R Notebook

Directional change in community composition based on treatment identity

California NutNet

Background

- Global changes related to resource limtation are a well-studied phenomenon in ecology. Chronic nutrient enrichment, for example, is often expected to drive changes in community composition by altering competitive interactions.
- Many experiments that explore global change factors do so on relatively short timescales. However, these effects may not hold constant over time.
- Interactions between multiple drivers of resource limitation may be expected to produce nonlinear shifts in community dynamics that may contrast with those observed in short-term manipulative experiments.
- In particular, the strength of directional change in community composition is expected to be dependent on the nature of artificial resource enrichment (press vs. pulse) + other sources of environmental heterogeneity in a given system (e.g. Smith et al. 2009).
- When chronic nutrient deposition affects the primary axis of resource competition in community assembly, consistent directional change in community composition may be expected.
- However, when nutrient deposition interacts strongly with other drivers of resource limitation (such as normal environmental fluctuations, or extreme events, such as drought), community change may be strongly nonlinear/idiosyncratic

Study sites - NutNet has the advantage of (relatively) long-term datasets of community change across a number of sites in the United States. - Within both California and across the Great Plains, there are sites containing nutrient enrichment treatments across a gradient of climatic conditions (precipitation/temperature)

- California Nutrient Network sites
- American perennial grassland sites? Konza/CdrCreek/etc.

Some expectations: - All sites show changes in ANPP as a function of Nutrient enrichment + climate - Sites with the greatest sensitivity to climate in ANPP will show the least directional change - Sites with an annual life history (greater sensitivity / variability) will show less directional change - In all sites, nutrient enrichment will cause segregation of communities with respect to one another over time - Strength of nutrient enrichment in explaining multivariate dissimilaritiy between communities will depend on climate sensitivity

Steps:

1. Evaluate effects of nutrient enrichment on ANPP over time **(Siddharth, you have this data readily available?)**
2. Evaluate community directional change in response to nutrient enrichment over time.
3. Run ordination of multivariate community composition
4. PermDISP analysis of increasing dispersion over time
5. Evaluate significance of nutrient identity factors on community variance (CAP may be the best choice)

Data preprocessing

```
################################################################################
# Loading necessary packages
library(codyn) # Temporal analysis
```

```
## Warning: package 'codyn' was built under R version 3.4.3
```

```r
library(ggplot2) # Figure plotting
library(tidyverse) # Data manipulation
library(lubridate)
library(data.table)
library(vegetarian) # Exponentiated diversity indices (Hill Numbers)
library(lme4) # Linear mixed effects models
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 3.4.3
```

```r
###############################################################################
# Loading in dataset (up to 2017 data)
cov.long <- fread('C:/Users/ebatzer/Dropbox/NutNet Data/full-cover-04-December-2017.csv',
                  na.strings = c('NA','NULL'))

# Subsetting to just California sites
site.subset <- c("mcla.us", "hopl.us", "sier.us", "elliot.us", "sedg.us",
                 "cdcr.us", "konz.us", "cbgb.us", "trel.us", "cdpt.us")
cov.long <- cov.long[cov.long$site_code %in% site.subset,]

# Choose identifying variables
ids <- c('site_code','year','year_trt', 'block','plot','trt')
  cov.long[,unique(.SD),.SDcols=ids]
```

```
##        site_code year year_trt block plot        trt
##    1:    cdcr.us 2007        0     1    1  NPK+Fence
##    2:    cdcr.us 2007        0     1    2         NP
##    3:    cdcr.us 2007        0     1    3        NPK
##    4:    cdcr.us 2007        0     1    4          K
##    5:    cdcr.us 2007        0     1    6         PK
##   ---
## 3562:    trel.us 2013        5     3   26         NP
## 3563:    trel.us 2013        5     3   27         NK
## 3564:    trel.us 2013        5     3   28  NPK+Fence
## 3565:    trel.us 2013        5     3   29          P
## 3566:    trel.us 2013        5     3   30          K
```

```r
# Remove non-live percent cover esimates
cov.long[,max_cover:=as.numeric(max_cover)]
  cov.long <- cov.long[live==1]

# Cast long into wide
plot.sp.mat <- dcast(cov.long,site_code+year+block+plot+trt+year_trt ~ Taxon,value.var='max_cover',
                     fun.aggregate = sum,drop=T,fill=0)

# Checking total no. of observations and unique species IDs
dim(plot.sp.mat)
```

```
## [1] 3541  472
```

```r
###############################################################################
# Loading in climate data
```

