220 176 -3.14458  0.0020
## Habitat.typeruderal.grass -0.113853 0.07240569 176 -1.57243  0.1176
## Habitat.typetall.herbs     -0.418886 0.07631617 176 -5.48882  0.0000
## Habitat.typewasteland      -0.154868 0.10070796 176 -1.53779  0.1259
## Habitat.typewoodland       -0.471932 0.09683872 176 -4.87338  0.0000
##  Correlation:
##                            (Intr) sc(H.) Hbtt.typr. Hbtt.typt.
Hbtt.typws
## scale(Hogweed.cover)        0.240
## Habitat.typeruderal.grass -0.523 -0.343
## Habitat.typetall.herbs     -0.507 -0.409  0.561
## Habitat.typewasteland      -0.337  0.055  0.408      0.299
## Habitat.typewoodland       -0.357 -0.072  0.368      0.440       0.260
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -1.9455147 -0.7636449 -0.1452796  0.6615598  2.3691106
##
## Number of Observations: 201
## Number of Groups: 20
```

Since the main statistic of interest is the Wald approach (t for PQL) for the fixed effects parameters, we can firstly fit a crude Wald. The summary of the model gives us crude (Wald) estimates of the p-values for each individual parameter:

```
coef(summary(RichnessPQL1))
```

```
##                                Value  Std.Error  DF   t-value
## (Intercept)                 3.17934701 0.08077289 176 39.361559
## scale(Hogweed.cover)       -0.08497357 0.02702220 176 -3.144583
## Habitat.typeruderal.grass -0.11385291 0.07240569 176 -1.572430
```

```
## Habitat.typetall.herbs    -0.41888568 0.07631617 176 -5.488820
## Habitat.typewasteland     -0.15486750 0.10070796 176 -1.537788
## Habitat.typewoodland      -0.47193166 0.09683872 176 -4.873378
##                                  p-value
## (Intercept)               3.647255e-89
## scale(Hogweed.cover)      1.952741e-03
## Habitat.typeruderal.grass 1.176467e-01
## Habitat.typetall.herbs    1.393556e-07
## Habitat.typewasteland     1.258963e-01
## Habitat.typewoodland      2.436558e-06
```

One could be interested in the investigation of the main effects as a whole. Thus, we use the function "wald.test" of the package aod in order test the influence of the factor as whole using the Wald Z and X^2 (Wald Chi-squared) test, which is an approach analogous to an ANOVA. In function "wald.test" the following parameters are used:

fixed effects parameter estimates (b) the variance-covariance matrix (Sigma) and (c) a specification of which fixed factor terms (Terms) to combine for the Wald statistic. For more information, please, read the R documentation of the package aod in the wald.test section.

You define the terms by designating the order in which the coefficients of interest appear in the summary of the model. For instance, the predictor scale(Hogweed.cover) is the second coefficient after the intercept and Habitat.typewoodland is sixth and last. If we are interested in the main effects of the groups of parameters as whole, then we write 'Terms=2:6'. It is important to notice that the Wald X^2 test is suitable only in the absence of overdispersion in the model. When the model is overdispersed the suitable approach is to use Wald F and X^2 tests.

```
# install.packages("aod")
library(aod)

wald<-wald.test(b=fixef(RichnessPQL1),
                Sigma=vcov(RichnessPQL1),Terms=2:6)

wald
```

```
## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 74.4, df = 5, P(> X2) = 1.2e-14
```

The global p-value of Wald confirms the overall significant effect of the numeric (Hogweed.cover) and categorical (Habitat.type) predictors, as found in the other models (glmmPQL and lme), with Species.richness as response variable.

To assess the confidence intervals for model estimates based on Wald statistics.

```r
library(gmodels)
ci(RichnessPQL1, method="Wald")
```

```
##                                Estimate   CI lower    CI upper Std.
Error
## (Intercept)                3.17934701  3.0199389  3.33875510
0.08077289
## scale(Hogweed.cover)      -0.08497357 -0.1383028 -0.03164432
0.02702220
## Habitat.typeruderal.grass -0.11385291 -0.2567480  0.02904221
0.07240569
## Habitat.typetall.herbs    -0.41888568 -0.5694983 -0.26827310
0.07631617
## Habitat.typewasteland     -0.15486750 -0.3536181  0.04388312
0.10070796
## Habitat.typewoodland      -0.47193166 -0.6630462 -0.28081712
0.09683872
##                             DF      p-value
## (Intercept)                176 3.647255e-89
## scale(Hogweed.cover)       176 1.952741e-03
## Habitat.typeruderal.grass 176 1.176467e-01
## Habitat.typetall.herbs     176 1.393556e-07
## Habitat.typewasteland      176 1.258963e-01
## Habitat.typewoodland       176 2.436558e-06
```

GLMM - PQL: Spatial autocorrelation

```r
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4)
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
```

```
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```
library(MASS) # PQL Estimation Of Generalized Linear Mixed Models
(glmmPQL)
library(nlme) # corExp (autocorrelation structure of order 1.
              # For temporal autocorrelation correction)
library(lme4) # glmer
```

```
RichnessPQL2 <- glmmPQL(Richness ~ Mortality + Recruitment, random=~1|
                        Site, data=BIOVEG, family=poisson(),
                        correlation = corExp())
```

```
## iteration 1

## iteration 2

## iteration 3
```

```
summary(RichnessPQL2)
```

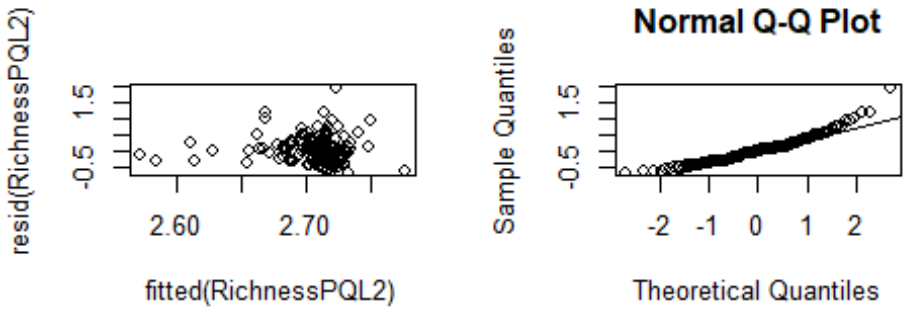
```
## Linear mixed-effects model fit by maximum likelihood
##  Data: BIOVEG
##   AIC BIC logLik
##    NA  NA     NA
##
## Random effects:
##  Formula: ~1 | Site
##         (Intercept) Residual
## StdDev: 2.513287e-05 1.568849
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~1 | Site
##  Parameter estimate(s):
##    range
## 2.114817
## Variance function:
##  Structure: fixed weights
##  Formula: ~invwt
## Fixed effects: Richness ~ Mortality + Recruitment
##                  Value  Std.Error  DF  t-value p-value
## (Intercept)  2.7193377 0.07676437 145 35.42448  0.0000
## Mortality   -0.0076205 0.00877996 145 -0.86795  0.3869
## Recruitment  0.0044188 0.01109908 145  0.39812  0.6911
##  Correlation:
##             (Intr) Mrtlty
## Mortality   -0.290
```

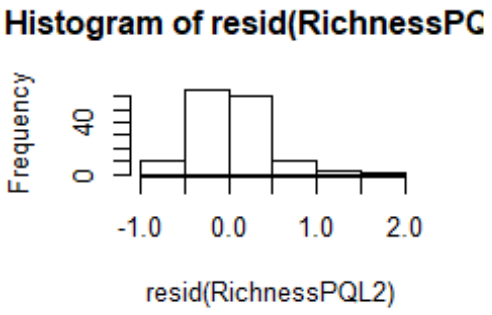
```
## Recruitment -0.366 -0.075
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.68788217 -0.78368147 -0.02639946  0.48572389  4.85960190
##
## Number of Observations: 150
## Number of Groups: 3
```

```
class(RichnessPQL2)="lme"
anova(RichnessPQL2,test="Chisq")
```

```
##             numDF denDF   F-value p-value
## (Intercept)     1   145 1629.6022  <.0001
## Mortality       1   145    0.7061  0.4021
## Recruitment     1   145    0.1585  0.6911
```

```
# Residuals

par(mfrow=c(2,2))
plot(fitted(RichnessPQL2), resid(RichnessPQL2))
qqnorm(resid(RichnessPQL2))
qqline(resid(RichnessPQL2))
hist(resid(RichnessPQL2))
```





The model RichnessPQL2 above did not show an acceptable residual fit in the Q.Q Plot and Histogram of residuals. In this case we then need to calculate a glmmPQL negative

binomial. Firstly, we compute a glm model for the same set of fixed effect variables to fit the Theta parameter of negative binomial dispersion.

```
RichnessPQL2.1 <- glm.nb(Richness ~ Mortality + Recruitment, data=BIOVEG)
theta<-RichnessPQL2.1$theta

RichnessPQL2.1.1 <- glmmPQL(Richness ~ Mortality + Recruitment,
random=~1|
                         Site, data=BIOVEG, family=quasipoisson(),
                       correlation = corExp())

## iteration 1

## iteration 2

## iteration 3

summary(RichnessPQL2.1.1)

## Linear mixed-effects model fit by maximum likelihood
##  Data: BIOVEG
##    AIC BIC logLik
##     NA  NA     NA
##
## Random effects:
##  Formula: ~1 | Site
##          (Intercept) Residual
## StdDev: 2.513287e-05 1.568849
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~1 | Site
##  Parameter estimate(s):
##    range
## 2.114817
## Variance function:
##  Structure: fixed weights
##  Formula: ~invwt
## Fixed effects: Richness ~ Mortality + Recruitment
##                  Value  Std.Error  DF  t-value p-value
## (Intercept)  2.7193377 0.07676437 145 35.42448  0.0000
## Mortality   -0.0076205 0.00877996 145 -0.86795  0.3869
## Recruitment  0.0044188 0.01109908 145  0.39812  0.6911
##  Correlation:
##             (Intr) Mrtlty
## Mortality   -0.290
## Recruitment -0.366 -0.075
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.68788217 -0.78368147 -0.02639946  0.48572389  4.85960190
##
```

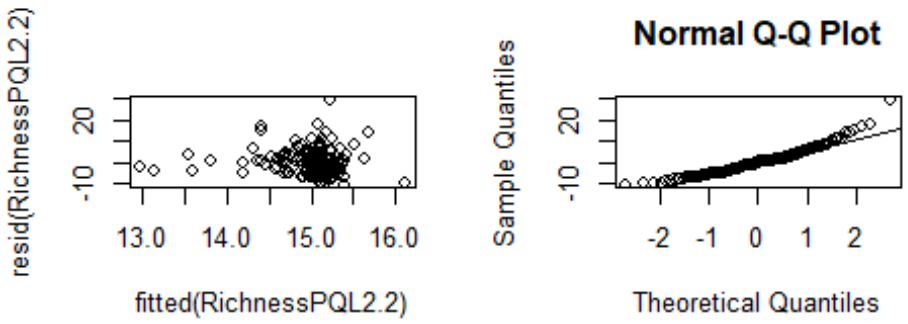
```
## Number of Observations: 150
## Number of Groups: 3

class(RichnessPQL2.1.1)="lme"
anova(object=RichnessPQL2.1.1,test="Chisq")

##             numDF denDF   F-value p-value
## (Intercept)     1   145 1629.6022  <.0001
## Mortality       1   145    0.7061  0.4021
## Recruitment     1   145    0.1585  0.6911
```

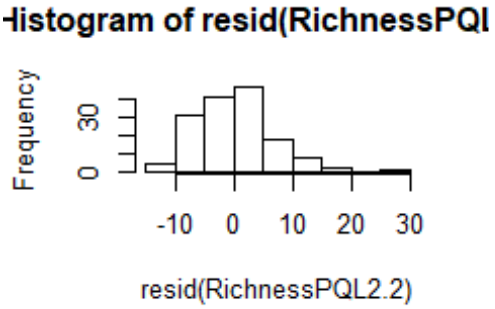
The outcomes of both the glmmPQL model with Poisson and Negative binomial dispersion were the same.

Similar to the first example of glmmPQL above, we run a lme model for the same set of variables and compare the residuals and anova outcomes of both models. Despite the fact that lme assumes a normal distribution, we can still consider this model if the residuals reasonably conform with a normal fit.

```
RichnessPQL2.2 <- lme(Richness ~ Mortality + Recruitment, random=~1|
                        Site, data=BIOVEG, correlation
                      = corExp())
summary(RichnessPQL2.2)

## Linear mixed-effects model fit by REML
##  Data: BIOVEG
##        AIC      BIC    logLik
##   909.0265 926.9691 -448.5133
##
## Random effects:
##  Formula: ~1 | Site
##         (Intercept) Residual
## StdDev: 0.003170964 6.205825
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~1 | Site
##  Parameter estimate(s):
##   range
## 2.19089
## Fixed effects: Richness ~ Mortality + Recruitment
##                 Value Std.Error  DF   t-value p-value
## (Intercept) 15.147875 1.1779626 145 12.859385  0.0000
## Mortality   -0.113682 0.1260718 145 -0.901720  0.3687
## Recruitment  0.072715 0.1686360 145  0.431194  0.6670
##  Correlation:
##             (Intr) Mrtlty
## Mortality   -0.298
## Recruitment -0.350 -0.076
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
```

```
## -1.67557693 -0.75056004 -0.02212395  0.47904130  4.79686539
##
## Number of Observations: 150
## Number of Groups: 3

anova(RichnessPQL2.2)

##             numDF denDF   F-value p-value
## (Intercept)     1   145 209.95041  <.0001
## Mortality       1   145   0.75942   0.385
## Recruitment     1   145   0.18593   0.667

# Residuals

par(mfrow=c(2,2))
plot(fitted(RichnessPQL2.2), resid(RichnessPQL2.2))
qqnorm(resid(RichnessPQL2.2))
qqline(resid(RichnessPQL2.2))
hist(resid(RichnessPQL2.2))
```





The anova output of the lme model, similar to those of the glmmPQL with Richness as response variable, shows that none of the predictors are significantly related to this response variable. However, the residual fit of this lme model is also not as good as those of the glmmPQL models for this response variable. Thus, we can try to log-transform Richness, though log transformations of discrete data are largely not advised and their use demands a cautious approach.

```
RichnessPQL2.2.2 <- lme(log(Richness) ~ Mortality + Recruitment,
random=~1|
                       Site, data=BIOVEG, correlation
                     = corExp())
summary(RichnessPQL2.2.2)
```

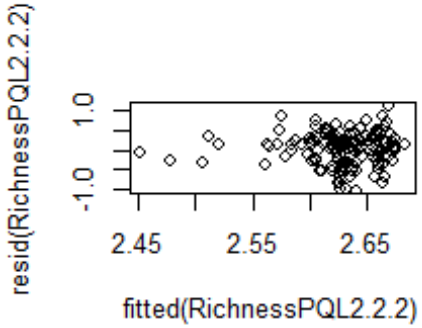
```
## Linear mixed-effects model fit by REML
##  Data: BIOVEG
##       AIC      BIC    logLik
##   121.274 139.2166 -54.63701
##
## Random effects:
##  Formula: ~1 | Site
##         (Intercept)  Residual
## StdDev:  0.04515893 0.4084216
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~1 | Site
##  Parameter estimate(s):
##    range
## 1.907718
## Fixed effects: log(Richness) ~ Mortality + Recruitment
##                  Value  Std.Error  DF  t-value p-value
## (Intercept)  2.6515169 0.07939254 145 33.39756  0.0000
## Mortality   -0.0092208 0.00874206 145 -1.05476  0.2933
## Recruitment  0.0025622 0.01170855 145  0.21883  0.8271
##  Correlation:
##             (Intr) Mrtlty
## Mortality   -0.308
## Recruitment -0.359 -0.074
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -2.5263531 -0.7349958  0.1569121  0.6254959  2.7853229
##
## Number of Observations: 150
## Number of Groups: 3
```

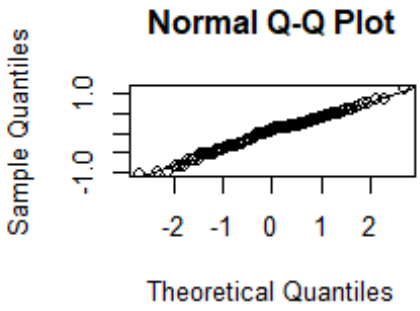
```
anova(RichnessPQL2.2.2)
```

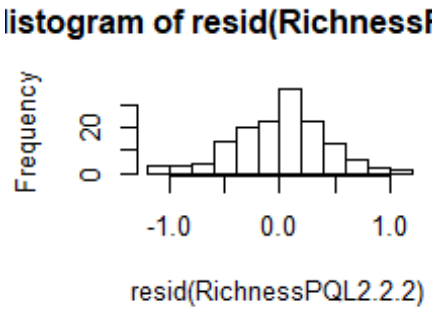
```
##             numDF denDF   F-value p-value
## (Intercept)     1   145 1446.6712  <.0001
## Mortality       1   145    1.0846  0.2994
## Recruitment     1   145    0.0479  0.8271
```

```
# Residuals

par(mfrow=c(2,2))
plot(fitted(RichnessPQL2.2.2), resid(RichnessPQL2.2.2))
qqnorm(resid(RichnessPQL2.2.2))
```

```
qqline(resid(RichnessPQL2.2.2))
hist(resid(RichnessPQL2.2.2))
```







For this lme model, the log transformation of Richness worked well. The residuals are better fitted and the anova output maintains non-significance for the predictor variables, similar to the previous glmmPQL and lme models. This suggests that there is no great distortion of the empirical condition of the data in the model after the log transformation.

Wald Test

Now, let's compute the Wald test for the model "RichnessPQL2.1.1"

```
summary(RichnessPQL2.1.1)
```

```
## Linear mixed-effects model fit by maximum likelihood
##  Data: BIOVEG
##    AIC BIC logLik
##     NA  NA     NA
##
## Random effects:
##  Formula: ~1 | Site
##          (Intercept) Residual
## StdDev: 2.513287e-05 1.568849
##
```

```
## Correlation Structure: Exponential spatial correlation
##  Formula: ~1 | Site
##  Parameter estimate(s):
##    range
## 2.114817
## Variance function:
##  Structure: fixed weights
##  Formula: ~invwt
## Fixed effects: Richness ~ Mortality + Recruitment
##                  Value  Std.Error  DF  t-value p-value
## (Intercept)  2.7193377 0.07676437 145 35.42448  0.0000
## Mortality   -0.0076205 0.00877996 145 -0.86795  0.3869
## Recruitment  0.0044188 0.01109908 145  0.39812  0.6911
##  Correlation:
##             (Intr) Mrtlty
## Mortality   -0.290
## Recruitment -0.366 -0.075
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.68788217 -0.78368147 -0.02639946  0.48572389  4.85960190
##
## Number of Observations: 150
## Number of Groups: 3
```

```
wald2<-wald.test(b=fixef(RichnessPQL2.1.1),
                 Sigma=vcov(RichnessPQL2.1.1),Terms=2:3)

wald2
```

```
## Wald test:
## ----------
##
## Chi-squared test:
## X2 = 0.88, df = 2, P(> X2) = 0.64
```

The global p-value of Wald confirms the non-significant effects of the predictors (Mortality and Recruitment) as found in the previous glmmPQL and lme models for this set of variables.

```
# Confidence Interval under Wald fit.

ci(RichnessPQL2.1.1, method=Wald)
```

```
##                 Estimate    CI lower    CI upper  Std. Error  DF
## (Intercept)  2.719337688  2.56761601 2.871059367 0.076764373 145
## Mortality   -0.007620525 -0.02497375 0.009732702 0.008779955 145
## Recruitment  0.004418759 -0.01751812 0.026355633 0.011099076 145
##                  p-value
## (Intercept) 2.826205e-73
```

```
## Mortality   3.868582e-01
## Recruitment 6.911276e-01
```

Useful links and examples:

https://rpubs.com/bbolker/glmmchapter

http://www.flutterbys.com.au/stats/tut/tut11.2a.html

https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html

https://bbolker.github.io/mixedmodels-misc/ecostats_chap.html

https://www.rdocumentation.org/packages/MASS/versions/7.3-47/topics/glmmPQL

Recommended Reading:

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 235, 397.

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

LOGISTIC REGRESSION

Hypothesis test: in a period of 5 years do the continuous variables (mean diameter and mean precipitation) affect the likelihood of tree recruitment, i.e., survival, growth and achieve a minimum diameter criteria (e.g. > 15 cm). That is, we want to know if in a five years-period of forest monitoring, do two continuous variables (Mean_diameter + Precipitation_mean) and one categorical (type of vegetation) determine the success of a trees individual likelihood of recruitment (0 indicates the absence of recruitment in a subplot and 1 the presence).

```
Lreg <- read.table("Logit2.csv", header=T, sep=";", dec=".")
head(Lreg,4)
```

```
##          type1  Site Mean_diameter Precipitation_mean Rec.binar
## 1 Ombrophilous AREA1        11.657               1142         1
## 2 Ombrophilous AREA1        13.793               1142         1
## 3 Ombrophilous AREA1        17.928               1142         1
## 4 Ombrophilous AREA1        12.212               1142         1
```

```
Recrut.binar<- glm(Rec.binar ~ Mean_diameter + Precipitation_mean +
                                type1, data=Lreg,family="binomial")
Recrut.binar

##
## Call:  glm(formula = Rec.binar ~ Mean_diameter + Precipitation_mean +
##     type1, family = "binomial", data = Lreg)
##
## Coefficients:
##        (Intercept)       Mean_diameter  Precipitation_mean
##           4.431746           -0.143722           -0.001657
##  type1Ombrophilous   type1Semideciduos
##          -0.825271           -0.120710
##
## Degrees of Freedom: 449 Total (i.e. Null);  445 Residual
## Null Deviance:       586.9
## Residual Deviance: 553.5     AIC: 563.5
```

According to the output, the model is logit(pi) = 4.43 + -0.14*Mean_diameter + 0.001*Precipitation_mean - -0.82*typeOmbrophilous + 0.12*typeSemideciduos

LRT (likelihood ratio test)

To test the overall model fit and hypothesis

LRT compares the full model with a reduced model where the explanatory variables of interest are omitted and provides p-values of the tests calculated using Chi-squared distribution.

```
Rec.bin.reduced<- glm(Rec.binar ~ 1, data=Lreg, family="binomial")
anova(Rec.bin.reduced,Recrut.binar, test="Chisq")

## Analysis of Deviance Table
##
## Model 1: Rec.binar ~ 1
## Model 2: Rec.binar ~ Mean_diameter + Precipitation_mean + type1
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1       449     586.92
## 2       445     553.52  4     33.4 9.893e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The LRT is 33.399 with a p-value 9.895e-07. Thus, we have strong evidence, based on high significance, that there is influence of some of the predictors in the success or failure of tree recruitment.

Perform tests on the individual regression parameters:

```
summary(Recrut.binar)

##
## Call:
```

```
## glm(formula = Rec.binar ~ Mean_diameter + Precipitation_mean +
##     type1, family = "binomial", data = Lreg)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8080  -1.2327   0.7476   0.9216   1.9004
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          4.431746   1.742508   2.543  0.01098 *
## Mean_diameter       -0.143722   0.035671  -4.029  5.6e-05 ***
## Precipitation_mean -0.001657   0.001402  -1.182  0.23730
## type1Ombrophilous   -0.825271   0.314016  -2.628  0.00859 **
## type1Semideciduos   -0.120710   0.280880  -0.430  0.66737
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 586.92  on 449  degrees of freedom
## Residual deviance: 553.52  on 445  degrees of freedom
## AIC: 563.52
##
## Number of Fisher Scoring iterations: 4
```

We can see that mean diameter (z = -4.029 and p=5.6e-05) appears to have a significant impact on the likelihood of recruitment success or failure of the trees. The same way the vegetation type Ombrophilous (z = -2.628 and p=0.00859) seems to have significant negative impact (Estimate = -0.825271) on the recruitment success. Semideciduous forest (z = -2.628 and p = 0.00859 **)does not seem to have a significant effect on recruitment, once mean diameter and ombrophilous are included in the model. The same can be said about the effect of mean precipitation (z =-1.505 and p = 0.13224) on recruitment, since it's effect is controlled by the stronger influence of mean diameter and ombrophilous type.

We can check for significance of influence from the predictors by executing a test for the full model.

```
anova(Recrut.binar, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: Rec.binar
##
## Terms added sequentially (first to last)
##
##
##                    Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
```

```
## NULL                                  449     586.92
## Mean_diameter       1  23.8193       448     563.10 1.058e-06 ***
## Precipitation_mean  1   0.1662       447     562.93  0.683539
## type1               2   9.4142       445     553.52  0.009031 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# To compute the odds of successful tree recruitment as a function of
mean diameter
# and ombrophilous type

exp(coef(Recrut.binar))
```

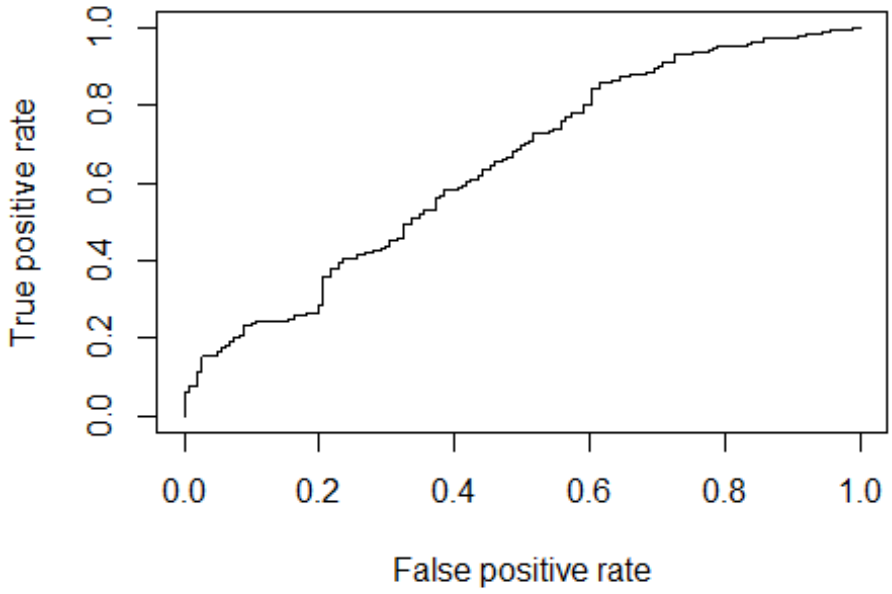
```
##        (Intercept)      Mean_diameter Precipitation_mean
##         84.0780806          0.8661288          0.9983448
##  type1Ombrophilous  type1Semideciduos
##          0.4381162          0.8862912

## To create a 95% confidence interval for the estimate, type:

exp(confint.default(Recrut.binar))
```

```
##                          2.5 %       97.5 %
## (Intercept)         2.7634844 2558.0472670
## Mean_diameter       0.8076423    0.9288507
## Precipitation_mean 0.9956056    1.0010915
## type1Ombrophilous   0.2367547    0.8107368
## type1Semideciduos   0.5110827    1.5369570
```

We see that the odds ratio corresponding to mean diameter is 0.87 (95% CI: (0.80, 0.92)) and Ombrophilous is 0.43 (95% CI: (0.23, 0.811))

To use the fitted logistic regression curve to estimate the predictive power and accuracy of the model. The most commonly used way to check the predictive ability of a logistic model is to fit the ROC curve and its AUC (area under the curve), which are typical performance measurements for a binary classifier. The ROC is a curve which plots the true positive rate (TPR) against the false positive rate (FPR) at various threshold settings, whereas the AUC is the area under the ROC curve. A commonly used rule to assess the robustness of predictive power of the model, is to consider a good predictive ability when AUC is closer to 1 (1 is ideal) than to 0.5.

```
# install.packages("ROCR")
library(ROCR)

p <- predict(Recrut.binar, type="response") # predict scorees
pr <- prediction(p, Lreg$Rec.binar)
prf <- performance(pr, measure = "tpr", x.measure = "fpr")
plot(prf)
```

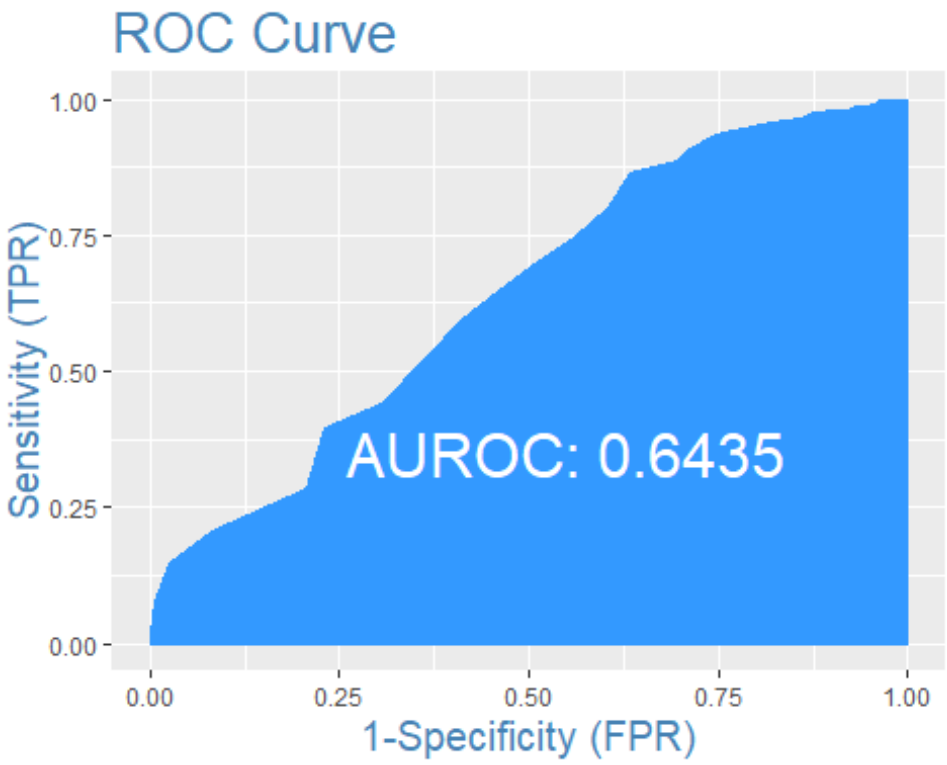



```
auc <- performance(pr, measure = "auc")
auc <- auc@y.values[[1]]
auc

## [1] 0.6462206
```

Or we can use the package plotROC for a better presentation of the AUC and true and false positive rates.

install.packages("InformationValue") # To plot ROC curve

```
library(InformationValue)

P<- plotROC(Lreg$Rec.binar, p)
```



Here we got a reasonable predictive accuracy (0.64), but it could be better (e.g. > 0.70).

