Analysis_birdsdata

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4/7/2021

This document have been created to include all relevant parts in the analysis of our animal diversity project.

##Data preparation and data observation

The first code's chunk will be used to load all libraries needed to proceed.

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.0.5

## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.2     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   2.0.1     v forcats 0.5.1

## Warning: package 'ggplot2' was built under R version 4.0.5

## Warning: package 'tibble' was built under R version 4.0.5

## Warning: package 'tidyr' was built under R version 4.0.5

## Warning: package 'readr' was built under R version 4.0.5

## Warning: package 'forcats' was built under R version 4.0.5

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 4.0.4

## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.5-7
```

```
library(nlme)
```

```
## Warning: package 'nlme' was built under R version 4.0.5
```

```
##
## Attaching package: 'nlme'
```

```
## The following object is masked from 'package:dplyr':
##
##     collapse
```

```
library(MASS)
```

```
## Warning: package 'MASS' was built under R version 4.0.5
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```
library(MuMIn)
```

```
## Warning: package 'MuMIn' was built under R version 4.0.5
```

In this second chunk, the data to be used will be loaded into a data frame and transferred into adequate data types.

```
dat <- read.csv("data/birds_dataset.csv", sep=";")
dat$category <- as.factor(dat$category)
dat$site <- as.factor(dat$site)
```

Following, species richness, species abundance and rarefied richness of species will be calculated.

```
dat$species_richness <- specnumber(dat[,4:31]) #species richness
dat$species_abund <- rowSums(dat[,4:31]) #abundances
dat$rarefied_richness <- rarefy(dat[,4:31],min(dat$species_abund)) #rarefied richness based on the subs
```

subsets for forest and park + median, mean, min max…

```
forest <- subset(dat, category=="forest")
park <- subset(dat, category=="park")
median(forest$species_abund)
```

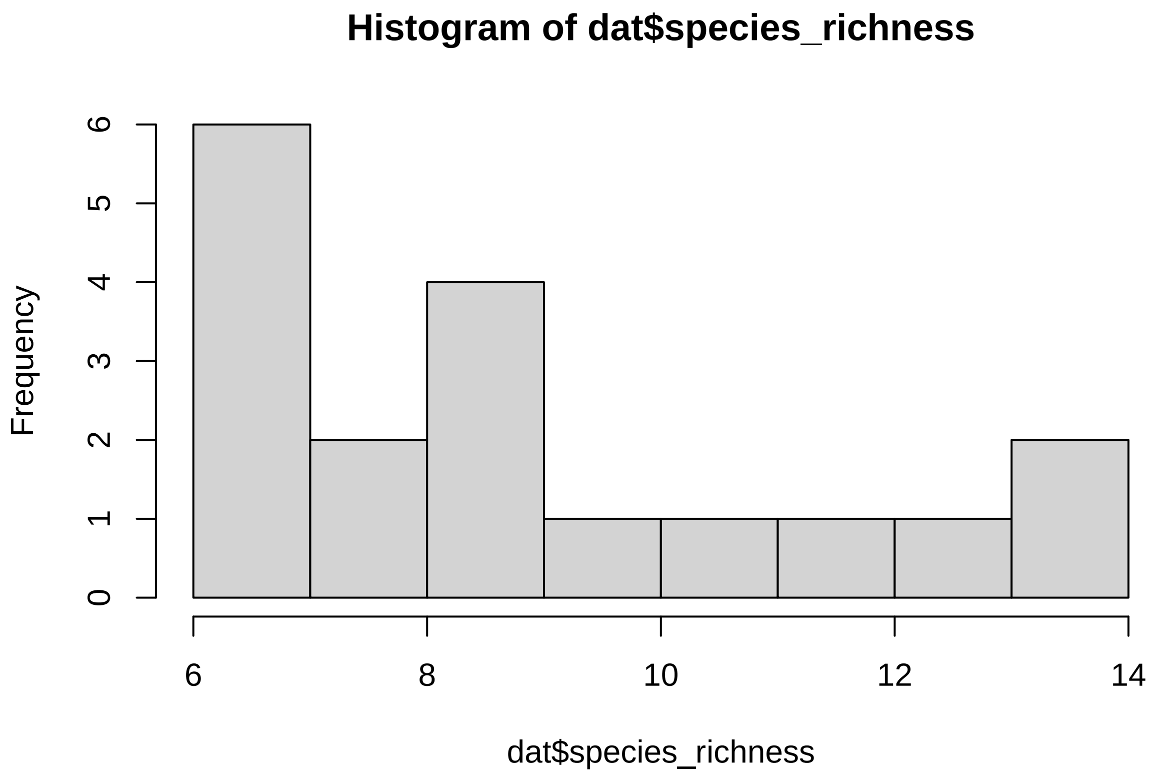
```
## [1] 16
```

```
median(park$species_abund)
```

```
## [1] 24
```

After, data is observed comparing the plots from parks and forests.

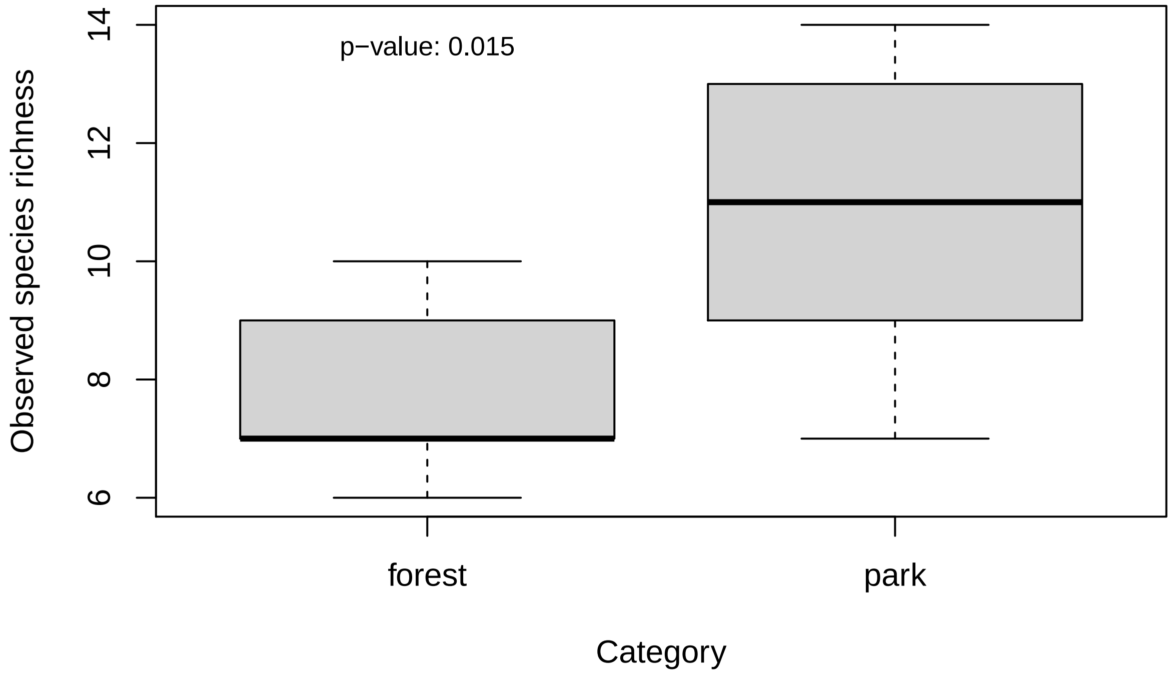
```
hist(dat$species_richness) # not normally distributed
```



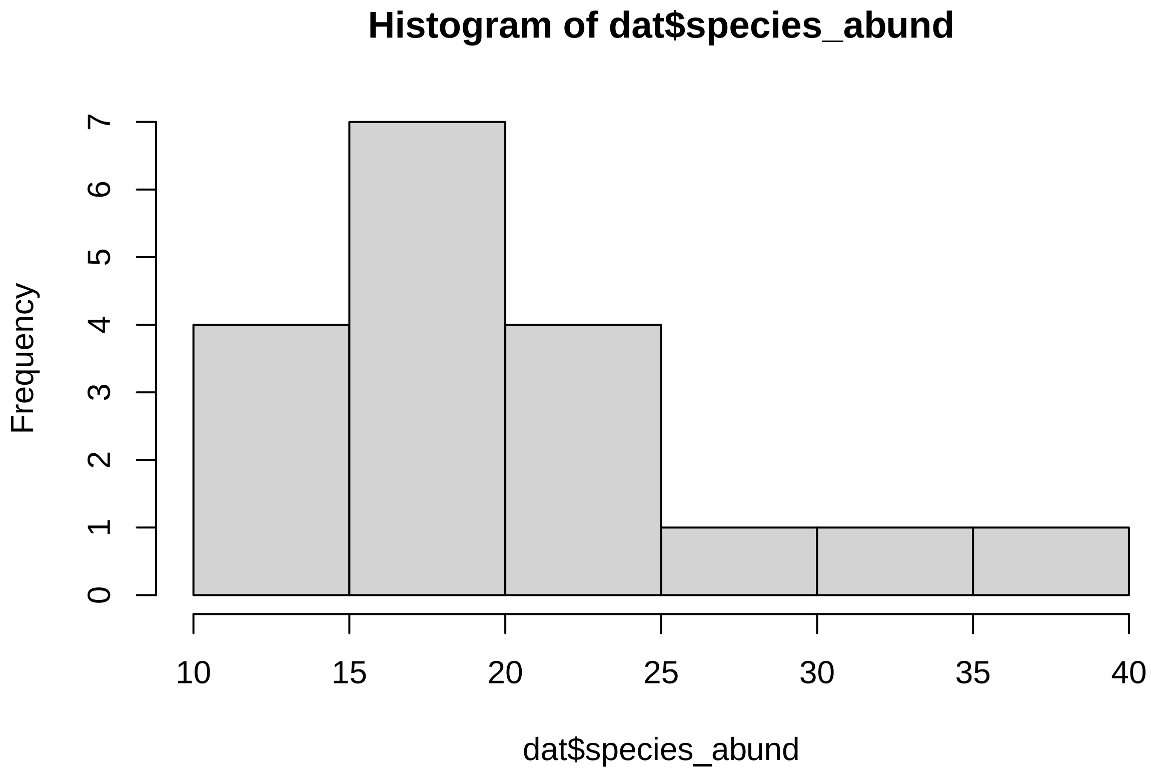
```
kruskal.test(dat$species_richness, dat$category) #p-value = 0.01533
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dat$species_richness and dat$category
## Kruskal-Wallis chi-squared = 5.8783, df = 1, p-value = 0.01533
```

```
boxplot(species_richness~category, data=dat, xlab= "Category", ylab= "Observed species richness")
text(1,13.6,labels = "p-value: 0.015", cex = 0.8)
```



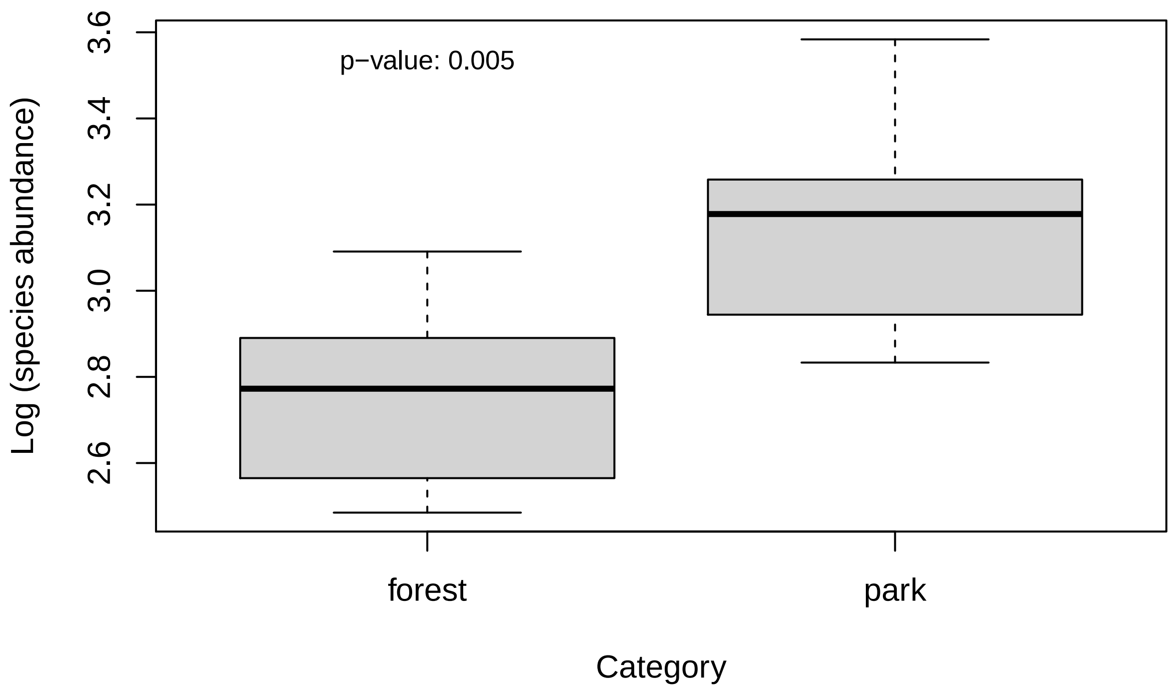
```
hist(dat$species_abund) # not normally distributed
```



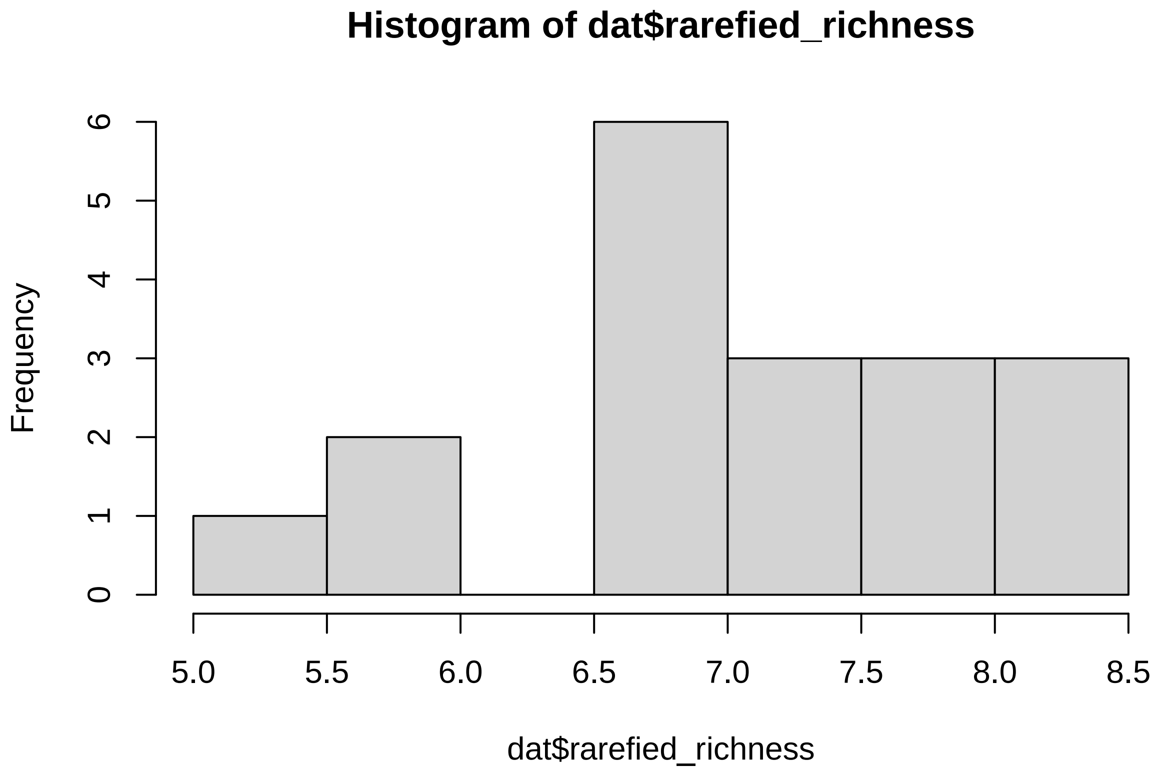
```
kruskal.test(dat$species_abund, dat$category) #p-value = 0.0046
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dat$species_abund and dat$category
## Kruskal-Wallis chi-squared = 8.0175, df = 1, p-value = 0.004633
```

```
boxplot(log(species_abund)~category, data=dat, xlab= "Category", ylab= "Log (species abundance)")
text(1,3.53,labels = "p-value: 0.005", cex = 0.8)
```



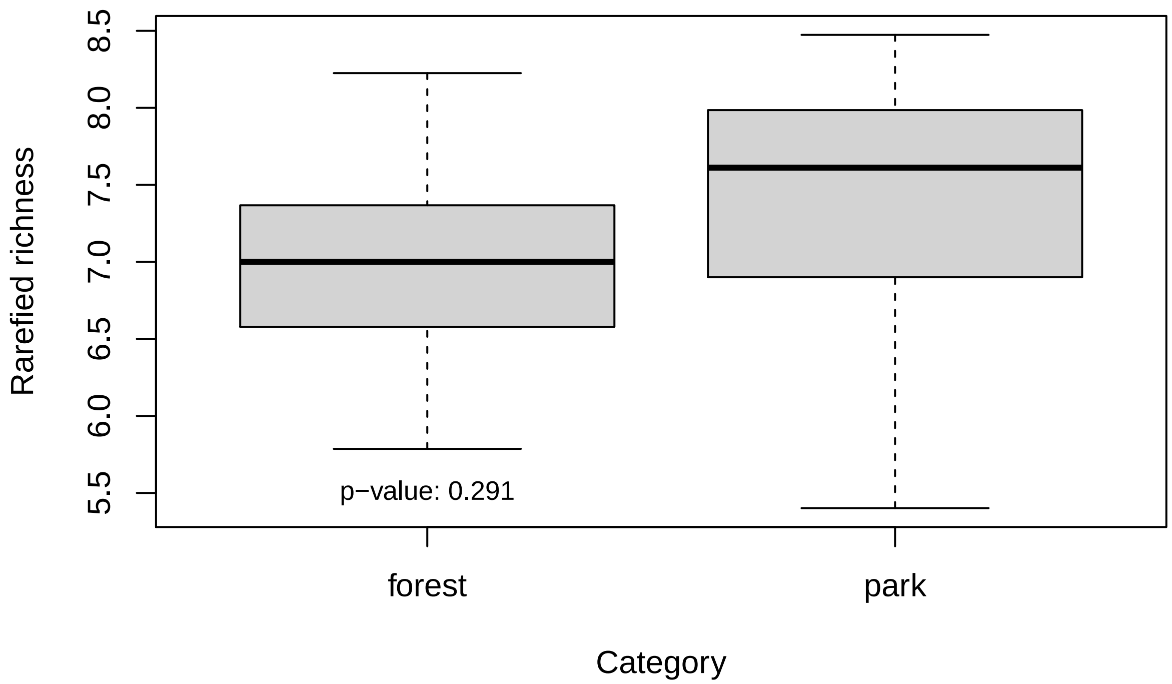
```
hist(dat$rarefied_richness) # normally distributed
```



```
mod<-aov(dat$rarefied_richness ~ dat$category)
summary(mod) #p-value: 0.291
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## dat$category  1  0.941  0.9405   1.194  0.291
## Residuals    16 12.605  0.7878
```

```
boxplot(rarefied_richness~category, data=dat, xlab= "Category", ylab= "Rarefied richness")
text(1,5.5,labels = "p-value: 0.291", cex = 0.8)
```



##Now let's begin with the data analysis

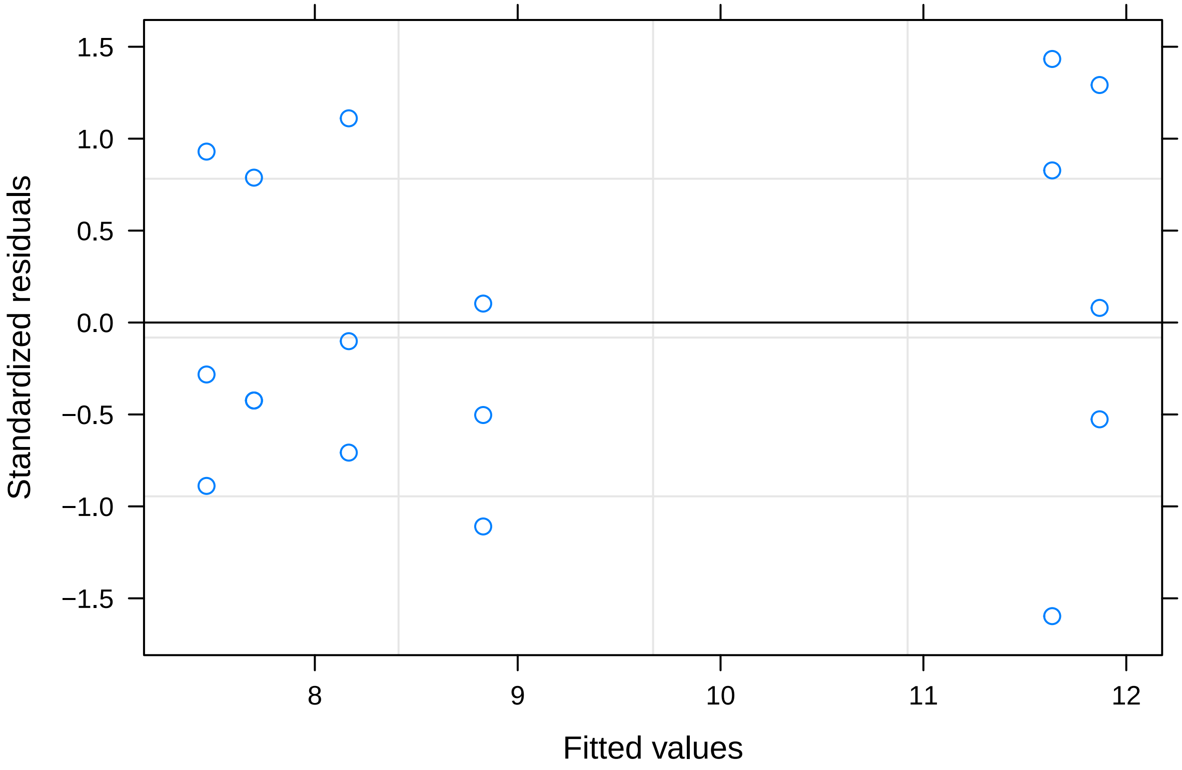
#2a linear models: to check for difference between habitat types with the implementation of mixed effect models.