**Constructing estimates of change in abundance-weighted diversity**

```r
# Defines the "jostAlpha" function to calculate Hill diversities
# I don't like the vegetarian function call of "d"
jostAlpha <- function(x, q){
  return(d(x, lev = "alpha", q = q, wts = FALSE))
}

# Apply alpha diversity calculation over all rows
# q = 2 (inverse simpson)
alpha.div2 <- apply(MARGIN = 1,
                    plot.sp.mat[,-(1:6)],
                    jostAlpha,
                    q = 2)

# q = 1 (exponentiated shannon)
alpha.div1 <- apply(MARGIN = 1,
                    plot.sp.mat[,-(1:6)],
                    jostAlpha,
                    q = 1)

# q = 0 (species richness)
alpha.div0 <- apply(MARGIN = 1,
                    plot.sp.mat[,-(1:6)],
                    jostAlpha,
                    q = 0)

# Combine into a single dataframe for plotting
alpha.byplot <- cbind(plot.sp.mat[,1:6],
                      alpha.div2,
                      alpha.div1,
                      alpha.div0)
```
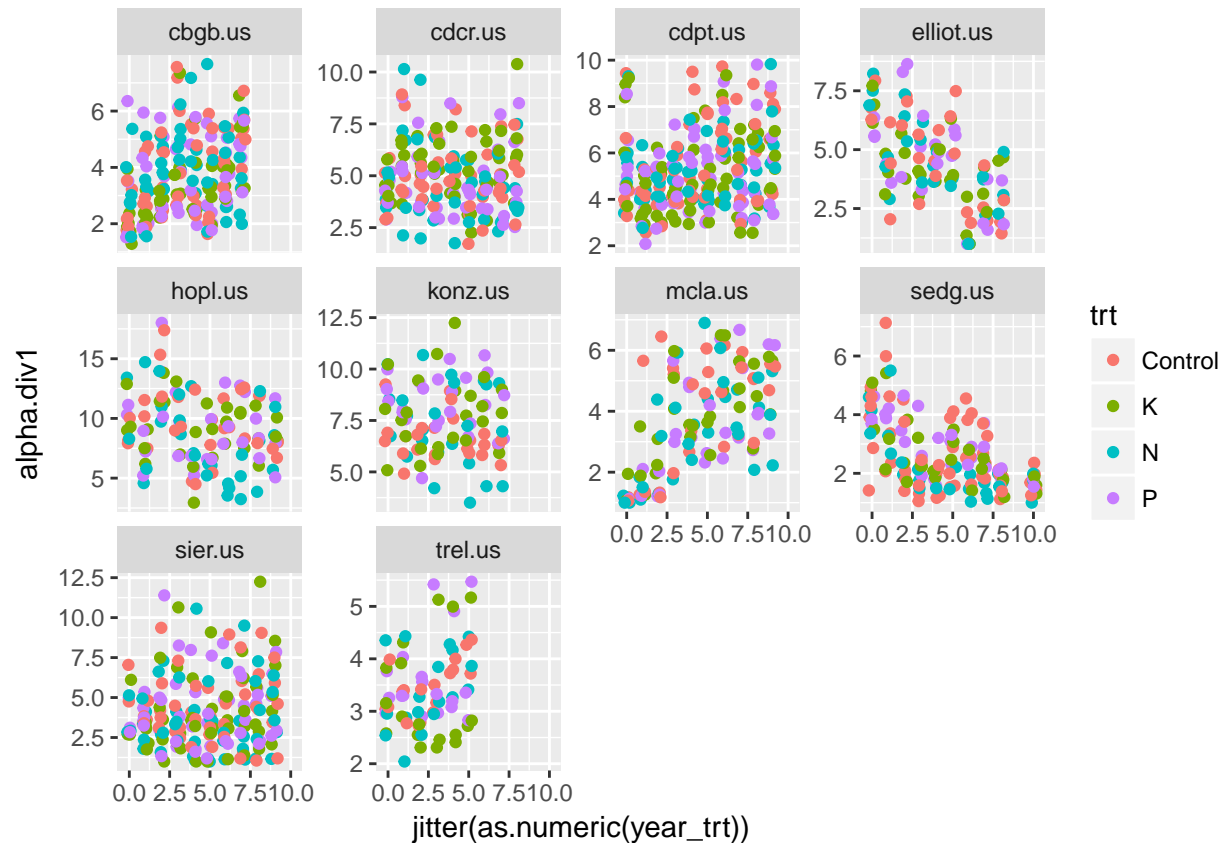
I was a little surprised by this result, so double-checked the shannon diversity richness values that are provided in the dropbox.

```
divstats <- read.csv("C:/Users/ebatzer/Dropbox/NutNet Data/plot_diversity_stats2-04-Dec-2017.csv")
trtlabels <- read.csv("C:/Users/ebatzer/Dropbox/NutNet Data/all-plot-descriptions-1-December-2017.csv")