Moran's I: spatial autocorrelation test

Spatial autocorrelation refers to the correlation between the values of a variable due their proximity in geographical space. This violates the assumption that they are from independent observations.

The function "moransI" of the package "lctools" allows us to estimate the local spatial correlation of the residuals from a linear model.

In order to execute the classical Moran's I test with this function, we first must calculate and provide metric coordinates, such as UTM coordinates, for each row of data. Firstly you must convert the geographical coordinates belonging to your data to UTM. After this, if you are using subplots (e.g. treatment with 50 subplots of 10 meters per 10 meters) you must add the distance of each subplot from the reference point of the site to the UTM coordinates of the site. This is done separately for X direction (East-West) and Y direction (North-South). If the reference point is the South-West corner of the site, you add the distances of the subplot in W-E and S-N direction to the site coordinates (e.g. 10 m and 30 m). But, if the reference point is the North-East corner, you subtract the distances from the site coordinates.

Each row of your data will contain real coordinates based on the sample units (here represented by subplot) and you will be able to estimate spatial autocorrelation in your linear model.

It is also important to note that Moran's I ranges from -1 to 1. Values close to -1 imply negative spatial autocorrelation (low values tend to have neighbours with high values and vice versa) and values close to 1 represent positive spatial autocorrelation (spatial clusters of similarly low or high values among neighbour subplots, as in the present example).

The function "moransI" provides the Moran's I value (named as "Morans.I") and the two tailed p-value (named "p.value.resampling" in the output) to test the significance of Moran's I and, consequently, significance of spatial autocorrelation.

In order to graphically demonstrate the results for Moran's I, you can create a correlogram with the function "correlog" of the package "ncf" as shown in the example below. There, a univariate spatial correlogram based on the spatial distances between the subplots is provided. Additionally, a plot with the corresponding p-values of the Moran's I statistic is drawn, including a line of the threshold (p=0.05) to facilitate assessment of significance.

```
# install.packages("lctools")
# install.packages("ncf")

library(lctools) # Moran's I
library(ncf) # correlogram

BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG, 4)
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
```

```
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

LM to base the Moran's I computation:

```
Mean.Diameter.pre <- lm(Mean_diameter ~ Mortality + Recruitment +
                                                Site, data=BIOVEG)
```

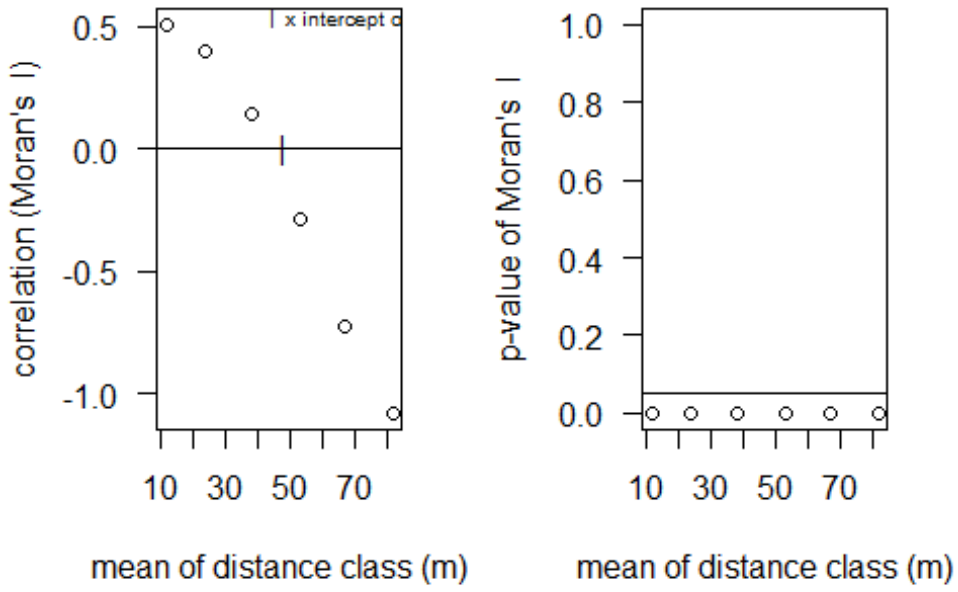
Moran's I

```
Moran.M.diameter <- moransI(Coords=cbind(BIOVEG$local.utm.x,
BIOVEG$local.utm.y),
                   Bandwidth=4, resid(Mean.Diameter.pre), WType="Binary")

Moran.M.diameter$Morans.I

##         1
## 0.6320286

Moran.M.diameter$p.value.resampling # significance of the Moran's I

##            1
## 9.537331e-37

Moran.M.diameter$p.value.randomization # another variant of p-value

##            1
## 1.065647e-36
```

Graph (Correlogram):

```
Cor.Mean_diameter <- correlog(x=BIOVEG$local.utm.x, y=BIOVEG$local.utm.y,
                        as.vector(resid(Mean.Diameter.pre)), increment=15,
resamp=1000)

## 100  of  1000
200  of  1000
300  of  1000
400  of  1000
500  of  1000
600  of  1000
700  of  1000
800  of  1000
900  of  1000
1000  of  1000

x11(width=12, height=12) ####
par(mfrow=c(1,2))
plot(Cor.Mean_diameter$mean.of.class[1:6],
Cor.Mean_diameter$correlation[1:6],
```

```
  xlab="mean of distance class (m)", ylab="correlation (Moran's  I)",
las=1)
abline(0, 0)
points(Cor.Mean_diameter$x.intercept, 0, pch="|")
legend("topright", "x intercept of autocorrelation", pch="|", bty="n",
cex=0.6)
 plot(Cor.Mean_diameter$mean.of.class[1:6], Cor.Mean_diameter$p[1:6],
ylim=c(0,1),
  xlab="mean of distance class (m)", ylab="p-value of Moran's  I", las=1)
abline(0.05, 0)
```




```
# dev.off() # turn off the graphics device
```

LME (Linear Mixed Effects)

With spatial autocorrelation's correction included

A LME model is a mixed model is implemented to deal with pseudoreplicates by including random effects of, e.g., sites that meet the assumption of normal distribution of residuals. In addition to random effects, it can handle spatial autocorrelation. Therefore, if in a previous test (e.g. Moran's I) you find significant spatial autocorrelation in a Linear Mixed Model (LMM; with random and fixed effects and normal distribution), you must use LME with a spatial correlation strucure in the model. If you have non-normal data with spatial auto-correlation please check the

function glmmPQL of the package MASS to calculate a GLMM with a spatial correlation structure.

There are different variants of spatial correlation structures. One good example is Exponential correlation (function "corExp"). The correlation structure must be included in the syntax of the lme command as in the analyses below. If you don't include a correlation function (e.g. corExp) in the LME model, it is just like a common LMM. However, like GLMM, this would not be enough to resolve the autocorrelation and provide reliable p-values. In order to test spatial autocorrelation by Moran's I, you must first construct a LM with the same predictors that will be used in the LME (see LM model used in the section Linearity Tests and Moran's I). To better understand this approach of handling spatial autocorrelation using the proper regression models, read Dormann et al. (2007).

Dormann, C.F., M. McPherson, J., B. Araújo, M., Bivand, R., Bolliger, J., Carl, G.et al. (2007). Methods to account for spatial autocorrelation in the analysis of species distributional data: A review. Ecography (Cop.)., 30, 609–628

Note 1: LMM can be calculated using either Maximum Likelihood (ML) or Restricted Maximum Likelihood (REML). If we are focusing on estimation and testing of fixed effects, we choose "ML". In addition to correlation of the residuals, lme can also deal with heterogeneous variance of residuals (heteroscedasticity), e.g. when variances differ among groups, such as sites. For this purpose, we can use the "weights" argument.

```
# install.packages("nlme")
# install.packages("car")

library(nlme) # LME models
library(car) # Anova type II gives the predictors the same chance of
             # being significant

BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG,4)
```

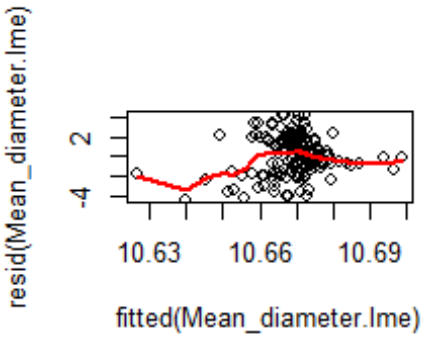
```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
```

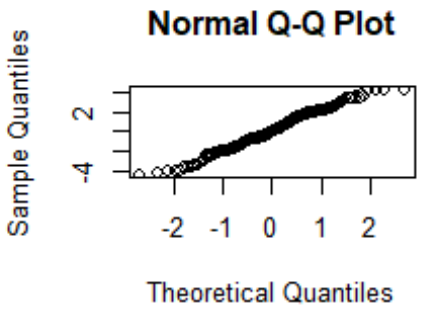
```
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

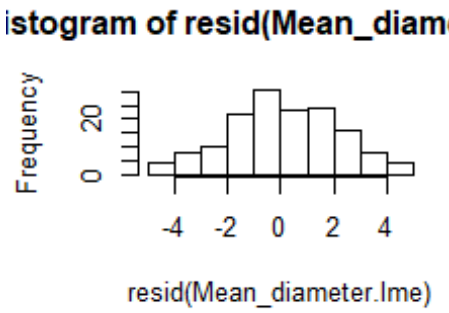
```
Mean_diameter.lme<- lme(Mean_diameter ~ Mortality + Recruitment,
data=BIOVEG,
              method="ML", random= ~1|Site,
corr=corExp(form=~local.utm.x+
              local.utm.y|Site), weights=varIdent(form=~1|Site),
na.action=na.omit)

summary(Mean_diameter.lme)
```

```
## Linear mixed-effects model fit by maximum likelihood
##  Data: BIOVEG
##        AIC      BIC   logLik
##   97.1106 121.1957 -40.5553
##
## Random effects:
##  Formula: ~1 | Site
##          (Intercept) Residual
## StdDev: 0.0001718405 2.831905
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~local.utm.x + local.utm.y | Site
##  Parameter estimate(s):
##    range
## 999.8204
## Variance function:
##  Structure: Different standard deviations per stratum
##  Formula: ~1 | Site
##  Parameter estimates:
##     AREA1     AREA2     AREA3
## 1.0000000 0.3103472 2.6947936
## Fixed effects: Mean_diameter ~ Mortality + Recruitment
##                 Value Std.Error  DF   t-value p-value
## (Intercept) 10.672167 0.8185581 145 13.037763  0.0000
## Mortality    0.001605 0.0032656 145  0.491505  0.6238
## Recruitment -0.003023 0.0091995 145 -0.328623  0.7429
##  Correlation:
##             (Intr) Mrtlty
## Mortality   -0.006
## Recruitment -0.032 -0.053
```

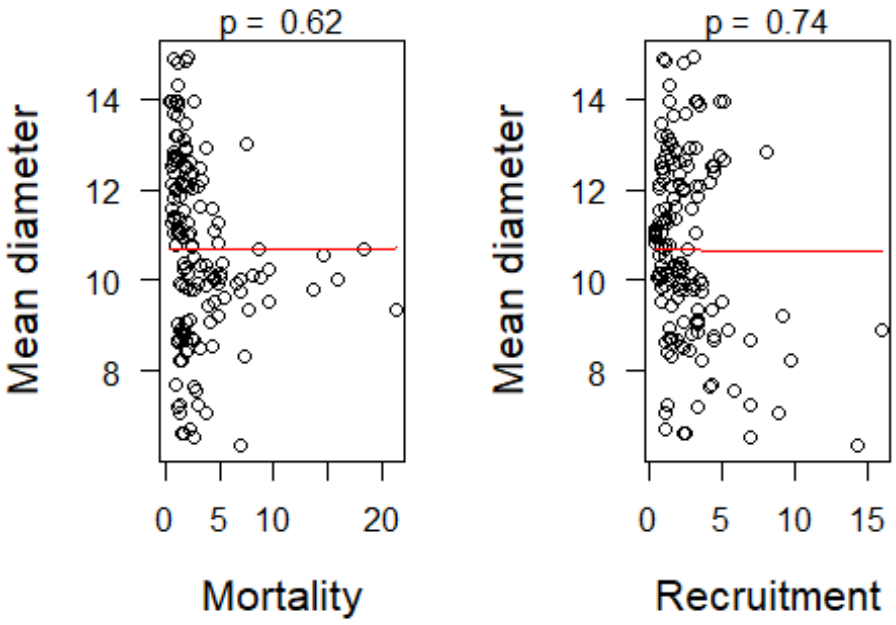
```
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.51239300 -0.68377730 -0.01067181  0.29650175  1.46812947
##
## Number of Observations: 150
## Number of Groups: 3

## Anova from car package

An<- Anova(Mean_diameter.lme, Type = II)
An

## Analysis of Deviance Table (Type II tests)
##
## Response: Mean_diameter
##              Chisq Df Pr(>Chisq)
## Mortality   0.2465  1     0.6195
## Recruitment 0.1102  1     0.7399

## Residuals

x11(width=12, height=12) ####
par(mfrow=c(2,2))
plot(fitted(Mean_diameter.lme), resid(Mean_diameter.lme))
lines(smooth.spline(fitted(Mean_diameter.lme), resid(Mean_diameter.lme),
                                          spar=c(1)), col="red", lwd=2)
qqnorm(resid(Mean_diameter.lme))
qqline(resid(Mean_diameter.lme))
hist(resid(Mean_diameter.lme))
#dev.off() ## turn off the graphics device
```








```
## Scatterplot

b.0.Mean_diameter<- Mean_diameter.lme$coefficients$fixed[1]
b.1.Mean_diameter<- Mean_diameter.lme$coefficients$fixed[2]
b.2.Mean_diameter<- Mean_diameter.lme$coefficients$fixed[3]

x11(width=14, height=8)
par(mfrow=c(1,2))
plot(BIOVEG$Mean_diameter ~ BIOVEG$Mortality, las=1, ylab="Mean
diameter", xlab="Mortality",
     cex.lab=1.3)
curve(b.0.Mean_diameter + b.1.Mean_diameter*x, add=TRUE, col="red")
mtext(ifelse(An[1,3]<0.001, "p < 0.001", paste("p = ",
round(An[1,3],3))))
plot(BIOVEG$Mean_diameter ~ BIOVEG$Recruitment, las=1, ylab="Mean
diameter", xlab="Recruitment",
     cex.lab=1.3)
curve(b.0.Mean_diameter + b.2.Mean_diameter*x, add=TRUE, col="red")
mtext(ifelse(An[2,3]<0.001, "p < 0.001", paste("p = ",
round(An[2,3],3))))
```




```
#dev.off() ## turn off the graphics device
```

GLS (Generalized Least Squares)

GLS is another variant of linear regression. It is mostly used to perform analysis when there is significant spatial (or temporal) correlation between the residuals (or if there is heteroscedasticity), but you do not have any random effect in the model. In the absence of random effects, you cannot use lme, but you can use gls. GLS models fit correlation structures of the variance-covariance matrix to model the (spatial) dependence of observations, just as LME models do. Thus, gls is an efficient tool to deal with spatial autocorrelation when you would otherwise use lm (read Dormann et al. 2007).

Dormann et al. Methods to account for spatial autocorrelation in the analysis of species distributional data: a review. Ecography 30: 609-628, 2007.

N.B. GLS assumes a normal distribution.

In cases such as in the example below, when you just want to know whether there is variation of a variable among treatments and study sites, for instance, but your data comes from pseudoreplicates (e.g. subplots in our example below), GLS is a good option. Notice that in this case, you use site as a fixed effect. Otherwise, if you want to include site as a random effect, you must use a mixed effect model (GLMM or LME). Before calculating a GLS model, you should use Moran's I to check the significance of

spatial autocorrelation. If significant autocorrelation is found, you must include a correlation structure in the model (e.g. correlation=corExp).

```
## Pre-test: Spatial autocorrelation (Moran'I)

BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG,4)

##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727

## LM

Mean.Diameter.pre <- lm(Mean_diameter ~ Site, data=BIOVEG)
summary(Mean.Diameter.pre)

##
## Call:
## lm(formula = Mean_diameter ~ Site, data = BIOVEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.14642 -0.57963 -0.01675  0.58659  1.94452
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   8.5034     0.1168   72.81   <2e-16 ***
## SiteAREA2     2.1837     0.1652   13.22   <2e-16 ***
```

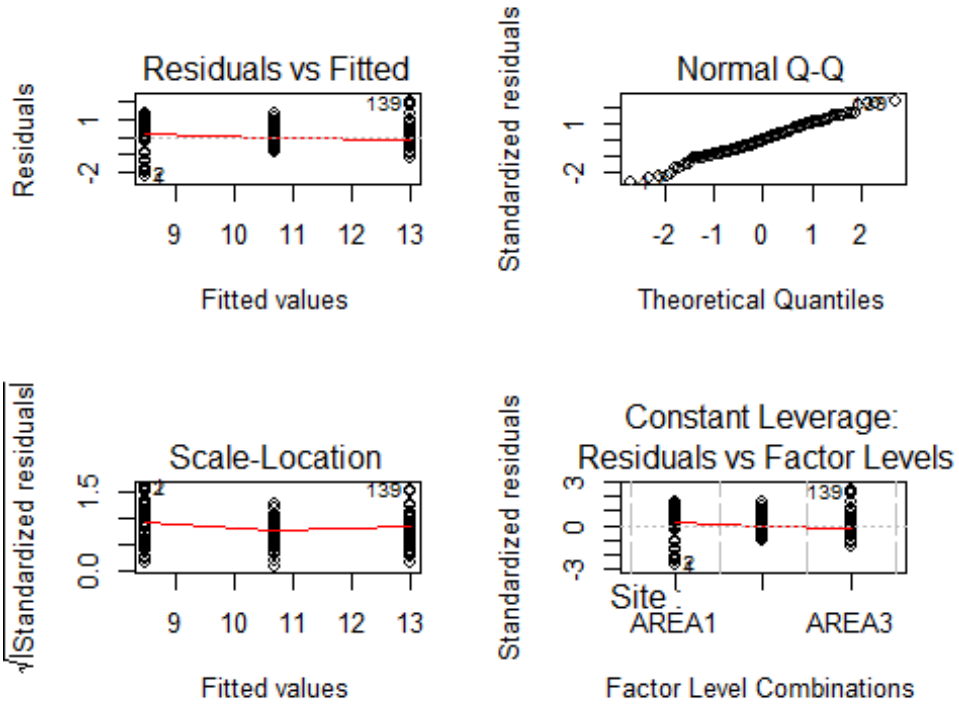
```
## SiteAREA3     4.4821     0.1652   27.14   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8258 on 147 degrees of freedom
## Multiple R-squared:  0.8336, Adjusted R-squared:  0.8314
## F-statistic: 368.3 on 2 and 147 DF,  p-value: < 2.2e-16
```

```
shapiro.test(BIOVEG$Mean_diameter)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  BIOVEG$Mean_diameter
## W = 0.98496, p-value = 0.1022
```

```
# Residuals
```

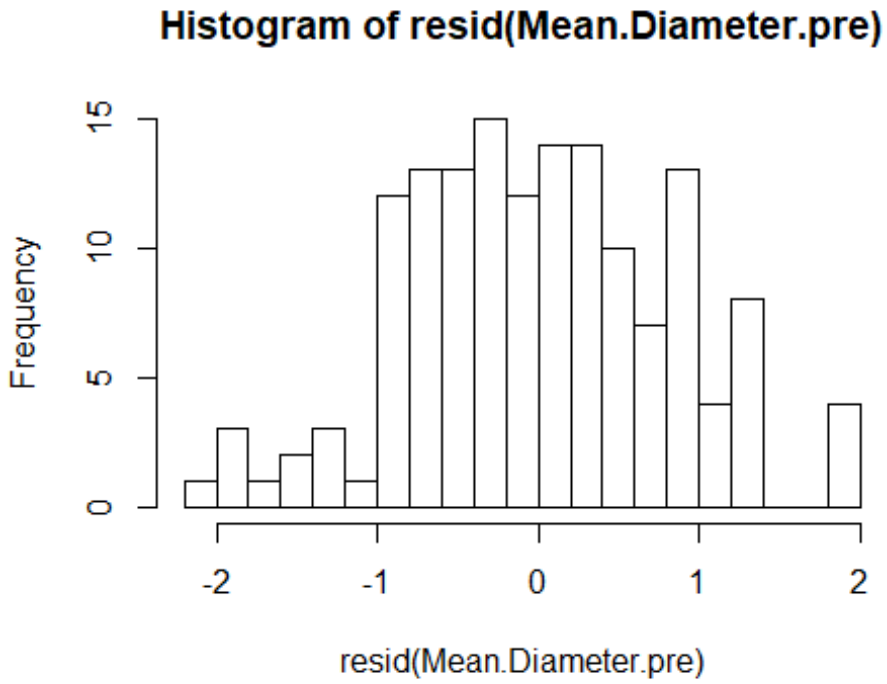
```
x11(width=12, height=12)
par(mfrow=c(2,2))
plot(Mean.Diameter.pre)
```




```
dev.off() ## turn off the graphics device
```

```
## png
##   2
```

```r
x11(width=12, height=12)
hist(resid(Mean.Diameter.pre),breaks=20)
```




```r
# dev.off() ## turn off the graphics device

## Moran's I

library(lctools) # Moran's I

Moran.M.diameter <- moransI(Coords=cbind(BIOVEG$local.utm.x,
BIOVEG$local.utm.y),
                   Bandwidth=4, resid(Mean.Diameter.pre), WType="Binary")

Moran.M.diameter$Morans.I

##         1
## 0.6691855

Moran.M.diameter$p.value.resampling # significance of the Moran's I

##            1
## 6.116947e-41

Moran.M.diameter$p.value.randomization

##            1
## 6.556257e-41
```

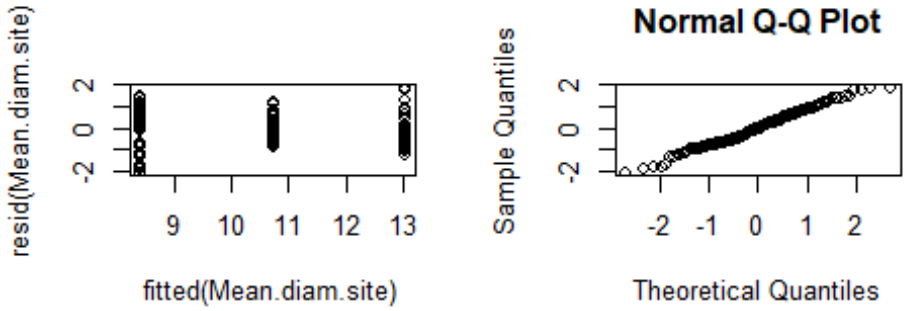
GLS model

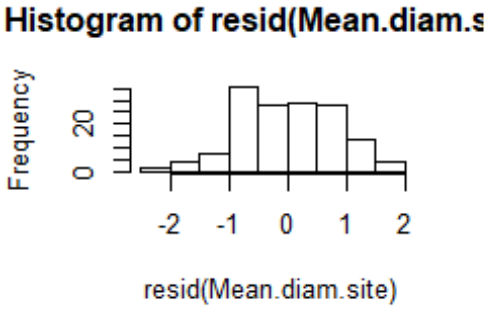
Since we found significant spatial autocorrelation in the pre-test with Moran's I, a correlation (corExp) structure must be added in the syntax of the model

```
library(nlme)
library(car)

Mean.diam.site<- gls(Mean_diameter ~ Site,
correlation=corExp(form=~1|Site),
                     data=BIOVEG)

summary(Mean.diam.site)

## Generalized least squares fit by REML
##   Model: Mean_diameter ~ Site
##   Data: BIOVEG
##        AIC      BIC    logLik
##   204.1488 219.1009 -97.07439
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~1 | Site
##  Parameter estimate(s):
##    range
## 10.55233
##
## Coefficients:
##                Value Std.Error   t-value p-value
## (Intercept) 8.391105 0.6110569 13.732118  0.0000
## SiteAREA2   2.361087 0.8641649  2.732218  0.0071
## SiteAREA3   4.646891 0.8641649  5.377319  0.0000
##
##  Correlation:
##           (Intr) SAREA2
## SiteAREA2 -0.707
## SiteAREA3 -0.707  0.500
##
## Standardized residuals:
##         Min          Q1         Med          Q3         Max
## -1.82692630 -0.57058862 -0.03421433  0.53862327  1.69929827
##
## Residual standard error: 1.113403
## Degrees of freedom: 150 total; 147 residual

An<- Anova(Mean.diam.site)
An

## Analysis of Deviance Table (Type II tests)
##
```

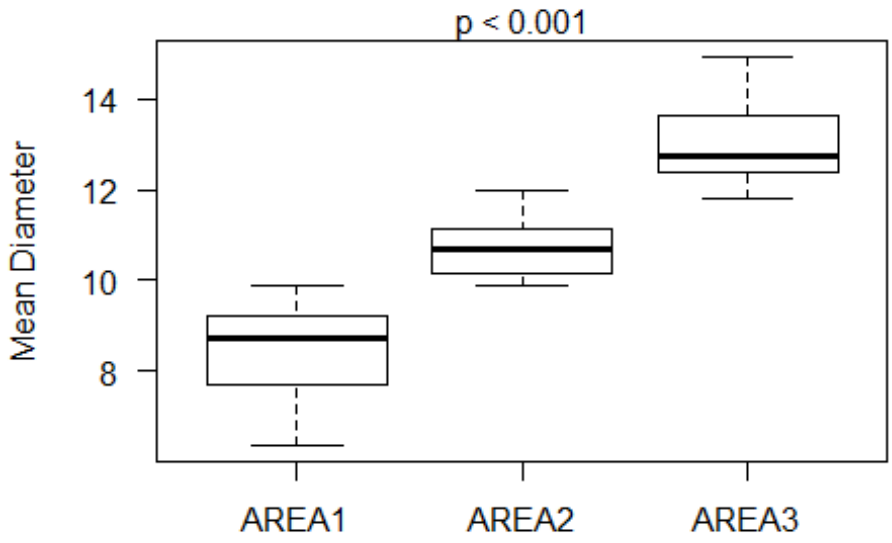
```
## Response: Mean_diameter
##      Df  Chisq Pr(>Chisq)
## Site  2 28.918  5.254e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Residuals

x11(width=12, height=12)
par(mfrow=c(2,2))
plot(fitted(Mean.diam.site), resid(Mean.diam.site))
qqnorm(resid(Mean.diam.site))
hist(resid(Mean.diam.site))
# dev.off()
```






```
# Boxplot

x11(width=12, height=12)
par(mfrow=c(1,1))
boxplot(BIOVEG$Mean_diameter ~ BIOVEG$Site, las=1, ylab="Mean Diameter")
mtext(ifelse(An[1,3]<0.001, "p < 0.001", paste("p = ",
round(An[1,3],3))))
```




```
# dev.off()
```

QUADRATIC MODEL

A quadratic regression is an extension of simple linear regression aiming to find the best fit equation a set of data (dependent and predictor variables) shaped like a parabola (e.g. U-shape curve). A quadratic fit is useful When the coefficients and, consequently, the curve appear to fit the data better than the linear model does.

