Sensitivity analyses for: Decoupled erosion of amphibians' phylogenetic and functional diversity from extinction

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This code simulates phylogenies and trait data.
Phylogenies are simulated following a birth-death model, and traits are allowed to evolve in simulated trees following a brownian motion model.

From simulated phylogenies and traits, phylogenetic diversity (PD) and functional diversity (FD) metrics are calculated. For PD, we use the sum across all the branches (Faith 1992), and for FD we used the convex hull (aka functional richness, Cornwell et al. 2006) and the hypervolume (Blonder et al. 2014) approaches.

1. Simulate phylogenies and trait data with sizes ranging from 5 to 500 species.

This tests whether hypervolume and convex hulls are correlated with PD. A lack of correlation between PD and both metrics of FD suggests that these metrics should not be used for testing for the coupling/decoupling between PD and FD.

```r
sim_tree_traits <- function(x) {

  tree <- sim.bdtree(n = x, stop="taxa", extinct=FALSE)

  tree <- drop.extinct(tree)
  for (y in 1: length(tree$edge.length)) {
    if (tree$edge.length[y] == 0.00000000 ) # if a branch length is zero...
      tree$edge.length[y] = 0.01   # ... set the length to 0.01.
  }

  rich <- length(tree$tip.label)

  PD <- sum(tree$edge.length)

  traits <- sim.traits(ntaxa = x, ntraits = 4, nreps = 1, tree=tree)

  traits <- traits$trait_data

  convex <- convhulln(as.matrix(traits), "FA")$vol

  hyper_ <- hypervolume_gaussian(traits,
                        samples.per.point = 1000,
                        kde.bandwidth = c(.1, .1, .1, .1),
                        verbose = F)

  hyper <- get_volume(hyper_)
```

```
  return(data.frame(rich = rich, PD = PD, hyper = hyper, convex = convex))
}

rich_ <- seq(5,200,10)

simula_pdfd <- pblapply(rich_, function(x) sim_tree_traits(x))
simula_pdfd <- do.call(rbind, simula_pdfd)
```
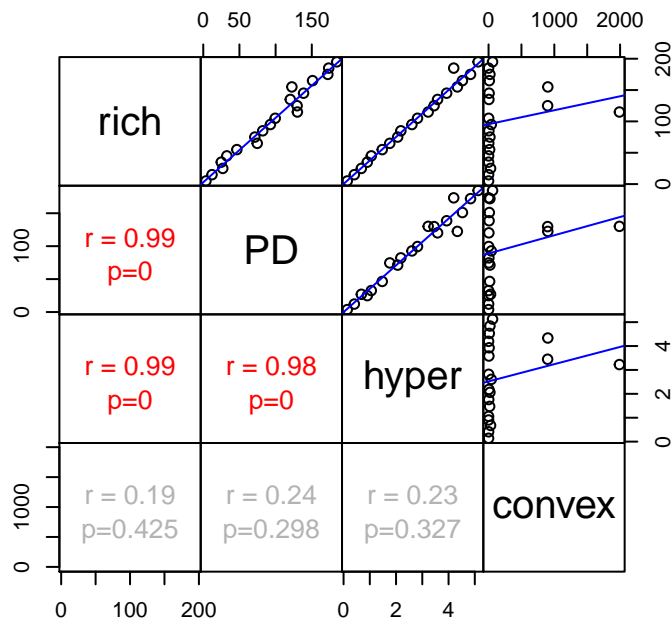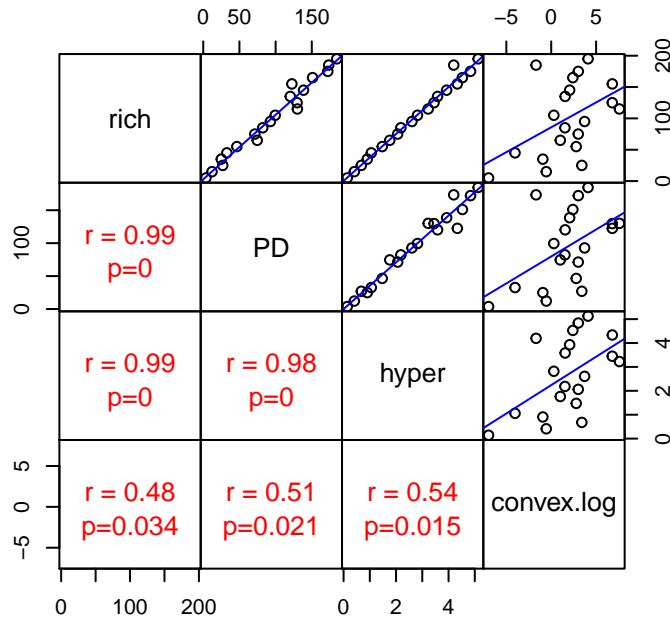
1.1. Check for correlations

```
pairsrp(simula_pdfd, meth = "pearson")
```


Pearson's product–moment correlation

```
pairsrp(data.frame(simula_pdfd[,-4],convex.log=log(simula_pdfd$convex)), meth = "pearson")
```

Pearson's product–moment correlation

PD and hypervolumes show similar sensitivity to richness. While both hypervolumes and convex hulls correlate with PD, the correlation between PD and hypervolume is much stronger than the correlation between PD and convex hull.