divstats <- left_join(divstats, trtlabels)

## Joining, by = c("site_code", "block", "plot")

ggplot(aes(x = as.numeric(year),
           y = shan,
           color = Treatment),
       data = divstats[divstats$site_code %in% site.subset &
                         divstats$Treatment %in% trts,]) +
  facet_wrap(~site_code, scales = "free_y") +
  geom_point()
```
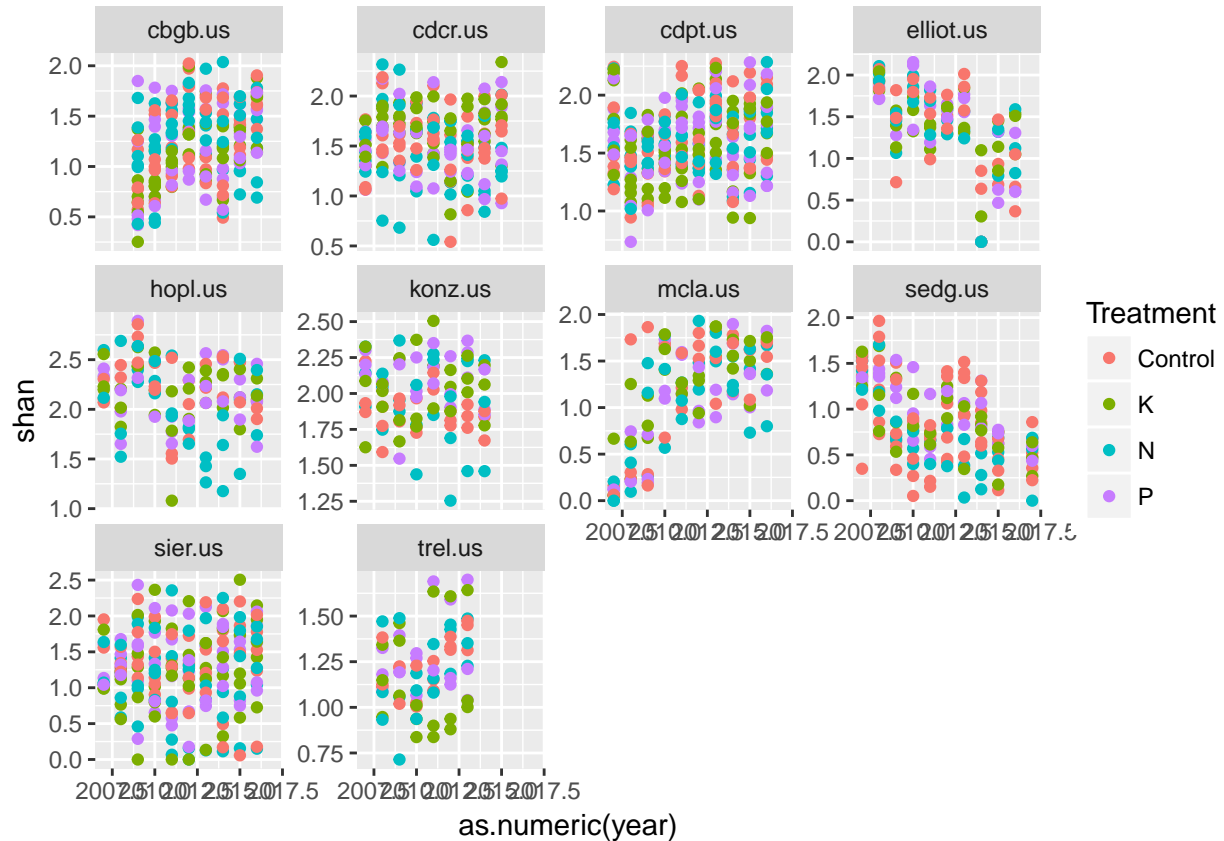
Conducting analysis of temporal change

```r
# Codyn package requires long-format data, so we'll stick with the cov.long dataset
# Subsetting to just include live taxa
tempvar.dat <- cov.long[cov.long$live == 1,]
tempvar.dat$year_trt <- as.numeric(tempvar.dat$year_trt)
tempvar.dat$max_cover <- sqrt(tempvar.dat$max_cover)

calcRateChange <- function(x){
  rc <- codyn::rate_change_interval(x,
                    time.var = "year_trt",
                    species.var = "Taxon",
                    abundance.var = "max_cover")
  return(rc)
}

calcRateChange_bray <- function(comdf, comvar, abundvar, timevar){
  # Take dataframe,
  # Cast by species variable and abundance
  # Take just numeric values
  # Assign to commat
  ssdf <- comdf[,colnames(comdf) %in% c(comvar, abundvar, timevar)]
  commat <- spread(data.frame(ssdf),
                   comvar,
```

```r
                       max_cover,
                       drop = TRUE,
                       fill = 0)

