

## Suppl. Doc. 4 – Directional analysis of the Doubs fish data

### # Real ecological example – The Doubs River fish data available in package ade4

# The data matrix contains 30 sites from the source of the river downwards, till the point where the Doubs River, in southern France, flows into the Saone River. The data were collected by J. Verneaux for his doctoral thesis in 1973. No fish had been caught by Verneaux at site 8, probably due to sampling variation. That site is thus excluded from all analyses. The 27 species abundances are coded on a semi-quantitative scale from 0 (absent) to 5 (the most abundant).

# The fish community forms a nice coenocline along the course of the river. The coenocline is not entirely smooth, as shown in the plot of species richness along the course of the river (on p. 2). There are also three polluted sites, #23–25 in the original data file (relabelled #22–24 in the present analysis), where most species were absent, which broke the directionality of the community change. These irregularities will be useful in our paper to show how the indices react to these situations.

```
library(ade4)
data(doubs)                # The Doubs River fish data are available in ade4
dim(doubs$fish)             # 30 sites, 27 species
fish <- doubs$fish[-8,]     # No fish had been caught at site 8; that site is removed
```

# We will run the `directional.response.R` function (Suppl. Doc 2) to compute matrices of directional indices. Function `sub.diag.R` (Suppl. Doc 3) computes the square matrix of directional response indices by calling function `directional.response.R`, then it extracts the sub-diagonal of that matrix. That vector contains the indices estimated *between adjacent sites* along the transect or time series, in the direction given by the order of the sites in the data matrix. For  $n$  sites, that vector contains  $(n-1)$  indices.

The **lower triangular matrix** of directional indices can be obtained by running function `directional.response.R` directly on the fish data, then extracting element "mat.out" from the output file. Example:

```
doubs.out = directional.response(fish, method="gaining.turnover", relativize="J")
summary(doubs.out)
mat1 <- as.dist(doubs.out$mat.out)
```

```
# ----
```

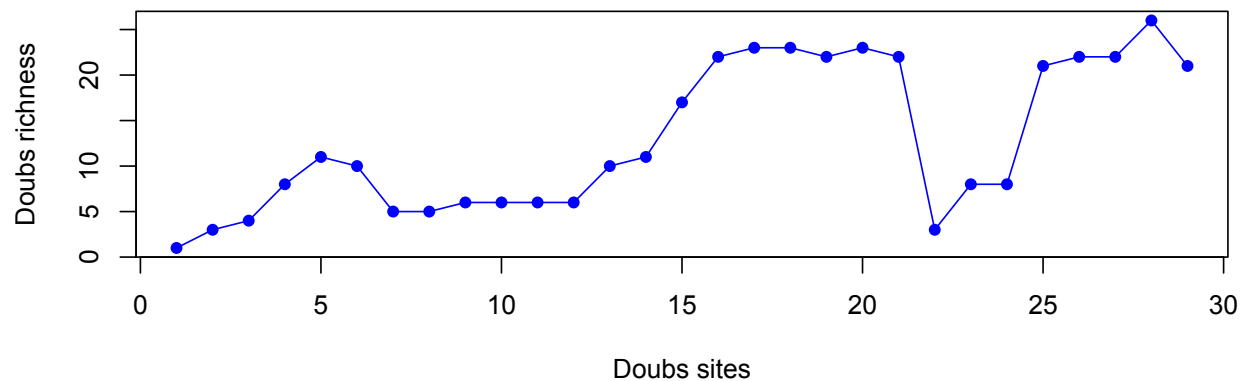
# One can also extract the **upper triangular matrix** in order to analyse a gradient in the direction opposite to the order of the sampling units in the data matrix. Example of extraction of the upper triangular portion of matrix `doubs.out$mat.out`, written to object `mat2` with class *dist* :

```
mat2 <- as.dist(t(doubs.out$mat.out))
# ----
```

# Compute and plot *species richness* along the Doubs River from the source of the river (site #1) to the confluence with the Saone River (site #29 in the data matrix used here). Remember, site #8 was removed from the data matrix. It is not present in the list of 29 sites used here.

```
fish.pa = ifelse(fish>0, 1, 0)           # Transform to absence-presence (0-1) data
Doubs.rich = apply(fish.pa, 1, sum)      # Compute species richness
as.vector(Doubs.rich)                   # Length of species richness vector: 29 sites
[1] 1 3 4 8 11 10 5 5 6 6 6 6 10 11 17 22 23 23 22 23 22 3 8 8 21 22 22 26 21
```

```
plot(Doubs.rich, xlab="Doubs sites", ylab="Doubs richness", pch=16, col="blue")
lines(1:29, Doubs.rich, type="l", col="blue")
```



Along the abscissa of this plot, sites are numbered 1 to 29. These numbers correspond to sites #1 to #7, then #9 to #30 in the original data file of Verneaux. The three polluted sites (#23-24-25) have numbers {22,23,24} in this and the following graphs; their species richness is very low.