```
mod1 <- lme(species_richness~category, random = (~1|site), data=dat) #model structure, random=... speci
summary(mod1) #model output - important is the "fixed effects" part. Here "forest" is hiding in the "In
```

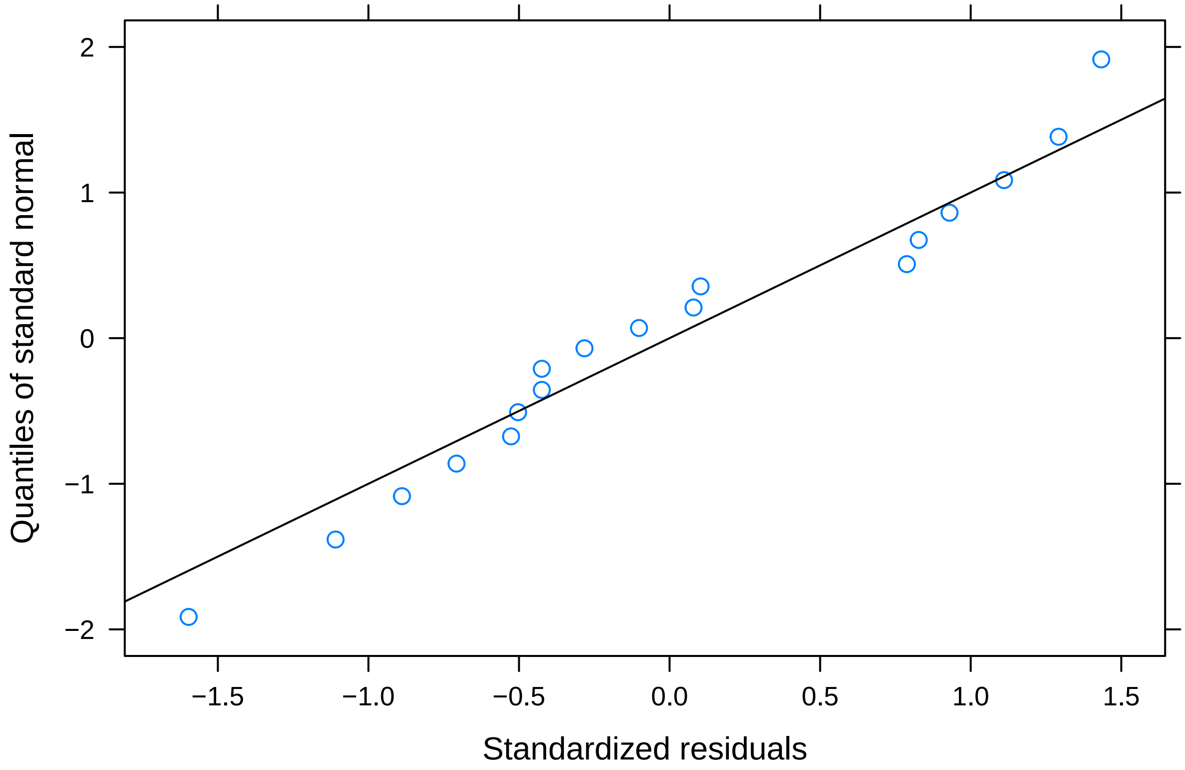
```
## Linear mixed-effects model fit by REML
##   Data: dat
##        AIC     BIC    logLik
##   78.65584 81.7462 -35.32792
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept) Residual
## StdDev:    1.459325 1.649916
##
## Fixed effects:  species_richness ~ category
##                    Value Std.Error DF  t-value p-value
## (Intercept)  7.777778  1.006154 12 7.730207  0.0000
## categorypark 3.000000  1.422916  4 2.108346  0.1027
##  Correlation:
##              (Intr)
## categorypark -0.707
##
```

```
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -1.5969444 -0.5205776 -0.1919700  0.8175666  1.4335132
##
## Number of Observations: 18
## Number of Groups: 6
```

```
plot(mod1) #check for homogeneity of variances (data points should have similar vertical spread along t
```



```
qqnorm(mod1, ~resid(.,type="p"), abline = c(0,1)) #check for normality of residuals (should not be comp
```



#2b linear models to include environmental variables and see the variation of the data with each of them.

```
### MIXED EFFECTS MODEL WITH SPECIES RICHNESS

round(cor(dat[,32:45]),2) #check which predictor variables are strongly correlated (below -0.7 or above
```

```
##                 canopy_cover n_tree_spec n_tree_ind dbh_min dbh_min5 dbh_mean
## canopy_cover            1.00       -0.68       0.22   -0.43    -0.38    -0.42
## n_tree_spec            -0.68        1.00      -0.42    0.30     0.18     0.31
## n_tree_ind              0.22       -0.42       1.00   -0.12    -0.51    -0.49
## dbh_min                -0.43        0.30      -0.12    1.00     0.37     0.68
## dbh_min5               -0.38        0.18      -0.51    0.37     1.00     0.71
## dbh_mean               -0.42        0.31      -0.49    0.68     0.71     1.00
## dbh_max                -0.33        0.23      -0.52    0.26     0.57     0.83
## dbh_median             -0.29        0.29      -0.56    0.30     0.89     0.74
## dbh_sd                 -0.69        0.78      -0.63    0.09     0.39     0.36
## n_microhabitats         0.30       -0.42      -0.12   -0.06     0.44     0.27
## latitude                0.30       -0.60       0.22   -0.23     0.04    -0.08
## longitude               0.71       -0.64       0.32   -0.57    -0.50    -0.42
## size                    0.64       -0.52       0.35   -0.33    -0.55    -0.52
## temperature            -0.02        0.03       0.44   -0.29    -0.49    -0.26
##                 dbh_max dbh_median dbh_sd n_microhabitats latitude longitude
## canopy_cover      -0.33      -0.29  -0.69            0.30     0.30      0.71
## n_tree_spec        0.23       0.29   0.78           -0.42    -0.60     -0.64
## n_tree_ind        -0.52      -0.56  -0.63           -0.12     0.22      0.32
## dbh_min            0.26       0.30   0.09           -0.06    -0.23     -0.57
## dbh_min5           0.57       0.89   0.39            0.44     0.04     -0.50
## dbh_mean           0.83       0.74   0.36            0.27    -0.08     -0.42
## dbh_max            1.00       0.57   0.47            0.14     0.03     -0.19
## dbh_median         0.57       1.00   0.44            0.49    -0.06     -0.39
## dbh_sd             0.47       0.44   1.00           -0.32    -0.40     -0.58
## n_microhabitats    0.14       0.49  -0.32            1.00     0.30      0.21
## latitude           0.03      -0.06  -0.40            0.30     1.00      0.14
## longitude         -0.19      -0.39  -0.58            0.21     0.14      1.00
## size              -0.52      -0.48  -0.61            0.22    -0.09      0.80
## temperature       -0.06      -0.38  -0.02           -0.45     0.05      0.23
##                  size temperature
## canopy_cover     0.64       -0.02
## n_tree_spec     -0.52        0.03
## n_tree_ind       0.35        0.44
## dbh_min         -0.33       -0.29
## dbh_min5        -0.55       -0.49
## dbh_mean        -0.52       -0.26
## dbh_max         -0.52       -0.06
## dbh_median      -0.48       -0.38
## dbh_sd          -0.61       -0.02
## n_microhabitats  0.22       -0.45
## latitude        -0.09        0.05
## longitude        0.80        0.23
## size             1.00       -0.07
## temperature     -0.07        1.00
```

```
mod1 <- lme(species_richness ~ category*size + canopy_cover + n_tree_spec + n_tree_ind + log(dbh_min) +
summary(mod1)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC   logLik
##   79.34161 90.91644 -26.6708
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept) Residual
## StdDev: 4.101158e-05 1.064785
##
## Fixed effects:  species_richness ~ category * size + canopy_cover + n_tree_spec +      n_tree_ind + l
##                       Value Std.Error DF    t-value p-value
## (Intercept)       13.449991  5.833096  6  2.3058067  0.0606
## categorypark       0.925977  3.442663  1  0.2689712  0.8327
## size              -0.004229  0.011728  1 -0.3606218  0.7797
## canopy_cover      -0.042049  0.027271  6 -1.5418946  0.1740
## n_tree_spec       -0.372451  0.390288  6 -0.9542969  0.3768
## n_tree_ind        -0.015531  0.161447  6 -0.0961977  0.9265
## log(dbh_min)       1.622178  0.851637  6  1.9047752  0.1055
## dbh_min5          -0.051502  0.070771  6 -0.7277286  0.4942
## n_microhabitats    0.029756  0.114604  6  0.2596375  0.8038
## temperature       -0.201717  0.171316  1 -1.1774589  0.4482
## categorypark:size  0.004324  0.062229  1  0.0694820  0.9558
##  Correlation:
##                   (Intr) ctgryp size   cnpy_c n_tr_s n_tr_n lg(d_) dbh_m5
## categorypark      -0.139
## size              -0.306  0.593
## canopy_cover      -0.552  0.312  0.025
## n_tree_spec       -0.447 -0.589 -0.291  0.096
## n_tree_ind        -0.481  0.067 -0.027  0.134  0.430
## log(dbh_min)      -0.401 -0.217 -0.125  0.033  0.261  0.049
## dbh_min5          -0.169 -0.578  0.013 -0.050  0.412  0.135 -0.207
## n_microhabitats   -0.099  0.425  0.029  0.093 -0.257 -0.176  0.020 -0.663
## temperature       -0.335  0.142  0.333  0.151 -0.282 -0.499  0.074  0.045
## categorypark:size  0.200  0.045  0.019  0.163 -0.424 -0.503 -0.438  0.032
##                   n_mcrh tmprtr
## categorypark
## size
## canopy_cover
## n_tree_spec
## n_tree_ind
## log(dbh_min)
## dbh_min5
## n_microhabitats
## temperature        0.328
## categorypark:size  0.299  0.468
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -1.4774299 -0.8641612 -0.1156606  0.4119055  2.3217607
##
## Number of Observations: 18
## Number of Groups: 6
```

```
mod1.1 <- stepAIC(mod1) #model simplification based on AIC-value of the model
```

```
## Start:  AIC=79.34
## species_richness ~ category * size + canopy_cover + n_tree_spec +
##     n_tree_ind + log(dbh_min) + dbh_min5 + n_microhabitats +
##     temperature
##
##                   Df    AIC
## - category:size    1 77.354
## - n_tree_ind       1 77.365
## - n_microhabitats  1 77.514
## - dbh_min5         1 78.654
## <none>              79.342
## - n_tree_spec      1 79.543
## - temperature      1 80.594
## - canopy_cover     1 82.605
## - log(dbh_min)     1 84.858
##
## Step:  AIC=77.35
## species_richness ~ category + size + canopy_cover + n_tree_spec +
##     n_tree_ind + log(dbh_min) + dbh_min5 + n_microhabitats +
##     temperature
##
##                   Df    AIC
## - n_tree_ind       1 75.367
## - n_microhabitats  1 75.514
## - category         1 75.535
## - size             1 75.688
## - dbh_min5         1 76.675
## <none>               77.354
## - n_tree_spec      1 77.852
## - temperature      1 79.622
## - canopy_cover     1 80.806
## - log(dbh_min)     1 84.496
##
## Step:  AIC=75.37
## species_richness ~ category + size + canopy_cover + n_tree_spec +
##     log(dbh_min) + dbh_min5 + n_microhabitats + temperature
##
##                   Df    AIC
## - n_microhabitats  1 73.524
## - category         1 73.560
## - size             1 73.703
## - dbh_min5         1 74.683
## <none>               75.367
## - n_tree_spec      1 75.961
## - temperature      1 78.287
## - canopy_cover     1 79.003
## - log(dbh_min)     1 82.760
##
## Step:  AIC=73.52
## species_richness ~ category + size + canopy_cover + n_tree_spec +
##     log(dbh_min) + dbh_min5 + temperature
##
##                Df    AIC
## - category      1 71.611
## - size          1 71.869
## - dbh_min5      1 73.033
## <none>            73.524
## - n_tree_spec   1 73.980
## - temperature   1 76.975
## - canopy_cover  1 77.237
## - log(dbh_min)  1 80.787
##
## Step:  AIC=71.61
## species_richness ~ size + canopy_cover + n_tree_spec + log(dbh_min) +
##     dbh_min5 + temperature
##
##                Df    AIC
## - size          1 70.645
## - dbh_min5      1 71.139
## <none>            71.611
## - n_tree_spec   1 72.982
## - temperature   1 75.195
## - canopy_cover  1 76.107
## - log(dbh_min)  1 80.025
##
## Step:  AIC=70.65
## species_richness ~ canopy_cover + n_tree_spec + log(dbh_min) +
##     dbh_min5 + temperature
##
##                 Df    AIC
## - dbh_min5      1 69.299
## <none>            70.645
## - n_tree_spec   1 71.260
## - temperature   1 73.198
## - canopy_cover  1 76.119
## - log(dbh_min)  1 79.032
##
## Step:  AIC=69.3
## species_richness ~ canopy_cover + n_tree_spec + log(dbh_min) +
##     temperature
##
##                 Df    AIC
## <none>            69.299
## - n_tree_spec   1 69.688
## - temperature   1 71.200
## - canopy_cover  1 74.131
## - log(dbh_min)  1 77.308
```

```
summary(mod1.1) #final model which includes only the most important predictors
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   69.29947 75.53207 -27.64974
##
## Random effects:
##  Formula: ~1 | site
##          (Intercept) Residual
## StdDev: 2.762129e-05 1.124297
##
## Fixed effects:  species_richness ~ canopy_cover + n_tree_spec + log(dbh_min) +      temperature
##                  Value Std.Error DF   t-value p-value
## (Intercept)  11.366118  3.314519  9  3.429190  0.0075
## canopy_cover -0.044574  0.018196  9 -2.449668  0.0368
## n_tree_spec  -0.241219  0.177235  9 -1.361014  0.2066
## log(dbh_min)  1.542315  0.496008  9  3.109455  0.0125
## temperature  -0.160682  0.090601  4 -1.773506  0.1508
##  Correlation:
##              (Intr) cnpy_c n_tr_s lg(d_)
## canopy_cover -0.791
## n_tree_spec  -0.495  0.595
## log(dbh_min) -0.759  0.467 -0.013
## temperature  -0.681  0.241 -0.024  0.519
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.67276372 -0.80102592 -0.08660587  0.68432847  2.15093491
##
## Number of Observations: 18
## Number of Groups: 6
```

```
mod1.2 <- update(mod1.1, ~.-n_tree_spec)
summary(mod1.2)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   69.68834 75.03057 -28.84417
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept) Residual
## StdDev:   0.1799486 1.188182
##
## Fixed effects:  species_richness ~ canopy_cover + log(dbh_min) + temperature
##                   Value Std.Error DF   t-value p-value
## (Intercept)   9.140053 2.9508347 10  3.097447  0.0113
## canopy_cover -0.029890 0.0150141 10 -1.990770  0.0745
## log(dbh_min)  1.532576 0.5067240 10  3.024479  0.0128
## temperature  -0.163764 0.0945977  4 -1.731167  0.1585
##  Correlation:
##               (Intr) cnpy_c lg(d_)
## canopy_cover -0.700
## log(dbh_min) -0.875  0.574
## temperature  -0.797  0.303  0.507
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.47877950 -0.81708368  0.01400286  0.42067808  2.51962252
##
## Number of Observations: 18
## Number of Groups: 6
```

```
anova(mod1.1, mod1.2)
```

```
##        Model df      AIC      BIC    logLik   Test L.Ratio p-value
## mod1.1     1  7 69.29947 75.53207 -27.64973
## mod1.2     2  6 69.68834 75.03057 -28.84417 1 vs 2 2.38887  0.1222
```

```
mod1.3 <- update(mod1.2, ~.-temperature)
summary(mod1.3)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   70.90548 75.35733 -30.45274
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept) Residual
## StdDev:    0.550221 1.212528
##
## Fixed effects:  species_richness ~ canopy_cover + log(dbh_min)
##                   Value Std.Error DF   t-value p-value
## (Intercept)   5.562682 1.8467347 10  3.012172  0.0131
## canopy_cover -0.025139 0.0152642 10 -1.646896  0.1306
## log(dbh_min)  1.862918 0.4588731 10  4.059768  0.0023
##  Correlation:
##              (Intr) cnpy_c
## canopy_cover -0.756
## log(dbh_min) -0.882  0.427
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -1.6480211 -0.6031499 -0.2136438  0.7787394  1.8252090
##
## Number of Observations: 18
## Number of Groups: 6
```

```
anova(mod1.2, mod1.3) #close to significcance effect with these variables (species increasing with incr
```

```
##        Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## mod1.2     1  6 69.68834 75.03057 -28.84417
## mod1.3     2  5 70.90548 75.35733 -30.45274 1 vs 2 3.217136  0.0729
```

```
mod1.4 <- update(mod1.3, ~.-canopy_cover)
summary(mod1.4)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   71.50383 75.06532 -31.75191
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept) Residual
## StdDev: 0.0001335345  1.41207
##
## Fixed effects:  species_richness ~ log(dbh_min)
##                  Value Std.Error DF  t-value p-value
## (Intercept)  2.833014 1.1783306 11 2.404261  0.0350
## log(dbh_min) 2.342352 0.4085936 11 5.732719  0.0001
##  Correlation:
##              (Intr)
## log(dbh_min) -0.954
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.06423425 -0.69965226  0.06165372  0.63232038  1.83834164
##
## Number of Observations: 18
## Number of Groups: 6
```