  # Calculate vegetation distance
  vd <- vegdist(commat[,-1], method = "bray")
  td <- dist(commat[,colnames(commat) == timevar])
  output <- cbind(interval = c(td), distance = c(vd))
  return(data.frame(output))
}

temp_ratechange_bray <- data.frame(tempvar.dat) %>% group_by(site_code, block, plot, trt) %>%
  do(calcRateChange_bray(., timevar = "year_trt",
                            comvar = "Taxon",
                            abundvar = "max_cover"))

# To confirm that the function is working properly:
newdf = tempvar.dat[tempvar.dat$site_code == "mcla.us" &
                        tempvar.dat$block == 1 &
                        tempvar.dat$plot == 1,]

ratechange_errorchecking <- calcRateChange_bray(data.frame(newdf),
                                                  timevar = "year_trt",
                                                  comvar = "Taxon",
                                                  abundvar = "max_cover")


# Plotting results
ggplot(aes(x = interval,
           y = distance,
           color = trt),
       data = temp_ratechange_bray[temp_ratechange_bray$trt %in% trts,]) +
  geom_point(alpha = .1) +
  facet_wrap(~site_code, scales = "free") +
  stat_smooth(method = "lm", se = FALSE)
```
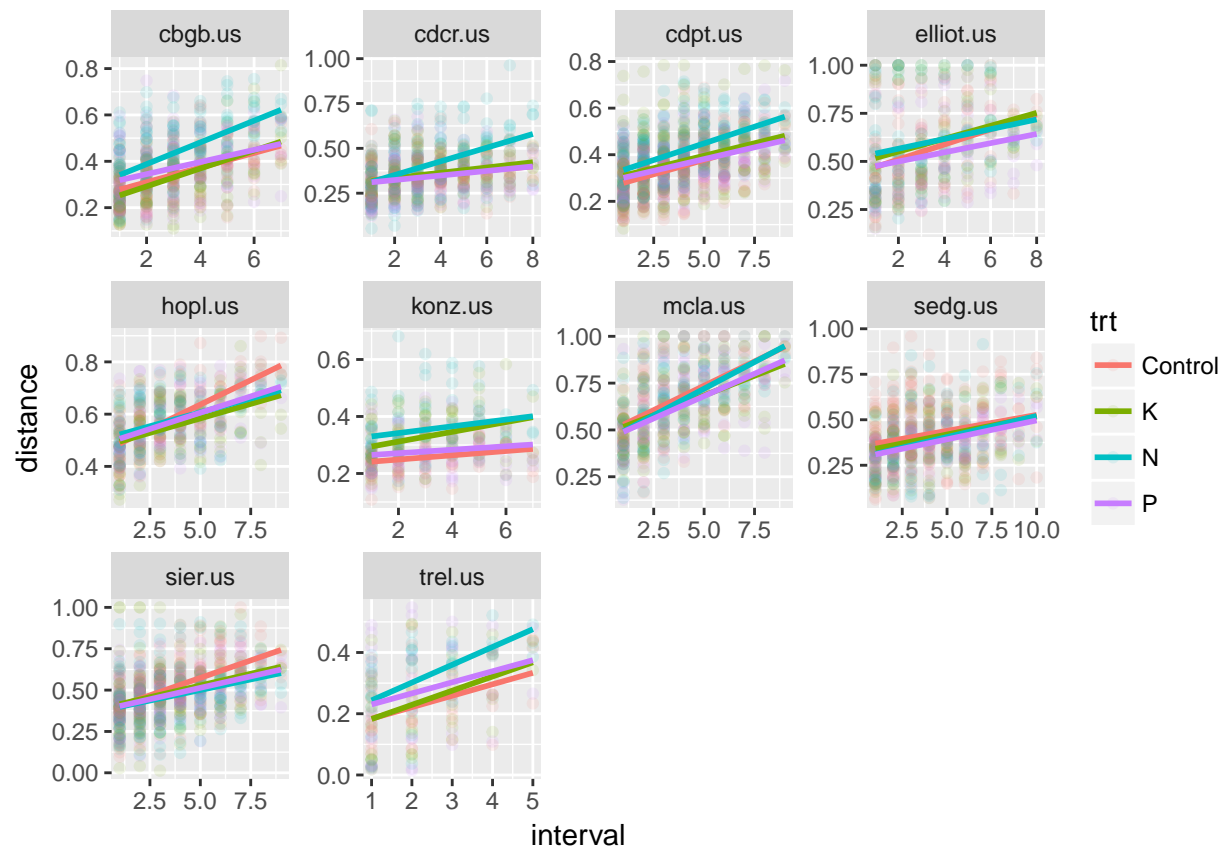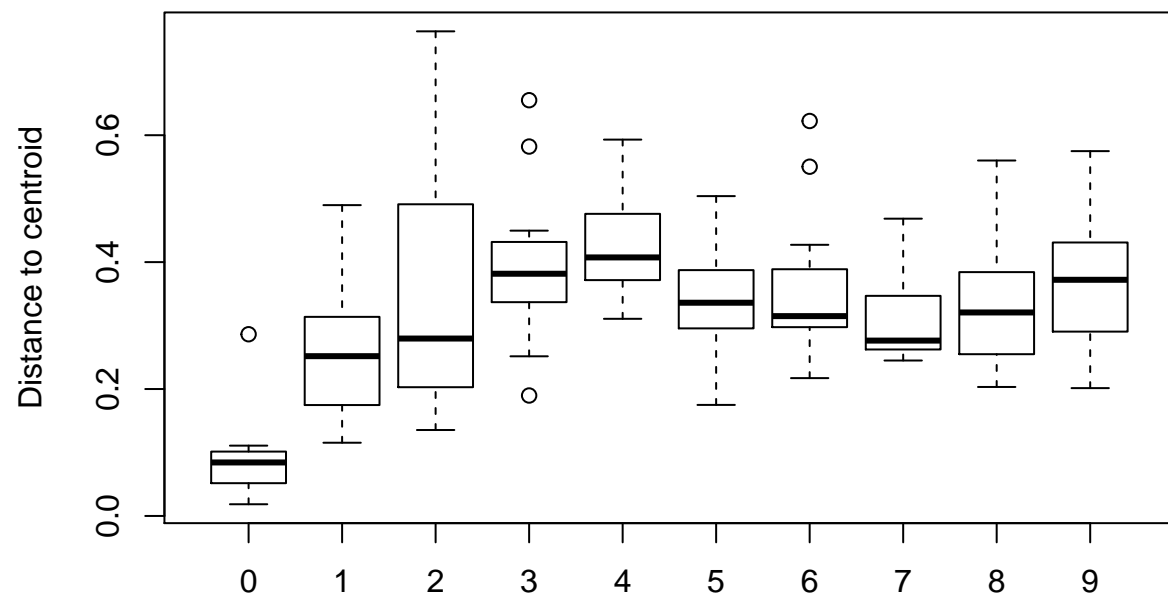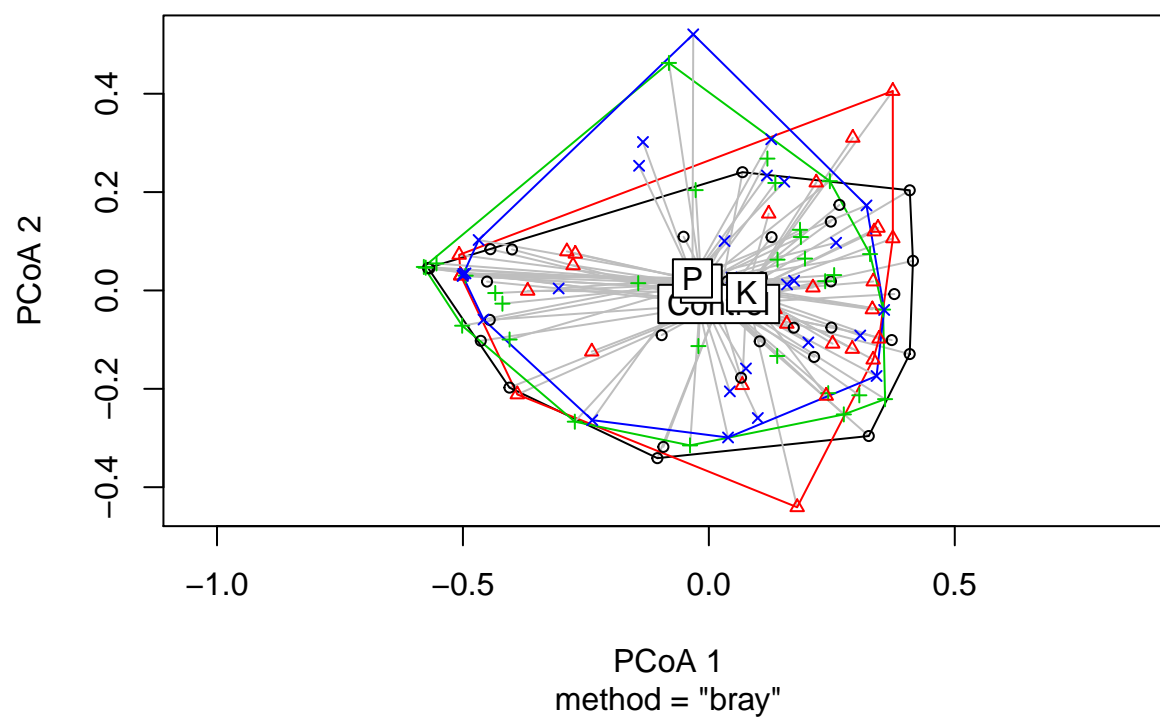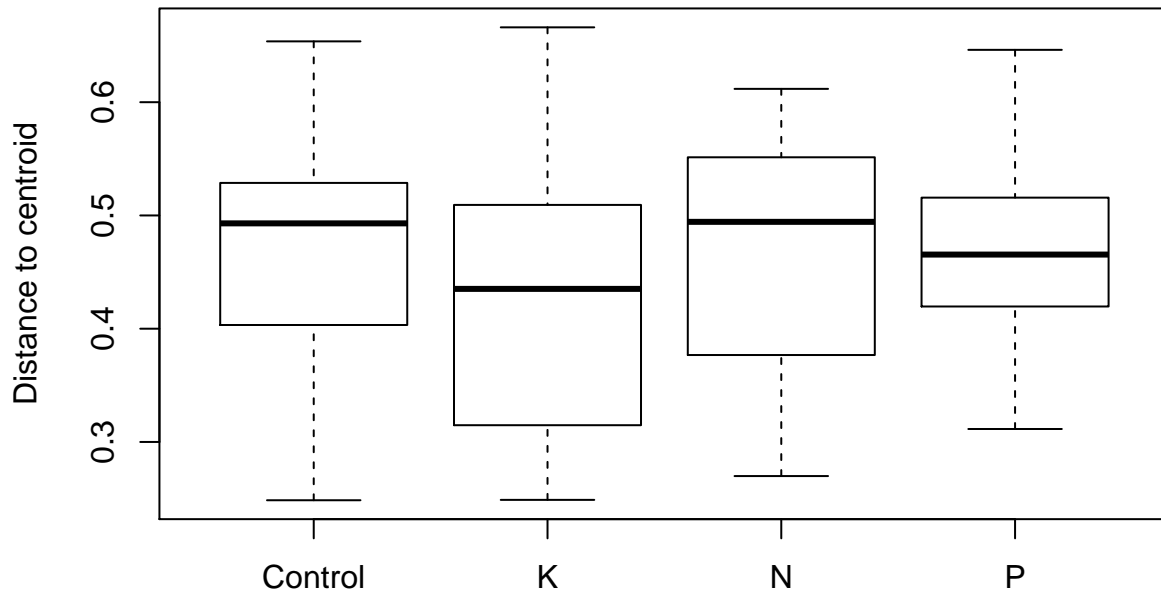
mcla.us Bray_Curtis PCoA by Year