# =====

### Reference

Verneaux, J. 1973. *Cours d'eau de Franche-Comté (Massif du Jura). Recherches écologiques sur le réseau hydrographique du Doubs. Essai de biotypologie*. Thèse d'État, Besançon. 1–257.

# =====

## Part 1 – Directional beta diversity indices

# Examine the partitioning of turnover into gain.t, loss.t and neutral.t.

# Turnover – The change in species composition between two sites along a gradient.

```
( gaining.t = sub.diag(fish, method= "gaining.turnover", relativize=NULL)$sub.diag )
```

```
# Method: gaining.turnover
```

```
[1] 2 1 4 3 0 0 4 5 4 0 2 4 3 8 5 1 6 0 1 0 0 5 6 13 1 0 4 0 # Length 28 point pairs
```

```
( gaining.t.J = sub.diag(fish, method= "gaining.turnover", relativize="J")$sub.diag )
```

```
# Method: gaining.turnover
```

```
# Relativize with denominator: Jaccard
```

```
[1] 0.66666667 0.25000000 0.50000000 0.27272727 0.00000000 0.00000000 0.57142857
```

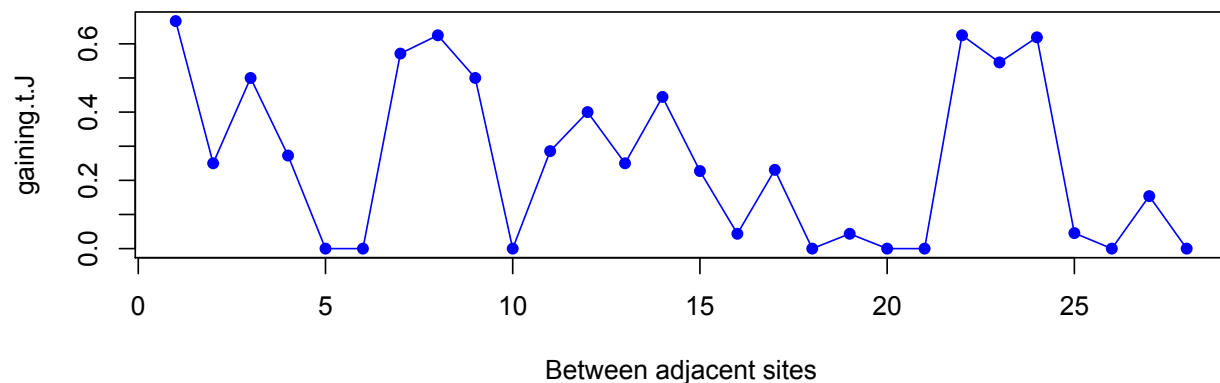
```
[8] 0.62500000 0.50000000 0.00000000 0.28571429 0.40000000 0.25000000 0.44444444
```

```
[15] 0.22727273 0.04347826 0.23076923 0.00000000 0.04347826 0.00000000 0.00000000
```

```
[22] 0.62500000 0.54545455 0.61904762 0.04545455 0.00000000 0.15384615 0.00000000
```

```
plot(gaining.t.J, xlab="Between adjacent sites", pch=16, col="blue")
```

```
lines(1:28, gaining.t.J, type="l", col="blue")
```



# Sites {22,23,24} in the graph are the three polluted sites. [They correspond to sites {23,24,25} in the original labelling of the Doubs River sites.] Before our analyses, site #8 has been removed from the data set. Our analyses thus involve 29 sites instead of the original 30 sites. Our results show that gaining turnover decreases along the gradient in general. However, the three polluted sites show a high proportion of gaining turnover.

# ----

```
( losing.t = sub.diag(fish, method= "losing.turnover", relativize=NULL)$sub.diag )
```

```
# Method: losing.turnover
```

```
[1] 0 0 0 0 1 5 4 4 4 0 2 0 2 2 0 0 6 1 0 1 19 0 6 0 0 0 0 5
```

```
( losing.t.J = sub.diag(fish, method= "losing.turnover", relativize="J")$sub.diag )
```

