

Simulates assemblages and calculate FD metrics.  
Supplementary material in: Species and functional diversity accumulate differently in terrestrial mammals

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This document follows the principles of reproducible research (Peng, 2011). This document was generated in **R studio** with **kintr** package.

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## 1. Packages versions:

We used R version 3.2.2 (2015-08-14) and the following packages:

```
library(FD)
```

## 2. Load functions:

```
# modified version of simul_dbFD function from FD packages
source("simul_dbFB_mod.R")

# Pairs correlation
# P-value and r coefficient
panel.cor <- function(x, y, digits=2, cex.cor)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r <- abs(cor(x, y))
  txt <- format(c(r, 0.123456789), digits=digits)[1]
  test <- cor.test(x,y)
  Signif <- ifelse(round(test$p.value,3)<0.001,"p<0.001",paste("p=",round(test$p.value,3)))
  text(0.5, 0.25, paste("r=",txt))
  text(.5, .75, Signif)
}
# Apply smooth regression line
panel.smooth<-function (x, y, col = "black", bg = NA, pch = 18,
                         cex = 0.8, col.smooth = "red", span = 2/3, iter = 3, ...)
{
  points(x, y, pch = pch, col = col, bg = bg, cex = cex)
  ok <- is.finite(x) & is.finite(y)
  if (any(ok))
    lines(stats:::lowess(x[ok], y[ok], f = span, iter = iter),
          col = col.smooth, ...)
}
# Add histogram to the diagonal
panel.hist <- function(x, ...)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(usr[1:2], 0, 1.5) )
  h <- hist(x, plot = FALSE)
  breaks <- h$breaks; nB <- length(breaks)
  y <- h$counts; y <- y/max(y)
  rect(breaks[-nB], 0, breaks[-1], y, col="white", ...)
}
```

## 3. Simulate assemblages and calculate FD metrics:

3.1 *Experiment 1*: Simulate trait values following a normal distribution and using parameters extracted from the distribution of body mass observed across mammals

P.S.: In this first experiment lets use a modified version of the simul.dbFD function from FD package. With this function it is possible to give parameters to generate trait values.

---

```
# s - vector listing the different levels of species richness used in the simulations
# t - number of traits
# r - number of replicates per species richness level
# p - number of species in the common species pool
# tr.method - character string indicating the sampling distribution for the traits. "unif" is a uniform
# abun.method - character string indicating the sampling distribution for the species abundances. Sam
# w.abun - logical; should FDis, FEve, FDiv, and Rao's quadratic entropy (Q) be weighted by species abu
```

```
res1 <- simul.dbFD.mod(s = c(5,10,15,20,25,30,35,40,45,50,55,60,65,70,75,80,85,90,95,100), t = 5, r = 1000,
```

```
results1 <- data.frame(res1$results)
colnames(results1)[1] <- "Richness"
```

### 3.2 *Experiment 2:* Simulate trait values following a normal distribution

```
res2 <- simul.dbFD(s = c(5,10,15,20,25,30,35,40,45,50,55,60,65,70,75,80,85,90,95,100), t = 5, r = 1000,
```

```
results2 <- data.frame(res2$results)
colnames(results2)[1] <- "Richness"
```

### 3.3 *Experiment 3:* Simulate trait values following a log normal distribution

```
res3 <- simul.dbFD(s = c(5,10,15,20,25,30,35,40,45,50,55,60,65,70,75,80,85,90,95,100), t = 5, r = 1000,
```

```
results3 <- data.frame(res3$results)
colnames(results3)[1] <- "Richness"
```

## 4. Get standard deviation and range of simulates traits in assemblages:

### 4.1 *Experiment 1:*

```
res1$abun[res1$abun > 0] <- 1
```

```
SD <- NA
amp <- NA
for(i in 1:nrow(res1$abun)){
  tmp <- res1$traits[which(res1$abun[i,]==1)]
  SD[i] <- sd(tmp)
  amp[i] <- max(tmp)-min(tmp)
}

experiment1 <- cbind(SD, amp, results1)
```

## 4.2 Experiment 2:

```
res2$abun[res2$abun > 0] <- 1

SD <- NA
amp <- NA
for(i in 1:nrow(res2$abun)){
  tmp <- res2$traits[which(res2$abun[i,]==1)]
  SD[i] <- sd(tmp)
  amp[i] <- max(tmp)-min(tmp)
}

experiment2 <- cbind(SD, amp, results2)
```