2. Keep species number constant and simulate traits with varying levels of dispersion

This tests whether hypervolumes and convex hulls are sensitive to an increase in trait space.

```
sim_traits <- function(nsps=50,dispersion) {

  traits <- data.frame(axis1 = rnorm(nsps,sd=dispersion),
                       axis2 = rnorm(nsps,sd=dispersion),
                       axis3 = rnorm(nsps,sd=dispersion))

  convex <- convhulln(as.matrix(traits), "FA")$vol

  hyper_ <- hypervolume_gaussian(traits,
                                 samples.per.point = 1000,
                                 kde.bandwidth = c(.1, .1, .1),
                                 verbose = F)

  hyper <- get_volume(hyper_)

  return(data.frame(dispersion = dispersion, hyper = hyper, convex = convex))
}
```
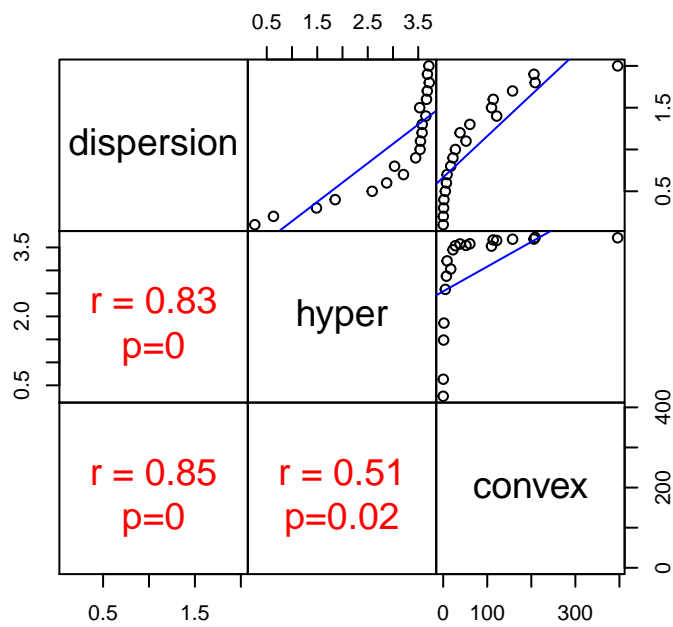
```
disl <- seq(.1,2,.1)

simula_fd <- pblapply(disl, function(x) sim_traits(dispersion=x))
simula_fd <- do.call(rbind, simula_fd)
```
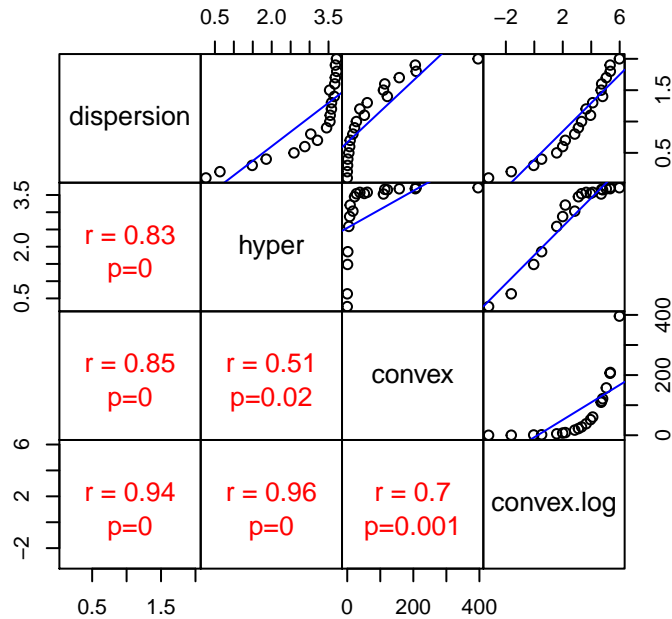
2.2. Check for correlations

```
pairsrp(simula_fd, meth = "pearson")
```

Pearson's product–moment correlation


```
pairsrp(data.frame(simula_fd[,-4],convex.log=log(simula_fd$convex)), meth = "pearson")
```

Pearson's product–moment correlation

Both hypervolumes and convex hulls were sensitive to increasing variance in trait values.

