

dcCAWisconsin.r

```
rm(list=ls(all=TRUE)) # remove all existing items from the workspace

resp<- read.csv("data/Wisconsin_response.csv")
names(resp)[1:10]

## [1] "X"          "Actaepachy" "Adianpedat" "Ageraaltis" "Agrimgrypo"
## [6] "Alliapetio" "Alliutrico" "Ambroartem" "Ambrotrifi" "Amphibract"

Y <- resp[, -1]; rownames(resp) <- resp[, "X"]
envir<- read.csv("data/Wisconsin_envir.csv")[, -1]
envir$site<- paste0("site", round(envir$site,0))
traits<- read.csv("data/Wisconsin_traits.csv")
names(envir)

## [1] "site" "quads" "Lat" "Long" "MAT" "MAP" "TSD"
## [8] "PCV" "X.Sand" "X.N" "BA"

names(traits)

## [1] "X" "sp" "SLA" "VH" "LCC" "LS" "CN" "LT" "LNC"
## [10] "LDMC"

envir$BA <- sqrt(envir$BA)
envir$X.N <- log(envir$X.N)
summary(traits)

##           X           sp           SLA           VH
## Min.      : 1   Length:185   Min.      : 102.8   Min.      : 5.333
## 1st Qu.: 47   Class :character 1st Qu.: 273.6   1st Qu.: 21.750
## Median : 93   Mode  :character Median : 362.1   Median : 42.667
## Mean      : 93                Mean      : 389.5   Mean      : 49.636
## 3rd Qu.:139                3rd Qu.: 473.3   3rd Qu.: 65.417
## Max.      :185                Max.      :1140.8   Max.      :285.667
##           LCC           LS           CN
## Min.      :37.41   Min.      : 0.0486   Min.      : 7.609
## 1st Qu.:42.77   1st Qu.: 13.7969   1st Qu.:13.606
## Median :44.33   Median : 31.2816   Median :16.742
## Mean      :44.16   Mean      :110.0357   Mean      :17.727
## 3rd Qu.:45.83   3rd Qu.: 80.6262   3rd Qu.:20.738
## Max.      :48.27   Max.      :2472.8583   Max.      :43.459
##           LT           LNC           LDMC
## Min.      :0.07106   Min.      :0.01036   Min.      :0.06807
## 1st Qu.:0.15967   1st Qu.:0.02146   1st Qu.:0.17952
## Median :0.20324   Median :0.02571   Median :0.22549
## Mean      :0.22066   Mean      :0.02738   Mean      :0.23668
## 3rd Qu.:0.25200   3rd Qu.:0.03308   3rd Qu.:0.29316
## Max.      :0.68700   Max.      :0.06047   Max.      :0.54234
```

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nams<- c("SLA","VH","LS","CN","LT") #log transformed
for (k in nams) traits[[k]] <- log(traits[[k]])
names(traits)[3] <- "LMA"; traits[,3] <- - traits[,3]
names(traits)

## [1] "X"      "sp"     "LMA"    "VH"     "LCC"    "LS"     "CN"     "LT"     "LNC"
## [10] "LDMC"

keytraits <- c("VH","LS","LMA","LCC")
keyenv <- c("MAT","MAP","TSD","X.Sand","X.N","BA")

formulaEnvkey <- as.formula(paste0("~", paste(keyenv,collapse = "+")))
formulaTraitskey <- as.formula(paste0("~", paste(keytraits,collapse = "+")))

library(douconca)
divide = TRUE
mod1 <- dc_CA(formulaEnv = formulaEnvkey,formulaTraits = formulaTraitskey,
               response = Y, dataEnv = enviro, dataTraits = traits,
               divideBySiteTotals = divide)