PCoA 2

PCoA 1
method = "bray"

# mcla.us Bray_Curtis PCoA by Treatment

PCoA 1
method = "bray"
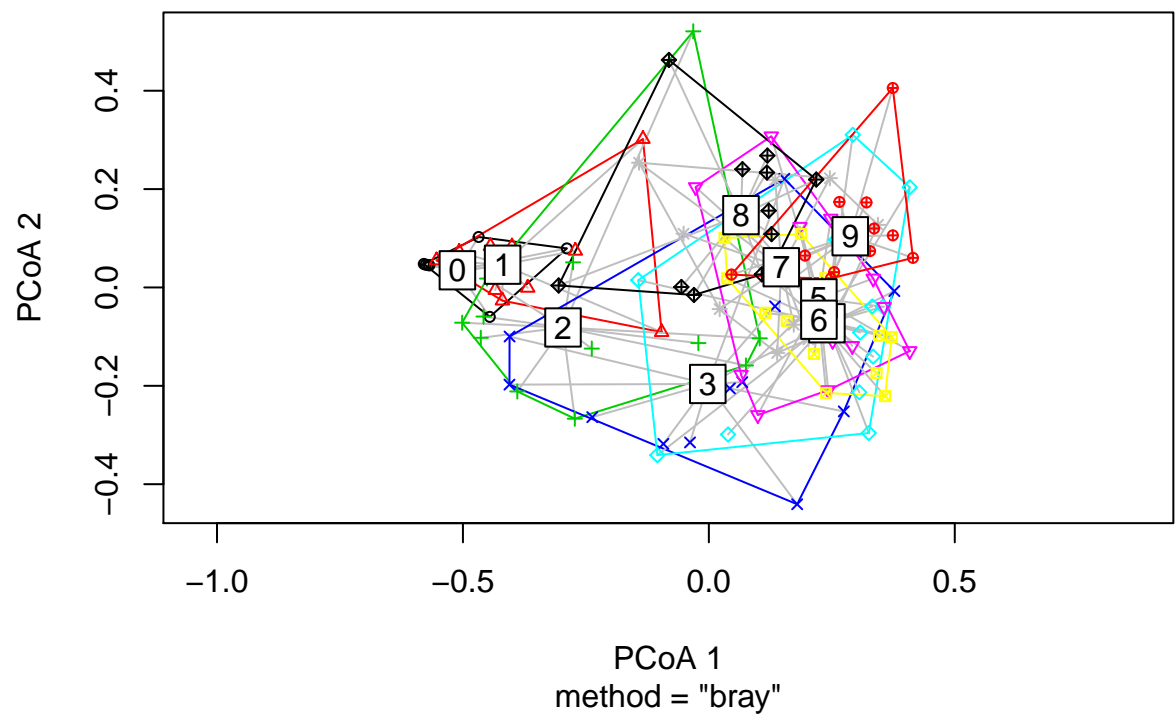
```
cap.full <- capscale(sp.mat ~ trt * as.numeric(year_trt) + as.factor(block),
        env.mat,
        distance = distmethod)

cap.full
```

```
## Call: capscale(formula = sp.mat ~ trt * as.numeric(year_trt) +
## as.factor(block), data = env.mat, distance = distmethod)
##
##               Inertia Proportion Eigenvals Rank
## Total         28.6210     1.0000   35.2701
## Constrained    8.8799     0.3103    9.2978     9
## Unconstrained 19.7410     0.6897   25.9724    49
## Imaginary                          -6.6492    69
## Inertia is squared Bray distance
##
## Eigenvalues for constrained axes:
##  CAP1  CAP2  CAP3  CAP4  CAP5  CAP6  CAP7  CAP8  CAP9
## 6.463 1.288 0.804 0.219 0.152 0.134 0.090 0.078 0.071
##
## Eigenvalues for unconstrained axes:
##  MDS1  MDS2  MDS3  MDS4  MDS5  MDS6  MDS7  MDS8
## 5.837 2.747 2.601 1.705 1.577 1.532 1.072 0.862
## (Showed only 8 of all 49 unconstrained eigenvalues)
```

```
screeplot(cap.full)
```