## 4.3 Experiment 3:

```
res3$abun[res3$abun > 0] <- 1

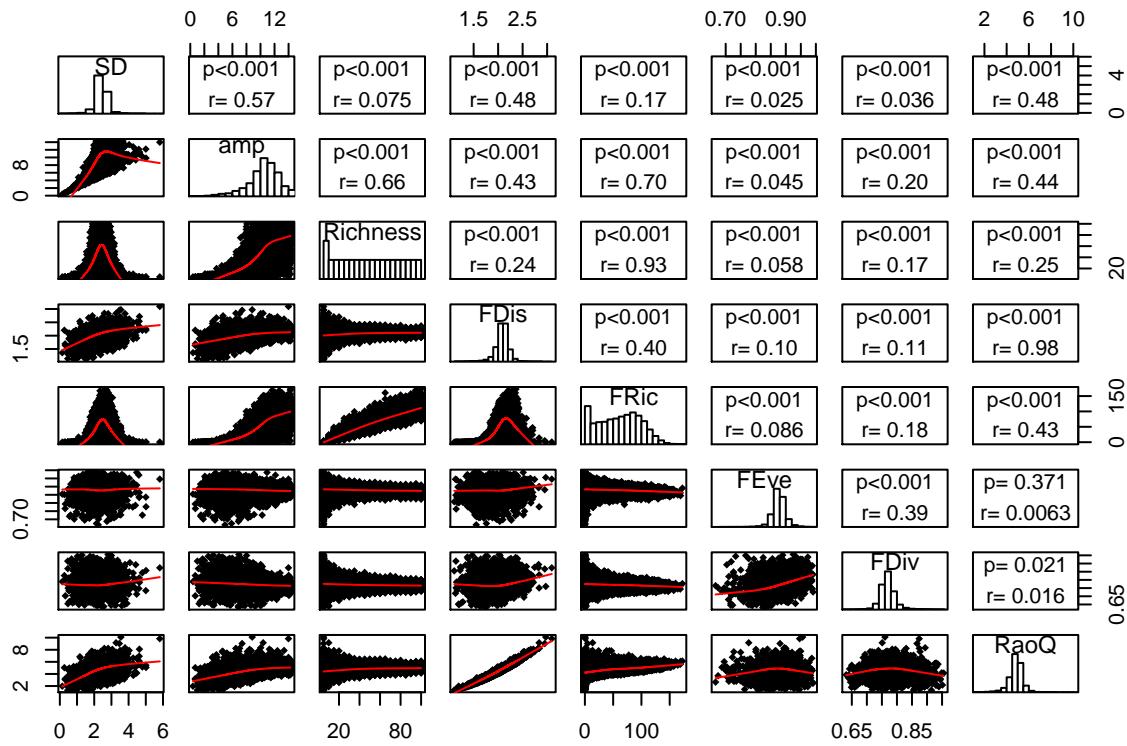
SD <- NA
amp <- NA
for(i in 1:nrow(res3$abun)){
  tmp <- res3$traits[which(res3$abun[i,]==1)]
  SD[i] <- sd(tmp)
  amp[i] <- max(tmp)-min(tmp)
}

experiment3 <- cbind(SD, amp, results3)
```

## 5. Plot results:

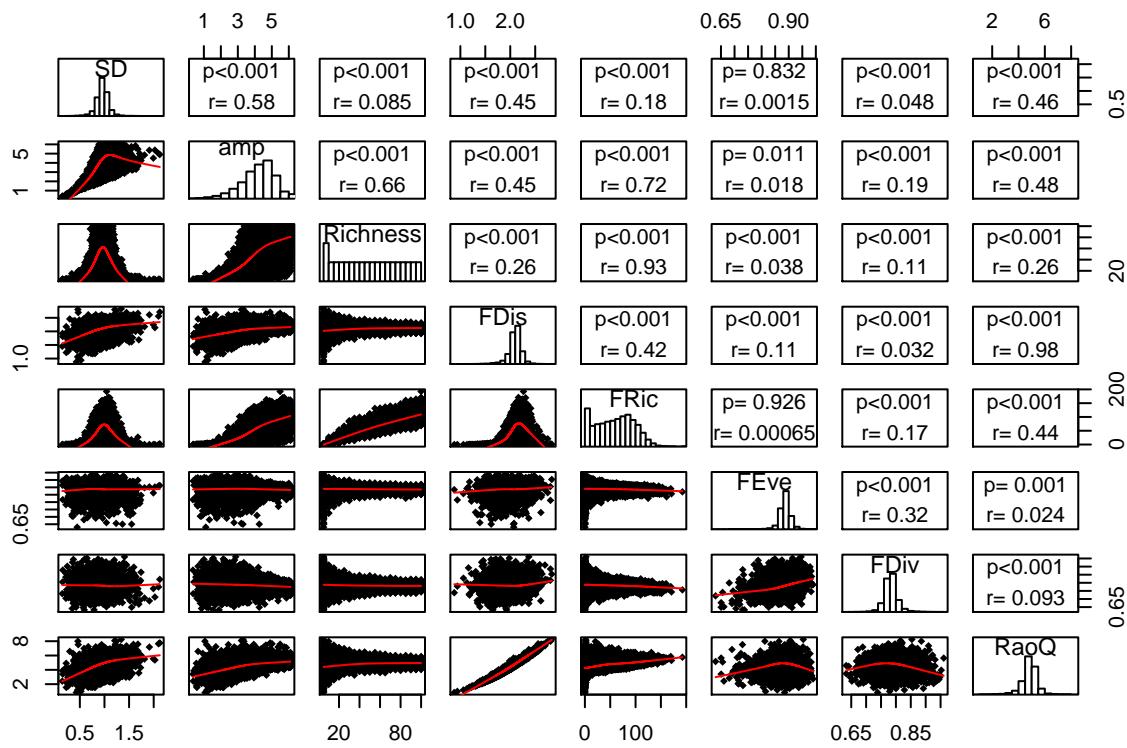
### 4.1 Experiment 1:

```
pairs(experiment1,
      lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel=panel.hist)
```



