Training in ade4 in R - Module I: Basic methods

Correspondence analysis and Principal Coordinates Analysis

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Data structure

- One table with *n* rows and *m* columns
- Data are counts of individuals (sums by row and columns are meaningful)
- For instance
  - sites $\times$ species

Objectives

- Identify what is the main information contained in the table
    - Identify the principal differences/similarities between row categories
    - Identify the principal differences/similarities between column categories
    - Identify the principal differences/similarities between row and column categories

Data

We consider the `meaudret` data set

```
library(ade4)
data(meaudret)
names(meaudret)
```

```
## [1] "env"       "design"    "spe"       "spe.names"
```

```
dim(meaudret$spe)
```

```
## [1] 20 13
```

```
head(meaudret$spe.names)
```

```
## [1] "Ephemera_danica" "Baetis_sp"       "Baetis_rhodani"  "Baetis_niger"
## [5] "Baetis_muticus"  "Centroptilum_sp"
```

The data set contains the abundances of 13 Ephemeroptera species in 20 samples. The measurements have been made in 5 sites at each season along a small French stream (see `?meaudret`)

```
head(meaudret$design)
```

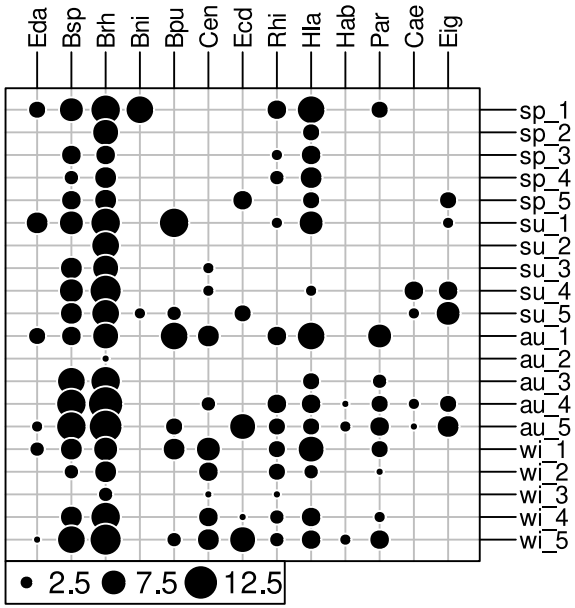
```
##      season site
## sp_1 spring   S1
## sp_2 spring   S2
## sp_3 spring   S3
## sp_4 spring   S4
## sp_5 spring   S5
## su_1 summer   S1
```

We want to know

- which species have similar distributions
- which sites have similar composition
- which species are mainly present in which sites

Contingency table

```
library(adegraphics)
table.value(meaudret$spe, symbol
```




```
head(rowSums(meaudret$spe))
```

```
## sp_1 sp_2 sp_3 sp_4 sp_5 su_1
##   48   12   17   18   24   44
```

```
head(colSums(meaudret$spe))
```

```
## Eda Bsp Brh Bni Bpu Cen
##  20 104 163  11  35  37
```

```
sum(meaudret$spe)
```

```
## [1] 595
```

Chi-square test

The χ^2 test allows to measure and evaluate the significance of the association between species and sites (the null hypothesis is the random distribution)