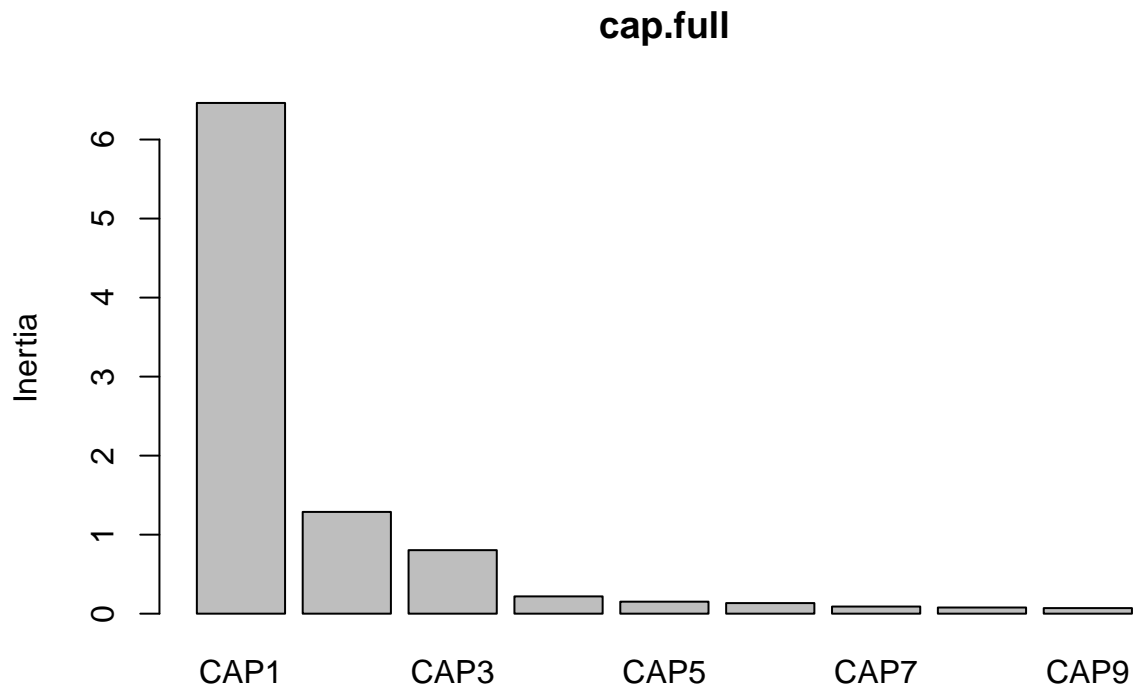
cap.full


```
varpart(sp.mat, ~ trt, ~ year_trt, data = env.mat)
```

```
##
## Partition of variance in RDA
##
## Call: varpart(Y = sp.mat, X = ~trt, ~year_trt, data = env.mat)
##
## Explanatory tables:
## X1:  ~trt
## X2:  ~year_trt
##
## No. of explanatory tables: 2
## Total variation (SS): 7124.2
##           Variance: 59.867
## No. of observations: 120
##
## Partition table:
##                 Df R.squared Adj.R.squared Testable
## [a+b] = X1        3   0.05779      0.03342    TRUE
## [b+c] = X2        9   0.36822      0.31653    TRUE
## [a+b+c] = X1+X2  12   0.42601      0.36164    TRUE
## Individual fractions
## [a] = X1|X2       3                0.04511    TRUE
## [b]               0               -0.01169    FALSE
```
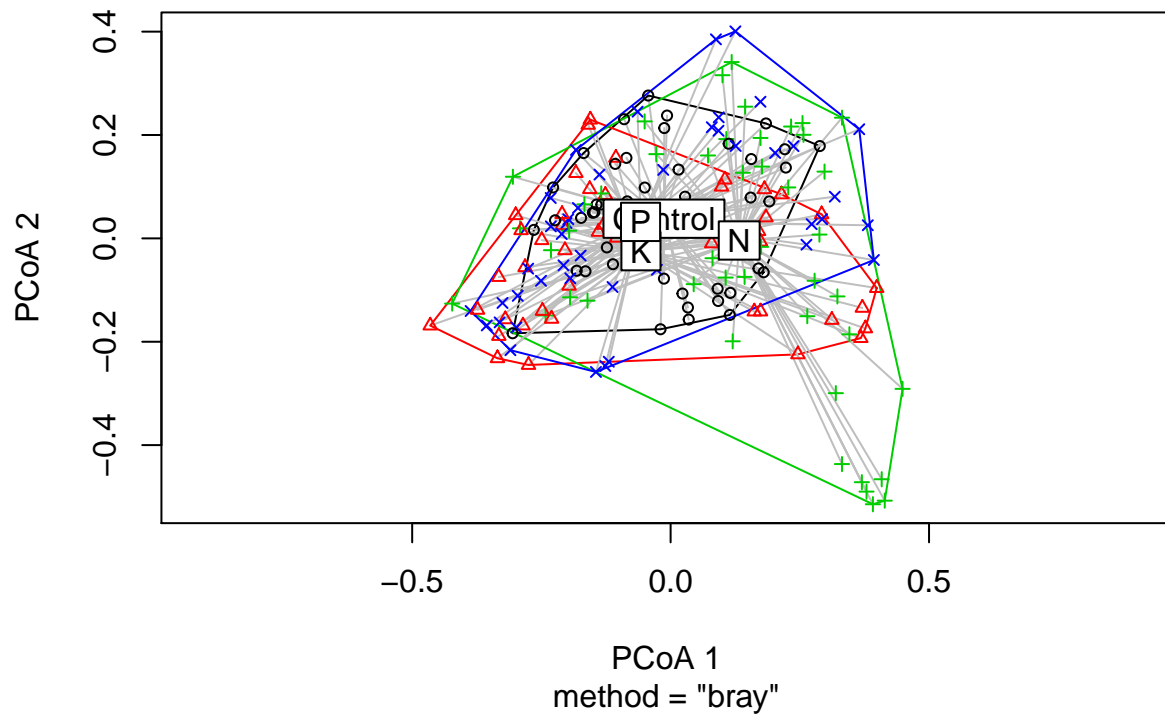
```
## [c] = X2|X1            9                 0.32822      TRUE
## [d] = Residuals                          0.63836      FALSE
## ---
## Use function 'rda' to test significance of fractions of interest
```
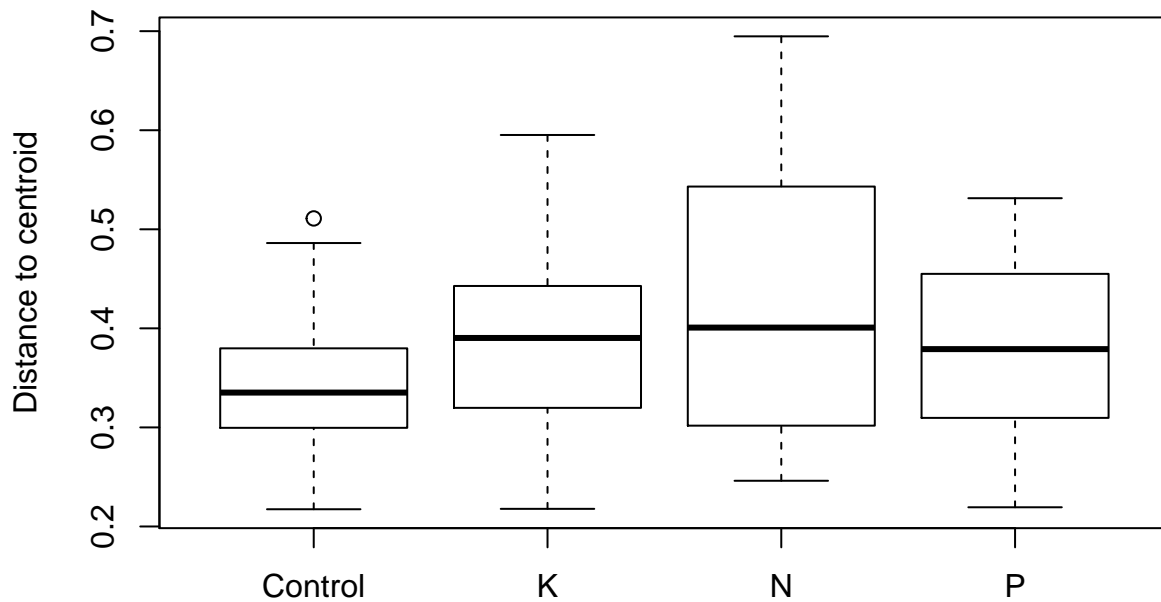
cdcr.us Bray_Curtis PCoA by Year