## 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 ~ VH + LS + LMA + LCC, data = dataTraits)
##
## -- Model Summary --
##
##              Inertia Proportion Rank
## Total          8.00948    1.00000
## Constrained    0.69794    0.08714    4
## Unconstrained  7.31154    0.91286   179
##
## Inertia is scaled Chi-square
##
## -- Eigenvalues --
##
## Eigenvalues for constrained axes:
##   CCA1  CCA2  CCA3  CCA4
## 0.4492 0.1395 0.0700 0.0392
##
## Eigenvalues for unconstrained axes:
##   CA1  CA2  CA3  CA4  CA5  CA6  CA7  CA8
## 0.5359 0.4100 0.3389 0.2853 0.2578 0.2482 0.2342 0.2172
## (Showing 8 of 179 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 ~ MAT + MAP + TSD

```

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## + X.Sand + X.N + BA, data = out1$data$dataEnv)
##
## -- Model Summary --
##
##              Inertia Proportion Rank
## Total          0.6979      1.0000
## Constrained    0.3731      0.5346    4
## Unconstrained  0.3248      0.4654    4
##
## Inertia is variance
##
## -- Eigenvalues --
##
## Eigenvalues for constrained axes:
##   RDA1   RDA2   RDA3   RDA4
## 0.3358 0.0315 0.0055 0.0003
##
## Eigenvalues for unconstrained axes:
##   PC1    PC2    PC3    PC4
## 0.11926 0.10911 0.06018 0.03626
##
## mean, sd, VIF and canonical coefficients with their optimistic [!] t-
values:
##           Avg      SDS      VIF   Regr1   tval1
## MAT       7.4346  18.6444  1.8605 -0.4633 -13.6170
## MAP      871.1496 671.3967  1.3141 -0.0373  -1.3032
## TSD       11.1728   6.1386  1.3080 -0.1323  -4.6380
## X.Sand    51.3152 290.7371  1.5450  0.0704   2.2707
## X.N       -1.3053   7.2435  1.4969 -0.1861  -6.0980
## BA         4.8269  12.2454  1.0815  0.0184   0.7076
##           Avg      SDS      VIF   Regr1   tval1
## VH       3.4328  0.6483  1.2462 -0.5975  -7.7126
## LS       4.0828  1.5063  1.3598 -0.0276  -0.3414
## LMA     -6.0860  0.3689  1.0817  0.5688   7.8794
## LCC     44.4614  2.0866  1.1830  0.3462   4.5858
##
##           weighted variance
## total                8.009
## traits_explain        0.698
## constraintsTE          0.373
## attr(,"meaning")
##           meaning
## total          "total inertia"
## traits_explain "trait-constrained inertia"
## constraintsTE  "trait-constrained inertia explained by the predictors in
formulaEnv"