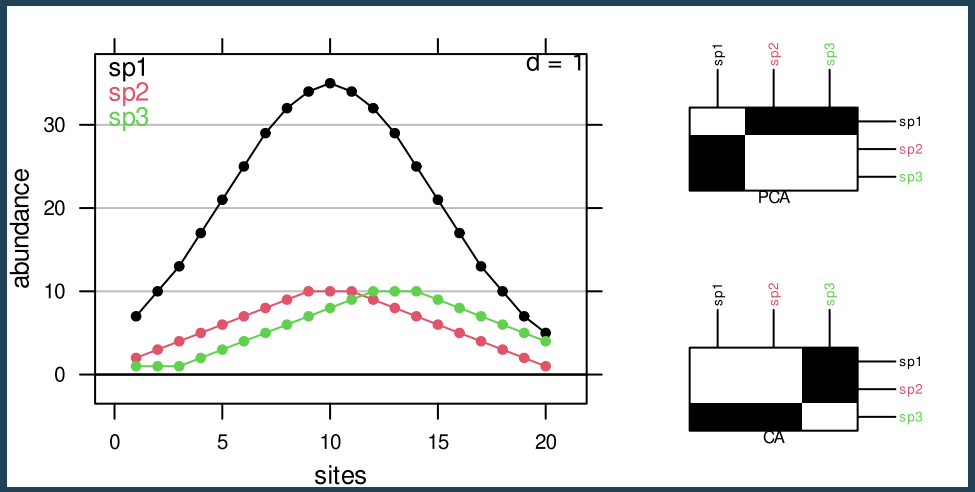
$$\chi^2_{obs} = \sum_{i=1}^{I}\sum_{j=1}^{J} \frac{\left(y_{ij} - \frac{y_{i.}\, y_{.j}}{y_{..}}\right)^2}{\frac{y_{i.}\, y_{.j}}{y_{..}}}$$

```
chisq.test(meaudret$spe)
```

```
## Warning in chisq.test(meaudret$spe): L'approximation du Chi-2 est peut-êtr
## incorrecte

##
##     Pearson's Chi-squared test
##
## data:  meaudret$spe
## X-squared = 534.52, df = 228, p-value < 2.2e-16
```

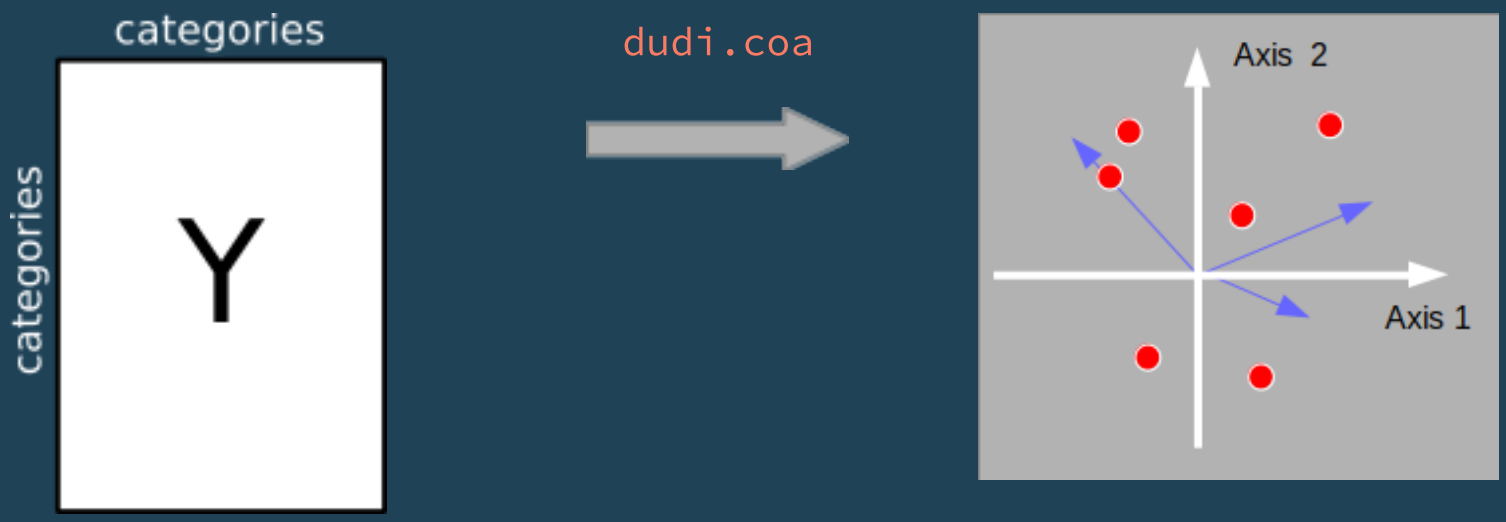
Absolute and relative frequencies



- In PCA (Euclidean distances), species 2 and 3 are closer
- In COA (χ^2 distances), species 1 and 2 are closer (null distance)