cdcr.us Bray_Curtis PCoA by Treatment

PCoA 1
method = "bray"
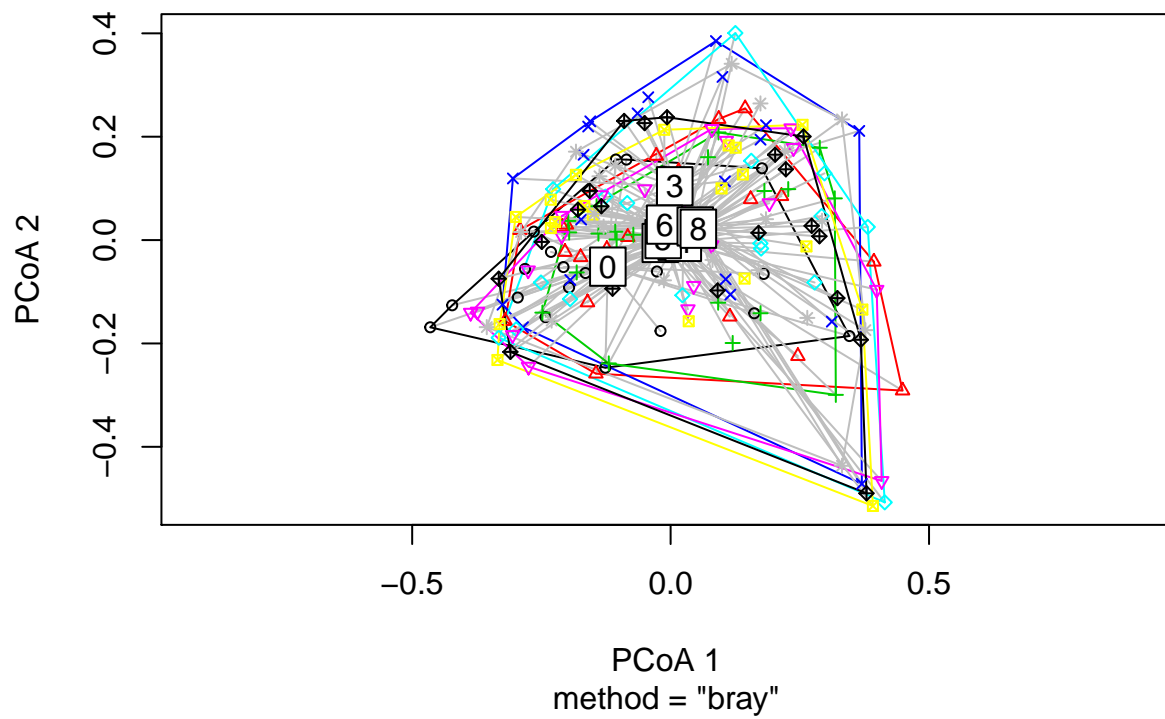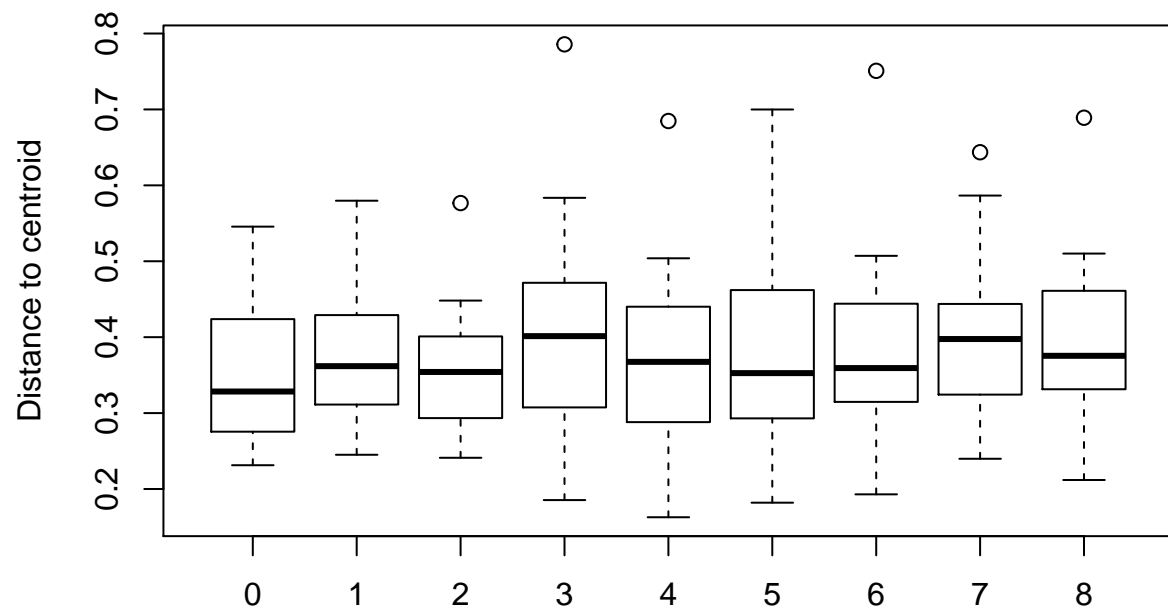
```
cap.full <- capscale(sp.mat ~ trt * year_trt + as.factor(block),
        env.mat,
        distance = distmethod)

cap.full
```
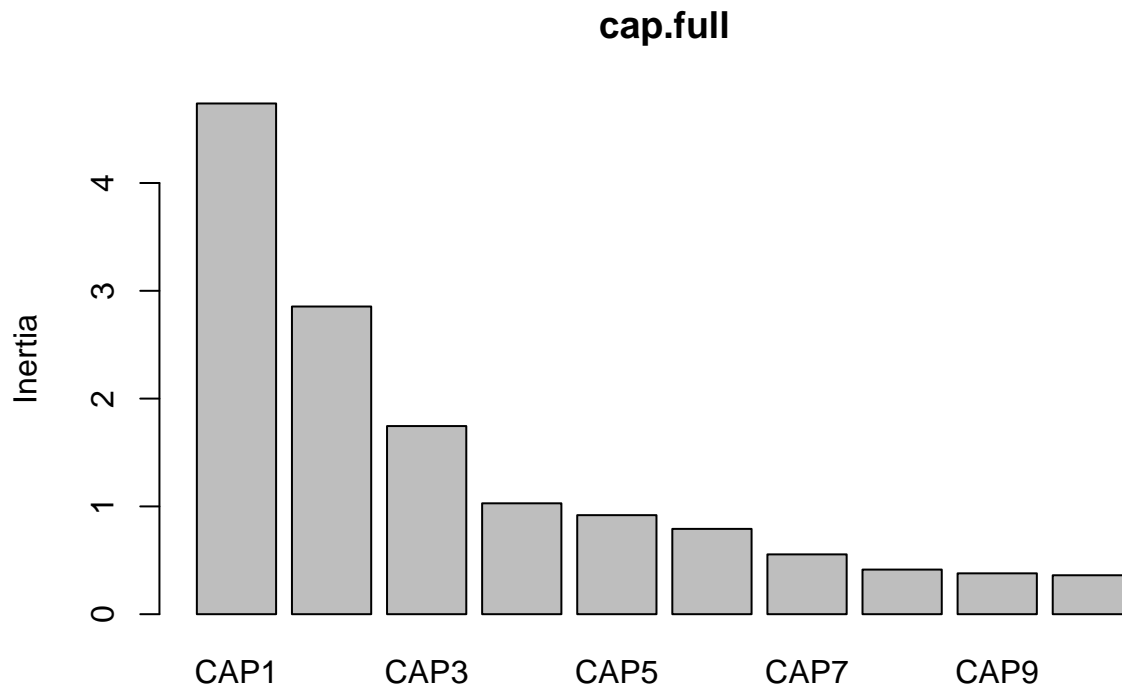
```
## Call: capscale(formula = sp.mat ~ trt * year_trt +
## as.factor(block), data = env.mat, distance = distmethod)
##
##                 Inertia Proportion Eigenvals Rank
## Total           30.7501     1.0000   39.8972
## Constrained     14.0031     0.4554   15.8340   39
## Unconstrained   16.7470     0.5446   24.0632   71
## Imaginary                             -9.1472  108
## Inertia is squared Bray distance
##
## Eigenvalues for constrained axes:
##   CAP1  CAP2  CAP3  CAP4  CAP5  CAP6  CAP7  CAP8  CAP9 CAP10 CAP11 CAP12
## 4.738 2.854 1.745 1.029 0.919 0.791 0.555 0.414 0.379 0.361 0.276 0.252
## CAP13 CAP14 CAP15 CAP16 CAP17 CAP18 CAP19 CAP20 CAP21 CAP22 CAP23 CAP24
## 0.213 0.180 0.152 0.121 0.116 0.096 0.082 0.078 0.062 0.056 0.049 0.043
## CAP25 CAP26 CAP27 CAP28 CAP29 CAP30 CAP31 CAP32 CAP33 CAP34 CAP35 CAP36
## 0.039 0.032 0.031 0.029 0.025 0.022 0.020 0.016 0.014 0.013 0.010 0.008
## CAP37 CAP38 CAP39
## 0.007 0.005 0.004
##
```