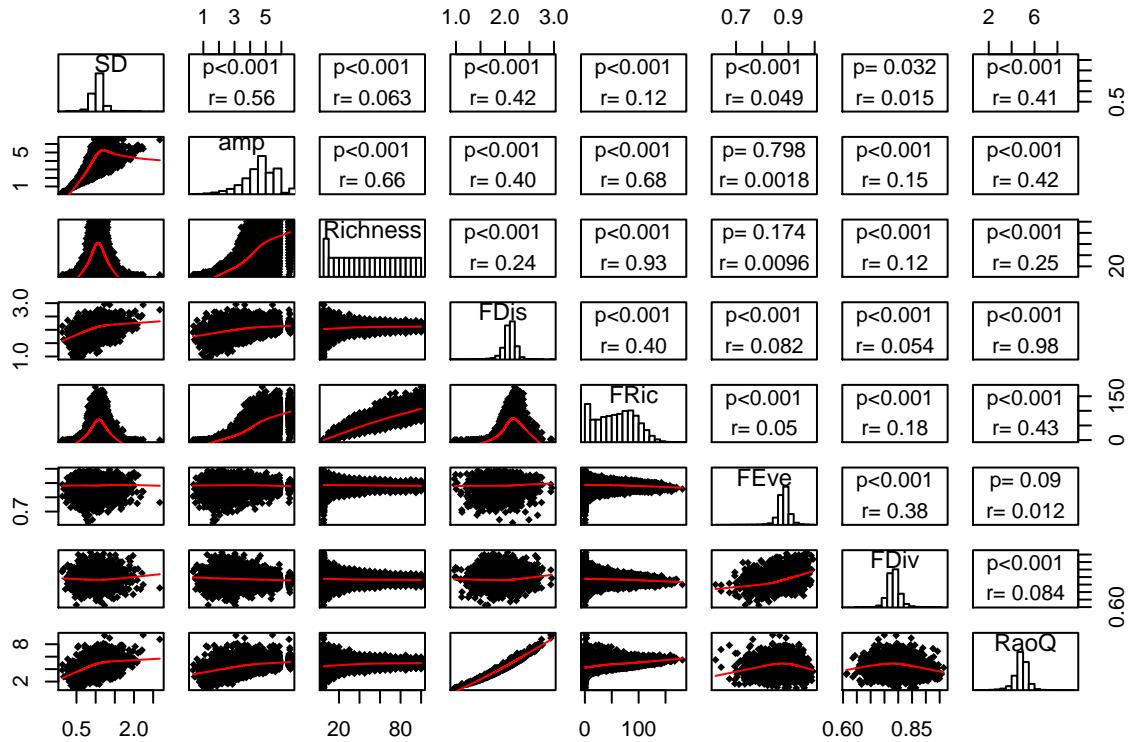
## 4.2 Experiment 2:

```
pairs(experiment2,
      lower.panel=panel.smooth, upper.panel=panel.cor, diag.panel=panel.hist)
```



### 4.3 Experiment 3:

```
pairs(experiment3,
      lower.panel=panel.smooth, upper.panel=panel.cor, diag.panel=panel.hist)
```



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Contact [brunno.oliveira@me.com](mailto:brunno.oliveira@me.com) for any further information.