Create linear model of species richness vs. Hogweed cover

```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
```

```
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
```

```
M.lin <- glm(Species.richness ~ Hogweed.cover + Habitat.type,
data=Hogweed,
             family="quasipoisson")
summary(M.lin)
```

```
##
## Call:
## glm(formula = Species.richness ~ Hogweed.cover + Habitat.type,
##     family = "quasipoisson", data = Hogweed)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.3435  -1.2231  -0.2592   1.2230   4.0514
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 3.248210   0.059719  54.392  < 2e-16 ***
## Hogweed.cover              -0.003072   0.001094  -2.807  0.00551 **
## Habitat.typeruderal.grass -0.022699   0.080921  -0.281  0.77938
## Habitat.typetall.herbs    -0.428306   0.083712  -5.116 7.43e-07 ***
## Habitat.typewasteland     -0.101591   0.106856  -0.951  0.34292
## Habitat.typewoodland      -0.354923   0.111048  -3.196  0.00163 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 2.884375)
##
##     Null deviance: 775.16  on 200  degrees of freedom
## Residual deviance: 571.60  on 195  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

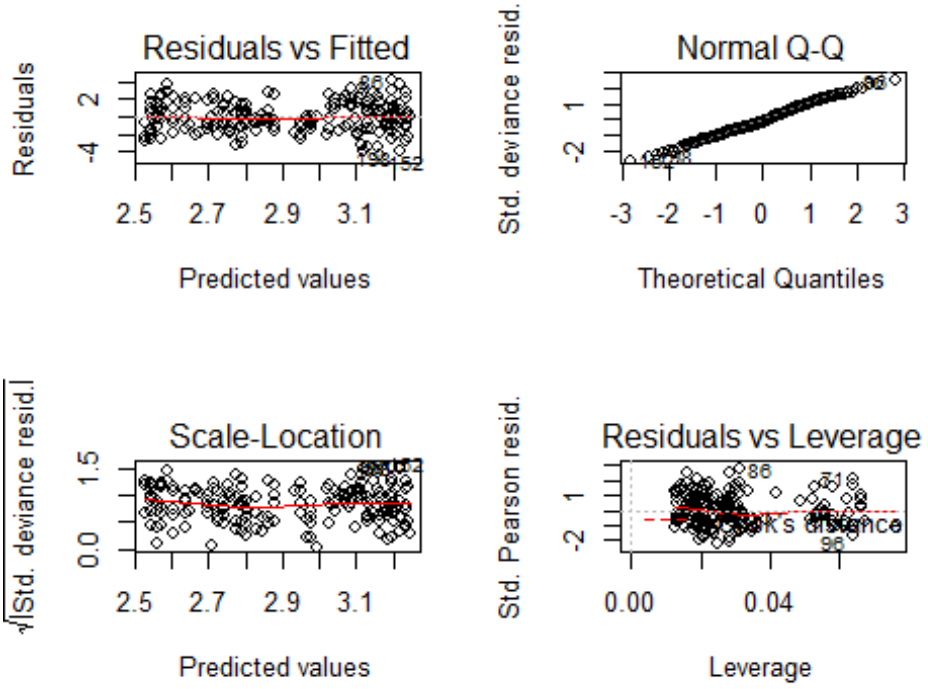
```
anova(M.lin, test = "F")
```

```
## Analysis of Deviance Table
##
```

```
## Model: quasipoisson, link: log
##
## Response: Species.richness
##
## Terms added sequentially (first to last)
##
##
##                Df Deviance Resid. Df Resid. Dev      F    Pr(>F)
## NULL                             200     775.16
## Hogweed.cover   1   70.215       199     704.94 24.343 1.723e-06 ***
## Habitat.type    4  133.345       195     571.60 11.557 1.929e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hogweed cover has a significant negative linear effect on species richness

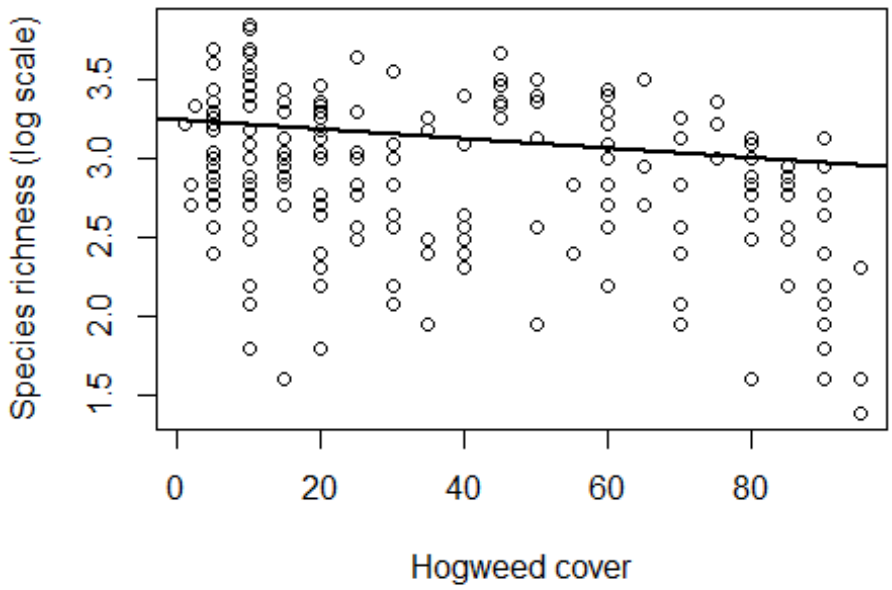
```
# Model diangostics

par(mfrow = c(2, 2))
plot(M.lin)
```



The diagnostic graphs look ok.

```
# Plot the data and the regression line

par(mfrow = c(1, 1))
plot(log(Species.richness) ~ Hogweed.cover, data = Hogweed,
```

```
     xlab = "Hogweed cover", ylab = "Species richness (log scale)")
abline(glm(Species.richness ~ Hogweed.cover + Habitat.type, data=Hogweed,
           family="quasipoisson"), lwd = 2)
```



The plot suggests that a quadartic model mignt fit the data even better

```
# Create variable of centered and squared Hogweed cover

Mean.cover <- mean(Hogweed$Hogweed.cover)
Hogweed.cover.sq <- (Hogweed$Hogweed.cover - Mean.cover)^2
```

Calculate the model with original and, additionally, squared Hogweed cover

```
M.quad <- glm(Species.richness ~ Hogweed.cover + Hogweed.cover.sq +
Habitat.type,
              data=Hogweed, family="quasipoisson")
summary(M.quad)

##
## Call:
## glm(formula = Species.richness ~ Hogweed.cover + Hogweed.cover.sq +
##     Habitat.type, family = "quasipoisson", data = Hogweed)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.3890  -1.3328  -0.2187   1.0562   4.2712
##
## Coefficients:
```

```
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 3.286e+00  6.258e-02  52.502  < 2e-16 ***
## Hogweed.cover              -1.718e-03  1.303e-03  -1.319 0.188639
## Hogweed.cover.sq           -8.413e-05  4.408e-05  -1.908 0.057825 .
## Habitat.typeruderal.grass -5.146e-02  8.144e-02  -0.632 0.528221
## Habitat.typetall.herbs    -4.418e-01  8.299e-02  -5.324 2.79e-07 ***
## Habitat.typewasteland     -1.010e-01  1.060e-01  -0.952 0.342054
## Habitat.typewoodland      -3.748e-01  1.107e-01  -3.387 0.000855 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 2.838361)
##
##     Null deviance: 775.16  on 200  degrees of freedom
## Residual deviance: 561.23  on 194  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
anova(M.quad, test="F")
```

```
## Analysis of Deviance Table
##
## Model: quasipoisson, link: log
##
## Response: Species.richness
##
## Terms added sequentially (first to last)
##
##
##                   Df Deviance Resid. Df Resid. Dev       F    Pr(>F)
## NULL                                200     775.16
## Hogweed.cover      1   70.215       199     704.94 24.7377 1.442e-06
***
## Hogweed.cover.sq   1   10.471       198     694.47  3.6891   0.05623 .
## Habitat.type       4  133.242       194     561.23 11.7358 1.479e-08
***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Compare linear and quadratic model

```
anova(M.lin, M.quad, test = "F")
```

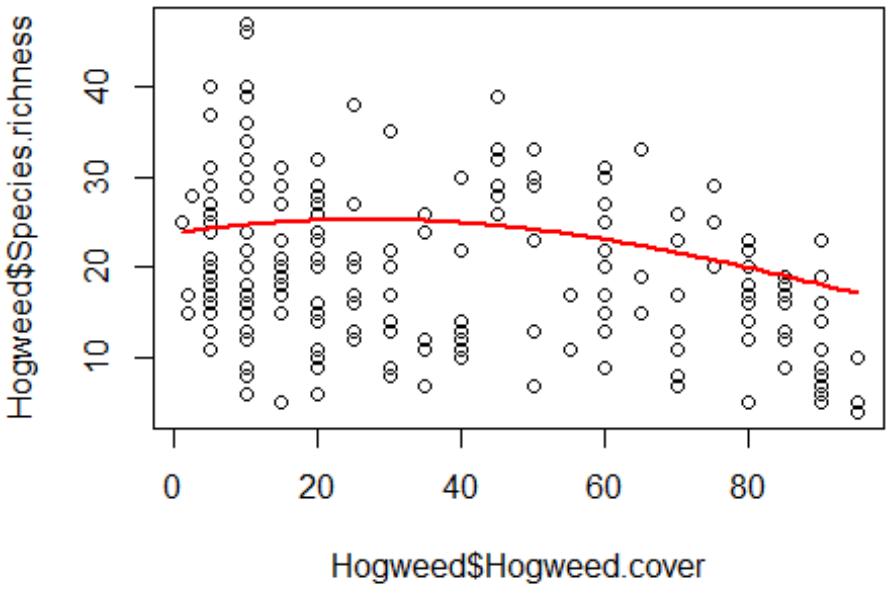
```
## Analysis of Deviance Table
##
## Model 1: Species.richness ~ Hogweed.cover + Habitat.type
## Model 2: Species.richness ~ Hogweed.cover + Hogweed.cover.sq +
Habitat.type
##   Resid. Df Resid. Dev Df Deviance      F  Pr(>F)
## 1       195     571.60
```

```
## 2       194     561.23  1   10.368 3.6527 0.05745 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Squared hogweed cover is (marginally) not significant.

Anyway, let's create a scatter plot with regression curve.

```
plot(Hogweed$Species.richness ~ Hogweed$Hogweed.cover)

b0 <- coef(M.quad)[1] # Intercept
b1 <- coef(M.quad)[2] # Hogweed cover linear
b2 <- coef(M.quad)[3] # Hogwee cover squared
# In the curve syntax, we need to center and square "x" before
multiplying it with
# the coefficient of Hogweed.cover.sq.
curve(exp(b0 + b1*x + b2*(x-Mean.cover)^2), add=T, col="red", lwd=2)
```



GNM (Generalized Nonlinear Models)

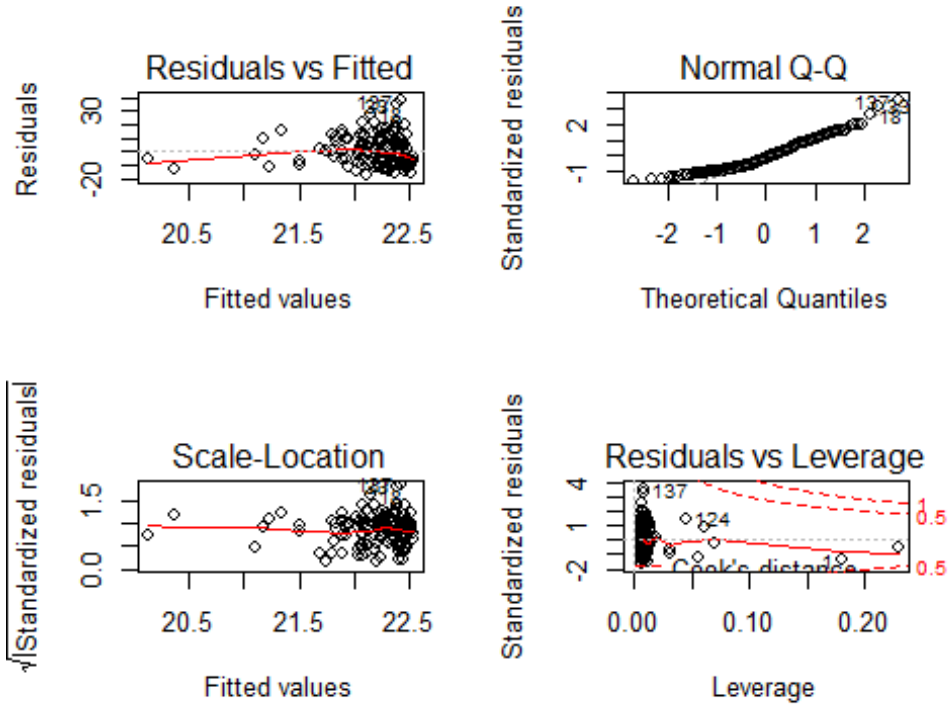
If you find significant non-linear relationships among variables, you can first try transforming (e.g. log, square) the predictor variable. This will not always be enough to resolve non-linearity issues and it can turn p-values of the linearity tests non-significant. If non-linearity is not resolved using this procedure, models such as LM, GLM and GLS are not the appropriate model for this purpose. Indeed, a better way to

deal with non-linearity may be to apply a model that uses a nonlinear function of the predictor variables, i.e. on the right-hand side of the model formula. GNM models still require you to specify the distribution family of the dependent variable (e.g. Gaussian, Poisson, Quasi-poisson). Furthermore, it is possible to use an option to coerce a GLM model to a GNM model, as explained at the end of this section.

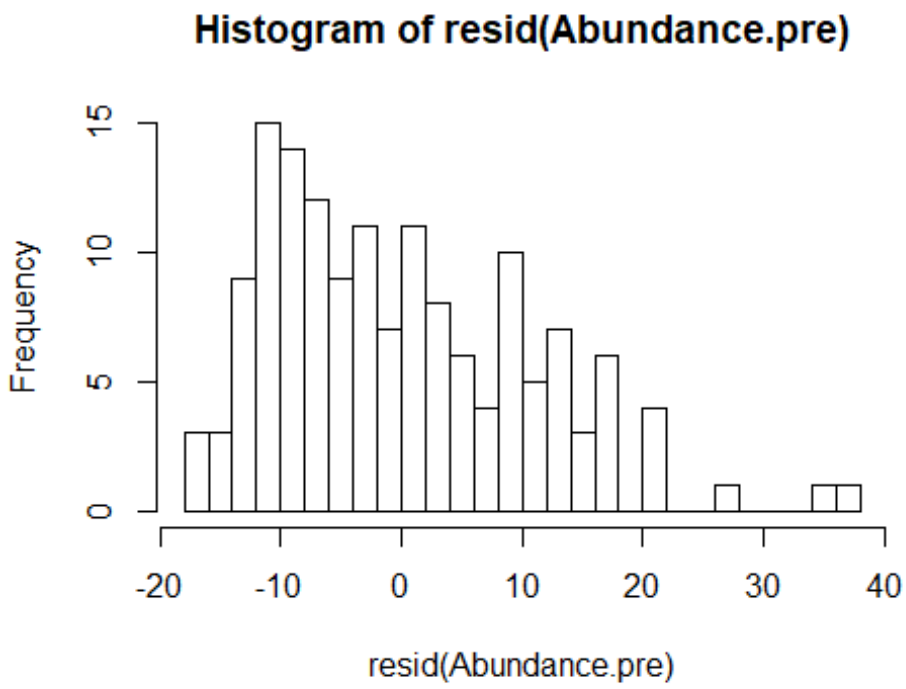
If the relationship between some of the predictor and the dependent variables is nonlinear, is necessary to use a proper model that accounts for the nonlinear effects.

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG,4)

##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727

## Base LM model to apply linearity test

Abundance.pre <- lm(Abundance ~ Recruitment, data=BIOVEG)
summary(Abundance.pre)

##
## Call:
## lm(formula = Abundance ~ Recruitment, data = BIOVEG)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -17.110  -9.205  -2.062   8.069  37.590
##
```

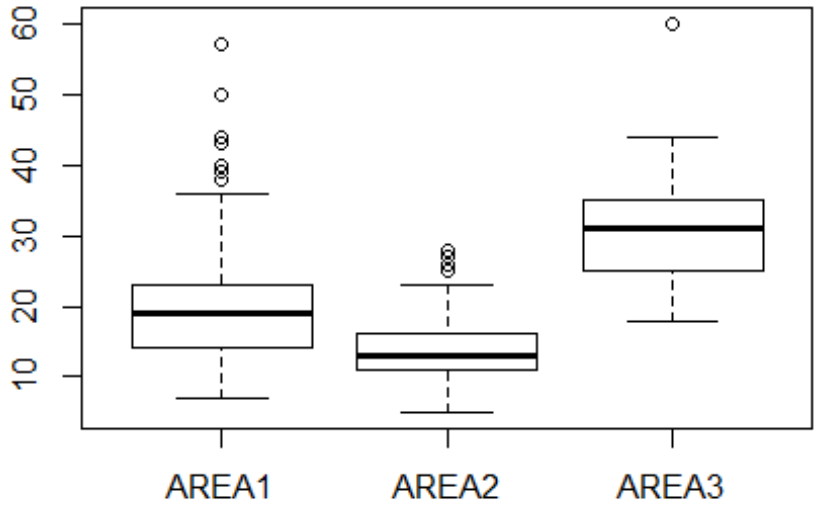
```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  22.5720     1.3076  17.262   <2e-16 ***
## Recruitment  -0.1530     0.3819  -0.401    0.689
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.85 on 148 degrees of freedom
## Multiple R-squared:  0.001083,   Adjusted R-squared:  -0.005667
## F-statistic: 0.1604 on 1 and 148 DF,  p-value: 0.6894

## Residuals

x11(width=12, height=12)
par(mfrow=c(2,2))
plot(Abundance.pre)
```



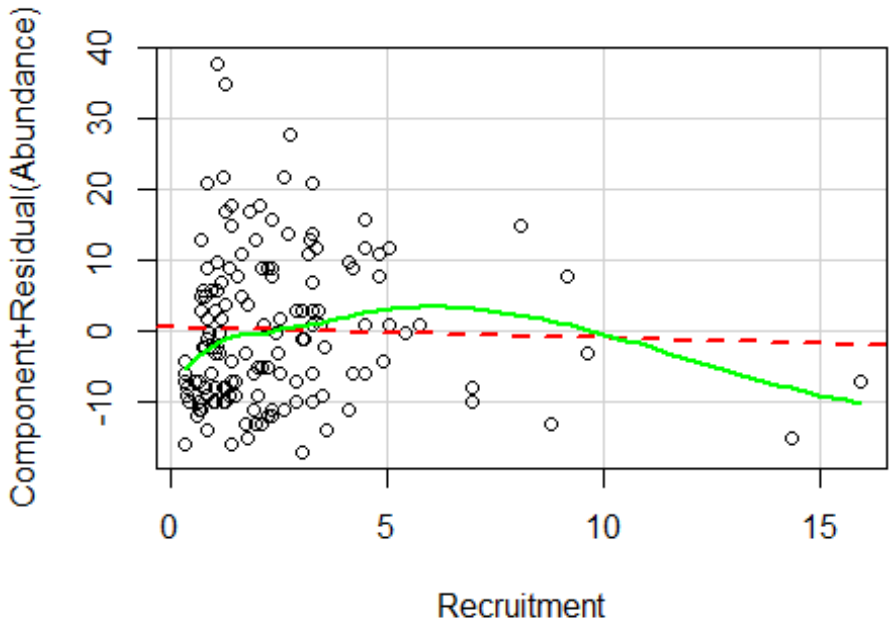

```
# dev.off() ## turn off the graphics device

hist(resid(Abundance.pre),breaks=20)
```




```r
# dev.off() ## turn off the graphics device
plot(BIOVEG$Site, BIOVEG$Abundance) # variation among sites
```



```
### Tests of linearity

library(car)

crPlots(Abundance.pre, col.lines=c("red", "green"))
```



If one find some nonlinear relationship between predictor and dependent variable using the diagnostic for linearity showed previously here, thus a model that account for nonlinear terms is necessary to carry the statistical prediction.

GNM model

```
# install.packages("gnm")
library(gnm)


Exp <- function(expression, inst = NULL){list(predictors =
list(substitute
(expression)), term = function(predictors, ...) {paste("exp(",
predictors, ")",
                    sep = "")}, call = as.expression(match.call()), match
= 1)}
class(Exp) <- "nonlin"
```

```r
N.gnm<- gnm(Abundance ~ Exp(Recruitment), data=BIOVEG, method = "gnmFit",
start = NULL, checkLinear = TRUE, verbose = FALSE, family="quasipoisson")

summary(N.gnm)
```

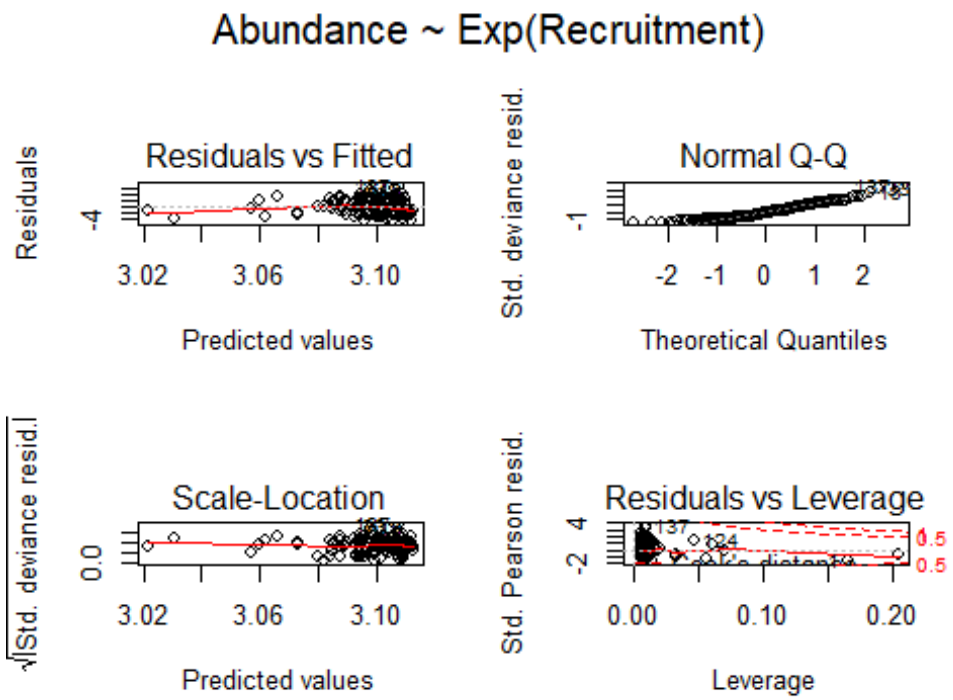
```
##
## Call:
##
## gnm(formula = Abundance ~ Exp(Recruitment), family = "quasipoisson",
##     data = BIOVEG, method = "gnmFit", checkLinear = TRUE, start =
NULL,
##     verbose = FALSE)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.4003  -2.1178  -0.4718   1.6239   6.5653
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)          2.114609   0.060506  34.949   <2e-16 ***
## Exp(.).Recruitment -0.006124   0.018796  -0.326    0.745
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 5.297747)
##
## Residual deviance: 758.18 on 148 degrees of freedom
## AIC: NA
##
## Number of iterations: 10
```

```r
An <- anova(N.gnm, test = "F")
An
```

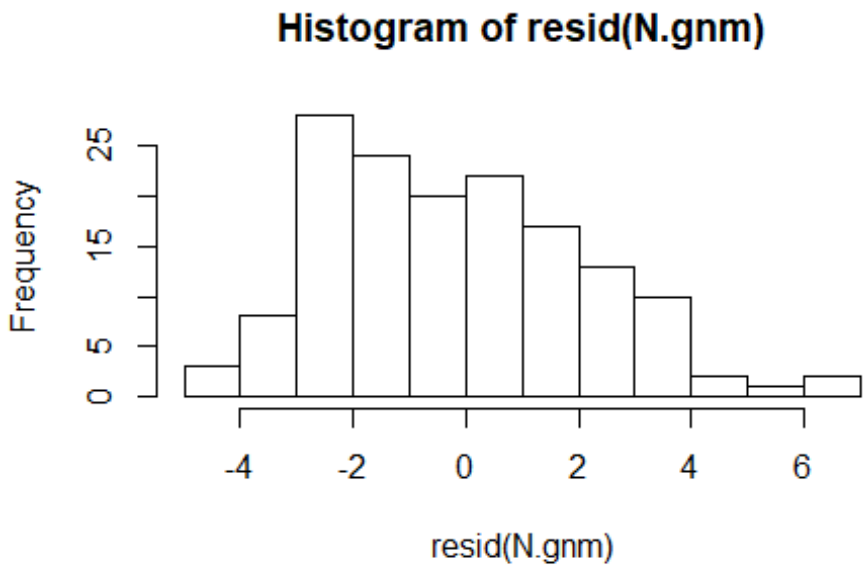
```
## Analysis of Deviance Table
##
## Model: quasipoisson, link: log
##
## Response: Abundance
##
## Terms added sequentially (first to last)
##
##
##                  Df Deviance Resid. Df Resid. Dev      F Pr(>F)
## NULL                                149     758.90
## Exp(Recruitment)  1  0.72765       148     758.18 0.1374 0.7115

## Residuals
```

```r
x11(width=12, height=12)
par(mfrow = c(2,2), oma = c(0, 0, 3, 0))
```

```
title <- paste(deparse(N.gnm$formula, width.cutoff = 50), collapse =
"\n")
plot(N.gnm, sub.caption = title)
```




```
par(mfrow = c(1,1))
hist(resid(N.gnm))
```

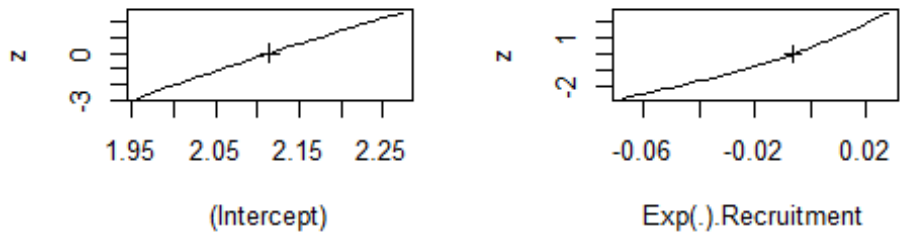



```
## Deviance profile (optional) - just similar to a summary

prof<- profile(N.gnm, which = ofInterest(N.gnm), alpha = 0.05, trace =
TRUE)

##
## Parameter: (Intercept) down
##
## Parameter: (Intercept) up
##
## Parameter: Exp(.).Recruitment down
##
## Parameter: Exp(.).Recruitment up

prof

## $`(Intercept)`
##            z par.vals.(Intercept) par.vals.Exp(.).Recruitment
## 1 -2.8403065          1.956489871                  0.020592763
## 2 -2.1157986          1.996019742                  0.015066410
## 3 -1.3995734          2.035549613                  0.008855133
## 4 -0.6935905          2.075079484                  0.001838984
## 5  0.0000000          2.114609355                 -0.006123605
## 6  0.6788685          2.154139226                 -0.015198816
## 7  1.3405281          2.193669097                 -0.025580770
## 8  1.9823610          2.233198968                 -0.037495562
## 9  2.6016481          2.272728839                 -0.051206839
```

```
##
## $`Exp(.).Recruitment`
##             z par.vals.(Intercept) par.vals.Exp(.).Recruitment
## 1  -2.6375990          2.241123018                -0.067522297
## 2  -2.2261319          2.218699511                -0.055242559
## 3  -1.7670464          2.195032442                -0.042962820
## 4  -1.2514221          2.169952893                -0.030683082
## 5  -0.6676060          2.143242561                -0.018403343
## 6   0.0000000          2.114609355                -0.006123605
## 7   0.2912927          2.102683614                -0.001272529
## 8   0.6005749          2.090364248                 0.003578546
## 9   0.9297606          2.077613865                 0.008429621
## 10  1.2810713          2.064388272                 0.013280696
## 11  1.6571012          2.050634724                 0.018131772
## 12  2.0608991          2.036289619                 0.022982847
## 13  2.4960714          2.021275411                 0.027833922
##
## attr(,"original.fit")
##
## Call:
##
## gnm(formula = Abundance ~ Exp(Recruitment), family = "quasipoisson",
##     data = BIOVEG, method = "gnmFit", checkLinear = TRUE, start =
NULL,
##     verbose = FALSE)
##
## Coefficients:
##        (Intercept)  Exp(.).Recruitment
##        2.114609355        -0.006123605
##
## Deviance:            758.1769
## Pearson chi-squared: 784.0666
## Residual df:         148
## attr(,"summary")
##
## Call:
##
## gnm(formula = Abundance ~ Exp(Recruitment), family = "quasipoisson",
##     data = BIOVEG, method = "gnmFit", checkLinear = TRUE, start =
NULL,
##     verbose = FALSE)
##
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -4.4003229  -2.1178163  -0.4718448   1.6238609   6.5653146
##
## Coefficients:
##                         Estimate   Std. Error  t value Pr(>|t|)
## (Intercept)         2.114609355  0.060506016 34.94875  < 2e-16 ***
## Exp(.).Recruitment -0.006123605  0.018795864 -0.32580  0.74504
```

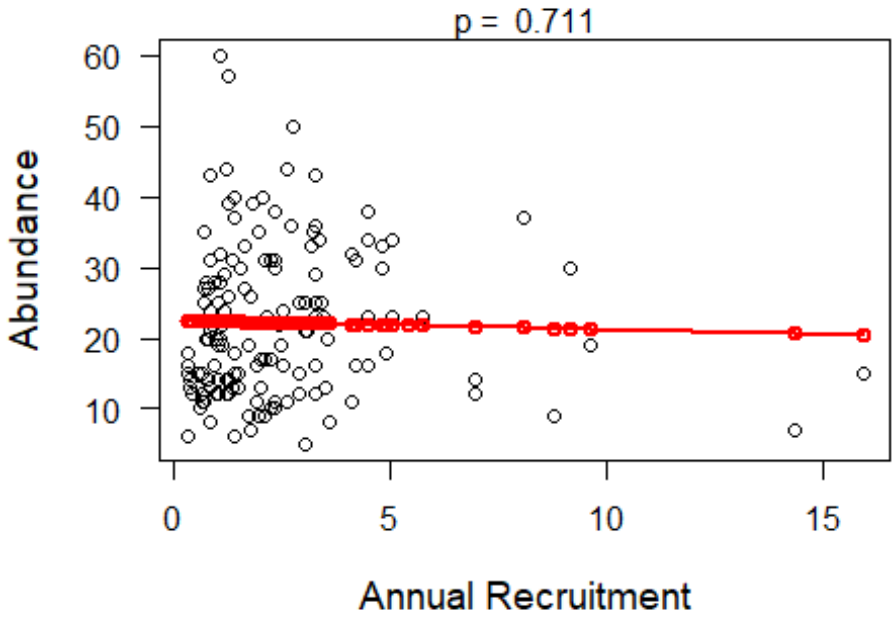
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 5.297747)
##
## Residual deviance: 758.17689 on 148 degrees of freedom
## AIC: NA
##
## Number of iterations: 10
##
## attr(,"class")
## [1] "profile.gnm" "profile.glm" "profile"
```

```
x11(width=12, height=8)
plot(prof)
```




```
# dev.off()

## scatterplot


x11(width=12, height=12)
plot(BIOVEG$Abundance ~ BIOVEG$Recruitment, ylab="Abundance",
xlab= "Annual Recruitment", las = 1, cex.lab=1.2)
points(BIOVEG$Recruitment, fitted(N.gnm), col = "red", lwd = 2)
Smooth <- smooth.spline(BIOVEG$Recruitment, fitted(N.gnm))
lines(Smooth, col = "red", lwd = 2)
```

```
mtext(ifelse(An[2,6]<0.001, "p < 0.001", paste("p = ",
round(An[2,6],3))))
```




```
# dev.off()
```

Note 1: If you need to coerce objects of class “glm” to an object of class “gnm” follow the procedure below.

```
Nall.glm<- glm(Abundance ~ Recruitment, data=BIOVEG,
family="quasipoisson")
N.gnm2<- update(asGnm(Nall.glm))
N.gnm2

##
## Call:
## gnm(formula = Abundance ~ Recruitment, family = "quasipoisson",
##     data = BIOVEG)
##
## Coefficients:
## (Intercept)  Recruitment
##    3.117131    -0.007054
##
## Deviance:            758.0411
## Pearson chi-squared: 783.8135
## Residual df:         148

anova(N.gnm2, test = "F")
```

```
## Analysis of Deviance Table
##
## Model: quasipoisson, link: log
##
## Response: Abundance
##
## Terms added sequentially (first to last)
##
##
##             Df Deviance Resid. Df Resid. Dev     F Pr(>F)
## NULL                          149     758.90
## Recruitment  1  0.86347       148     758.04 0.163  0.687
```

```
summary(N.gnm2)
```

```
##
## Call:
## gnm(formula = Abundance ~ Recruitment, family = "quasipoisson",
##     data = BIOVEG)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -4.399  -2.119  -0.451   1.632   6.557
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.117131   0.059166  52.684   <2e-16 ***
## Recruitment -0.007054   0.017604  -0.401    0.689
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 5.296138)
##
## Residual deviance: 758.04 on 148 degrees of freedom
## AIC: NA
##
## Number of iterations: 4
```

GAM (Generalized Aditive Models)