```
anova(mod1.3,mod1.4)
```

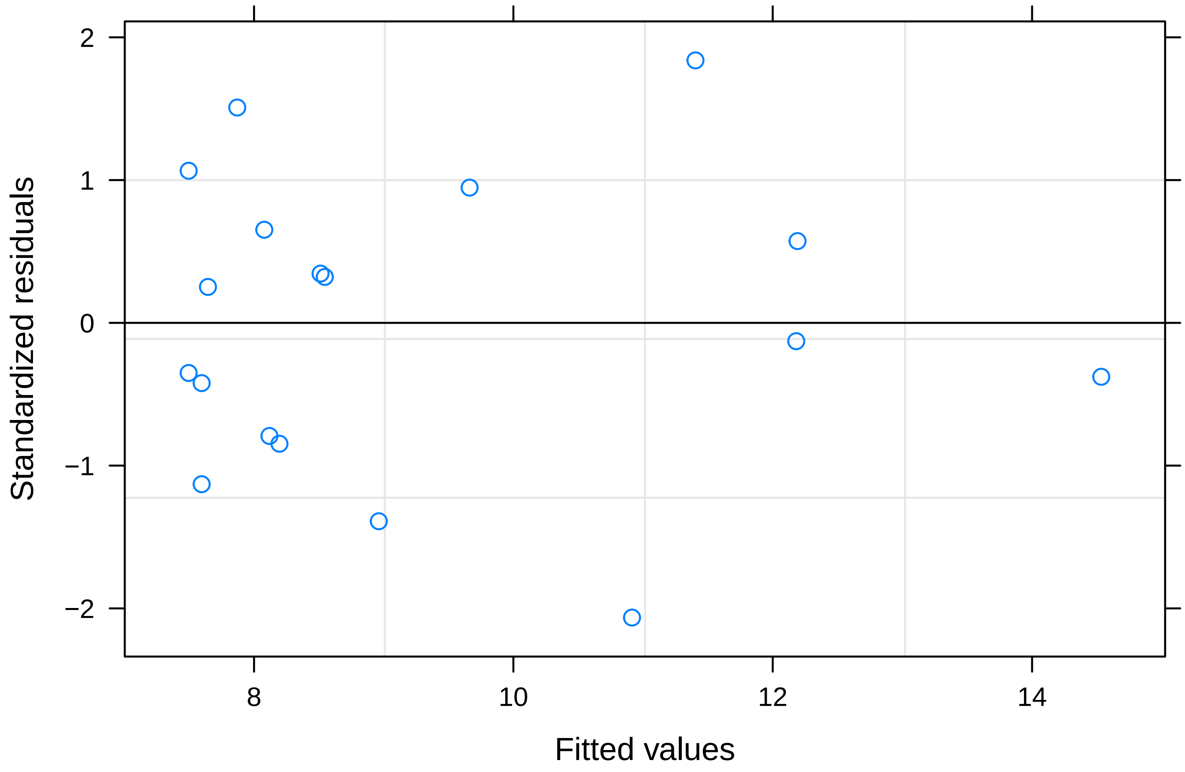
```
##         Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## mod1.3     1  5 70.90548 75.35733 -30.45274
## mod1.4     2  4 71.50383 75.06532 -31.75191 1 vs 2 2.598353   0.107
```

```
#final model:
#lme(species_richness ~ log(dbh_min), random = (~1|site), data=dat, method="ML")
#https://jonlefcheck.net/2013/03/13/r2-for-linear-mixed-effects-models/
r.squaredGLMM(mod1.4)
```

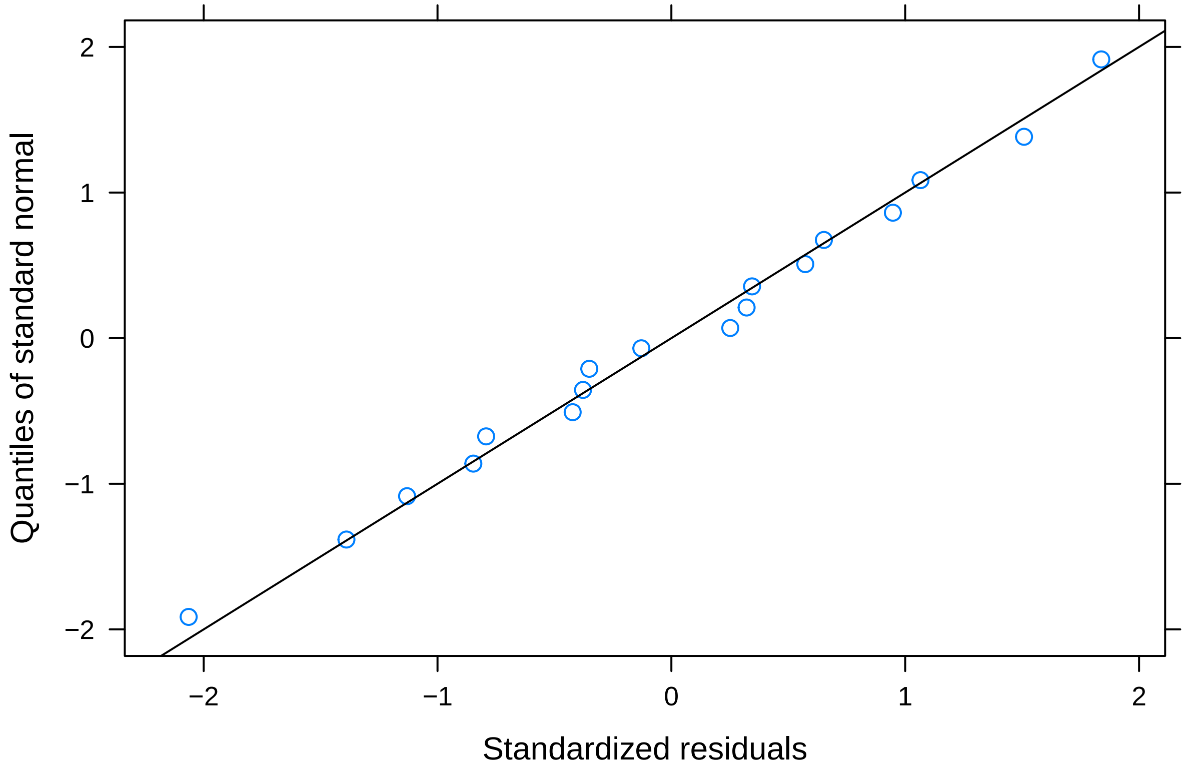
```
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.
```

```
##            R2m       R2c
## [1,] 0.6850223 0.6850223
```

```
plot(mod1.4) #check for homogeneity of variances (data points should have similar vertical spread along
```



```
qqnorm(mod1.4, ~resid(.,type="p"), abline=c(0,1)) #check for normality of residuals (should not be comp
```



```r
#standard deviation, coefficient of variation (sd/mean) to make variation independent from out mean val

#dat$sddbh_mean <- sd() we can try as alternative
library(car)
```

```
## Warning: package 'car' was built under R version 4.0.5

## Loading required package: carData

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some
```

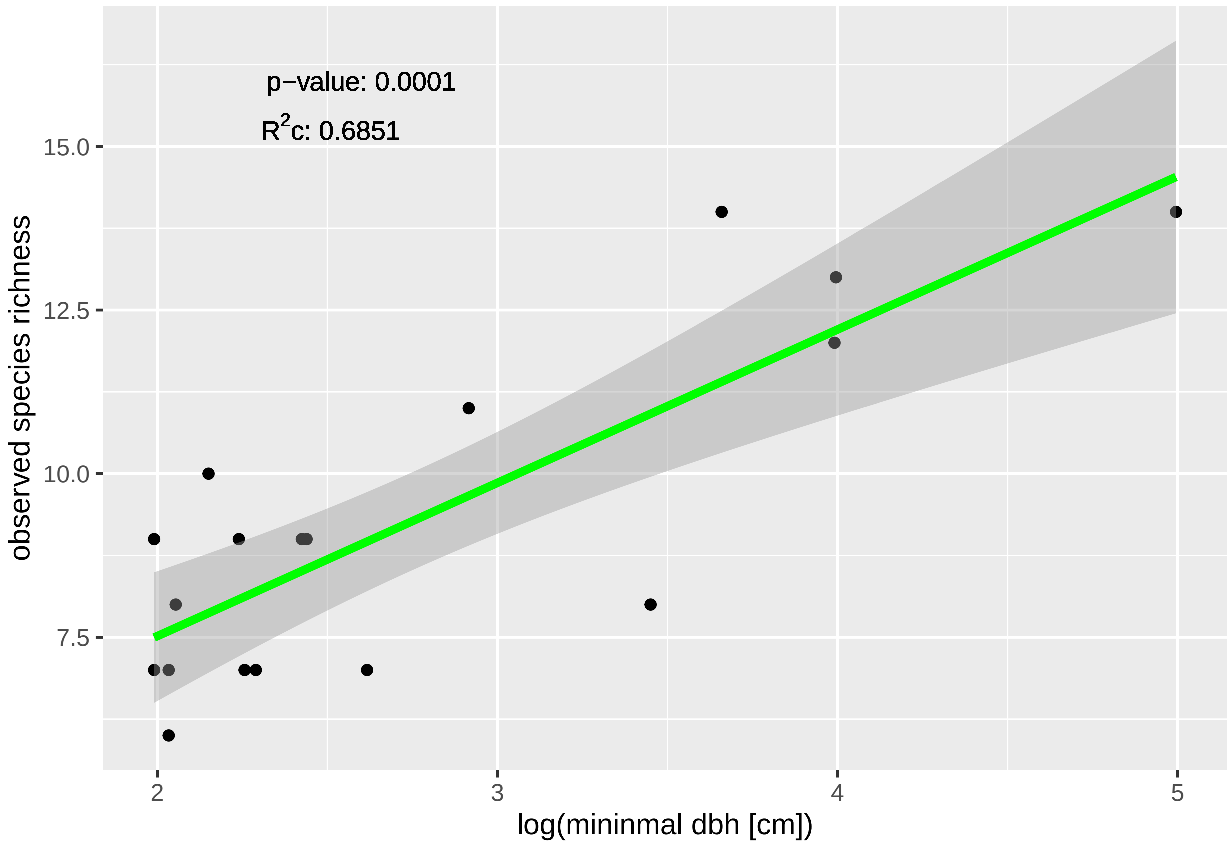
```r
vif(mod1.2)
```

```
## canopy_cover log(dbh_min)  temperature
##     1.492654     1.824734     1.346892
```

```
ggplot(dat, aes(x = log(dbh_min), y = species_richness))+
  geom_point() +
  geom_smooth(method = lm,se = TRUE, colour = 'green', size = 1.5) +
  geom_text(x=2.6, y=16, label="p-value: 0.0001", size=3.5) +
  geom_text(x=2.51,y=15.3,label=expression(paste("R"^2,"c: 0.6851")), size=3.5) +
  labs(x="log(mininmal dbh [cm])", y="observed species richness")
```

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning in is.na(x): is.na() aplicado a un objeto que no es (lista o vector) de
## tipo 'expression
```



#2c Linear Mixed Effect models

```
### MIXED EFFECTS MODEL WITH BIRD ABUNDANCE
mod2.1 <- lme(species_abund ~ category*size + canopy_cover + n_tree_spec + n_tree_ind + log(dbh_min) + c
summary(mod2.1)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   110.9826 122.5575 -42.49131
##
## Random effects:
```

```
##  Formula: ~1 | site
##         (Intercept) Residual
## StdDev: 5.575945e-05 2.564311
##
## Fixed effects:  species_abund ~ category * size + canopy_cover + n_tree_spec +      n_tree_ind + log
##                           Value Std.Error DF    t-value p-value
## (Intercept)          18.087181 17.052295  6  1.0606890  0.3296
## categorypark          1.639039  8.730317  1  0.1877410  0.8819
## size                 -0.018921  0.028943  1 -0.6537125  0.6314
## canopy_cover         -0.092920  0.069269  6 -1.3414462  0.2283
## n_tree_spec          -0.246951  0.918143  6 -0.2689682  0.7970
## n_tree_ind            0.022661  0.386631  6  0.0586127  0.9552
## log(dbh_min)          2.407254  2.053033  6  1.1725356  0.2854
## dbh_min5              0.047614  0.138542  6  0.3436810  0.7428
## log(n_microhabitats)  2.742905  2.485440  6  1.1035893  0.3121
## temperature          -0.208719  0.485090  1 -0.4302687  0.7413
## categorypark:size    -0.005155  0.182488  1 -0.0282467  0.9820
##  Correlation:
##                      (Intr) ctgryp size   cnpy_c n_tr_s n_tr_n lg(d_) dbh_m5
## categorypark         -0.369
## size                 -0.369  0.650
## canopy_cover         -0.613  0.414  0.094
## n_tree_spec          -0.314 -0.541 -0.315  0.068
## n_tree_ind           -0.332  0.063 -0.053  0.097  0.417
## log(dbh_min)         -0.301 -0.239 -0.133  0.014  0.279  0.059
## dbh_min5             -0.014 -0.545 -0.047 -0.115  0.361  0.077 -0.219
## log(n_microhabitats) -0.573  0.511  0.220  0.330 -0.146 -0.141 -0.049 -0.390
## temperature          -0.553  0.306  0.399  0.293 -0.259 -0.461  0.028  0.042
## categorypark:size    -0.200  0.254  0.145  0.310 -0.383 -0.460 -0.395 -0.010
##                      lg(n_) tmprtr
## categorypark
## size
## canopy_cover
## n_tree_spec
## n_tree_ind
## log(dbh_min)
## dbh_min5
## log(n_microhabitats)
## temperature           0.595
## categorypark:size     0.621  0.628
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -1.6063561 -0.7198577 -0.2194506  0.9435601  1.8810180
##
## Number of Observations: 18
## Number of Groups: 6
```

```
mod2.2 <- stepAIC(mod2.1) #model simplification based on AIC-value of the model
```

```
## Start:  AIC=110.98
## species_abund ~ category * size + canopy_cover + n_tree_spec +
##     n_tree_ind + log(dbh_min) + dbh_min5 + log(n_microhabitats) +
##     temperature
```

```
##
##                         Df    AIC
## - category:size          1 108.98
## - n_tree_ind             1 108.99
## - n_tree_spec            1 109.17
## - dbh_min5               1 109.28
## - temperature            1 109.45
## <none>                     110.98
## - log(n_microhabitats)  1 111.87
## - log(dbh_min)           1 112.21
## - canopy_cover           1 113.10
##
## Step:  AIC=108.98
## species_abund ~ category + size + canopy_cover + n_tree_spec +
##     n_tree_ind + log(dbh_min) + dbh_min5 + log(n_microhabitats) +
##     temperature
##
##                         Df    AIC
## - n_tree_ind             1 106.99
## - category               1 107.09
## - n_tree_spec            1 107.22
## - dbh_min5               1 107.28
## - temperature            1 107.69
## - size                   1 108.06
## <none>                     108.98
## - log(dbh_min)           1 110.69
## - canopy_cover           1 111.44
## - log(n_microhabitats)  1 111.60
##
## Step:  AIC=106.99
## species_abund ~ category + size + canopy_cover + n_tree_spec +
##     log(dbh_min) + dbh_min5 + log(n_microhabitats) + temperature
##
##                         Df    AIC
## - category               1 105.09
## - n_tree_spec            1 105.27
## - dbh_min5               1 105.29
## - temperature            1 105.71
## - size                   1 106.07
## <none>                     106.99
## - log(dbh_min)           1 108.81
## - log(n_microhabitats)  1 109.73
## - canopy_cover           1 109.87
##
## Step:  AIC=105.09
## species_abund ~ size + canopy_cover + n_tree_spec + log(dbh_min) +
##     dbh_min5 + log(n_microhabitats) + temperature
##
##                         Df    AIC
## - n_tree_spec            1 103.27
## - dbh_min5               1 103.89
## - temperature            1 104.00
## <none>                     105.09
## - size                   1 105.64
## - log(dbh_min)          1 107.08
## - log(n_microhabitats)  1 108.21
## - canopy_cover          1 108.85
##
## Step:  AIC=103.27
## species_abund ~ size + canopy_cover + log(dbh_min) + dbh_min5 +
##     log(n_microhabitats) + temperature
##
##                        Df    AIC
## - temperature           1 102.03
## - dbh_min5              1 102.10
## <none>                    103.27
## - size                  1 103.67
## - log(dbh_min)          1 105.57
## - canopy_cover          1 107.32
## - log(n_microhabitats)  1 108.41
##
## Step:  AIC=102.04
## species_abund ~ size + canopy_cover + log(dbh_min) + dbh_min5 +
##     log(n_microhabitats)
##
##                        Df    AIC
## - dbh_min5              1 101.49
## - size                  1 101.81
## <none>                    102.03
## - canopy_cover          1 105.76
## - log(dbh_min)          1 106.20
## - log(n_microhabitats)  1 108.22
##
## Step:  AIC=101.49
## species_abund ~ size + canopy_cover + log(dbh_min) + log(n_microhabitats)
##
##                        Df    AIC
## <none>                    101.49
## - size                  1 103.86
## - canopy_cover          1 105.00
## - log(dbh_min)          1 111.47
## - log(n_microhabitats)  1 112.79
```

```
summary(mod2.2) #final model which includes only the most important predictors
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   101.4876 107.7202 -43.74381
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept) Residual
## StdDev: 6.353355e-05 2.749099
##
## Fixed effects:  species_abund ~ size + canopy_cover + log(dbh_min) + log(n_microhabitats)
##                           Value Std.Error DF   t-value p-value
## (Intercept)           11.127950  4.317066  9  2.577665  0.0298
## size                  -0.026102  0.013803  4 -1.891107  0.1316
## canopy_cover          -0.090785  0.042043  9 -2.159361  0.0591
## log(dbh_min)           3.715107  1.059513  9  3.506431  0.0067
## log(n_microhabitats)  3.660144  0.964060  9  3.796592  0.0042
##  Correlation:
##                       (Intr) size   cnpy_c lg(d_)
## size                  -0.087
## canopy_cover          -0.533 -0.439
## log(dbh_min)          -0.896  0.203  0.311
## log(n_microhabitats) -0.143 -0.152 -0.326  0.003
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.66990039 -0.84208140  0.03715311  0.85684838  1.71424488
##
## Number of Observations: 18
## Number of Groups: 6
```

```
anova(mod2.1, mod2.2)
```

```
##        Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## mod2.1     1 13 110.9826 122.5575 -42.49131
## mod2.2     2  7 101.4876 107.7202 -43.74381 1 vs 2 2.505011  0.8679
```

```
#mod2.3 <- update(mod2.2, ~.-size)
#summary(mod2.3)
#anova(mod2.2, mod2.3)

#mod2.4<-update(mod2.3, ~.-canopy_cover)
#summary(mod2.4)
#anova(mod2.3,mod2.4)
```