Correspondence analysis

- $\mathbf{X} = \mathbf{D}_n^{-1}\mathbf{P}\mathbf{D}_m^{-1} - \mathbf{1}_n\mathbf{1}_m{}^\top$ is the transformed and centred table of relative frequencies with $\mathbf{P} = [y_{ij}/y_{..}]$
- $\mathbf{Q} = \mathbf{D}_m$ where $\mathbf{D}_m = diag(\mathbf{P}^\top\mathbf{1}_n)$ contains the column category frequencies
- $\mathbf{D} = \mathbf{D}_n$ where $\mathbf{D}_n = diag(\mathbf{P}\mathbf{1}_m)$ contains the row category frequencies



Maximized criteria

- For rows

$$Q(\mathbf{a}) = \|\mathbf{D}_n^{-1}\mathbf{P}_0\mathbf{D}_m^{-1}\mathbf{D}_m\mathbf{a}\|^2_{\mathbf{D}_n} = \|\mathbf{D}_n^{-1}\mathbf{P}_0\mathbf{a}\|^2_{\mathbf{D}_n}$$

In this viewpoint, columns have a unit-variance score $\mathbf{a}$ that maximises the variance between the row barycenters.

- For columns

$$\|\mathbf{D}_m^{-1}\mathbf{P}_0{}^\top\mathbf{D}_n^{-1}\mathbf{D}_n\mathbf{b}\|^2_{\mathbf{D}_m} = \|\mathbf{D}_m^{-1}\mathbf{P}_0{}^\top\mathbf{b}\|^2_{\mathbf{D}_m}$$

  In this viewpoint, rows have a unit-variance score $\mathbf{b}$ that maximises the variance between the column barycenters.

The `dudi.coa` function

Arguments

```
args(dudi.coa)
```

```
## function (df, scannf = TRUE, nf = 2)
## NULL
```

- `df` is a `data.frame` with the positive values (counts)
- `scannf` and `nf` allow to set the number of dimensions to interpret

```
coa.meau <- dudi.coa(meaudret$spe, scannf = FALSE)
```

Returned values

```
names(coa.meau)
```

```
##  [1] "tab"  "cw"   "lw"   "eig"  "rank" "nf"   "c1"   "li"   "co"   "l1"
## [12] "N"
```

It returns an object of class `dudi` containing:

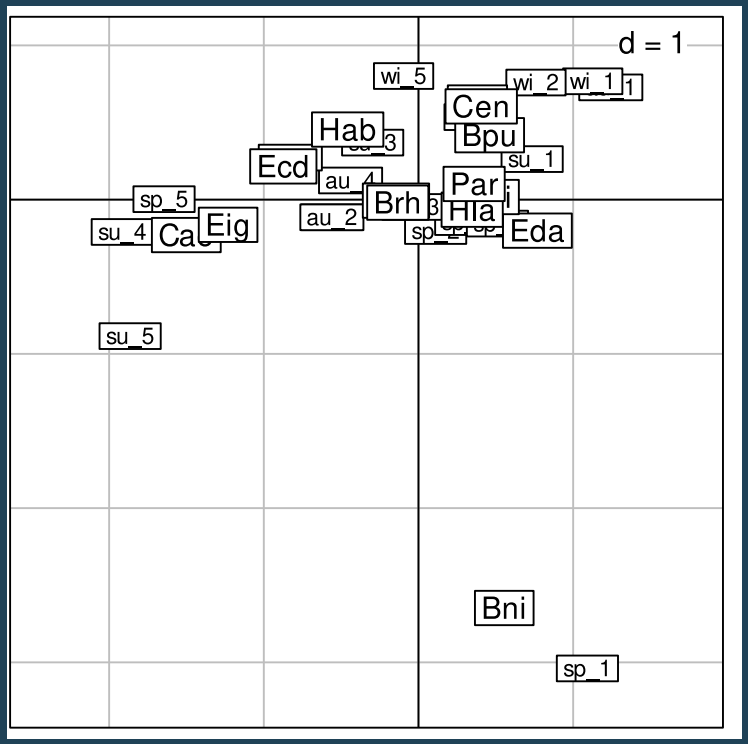
- `$eig`: eigenvalues ($\mathbf{\Lambda}$)
- `$cw`: column weights ($\mathbf{D}_m$)
- `$lw`: row weights ($\mathbf{D}_n$)
- `$tab`: centred relative frequencies table ($\mathbf{D}_n^{-1}\mathbf{P}_0\mathbf{D}_m^{-1}$)
- `$c1`: unit-variance column scores ($\mathbf{A}$)
- `$li`: row scores as weighted averages ($\mathbf{L} = \mathbf{D}_n^{-1}\mathbf{P}_0\mathbf{A}$)
- `$l1`: unit-variance row scores ($\mathbf{B}$)
- `$co`: column scores as weighted averages ($\mathbf{C} = \mathbf{D}_m^{-1}{\mathbf{P}_0}^\top\mathbf{B}$)
- `$N`: total sum ($y_{..}$)