For a GAM model example, let's assume that we only have fixed effects data(e.g. vegetation type). We will use the same variables as used for the model in a pre- test for linearity ,using the function "crPlots" of the package "car". Since "P_mg_100g" and "K_mg_100g" demonstrated the greatest deviation from linearity, we apply a smoothing term (s) for them in the model.

```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)
```

```
##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
```

```r
# install.packages("mgcv")
library(mgcv) # carry out GAM model

spp.gam<- gam(log(Species.richness) ~ s(P_mg_100g) + s(K_mg_100g) +
Veg.cover,
                                        data=Hogweed,
family="gaussian")

summary(spp.gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## log(Species.richness) ~ s(P_mg_100g) + s(K_mg_100g) + Veg.cover
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.504829   0.075790  33.050  < 2e-16 ***
## Veg.cover   0.005250   0.001095   4.795 3.32e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Approximate significance of smooth terms:
##                edf Ref.df     F  p-value
## s(P_mg_100g) 5.987  6.993 3.956 0.000447 ***
## s(K_mg_100g) 7.544  8.421 2.087 0.050678 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.267   Deviance explained =   32%
## GCV = 0.19193  Scale est. = 0.1771    n = 201
```

In the summary, we can see two types of output: parametric coefficients, i.e., the slope of the predictor that indicated a linear relationship and was not subjected to smoothing and the non-linear predictors which were smoothed, showing their F and p-values for significance. The edf refers to the estimated degrees of freedom and basically, the larger the number, the wigglier the fitted model. Values close to 1 indicate a linear term.

```
anova(spp.gam) # the output is quite similar to the summary
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## log(Species.richness) ~ s(P_mg_100g) + s(K_mg_100g) + Veg.cover
##
## Parametric Terms:
##           df  F  p-value
## Veg.cover  1 23 3.32e-06
##
## Approximate significance of smooth terms:
##                edf Ref.df     F  p-value
## s(P_mg_100g) 5.987  6.993 3.956 0.000447
## s(K_mg_100g) 7.544  8.421 2.087 0.050678
```

Below we calculate a measure for correlation (analogous to collinearity) known as concurvity, between the predictors in the model, to consider non-linear correlations. The range is from 0 to 1. The closer the value is to 1, the higher the correlation. To know more about concurvity read:

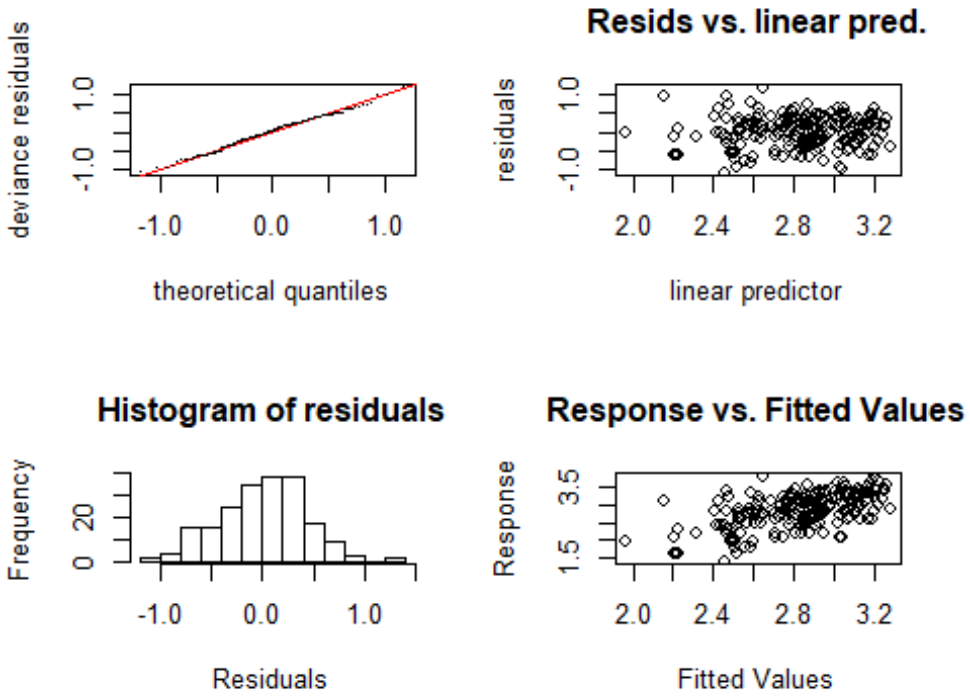
Marra, G. & Wood, S. N. Practical variable selection for generalized additive models. Comput. Stat. Data Anal. 55, 2372-2387 (2011).

```
concurvity(spp.gam, full=FALSE)
```

```
## $worst
##                       para s(P_mg_100g) s(K_mg_100g)
## para          1.000000e+00 1.496793e-25 4.372779e-26
## s(P_mg_100g) 1.509192e-25 1.000000e+00 9.988476e-01
## s(K_mg_100g) 4.316333e-26 9.988476e-01 1.000000e+00
##
```

```
## $observed
##                       para s(P_mg_100g) s(K_mg_100g)
## para          1.000000e+00 5.574905e-28 3.880743e-27
## s(P_mg_100g) 1.509192e-25 1.000000e+00 5.477266e-01
## s(K_mg_100g) 4.316333e-26 3.313584e-01 1.000000e+00
##
## $estimate
##                       para s(P_mg_100g) s(K_mg_100g)
## para          1.000000e+00  2.91690e-28 2.149244e-28
## s(P_mg_100g) 1.509192e-25  1.00000e+00 5.080148e-01
## s(K_mg_100g) 4.316333e-26  4.49389e-01 1.000000e+00
```

```
# Residuals

par(mfrow = c(2,2))
gam.check(spp.gam)
```




```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 8 iterations.
## The RMS GCV score gradient at convergence was 2.668476e-06 .
## The Hessian was positive definite.
## Model rank =  20 / 20
##
## 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(P_mg_100g) 9.00 5.99    1.09    0.83
## s(K_mg_100g) 9.00 7.54    1.14    0.95
```

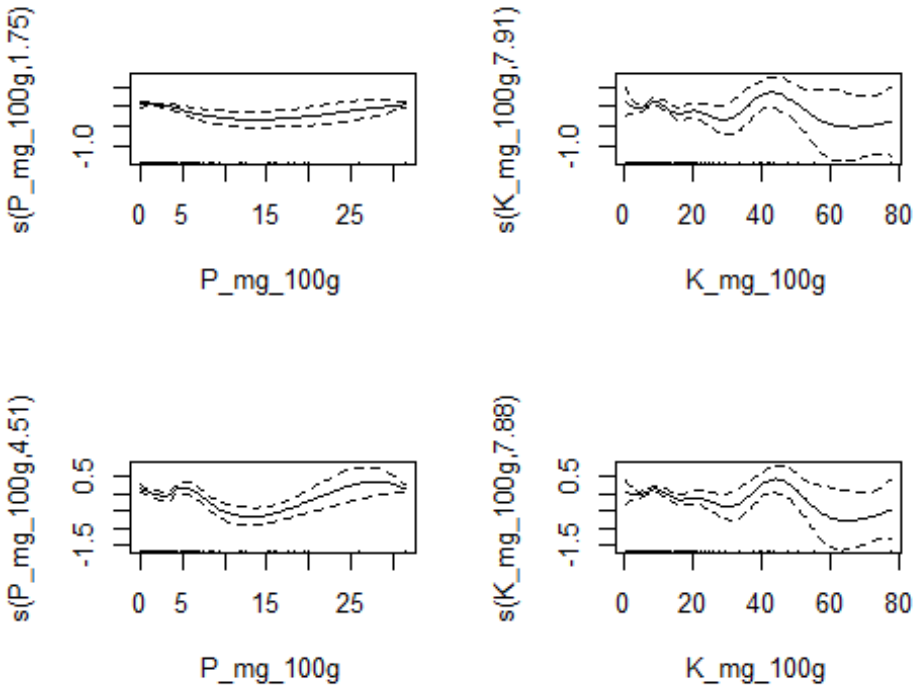
Here the graphical residuals look generally acceptable, since the histogram is not that nice (i.e. symmetrical).

Together with the graphical residuals, the model returns a written output that shows parameters for each predictor with its smoothing term e.g. “k”, “edf”, “K-index” and its p-value. “k-index” is the ratio of neighbor differencing scale estimate to fitted model scale estimate; “edf” is the previously mentioned estimated degrees of freedom and “k’” is the maximum possible EDF for the term. These parameters test whether the basis dimension for smoothing is adequate for the predictor.

For further details regarding this kind of residual diagnostic, please consult the documentation of the function “gam.check” of the package “mgcv”. One way to correctly apply a smoothing term for the predictor is to choose the most appropriate and insert it into the model using the argument “bs”. Look for “smooth.terms” in the mgcv documentation.

In order to test for improvement of the fit of the model, we included the type of smoothing with the argument “bs” and used “K” to choose the number of knots (k) once cubic regression splines have a set number of knots. The default of knots automatically defined by the model “spp.gam” was 9. Let’s test the model fit with 6 and 9 knots. Here we apply “cc” (cyclic cubic regression splines) smoothing to “bs” because of the observed tendency of non-linear fitting in a pre-diangostic graph with the function “crPLots” of package “car”. Here we test of redefine the knots for the predictor P_mg_100g because it was diagnosed as being the most non-linear, and improving its fit also may improve the overall fit of the model.

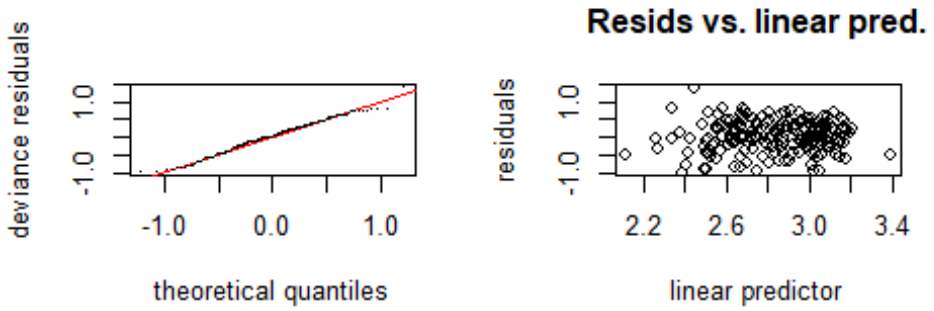
```
par(mfrow = c(2, 2))
spp.gam2<- gam(log(Species.richness) ~ s(P_mg_100g, bs='cc', k=6) +
               s(K_mg_100g) + Veg.cover, data=Hogweed, family="gaussian")
plot(spp.gam2)
spp.gam3<- gam(log(Species.richness) ~ s(P_mg_100g, bs='cc', k=9) +
                 s(K_mg_100g) + Veg.cover, data=Hogweed,
family="gaussian")
plot(spp.gam3)
```

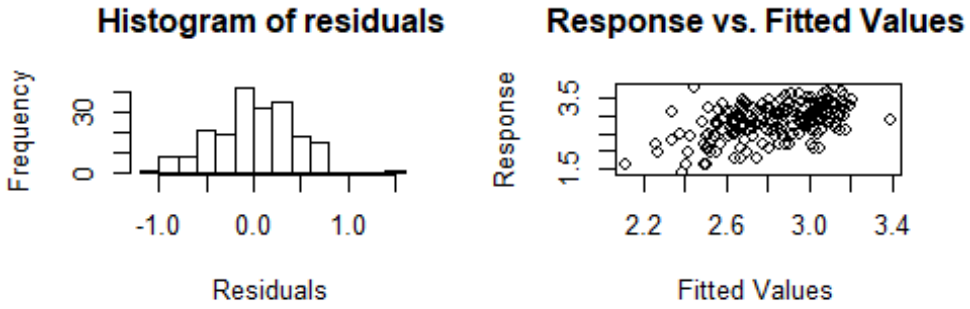


We can see that setting models with 6 and 9 knots provides similar model fitting. Thus, the first model (spp.gam) with 9 knots defined automatically by the model is already sufficient for a good model fit.

If we still call the residuals for each model test (6 and 9 knots), the degrees of freedom (EDF) of the smoothers are close especially for the predictor "K_mg_100g" and they k-index is nonsignificant.

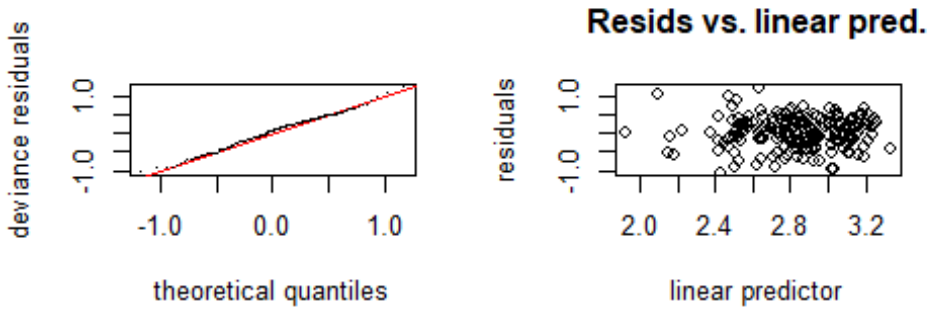
```
par(mfrow = c(2,2))
gam.check(spp.gam2)
```

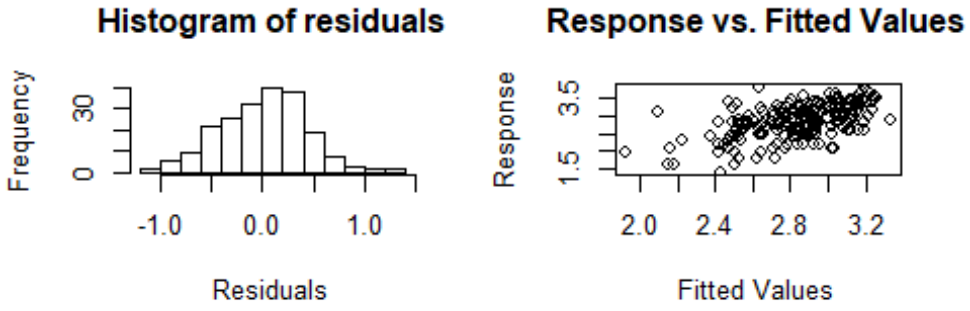





```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 11 iterations.
## The RMS GCV score gradient at convergence was 1.500108e-07 .
## The Hessian was positive definite.
## Model rank =  15 / 15
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                 k'  edf k-index p-value
## s(P_mg_100g) 4.00 1.75    0.99    0.44
## s(K_mg_100g) 9.00 7.91    1.18    0.99
```

```
par(mfrow = c(2,2))
gam.check(spp.gam3)
```






```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 6 iterations.
## The RMS GCV score gradient at convergence was 1.702051e-07 .
## The Hessian was positive definite.
## Model rank =  18 / 18
##
## 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(P_mg_100g) 7.00 4.51    1.08    0.85
## s(K_mg_100g) 9.00 7.88    1.15    0.99
```

GAMM (Generalized Aditive Mixed Models)

To simulate a GAMM model we take the dependent and almost all predictor variables as we used in the previous GAM example. Our intention here is to also include random effects in our modeling, rather than only fixed effects as we did in GAM analysis.

```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
```

```
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
```

```
library(mgcv) # carry out GAMM model

spp.gamm<- gamm(log(Species.richness) ~ s(Hogweed.cover) + s(P_mg_100g),
random =
                          list(Study.area = ~ 1), data=Hogweed,
family="gaussian")

summary(spp.gamm)
```

```
##     Length Class Mode
## lme 18     lme   list
## gam 31     gam   list
```

Similar to the summary of the GAM model, we have two types of output: parametric coefficients i.e., the slope of the predictor that indicated a linear relationship and was not smoothed and the non-linear predictors with smoothing and their F and p-values for significance.

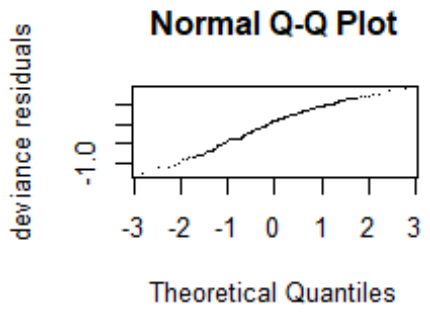
```
anova(spp.gamm$gam)
```

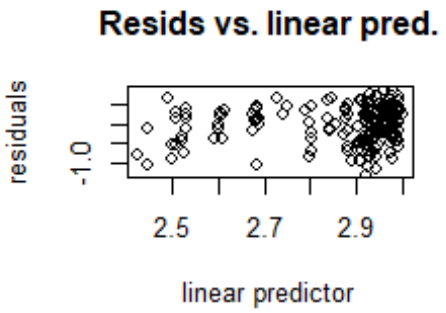
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## log(Species.richness) ~ s(Hogweed.cover) + s(P_mg_100g)
##
```

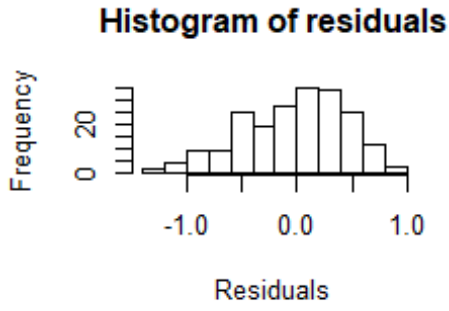
```
## Approximate significance of smooth terms:
##                     edf Ref.df      F  p-value
## s(Hogweed.cover) 2.528  2.528 11.014 4.22e-06
## s(P_mg_100g)     1.000  1.000  0.133    0.715
```

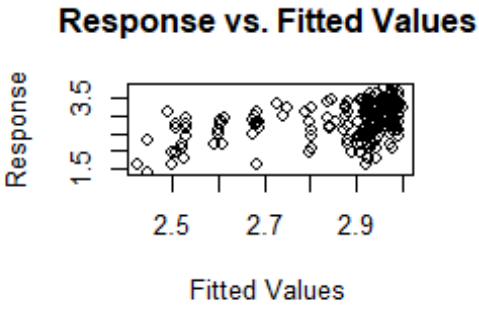
Below we again conduct a measure for by concurvity between the predictors in the model, to consider non-linear correlations.

```
concurvity(spp.gamm$gam, full=FALSE)

## $worst
##                          para s(Hogweed.cover) s(P_mg_100g)
## para             1.000000e+00     5.664068e-17 1.496793e-25
## s(Hogweed.cover) 5.664067e-17     1.000000e+00 1.688794e-01
## s(P_mg_100g)     1.479572e-25     1.688794e-01 1.000000e+00
##
## $observed
##                          para s(Hogweed.cover) s(P_mg_100g)
## para             1.000000e+00     4.617211e-23 4.695046e-33
## s(Hogweed.cover) 5.664067e-17     1.000000e+00 5.838020e-02
## s(P_mg_100g)     1.479572e-25     1.101885e-01 1.000000e+00
##
## $estimate
##                          para s(Hogweed.cover) s(P_mg_100g)
## para             1.000000e+00     9.403869e-20 2.916900e-28
## s(Hogweed.cover) 5.664067e-17     1.000000e+00 4.726491e-02
## s(P_mg_100g)     1.479572e-25     8.170693e-02 1.000000e+00

# Residuals
par(mfrow = c(2,2))
gam.check(spp.gamm$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(Hogweed.cover) 9.00 2.53    0.78   0.005 **
## s(P_mg_100g)     9.00 1.00    0.90   0.080 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Here the graphical residuals looks fine in general. However, the predictor "Hogweed.cover" has significant low p-value for k. In order to remember: "k-index" is the ratio of the neighbor differencing scale estimate to fitted model scale estimate; "edf" is the previously mentioned estimated degrees of freedom and "k" is the maximum possible EDF for the term. These parameters test whether the basis dimension for a smoothing is adequate for the predictor.Therefore, here you can try to improve the model by setting different number of knots (k) and maybe choosing another smooth term for this predictor (e.g. "gp" (Gaussian process), "tp" (Thin plate regression splines) and others. Please, check this out searching for "smooth.terms" documentation of the package mgcv.

SUPERVISED LEARNING

Random Forest

The Random Forest model is a supervised learning technique that generates multiple models from a training dataset on the given data and then simply combines their output rules (predictive variables), thus generating a robust high performance model that corrects overfitting and balances variance inequalities. That is, this model improves the predictive power from decision trees, reducing their variances by calculating their averages. The decision tree is a type of modeling that operates with information gain on each node, classifying data points with greater information increment on each node. When all nodes are depleted for their information gain ratings, the model achieves its optimal performance result. Thus, the Random Forest model is considered, in many cases, to be the most robust decision tree approach.

In its results, the Random Forest provides a percentage explanation of the Y variance from the whole set of predictors considered. It also provides the mean square residual error in the predictions from an approach called "Out of Bag Error Estimation (OBB)", a robust and efficient method of fitting and error estimation.

```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
Hogweed$Plot <- as.integer(Hogweed$Plot) # Transform predictor Plot that
is factor
                                        # in integer, since random Forest
cannot
                                        # handle more the 53 categories
head(Hogweed,4)
```

```
##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1    1        VOL ruderal.grass 2002        0.5        70
18
## 2  110        VOL ruderal.grass 2002        0.7        65
19
## 3  126        VOL ruderal.grass 2002        0.4        30
16
## 4  137        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
```

```
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34

# install.packages("randomForest")

library(randomForest)
```

Below we split our data in train (70% of data) and test (30% of data) sets.

```
set.seed(100)
train <- sample(nrow(Hogweed), 0.7*nrow(Hogweed), replace = FALSE)
train <- sort(train)
TrainSet <- Hogweed[train,] # split the data in train set
TestSet <- Hogweed[-train,] # split the data in test set
head(TrainSet)# visualize if all variables are present in train set

##    Plot Study.area  Habitat.type Year Veg.height Veg.cover
## 2   110        VOL ruderal.grass 2002        0.7        65
## 3   126        VOL ruderal.grass 2002        0.4        30
## 4   137        VOL ruderal.grass 2002        0.9        90
## 5   148        VOL ruderal.grass 2002        0.7        75
## 8   181        REN ruderal.grass 2002        0.8        90
## 12   22        REN agr.grassland 2002        0.7        95
##    Species.richness Hogweed.height Hogweed.cover    Land.use
Disturbance
## 2                19            1.4            65        NONE
TREESHRUB
## 3                16            1.7            90        NONE
TREESHRUB
## 4                23            1.0            20        NONE
NONE
## 5                27            0.8            20        NONE
NONE
## 8                32            1.1            45 MAINTENANCE
NONE
## 12               27            0.6             5   GRASSLAND
NONE
##    Altitude Inclination Exposition N_perc P_mg_100g K_mg_100g
## 2   295.653           2          W   0.19      3.56     12.49
## 3   295.653           2          W   0.19      8.44     39.95
## 4   292.112           2          W   0.12      2.53     12.34
## 5   292.112           2          W   0.12      2.53     12.34
## 8   371.930           2          S   0.21      0.55      6.97
## 12  377.433           1          S   0.22      7.44     18.27

head(TestSet)# visualize if all variables are present in test set
```

```
##    Plot Study.area  Habitat.type Year Veg.height Veg.cover
## 1     1        VOL ruderal.grass 2002        0.5        70
## 6   159        VOL      woodland 2002        0.2         5
## 7   170        REN agr.grassland 2002        0.8        95
## 9   191        REN ruderal.grass 2002        0.8        90
## 10    2        REN agr.grassland 2002        0.7        90
## 11   11        REN    tall.herbs 2002        0.5        20
##    Species.richness Hogweed.height Hogweed.cover    Land.use
Disturbance
## 1                18            0.9            80        NONE
TREESHRUB
## 6                16            0.8            10        NONE
NONE
## 7                33            1.0            45   GRASSLAND
SOILDIS
## 9                19            1.1            85 MAINTENANCE
NONE
## 10               28            0.8            10   GRASSLAND
NONE
## 11               16            1.8            90        NONE
SOILDIS
##    Altitude Inclination Exposition N_perc P_mg_100g K_mg_100g
## 1   295.653           2          W   0.19      3.99     22.27
## 6   298.394           2         NW   0.16      2.62     10.77
## 7   394.018           2          S   0.24      5.42     20.46
## 9   371.930           2          S   0.21      0.55      6.97
## 10  374.018           0          0   0.22      5.86     15.13
## 11  379.444           0          0   0.38      0.96     20.34
```

```
summary(TrainSet)# visualize if all data for train set is correct, i.e.
```

```
##       Plot          Study.area        Habitat.type      Year
##  Min.   :  4.00   NIE    :14   agr.grassland:28    Min.   :2002
##  1st Qu.: 55.75   RUH    :14   ruderal.grass:38    1st Qu.:2002
##  Median :103.00   HEL    :13   tall.herbs   :46    Median :2002
##  Mean   :103.11   ENG    :11   wasteland    :13    Mean   :2002
##  3rd Qu.:150.25   DOM    :10   woodland     :15    3rd Qu.:2003
##  Max.   :200.00   BRE    : 9                      Max.   :2003
##                   (Other):69
##    Veg.height       Veg.cover     Species.richness Hogweed.height
##  Min.   :0.1000   Min.   : 1.00   Min.   : 4.00    Min.   :0.2500
##  1st Qu.:0.3500   1st Qu.:40.00   1st Qu.:13.00    1st Qu.:0.6875
##  Median :0.5000   Median :80.00   Median :18.00    Median :0.9000
##  Mean   :0.5539   Mean   :64.49   Mean   :19.44    Mean   :0.9246
##  3rd Qu.:0.7000   3rd Qu.:90.00   3rd Qu.:25.25    3rd Qu.:1.1000
##  Max.   :1.7000   Max.   :99.00   Max.   :47.00    Max.   :1.9000
##
##  Hogweed.cover          Land.use     Disturbance    Altitude
##  Min.   : 1.00   GRASSLAND  :18   DEPORG   : 6   Min.   :127.6
##  1st Qu.:10.00   MAINTENANCE:26   FLOOD    :13   1st Qu.:208.0
```

```
##  Median :20.00   NONE       :96   NONE     :99   Median :322.0
##  Mean   :34.55                    SOILDIS  : 7   Mean   :357.9
##  3rd Qu.:60.00                    TREESHRUB:15   3rd Qu.:439.5
##  Max.   :95.00                                   Max.   :977.0
##
##   Inclination     Exposition     N_perc         P_mg_100g
##  Min.   : 0.0   0      :95   Min.   :0.0400   Min.   : 0.000
##  1st Qu.: 0.0   W      :12   1st Qu.:0.2100   1st Qu.: 0.525
##  Median : 0.0   E      :10   Median :0.2700   Median : 1.405
##  Mean   : 1.4   SW     : 8   Mean   :0.2853   Mean   : 3.128
##  3rd Qu.: 2.0   S      : 5   3rd Qu.:0.3425   3rd Qu.: 3.377
##  Max.   :30.0   N      : 4   Max.   :1.0300   Max.   :31.420
##                 (Other): 6
##    K_mg_100g
##  Min.   : 1.440
##  1st Qu.: 5.728
##  Median : 8.329
##  Mean   :11.639
##  3rd Qu.:13.135
##  Max.   :77.769
##
```

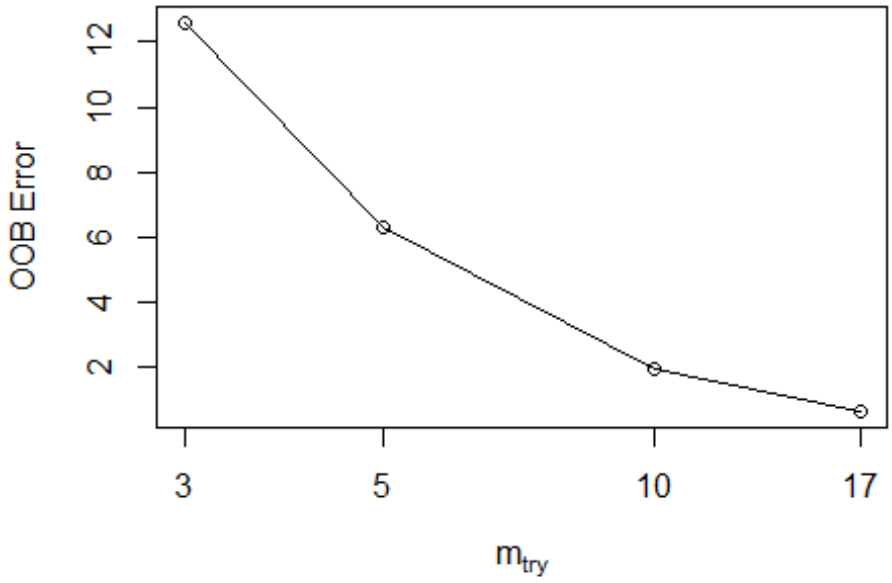
```
# Min, Median, Mean, Max...
summary(TestSet) # visualize if all data for test set is correct
```

```
##       Plot          Study.area        Habitat.type      Year
##  Min.   :  1.00   GOE    : 6   agr.grassland: 8    Min.   :2002
##  1st Qu.: 46.00   NIE    : 6   ruderal.grass:15    1st Qu.:2002
##  Median :100.00   WAT    : 6   tall.herbs    :31    Median :2002
##  Mean   : 96.16   RUH    : 5   wasteland     : 3    Mean   :2002
##  3rd Qu.:156.00   WEN    : 5   woodland      : 4    3rd Qu.:2003
##  Max.   :201.00   DAH    : 4                        Max.   :2003
##                   (Other):29
##    Veg.height       Veg.cover    Species.richness Hogweed.height
##  Min.   :0.2000   Min.   : 5.0   Min.   : 5.00    Min.   :0.300
##  1st Qu.:0.4000   1st Qu.:40.0   1st Qu.:13.00    1st Qu.:0.800
##  Median :0.5000   Median :70.0   Median :17.00    Median :1.000
##  Mean   :0.5893   Mean   :61.9   Mean   :18.33    Mean   :1.023
##  3rd Qu.:0.7000   3rd Qu.:90.0   3rd Qu.:24.00    3rd Qu.:1.200
##  Max.   :1.4000   Max.   :98.0   Max.   :46.00    Max.   :2.400
##
##  Hogweed.cover          Land.use     Disturbance    Altitude
##  Min.   : 5.00   GRASSLAND  : 6   DEPORG   : 5   Min.   :104.5
##  1st Qu.:15.00   MAINTENANCE: 7   FLOOD    : 8   1st Qu.:206.9
##  Median :40.00   NONE       :48   NONE     :36   Median :316.1
##  Mean   :43.11                    SOILDIS  : 7   Mean   :329.7
##  3rd Qu.:75.00                    TREESHRUB: 5   3rd Qu.:355.0
##  Max.   :90.00                                   Max.   :978.0
##
##   Inclination       Exposition     N_perc         P_mg_100g
```

```
##  Min.   : 0.000   0      :28   Min.   :0.0900   Min.   : 0.020
##  1st Qu.: 0.000   S      : 8   1st Qu.:0.2000   1st Qu.: 0.820
##  Median : 1.000   W      : 8   Median :0.2500   Median : 2.280
##  Mean   : 1.918   E      : 5   Mean   :0.2721   Mean   : 3.431
##  3rd Qu.: 2.000   N      : 5   3rd Qu.:0.3400   3rd Qu.: 4.040
##  Max.   :25.000   NW     : 2   Max.   :0.7200   Max.   :26.010
##                   (Other): 5
##    K_mg_100g
##  Min.   : 0.75
##  1st Qu.: 6.32
##  Median : 7.90
##  Mean   :12.39
##  3rd Qu.:14.78
##  Max.   :47.74
##
```

Verify the best number of predictors (mtry) per node (split) in the branches of the decision trees. The function "mtry" shows from which number of predictors per node the prediction errors are lower, based on OBB error (Out of bag) estimation.

```
# check how many predictors per node reduce error:

tuneRF(Hogweed, Hogweed$Species.richness)

## mtry = 5  OOB error = 6.304418
## Searching left ...
## mtry = 3     OOB error = 12.58651
## -0.9964583 0.05
## Searching right ...
## mtry = 10    OOB error = 1.960619
## 0.6890087 0.05
## mtry = 17    OOB error = 0.6492911
## 0.6688337 0.05
```




```
##    mtry   OOBError
## 3     3 12.5865073
## 5     5  6.3044180
## 10   10  1.9606194
## 17   17  0.6492911
```

The outcome shows that increasing the number of predictors per node of the trees decreases the error. Thus, we include all predictors (16) per node in the model.