#2d Plotting

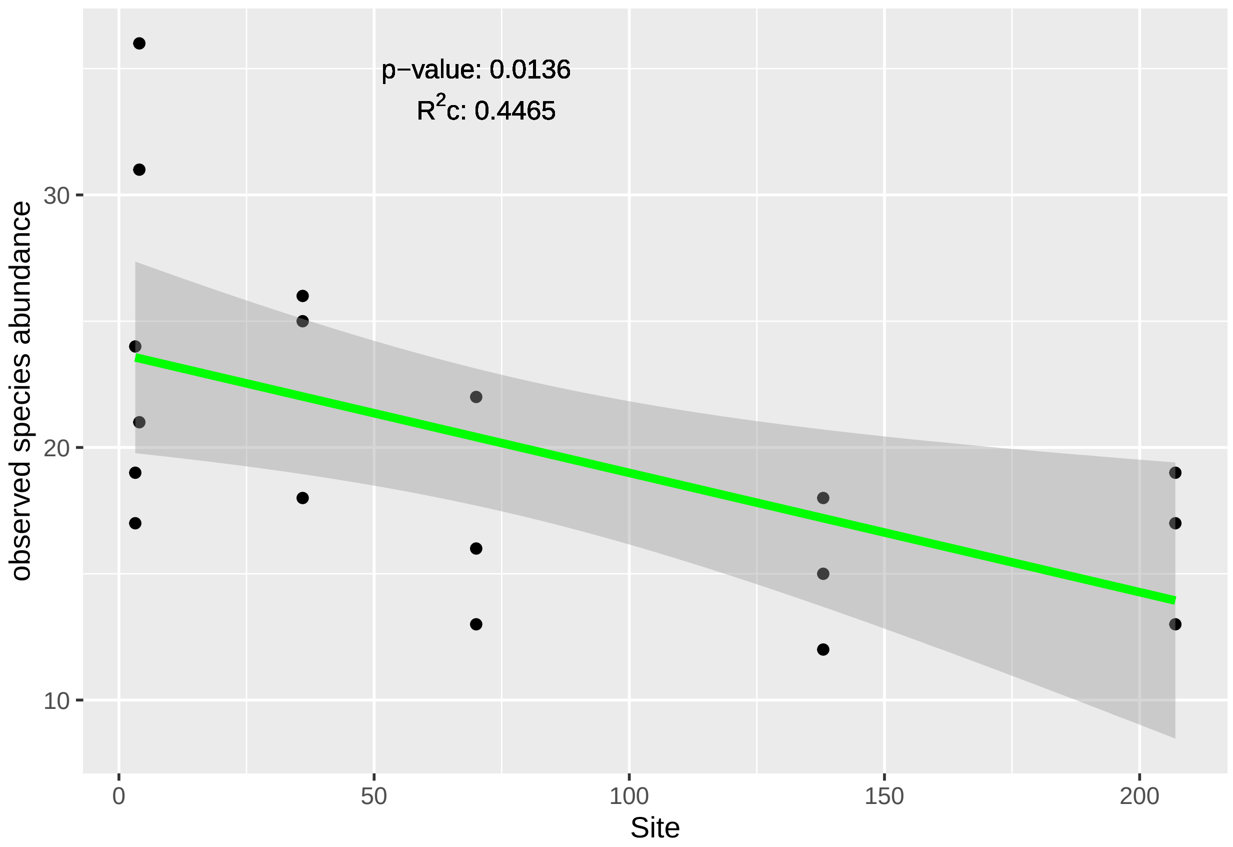
```
# plot model for abundance vs. size
mod_size<-lme(species_abund ~ size, random = (~1|site), data=dat, method="ML")
r.squaredGLMM(mod_size)
```

```
##            R2m       R2c
## [1,] 0.3340045 0.4465148
```

```
ggplot(dat, aes(x = size, y = species_abund))+
  geom_point() +
  geom_smooth(method = lm, se = TRUE, colour = 'green', size = 1.5) +
  geom_text(x=70, y=35, label="p-value: 0.0136", size=3.5) +
  geom_text(x=72,y=33.5, label=expression(paste("R"^2,"c: 0.4465")), size=3.5) +
  labs(x="Site", y="observed species abundance")
```

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning in is.na(x): is.na() aplicado a un objeto que no es (lista o vector) de
## tipo 'expression
```



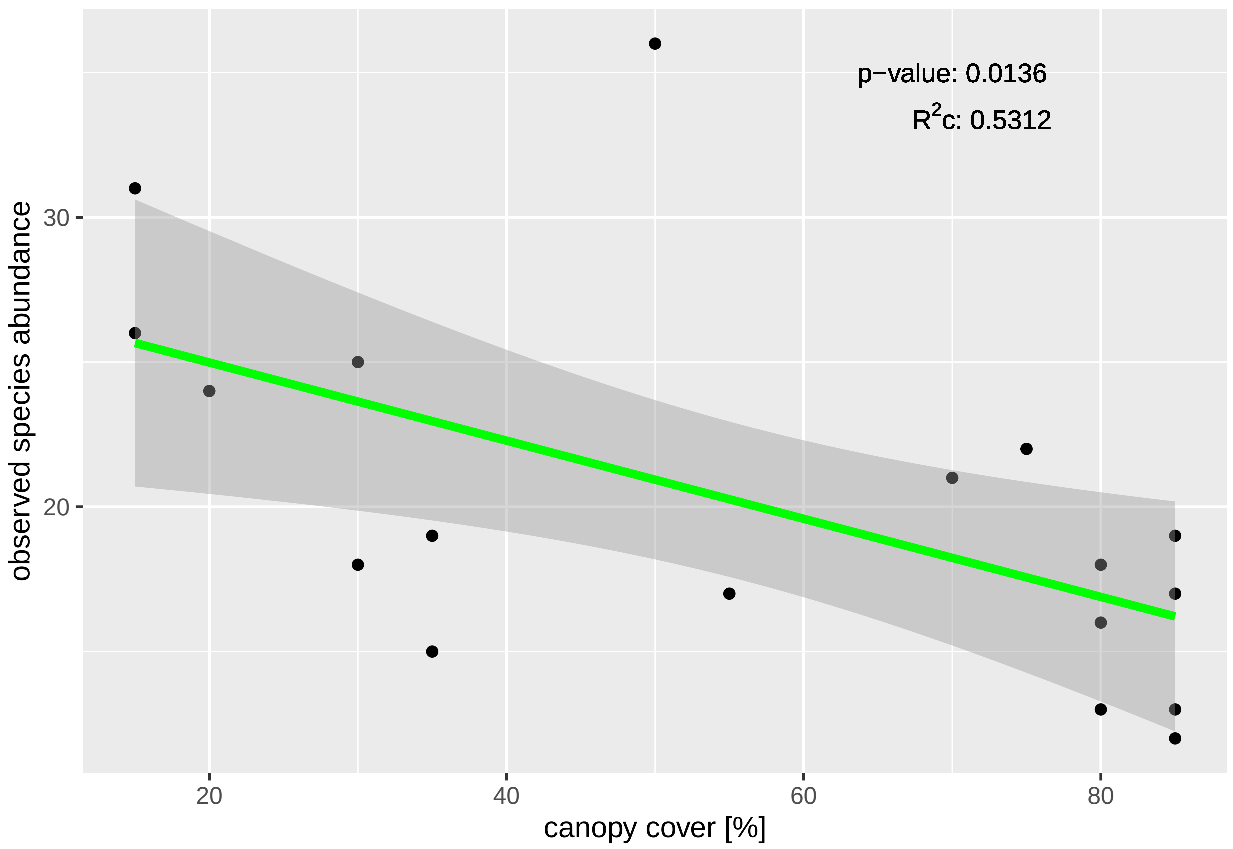
```
# plot model for abundance vs. canopy cover
mod_can<-lme(species_abund ~ canopy_cover, random = (~1|site), data=dat, method="ML")
r.squaredGLMM(mod_can)
```

```
##            R2m       R2c
## [1,] 0.3208035 0.5312365
```

```
ggplot(dat, aes(x = canopy_cover, y = species_abund))+
  geom_point() +
  geom_smooth(method = lm, se = TRUE, colour = 'green', size = 1.5) +
  geom_text(x=70, y=35, label="p-value: 0.0136", size=3.5) +
  geom_text(x=72,y=33.5, label=expression(paste("R"^2,"c: 0.5312")), size=3.5) +
  labs(x="canopy cover [%]", y="observed species abundance")
```

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning in is.na(x): is.na() aplicado a un objeto que no es (lista o vector) de
## tipo 'expression
```



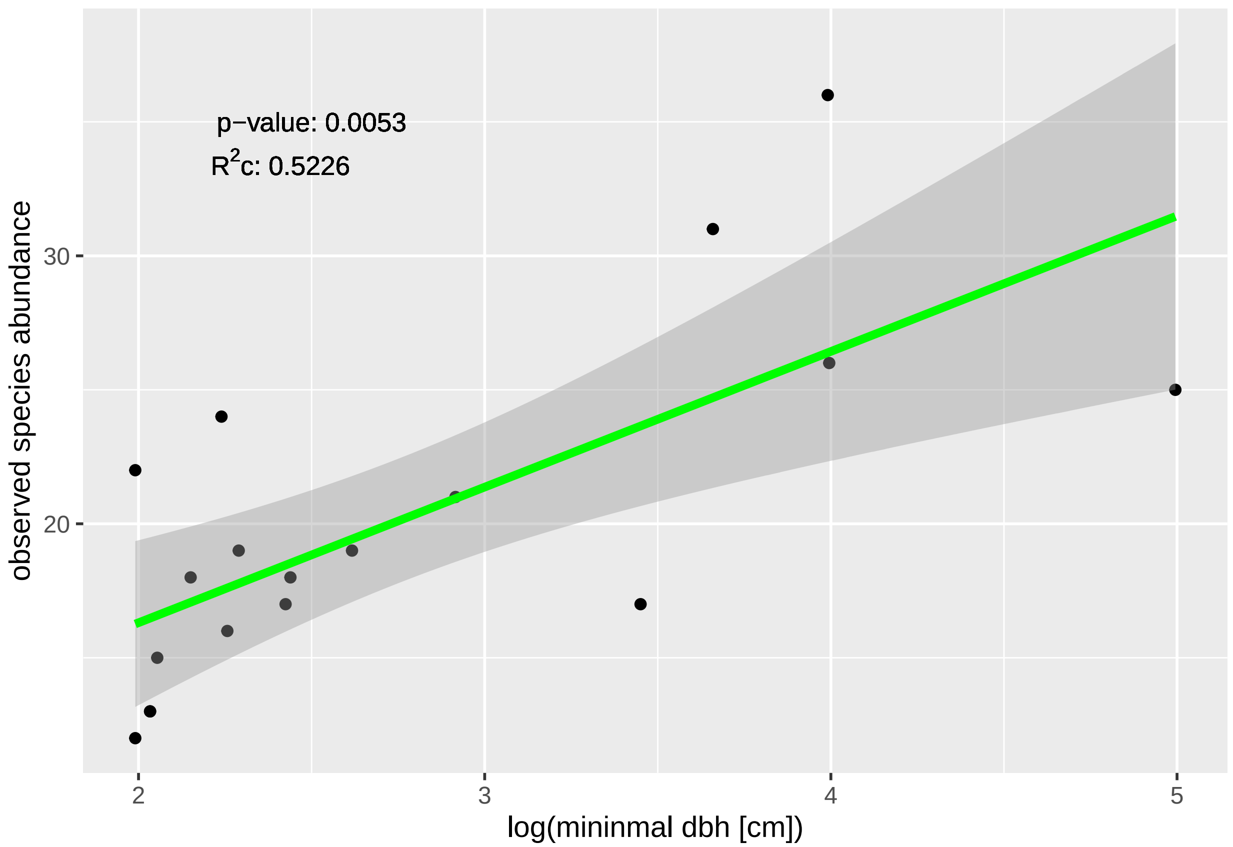
```
#plot model for abundance vs. minimal dbh
mod_dbh<-lme(species_abund ~ log(dbh_min), random = (~1|site), data=dat, method="ML")
r.squaredGLMM(mod_dbh)
```

```
##            R2m       R2c
## [1,] 0.506479 0.5225862
```

```
ggplot(dat, aes(x = log(dbh_min), y = species_abund))+
  geom_point() +
  geom_smooth(method = lm, se = TRUE, colour = 'green', size = 1.5) +
  geom_text(x=2.5, y=35, label="p-value: 0.0053", size=3.5) +
  geom_text(x=2.41,y=33.5, label=expression(paste("R"^2,"c: 0.5226")), size=3.5) +
  labs(x="log(mininmal dbh [cm])", y="observed species abundance")
```

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning in is.na(x): is.na() aplicado a un objeto que no es (lista o vector) de
## tipo 'expression
```



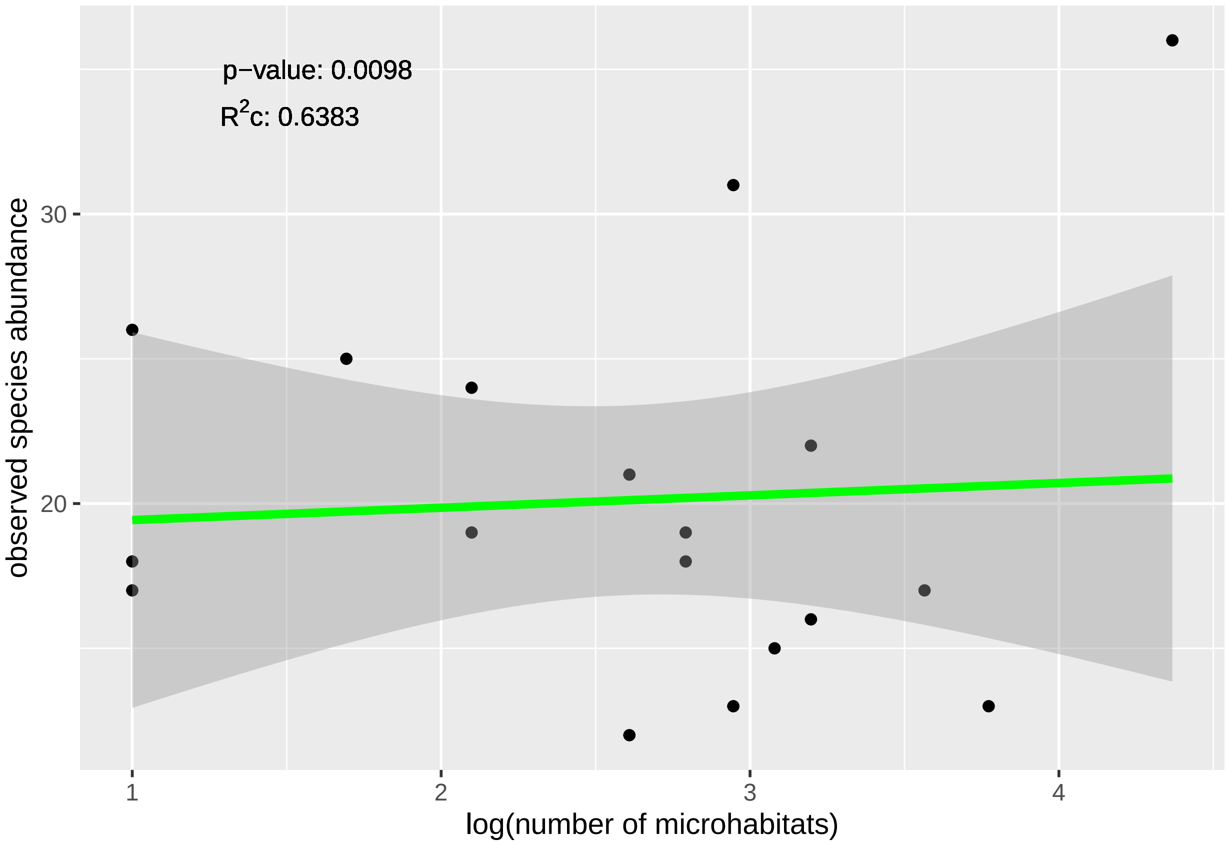
```
# plot model for abundance vs. microhabitats
mod_mic<-lme(species_abund ~ log(n_microhabitats), random = (~1|site), data=dat, method="ML")
r.squaredGLMM(mod_mic)
```

```
##            R2m       R2c
## [1,] 0.1144617 0.6382438
```

```
ggplot(dat, aes(x = log(n_microhabitats)+1, y = species_abund))+
  geom_point() +
  geom_smooth(method = lm, se = TRUE, colour = 'green', size = 1.5) +
  geom_text(x=1.6, y=35, label="p-value: 0.0098", size=3.5) +
  geom_text(x=1.51,y=33.5, label=expression(paste("R"^2,"c: 0.6383")), size=3.5) +
  labs(x="log(number of microhabitats)", y="observed species abundance")
```

```
## ‘geom_smooth()‘ using formula ’y ~ x’
```

```
## Warning in is.na(x): is.na() aplicado a un objeto que no es (lista o vector) de
## tipo ’expression
```



```
### MIXED EFFECTS MODEL WITH RAREFIED RICHNESS
mod3 <- lme(rarefied_richness ~ category*size + canopy_cover + n_tree_spec + n_tree_ind + log(dbh_min) +
summary(mod3)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   58.56492 69.24938 -17.28246
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept)  Residual
## StdDev: 2.442777e-05 0.6320405
##
## Fixed effects:  rarefied_richness ~ category * size + canopy_cover + n_tree_spec +      n_tree_ind +
##                        Value Std.Error DF    t-value p-value
## (Intercept)         8.419457  3.192485  7  2.6372736  0.0336
## categorypark       -0.269752  1.559754  1 -0.1729449  0.8910
## size               -0.000680  0.006511  1 -0.1044220  0.9338
## canopy_cover       -0.009324  0.015123  7 -0.6165055  0.5571
## n_tree_spec        -0.193305  0.197460  7 -0.9789587  0.3602
## n_tree_ind         -0.026853  0.088828  7 -0.3022983  0.7712
## log(dbh_min)        0.459643  0.462676  7  0.9934439  0.3536
## n_microhabitats    -0.007390  0.047624  7 -0.1551677  0.8811
## temperature        -0.019742  0.095026  1 -0.2077477  0.8696
## categorypark:size   0.017530  0.034535  1  0.5076063  0.7010
##  Correlation:
##                   (Intr) ctgryp size   cnpy_c n_tr_s n_tr_n lg(d_) n_mcrh
## categorypark      -0.294
## size              -0.308  0.736
## canopy_cover      -0.569  0.348  0.026
## n_tree_spec       -0.420 -0.472 -0.325  0.128
## n_tree_ind        -0.469  0.179 -0.029  0.142  0.415
## log(dbh_min)      -0.452 -0.421 -0.125  0.023  0.388  0.079
## n_microhabitats   -0.285  0.068  0.051  0.079  0.023 -0.117 -0.160
## temperature       -0.333  0.206  0.332  0.154 -0.330 -0.510  0.085  0.478
## categorypark:size  0.209  0.078  0.018  0.165 -0.480 -0.512 -0.441  0.428
##                   tmprtr
## categorypark
## size
## canopy_cover
## n_tree_spec
## n_tree_ind
## log(dbh_min)
## n_microhabitats
## temperature
## categorypark:size  0.467
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -2.1905486 -0.3771982  0.1406606  0.6747755  1.9225911
##
## Number of Observations: 18
## Number of Groups: 6
```

```
mod3.1 <- stepAIC(mod3) #model simplification based on AIC-value of the model
```

```
## Start:  AIC=58.56
## rarefied_richness ~ category * size + canopy_cover + n_tree_spec +
##     n_tree_ind + log(dbh_min) + n_microhabitats + temperature
##
##                   Df    AIC
## - n_microhabitats  1 56.619
## - temperature      1 56.662
## - n_tree_ind       1 56.769
## - category:size    1 57.136
## - canopy_cover     1 57.400
## - n_tree_spec      1 58.543
## <none>               58.565
## - log(dbh_min)     1 58.659
##
## Step:  AIC=56.62
## rarefied_richness ~ category + size + canopy_cover + n_tree_spec +
##     n_tree_ind + log(dbh_min) + temperature + category:size
##
##                 Df    AIC
## - temperature    1 54.671
## - n_tree_ind     1 54.851
## - canopy_cover   1 55.425
## - category:size  1 55.502
## - n_tree_spec    1 56.591
## <none>             56.619
## - log(dbh_min)   1 56.659
##
## Step:  AIC=54.67
## rarefied_richness ~ category + size + canopy_cover + n_tree_spec +
##     n_tree_ind + log(dbh_min) + category:size
##
##                 Df    AIC
## - n_tree_ind     1 53.159
## - canopy_cover   1 53.436
## - category:size  1 53.814
## <none>             54.671
## - log(dbh_min)   1 54.890
## - n_tree_spec    1 55.119
##
## Step:  AIC=53.16
## rarefied_richness ~ category + size + canopy_cover + n_tree_spec +
##     log(dbh_min) + category:size
##
##                 Df    AIC
## - canopy_cover   1 51.664
## - category:size  1 51.880
## <none>             53.159
## - n_tree_spec    1 53.213
## - log(dbh_min)   1 53.774
##
## Step:  AIC=51.66
## rarefied_richness ~ category + size + n_tree_spec + log(dbh_min) +
##     category:size
##
##                 Df    AIC
## - category:size  1 50.738
## - n_tree_spec    1 51.381
## <none>             51.664
## - log(dbh_min)   1 52.136
##
## Step:  AIC=50.74
## rarefied_richness ~ category + size + n_tree_spec + log(dbh_min)
##
##                Df    AIC
## - size          1 48.740
## - category      1 48.753
## - n_tree_spec   1 49.576
## <none>            50.738
## - log(dbh_min)  1 53.379
##
## Step:  AIC=48.74
## rarefied_richness ~ category + n_tree_spec + log(dbh_min)
##
##                Df    AIC
## - category      1 46.758
## - n_tree_spec   1 47.633
## <none>            48.740
## - log(dbh_min)  1 51.712
##
## Step:  AIC=46.76
## rarefied_richness ~ n_tree_spec + log(dbh_min)
##
##                Df    AIC
## - n_tree_spec   1 46.091
## <none>            46.758
## - log(dbh_min)  1 52.240
##
## Step:  AIC=46.09
## rarefied_richness ~ log(dbh_min)
##
##                Df    AIC
## <none>            46.091
## - log(dbh_min)  1 50.433
```