```
## Eigenvalues for unconstrained axes:
##  MDS1  MDS2  MDS3  MDS4  MDS5  MDS6  MDS7  MDS8
## 5.144 3.269 1.466 1.216 1.078 0.960 0.828 0.784
## (Showed only 8 of all 71 unconstrained eigenvalues)
```

```r
screeplot(cap.full)
```

cap.full


```r
varpart(sp.mat, ~ trt, ~ year_trt, data = env.mat)
```

```
##
## Partition of variance in RDA
##
## Call: varpart(Y = sp.mat, X = ~trt, ~year_trt, data = env.mat)
##
## Explanatory tables:
## X1:  ~trt
## X2:  ~year_trt
##
## No. of explanatory tables: 2
## Total variation (SS): 8272.4
##             Variance: 46.214
## No. of observations: 180
##
## Partition table:
##                 Df R.squared Adj.R.squared Testable
## [a+b] = X1       3   0.06242       0.04644     TRUE
## [b+c] = X2       8   0.08313       0.04023     TRUE
```

```
## [a+b+c] = X1+X2      11   0.14555        0.08960     TRUE
## Individual fractions
## [a] = X1|X2           3                  0.04937     TRUE
## [b]                   0                 -0.00293     FALSE
## [c] = X2|X1           8                  0.04316     TRUE
## [d] = Residuals                          0.91040     FALSE
## ---
## Use function 'rda' to test significance of fractions of interest
```