dcCADune.r

```r
rm(list=ls())
library(douconca)
data("dune_trait_env")

abun <-dune_trait_env$comm[, -1]  # must delete column/variable "Sites"
envData <- dune_trait_env$envir
traitData <- dune_trait_env$traits
names(envData)[c(3,4)] <- c("Moisture","Management")

mod_funct_traits <- dc_CA(
  formulaEnv = ~ Moisture + Management,
  formulaTraits = ~ SLA + Height + LDMC + Seedmass + Lifespan,
  response = abun, envData, traitData)

## Step 1: the CCA ordination of the transposed matrix with trait
constraints,
##          useful in itself and also yielding CWMs of the orthonormalized
traits for step 2.
## Call: cca(formula = tY ~ SLA + Height + LDMC +
## Seedmass + Lifespan, data = dataTraits)
##
## -- Model Summary --
##
##               Inertia Proportion Rank
## Total           2.3490     1.0000
## Constrained     0.6776     0.2885     5
## Unconstrained   1.6714     0.7115    19
##
## Inertia is scaled Chi-square
##
## -- Eigenvalues --
##
## Eigenvalues for constrained axes:
##    CCA1    CCA2    CCA3    CCA4    CCA5
## 0.26839 0.19597 0.12356 0.07003 0.01967
##
## Eigenvalues for unconstrained axes:
##    CA1    CA2    CA3    CA4    CA5    CA6    CA7    CA8
## 0.4386 0.2396 0.1938 0.1750 0.1429 0.1112 0.0854 0.0601
## (Showing 8 of 19 unconstrained eigenvalues)
##
## Step 2: the RDA ordination of CWMs of the orthonormalized traits
##         of step 1 with environmental constraints:
## Call: rda(formula = out1$CWMs_orthonormal_traits ~
## Moisture + Management, data = out1$data$dataEnv)
##
```

```
## -- Model Summary --
##
##               Inertia Proportion Rank
## Total          0.6776     1.0000
## Constrained    0.3485     0.5143    4
## Unconstrained  0.3291     0.4857    5
##
## Inertia is variance
##
## -- Eigenvalues --
##
## Eigenvalues for constrained axes:
##    RDA1    RDA2    RDA3    RDA4
## 0.23379 0.09752 0.01330 0.00387
##
## Eigenvalues for unconstrained axes:
##     PC1     PC2     PC3     PC4     PC5
## 0.15878 0.07151 0.05197 0.02864 0.01823
##
## mean, sd, VIF and canonical coefficients with their optimistic [!] t-
values:
##                Avg    SDS    VIF  Regr1  tval1
## Moisture      2.90 7.8613 1.3001 0.3391 6.3237
## ManagementBF 0.15 1.5969 1.4553 0.0348 0.6131
## ManagementHF 0.25 1.9365 1.4214 0.0402 0.7170
## ManagementNM 0.30 2.0494 1.4393 0.2792 4.9488
##                        Avg     SDS    VIF   Regr1
## SLA                24.6468  6.3438 1.1888 -0.8181
## Height             25.1272 15.6848 1.3033 -0.1122
## LDMC              244.5084 70.9729 1.1791 -0.0821
## Seedmass            0.6543  0.6688 1.0784 -0.7661
## Lifespanperennial   0.9607  0.1944 1.0964  0.1399
##                      tval1
## SLA                -3.5373
## Height             -0.4635
## LDMC               -0.3562
## Seedmass           -3.4781
## Lifespanperennial   0.6301
##
##                 weighted variance
## total                       2.349
## traits_explain              0.678
## constraintsTE               0.348
## attr(,"meaning")
##                 meaning
## total           "total inertia"
## traits_explain "trait-constrained inertia"
## constraintsTE  "trait-constrained inertia explained by the predictors in
formulaEnv"
```

```r
mod_ecol_traits <- dc_CA(
  formulaEnv = ~ Moisture + Management,
  formulaTraits = ~F+R+N+L,
  response = abun, envData, traitData, verbose = FALSE)
Y <- abun / rowSums(abun)
mod_cca <-cca(Y~Moisture+Management, data = envData)
mod_CCA <- dc_CA(formulaEnv = ~ Moisture+Management,
                 formulaTraits = ~Species,
                 response = abun, envData, traitData, verbose = FALSE)

##
## The model is overfitted with no unconstrained
## (residual) component

sum(eigenvals(mod_cca, model = "constrained")) # 0.967