Random Forest Model

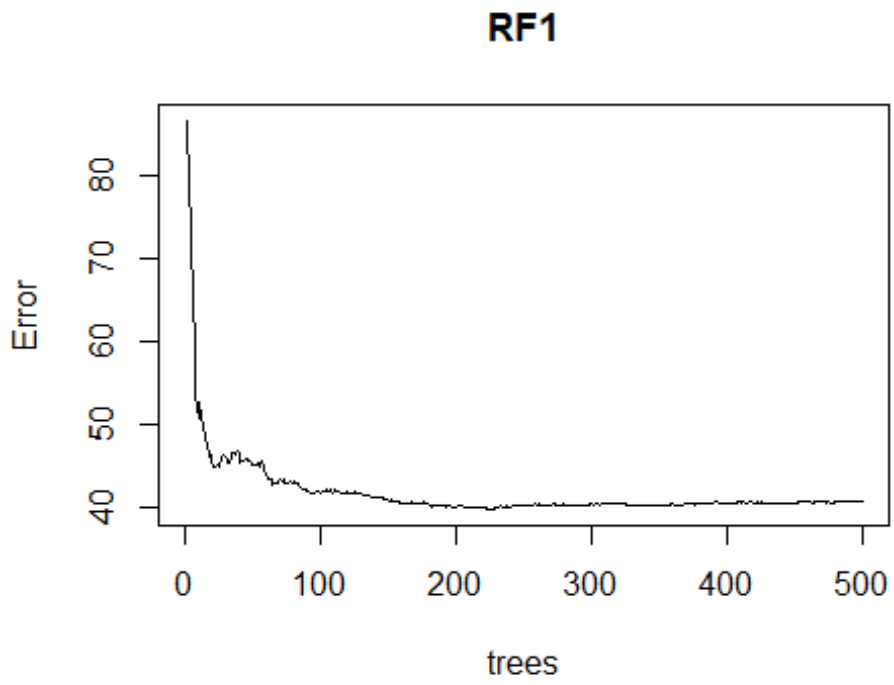
```
set.seed(100)
RF1 <- randomForest(Species.richness ~ ., data=Hogweed,
                    subset=train, mtry = 16, importance=TRUE, ntree=500)

print(RF1)

##
## Call:
##  randomForest(formula = Species.richness ~ ., data = Hogweed,
mtry = 16, importance = TRUE, ntree = 500, subset = train)
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 16
##
```

```
##           Mean of squared residuals: 40.6848
##                     % Var explained: 47.48
```

The model with train subset performed poorly regarding the percentage of variance explained in the prediction of species richness by the selected set of predictors.

Let's see if the number of decision (500) chosen for the model were enough to reduce the errors:

```
plot(RF1)
```



The output shows that 500 trees are sufficient to reduce error, since from approximately 100 trees, the error starts to decrease.

Importance of predictors

Here we check which predictors are the least and most important when predicting the variation of the dependent variable. The variable importance in Random Forest is computed based on Node Purity and Mean squared error. Node purity measures the total decrease of impurities in the nodes (splits) by computing the average of each predictor over the nodes of all trees, being measured, in regression, by the sum of the squares residuals. Of these two approaches for importance, Mean squared error (%IncMSE) is the most robust and informative measure, where the higher number, the more important the variable. Conversely, IncNodePurity is biased and should only be used if the extra computation time of calculating %IncMSE is challenging. Since the

%IncMSE is calculated based on OBB estimation, the expectation is that the MSE will increase, especially if the variable has some importance, thus the label "% IncMSE".

```
import<- importance(RF1)
import

##                   %IncMSE IncNodePurity
## Plot            5.5707559     294.35118
## Study.area     37.1460387    5757.91498
## Habitat.type   10.9296666     558.60044
## Year            1.7781753       5.62926
## Veg.height      4.6763764     250.32433
## Veg.cover      12.7326538     652.26748
## Hogweed.height 10.7277820     627.23769
## Hogweed.cover   2.2307121     341.24214
## Land.use       -0.8118798      27.13485
## Disturbance     8.2167514     221.78219
## Altitude        6.3721603     387.67738
## Inclination     1.0159853      66.17019
## Exposition      6.1613376     228.69195
## N_perc          0.4512169     389.86253
## P_mg_100g       3.2757968     362.76719
## K_mg_100g       3.2115987     378.80948
```

The outcome states that the most important predictors based on %IncMSE. Remember that the higher number, the more important the variable.

```
### save output of importance

write.table(import, "Importance.csv", row.names=T, sep=",", dec=".")
```

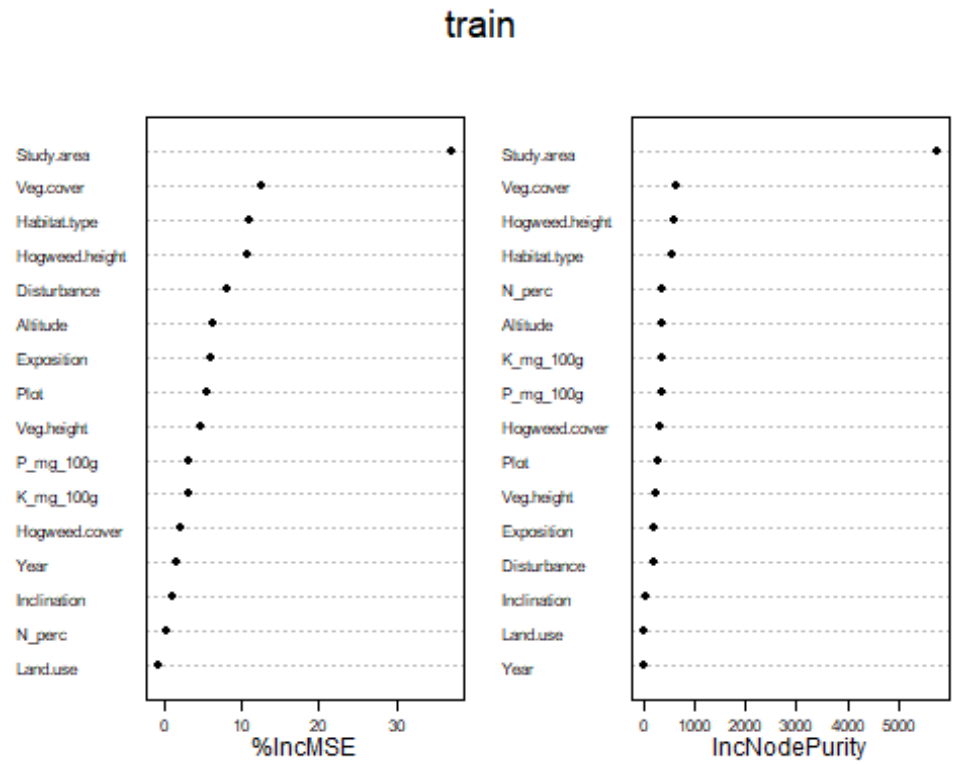
Note: Prior to selecting the predictor variables for the Random Forest model, verify whether there is high correlation among them. The presence of highly correlated predictors may bias the computation of importance of each one, for predicting the dependent variable, leading to suboptimal predictor variables being artificially and arbitrarily preferred. For more information about this topic, please read the recommended papers below:

Strobl C, Boulesteix AL, Zeileis A, Hothorn T.Bias in random forest variable importance measures: illustrations, sources and a solution. BMC Bioinformatics, 2007 Jan 25;8:25

Strobl C et al. Conditional variable importance for random forests. BMC Bioinformatics, BMC Bioinformatics. 2008 Jul 11;9:307

```
# Shows and save importance graphically

# library(lattice) # save the figure:
# tiff(filename="Fig_IMPORTANCE2019.jpg", width=180, height=80,
units="mm", res=300)
```

```
varImpPlot(RF1, sort=TRUE, main=deparse(substitute(train)),
           cex.lab=1.5, las=1, bty="n", cex=0.5,pch=19, col='black')
```




```
# dev.off() ## turn off the graphics device
```

Comparison of the level of error

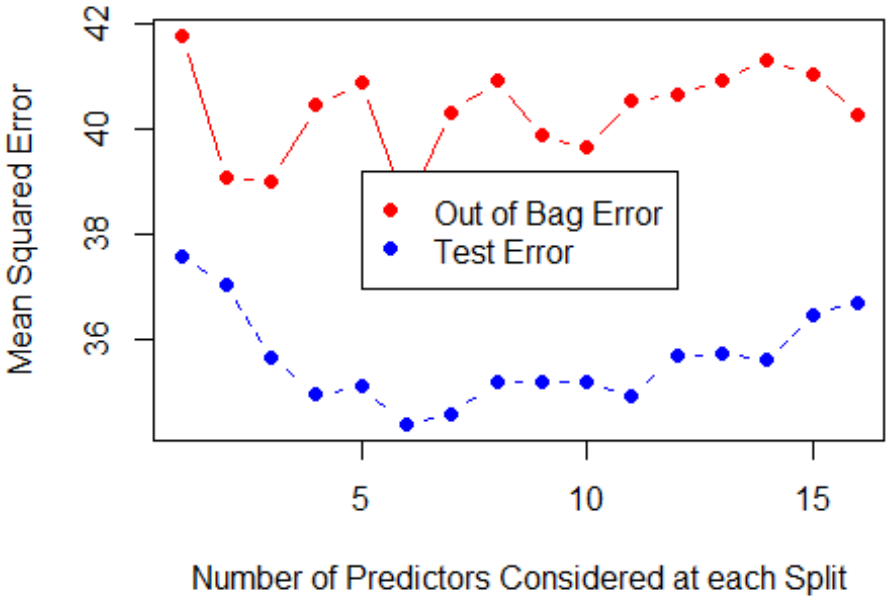
Here we compare the level of error of the model in relation to the number of predictors per node for the train (70%) and test (30%) set.

The OBB (out of bag error estimation) is computed to the train set and compared to the test set (test.err).

Here we simulate whether the inclusion of all predictors per node of the trees delivers a better or worse performance for the random forest prediction of both train and test set. Then, we reduce the number of trees from 500 to 400 to better fit the whole number of predictors per node.

```
oob.err=double(16) # 16 regards to total number of predictors
test.err=double(16)

for(mtry in 1:16)
{
  rf=randomForest(Species.richness ~ . , data = Hogweed , subset =
train,mtry=mtry,ntree=400)
  oob.err[mtry] = rf$mse[400] # Error of all trees adjusted
```

```
  pred<-predict(rf,Hogweed[-train,]) # Prediction in test set for each
tree
  # Mean Squared Test Error:
  test.err[mtry]= with(Hogweed[-train,], mean( (Species.richness -
pred)^2))

  cat(mtry," ") # show the outcome in R console

}

## 1  2  3  4  5  6  7  8  9  10  11  12  13  14  15  16

test.err

##  [1] 37.56997 37.04643 35.65082 34.96186 35.11245 34.40052 34.58925
##  [8] 35.19916 35.18508 35.20572 34.94613 35.69522 35.74131 35.61271
## [15] 36.48326 36.70819

oob.err

##  [1] 41.77874 39.09036 39.01873 40.45448 40.88128 38.47648 40.33007
##  [8] 40.92160 39.89282 39.65230 40.56144 40.65620 40.93758 41.32343
## [15] 41.05698 40.28447

matplot(1:mtry , cbind(oob.err,test.err), pch=19 ,
col=c("red","blue"),type="b",
        ylab="Mean Squared Error",xlab="Number of Predictors Considered
at each Split")
legend("center",legend=c("Out of Bag Error","Test Error"),pch=19,
col=c("red","blue"))
```



The graph shows that the mean squared error increases slightly in both Out of bag error and test error as the number of predictors increases at each split (node).

In addition, we can check the performance using cross-validation prediction of models with the number of predictors reducing sequentially. In such reduction, the predictors are ranked by variable importance via a nested cross-validation procedure.

```
rfcv(Hogweed, Hogweed$Species.richness, cv.fold=5)
```

```
## $n.var
## [1] 17  8  4  2  1
##
## $error.cv
##        17         8         4         2         1
## 8.1906159 7.5375960 2.3589484 2.8383323 0.2002621
##
## $predicted
## $predicted$`17`
##   [1] 17.672433 18.030300 15.337233 22.282800 24.021633 16.897033
28.913267
##   [8] 30.135833 21.520233 26.856300 16.746733 27.260633 15.721633
13.453567
##  [15] 16.507900 19.716600 19.747133 15.485233 23.652200 16.815933
24.503100
##  [22] 22.552900 17.388367 14.350433 20.736033 19.691367 17.359300
22.121633
##  [29] 23.384767 16.301267 18.328810 16.987533 21.580133 28.771967
```

```
29.188067
##  [36] 26.065800 26.761333 26.772533 17.291400 14.992867 17.186533
17.125033
##  [43] 15.659167 27.405367 25.042533 18.814633 26.539867 24.301533
23.922633
##  [50] 16.988333 23.194133 18.075133 20.801600 20.664733 13.250767
21.020300
##  [57] 16.391500 23.097700 15.034967 23.521000 19.750467 19.035967
19.168633
##  [64] 12.197600 34.648433 37.296667 34.424167 35.882700 18.934800
18.836767
##  [71] 33.501167 33.183117 33.556867 35.460467 32.355019 31.523833
31.131150
##  [78] 35.963300 34.821252 24.151800 18.554567 19.276467 26.590133
17.334467
##  [85] 23.964333 33.287267 34.879767 30.707700 28.321700 11.301900
27.049000
##  [92] 20.093867 15.456833 21.126567 26.666367 17.503700 11.657867
10.735600
##  [99] 25.840033 12.995600 24.447533 13.827533 17.571000 13.038833
13.499533
## [106] 25.906633 13.412100 12.218733 12.546467 17.482067 16.671900
11.202300
## [113] 19.190967 21.911667 16.418367 25.308133 25.034100 18.914567
12.792400
## [120] 15.181300 16.227733 13.116067 16.928833 13.013033  9.636533
19.637000
## [127] 20.578267 20.131900 21.181867 14.218033 16.712400 12.863433
12.921967
## [134] 13.020267 10.116367 23.466033 20.984467 19.057300 10.998900
10.120700
## [141]  9.287533 18.225333  9.547233  9.134967  8.096767 10.089367
8.693533
## [148] 10.924900  9.687600 24.000233 14.142300 13.719800 12.156467
12.001210
## [155] 20.968167 20.483967 15.667233 11.203767 19.519567 12.295833
13.258667
## [162] 13.845200 14.621967 15.481133 19.361033 12.083700 19.578633
13.317233
## [169] 14.865433  9.688533 15.565467 22.156700 13.765967 13.456500
18.772900
## [176] 19.198500 24.825433 24.813933 24.400967 15.700033 15.560467
12.014700
## [183] 12.644733 16.194233 11.878667 13.769267 24.687300 17.350267
17.200533
## [190] 15.981167 23.297533 17.945867 16.097367 24.255900 17.967033
11.776433
## [197]  8.376100 10.382467  9.064367 13.487167  9.122070
##
## $predicted$`8`
```

```
##   [1] 18.116733 18.126933 15.723933 22.454233 24.285667 16.398400
29.517467
##   [8] 29.963467 22.252033 27.218952 17.309400 27.075233 15.536100
12.620533
##  [15] 16.625233 20.241433 19.972967 15.291467 24.122667 16.771933
24.833400
##  [22] 22.103367 16.993800 14.029033 21.285200 19.938267 17.170667
21.810833
##  [29] 23.199733 16.683500 18.138267 16.906467 21.281517 29.320400
29.480067
##  [36] 26.056467 27.337767 26.539644 17.502833 14.980733 17.348533
17.096700
##  [43] 16.152967 26.927667 24.674417 17.953719 26.677167 24.512167
23.674633
##  [50] 16.476633 23.604467 18.917233 20.689300 21.145200 14.290233
21.287433
##  [57] 16.929605 22.788733 14.713551 23.325417 19.193729 19.671600
19.142833
##  [64] 11.580233 34.646300 37.674133 33.600860 36.438800 18.194833
17.889467
##  [71] 34.581089 33.990619 33.871003 35.782237 31.630133 31.568895
30.632357
##  [78] 36.010570 35.352333 23.402848 17.586800 18.367733 27.925500
17.136033
##  [85] 23.778133 33.513500 35.149200 30.216333 28.386048 11.168900
26.099367
##  [92] 20.632433 15.224500 20.282500 26.349352 16.572314 10.853590
10.018400
##  [99] 26.105267 12.398033 24.829967 13.971211 17.908500 12.965700
12.644400
## [106] 25.938133 12.814267 11.794100 12.365571 17.487189 16.183822
10.824133
## [113] 19.566083 21.403833 16.790533 25.751767 25.046300 18.981100
12.734217
## [120] 15.307400 16.545148 13.253267 17.106744 12.791500  9.175417
19.800333
## [127] 20.900289 19.650748 20.956702 13.157933 16.599721 12.890300
13.050700
## [134] 13.447033 10.493267 23.443367 20.432548 18.341200 10.189233
9.109056
## [141]  8.470224 17.970205  8.876167  8.468467  7.727737  9.864000
7.637333
## [148] 11.161133 10.037378 23.758833 13.002300 12.467600 13.099267
11.540633
## [155] 20.825200 20.320633 15.355167 11.915652 20.090500 12.285867
13.461900
## [162] 14.167667 15.082633 15.264667 19.589133 12.044767 19.478533
12.663900
## [169] 14.029000  9.381533 15.104767 22.091367 13.700367 12.204567
19.020767
```

```
## [176] 18.804800 26.312500 25.430600 24.673867 15.513867 15.223122
11.019733
## [183] 11.540633 16.449700 11.563200 13.683000 24.501300 17.617633
17.253200
## [190] 16.538467 23.473733 18.063133 16.176200 23.753533 18.022900
11.770067
## [197]  8.699633 11.045514  8.279405 12.382867  8.730467
##
## $predicted$`4`
##   [1] 17.750167 18.466400 16.463486 22.696867 25.482767 16.509300
30.831333
##   [8] 31.563824 19.849000 27.984700 17.509233 27.711600 16.321033
12.082710
##  [15] 16.505933 19.929367 19.960767 13.345500 24.779633 16.891033
25.840567
##  [22] 23.781867 18.819767 13.786767 22.185633 19.621900 18.111729
22.974833
##  [29] 23.548717 14.315633 17.749367 17.434067 22.896033 30.233400
30.114533
##  [36] 24.698967 27.248367 28.303600 16.544633 14.148200 13.839567
15.686333
##  [43] 15.941600 28.901067 24.559567 16.581233 28.406767 24.902133
23.747433
##  [50] 15.290767 23.963933 18.996833 20.171867 20.638967 10.823533
22.096967
##  [57] 15.988533 23.364100 12.915667 24.937500 19.775067 19.495833
19.332933
##  [64] 10.041567 38.423719 39.251933 33.473267 37.672843 17.778433
17.875167
##  [71] 36.410476 32.496133 33.923733 37.679667 32.597395 32.953867
29.819300
##  [78] 37.929033 37.975662 27.130800 16.481833 17.497656 27.634400
14.211567
##  [85] 26.671700 36.368010 33.783367 31.540433 30.491233  7.590767
29.423967
##  [92] 20.375567 14.521233 23.098233 27.788167 11.939467  8.732333
7.345867
##  [99] 27.775033 10.179133 24.565400 12.338067 14.354389 13.715000
11.535067
## [106] 27.672767 12.465609  9.570033 11.614776 17.443833 17.251300
10.133972
## [113] 19.850408 22.378731 18.067008 28.004567 25.957386 19.995667
13.836188
## [120] 14.856810 16.913900 13.061010 17.246547 12.163976 10.102440
22.359767
## [127] 21.681471 20.255424 21.866667 12.123310 17.356333 11.366974
11.571700
## [134] 12.514600  8.733243 25.397267 22.448857 18.832767 11.164756
9.326433
## [141]  7.127914 20.512133  7.124732  8.702437  6.914995  9.219770
```

```
6.767932
## [148]  8.740200 10.283953 26.025367 13.127467  8.618733 11.518867
12.318400
## [155] 21.395200 20.650800 14.775233 11.834176 20.594133  8.933057
11.965867
## [162] 12.787900 14.311533 15.684467 19.305100 11.397092 20.404967
13.187200
## [169] 12.799267  7.679048 16.472038 23.254933 14.022300  8.728633
19.046300
## [176] 19.552300 27.749967 27.810200 24.189333 15.367367 14.879600
10.721067
## [183] 12.573667 15.732900  9.634867 12.902543 28.063500 17.034067
16.789124
## [190] 16.160500 24.752733 17.044157 15.420533 26.447033 18.000033
9.768800
## [197]  6.171900  8.501300  6.115067  9.768800  8.204167
##
## $predicted$`2`
##   [1] 17.787040 18.181932 16.632162 21.921698 24.699109 16.639488
30.531218
##   [8] 30.576731 19.284859 28.418904 19.138840 27.493669 16.360752
12.651008
##  [15] 16.861102 19.802243 19.869078 13.436114 24.217259 16.995212
25.390292
##  [22] 24.036283 18.841096 13.961400 21.874063 19.720772 18.089957
22.938552
##  [29] 23.477464 14.321937 17.238112 17.238112 22.868158 29.968024
29.862916
##  [36] 24.681682 27.274289 28.606017 16.974477 14.218342 14.465759
15.687248
##  [43] 16.230523 29.081856 24.696822 16.974477 28.424022 25.165656
23.877056
##  [50] 15.290838 23.792054 18.852658 20.010010 20.522011 10.359489
21.901176
##  [57] 15.802248 23.725885 13.380539 25.235175 19.920152 19.797138
19.091288
##  [64] 10.213443 38.705436 38.274362 33.322843 37.466634 18.894488
19.215907
##  [71] 38.074276 33.121619 33.941686 37.535152 32.143752 33.168057
30.853352
##  [78] 37.720419 37.777322 27.926648 16.635544 17.820417 28.139450
14.936017
##  [85] 25.674017 35.336478 33.607119 31.410933 30.327167  7.934058
28.560792
##  [92] 20.719517 13.810440 23.403379 27.331679  8.948105  8.740511
7.679971
##  [99] 27.913372 10.369589 24.586772 12.220422 12.651138 13.686083
11.401056
## [106] 27.372650 12.813737 10.025589 11.155855 17.727375 17.727375
9.724002
```

```
## [113] 20.101996 22.572533 17.975740 28.094633 25.906639 19.967648
13.582827
## [120] 14.807249 16.818869 13.143854 16.775789 12.199573  9.769508
22.605948
## [127] 21.846125 20.277087 21.746721 12.199573 17.196954 11.310406
11.454073
## [134] 12.929044  9.541178 24.918511 22.396997 18.344693 11.028118
9.097739
## [141]  6.729909 20.460728  7.251395  8.802724  7.049811  9.287457
6.709190
## [148]  7.206243 10.301729 25.372677 12.463781  8.442183 11.521914
12.463781
## [155] 21.181562 21.002762 14.363596 11.591981 20.918180  8.727583
11.729165
## [162] 12.387132 13.879798 15.816133 19.492891 11.671132 19.900694
12.813791
## [169] 13.014660  8.331275 16.447662 22.042219 13.222043  9.309317
18.484167
## [176] 19.805973 27.394183 27.616381 23.723647 14.920914 14.891754
11.314526
## [183] 12.995476 16.192886 10.997498 13.652834 27.724741 16.894200
16.743327
## [190] 16.082700 25.050559 16.743327 15.487371 27.632429 17.422239
8.728471
## [197]  6.789937  7.802499  6.277764  8.728471  8.423148
##
## $predicted$`1`
##   [1] 18.007267 18.912267 15.998000 22.984867 26.946633 16.000000
32.948233
##   [8] 32.009600 18.971067 27.851233 15.992667 26.982400 16.000000
10.992200
##  [15] 17.000000 19.999500 19.999200 13.002000 25.020267 17.000400
26.946633
##  [22] 25.028800 18.966167 12.999200 21.998867 19.999500 18.013467
22.999200
##  [29] 24.012667 13.974700 17.000400 17.000400 22.991733 32.012933
31.018900
##  [36] 24.000933 26.982133 29.001433 16.999400 14.008900 12.999200
14.998700
##  [43] 15.992667 28.984400 23.994333 16.999400 27.915000 25.986633
24.002633
##  [50] 14.998700 24.012667 18.912267 19.999200 20.884667  9.009600
21.993033
##  [57] 15.992667 24.000933 13.002000 25.941600 19.999500 20.000000
18.963867
##  [64]  7.966500 43.760033 39.087567 30.010533 39.282800 15.992667
14.978900
##  [71] 39.685600 30.956600 32.883100 39.025367 31.963233 33.236500
25.941600
##  [78] 39.282067 37.749400 28.998067 16.000000 17.000000 29.956367
```

```
11.998000
##  [85] 25.985967 42.349167 33.008267 32.861333 30.988533  6.728400
35.017633
##  [92] 20.884667 14.995767 22.991733 27.851233  8.999900  9.009600
5.289000
##  [99] 29.009233  9.009600 24.980967 11.996400 12.997300 14.001100
10.983067
## [106] 27.905300 13.000000  7.996067 10.967867 18.008267 18.008267
9.667167
## [113] 19.993600 21.997967 18.019567 30.014967 25.982000 19.999200
13.991600
## [120] 15.000000 17.000400 12.999200 16.999400 11.996800  9.667167
22.993633
## [127] 21.998867 20.884667 22.007867 11.996800 18.008267 10.986467
10.992200
## [134] 12.997300  5.289000 27.031100 22.996033 19.993600 11.995333
9.009600
## [141]  5.806033 21.994767  6.728400  9.002433  6.927633  9.892267
5.101500
## [148]  6.864700 10.986467 29.009333 12.997300  5.725900 10.967867
12.997300
## [155] 21.994767 20.993000 14.999600 12.002500 20.884667  7.978767
10.983067
## [162] 11.996400 14.008900 15.992667 19.993600 10.967867 20.993000
12.999200
## [169] 12.997300  5.756767 16.999400 24.998867 13.974700  7.966500
19.999500
## [176] 19.993600 28.998067 29.956367 23.994333 14.995767 14.978900
7.960967
## [183] 13.000000 17.000000  6.728400 12.002500 29.001433 17.000000
16.999400
## [190] 15.998000 24.990767 16.999400 14.978900 29.009233 19.993600
9.002433
## [197]  5.101500  7.985400  4.953067  9.002433  8.997300
```

The section "$error.cv" in the output show us that reducing number of predictors decreases the rates of error in the performance of the model. This outcome make sense and is congruent with large amount of predictors with low importance for the model prediction observed above.

Prediction performance

In order to verify the percentage of explanation for the Random Forest model we can adjust a linear model to get a value for R-squared. We do this for the test set created above. If 30% of data from the test produces a high performance, your prediction is good.

```
predTest <- predict(RF1, TestSet)
r2_test <- lm(predTest ~ TestSet$Species.richness)
summary(r2_test)
```

```
##
## Call:
## lm(formula = predTest ~ TestSet$Species.richness)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.3940 -3.0597 -0.1885  2.3862 10.6701
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                11.04786    1.25847   8.779 2.67e-12 ***
## TestSet$Species.richness  0.44538    0.06282   7.090 1.91e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.968 on 59 degrees of freedom
## Multiple R-squared:   0.46,  Adjusted R-squared:  0.4509
## F-statistic: 50.26 on 1 and 59 DF,  p-value: 1.907e-09
```

The adjusted R-squared shows that the prediction performance of the model is not good, since it predicts less than 50 % of the dependent variable.

Nevertheless, you do not need necessarily to use a linear model to check on prediction performance. You could also calculate the correlation coefficient and, then, square it:

```
cor(predTest, TestSet$Species.richness) ^ 2
```

```
## [1] 0.4600236
```

RMSE

We can adjust a RMSE (Root mean squared error) for the model. The RMSE is particularly useful when it is compared with other models to see if it performs better or worse depending if it has a higher or lower error of prediction.

```
rfvalpred = predict(RF1,newdata=TestSet)
rmse = sqrt(mean((TestSet$Species.richness-rfvalpred)^2))
rmse
```

```
## [1] 6.010385
```

Model Selection (Akaike)

For both Akaike and GLM / GLMM the predictor variables must be tested for the degree of correlation, because if these variables are highly correlated, it implies collinearity, and the real contributions of each predictor to the dependent variable may be confounded. One conventional way to test correlation, and collinearity, is the Pearson's correlation (described in this script). Pearson correlation coefficients can be between -1 and 1, and the accepted limit for collinearity is |0.60|. Correlations above 0.60 indicate too much collinearity between predictors. On the other hand, many authors accept correlations up to 0.70 and use variables with this degree of correlation in the model.

Akaike's function: select the best regression model according to the relationship between the dependent and predictor variables. The best model is normally assumed to be the one with the lowest AICc value. However, the quantity of models considered to be good does not necessarily follow a specific rule, since it depends on your purpose and research approach. It also can depend on the statistical line you follow. Some researchers suggest that a difference between AIC values smaller than 2 (i.e. delta AIC =< 2) indicates that the models are almost equally good. Others use a threshold level of delta AIC =< 4.

