

Multivariate Statistics in Ecology and Quantitative Genetics

Canonical correspondence analysis

Dirk Metzler & Noémie Becker

http://evol.bio.lmu.de/_statgen

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- 1 Canonical correspondence analysis
 - Setting
 - Mathematical background
 - The CCA triplot
 - Example: Mexican plant data
 - When to use PCA, RDA, CA or CCA

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 $Y[i, \cdot]$ are the observations of species i
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Assumption: There is a niche dependence of the species on environmental factors

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Let Y have M rows and N columns and let X have M rows and Q columns. The site scores (l_1, l_2, \dots, l_M) in the Gaussian response model

$$Y[i, k] \approx C_k \exp\left(-\frac{(l_i - u_k)^2}{2t_k^2}\right)$$

are now assumed to be a linear combination of our environmental variables, that is,

$$l_i = \sum_{p=1}^Q X[i, p] \alpha[p].$$

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Canonical correspondence analysis is realized by a correspondence analysis in which weighted multiple regression is used to represent the axes as linear combination of the explanatory variables.

So CCA is a CA with the axes being linear combinations of the explanatory variables.

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The species scores, the site scores and the environmental scores are plotted in a figure called a triplot (confer with triplots in RDA). These triplots are the biplots from CA with additionally the explanatory variables plotted as lines.

Again the position of a species represents the optimum value in terms of the Gaussian response model (niche) along the first and second axes. For this reason, species scores are represented as labels or points.

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Again the position of a species represents the optimum value in terms of the Gaussian response model (niche) along the first and second axes. For this reason, species scores are represented as labels or points.

In addition: Species can be projected perpendicular (=orthogonally) on the lines showing the species optima of the respective explanatory variables (in the respective scaling). Projecting sites perpendicular on the lines results in the values of the respective environmental variable at those sites.

The angle between lines does NOT represent correlation between the variables. Instead if the tip of a line is projected on another line or an axis then the resulting value represents a weighted correlation.

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The data has been explained in part on the slides on CA.

```
mplants<-read.table("MexicanPlants.txt",h=T,sep="\t")
species<-mplants[,c("ac","as","co","com","cy","eu",
                    "grcyn","grresto","la","le","ma",
                    "ru","so","vi","vit")]
env_var<-mplants[,c("MAXVEGHEIGHT","AGE",
                    "ALTITUDE","BAREDSOIL")]

library(vegan)
mplants_CCA<-cca(species, env_var)
```

```
# the total variation in the data is: 0.33
round(mplants_CCA$tot.chi, 2)

# the sum of all canonical eigenvalues: 0.15
round(mplants_CCA$CCA$tot.chi, 2)

# all four explanatory variables explain
cat(round(mplants_CCA$CCA$tot.chi
        /mplants_CCA$tot.chi*100), "% of data", "\n")
# 46% of the total variation in the data

# the first two (canonical) eigenvalues are: 0.10, 0.02
round(mplants_CCA$CCA$eig[1:2], 2)
```

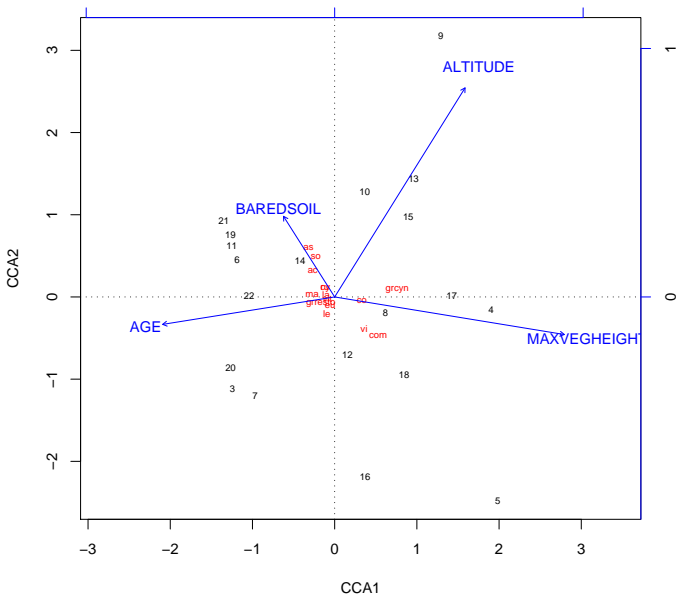


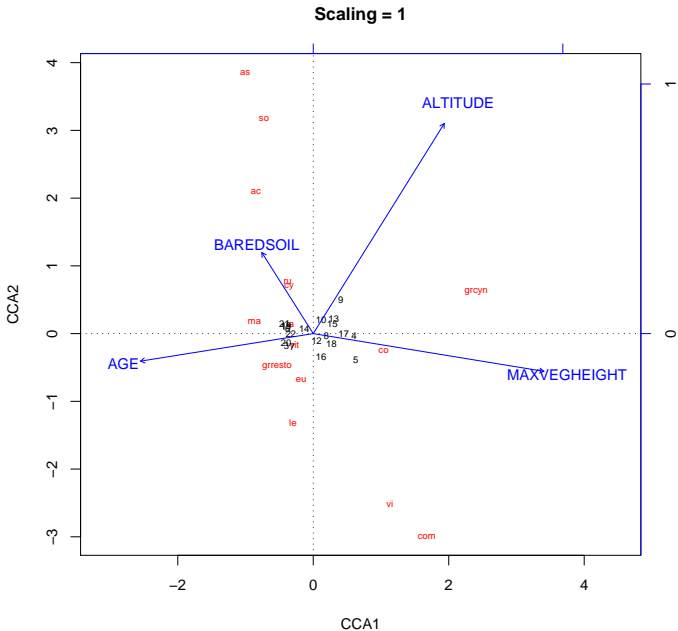
```
# so the first two canonical axes explain:
cat(round(sum(mplants_CCA$CCA$eig[1:2])
      /mplants_CCA$CCA$tot.chi*100), "%", "\n")
# 82% of the variation that can be explained
# with the four environmental variables

# but this is (the first two canonical axes explain):
cat(round(sum(mplants_CCA$CCA$eig[1:2])
      /mplants_CCA$tot.chi*100), "%", "\n")
# 37% of the total variation in the data

plot(mplants_CCA, scaling = 2, main="Scaling2")
plot(mplants_CCA, scaling = 1, main="Scaling1")
```

Scaling = 2





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When PCA, RDA, CA, CCA?

Summary of methods:

- Relationships in PCA and RDA are linear.
- In RDA and CCA two sets of variables are used, and a cause-effect relationship is assumed.

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	Pure ordination	Cause-effect relation
Linear model	PCA	RDA
Unimodal model	CA	CCA