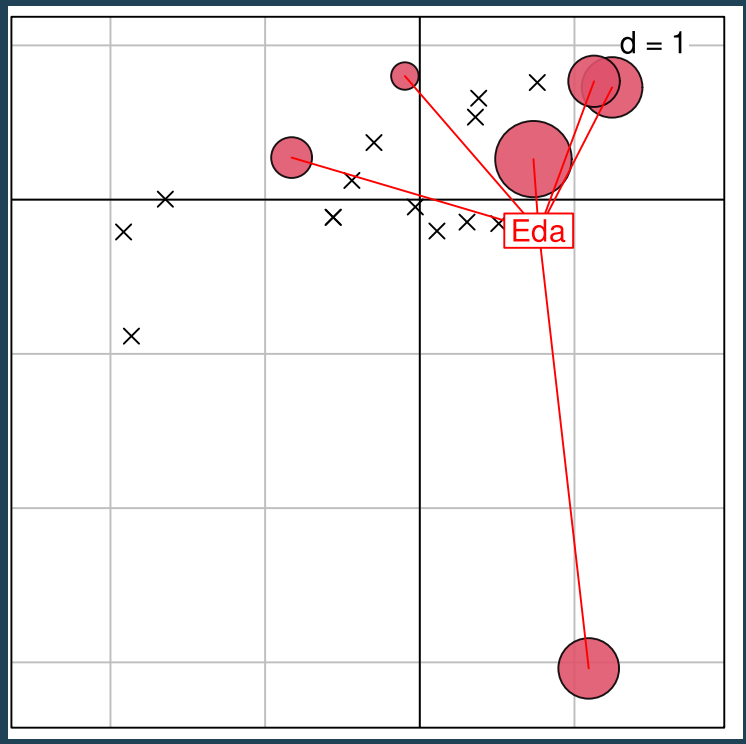
Graphical representations

Biplot can be produced for CA using the `biplot` function. Three types of biplots can be produced using the argument `method`

- If `method = 2`, species are positioned by a unit-variance score (`$c1`) and sites by weighted averaging (`li`).
- If `method = 3`, sites are positioned by a unit-variance score (`$l1`) and species by weighted averaging (`$co`).
- By default, `method = 1` corresponds to a compromise between these two representations (`$li` and `$co`).