GLM's Akaike selection

```
## Akaike: basic syntax

## install and load "MuMIn" package

# Usage

Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
```

```
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
```

```
# install.packages("MuMIn")
library(MuMIn)
options(na.action = "na.fail")
div <- glm(Veg.height ~ P_mg_100g + K_mg_100g + Land.use,
family=gaussian,
           data=Hogweed)
tested.div1 <- dredge(div)
tested.div1
```

```
## Global model call: glm(formula = Veg.height ~ P_mg_100g + K_mg_100g +
Land.use,
##     family = gaussian, data = Hogweed)
## ---
## Model selection table
##    (Int)   K_mg_100 Lnd.use P_mg_100 df  logLik AICc delta weight
## 7 0.3256                 + 0.006875  5 -23.238 56.8  0.00  0.414
## 3 0.3396                 +           4 -24.592 57.4  0.60  0.306
## 8 0.3330 -0.0011540      + 0.008192  6 -23.093 58.6  1.83  0.165
## 4 0.3336  0.0006829      +           5 -24.525 59.4  2.57  0.114
## 5 0.5353                   0.009135  3 -32.343 70.8 14.02  0.000
## 6 0.5399 -0.0005695        0.009789  4 -32.310 72.8 16.04  0.000
## 1 0.5647                             2 -34.565 73.2 16.41  0.000
## 2 0.5450  0.0016610                  3 -34.197 74.5 17.73  0.000
## Models ranked by AICc(x)
```

LME's Akaike selection

Firstly you must carry out the pre-tests with LM in the model to be executed as LME model. If normality and linearity are accepted, then, you check for spatial autocorrelation by Moran's I. If there is significant autocorrelation you must model include a spatial correlation structure (e.g. corExp) within the global LME that will be submited to selection by Akaike such as the example below.

Example of LM model to check for linearity and autocorrelation for the global LME model to execute Akaike's selection:

Firstly you must conduct pre-tests with LMs in the model to be executed as LME model. If normality and linearity are acceptable, you must then check for spatial autocorrelation by Moran's I. If there is significant autocorrelation your model must

include a spatial correlation structure (e.g. corExp) within the global LME, which will be submitted to selection by Akaike criteria, as described in the example below.

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG,4)

##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727

Mean.Diameter.pre <- lm(Mean_diameter ~ Mortality + Recruitment +
Richness + Site,

data=BIOVEG)

## LME's Akaike selection

library(nlme) # LME models
library(MuMIn) # Dredge function to execute the selection

options(na.action = "na.fail")
div <- lme(Mean_diameter ~ Mortality + Recruitment + Richness,
data=BIOVEG, method="ML", random= ~1|Site,
corr=corExp(form=~local.utm.x+local.utm.y|Site),
                                weights=varIdent(form=~1|Site),
na.action=na.fail)
```

```
tested.div1 <- dredge(div)
tested.div1

## Global model call: lme.formula(fixed = Mean_diameter ~ Mortality +
Recruitment +
##     Richness, data = BIOVEG, random = ~1 | Site, correlation =
corExp(form = ~local.utm.x +
##     local.utm.y | Site), weights = varIdent(form = ~1 | Site),
##     method = "ML", na.action = na.fail)
## ---
## Model selection table
##   (Intrc)    Mrtlt     Rcrtm      Rchns df  logLik  AICc delta weight
## 1   10.67                                6 -40.724  94.0  0.00  0.403
## 2   10.67 0.001550                       7 -40.609  96.0  1.97  0.150
## 3   10.67          -0.002797             7 -40.678  96.1  2.11  0.140
## 5   10.68                     -0.0007914  7 -40.686  96.2  2.13  0.139
## 4   10.67 0.001605 -0.003023             8 -40.555  98.1  4.10  0.052
## 6   10.67 0.001428           -0.0005343  8 -40.593  98.2  4.17  0.050
## 7   10.69          -0.002982 -0.0008561  8 -40.634  98.3  4.25  0.048
## 8   10.68 0.001472 -0.003134 -0.0005951  9 -40.535 100.4  6.32  0.017
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | Site'
```

QAIC - QUASI Akaike

When the generalized model shows oversdispersion, the typical AIC value cannot be computed using the dredge function. Instead, the QAIC value needs to be computed. With the function "QAIC" (Quasi AIC) of the package MuMIn, calculated a modification of Akaike's Information Criterion for overdispersed count data (e.g. quasipoisson model) can be calculated, but it also may also be used to compute QAIC for binomial data (e.g. quasipoisson).

QAIC - Quasipoisson

```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
```

```
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34

# install.packages("MuMIn")
library(MuMIn)
options(na.action = "na.fail")
```

Fist, we execute the function for "x.quasipossion" constructor, which allows for quasipoisson family objects, for ML estimation.

```
x.quasipoisson <- function(...) {
  res <- quasipoisson(...)
  res$aic <- poisson(...)$aic
  res
}

riqueza.glm2<- glm(Species.richness ~ P_mg_100g + Land.use + K_mg_100g
                + Hogweed.height, data=Hogweed, family="x.quasipoisson")
```

To compute the variance inflation factor based on residuals of Pearson, where it is necessary to use the "dredge" function to compute the QAIC values and its parameters. There is a discussion among statisticians regarding whether residuals of Pearson are suitable for models (e.g. Poisson and Binomial) based on Chisq, but there are various examples where it provides a robust and reliable fit.

```
chat<-sum(residuals(riqueza.glm2,"pearson")^2)/riqueza.glm2$df.residual
chat

## [1] 3.231642

riqueza.QAIC <- dredge(riqueza.glm2, rank = "QAIC", chat = chat)

## Fixed term is "(Intercept)"

riqueza.QAIC

## Global model call: glm(formula = Species.richness ~ P_mg_100g +
Land.use + K_mg_100g +
##     Hogweed.height, family = "x.quasipoisson", data = Hogweed)
```

```
## ---
## Model selection table
##    (Int) Hgw.hgh  K_mg_100 Lnd.use P_mg_100 df   logLik  QAIC delta
weight
## 10 3.412 -0.4344                   -0.02074  3 -788.820 496.2  0.00
0.478
## 12 3.432 -0.4319 -0.002688         -0.01770  4 -787.878 497.6  1.42
0.235
## 14 3.433 -0.3805                 + -0.01978  5 -786.527 498.8  2.58
0.131
## 16 3.449 -0.3805 -0.002554       + -0.01689  6 -785.687 500.2  4.06
0.063
## 4  3.433 -0.4422 -0.006557                   3 -795.857 500.5  4.35
0.054
## 8  3.450 -0.3837 -0.006229       +           5 -792.800 502.6  6.46
0.019
## 2  3.368 -0.4539                             2 -803.606 503.3  7.15
0.013
## 6  3.396 -0.3839                 +           4 -799.668 504.9  8.71
0.006
## 13 3.263                         + -0.02047  4 -814.401 514.0 17.83
0.000
## 15 3.280         -0.002651       + -0.01747  5 -813.488 515.5 19.27
0.000
## 7  3.277         -0.006323       +           4 -820.933 518.1 21.87
0.000
## 5  3.222                         +           3 -827.998 520.4 24.25
0.000
## 9  3.022                           -0.02408  2 -839.309 525.4 29.25
0.000
## 11 3.050         -0.003526         -0.02014  3 -837.648 526.4 30.22
0.000
## 3  3.038         -0.007717                   2 -847.930 530.8 34.58
0.000
## 1  2.950                                     1 -858.742 535.5 39.27
0.000
## Models ranked by QAIC(x, chat = 3.23164202774229)
```

We can compare the QAIC selection by using Pearson's residuals to fit variance inflation factor, by dividing the deviance by residual degrees of freedom.

```
chat2=(deviance(riqueza.glm2) / df.residual(riqueza.glm2))

riqueza2.QAIC <- dredge(riqueza.glm2, rank = "QAIC", chat = chat2)

## Fixed term is "(Intercept)"

riqueza2.QAIC

## Global model call: glm(formula = Species.richness ~ P_mg_100g +
Land.use + K_mg_100g +
```

```
##     Hogweed.height, family = "x.quasipoisson", data = Hogweed)
## ---
## Model selection table
##    (Int) Hgw.hgh  K_mg_100 Lnd.use P_mg_100 df   logLik  QAIC delta
weight
## 10 3.412 -0.4344                   -0.02074  3 -788.820 497.1  0.00
0.478
## 12 3.432 -0.4319 -0.002688         -0.01770  4 -787.878 498.5  1.42
0.235
## 14 3.433 -0.3805                 + -0.01978  5 -786.527 499.6  2.58
0.132
## 16 3.449 -0.3805 -0.002554       + -0.01689  6 -785.687 501.1  4.06
0.063
## 4  3.433 -0.4422 -0.006557                   3 -795.857 501.4  4.36
0.054
## 8  3.450 -0.3837 -0.006229       +           5 -792.800 503.5  6.47
0.019
## 2  3.368 -0.4539                             2 -803.606 504.2  7.17
0.013
## 6  3.396 -0.3839                 +           4 -799.668 505.8  8.73
0.006
## 13 3.263                         + -0.02047  4 -814.401 514.9 17.86
0.000
## 15 3.280         -0.002651       + -0.01747  5 -813.488 516.3 19.29
0.000
## 7  3.277         -0.006323       +           4 -820.933 519.0 21.91
0.000
## 5  3.222                         +           3 -827.998 521.3 24.29
0.000
## 9  3.022                           -0.02408  2 -839.309 526.4 29.30
0.000
## 11 3.050         -0.003526         -0.02014  3 -837.648 527.3 30.27
0.000
## 3  3.038         -0.007717                   2 -847.930 531.7 34.65
0.000
## 1  2.950                                     1 -858.742 536.4 39.35
0.000
## Models ranked by QAIC(x, chat = 3.2258850123267)
```

We see that the outcomes of QAIC selection using the two approaches above, to compute 'chat' as the variance inflation factors, results in virtually the same outcomes.

QAIC - Quasibinomial

```
# install.packages("MuMIn")
library(MuMIn)
```

```
Hogweed <- read.table("Hogweed.csv", header=T, sep=",", dec=".")
head(Hogweed,4)

##   Plot Study.area  Habitat.type Year Veg.height Veg.cover
Species.richness
## 1   s1        VOL ruderal.grass 2002        0.5        70
18
## 2   s2        VOL ruderal.grass 2002        0.7        65
19
## 3   s3        VOL ruderal.grass 2002        0.4        30
16
## 4   s4        VOL ruderal.grass 2002        0.9        90
23
##   Hogweed.height Hogweed.cover Land.use Disturbance Altitude
Inclination
## 1            0.9            80     NONE   TREESHRUB  295.653
2
## 2            1.4            65     NONE   TREESHRUB  295.653
2
## 3            1.7            90     NONE   TREESHRUB  295.653
2
## 4            1.0            20     NONE        NONE  292.112
2
##   Exposition N_perc P_mg_100g K_mg_100g
## 1          W   0.19      3.99     22.27
## 2          W   0.19      3.56     12.49
## 3          W   0.19      8.44     39.95
## 4          W   0.12      2.53     12.34
```

First, let's execute a 'hacked' constructor for quasibinomial family object for ML estimation

```
x.quasibinomial  <- function(...) {
  res <- quasibinomial(...)
  res$aic <- binomial(...)$aic
  res
}

coverHog.glm1 <- glm(Hogweed.cover/100 ~ Veg.height + N_perc +
                       Habitat.type + Land.use + P_mg_100g,
                     data=Hogweed,family="x.quasibinomial")

chat3=(deviance(coverHog.glm1) / df.residual(coverHog.glm1))

options(na.action = "na.fail")
AICselectCover <- dredge(coverHog.glm1)

## Fixed term is "(Intercept)"

AICselectCover
```

```
## Global model call: glm(formula = Hogweed.cover/100 ~ Veg.height +
N_perc + Habitat.type +
##     Land.use + P_mg_100g, family = "x.quasibinomial", data = Hogweed)
## ---
## Model selection table
##      (Int) Hbt.typ Lnd.use    N_prc   P_mg_100 Veg.hgh df   logLik
AICc
## 18 -1.0670       +                             -1.4490  6 -103.960
220.4
## 22 -0.9835       +         -0.26910            -1.4480  7 -103.885
222.3
## 26 -1.0640       +                  -0.0021020 -1.4450  7 -103.923
222.4
## 30 -0.9841       +         -0.26550 -0.0003552 -1.4470  8 -103.880
224.5
## 20 -1.2730       +       +                     -1.5110  8 -104.183
225.1
## 28 -1.2680       +       +          -0.0035190 -1.5050  9 -104.119
227.2
## 24 -1.2030       +       + -0.22390            -1.5090  9 -104.125
227.2
## 32 -1.2070       +       + -0.20140 -0.0021360 -1.5050 10 -104.093
229.3
## 2  -1.6180       +                                    5 -111.991
234.3
## 10 -1.5930       +                  -0.0112400        6 -111.663
235.8
## 6  -1.5310       +         -0.28200                   6 -111.911
236.3
## 14 -1.5390       +         -0.18180 -0.0099980        7 -111.649
237.9
## 4  -1.7550       +       +                            7 -112.295
239.2
## 12 -1.7290       +       +          -0.0121200        8 -111.946
240.6
## 8  -1.6720       +       + -0.27060                   8 -112.220
241.2
## 16 -1.6840       +       + -0.15350 -0.0110100        9 -111.937
242.8
## 19 -1.3360               +                     -1.0910  4 -118.099
244.4
## 23 -1.5340               +  0.66320            -1.1130  5 -117.915
246.1
## 27 -1.3480               +           0.0093530 -1.1100  5 -118.169
246.6
## 31 -1.5250               +  0.61040  0.0053720 -1.1220  6 -117.969
248.4
## 17 -0.2031                                    -0.5782  2 -123.782
251.6
## 3  -1.6940               +                            3 -122.882
```

```
251.9
## 21 -0.2390                  0.12860            -0.5786  3 -123.786
253.7
## 25 -0.2347                           0.0172700 -0.6221  3 -123.797
253.7
## 7  -1.8480               +  0.50420                     4 -122.812
253.8
## 1  -0.5257                                              1 -125.948
253.9
## 11 -1.6990               +           0.0023620          4 -122.920
254.0
## 29 -0.2312                 -0.01305  0.0173400 -0.6222  4 -123.796
255.8
## 15 -1.8490               +  0.51560 -0.0011110          5 -122.792
255.9
## 5  -0.5598                  0.12110                     2 -125.954
256.0
## 9  -0.5636                           0.0116700          2 -126.068
256.2
## 13 -0.5699                  0.02369  0.0115400          3 -126.068
258.3
##    delta weight
## 18  0.00  0.495
## 22  2.00  0.182
## 26  2.07  0.176
## 30  4.16  0.062
## 20  4.76  0.046
## 28  6.83  0.016
## 24  6.84  0.016
## 32  8.99  0.006
## 2  13.94  0.000
## 10 15.41  0.000
## 6  15.90  0.000
## 14 17.53  0.000
## 4  18.82  0.000
## 12 20.29  0.000
## 8  20.84  0.000
## 16 22.46  0.000
## 19 24.05  0.000
## 23 25.79  0.000
## 27 26.29  0.000
## 31 28.02  0.000
## 17 31.27  0.000
## 3  31.53  0.000
## 21 33.34  0.000
## 25 33.36  0.000
## 7  33.48  0.000
## 1  33.56  0.000
## 11 33.69  0.000
## 29 35.44  0.000
```

```
## 15 35.54  0.000
## 5  35.62  0.000
## 9  35.85  0.000
## 13 37.91  0.000
## Models ranked by AICc(x)
```

MODEL AVERAGING

With the function "model.avg" of the package MuMIn we can compute model averaging based on an information criterion (e.g. AIC (Akaike) or BIC (Baysean)).

```
BIOVEG <- read.table("BIOVEG3.csv", header=TRUE, sep=",", dec=".")
head(BIOVEG, 4)
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727
```

```
library(MuMIn)
options(na.action = "na.fail")
riqueza <- glm(Richness ~ Mortality + Recruitment + Diameter
               + Temperature_mean, family=gaussian, data=BIOVEG)
riqueza.AICc <- dredge(riqueza)

## Fixed term is "(Intercept)"

riqueza.AICc
```

```
## Global model call: glm(formula = Richness ~ Mortality + Recruitment +
Diameter +
##     Temperature_mean, family = gaussian, data = BIOVEG)
## ---
## Model selection table
##     (Int)     Dmt     Mrt     Rcr Tmp_men df   logLik  AICc delta
weight
## 5  15.920                 -0.3395          3 -483.219 972.6  0.00
0.140
## 1  15.060                                  2 -484.472 973.0  0.42
0.113
## 6  14.730 0.04540         -0.3990          4 -482.416 973.1  0.50
0.108
## 13  5.449                 -0.4582 0.47360  4 -482.436 973.1  0.55
0.106
## 7  16.350         -0.1435 -0.3391          4 -482.774 973.8  1.22
0.076
## 14  5.844 0.03940         -0.4936 0.40910  5 -481.840 974.1  1.49
0.066
## 3  15.500         -0.1440                  3 -484.031 974.2  1.62
0.062
## 2  14.140 0.03131                          3 -484.079 974.3  1.72
0.059
## 8  15.180 0.04361 -0.1330 -0.3963          5 -482.031 974.5  1.88
0.055
## 15  6.374         -0.1302 -0.4518 0.44970  5 -482.068 974.6  1.95
0.053
## 9  11.170                         0.17120  3 -484.352 974.9  2.27
0.045
## 16  6.704 0.03805 -0.1229 -0.4864 0.38880  6 -481.511 975.6  3.01
0.031
## 4  14.610 0.02957 -0.1369                  4 -483.680 975.6  3.03
0.031
## 11 12.080         -0.1396         0.15010  4 -483.939 976.2  3.55
0.024
## 10 11.780 0.02887                 0.10680  4 -484.035 976.3  3.74
0.021
## 12 12.630 0.02755 -0.1348         0.08937  5 -483.649 977.7  5.11
0.011
## Models ranked by AICc(x)
```

Average of the best modes under delta < 4

```
summary(model.avg(riqueza.AICc, subset = delta < 4))

##
## Call:
## model.avg(object = riqueza.AICc, subset = delta < 4)
##
```

```
## Component model call:
## glm(formula = Richness ~ <15 unique rhs>, family = gaussian, data
##      = BIOVEG)
##
## Component models:
##        df  logLik   AICc delta weight
## 3       3 -483.22 972.60  0.00   0.14
## (Null)  2 -484.47 973.03  0.42   0.11
## 13      4 -482.42 973.11  0.50   0.11
## 34      4 -482.44 973.15  0.55   0.11
## 23      4 -482.77 973.82  1.22   0.08
## 134     5 -481.84 974.10  1.49   0.07
## 2       3 -484.03 974.23  1.62   0.06
## 1       3 -484.08 974.32  1.72   0.06
## 123     5 -482.03 974.48  1.88   0.06
## 234     5 -482.07 974.55  1.95   0.05
## 4       3 -484.35 974.87  2.27   0.05
## 1234    6 -481.51 975.61  3.01   0.03
## 12      4 -483.68 975.64  3.03   0.03
## 24      4 -483.94 976.15  3.55   0.02
## 14      4 -484.03 976.35  3.74   0.02
##
## Term codes:
##         Diameter        Mortality      Recruitment Temperature_mean
##                1                2                3                4
##
## Model-averaged coefficients:
## (full average)
##                   Estimate Std. Error Adjusted SE z value Pr(>|z|)
## (Intercept)      12.51626    6.47186     6.50420   1.924   0.0543 .
## Recruitment      -0.26106    0.26949     0.27049   0.965   0.3345
## Diameter          0.01462    0.02932     0.02946   0.496   0.6196
## Temperature_mean  0.12805    0.29325     0.29466   0.435   0.6639
## Mortality        -0.04573    0.10993     0.11053   0.414   0.6791
##
## (conditional average)
##                   Estimate Std. Error Adjusted SE z value Pr(>|z|)
## (Intercept)      12.51626    6.47186     6.50420   1.924   0.0543 .
## Recruitment      -0.40696    0.23202     0.23383   1.740   0.0818 .
## Diameter          0.03895    0.03664     0.03693   1.055   0.2916
## Temperature_mean  0.36591    0.39838     0.40134   0.912   0.3619
## Mortality        -0.13691    0.15394     0.15522   0.882   0.3777
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

POST-HOC TEST TO REGRESSION MODELS

A common necessity when using GLM, LM or GLMM using categorical (factor variable) predictors, is to conduct multiple comparison of means among the pairs of categories. Such comparison using regression models is still being developed and improved. For instance, there are currently no 100% robust, standard unbiased post-hoc tests which can be applied in Mixed Models (e.g. GLMM, LME). Below we provide examples of two of the most commonly used post-hoc methods applied in Ecology but we highly advise you to read about their application and carefully consider whether their use is appropriate for your analysis.

If after you run your model, you find a significant difference of the means among categories (as shown by fitting ANOVA to count data in this GLM model example with species richness as target variable), then you need a post-hoc (posteriori) test to show you between which categories the difference occurred. Post-hoc tests on Linear Models become even more important the more predictor variables you use. If you want to run an a posteriori comparison of the model, knowing that there are significant differences among categories as there are in this example, this comparison will consider the weight of other predictor variables (e.g. k, ca, light).

TUKEY'S POST HOC TEST (Tukey's HSD (honest significant difference) test)

```
BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG,4)
```

```
##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
## 4         6.626      0.128        19               1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
```

```
## 3     7807727
## 4     7807727

# Usage

# install.packages("multcomp")
library(multcomp)


richtype <- glm(Richness ~ type, data=BIOVEG, family=poisson)
summary(richtype)

##
## Call:
## glm(formula = Richness ~ type, family = poisson, data = BIOVEG)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8720  -1.2326  -0.1111   0.8646   5.5989
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)       2.61593    0.03824  68.416  < 2e-16 ***
## typeOmbrofila     0.22197    0.05131   4.326 1.52e-05 ***
## typeSemidecidual  0.05268    0.05338   0.987    0.324
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 350.25  on 149  degrees of freedom
## Residual deviance: 329.36  on 147  degrees of freedom
## AIC: 1007.9
##
## Number of Fisher Scoring iterations: 4

summary(glht(richtype, linfct=mcp(type = "Tukey")))

##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: glm(formula = Richness ~ type, family = poisson, data = BIOVEG)
##
## Linear Hypotheses:
##                               Estimate Std. Error z value Pr(>|z|)
## Ombrofila - Aluvial == 0       0.22197    0.05131   4.326  < 0.001 ***
## Semidecidual - Aluvial == 0    0.05268    0.05338   0.987  0.58493
## Semidecidual - Ombrofila == 0 -0.16929    0.05058  -3.347  0.00247 **
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

cldm0 <- cld(glht(richtype, linfct=mcp(type = "Tukey")))
cldm0 # here show between each pairs of type there is the significant
difference

##      Aluvial    Ombrofila Semidecidual
##          "a"          "b"          "a"
```

LMERTEST

This test is used for mixed models (e.g. GLMM, LME) which have Pseudoreplication (when your data is distributed in subplots within each site. E.g. 3 sites with 50 10 m x 10 m plots) and you need to consider this effect (normally called random effect, but be careful when reading about this subject since there remains some disagreement between statisticians). For instance, if you need to not only consider data values per site or fragment, but also data values per subplot within each site. Suppose you need to know the phylogenetic diversity per subplot within each site, you need to recognize that the subplots are not real replicates and so you need to use a mixed model.

Atention: The "lmer test" from the package of the same name is one of the most commonly used post-hoc tests in this case, but there remain disagreements among statisticians about its robustness when homogeneity of variance and normality are violated. Read about this method and carefully consider whether it is appropriate for your analysis. The "lmerTest" package calculate p-values of differences of means among categories.

```
# install.packages("lmerTest")
library(lmerTest)

BIOVEG <- read.table("BIOVEG3.csv", header=T, sep=",", dec=".")
head(BIOVEG,4)

##           type Plot  Site                Species Richness Diameter
## 1 Semidecidual p001 AREA1 Alchornea_triplinervia        8    27.12
## 2 Semidecidual p002 AREA1     Amaioua_intermedia       10    39.15
## 3 Semidecidual p003 AREA1          Aniba_firmula       10    33.93
## 4 Semidecidual p004 AREA1          Annona_cacans       10    40.43
##   Mean_diameter Basal.area Abundance Precipitation_mean
Temperature_mean
## 1         6.357      0.058         7               1250
24.4
## 2         6.524      0.120        12               1250
24.4
## 3         6.632      0.090        10               1250
24.4
```

```
## 4         6.626      0.128        19                1250
24.4
##   Mortality Recruitment local.x local.y  utm.x   utm.y local.utm.x
## 1      6.94       14.34       0       0 747923 7807727      747923
## 2      2.74        6.94     -10       0 747923 7807727      747913
## 3      1.71        2.35     -20       0 747923 7807727      747903
## 4      1.60        2.47     -30       0 747923 7807727      747893
##   local.utm.y
## 1     7807727
## 2     7807727
## 3     7807727
## 4     7807727

## use to Continuos data

# call the function "glmer" from package "lme4"
DIAM<-lmer(Diameter ~ type + (1|Site), REML=FALSE, data=BIOVEG)

difflsmeans(DIAM, test.effs="type")

## Least Squares Means table:
##
##                                  Estimate Std. Error  df t value
lower
## typeAluvial - typeOmbrofila       -0.8800     2.7343 150 -0.3218  -
6.2828
## typeAluvial - typeSemidecidual    -7.8790     2.7343 150 -2.8815 -
13.2818
## typeOmbrofila - typeSemidecidual  -6.9990     2.7343 150 -2.5597 -
12.4018
##                                    upper Pr(>|t|)
## typeAluvial - typeOmbrofila        4.5228 0.748026
## typeAluvial - typeSemidecidual    -2.4762 0.004539 **
## typeOmbrofila - typeSemidecidual  -1.5962 0.011466 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##   Confidence level: 95%
##   Degrees of freedom method: Satterthwaite
```

MULTIVARIATE ANALYSIS

This approach is indicated to analyze more than one statistical outcome variable at a time. Usually, multivariate analysis to establish relationships among variables, where they were sampled by multiple measurements in sample or experimental units, and their sampling design.

NMDS - Non-metric multidimensional scaling

NMDS is used to robustly demonstrate the original position of data in multidimensional space using a reduced number of dimensions that can be easily plotted and visualized.

```
# use "vegan" package:

# install.packages("vegan")
library("vegan")

# Adapted NMDS template option:

matrix<- read.table("matrixspp.txt", header=T, sep="\t")
matrix[1:5,1:4] # shows only part of the data
```

```
##   abarema_brachystachya abarema_villosa acanthocladus_pulcherrimus
## 1                     0               0                           0
## 2                     0               0                           0
## 3                     0               0                           0
## 4                     0               0                           0
## 5                     0               0                           0
##   alchornea_glandulosa
## 1                    0
## 2                    0
## 3                    0
## 4                    0
## 5                    0
```

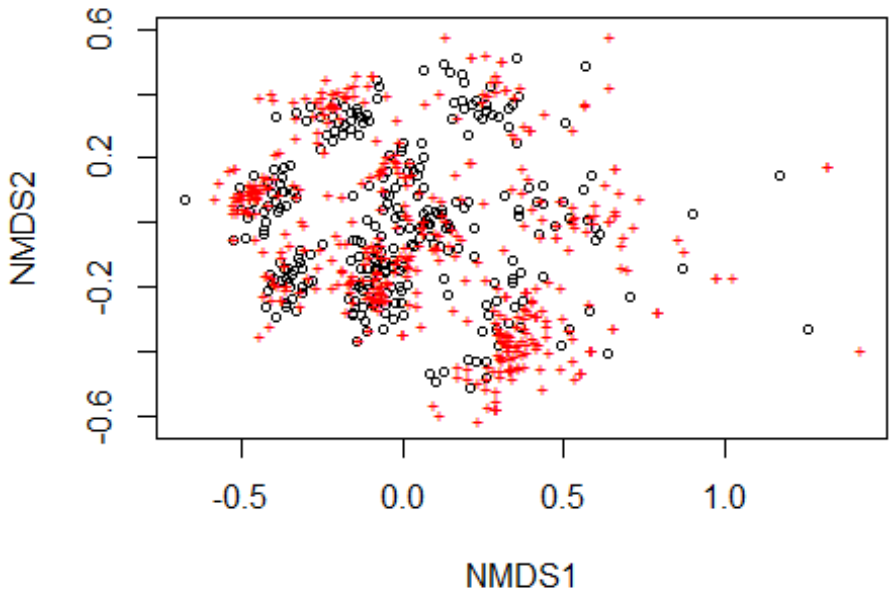
```
# NMDS

NMDS_bray<- metaMDS(matrix, k=2, distance="bray")
```

```
## Wisconsin double standardization
## Run 0 stress 0.2198643
## Run 1 stress 0.2216841
## Run 2 stress 0.2198769
## ... Procrustes: rmse 0.00288897  max resid 0.0325339
## Run 3 stress 0.2217402
## Run 4 stress 0.2215109
## Run 5 stress 0.2187916
## ... New best solution
## ... Procrustes: rmse 0.04319214  max resid 0.1200068
## Run 6 stress 0.2216311
## Run 7 stress 0.2194974
## Run 8 stress 0.2198929
## Run 9 stress 0.2205943
## Run 10 stress 0.2183727
## ... New best solution
## ... Procrustes: rmse 0.0179176  max resid 0.07948068
## Run 11 stress 0.2194878
```

```
## Run 12 stress 0.21851
## ... Procrustes: rmse 0.005008619  max resid 0.06515672
## Run 13 stress 0.221705
## Run 14 stress 0.2210081
## Run 15 stress 0.2198895
## Run 16 stress 0.2188199
## ... Procrustes: rmse 0.01624568  max resid 0.07908814
## Run 17 stress 0.2187936
## ... Procrustes: rmse 0.01789406  max resid 0.08045457
## Run 18 stress 0.2188017
## ... Procrustes: rmse 0.01777192  max resid 0.08036169
## Run 19 stress 0.2265645
## Run 20 stress 0.2312948
## *** No convergence -- monoMDS stopping criteria:
##      1: no. of iterations >= maxit
##     19: stress ratio > sratmax

NMDS_bray$stress ## < 0.3:  check if  it was lower like this in your
analysis

## [1] 0.2183727
```

If stress < 0.3 the program returns "TRUE" which indicates acceptable levels of stress within your model. It implies how robust your analysis' result was.

```
plot(NMDS_bray) ### ordinary graph, just distinction in 2 colors and
symbols
```



```
# Save scores

write.table(NMDS_bray$points, "sitesR.txt", row.names=T, sep="\t")
write.table(NMDS_bray$species, "species.txt", row.names=F, sep="\t")
```

WARNING: The data sets used here are for training purposes only. The two matrices from test dataset don't represent a realistic species composition of the vegetation types described here. We collated species # data from our personal datasets and shuffled them into the columns of the species matrix. For example, you mind find that species common in Semideciduous forest (SEMI) might instead be listed amongst Rain Forest (OMB) species.

