

```
library(vegan)
library(corrplot)
library(berryFunctions)
library(packfor) ##alternatively adespatial can be used

##PAIRWISE CORRELATIONS BETWEEN ENV.TAB VARIABLES-----

plot(env.tab$Altitude, env.tab$TRI)
plot(env.tab[,1:2], pch=16, col=densCols(env.tab[,1:2], colramp=
colorRampPalette(c("gray80", "gray20"))))

cor.test(env.tab$Altitude, env.tab$TRI)

cor(env.tab)

#plot correlation matrix
source("panelutils.R")
op <- par(mfrow=c(1,1), pty="s")
pairs(env.tab[1:4], lower.panel=panel.smooth, upper.panel=panel.cor,
diag.panel=panel.hist, main="Pearson correlation matrix")
par(op)

#another correlation matrix
cor.mat <- cor(env.tab)
head(cor.mat)

corrplot.mixed(cor.mat, lower = "number", upper = "ellipse", tl.pos = "lt",
               tl.cex=0.7, tl.col = "black", number.cex=0.7,
               title="Correlation matrix")

###EXPLORE RESPONSE VARIABLE-----
```

```
#map species richness
```

```
coord <- forest[, c("X", "Y")]
```

```
plot(coord$X, coord$Y)
```

```
colPoints(coord$X, coord$Y, forest$Diversity, add = F)
```

```
#specify my own color scale
```

```
my.col <- colorRampPalette(c("blue", "yellow", "red"))
```

```
colPoints(coord$X, coord$Y, forest$Diversity, add = F, col=my.col(100))
```

```
#statistics
```

```
summary(forest$Diversity)
```

```
boxplot(forest$Diversity)
```

```
hist(forest$Diversity)
```

```
plot(density(forest$Diversity))
```

```
hist(log(forest$Diversity))
```

```
#test normality
```

```
shapiro.test(forest$Diversity)
```

```
shapiro.test(log(forest$Diversity))
```

```
## N0 = výběr pochází normálně rozloženého souboru
```

```
###CORRELATION ANALYSIS OF DIVERSITY AND ENV.TAB VARIABLES-----
```

```
#correlate diversity and enviro variables
```

```
cor(forest$Diversity, env.tab)
```

```
plot(env.tab$Limestone, forest$Diversity, main="Limestone")
```

```
plot(env.tab$Arable.land, forest$Diversity, main="Arable land")
```

```
plot(env.tab$ForestAB, forest$Diversity, main="Natural forests")
cor(env.tab$ForestAB, forest$Diversity)
```

```
#loess smooth
```

```
l <- loess.smooth(env.tab$ForestAB, forest$Diversity)
lines(l, lwd=3, col="red")
```

```
##LINEAR REGRESSION-----
```

```
m <- lm(forest$Diversity ~ ForestAB, data=env.tab.s)
anova(m)
summary(m)
```

```
m <- lm(forest$Diversity ~ ForestAB + Altitude, data=env.tab.s)
anova(m)
summary(m)
```

```
m <- lm(forest$Diversity ~ ., data=env.tab.s)
m
```

```
anova(m)
summary(m)
```

```
m2 <- lm(forest$Diversity ~ ., data=env.tab.s[, sample(1:15)])
anova(m2)
summary(m2)
```

```
library("packfor")
```

```
####FORWARD SELECTION-----
```

```
#forward selection based on significance level
fs <- forward.sel(forest$Diversity, env.tab.s, alpha=0.05)
fs

m <- lm(forest$Diversity ~ Limestone + Arable.land + Altitude,
data=env.tab.s)

anova(m)
summary(m)

res <- resid(m)
pr <- predict(m)

#compare predicted and observed values
head(res)
head(pr)
head(forest$Diversity)

##calculate total variability in response variable
TSS <- sum((mean(forest$Diversity) - forest$Diversity)^2)

#extract residuals
RSS <- sum(resid(m)^2)

#calculate R2
1-(RSS/TSS)

#evaluate model
# plot(m)
hist(res)
```

```
#map residuals
```

```
forest$res <- res
```

```
colPoints(coord$X, coord$Y, res, add=F, col=my.col(100), main="Residuals")
```

```
#map fitted values
```

```
forest$pr <- pr
```

```
colPoints(coord$X, coord$Y, pr, add=F, col=my.col(100), main="Fitted")
```

```
###VARIATION PARTITIONING-----
```

```
library(vegan)
```

```
colnames(env.tab)
```

```
v <- varpart(forest$Diversity, env.tab.s[,5:6], env.tab.s[, 7:9],  
env.tab.s[,10:15])
```

```
plot(v)
```

```
showvarparts(3)
```