```
summary(mod3.1) #final model which includes only the most important predictors
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: dat
##        AIC      BIC    logLik
##   46.09053 49.65202 -19.04527
##
## Random effects:
##  Formula: ~1 | site
##         (Intercept)  Residual
## StdDev:   0.3015021 0.6402719
##
## Fixed effects:  rarefied_richness ~ log(dbh_min)
##                 Value Std.Error DF  t-value p-value
## (Intercept)  5.551859 0.6230627 11 8.910594  0.0000
## log(dbh_min) 0.567502 0.2136461 11 2.656270  0.0223
##  Correlation:
##              (Intr)
## log(dbh_min) -0.943
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.78828290 -0.39209673  0.05314066  0.66857616  1.81864161
##
## Number of Observations: 18
## Number of Groups: 6
```

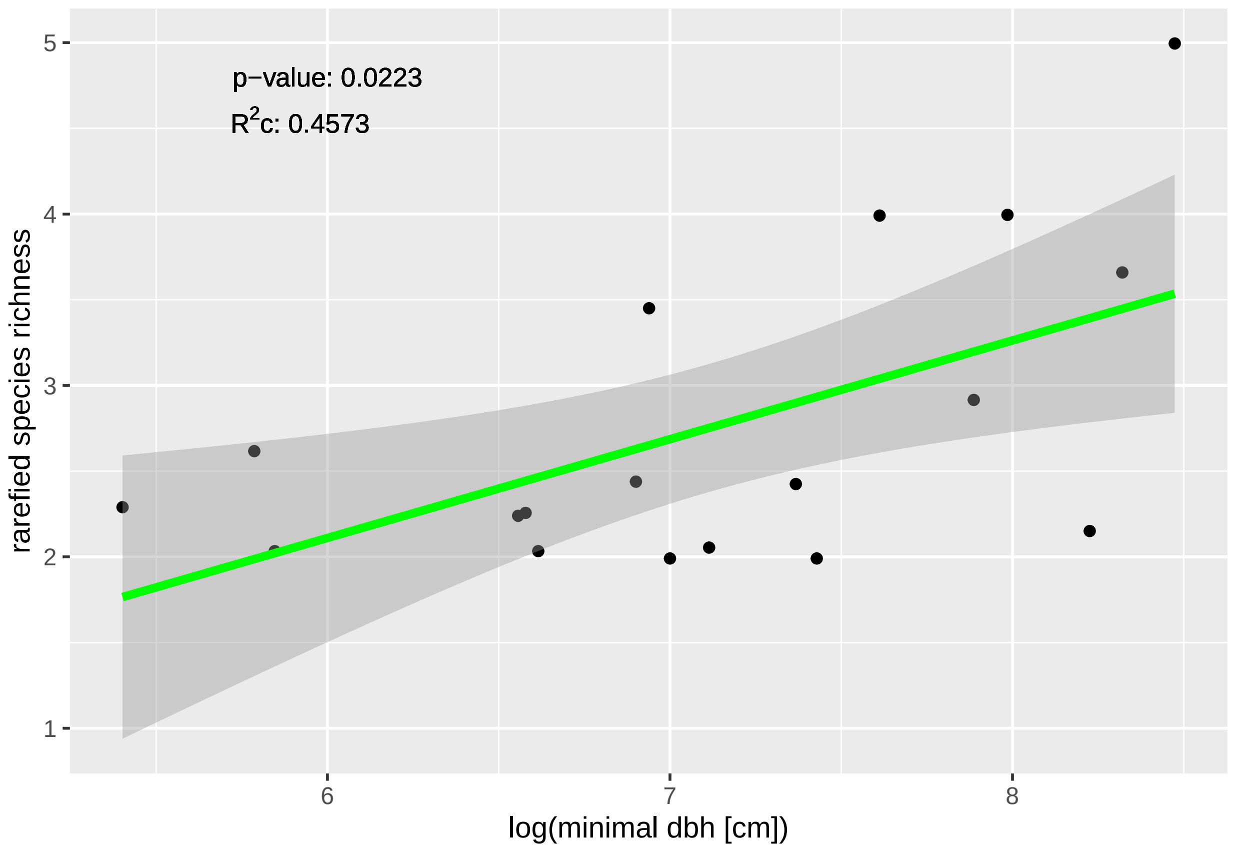
```
# plot model for rarefied richness vs. min dbh
mod_dbh<-lme(rarefied_richness ~ log(dbh_min), random = (~1|site), data=dat, method="ML")
r.squaredGLMM(mod3.1)
```

```
##          R2m       R2c
## [1,] 0.33697 0.4573085
```

```
ggplot(dat, aes(x = rarefied_richness, y = log(dbh_min)))+
  geom_point() +
  geom_smooth(method = lm, se = TRUE, colour = 'green', size = 1.5) +
  geom_text(x=6, y=4.8, label="p-value: 0.0223", size=3.5) +
  geom_text(x=5.92,y=4.55, label=expression(paste("R"^2,"c: 0.4573")), size=3.5) +
  labs(x="log(minimal dbh [cm])", y="rarefied species richness")
```

```
## ‘geom_smooth()‘ using formula ’y ~ x’
```

```
## Warning in is.na(x): is.na() aplicado a un objeto que no es (lista o vector) de
## tipo ’expression
```



```
#plot(log(dbh_min)~rarefied_richness, data=dat, ylim=c(0,5))
#mod<-lm(rarefied_richness ~ log(dbh_min), data=dat, poly(degree = 2))
```

##2c Ordination with NMDS (to look for differences in species composition)

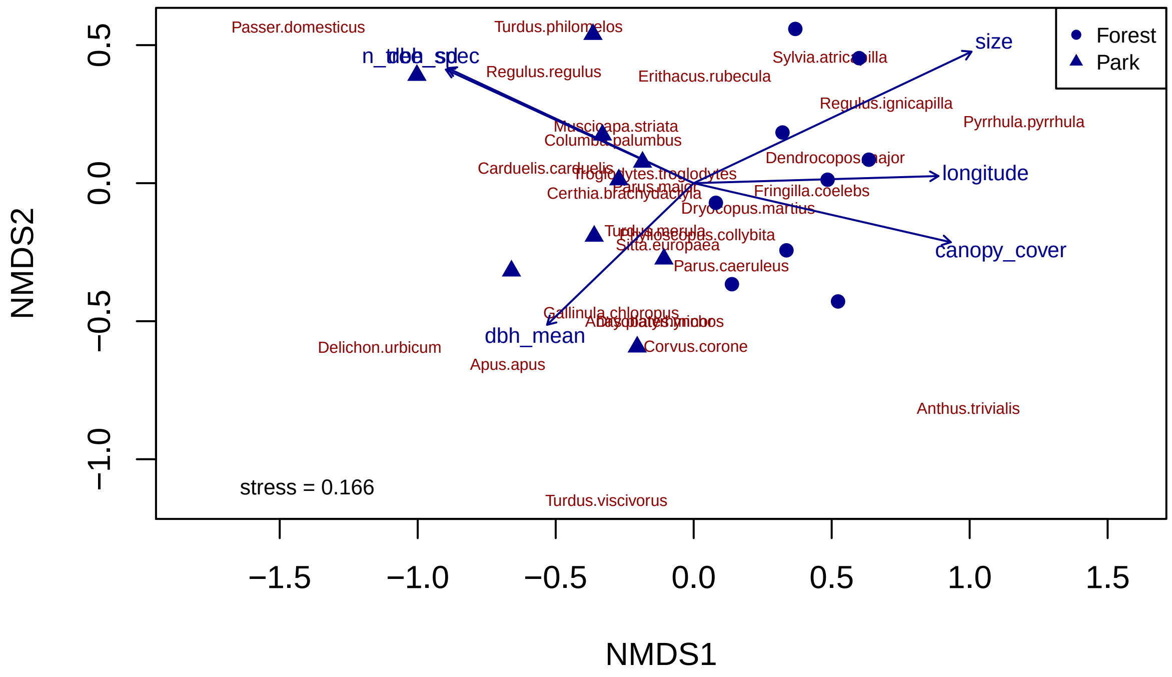
```
nmd1 <- metaMDS(dat[,4:31], distance="horn", k=2) #NMDS analysis based on Morisita-Horn-Index as a diss
```

```
## Run 0 stress 0.1663514
## Run 1 stress 0.1663514
## ... New best solution
## ... Procrustes: rmse 3.752698e-05  max resid 0.000102259
## ... Similar to previous best
## Run 2 stress 0.1663514
## ... Procrustes: rmse 2.047412e-05  max resid 6.742361e-05
## ... Similar to previous best
## Run 3 stress 0.2060524
## Run 4 stress 0.1663514
## ... Procrustes: rmse 2.359033e-05  max resid 7.896694e-05
## ... Similar to previous best
## Run 5 stress 0.267658
## Run 6 stress 0.1707767
## Run 7 stress 0.1663514
## ... New best solution
## ... Procrustes: rmse 1.455584e-06  max resid 3.333521e-06
## ... Similar to previous best
## Run 8 stress 0.1889469
## Run 9 stress 0.1828469
## Run 10 stress 0.1663514
## ... Procrustes: rmse 1.758373e-05  max resid 5.63743e-05
## ... Similar to previous best
## Run 11 stress 0.1777238
## Run 12 stress 0.1828469
## Run 13 stress 0.1663514
## ... Procrustes: rmse 1.542858e-05  max resid 5.18862e-05
## ... Similar to previous best
## Run 14 stress 0.182847
## Run 15 stress 0.1663514
## ... Procrustes: rmse 2.130293e-05  max resid 6.904612e-05
## ... Similar to previous best
## Run 16 stress 0.1777238
## Run 17 stress 0.1707767
## Run 18 stress 0.1707767
## Run 19 stress 0.1707767
## Run 20 stress 0.1777238
## *** Solution reached
```

```
# orditkplot(nmd1, display = "species", col = "darkred", fill = NA, border = NA, cex = 0.6)
ordiplot(nmd1, choices = c(1, 2), type = "n") # ylim = c(-0.75, 0.5), xlim = c(-1.25, 1.3))
ordilabel(nmd1, display = "species", col = "darkred", fill = NA, border = NA, cex = 0.5)
points(nmd1, pch=c(16, 17)[as.numeric(as.factor(dat$category))], col = "darkblue") #add sampling points
legend("topright", pch = c(16, 17), c("Forest","Park"), col = "darkblue", cex = 0.7) #add legend
text(-1.4, -1.1, labels = "stress = 0.166", cex = 0.7)

ef <- envfit(nmd1, dat[,32:44]) #check for correlation of dissimilarity gradients with environmental va
ef #results
```

```
##
## ***VECTORS
##
##                     NMDS1    NMDS2     r2 Pr(>r)
## canopy_cover      0.97464 -0.22379 0.5449  0.006 **
## n_tree_spec      -0.90908  0.41663 0.5815  0.001 ***
## n_tree_ind        0.98934 -0.14565 0.1254  0.361
## dbh_min          -0.96000 -0.28001 0.0958  0.480
## dbh_min5         -0.66028 -0.75102 0.2847  0.087 .
## dbh_mean        -0.71934 -0.69466 0.3251  0.050 *
## dbh_max         -0.75683 -0.65361 0.3293  0.055 .
## dbh_median      -0.64468 -0.76445 0.2933  0.076 .
## dbh_sd          -0.90587  0.42355 0.5773  0.005 **
## n_microhabitats  0.48725 -0.87326 0.2378  0.127
## latitude         0.66160 -0.74986 0.2294  0.125
## longitude        0.99958  0.02908 0.4694  0.011 *
## size             0.90394  0.42765 0.7395  0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
```

```
plot(ef, p.max=0.05, col = "darkblue", cex = 0.7) #add significant environmental variables to the NMDS
```



Now the species accumulation curve is shown.

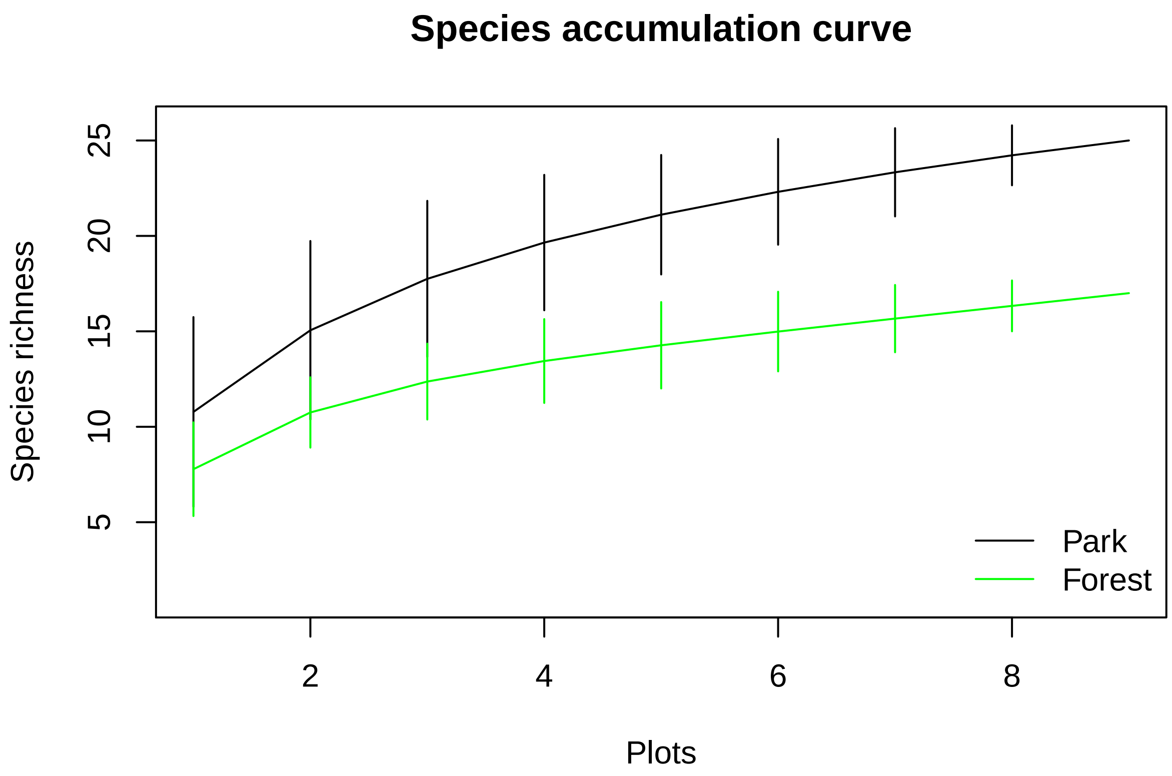
```
SAC_park <- specaccum(subset(dat[,4:31], dat$category == "park"))
```

```
## Warning in cor(x > 0): the standard deviation is zero
```

```
SAC_fore <- specaccum(subset(dat[,4:31], dat$category == "forest"))
```

```
## Warning in cor(x > 0): the standard deviation is zero
```

```
plot(SAC_park, xlab = "Plots", ylab = "Species richness", main="Species accumulation curve")

plot(SAC_fore, xlab = "Plots", ylab = "Species richness", main="Species accumulation curve", col="green
legend("bottomright", legend = c("Park","Forest"), col = c("black","green"), lwd=1, bty = "n")
```



Analysis of bird's diversity and the variables measured from these two types of ecosystems.

```
parks <- read.csv("data/parks.csv", sep=";")
forest <- read.csv("data/forest.csv", sep=";")
alpha <- specnumber(dat[,4:31]) # or use the binary site-species matrix
gamma <- ncol(dat[,colSums(dat[,4:31])>0])

##Lande's index  (beta) diversity
gamma - mean(alpha)
```

```
## [1] 38.72222
```

```
##Whittaker's index

#gamma/mean(alpha)


#For parks

alphap <- specnumber(parks[,4:31])
```

```
gammap <- ncol(parks[,colSums(parks[,4:31]) > 0])

##Lande's index
gammap - mean(alphap)
```

```
## [1] 28.22222
```

```
##Whittaker's index

#gammap/mean(alphap)

#For forest
alphaf <- specnumber(forest[,4:31])

gammaf <- ncol(parks[,colSums(parks[,4:31]) > 0])

##Lande's index
gammaf - mean(alphaf)
```

```
## [1] 31.22222
```

```
##Whittaker's index

#gammaf/mean(alphaf)
```

The number of shared and unique species for a given for the two plots combine and separated.