# 3. Identifying holes in the trait space

This tests the ability of convex hulls and hypervolumes for detecting extinctions that take place at center of trait space. The idea here is that when one needs to identify changes in trait space, the metric selected should be sensitive enough for capturing such a change.

```r
# Simulate 3 traits for 50 species
traits <- data.frame(axis1 = rnorm(50),
                     axis2 = rnorm(50),
                     axis3 = rnorm(50))

# Simulate extinctions in the center of the trait space
traits$survivor <- "live"
traits$survivor[which(traits$axis1<(1) & traits$axis1>(-1) &
                      traits$axis2<(1) & traits$axis2>(-1) &
                      traits$axis3<(1) & traits$axis3>(-1))] <- "die"
traits$survivor <- as.factor(traits$survivor)

# Visualize the simulated trait space
scatter3D(x = traits$axis1,
          y = traits$axis2,
          z = traits$axis3,
          colvar = as.integer(traits$survivor), col = c('red', 'blue'),
          pch = 16,ticktype = "detailed", bty = "b2",
          xlab = "Axis 1", ylab ="Axis 2", zlab = "Axis 3",
          colkey = list(at = c(1.25, 1.75),
```

```
                            addlines = TRUE, length = 0.3, width = 0.5,
                            labels = c("Die", "Survive")))
```
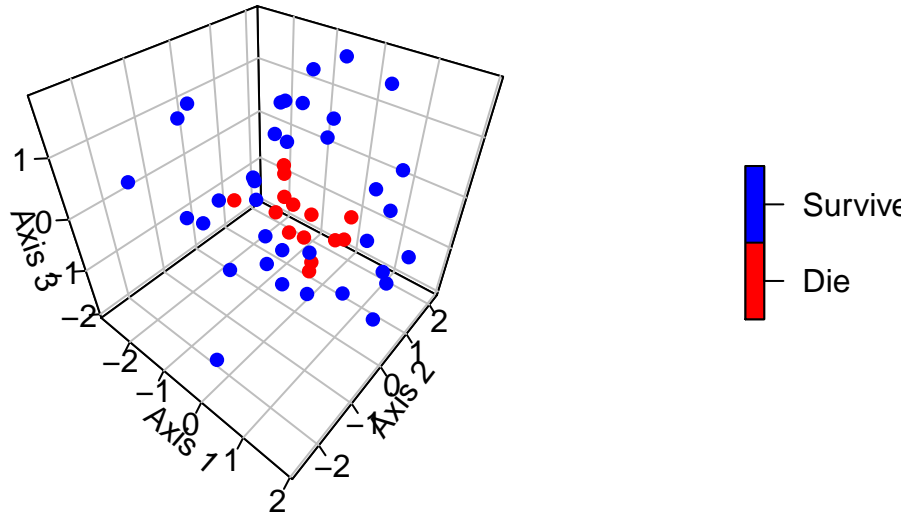


```
# Convex hull volume of the complete trait space
convex_complete <- convhulln(as.matrix(traits[,1:3]), "FA")
convex_complete$vol
```

```
## [1] 35.12198
```

```
# Convex hull volume of the trait space containing only survivors
convex_survivors <- convhulln(as.matrix(traits[-which(traits$survivor=="die"),1:3]), "FA")
convex_survivors$vol
```

```
## [1] 35.12198
```

```
# Hypervolume of the complete trait space
hyper_complete <- hypervolume_gaussian(traits[,1:3],
                            samples.per.point = 100,
                            kde.bandwidth = c(.1, .1, .1),
                            verbose = F)
get_volume(hyper_complete)
```

```
## untitled
## 3.585755
```

```
# Hypervolume of the trait space containing only survivors
hyper_survivors <- hypervolume_gaussian(traits[-which(traits$survivor=="die"),1:3],
                                        samples.per.point = 100,
                                        kde.bandwidth = c(.1, .1, .1),
                                        verbose = F)
get_volume(hyper_survivors)
```

```
## untitled
## 2.634919
```

The convex hull method was unable to identify changes in trait volume when these occur in the center of trait space. In contrast, the hypervolume prove to be sensitive to these changes, showing a reduction in hypervolume when data is removed from the center of trait space.

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

We used R version 3.6.0 (2019-04-26) and the following packages:

Package	version
kableExtra	1.1.0
plot3D	1.1.1
geiger	2.0.6.1
phylocurve	2.0.9
hypervolume	2.0.11
picante	1.8
phytools	0.6.60
pbapply	1.4.0
geometry	0.4.1
pgirmess	1.6.9

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