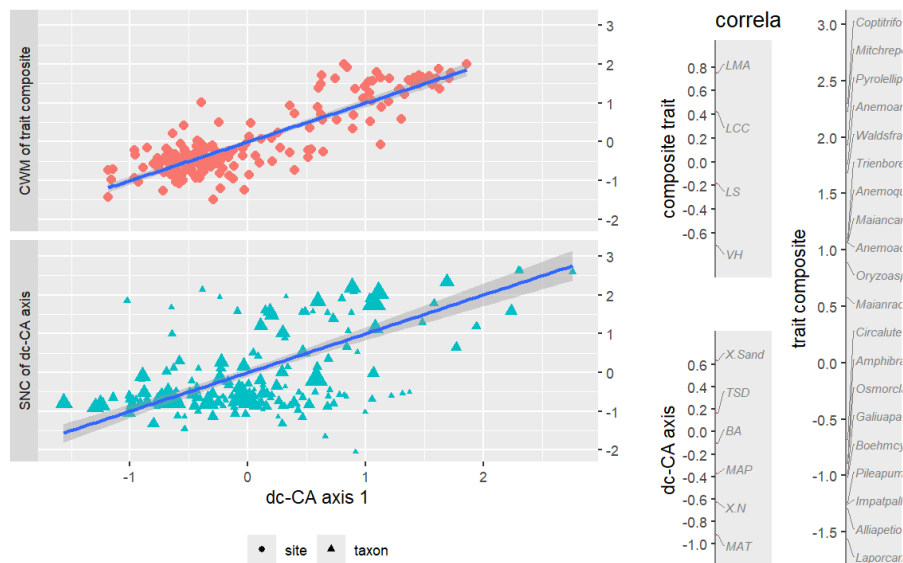
set.seed(1457)
anova(mod1,by="axis")
```

```

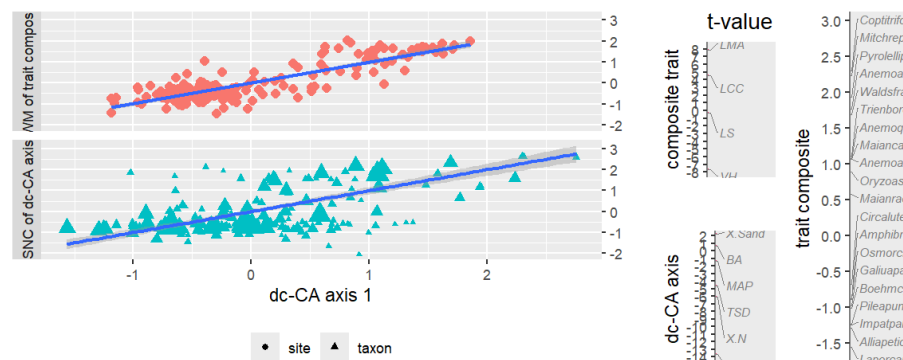
## $species
## Species-level permutation test using dc-CA
## Model: dc_CA(formulaEnv = formulaEnvkey, formulaTraits = formulaTraitskey,
response = Y, dataEnv = envir, dataTraits = traits, divideBySiteTotals =
divide)
## Residualized predictor permutation
##
##           df ChiSquare      R2      F Pr(>F)
## dcCA1      1   0.33581 0.259882 65.7702 0.001 ***
## dcCA2      1   0.03147 0.024356  6.1641 0.502
## dcCA3      1   0.00550 0.004253  1.0764 0.984
## dcCA4      1   0.00034 0.000262  0.0664 1.000
## Residual 180   0.91906
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $sites
##           Df ChiSquare      R2      F Pr(>F)
## dcCA1      1   0.33581 0.48115 190.2322 0.001 ***
## dcCA2      1   0.03147 0.04509  17.8288 0.001 ***
## dcCA3      1   0.00550 0.00787   3.1133 0.319
## dcCA4      1   0.00034 0.00049   0.1921 1.000
## Residual 184   0.32481
## ---
## 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 = formulaEnvkey, formulaTraits = formulaTraitskey,
response = Y, dataEnv = envir, dataTraits = traits, divideBySiteTotals =
divide)
##
## Taken from the species-level test:
## Residualized predictor permutation
## Permutation: free
## Number of permutations: 999
##
##           df ChiSquare      R2      F Pr(>F)
## dcCA1      1   0.33581 0.259882 65.7702 0.001 ***
## dcCA2      1   0.03147 0.024356  6.1641 0.502
## dcCA3      1   0.00550 0.004253  1.0764 0.984
## dcCA4      1   0.00034 0.000262  0.0664 1.000
## Residual 180   0.91906
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# the default plot
plot(mod1) # gradient_description = "correlation"

```



```
plot(mod1, gradient_description = "tvalues")
```



```
# nitty-gritty, adapt names, change widths, and flip the axis -----
# adapt names
newnames <- getPlotdata(mod1)$newNameList$newnames
newnames$env[4:5] <- c("%Sand", "%N")
plot(mod1, gradient_description = "tvalues", widths = c(3,1,1), newnames =
newnames, flip_axis = TRUE, expand = 1.5)
```