```
beta_virt <- betadiver(dat[,4:31], method = NA)
# a
beta_virt$a
```

```
##     1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
## 2   7
## 3   7  9
## 4   4  5  4
## 5   6  6  6  5
## 6   5  5  7  4  5
## 7   4  5  5  3  3  2
## 8   5  6  7  4  4  6  4
## 9   5  6  6  3  4  4  4  6
## 10  4  5  5  4  5  5  2  5  4
## 11  7  8  8  6  7  6  5  7  6  7
## 12  5  6  7  4  6  6  3  6  5  6  7
## 13  4  6  7  3  4  4  3  5  5  4  5  5
## 14  5  7  7  4  4  5  4  7  6  5  7  5  6
## 15  5  5  6  3  4  4  2  4  4  4  5  5  5  5
## 16  7  6  8  4  6  7  3  5  4  4  6  6  4  4  4
## 17  9  8  9  5  6  7  5  7  7  6  9  6  5  7  6  8
## 18  7  7  8  6  5  7  4  7  6  5  7  6  5  6  6  8 11
```

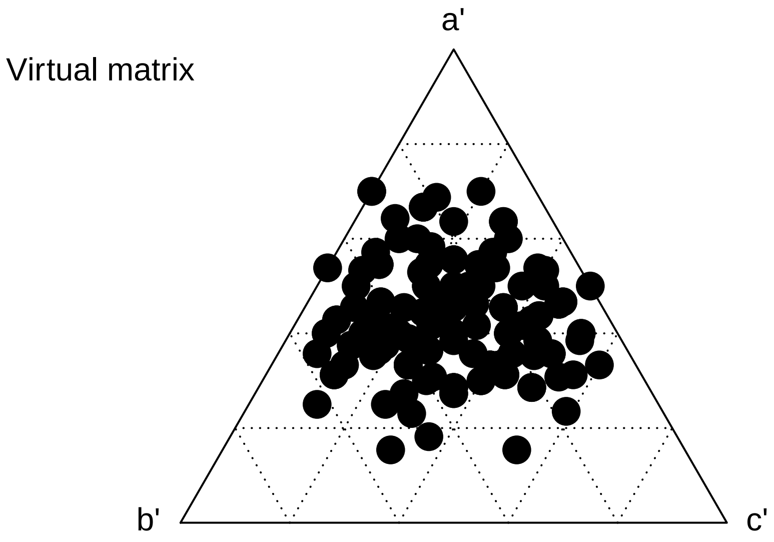
```r
beta_virt$b
```

```
##     1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
## 2   5                                                
## 3   7  5                                             
## 4   3  2  3                                          
## 5   1  1  1  2                                       
## 6   4  4  2  5  4                                    
## 7   2  1  1  3  3  4                                 
## 8   4  3  2  5  5  3  5                              
## 9   2  1  1  4  3  3  3  1                           
## 10  3  2  2  3  2  2  5  2  3                        
## 11  3  2  2  4  3  4  5  3  4  3                     
## 12  3  2  1  4  2  2  5  2  3  2  1                  
## 13  3  1  0  4  3  3  4  2  2  3  2  2               
## 14  3  1  1  4  4  3  4  1  2  3  1  3  2            
## 15  4  4  3  6  5  5  7  5  5  5  4  4  4  4         
## 16  2  3  1  5  3  2  6  4  5  5  3  3  5  5  5      
## 17  4  5  4  8  7  6  8  6  6  7  4  7  8  6  7  5   
## 18  7  7  6  8  9  7 10  7  8  9  7  8  9  8  8  6  3
```

```r
beta_virt$c
```

```
##     1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
## 2   4                                                
## 3   4  3                                             
## 4   7  7 10                                          
## 5   5  6  8  2                                       
## 6   6  7  7  3  2                                    
## 7   7  7  9  4  4  7                                 
## 8   6  6  7  3  3  3  2                              
## 9   6  6  8  4  3  5  2  3                           
## 10  7  7  9  3  2  4  4  4  3                        
## 11  4  4  6  1  0  3  1  2  1  0                     
## 12  6  6  7  3  1  3  3  3  2  1  3                  
## 13  7  6  7  4  3  5  3  4  2  3  5  3               
## 14  6  5  7  3  3  4  2  2  1  2  3  3  1            
## 15  6  7  8  4  3  5  4  5  3  3  5  3  2  3         
## 16  4  6  6  3  1  2  3  4  3  3  4  2  3  4  5      
## 17  2  4  5  2  1  2  1  2  0  1  1  2  2  1  3  1   
## 18  4  5  6  1  2  2  2  2  1  2  3  2  2  2  3  1  2
```

```r
plot(betadiver(dat[,4:31], method=NA), pch = 16, cex = 2,)
legend("topleft", legend = "Virtual matrix", bty = "n")
```



```
beta_virtp <- betadiver(parks, method = NA)
# a
beta_virtp$a
```

```
##    1  2  3  4  5  6  7  8
## 2 23
## 3 23 25
## 4 20 22 23
## 5 21 23 23 22
## 6 21 21 22 21 21
## 7 23 22 24 20 20 20
## 8 25 24 25 21 23 22 24
## 9 23 23 24 21 22 22 24 27
```

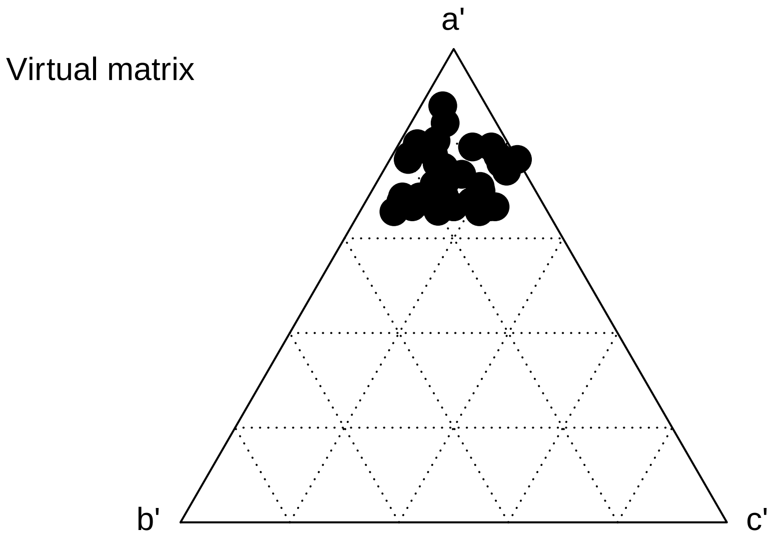
```
beta_virtp$b
```

```
##   1 2 3 4 5 6 7 8
## 2 5
## 3 7 5
## 4 3 1 0
## 5 3 1 1 2
## 6 4 4 3 4 4
## 7 2 3 1 5 5 5
## 8 4 5 4 8 6 7 5
## 9 7 7 6 9 8 8 6 3
```

```
beta_virtp$c
```

```
##   1 2 3 4 5 6 7 8
## 2 4
## 3 4 3
## 4 7 6 7
## 5 6 5 7 1
## 6 6 7 8 2 3
## 7 4 6 6 3 4 5
## 8 2 4 5 2 1 3 1
## 9 4 5 6 2 2 3 1 2
```

```
plot(betadiver(parks, method=NA), pch = 16, cex = 2,)
legend("topleft", legend = "Virtual matrix", bty = "n")
```

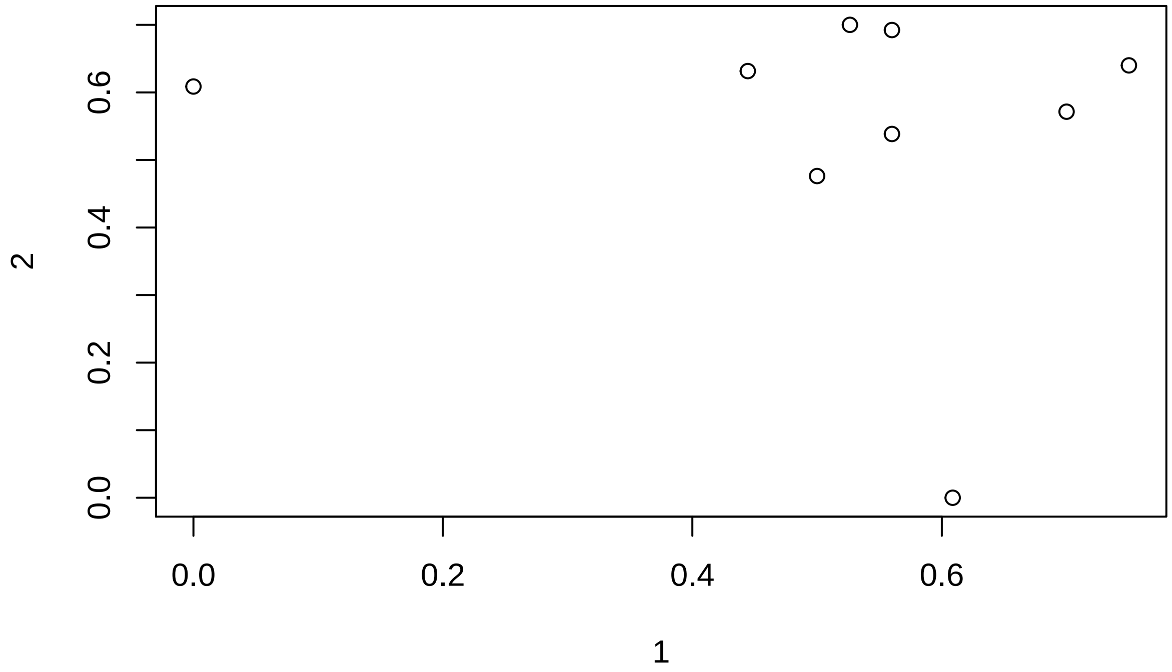


```
#vennd iagram <- as alternative to show the overlap of shared species
```

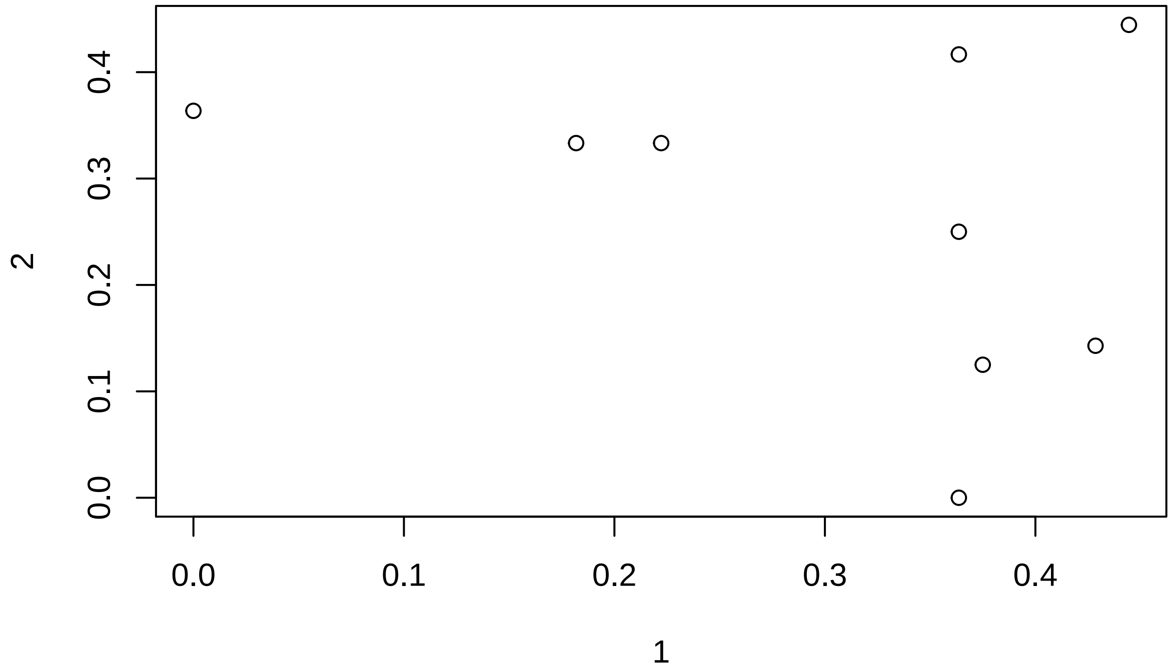
We can see how nice heterogeneity is present between the two ecosystems

Now the similarity between plots by Sorensen, Simpson and Jaccard

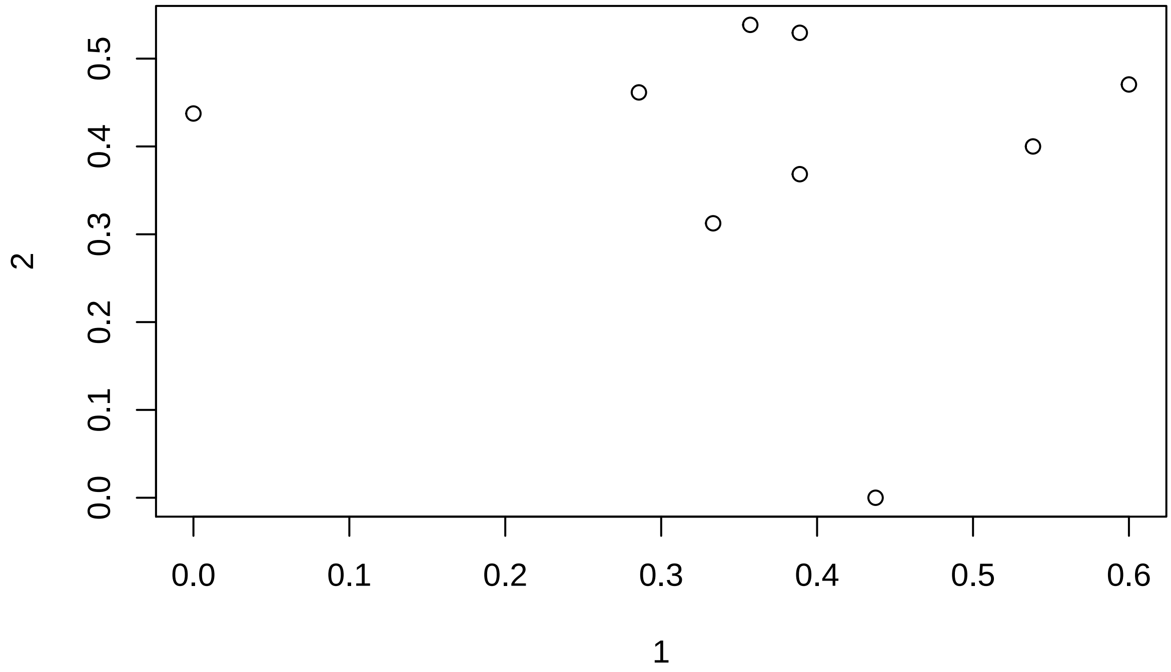
```
#Sorensen similarity
sorparks <-  betadiver(parks[,4:31], method = "sor")
sorensen <-  as.matrix(sorparks)[,]
plot(sorensen)
```



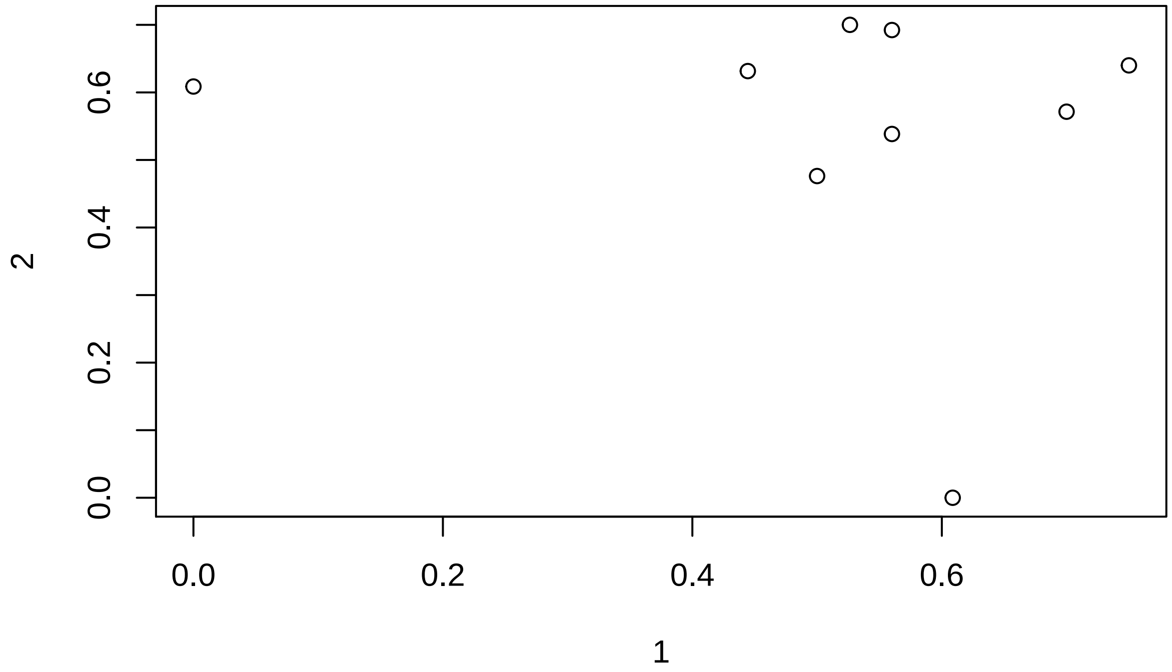
```
#Simpson similarity
simpark<- betadiver(parks[,4:31], method = "sim")
simpsonpark <- as.matrix(simpark)[,]
plot(simpsonpark)
```



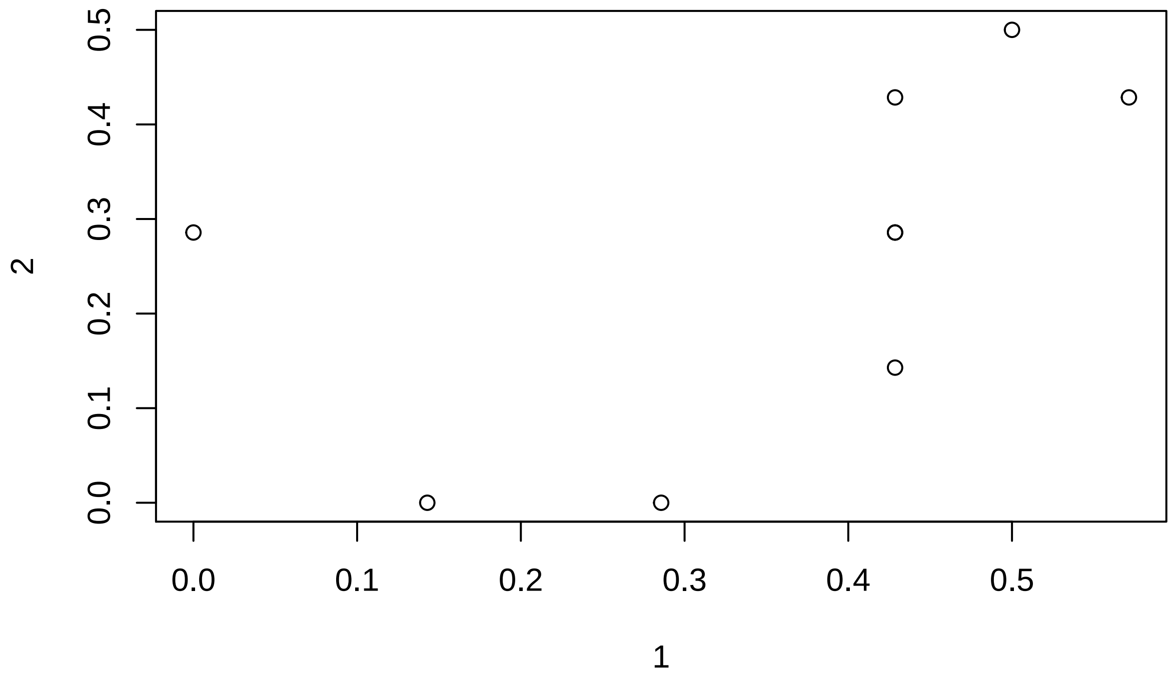
```
# Jaccard similarity
jparks <- betadiver(parks[,4:31], method = "j")
plot(as.matrix(jparks)[,])
```



```
#Sorensen similarity
sorforest <-  betadiver(forest[,4:31], method = "sor")
sorensenforest <-  as.matrix(sorforest)[,]
plot(sorensen)
```



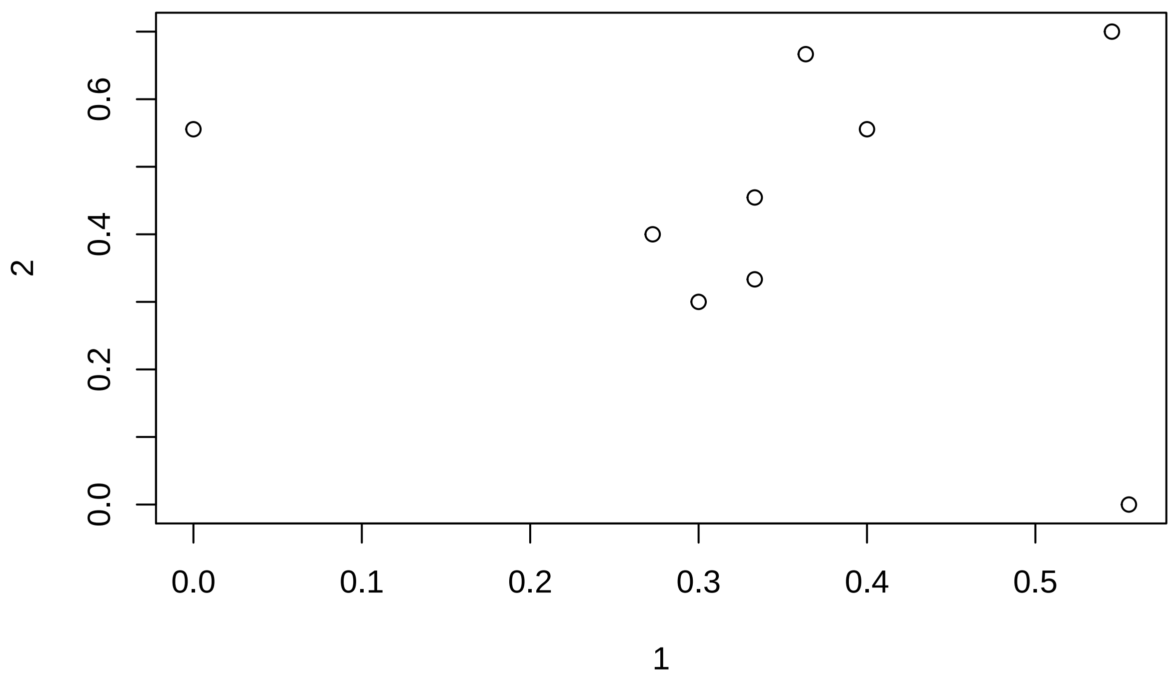
```
#Simpson similarity
simf <- betadiver(forest[,4:31], method = "sim")
simpson <- as.matrix(simf)[,]
plot(simpson)
```