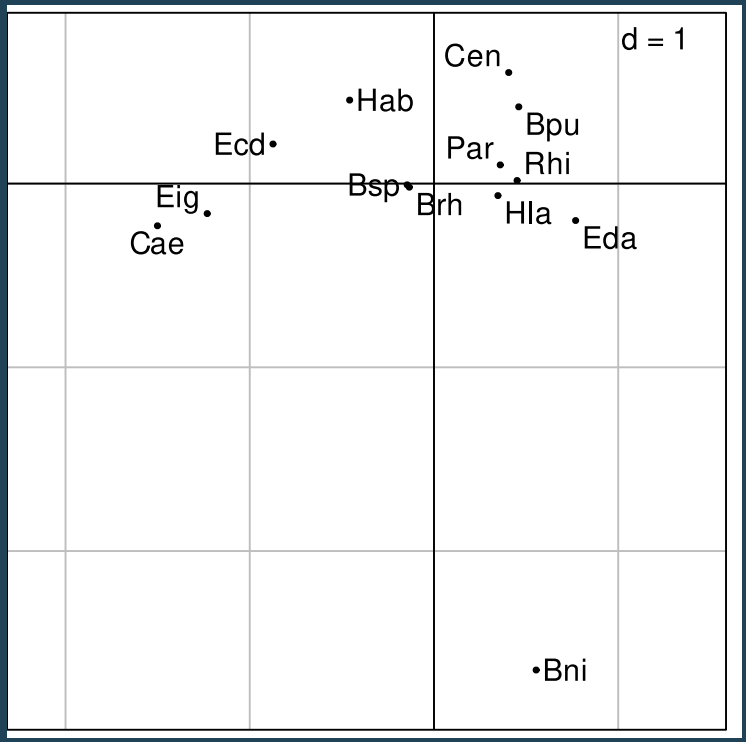
Weighted averaging



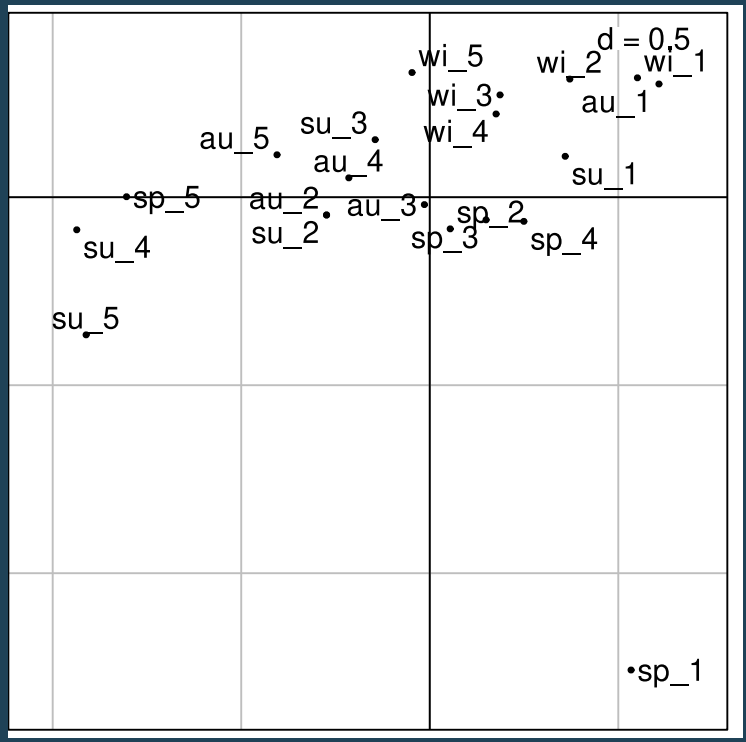


Separate representations

```
s.label(coa.meau$co, plabels.opti
```

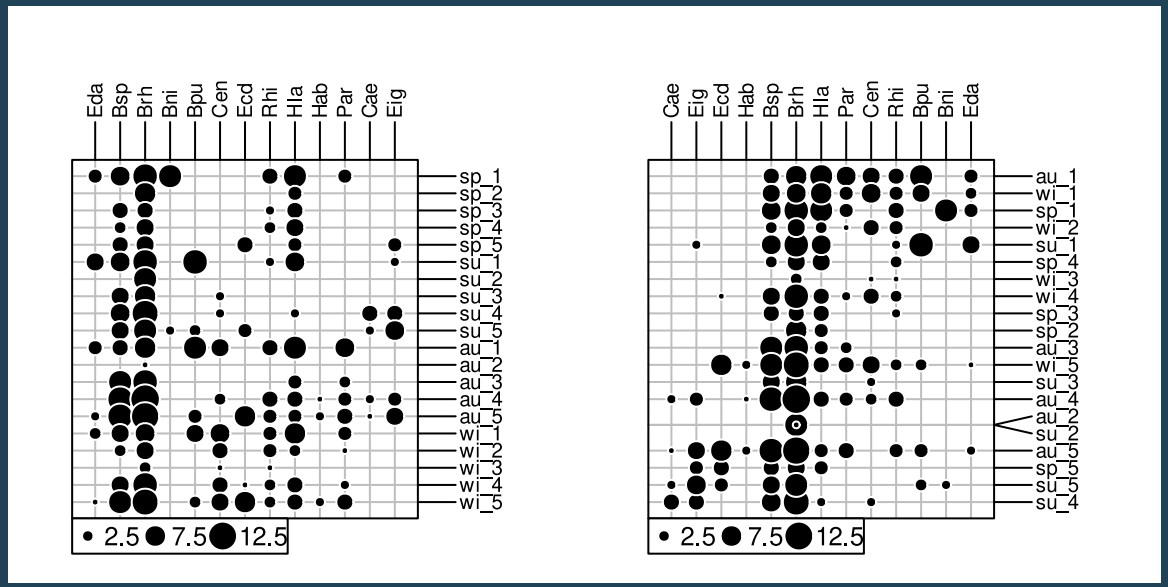



```
s.label(coa.meau$li, plabels.opti
```