## [1] 0.9670062

sum(mod_CCA$eigenvalues)                        # 0.967

## [1] 0.9670062

sum(mod_ecol_traits$eigenvalues)                # 0.567

## [1] 0.5674187

sum(mod_funct_traits$eigenvalues)               # 0.348

## [1] 0.3484763

#
set.seed(1457)
anova(mod_ecol_traits, by = "axis") # axis 1 P =  0.001 axis 2 0.003

## $species
## Species-level permutation test using dc-CA
## Model: dc_CA(formulaEnv = ~Moisture + Management, formulaTraits = ~F + R +
N + L, response = abun, dataEnv = envData, dataTraits = traitData, verbose =
FALSE)
## Residualized predictor permutation
##
##           df ChiSquare      R2        F Pr(>F)
## dcCA1      1   0.34359 0.35531 19.7768   0.001 ***
## dcCA2      1   0.21586 0.22322 12.4246   0.001 ***
## dcCA3      1   0.00790 0.00817  0.4547   0.964
## dcCA4      1   0.00007 0.00007  0.0042   1.000
## Residual 23   0.39959
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $sites
```

```
##            Df ChiSquare      R2        F Pr(>F)
## dcCA1      1   0.34359 0.39491 17.0301  0.001 ***
## dcCA2      1   0.21586 0.24810 10.6990  0.003 **
## dcCA3      1   0.00790 0.00908  0.3915  0.964
## dcCA4      1   0.00007 0.00008  0.0036  1.000
## Residual 15   0.30263
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $max
## Max test combining the community- and species- level tests
## Model: dc_CA(formulaEnv = ~Moisture + Management, formulaTraits = ~F + R +
N + L, response = abun, dataEnv = envData, dataTraits = traitData, verbose =
FALSE)
##
## a mix the species- (traits) and community- (environment) levels:
##
##            df ChiSquare       F traitP  envP Pr(>F)
## dcCA1      1   0.34359 17.0301  0.001 0.001  0.001 ***
## dcCA2      1   0.21586 12.4246  0.001 0.003  0.003 **
## dcCA3      1   0.00790  0.4547  0.964 0.964  0.964
## dcCA4      1   0.00007  0.0042  1.000 1.000  1.000
## Residual 23   0.39959
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
anova(mod_funct_traits, by = "axis")# axis 1 P =  0.048 axis 2 0.427
```

```
## $species
## Species-level permutation test using dc-CA
## Model: dc_CA(formulaEnv = ~Moisture + Management, formulaTraits = ~SLA +
Height + LDMC + Seedmass + Lifespan, response = abun, dataEnv = envData,
dataTraits = traitData)
## Residualized predictor permutation
##
##            df ChiSquare       R2        F Pr(>F)
## dcCA1      1   0.23379 0.241767 8.3155  0.048 *
## dcCA2      1   0.09752 0.100851 3.4687  0.427
## dcCA3      1   0.01330 0.013751 0.4730  0.998
## dcCA4      1   0.00387 0.003998 0.1375  1.000
## Residual 22   0.61853
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $sites
##            Df ChiSquare      R2        F Pr(>F)
## dcCA1      1   0.23379 0.34502 10.6545  0.001 ***
```

```
## dcCA2      1    0.09752 0.14392   4.4444   0.044 *
## dcCA3      1    0.01330 0.01962   0.6060   0.916
## dcCA4      1    0.00387 0.00571   0.1762   0.957
## Residual 15    0.32914
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $max
## Max test combining the community- and species- level tests
## Model: dc_CA(formulaEnv = ~Moisture + Management, formulaTraits = ~SLA +
## Height + LDMC + Seedmass + Lifespan, response = abun, dataEnv = envData,
## dataTraits = traitData)
##
## Taken from the species-level test:
## Residualized predictor permutation
## Permutation: free
## Number of permutations: 999
##
##            df ChiSquare       R2       F Pr(>F)
## dcCA1      1    0.23379 0.241767  8.3155   0.048 *
## dcCA2      1    0.09752 0.100851  3.4687   0.427
## dcCA3      1    0.01330 0.013751  0.4730   0.998
## dcCA4      1    0.00387 0.003998  0.1375   1.000
## Residual 22    0.61853
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```