```
# Jaccard similarity

jforest <- betadiver(forest[,4:31], method = "j")
as.matrix(jforest)[,]
```

```
##           1         2         3         4         5         6         7
## 1 0.0000000 0.5555556 0.3333333 0.3000000 0.3333333 0.2727273 0.4000000
## 2 0.5555556 0.0000000 0.4545455 0.3000000 0.3333333 0.4000000 0.5555556
## 3 0.3333333 0.4545455 0.0000000 0.1538462 0.5000000 0.3333333 0.4545455
## 4 0.3000000 0.3000000 0.1538462 0.0000000 0.3636364 0.4444444 0.1818182
## 5 0.3333333 0.3333333 0.5000000 0.3636364 0.0000000 0.6000000 0.4545455
## 6 0.2727273 0.4000000 0.3333333 0.4444444 0.6000000 0.0000000 0.4000000
## 7 0.4000000 0.5555556 0.4545455 0.1818182 0.4545455 0.4000000 0.0000000
## 8 0.5454545 0.7000000 0.4615385 0.4545455 0.5833333 0.5454545 0.7000000
## 9 0.3636364 0.6666667 0.5454545 0.2727273 0.5454545 0.5000000 0.6666667
##           8         9
## 1 0.5454545 0.3636364
## 2 0.7000000 0.6666667
## 3 0.4615385 0.5454545
## 4 0.4545455 0.2727273
## 5 0.5833333 0.5454545
## 6 0.5454545 0.5000000
## 7 0.7000000 0.6666667
## 8 0.0000000 0.6363636
## 9 0.6363636 0.0000000
```

```
plot(as.matrix(jforest)[,])
```



```
#calculate mean of these similarities indices and compare between sites
```

RANK abundance curve <- takes abundant species per site and plot it against relative species abundance rank

```
# Klosterpark
plot1_1 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[1,4:31]))
plot1_2 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[2,4:31]))
plot1_3 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[3,4:31]))

plot1_12 <- merge(plot1_1, plot1_2, by = "sp")
plot1 <- merge(plot1_12, plot1_3, by = "sp")
plot1$abun <- plot1$ab.x + plot1$ab.y + plot1$ab
plot1 <- plot1[which(plot1$abun!=0),]
dim(plot1)
```

```
## [1] 20  5
```

```
plot1$relabun <- plot1$abun * 100 / sum(plot1$abun)
plot1$rank <- rank(-plot1$relabun, ties.method = "random")
plot1 <- plot1[order(plot1$rank),]
```

```
# City Forest
plot2_1 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[4,4:31]))
plot2_2 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[5,4:31]))
plot2_3 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[6,4:31]))

plot2_12 <- merge(plot2_1, plot2_2, by = "sp")
plot2 <- merge(plot2_12, plot2_3, by = "sp")
plot2$abun <- plot2$ab.x + plot2$ab.y + plot2$ab
plot2 <- plot2[which(plot2$abun!=0),]
dim(plot2)
```

```
## [1] 12  5
```

```
plot2$relabun <- plot2$abun * 100 / sum(plot2$abun)
plot2$rank <- rank(-plot2$abun, ties.method = "random")
plot2 <- plot2[order(plot2$rank),]

# Forest Weende
plot3_1 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[7,4:31]))
plot3_2 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[8,4:31]))
plot3_3 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[9,4:31]))

plot3_12 <- merge(plot3_1, plot3_2, by = "sp")
plot3 <- merge(plot3_12, plot3_3, by = "sp")
plot3$abun <- plot3$ab.x + plot3$ab.y + plot3$ab
plot3 <- plot3[which(plot3$abun!=0),]
dim(plot3)
```

```
## [1] 12  5
```

```
plot3$relabun <- plot3$abun * 100 / sum(plot3$abun)
plot3$rank <- rank(-plot3$abun, ties.method = "random")
plot3 <- plot3[order(plot3$rank),]

# Forest Billingshäuser Schlucht
plot4_1 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[10,4:31]))
plot4_2 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[11,4:31]))
plot4_3 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[12,4:31]))

plot4_12 <- merge(plot4_1, plot4_2, by = "sp")
plot4 <- merge(plot4_12, plot4_3, by = "sp")
plot4$abun <- plot4$ab.x + plot4$ab.y + plot4$ab
plot4 <- plot4[which(plot4$abun!=0),]
dim(plot4)
```

```
## [1] 11  5
```

```
plot4$relabun <- plot4$abun * 100 / sum(plot4$abun)
plot4$rank <- rank(-plot4$abun, ties.method = "random")
plot4 <- plot4[order(plot4$rank),]
```

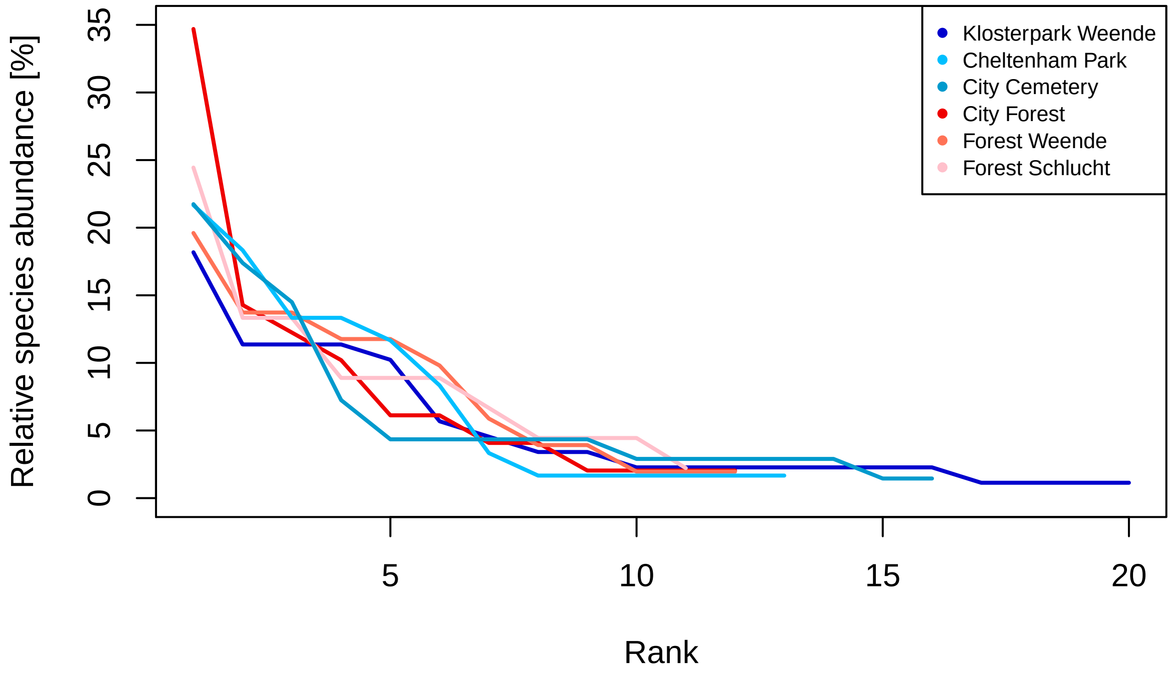
```
# Cheltenham Park
plot5_1 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[13,4:31]))
plot5_2 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[14,4:31]))
plot5_3 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[15,4:31]))

plot5_12 <- merge(plot5_1, plot5_2, by = "sp")
plot5 <- merge(plot5_12, plot5_3, by = "sp")
plot5$abun <- plot5$ab.x + plot5$ab.y + plot5$ab
plot5 <- plot5[which(plot5$abun!=0),]
dim(plot5)
```

```
## [1] 13  5
```

```
plot5$relabun <- plot5$abun * 100 / sum(plot5$abun)
plot5$rank <- rank(-plot5$abun, ties.method = "random")
plot5 <- plot5[order(plot5$rank),]

# City Cemetery
plot6_1 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[16,4:31]))
plot6_2 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[17,4:31]))
plot6_3 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[18,4:31]))

plot6_12 <- merge(plot6_1, plot6_2, by = "sp")
plot6 <- merge(plot6_12, plot6_3, by = "sp")
plot6$abun <- plot6$ab.x + plot6$ab.y + plot6$ab
plot6 <- plot6[which(plot6$abun!=0),]
dim(plot6)
```

```
## [1] 16  5
```

```
plot6$relabun <- plot6$abun * 100 / sum(plot6$abun)
plot6$rank <- rank(-plot6$abun, ties.method = "random")
plot6 <- plot6[order(plot6$rank),]

# Plotting
plot(plot1$rank, plot1$relabun, type = "l",
     col = "blue3", pch = 16, lwd = 2,
     ylim = c(0, 35),
     xlab = "Rank", ylab = "Relative species abundance [%]")
points(plot2$rank, plot2$relabun, type = "l",
       col = "red2", pch = 16, lwd = 2)
points(plot3$rank, plot3$relabun, type = "l",
       col = "coral1", pch = 16, lwd = 2)
points(plot4$rank, plot4$relabun, type = "l",
       col = "pink", pch = 16, lwd = 2)
points(plot5$rank, plot5$relabun, type = "l",
       col = "deepskyblue", pch = 16, lwd = 2)
points(plot6$rank, plot6$relabun, type = "l",
       col = "deepskyblue3", pch = 16, lwd = 2)
legend("topright",legend = c("Klosterpark Weende", "Cheltenham Park", "City Cemetery", "City Forest", "
```



```
#library(wesanderson)
#library("RColorBrewer")

#par(mfrow = c(1, 1))
#plot1_1 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[1,4:31]))

#plot1_1 <- plot1_1[which(plot1_1$ab!=0),]
#dim(plot1_1)

# Add rank of species in the first community
#plot1_1$rank <- rank(-plot1_1$ab, ties.method = "random")
# Ordering data before plotting
#plot1_1 <- plot1_1[order(plot1_1$rank), ]
# Plot
#plot(plot1_1$rank, plot1_1$ab, type = "b",
#    col = "coral", pch = 16, lwd = 1,
#    main = "RAD",
#    xlab = "Rank", ylab = "Abundances")



#plot1_2 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[2,4:31]))
#plot1_2 <- plot1_2[which(plot1_2$ab!=0),]
#dim(plot1_2)

#plot1_2$rank <- rank(-plot1_2$ab, ties.method = "random")
```

```
#plot1_2 <- plot1_2[order(plot1_2$rank), ]
#points(plot1_2$rank, plot1_2$ab, type = "both",   col = "coral2", pch = 16)

#plot1_3 <- data.frame(sp = colnames(dat[,4:31]), ab = as.numeric(dat[3,4:31]))

#plot1_3 <- plot1_3[which(plot1_3$ab!=0),]
#dim(plot1_3)
#plot1_3$rank <- rank(-plot1_3$ab, ties.method = "random")
#plot1_3 <- plot1_3[order(plot1_3$rank), ]
#points(plot1_3$rank, plot1_3$ab, type = "b",
# col = "coral3", pch = 16, lwd = 1)


#plot2_1 <- data.frame(sp = colnames(dat[,4:31]),
#                   ab = as.numeric(dat[4,4:31]))
#plot2_1 <- plot2_1[which(plot2_1$ab!=0),]
#dim(plot2_1)
#$rank <- rank(-plot2_1$ab, ties.method = "random")
#plot2_1 <- plot2_1[order(plot2_1$rank), ]
#points(plot2_1$rank, plot2_1$ab, type = "b",
#   col = "aquamarine", pch = 16, lwd = 1)



#plot2_2 <- data.frame(sp = colnames(dat[,4:31]),
#                     ab = as.numeric(dat[5,4:31]))
#plot2_2 <- plot2_2[which(plot2_2$ab!=0),]
#dim(plot2_2)
#plot2_2$rank <- rank(-plot2_2$ab, ties.method = "random")
#plot2_2 <- plot2_2[order(plot2_2$rank), ]
#points(plot2_2$rank, plot2_2$ab, type = "b",
#  col = "aquamarine3", pch = 16, lwd = 1)

#plot2_3 <- data.frame(sp = colnames(dat[,4:31]),
#                 ab = as.numeric(dat[6,4:31]))
#plot2_3 <- plot2_3[which(plot2_3$ab!=0),]
#dim(plot2_3)
#plot2_3$rank <- rank(-plot2_3$ab, ties.method = "random")
#plot2_3 <- plot2_3[order(plot2_3$rank), ]
#points(plot2_3$rank, plot2_3$ab, type = "b",
#  col = "aquamarine4", pch = 16, lwd = 1)

#plot3_1 <- data.frame(sp = colnames(dat[,4:31]),
#                     ab = as.numeric(dat[7,4:31]))
#plot3_1 <- plot3_1[which(plot3_1$ab!=0),]
#dim(plot3_1)
#plot3_1$rank <- rank(-plot3_1$ab, ties.method = "random")
#plot3_1 <- plot3_1[order(plot3_1$rank), ]
#points(plot3_1$rank, plot3_1$ab, type = "b",
#  col = "antiquewhite", pch = 16, lwd = 1)

#plot3_2 <- data.frame(sp = colnames(dat[,4:31]),
#                 ab = as.numeric(dat[8,4:31]))
```

```r
#plot3_2 <- plot3_2[which(plot3_1$ab!=0),]
#(plot3_2)
#plot3_2$rank <- rank(-plot3_2$ab, ties.method = "random")
#plot3_2 <- plot3_2[order(plot3_2$rank), ]
#points(plot3_2$rank, plot3_2$ab, type = "b",
#   col = "antiquewhite3", pch = 16, lwd = 1)


#plot3_3 <- data.frame(sp = colnames(dat[,4:31]),
#                   ab = as.numeric(dat[9,4:31]))
#plot3_3 <- plot3_3[which(plot3_1$ab!=0),]
#dim(plot3_3)
#plot3_3$rank <- rank(-plot3_3$ab, ties.method = "random")
#plot3_3 <- plot3_3[order(plot3_3$rank), ]
#points(plot3_3$rank, plot3_3$ab, type = "b",
#   col = "antiquewhite4", pch = 16, lwd = 1)


#plot4_1 <- data.frame(sp = colnames(dat[,4:31]),
#    ab = as.numeric(dat[10,4:31]))
#plot4_1 <- plot4_1[which(plot4_1$ab!=0),]
#dim(plot4_1)
#plot4_1$rank <- rank(-plot4_1$ab, ties.method = "random")
#plot4_1 <- plot4_1[order(plot4_1$rank), ]
#points(plot4_1$rank, plot4_1$ab, type = "b",
#    col = "brown1", pch = 16, lwd = 1)

#plot4_2 <- data.frame(sp = colnames(dat[,4:31]),
#                    ab = as.numeric(dat[11,4:31]))
#plot4_2 <- plot4_2[which(plot4_2$ab!=0),]
#dim(plot4_2)
#plot4_2$rank <- rank(-plot4_2$ab, ties.method = "random")
#plot4_2 <- plot4_2[order(plot4_1$rank), ]
#points(plot4_2$rank, plot4_2$ab, type = "b",
#   col = "brown4", pch = 16, lwd = 1)

#plot4_3 <- data.frame(sp = colnames(dat[,4:31]),
# ab = as.numeric(dat[12,4:31]))
#plot4_3 <- plot4_3[which(plot4_3$ab!=0),]
#dim(plot4_3)
#plot4_3$rank <- rank(-plot4_3$ab, ties.method = "random")
#plot4_3 <- plot4_3[order(plot4_3$rank), ]
#points(plot4_3$rank, plot4_3$ab, type = "b",
#     col = "brown2", pch = 16, lwd = 1)


#plot5_1 <- data.frame(sp = colnames(dat[,4:31]),
#                     ab = as.numeric(dat[13,4:31]))
#plot5_1 <- plot5_1[which(plot5_1$ab!=0),]
#dim(plot5_1)
#plot5_1$rank <- rank(-plot5_1$ab, ties.method = "random")
#plot5_1 <- plot5_1[order(plot5_1$rank), ]
#points(plot5_1$rank, plot5_1$ab, type = "b",
#   col = "chartreuse", pch = 16, lwd = 1)


#plot5_2 <- data.frame(sp = colnames(dat[,4:31]),
#                       ab = as.numeric(dat[14,4:31]))
#plot5_2 <- plot5_2[which(plot5_2$ab!=0),]
#dim(plot5_2)
#plot5_2$rank <- rank(-plot5_2$ab, ties.method = "random")
#plot5_2 <- plot5_2[order(plot5_2$rank), ]
#points(plot5_2$rank, plot5_2$ab, type = "b",
#   col = "chartreuse3", pch = 16, lwd = 1)

#plot5_3 <- data.frame(sp = colnames(dat[,4:31]),
#                      ab = as.numeric(dat[15,4:31]))
#plot5_3 <- plot5_3[which(plot5_3$ab!=0),]
#dim(plot5_3)
#plot5_3$rank <- rank(-plot5_3$ab, ties.method = "random")
#plot5_3 <- plot5_3[order(plot5_3$rank), ]
#points(plot5_3$rank, plot5_3$ab, type = "b",
#   col = "chartreuse4", pch = 16, lwd = 1)


#plot6_1 <- data.frame(sp = colnames(dat[,4:31]),
#                    ab = as.numeric(dat[16,4:31]))
#plot6_1 <- plot6_1[which(plot6_1$ab!=0),]
#dim(plot6_1)
#plot6_1$rank <- rank(-plot6_1$ab, ties.method = "random")
#plot6_1 <- plot6_1[order(plot6_1$rank), ]
#points(plot6_1$rank, plot6_1$ab, type = "b",
#    col = "cadetblue", pch = 16, lwd = 1)


#plot6_2 <- data.frame(sp = colnames(dat[,4:31]),
#                      ab = as.numeric(dat[17,4:31]))
#plot6_2 <- plot6_2[which(plot6_2$ab!=0),]
#dim(plot6_2)
#plot6_2$rank <- rank(-plot6_2$ab, ties.method = "random")
#plot6_2 <- plot6_2[order(plot6_2$rank), ]
#points(plot6_2$rank, plot6_2$ab, type = "b",
#   col = "cadetblue3", pch = 16, lwd = 1)


#plot6_3 <- data.frame(sp = colnames(dat[,4:31]),
#                      ab = as.numeric(dat[18,4:31]))
#plot6_3 <- plot6_3[which(plot6_3$ab!=0),]
#dim(plot6_3)
#plot6_3$rank <- rank(-plot6_3$ab, ties.method = "random")
#plot6_3 <- plot6_3[order(plot6_3$rank), ]
#points(plot6_3$rank, plot6_3$ab, type = "b",
#   col = "cadetblue4", pch = 16, lwd = 1)


#legend( "topright",legend=c("1_1 (11 species)", "1_2 (12 species)", "1_3 (14 species)", "2_1 (7 specie
```

```r
#datplot <- bind_rows(plot1_1,plot1_2,plot1_3)


#plot6_2$plot <- "plot6_2"

#plot1 <- cbind(plot1_1[,1:3], plot1_2[,1:3], plot1_3[,1:3])