Reordering of a table

```
g1 <- table.value(meaudret$spe, ppoint.cex = 0.5, symbol = "circle",
    plot = FALSE)
g2 <- table.value(meaudret$spe, ppoint.cex = 0.5, symbol = "circle",
    coordsx = rank(coa.meau$co[, 1]), coordsy = rank(coa.meau$li[,
        1]), plot = FALSE)
cbindADEg(g1, g2, plot = TRUE)
```



Principal coordinates analysis

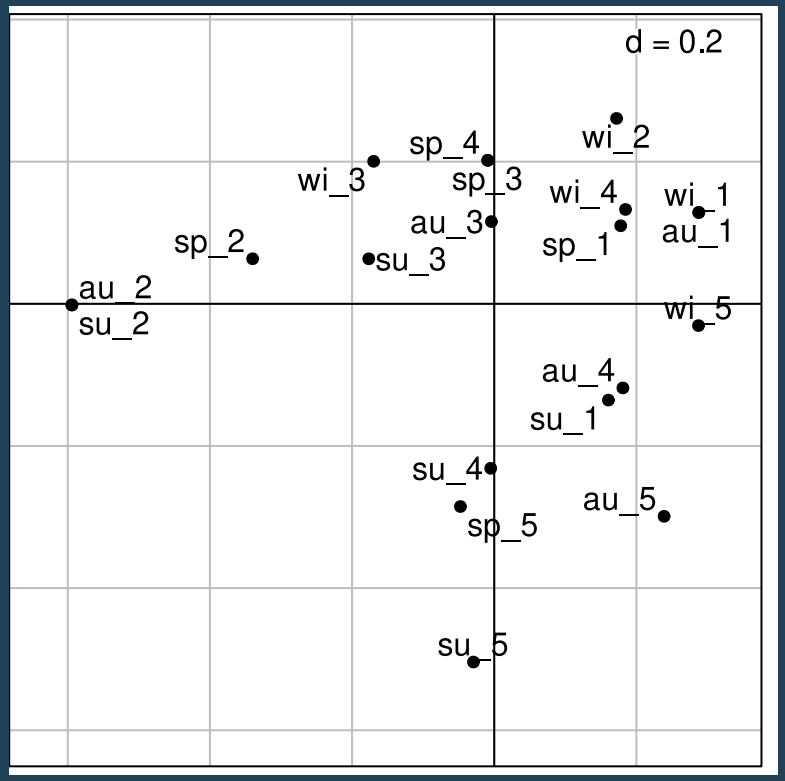
- PCA, CA methods induce implicitly a way to compute distances
- Several other distances have been proposed (e.g., genetic, presence-absence)
- PCoA takes a distance matrix as input and returns coordinates in a low dimensional space that best preserve the original distances.

- 😄 it allows to choose a particular distance measure between sites (or species).

- 😢 it focuses either on individuals or variables, not both.

- Useful if distances are directly recorded or computed from raw data tables

```
dJ <- dist.binary(meaudret$spe, method = 1)  # Jaccard
pcoJ <- dudi.pco(dJ, scannf = FALSE)
s.label(pcoJ$li, plabels.optim = TRUE)
```



COA in practice

Go to practical 4