Better NMDS graph: distinction between vegetation types (as in the following example: ssm, as, fo). You must to use 2 matrix files, one with species and another one with classification in vegetation types (e.g. if you just want to check species distribution between types) or environmental variables (e.g. soil: ph, Al...). In this example we just want to check the species distribution among vegetation types. Thus, you need the species matrix file (here it is the object "matrix") and another one with category (here it is "matrix4"). Each row number of "matrix4" corresponds to the same row number in "matrix". Therefore both matrices must have the same sequence and number of rows.

Note 1: again all of the these 3 matrices must have the same sequence and number of rows. Within each row you classify the soil variable value and element, or in case of vegetation the category.

Better Graph (separation among types: OMB, GAL, SEMI):

```
matrix<- read.table("matrixspp.txt", header=T, sep="\t")
matrix[1:5,1:4] # shows only part of the data

##   abarema_brachystachya abarema_villosa acanthocladus_pulcherrimus
## 1                     0              0                           0
## 2                     0              0                           0
## 3                     0              0                           0
## 4                     0              0                           0
## 5                     0              0                           0
##   alchornea_glandulosa
## 1                    0
## 2                    0
## 3                    0
## 4                    0
## 5                    0

matrix5<- read.table("matrixtype.txt", header=T, sep="\t")
head(matrix5) # shows by default only the first 6 rows of data

##   type codigos
## 1 OMBR     OMB
## 2 OMBR     OMB
```

```
## 3 OMBR     OMB
## 4 OMBR     OMB
## 5 OMBR     OMB
## 6 OMBR     OMB
```

```
forest.nmds <- metaMDS(matrix, distance="bray")
```

```
## Wisconsin double standardization
## Run 0 stress 0.2198643
## Run 1 stress 0.2192034
## ... New best solution
## ... Procrustes: rmse 0.04259014  max resid 0.1203069
## Run 2 stress 0.2190073
## ... New best solution
## ... Procrustes: rmse 0.005225512  max resid 0.05012064
## Run 3 stress 0.2214929
## Run 4 stress 0.2188155
## ... New best solution
## ... Procrustes: rmse 0.003405314  max resid 0.04596126
## Run 5 stress 0.2198851
## Run 6 stress 0.2317977
## Run 7 stress 0.2196541
## Run 8 stress 0.2205652
## Run 9 stress 0.2199014
## Run 10 stress 0.2194214
## Run 11 stress 0.219893
## Run 12 stress 0.2193951
## Run 13 stress 0.2198767
## Run 14 stress 0.2185807
## ... New best solution
## ... Procrustes: rmse 0.01736558  max resid 0.07833819
## Run 15 stress 0.2214877
## Run 16 stress 0.2206233
## Run 17 stress 0.2282496
## Run 18 stress 0.2189244
## ... Procrustes: rmse 0.01710657  max resid 0.07930599
## Run 19 stress 0.2199584
## Run 20 stress 0.2196082
## *** No convergence -- monoMDS stopping criteria:
##      1: no. of iterations >= maxit
##     19: stress ratio > sratmax
```

```
grupo<- matrix5$codigos
grupo.nivel <- levels(grupo)
head(grupo) # shows by default only the first 6 rows of data
```

```
## [1] OMB OMB OMB OMB OMB OMB
## Levels: GAL OMB SEMI
```

```
head(grupo.nivel) # shows by default only the first 6 rows of data
```

```
## [1] "GAL"  "OMB"  "SEMI"
```

```
escores.nmds <- scores(forest.nmds)
head(escores.nmds, 10) # shows only the scores of the first 10 rows
```

```
##          NMDS1       NMDS2
## 1  -0.43338491  0.06702318
## 2   0.16152959 -0.07929433
## 3  -0.14601269  0.30380524
## 4   0.12447163  0.45757042
## 5  -0.05114155  0.13083438
## 6   0.34695833 -0.14847638
## 7  -0.32401926 -0.13951549
## 8   0.41282420  0.05414265
## 9  -0.47627775  0.10440796
## 10  0.03482718 -0.07052191
```

```
forest.nmds$stress
```

```
## [1] 0.2185807
```

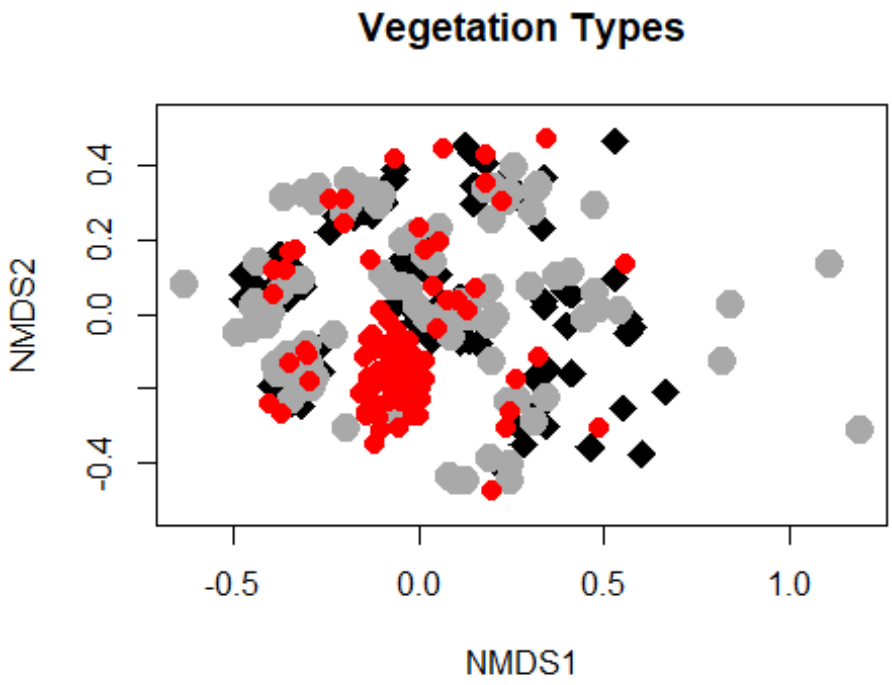
```
p <- ordiplot(escores.nmds, type="n", main="Vegetation Types")
```

```
## species scores not available
```

```
grupo.nivel
```

```
## [1] "GAL"  "OMB"  "SEMI"
```

```
points(escores.nmds[grupo=="OMB",], pch=(18), cex=2, col="black")
points(escores.nmds[grupo=="GAL",], pch=(19), cex=2, col="darkgrey")
points(escores.nmds[grupo=="SEMI",], pch=(20), cex=2, col="red")
```



Analysis of similarities (ANOSIM)

Basic template by "vegan"

The two matrices used here are the same as those used previously in NMDS analysis

```
# usage:

library(vegan)

# Data

matrix<- read.table("matrixspp.txt", header=T, sep="\t")
matrix[1:5,1:4] # shows only part of the data

##   abarema_brachystachya abarema_villosa acanthocladus_pulcherrimus
## 1                     0               0                           0
## 2                     0               0                           0
## 3                     0               0                           0
## 4                     0               0                           0
## 5                     0               0                           0
##   alchornea_glandulosa
## 1                    0
## 2                    0
## 3                    0
```

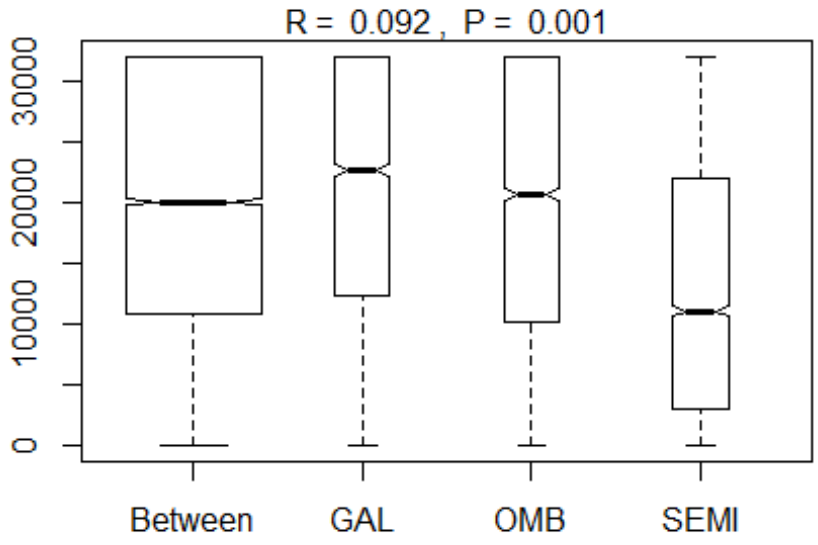
```
## 4                    0
## 5                    0

matrix5<- read.table("matrixtype.txt", header=T, sep="\t")
head(matrix5) # shows by default only the first 6 rows of data

##   type codigos
## 1 OMBR     OMB
## 2 OMBR     OMB
## 3 OMBR     OMB
## 4 OMBR     OMB
## 5 OMBR     OMB
## 6 OMBR     OMB
```

Analysis-ANOSIM

```
matrix[1:5,1:4] # shows only part of the data

##   abarema_brachystachya abarema_villosa acanthocladus_pulcherrimus
## 1                     0              0                           0
## 2                     0              0                           0
## 3                     0              0                           0
## 4                     0              0                           0
## 5                     0              0                           0
##   alchornea_glandulosa
## 1                    0
## 2                    0
## 3                    0
## 4                    0
## 5                    0

head(matrix5) # shows by default only the first 6 rows of data

##   type codigos
## 1 OMBR     OMB
## 2 OMBR     OMB
## 3 OMBR     OMB
## 4 OMBR     OMB
## 5 OMBR     OMB
## 6 OMBR     OMB

attach(matrix5)
forest.dist <- vegdist(matrix, "bray")
forest.ano <- anosim(matrix, matrix5$codigo)
summary(forest.ano)

##
## Call:
## anosim(x = matrix, grouping = matrix5$codigo)
## Dissimilarity: bray
##
```

```
## ANOSIM statistic R: 0.09155
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##     90%     95%   97.5%     99%
## 0.00741 0.01019 0.01246 0.01541
##
## Dissimilarity ranks between and within classes:
##         0%     25%   50%     75%  100%     N
## Between  3 10782.0 20070 32024.0 32024 26133
## GAL      4 12251.5 22714 32024.0 32024  4278
## OMB      2 10176.5 20662 32024.0 32024  4278
## SEMI     1  3031.5 11048 22024.5 32024  4371
```

```
plot(forest.ano)
```




```
forest.nmds$stress
```

```
## [1] 0.2185807
```

The graph described in NMDS analysis can also be used to illustrate the result of ANOSIM.

Important: This ANOSIM using R just provides the Global R statistics and p-value, i.e. whether there are differences or not. If you need to know between which pairs

there are significant differences, the most pratical and acessible way is to do ANOSIM in the “PAST” software. To do this you insert the names of the categories in the first column (grey), which corresponds to the rows , and the species’ names in the horizontal grey row, which corresponds to the columns. Your columns will contain the species’ names. In the rest of the cells are filled with the species abundance data per plot. The last step is to mark the first column with type names in different colors. Just go in edit and you’ll find how to insert different colors to specific lines. “Past” requires at least 2 different color groups to be defined. Lastly, just click on “Multivariatve” and select “ANOSIM-One way”. The output will return the Global and the pairwise values.

CCA (Canonical Correspondence Analysis)

CCA, also refered as constrained correspondence analysis, is one of the most commonly used multivariate analyses to model and to test effects of environmental variables (e.g. soil properties (ph, N, P, K etc) on species composition of plant communities.

```
# install.packages("vegan")
library(vegan)

# Usage:

# Species matrix

matrix<- read.table("matrixspp.txt", header=T, sep="\t")
matrix[1:5,1:4] # shows only part of the data

##   abarema_brachystachya abarema_villosa acanthocladus_pulcherrimus
## 1                     0               0                           0
## 2                     0               0                           0
## 3                     0               0                           0
## 4                     0               0                           0
## 5                     0               0                           0
##   alchornea_glandulosa
## 1                    0
## 2                    0
## 3                    0
## 4                    0
## 5                    0

# Environmental matrix

env<- read.table("matrixenv.txt", header=T, sep="\t")
head(env)

##    pH P  K  Ca  Mg  Al
## 1 4.5 4 39 0.1 0.1 2.6
## 2 4.5 4 45 0.1 0.1 3.3
```

```
## 3 4.4 3 39 0.2 0.1 3.2
## 4 4.2 4 44 0.2 0.1 2.2
## 5 4.0 5 36 0.2 0.1 4.1
## 6 4.3 4 28 0.1 0.1 2.1
```

```
forest.cca <- cca(matrix ~ pH + P + K + Ca + Mg + Al, env, na.action =
na.fail)
forest.cca
```

```
## Call: cca(formula = matrix ~ pH + P + K + Ca + Mg + Al, data =
## env, na.action = na.fail)
##
##                Inertia Proportion Rank
## Total         26.84694    1.00000
## Constrained    0.57015    0.02124    6
## Unconstrained 26.27679    0.97876  273
## Inertia is scaled Chi-square
## 73 species (variables) deleted due to missingness
##
## Eigenvalues for constrained axes:
##    CCA1    CCA2    CCA3    CCA4    CCA5    CCA6
## 0.13345 0.10707 0.09487 0.08878 0.07677 0.06921
##
## Eigenvalues for unconstrained axes:
##    CA1    CA2    CA3    CA4    CA5    CA6    CA7    CA8
## 0.7949 0.7109 0.6902 0.6704 0.6100 0.5536 0.5123 0.5007
## (Showing 8 of 273 unconstrained eigenvalues)
```

```
anova(forest.cca, by="margin")
```

```
## Permutation test for cca under reduced model
## Marginal effects of terms
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = matrix ~ pH + P + K + Ca + Mg + Al, data = env,
na.action = na.fail)
##           Df ChiSquare      F Pr(>F)
## pH         1    0.1070 1.1121  0.178
## P          1    0.1046 1.0862  0.262
## K          1    0.1015 1.0546  0.325
## Ca         1    0.0974 1.0120  0.432
## Mg         1    0.0815 0.8467  0.799
## Al         1    0.1020 1.0597  0.316
## Residual 273   26.2768
```

```
summary<- summary(forest.cca) # scores of CCA
head(summary) # shows by default only the first 6 rows of the scores
```

```
##
## Call:
```

```
## cca(formula = matrix ~ pH + P + K + Ca + Mg + Al, data = env,
na.action = na.fail)
##
## Partitioning of scaled Chi-square:
##               Inertia Proportion
## Total         26.8469    1.00000
## Constrained    0.5702    0.02124
## Unconstrained 26.2768    0.97876
##
## Eigenvalues, and their contribution to the scaled Chi-square
##
## Importance of components:
##                             CCA1     CCA2     CCA3     CCA4     CCA5
## Eigenvalue            0.133454 0.107067 0.094870 0.088783 0.076768
## Proportion Explained  0.004971 0.003988 0.003534 0.003307 0.002859
## Cumulative Proportion 0.004971 0.008959 0.012493 0.015800 0.018659
##                             CCA6     CA1     CA2     CA3     CA4     CA5
## Eigenvalue            0.069211 0.79491 0.71093 0.69017 0.67039 0.61000
## Proportion Explained  0.002578 0.02961 0.02648 0.02571 0.02497 0.02272
## Cumulative Proportion 0.021237 0.05085 0.07733 0.10303 0.12801 0.15073
##                             CA6     CA7     CA8     CA9    CA10    CA11
## Eigenvalue            0.55365 0.51231 0.50066 0.43055 0.37484 0.35749
## Proportion Explained  0.02062 0.01908 0.01865 0.01604 0.01396 0.01332
## Cumulative Proportion 0.17135 0.19043 0.20908 0.22512 0.23908 0.25240
##                            CA12    CA13    CA14    CA15    CA16    CA17
## Eigenvalue            0.33137 0.31731 0.31476 0.29647 0.29313 0.28059
## Proportion Explained  0.01234 0.01182 0.01172 0.01104 0.01092 0.01045
## Cumulative Proportion 0.26474 0.27656 0.28828 0.29932 0.31024 0.32069
##                            CA18     CA19     CA20     CA21     CA22
CA23
## Eigenvalue            0.27204 0.264399 0.257427 0.253720 0.247108
0.243790
## Proportion Explained  0.01013 0.009848 0.009589 0.009451 0.009204
0.009081
## Cumulative Proportion 0.33083 0.340676 0.350265 0.359715 0.368920
0.378000
##                             CA24     CA25     CA26    CA27     CA28
CA29
## Eigenvalue            0.243745 0.240429 0.229699 0.22041 0.216962
0.215906
## Proportion Explained  0.009079 0.008956 0.008556 0.00821 0.008081
0.008042
## Cumulative Proportion 0.387079 0.396035 0.404591 0.41280 0.420882
0.428924
##                             CA30     CA31    CA32    CA33     CA34
CA35
## Eigenvalue            0.212313 0.211601 0.21100 0.20539 0.202015
0.200763
## Proportion Explained  0.007908 0.007882 0.00786 0.00765 0.007525
0.007478
```

```
## Cumulative Proportion 0.436833 0.444714 0.45257 0.46022 0.467749
0.475227
##                            CA36     CA37     CA38    CA39     CA40
CA41
## Eigenvalue             0.197002 0.193546 0.191625 0.19034 0.183262
0.180381
## Proportion Explained  0.007338 0.007209 0.007138 0.00709 0.006826
0.006719
## Cumulative Proportion 0.482565 0.489774 0.496912 0.50400 0.510828
0.517547
##                            CA42     CA43     CA44     CA45     CA46
## Eigenvalue             0.179151 0.178841 0.172691 0.171183 0.168806
## Proportion Explained  0.006673 0.006661 0.006432 0.006376 0.006288
## Cumulative Proportion 0.524220 0.530881 0.537314 0.543690 0.549978
##                            CA47     CA48     CA49     CA50     CA51
## Eigenvalue             0.166302 0.164254 0.163920 0.162202 0.159697
## Proportion Explained  0.006194 0.006118 0.006106 0.006042 0.005948
## Cumulative Proportion 0.556172 0.562290 0.568396 0.574438 0.580386
##                            CA52     CA53     CA54     CA55     CA56
## Eigenvalue             0.158880 0.156539 0.152281 0.151755 0.150853
## Proportion Explained  0.005918 0.005831 0.005672 0.005653 0.005619
## Cumulative Proportion 0.586304 0.592135 0.597807 0.603460 0.609079
##                            CA57     CA58     CA59     CA60     CA61
## Eigenvalue             0.148587 0.145735 0.144786 0.144191 0.142750
## Proportion Explained  0.005535 0.005428 0.005393 0.005371 0.005317
## Cumulative Proportion 0.614613 0.620042 0.625435 0.630806 0.636123
##                            CA62     CA63     CA64     CA65     CA66
## Eigenvalue             0.141302 0.140067 0.139000 0.136403 0.135129
## Proportion Explained  0.005263 0.005217 0.005177 0.005081 0.005033
## Cumulative Proportion 0.641386 0.646603 0.651781 0.656862 0.661895
##                            CA67     CA68     CA69     CA70     CA71
## Eigenvalue             0.131766 0.130343 0.129344 0.127076 0.126107
## Proportion Explained  0.004908 0.004855 0.004818 0.004733 0.004697
## Cumulative Proportion 0.666803 0.671658 0.676476 0.681209 0.685906
##                            CA72     CA73     CA74     CA75    CA76
CA77
## Eigenvalue             0.124247 0.123811 0.122370 0.119772 0.11758
0.11705
## Proportion Explained  0.004628 0.004612 0.004558 0.004461 0.00438
0.00436
## Cumulative Proportion 0.690534 0.695146 0.699704 0.704165 0.70854
0.71290
##                            CA78     CA79     CA80     CA81     CA82
## Eigenvalue             0.115508 0.114218 0.112989 0.110408 0.109197
## Proportion Explained  0.004302 0.004254 0.004209 0.004113 0.004067
## Cumulative Proportion 0.717207 0.721462 0.725670 0.729783 0.733850
##                            CA83     CA84     CA85     CA86     CA87
## Eigenvalue             0.108409 0.108173 0.105441 0.104595 0.102905
## Proportion Explained  0.004038 0.004029 0.003927 0.003896 0.003833
## Cumulative Proportion 0.737888 0.741918 0.745845 0.749741 0.753574
```

```
##                            CA88     CA89     CA90     CA91     CA92
## Eigenvalue             0.101358 0.100752 0.100439 0.100086 0.097841
## Proportion Explained   0.003775 0.003753 0.003741 0.003728 0.003644
## Cumulative Proportion 0.757349 0.761102 0.764843 0.768571 0.772216
##                            CA93     CA94     CA95    CA96     CA97
CA98
## Eigenvalue             0.096959 0.096093 0.094704 0.09368 0.092814
0.092428
## Proportion Explained   0.003612 0.003579 0.003528 0.00349 0.003457
0.003443
## Cumulative Proportion 0.775827 0.779407 0.782934 0.78642 0.789881
0.793324
##                            CA99    CA100    CA101    CA102    CA103
## Eigenvalue             0.091093 0.089654 0.089457 0.087943 0.086575
## Proportion Explained   0.003393 0.003339 0.003332 0.003276 0.003225
## Cumulative Proportion 0.796717 0.800056 0.803388 0.806664 0.809889
##                           CA104    CA105    CA106    CA107    CA108
## Eigenvalue             0.085801 0.085266 0.084390 0.083684 0.083050
## Proportion Explained   0.003196 0.003176 0.003143 0.003117 0.003093
## Cumulative Proportion 0.813085 0.816261 0.819404 0.822521 0.825615
##                           CA109    CA110    CA111    CA112    CA113
## Eigenvalue             0.082650 0.081223 0.080599 0.079815 0.078284
## Proportion Explained   0.003079 0.003025 0.003002 0.002973 0.002916
## Cumulative Proportion 0.828693 0.831719 0.834721 0.837694 0.840610
##                           CA114    CA115    CA116    CA117   CA118
CA119
## Eigenvalue             0.077683 0.077200 0.076070 0.075753 0.07330
0.072731
## Proportion Explained   0.002894 0.002876 0.002833 0.002822 0.00273
0.002709
## Cumulative Proportion 0.843503 0.846379 0.849212 0.852034 0.85476
0.857473
##                           CA120    CA121    CA122   CA123    CA124
CA125
## Eigenvalue             0.071921 0.071254 0.069834 0.06928 0.068163
0.067691
## Proportion Explained   0.002679 0.002654 0.002601 0.00258 0.002539
0.002521
## Cumulative Proportion 0.860152 0.862806 0.865407 0.86799 0.870527
0.873048
##                           CA126    CA127    CA128    CA129    CA130
## Eigenvalue             0.066292 0.065208 0.064862 0.064022 0.063521
## Proportion Explained   0.002469 0.002429 0.002416 0.002385 0.002366
## Cumulative Proportion 0.875517 0.877946 0.880362 0.882747 0.885113
##                           CA131    CA132    CA133    CA134    CA135
## Eigenvalue             0.062631 0.061629 0.060607 0.059574 0.058172
## Proportion Explained   0.002333 0.002296 0.002258 0.002219 0.002167
## Cumulative Proportion 0.887446 0.889742 0.891999 0.894218 0.896385
##                           CA136    CA137    CA138    CA139    CA140
## Eigenvalue             0.057939 0.057631 0.056849 0.056001 0.054700
```