#ggplot()+
#  geom_line(aes(rank, ab, colour="plot1_1"), data=plot1_1)+
#geom_line(aes(rank, ab, colour="plot1_2"), data=plot1_2)+
#geom_line(aes(rank, ab, colour="plot1_3"), data=plot1_3)+
#geom_line(aes(rank, ab, colour="plot2_1"), data=plot2_1)+
#geom_line(aes(rank, ab, colour="plot2_2"), data=plot2_2)+
#geom_line(aes(rank, ab, colour="plot2_3"), data=plot2_3)+
#geom_line(aes(rank, ab, colour="plot3_1"), data=plot3_1)+
#geom_line(aes(rank, ab, colour="plot3_2"), data=plot3_2)+
#geom_line(aes(rank, ab, colour="plot3_3"), data=plot3_3)+
#geom_line(aes(rank, ab, colour="plot4_1"), data=plot4_1)+
#geom_line(aes(rank, ab, colour="plot4_2"), data=plot4_2)+
#geom_line(aes(rank, ab, colour="plot4_3"), data=plot4_3)+
#geom_line(aes(rank, ab, colour="plot5_1"), data=plot5_1)+
#geom_line(aes(rank, ab, colour="plot5_2"), data=plot5_2)+
#geom_line(aes(rank, ab, colour="plot5_3"), data=plot5_3)+
#geom_line(aes(rank, ab, colour="plot6_1"), data=plot6_1)+
#geom_line(aes(rank, ab, colour="plot6_2"), data=plot6_2)+
#geom_line(aes(rank, ab, colour="plot6_3"), data=plot6_3)+
#  labs(y = "Abundance", x = "Rank", color = "")

#rank abundance curve per site
#datsite<-aggregate(data=dat[,1:31],.~site, sum)
```

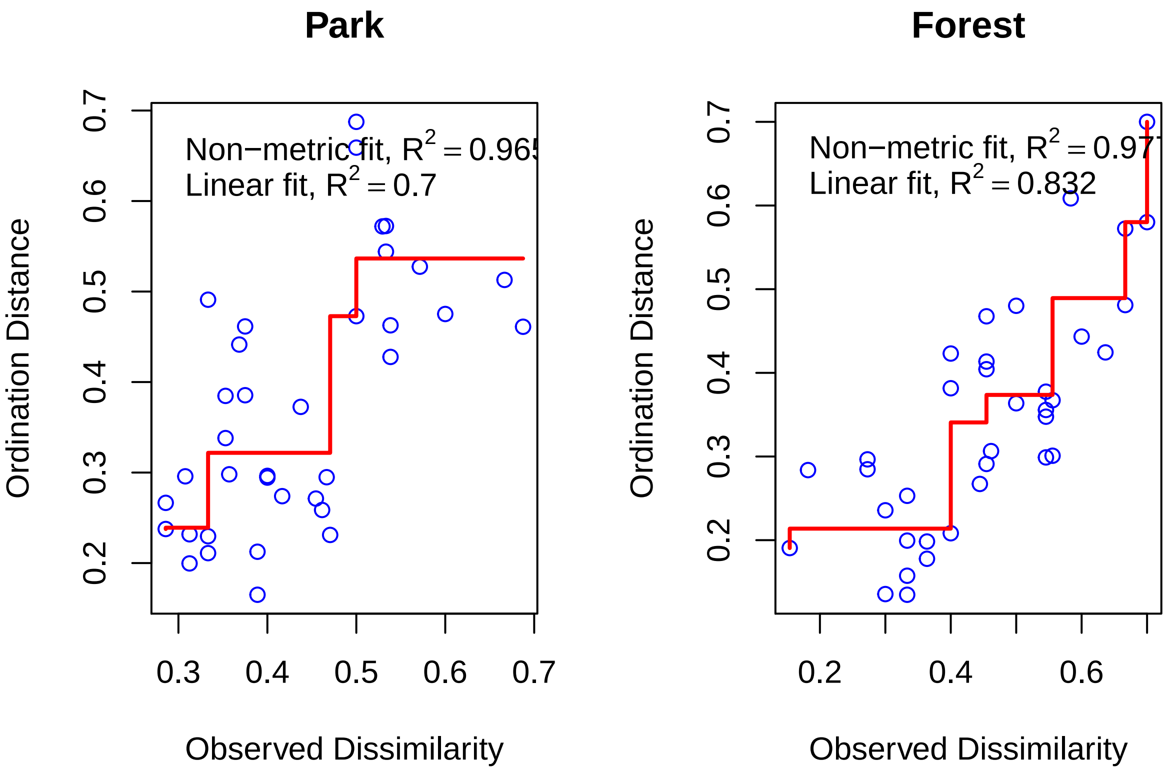
```r
datp_NMDS <- metaMDS(jparks, k = 2)
```

```
## Run 0 stress 0.1891579
## Run 1 stress 0.1891579
## ... New best solution
## ... Procrustes: rmse 9.895576e-05  max resid 0.0002141293
## ... Similar to previous best
## Run 2 stress 0.2117942
## Run 3 stress 0.2429486
## Run 4 stress 0.222101
## Run 5 stress 0.1891581
## ... Procrustes: rmse 0.000287844  max resid 0.000616197
## ... Similar to previous best
## Run 6 stress 0.2288515
## Run 7 stress 0.1881943
## ... New best solution
## ... Procrustes: rmse 0.1177482  max resid 0.2142563
## Run 8 stress 0.1881943
## ... New best solution
## ... Procrustes: rmse 3.48905e-05  max resid 5.59002e-05
## ... Similar to previous best
## Run 9 stress 0.2097903
## Run 10 stress 0.1888744
## Run 11 stress 0.301734
## Run 12 stress 0.1881943
## ... Procrustes: rmse 1.315319e-05  max resid 2.468345e-05
## ... Similar to previous best
## Run 13 stress 0.1958146
## Run 14 stress 0.21149
## Run 15 stress 0.2494831
## Run 16 stress 0.1888744
## Run 17 stress 0.2117942
## Run 18 stress 0.1891578
## Run 19 stress 0.2233721
## Run 20 stress 0.2278299
## *** Solution reached
```

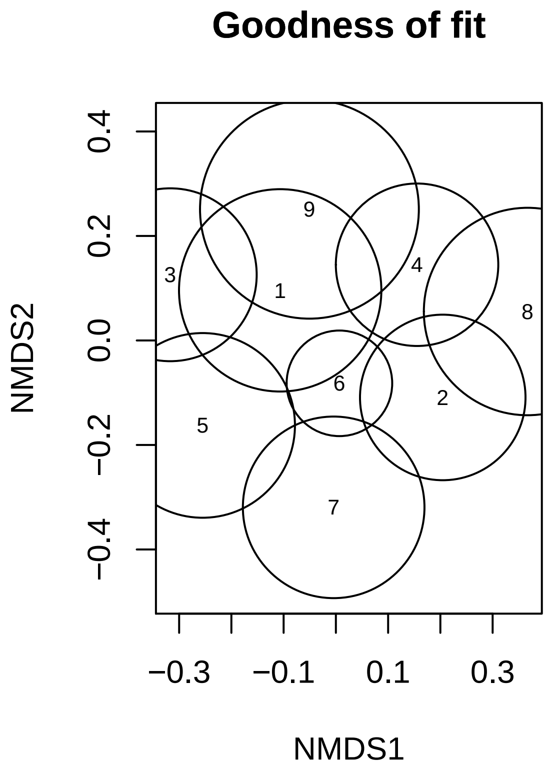
```r
datf_NMDS <- metaMDS(jforest, k=2)
```

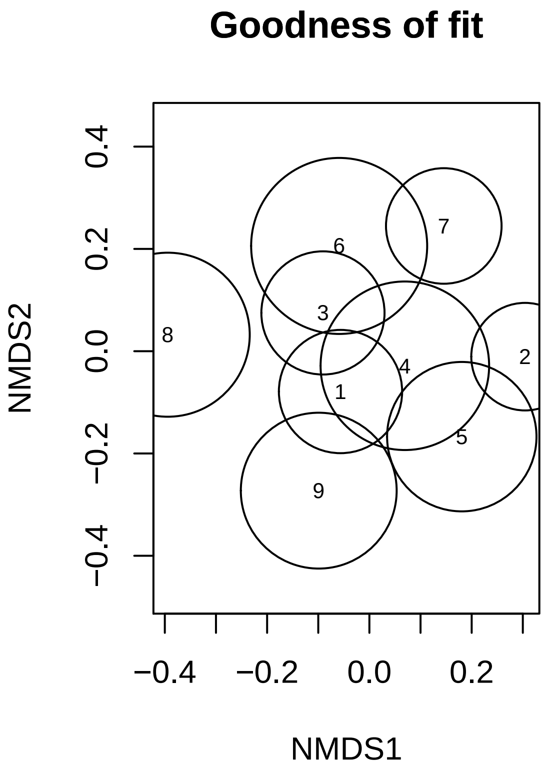
```
## Run 0 stress 0.174371
## Run 1 stress 0.1587959
## ... New best solution
## ... Procrustes: rmse 0.1690774  max resid 0.3616111
## Run 2 stress 0.1632269
## Run 3 stress 0.1634615
## Run 4 stress 0.1804467
## Run 5 stress 0.1707359
## Run 6 stress 0.1627734
## Run 7 stress 0.1769223
## Run 8 stress 0.1794955
## Run 9 stress 0.1996688
## Run 10 stress 0.1746112
## Run 11 stress 0.1746111
## Run 12 stress 0.1634615
## Run 13 stress 0.1506224
## ... New best solution
## ... Procrustes: rmse 0.2826296  max resid 0.4771843
## Run 14 stress 0.1644234
## Run 15 stress 0.1851013
## Run 16 stress 0.1634615
## Run 17 stress 0.1738528
## Run 18 stress 0.1634615
## Run 19 stress 0.1506224
## ... Procrustes: rmse 0.0001592443  max resid 0.0003175628
## ... Similar to previous best
## Run 20 stress 0.1738179
## *** Solution reached
```

```r
par(mfrow = c(1, 2))
stressplot(datp_NMDS, main = "Park")
stressplot(datf_NMDS, main = "Forest")
```

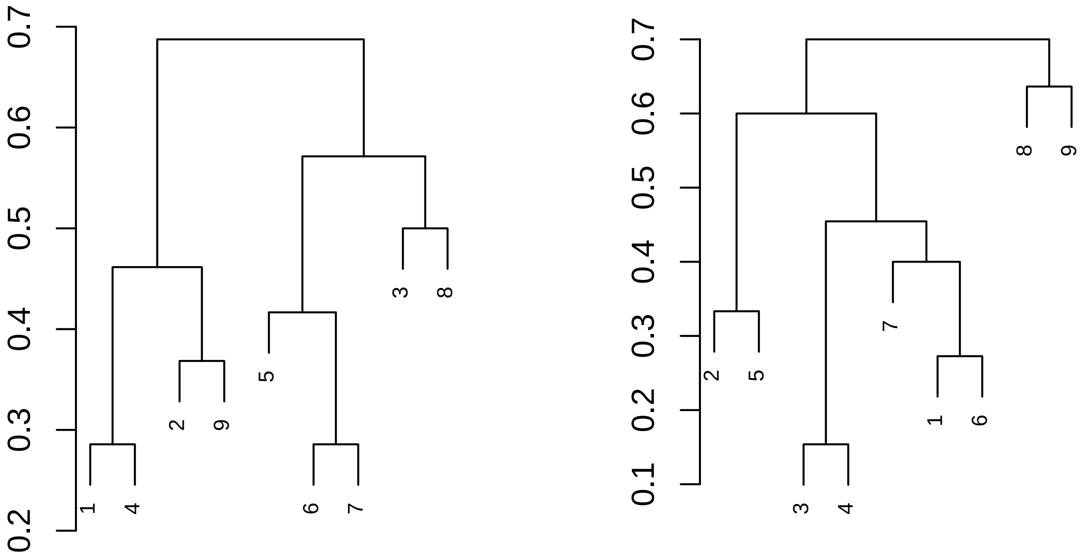


```
par(mfrow = c(1, 2))
plot(datp_NMDS, display = "sites", type = "t", main = "Goodness of fit")
points(datp_NMDS, display = "sites", cex = goodness(datp_NMDS)*200)
title(main = "Goodness of fit")

plot(datf_NMDS, display = "sites", type = "t", main = "Goodness of fit")
points(datf_NMDS, display = "sites", cex = goodness(datf_NMDS)*200)
title(main = "Goodness of fit")
```

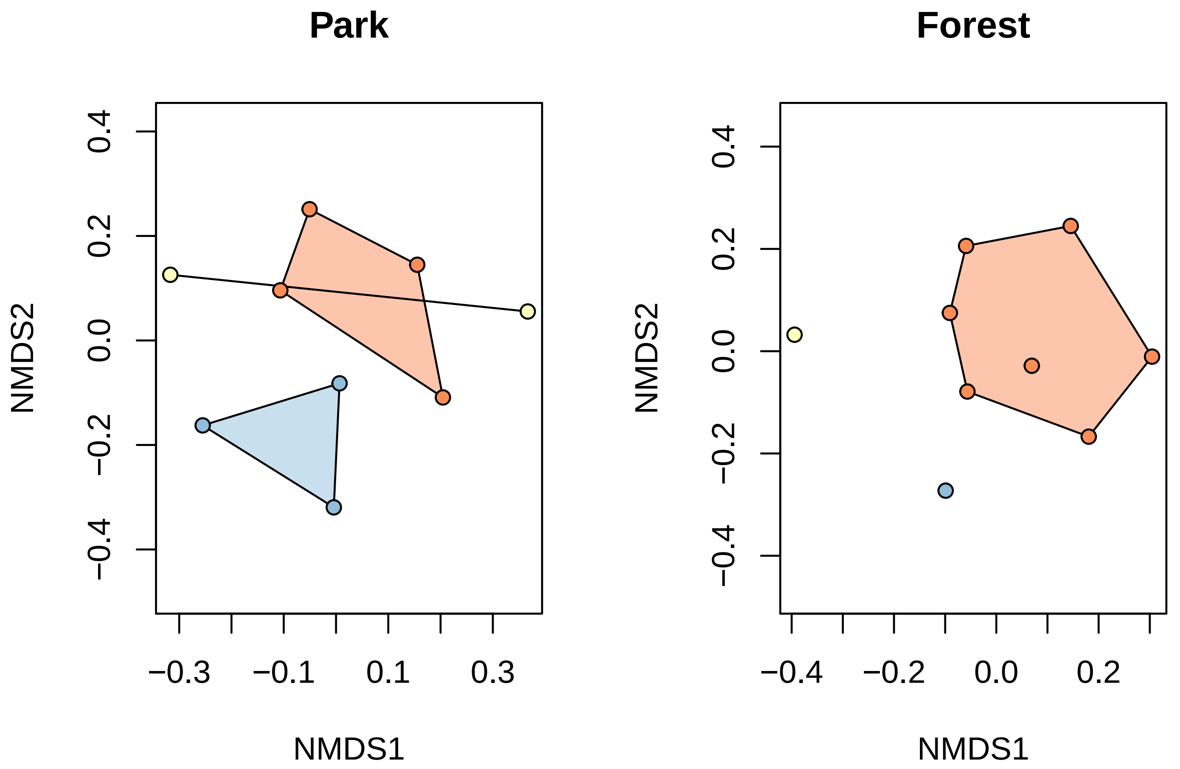




```
datpclust <- hclust(jparks, method = "complete")
plot(datpclust, xlab = "", cex = 0.7, ann = FALSE)
abline(h = 0.78, lwd = 2, col = "black", lty = 2)

datfclust <- hclust(jforest, method = "complete")
plot(datfclust, xlab = "", cex = 0.7, ann = FALSE)
abline(h = 0.78, lwd = 2, col = "black", lty = 2)
```

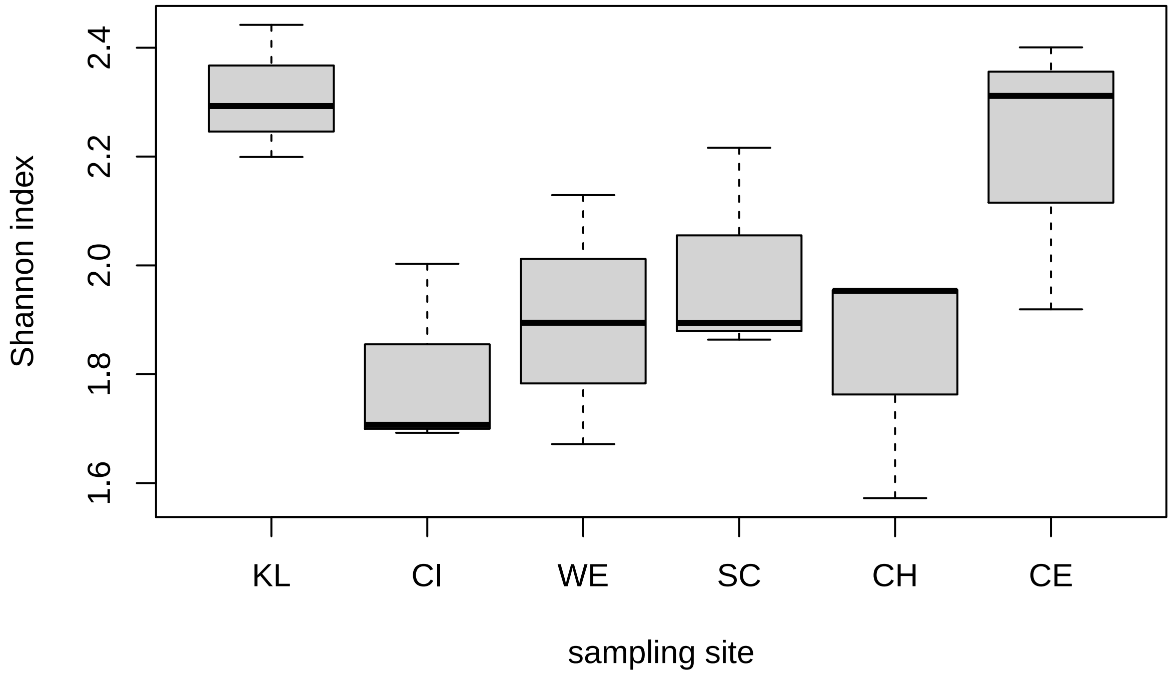


```
datpclust_3 <- cutree(datpclust, k = 3)

plot(datp_NMDS, display = "sites", type = "n", main = "Park")
ordihull(datp_NMDS, groups = datpclust_3,
         draw = "polygon", col = c("#fc8d59", "#ffffbf", "#91bfdb"),
         label = FALSE)
points(datp_NMDS, display = "sites", pch = 21, col = "black",
       bg = c("#fc8d59", "#ffffbf", "#91bfdb")[datpclust_3])
legend(x = 0.4, y = -0.2, legend = c(paste0("Cl. ", seq(1:3))),
       col = c("#fc8d59", "#ffffbf", "#91bfdb"), pch = 16)

datfclust_3 <- cutree(datfclust, k = 3)

plot(datf_NMDS, display = "sites", type = "n", main = "Forest")
ordihull(datf_NMDS, groups = datfclust_3,
         draw = "polygon", col = c("#fc8d59", "#ffffbf", "#91bfdb"),
         label = FALSE)
points(datf_NMDS, display = "sites", pch = 21, col = "black",
       bg = c("#fc8d59", "#ffffbf", "#91bfdb")[datfclust_3])
legend(x = 0.4, y = -0.2, legend = c(paste0("Cl. ", seq(1:3))),
       col = c("#fc8d59", "#ffffbf", "#91bfdb"), pch = 16)
```



Shannon diversity index

```
H <- diversity(dat[,4:31], index = "shannon")
plot(H~dat$site, xlab="sampling site", xaxt="n", ylab = "Shannon index")
axis(1, at=1:6, labels=c("KL","CI","WE","SC","CH","CE"))
```


Shannon index
2.4
2.2
2.0
1.8
1.6
KL
CI
WE
SC
CH
CE
sampling site