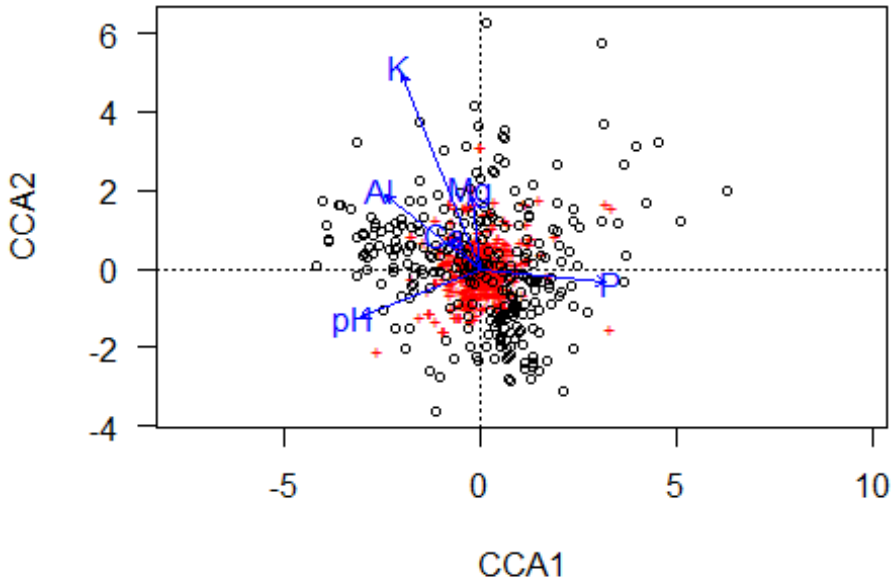
```
## Proportion Explained  0.002158 0.002147 0.002118 0.002086 0.002037
## Cumulative Proportion 0.898543 0.900690 0.902807 0.904893 0.906931
##                          CA141    CA142    CA143    CA144    CA145
## Eigenvalue            0.053797 0.052781 0.052687 0.052129 0.050532
## Proportion Explained  0.002004 0.001966 0.001962 0.001942 0.001882
## Cumulative Proportion 0.908934 0.910900 0.912863 0.914805 0.916687
##                          CA146    CA147    CA148    CA149    CA150
## Eigenvalue            0.050143 0.049893 0.048909 0.047714 0.046742
## Proportion Explained  0.001868 0.001858 0.001822 0.001777 0.001741
## Cumulative Proportion 0.918555 0.920413 0.922235 0.924012 0.925753
##                          CA151   CA152    CA153    CA154    CA155
CA156
## Eigenvalue            0.046119 0.04590 0.044665 0.044152 0.043621
0.043195
## Proportion Explained  0.001718 0.00171 0.001664 0.001645 0.001625
0.001609
## Cumulative Proportion 0.927471 0.92918 0.930844 0.932489 0.934114
0.935722
##                          CA157    CA158    CA159    CA160    CA161
## Eigenvalue            0.042589 0.040889 0.040483 0.039867 0.039142
## Proportion Explained  0.001586 0.001523 0.001508 0.001485 0.001458
## Cumulative Proportion 0.937309 0.938832 0.940340 0.941825 0.943283
##                          CA162    CA163    CA164    CA165    CA166
## Eigenvalue            0.038772 0.038209 0.036714 0.036433 0.035424
## Proportion Explained  0.001444 0.001423 0.001368 0.001357 0.001319
## Cumulative Proportion 0.944727 0.946150 0.947518 0.948875 0.950194
##                          CA167    CA168   CA169    CA170    CA171
CA172
## Eigenvalue            0.034841 0.034034 0.03357 0.032810 0.032202
0.031659
## Proportion Explained  0.001298 0.001268 0.00125 0.001222 0.001199
0.001179
## Cumulative Proportion 0.951492 0.952760 0.95401 0.955232 0.956432
0.957611
##                          CA173    CA174    CA175   CA176    CA177
CA178
## Eigenvalue            0.031358 0.030700 0.030271 0.03008 0.028924
0.028624
## Proportion Explained  0.001168 0.001144 0.001128 0.00112 0.001077
0.001066
## Cumulative Proportion 0.958779 0.959923 0.961050 0.96217 0.963248
0.964314
##                          CA179    CA180   CA181     CA182    CA183
## Eigenvalue            0.027961 0.027319 0.02710 0.0262734 0.026229
## Proportion Explained  0.001041 0.001018 0.00101 0.0009786 0.000977
## Cumulative Proportion 0.965355 0.966373 0.96738 0.9683612 0.969338
##                           CA184     CA185   CA186     CA187     CA188
## Eigenvalue            0.0255123 0.0247811 0.02443 0.0240143 0.0238019
## Proportion Explained  0.0009503 0.0009231 0.00091 0.0008945 0.0008866
## Cumulative Proportion 0.9702885 0.9712116 0.97212 0.9730160 0.9739026
```

```
##                            CA189     CA190     CA191     CA192
CA193
## Eigenvalue            0.0231740 0.0222444 0.0218978 0.0213761
0.0208438
## Proportion Explained  0.0008632 0.0008286 0.0008157 0.0007962
0.0007764
## Cumulative Proportion 0.9747658 0.9755944 0.9764100 0.9772062
0.9779826
##                            CA194     CA195     CA196     CA197
CA198
## Eigenvalue            0.0204801 0.0203209 0.0195663 0.0193642
0.0192158
## Proportion Explained  0.0007628 0.0007569 0.0007288 0.0007213
0.0007158
## Cumulative Proportion 0.9787455 0.9795024 0.9802312 0.9809525
0.9816682
##                            CA199     CA200     CA201     CA202
CA203
## Eigenvalue            0.0182656 0.0180880 0.0170441 0.0167410
0.0161192
## Proportion Explained  0.0006804 0.0006737 0.0006349 0.0006236
0.0006004
## Cumulative Proportion 0.9823486 0.9830223 0.9836572 0.9842808
0.9848812
##                            CA204     CA205     CA206     CA207
CA208
## Eigenvalue            0.0160310 0.0155517 0.0149094 0.0142466
0.0141906
## Proportion Explained  0.0005971 0.0005793 0.0005553 0.0005307
0.0005286
## Cumulative Proportion 0.9854783 0.9860576 0.9866129 0.9871436
0.9876722
##                            CA209     CA210     CA211     CA212
CA213
## Eigenvalue            0.0137521 0.0135397 0.0131839 0.0125312
0.0123308
## Proportion Explained  0.0005122 0.0005043 0.0004911 0.0004668
0.0004593
## Cumulative Proportion 0.9881844 0.9886888 0.9891798 0.9896466
0.9901059
##                            CA214     CA215     CA216     CA217
CA218
## Eigenvalue            0.0119986 0.0118160 0.0112397 0.0110831
0.0109782
## Proportion Explained  0.0004469 0.0004401 0.0004187 0.0004128
0.0004089
## Cumulative Proportion 0.9905528 0.9909929 0.9914116 0.9918244
0.9922333
##                            CA219     CA220     CA221     CA222
CA223
```

```
## Eigenvalue            0.0105488 0.0100077 0.0096448 0.0092001
0.0089624
## Proportion Explained  0.0003929 0.0003728 0.0003593 0.0003427
0.0003338
## Cumulative Proportion 0.9926263 0.9929990 0.9933583 0.9937010
0.9940348
##                           CA224     CA225    CA226     CA227     CA228
## Eigenvalue            0.0089161 0.0086083 0.008053 0.0077037 0.0074697
## Proportion Explained  0.0003321 0.0003206 0.000300 0.0002869 0.0002782
## Cumulative Proportion 0.9943669 0.9946876 0.994988 0.9952745 0.9955527
##                           CA229     CA230     CA231     CA232
CA233
## Eigenvalue            0.0072798 0.0071658 0.0066610 0.0062860
0.0058629
## Proportion Explained  0.0002712 0.0002669 0.0002481 0.0002341
0.0002184
## Cumulative Proportion 0.9958239 0.9960908 0.9963389 0.9965730
0.9967914
##                          CA234     CA235     CA236     CA237    CA238
## Eigenvalue            0.005692 0.0056442 0.0052689 0.0050255 0.004779
## Proportion Explained  0.000212 0.0002102 0.0001963 0.0001872 0.000178
## Cumulative Proportion 0.997003 0.9972137 0.9974099 0.9975971 0.997775
##                           CA239    CA240    CA241     CA242     CA243
## Eigenvalue            0.0046528 0.004536 0.004027 0.0035879 0.0034546
## Proportion Explained  0.0001733 0.000169 0.000150 0.0001336 0.0001287
## Cumulative Proportion 0.9979484 0.998117 0.998267 0.9984010 0.9985297
##                           CA244    CA245     CA246     CA247     CA248
## Eigenvalue            0.0032627 0.003034 0.0028833 0.0027852 2.587e-03
## Proportion Explained  0.0001215 0.000113 0.0001074 0.0001037 9.638e-05
## Cumulative Proportion 0.9986512 0.998764 0.9988716 0.9989754 9.991e-01
##                           CA249     CA250     CA251     CA252
CA253
## Eigenvalue            2.432e-03 2.309e-03 2.199e-03 2.057e-03 1.994e-
03
## Proportion Explained  9.057e-05 8.602e-05 8.192e-05 7.662e-05 7.426e-
05
## Cumulative Proportion 9.992e-01 9.992e-01 9.993e-01 9.994e-01 9.995e-
01
##                           CA254     CA255     CA256     CA257
CA258
## Eigenvalue            0.0017532 1.531e-03 1.333e-03 1.243e-03
0.0010927
## Proportion Explained  0.0000653 5.702e-05 4.964e-05 4.629e-05
0.0000407
## Cumulative Proportion 0.9995465 9.996e-01 9.997e-01 9.997e-01
0.9997401
##                           CA259     CA260     CA261     CA262
CA263
## Eigenvalue            1.016e-03 9.462e-04 8.598e-04 8.044e-04 6.902e-
04
```

```
## Proportion Explained  3.784e-05 3.524e-05 3.203e-05 2.996e-05 2.571e-
05
## Cumulative Proportion 9.998e-01 9.998e-01 9.998e-01 9.999e-01 9.999e-
01
##                          CA264     CA265     CA266     CA267
CA268
## Eigenvalue            6.058e-04 4.842e-04 3.749e-04 2.771e-04 2.547e-
04
## Proportion Explained  2.257e-05 1.804e-05 1.396e-05 1.032e-05 9.485e-
06
## Cumulative Proportion 9.999e-01 9.999e-01 1.000e+00 1.000e+00
1.000e+00
##                          CA269     CA270     CA271     CA272
CA273
## Eigenvalue            2.293e-04 1.765e-04 1.570e-04 7.871e-05 2.199e-
05
## Proportion Explained  8.541e-06 6.574e-06 5.849e-06 2.932e-06 8.190e-
07
## Cumulative Proportion 1.000e+00 1.000e+00 1.000e+00 1.000e+00
1.000e+00
##
## Accumulated constrained eigenvalues
## Importance of components:
##                          CCA1   CCA2    CCA3    CCA4    CCA5    CCA6
## Eigenvalue            0.1335 0.1071 0.09487 0.08878 0.07677 0.06921
## Proportion Explained  0.2341 0.1878 0.16639 0.15572 0.13464 0.12139
## Cumulative Proportion 0.2341 0.4219 0.58825 0.74397 0.87861 1.00000
##
## Scaling 2 for species and site scores
## * Species are scaled proportional to eigenvalues
## * Sites are unscaled: weighted dispersion equal on all dimensions
##
##
## Species scores
##
##                                CCA1     CCA2     CCA3     CCA4
CCA5
## abarema_brachystachya      -0.08600  0.74307 -0.05159  0.91193
0.05159
## abarema_villosa            -0.15080  1.70220 -0.98401 -1.92075 -
1.03712
## acanthocladus_pulcherrimus  1.21131  0.22509 -0.50765  0.64935
0.01608
## alchornea_glandulosa       -0.91166 -0.24970 -0.07451  0.07332 -
0.26944
## alibertia_concolor          0.32728 -0.45372 -0.11631 -0.28745
0.42483
## alibertia_edulis            0.01383  0.05318  0.17868  0.25923
0.04599
## ....
```

```
##                                 CCA6
## abarema_brachystachya      -0.113733
## abarema_villosa            -0.675995
## acanthocladus_pulcherrimus  1.273453
## alchornea_glandulosa       -0.001909
## alibertia_concolor         -0.449355
## alibertia_edulis           -0.012734
## ....
##
##
## Site scores (weighted averages of species scores)
##
##          CCA1    CCA2    CCA3    CCA4    CCA5    CCA6
## row1  1.48951 -1.6420 -1.8624 -2.1549 -0.3991 -1.0164
## row2 -0.07990  1.1061 -1.2860 -3.2203  2.5605  0.9580
## row3  2.02275 -0.7063  0.4961 -1.3433  0.8617  0.3517
## row4  6.29102  2.0096 -1.4887 -0.5053  3.8836  3.0659
## row5  0.00129 -0.1397  1.8836 -1.8595  1.4453  3.1196
## row6  1.38952 -0.8245 -1.4034  1.5555  0.6720 -1.1118
## ....
##
##
## Site constraints (linear combinations of constraining variables)
##
##         CCA1     CCA2     CCA3     CCA4   CCA5      CCA6
## row1  0.5722 -0.12906 -0.64977 -1.18507 0.6791 -0.021241
## row2 -0.1000 -0.02029 -0.23062 -1.51626 0.7934  0.512563
## row3 -0.5512 -0.54413 -0.03378 -0.23777 0.2450  0.631624
## row4  1.5712  0.61372 -0.46802  0.08159 0.5547 -0.227517
## row5  0.5161 -0.62360  1.33765 -0.91375 0.2887  1.930741
## row6  1.4922 -0.40025 -0.81149 -0.48078 0.3170  0.009357
## ....
##
##
## Biplot scores for constraining variables
##
##        CCA1     CCA2     CCA3     CCA4     CCA5    CCA6
## pH -0.50007 -0.19882 -0.19379 -0.41096  0.06805 -0.7066
## P   0.52640 -0.05314  0.65806 -0.49648  0.10292 -0.1730
## K  -0.32880  0.82533  0.37257 -0.07746  0.04001 -0.2536
## Ca -0.11852  0.11749  0.72741  0.22325 -0.32501 -0.5362
## Mg -0.03656  0.30274  0.07982 -0.27226 -0.89713 -0.1472
## Al -0.39741  0.31070  0.40749 -0.22859  0.04560  0.7247

# ordinary plot
x11(width=12, height=12)
plot(forest.cca, las=1)
```




```
# dev.off()
```

PCA (Principal Component Analysis

PCA is a method commonly used to separate variables (e.g environmental data, such as soil conditions) in ordination before submitting them to further analysis.

To execute the PCA in the example below, we use the function rda, though other functions such as prcomp or princomp can also be used to calculate PCA. It's important to correctly interpret the PCA output before trying to understand values returned by the function "PCAsignificance" and the command "PC1.exp", which are explained below. The command PC1.exp shows the percentage of explanation of each axis. In the function "PCAsignificance" the result named "percentage of variance" shows the percentage of variation explained by axis 1. You can access further information about this, and other values, by requesting R help for this function by writing: ?PCAsignificance.

The output of rda, v, contains the scores of the "species" (here: soil variables) and sites on the ordination axes. These are not the same as the correlations of variables with the axes.

```
# install.packages("vegan")

library(vegan) # rda function for PCA analysis
```

```r
# Environmental matrix
env<- read.table("matrixenv.txt", header=T, sep="\t")
head(env)
```

```
##    pH P  K  Ca  Mg  Al
## 1 4.5 4 39 0.1 0.1 2.6
## 2 4.5 4 45 0.1 0.1 3.3
## 3 4.4 3 39 0.2 0.1 3.2
## 4 4.2 4 44 0.2 0.1 2.2
## 5 4.0 5 36 0.2 0.1 4.1
## 6 4.3 4 28 0.1 0.1 2.1
```

```r
# Usage:

pca.env <- rda(env, scale=TRUE) # scale = TRUE - to standardize the data
pca.env
```

```
## Call: rda(X = env, scale = TRUE)
##
##               Inertia Rank
## Total               6
## Unconstrained       6    6
## Inertia is correlations
##
## Eigenvalues for unconstrained axes:
##    PC1    PC2    PC3    PC4    PC5    PC6
## 1.9853 1.4433 1.0506 0.7259 0.5413 0.2536
```

```r
summary<- summary(pca.env)
head(summary) # shows by default only the first 6 rows of the scores
```

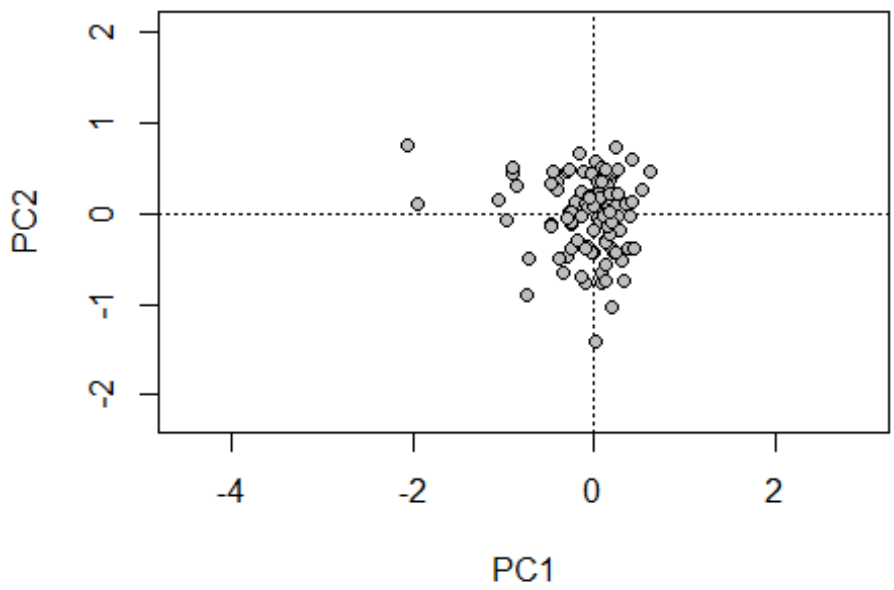
```
##
## Call:
## rda(X = env, scale = TRUE)
##
## Partitioning of correlations:
##               Inertia Proportion
## Total               6          1
## Unconstrained       6          1
##
## Eigenvalues, and their contribution to the correlations
##
## Importance of components:
##                            PC1    PC2    PC3    PC4     PC5     PC6
## Eigenvalue              1.9853 1.4433 1.0506 0.7259 0.54130 0.25355
## Proportion Explained    0.3309 0.2406 0.1751 0.1210 0.09022 0.04226
## Cumulative Proportion 0.3309 0.5714 0.7465 0.8675 0.95774 1.00000
##
## Scaling 2 for species and site scores
## * Species are scaled proportional to eigenvalues
## * Sites are unscaled: weighted dispersion equal on all dimensions
```

```
## * General scaling constant of scores:  6.396448
##
##
## Species scores
##
##        PC1     PC2     PC3       PC4     PC5      PC6
## pH -0.7012  2.0436 -0.3792  0.883221  1.0642  0.30809
## P  -0.9181 -0.4401  2.2376 -0.225144  0.8270 -0.20217
## K  -2.1470 -0.4973 -0.5432  0.972407 -0.2224 -0.81988
## Ca -2.1582  0.4553  0.6081 -0.001057 -1.0408  0.70784
## Mg -1.6190  0.1906 -0.9777 -1.712833  0.5125 -0.09719
## Al -0.5612 -2.2319 -0.6268  0.489924  0.6923  0.64071
##
##
## Site scores (weighted sums of species scores)
##
##         PC1       PC2      PC3      PC4     PC5     PC6
## sit1 0.2332  0.089598  0.17463  0.08095  0.4550 -0.2855
## sit2 0.1368 -0.145176  0.06386  0.24593  0.6126 -0.1015
## sit3 0.1862 -0.107166 -0.08787  0.13652  0.1706  0.2740
## sit4 0.1762  0.005016  0.30162 -0.10225 -0.1222 -0.5942
## sit5 0.1254 -0.741146  0.40371 -0.10187  0.3741  0.3728
## sit6 0.4021  0.131917  0.32129 -0.24087  0.1643 -0.3517
## ....
```

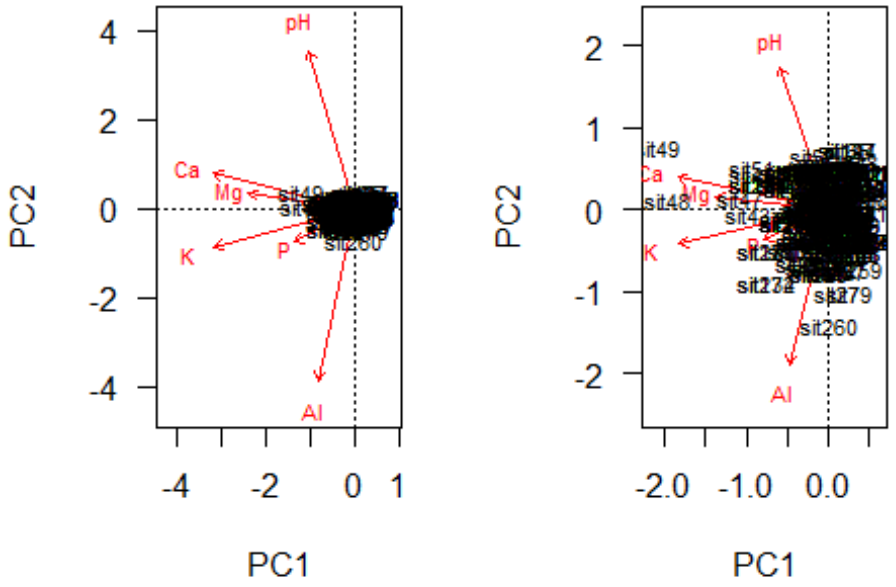
If you want to test for the signifance of PCA, you can either use the function PCAsignificance of the package BiodiversityR (e.g. PCAsignificance(pca.env, axes=6)) or to compute an anova under a rda.

```
(av <- pca.env$CA$eig) # av - inspects the eigenvalues. The sum of
eigenvalues

##       PC1       PC2       PC3       PC4       PC5       PC6
## 1.9852662 1.4433273 1.0506311 0.7259281 0.5412958 0.2535515

                       # represent the total percentage of explanation
assigned
                       # to each axis.
                       # pca.env$CA$":Relationship of each environmental
variable
                       # with the axes.The closer the result is to 1, the
larger
                       # the association with the positive or negative
axis, respectively.

sum.av <- sum(av)
PC1.exp <- 100*(av[1]/sum(av))  # calculate the percentage of explanation
of
PC1.exp                         # each axis. Here it shows the percentage
of the
```

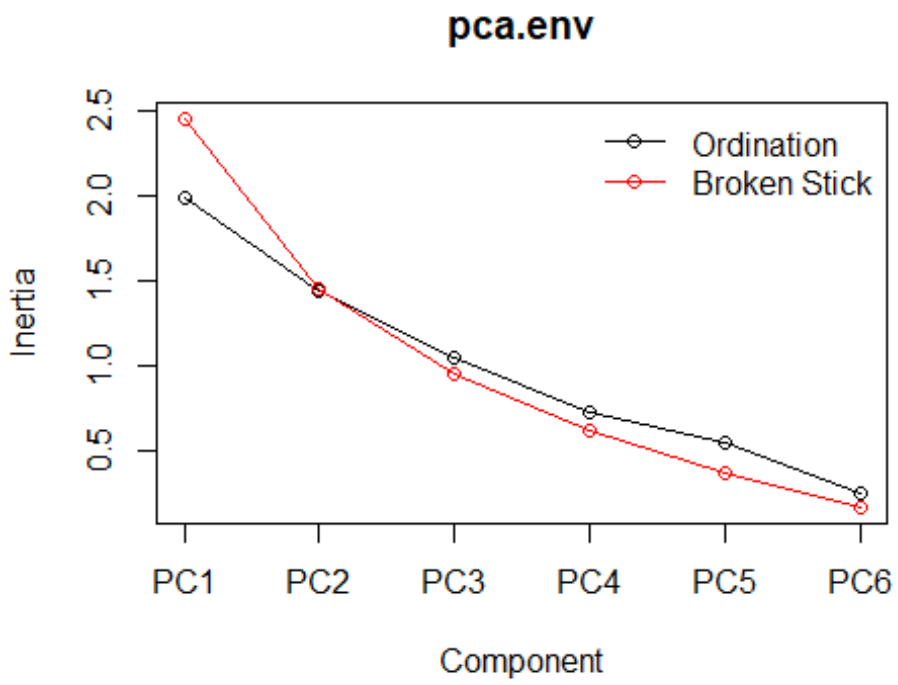
```
##      PC1
## 33.08777

round(PC1.exp, 2) # You can choose how many decimals after the point you
would

##   PC1
## 33.09

                  # like to keep. Here it is 2.

# Simple gragh

x11(width=12, height=12)
plot(pca.env, type="n")
points(pca.env, display = "sites", col=1, pch=21, cex=1, bg="grey")
```




```
# Biplot graph

par(mfrow=c(1,2))
plot1 <- biplot(pca.env, scaling=1, type="text", las=1) # sites scaled by
                                                        # eigenvalues
plot2 <- biplot(pca.env, scaling=2, type="text", las=1) # species scaled
by
```




```
                                                        # eigenvalues
# dev.off()

# Screeplots - select axes with values from the ordination that are
larger
# than the expected value under the Broken stick criteria.

screeplot(pca.env, bstick = TRUE, type = "lines")
```



Analysis of Indicator Species (INDVAL)

The association index named IndVal computed with the function "multipatt" of the package "indicspecies" is generated by combinations of the input clusters and comparison of each combination with the matrix species. Thus, each species receives the combination with the highest association value and the best matching patterns are tested for statistical significance of the associations. Thus this analysis is useful to indicate species that can be used to gather information about specific characteristics of habitats or environment (e.g. forest types; soil types; drought or wetter sites).

The name "type" within the command below refers to the categorical variable in the forest type matrix (matrixtype.txt). "codigos" are labels given to abbreviate forest type names: OMB = Rain (Ombrophilous) Forest; GAL = Gallery Forest and SEMI = Semideciduos forest.

```
# install.packages("indicspecies")

library(indicspecies)

# Species matrix
matrixspp<- read.table("matrixspp.txt", header=T, sep="\t")
matrixspp[1:5,1:4] # shows only part of the data

##   abarema_brachystachya abarema_villosa acanthocladus_pulcherrimus
## 1                     0              0                           0
```

```
## 2                      0                0                           0
## 3                      0                0                           0
## 4                      0                0                           0
## 5                      0                0                           0
##   alchornea_glandulosa
## 1                    0
## 2                    0
## 3                    0
## 4                    0
## 5                    0
```

```
# Vegetation type
type <- read.table("matrixtype.txt", header=T)
head(type)
```

```
##   type codigos
## 1 OMBR     OMB
## 2 OMBR     OMB
## 3 OMBR     OMB
## 4 OMBR     OMB
## 5 OMBR     OMB
## 6 OMBR     OMB
```

```
wetpt = multipatt(matrixspp, type$codigos) # Runs the combination
analysis
                                  # using IndVal.g as statistic
head(wetpt, 3) # shows by only the first 3 rows of the scores
```

```
## $call
## multipatt(x = matrixspp, cluster = type$codigos)
##
## $func
## [1] "IndVal.g"
##
## $cluster
##   [1] OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB
OMB
##  [15] OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB
OMB
##  [29] OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB
OMB
##  [43] OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB
OMB
##  [57] OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB
OMB
##  [71] OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB
OMB
##  [85] OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  OMB  GAL  GAL  GAL  GAL
GAL
##  [99] GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL
GAL
```

```
## [113] GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL
GAL
## [127] GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL
GAL
## [141] GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL
GAL
## [155] GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL
GAL
## [169] GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL  GAL
GAL
## [183] GAL  GAL  GAL  GAL  SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI
SEMI
## [197] SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI
SEMI
## [211] SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI
SEMI
## [225] SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI
SEMI
## [239] SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI
SEMI
## [253] SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI
SEMI
## [267] SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI SEMI
SEMI
## Levels: GAL OMB SEMI
```

```r
summary(wetpt) # Lists those species with significant association to one
combination
```

```
##
##  Multilevel pattern analysis
##  ---------------------------
##
##  Association function: IndVal.g
##  Significance level (alpha): 0.05
##
##  Total number of species: 532
##  Selected number of species: 62
##  Number of species associated to 1 group: 49
##  Number of species associated to 2 groups: 13
##
##  List of species associated to each combination:
##
##  Group GAL  #sps.  12
##                          stat p.value
## callisthene_major      0.360   0.005 **
## allagoptera_caudescens 0.302   0.005 **
## guazuma_ulmifolia      0.292   0.005 **
## alibertia_edulis       0.280   0.010 **
## miconia_cabucu         0.260   0.045 *
```

```
## dilodendron_bipinnatum 0.245   0.010 **
## protium_warmingiana    0.239   0.015 *
## diospyros_brasiliensis 0.239   0.005 **
## miconia_latecrenata    0.238   0.010 **
## parinari_parvifolia    0.232   0.005 **
## callisthene_minor      0.224   0.025 *
## psidium_oblongatum     0.207   0.015 *
##
##  Group OMB  #sps.  8
##                                  stat p.value
## licania_kunthiana               0.417   0.005 **
## phyllostemonodaphne_geminiflora 0.260   0.005 **
## styrax_ferrugineus              0.254   0.010 **
## ixora_gardneriana               0.232   0.025 *
## deguelia_hatschbachii           0.224   0.030 *
## virola_officinalis              0.223   0.045 *
## myrciaria_floribunda            0.217   0.015 *
## licania_spicata                 0.180   0.050 *
##
##  Group SEMI  #sps.  29
##                                stat p.value
## casearia_arborea             0.716   0.005 **
## lacistema_pubescens          0.632   0.005 **
## matayba_elaeagnoides         0.630   0.005 **
## xylopia_sericea              0.484   0.005 **
## erythroxylum_pelleterianum   0.469   0.005 **
## xylopia_aromatica            0.467   0.005 **
## miconia_calvescens           0.461   0.005 **
## myrcia_guianensis            0.461   0.005 **
## miconia_sellowiana           0.442   0.005 **
## pera_heteranthera            0.427   0.005 **
## himatanthus_phagedaenicus    0.425   0.005 **
## sacoglottis_mattogrossensis 0.396   0.005 **
## stryphnodendron_guianense    0.395   0.005 **
## siparuna_reginae             0.387   0.005 **
## jacaranda_macrantha          0.384   0.005 **
## gomidesia_tijucensis         0.372   0.005 **
## dalbergia_nigra              0.365   0.005 **
## guarea_pendula               0.358   0.005 **
## cryptocarya_aschersoniana    0.326   0.005 **
## vismia_martiana              0.315   0.005 **
## guatteria_gomeziana          0.309   0.010 **
## ocotea_diospyrifolia         0.273   0.010 **
## handroanthus_riodocensis     0.253   0.010 **
## duguetia_lanceolata          0.234   0.005 **
## hirtella_racemosa            0.231   0.030 *
## swartzia_polyphylla          0.231   0.010 **
## sloanea_guianensis           0.217   0.035 *
## alchornea_glandulosa         0.210   0.050 *
## vitex_megapotamica           0.206   0.030 *
```

```
##
##  Group GAL+OMB  #sps.  10
##                            stat p.value
## myrcia_sp                 0.502   0.005 **
## aspidosperma_discolor     0.415   0.030 *
## copaifera_langsdorffii    0.409   0.005 **
## senefeldera_verticillata 0.376   0.040 *
## protium_heptaphyllum      0.323   0.005 **
## clarisia_ilicifolia       0.293   0.005 **
## eschweilera_ovata         0.292   0.030 *
## terminalia_glabrescens    0.264   0.015 *
## ocotea_divaricata         0.220   0.050 *
## tabebuia_serratifolia     0.220   0.030 *
##
##  Group GAL+SEMI  #sps.  1
##                    stat p.value
## miconia_albicans 0.243    0.04 *
##
##  Group OMB+SEMI  #sps.  2
##                   stat p.value
## aniba_firmula   0.472   0.010 **
## ocotea_dispersa 0.317   0.025 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Permutational Analysis of variance (PERMANOVA)

PERMANOVA is a non-parametric multivariate statistical test used to compare groups of objects based on any measure of distance. Commonly this analysis is used to compare taxon in samples where the groups of samples are compared.

```
library(vegan)
library(permute)
library(lattice)

spp <- read.table("matrixspp.txt", header=T)
spp[1:5,10:13]

##   allophylus_racemosus alseis_floribunda amaioua_guianensis
## 1                    0                 0                  1
## 2                    0                 0                  0
## 3                    0                 0                  0
## 4                    0                 0                  0
## 5                    0                 0                  0
##   amaioua_intermedia
## 1                  0
## 2                  0
## 3                  0
```

```
## 4                   0
## 5                   0
```

```
log(spp+1)->spp2
spp2[1:5,10:13]
```

```
##   allophylus_racemosus alseis_floribunda amaioua_guianensis
## 1                    0                 0          0.6931472
## 2                    0                 0          0.0000000
## 3                    0                 0          0.0000000
## 4                    0                 0          0.0000000
## 5                    0                 0          0.0000000
##   amaioua_intermedia
## 1                  0
## 2                  0
## 3                  0
## 4                  0
## 5                  0
```

Usage:

Testing for species composition over different forest types: the name “type” within the command below is the categorical variable in the forest type matrix (matrixtype.txt). “codigos” are just labels given to abbreviate forest typenames: OMB = Rain (Ombrophilous) Forest; GAL = Gallery Forest and SEMI = Semideciduos forest.

```
type<- read.table("matrixtype.txt", header=T, sep="\t")
head(type)
```

```
##   type codigos
## 1 OMBR     OMB
## 2 OMBR     OMB
## 3 OMBR     OMB
## 4 OMBR     OMB
## 5 OMBR     OMB
## 6 OMBR     OMB
```

```
adonis(spp2 ~ codigos, data=type, permutations=999) -> perma.result1
perma.result1
```

```
##
## Call:
## adonis(formula = spp2 ~ codigos, data = type, permutations = 999)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##            Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## codigos     2     5.283 2.64162  6.5743 0.04532  0.001 ***
```

```
## Residuals 277   111.302 0.40181         0.95468
## Total     279   116.585                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Testing for soil influence in the tree species abundance: the names in the right side of the formula regard the soil variables contained in the environmental matrix ("matrixenv.txt"). The category "types" regard the forest type (OMB, GAL and SEMI).

```
env <- read.table("matrixenv.txt", header=T)
head(env)

##    pH P  K  Ca  Mg  Al
## 1 4.5 4 39 0.1 0.1 2.6
## 2 4.5 4 45 0.1 0.1 3.3
## 3 4.4 3 39 0.2 0.1 3.2
## 4 4.2 4 44 0.2 0.1 2.2
## 5 4.0 5 36 0.2 0.1 4.1
## 6 4.3 4 28 0.1 0.1 2.1

adonis(spp2 ~ pH + P + K + Ca + Mg + Al, data=env, permutations=999)->
perm.result
perm.result # Result to permanova pseudo-F, R2 e p.

##
## Call:
## adonis(formula = spp2 ~ pH + P + K + Ca + Mg + Al, data = env,
permutations = 999)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##            Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## pH          1     0.345 0.34542 0.82775 0.00296  0.703
## P           1     0.540 0.54033 1.29483 0.00463  0.152
## K           1     0.506 0.50551 1.21140 0.00434  0.193
## Ca          1     0.377 0.37685 0.90306 0.00323  0.587
## Mg          1     0.294 0.29425 0.70513 0.00252  0.874
## Al          1     0.600 0.60038 1.43874 0.00515  0.076 .
## Residuals 273   113.923 0.41730         0.97716
## Total     279   116.585                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

RECOMMENDED READING

Highlight:

GOTELLI, N.J.; ELLISON, A.M. A Primer of Ecological Statistics. Sinauer Associates Publishers, 2004. Version in Portuguese: GOTELLI, N.J.; ELLISON, A.M. Princípios de Estatística em Ecologia. Porto Alegre: Artmed, 2011. 527 p.

CRAWLEY, M.J. The R Book: Second Edtion. Chichester: Imperial College London at Silwood Park, John Wiley & Sons Ltd., 2012. 1051p.

BORCARD, D.; GILLET, F.; LEGENDRE, P. Numerical ecology with R. New York: Springer, 2011. 306 p.

FORTIN, M. J.; DALE, M. Spatial analysis: a guide for ecologists. Cambridge: Cambridge University, 2005. 365 p.

HINKLE, D.E.; WIERSMA, W. JURS, S.G. Applied Statistics for the Behavioral Sciences. 5th ed. Boston: Houghton Mifflin, 2003. 756 p.

LEGENDRE, P.; LEGENDRE, L. Numerical ecology. Third English edition. Amsterdam: Elsevier Science, 2012. 1006 p.

Complementary:

BEGON'S text book is highly recommendable reading on sampling design and statistical analysis in ecological studies (e.g. distribution, population growth, behaviour) of plants and animals.

BEGON, M.; TOWNSEND, C.R.; HARPER, J.L. Ecology: From Individuals to Ecosystems, 4th Edition. Wiley-Blackwell, 2005. 750 pages. Version in Portuguese: BEGON, M.; TOWNSEND, C.R.; HARPER, J.L. Ecologia: de indivíduos a ecossistemas. 4 ed. Porto Alegre: Artmed, 2007. 752 p.