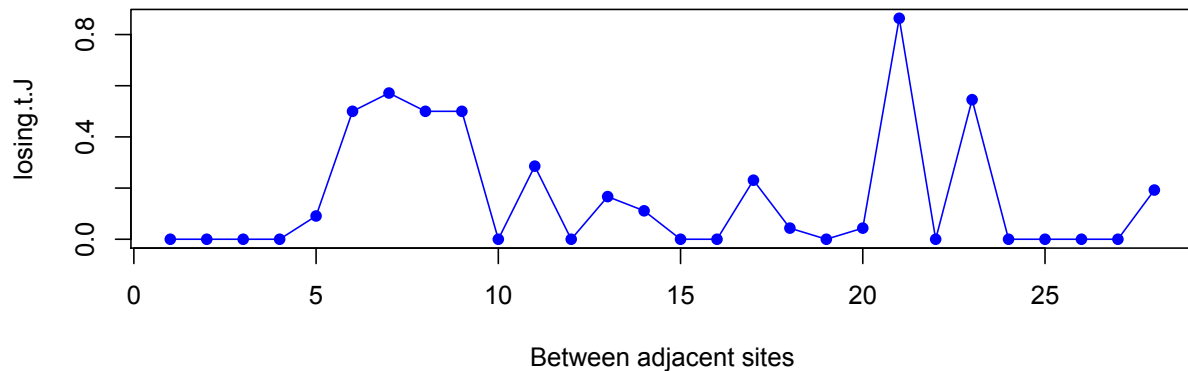
```
# Method: losing.turnover
```

```
# Relativize with denominator: Jaccard
```

```
[1] 0.00000000 0.00000000 0.00000000 0.00000000 0.09090909 0.50000000 0.57142857
```

```
[8] 0.50000000 0.50000000 0.00000000 0.28571429 0.00000000 0.16666667 0.11111111
[15] 0.00000000 0.00000000 0.23076923 0.04347826 0.00000000 0.04347826 0.86363636
[22] 0.00000000 0.54545455 0.00000000 0.00000000 0.00000000 0.00000000 0.19230769
```

```
plot(losing.t.J, xlab="Between adjacent sites", pch=16, col="blue")
lines(1:28, losing.t.J, type="l", col="blue")
```



# Losing turnover is moderate along the gradient. However, before the polluted sites (i.e. at site #21) and among the polluted sites (at site #23), we observe high values of losing turnover.

```
( neutral.t = sub.diag(fish, method= "neutral.turnover", relativize=NULL)$sub.diag )
```

```
# Method: neutral.turnover
```

```
[1] 0 0 0 0 0 4 4 4 0 2 0 2 2 0 0 6 0 0 0 0 0 6 0 0 0 0 0
```

```
( neutral.t.J = sub.diag(fish, method= "neutral.turnover", relativize="J")$sub.diag )
```

```
# Method: neutral.turnover
```

```
# Relativize with denominator: Jaccard
```

```
[1] 0.0000000 0.0000000 0.0000000 0.0000000 0.0000000 0.0000000 0.5714286
```

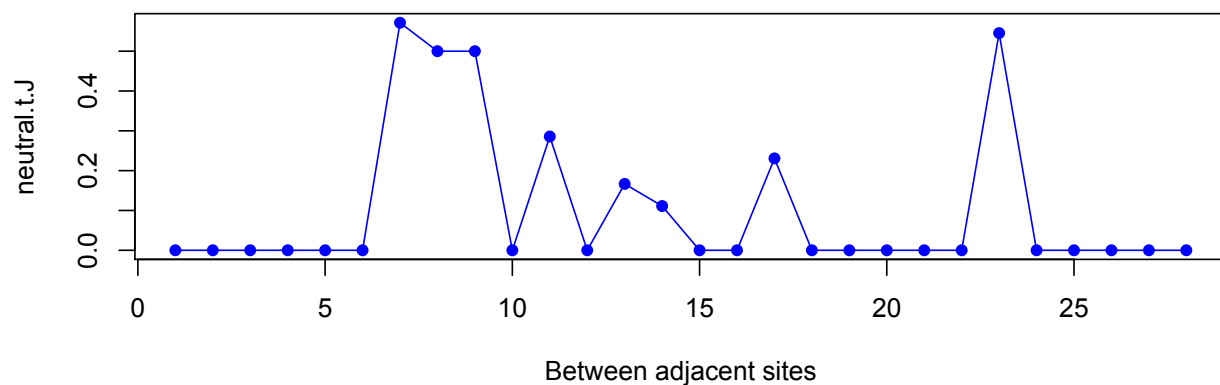
```
[8] 0.5000000 0.5000000 0.0000000 0.2857143 0.0000000 0.1666667 0.1111111
```

```
[15] 0.0000000 0.0000000 0.2307692 0.0000000 0.0000000 0.0000000 0.0000000
```

```
[22] 0.0000000 0.5454545 0.0000000 0.0000000 0.0000000 0.0000000 0.0000000
```

```
plot(neutral.t.J, xlab="Between adjacent sites", pch=16, col="blue")
```

```
lines(1:28, neutral.t.J, type="l", col="blue")
```



# Neutral turnover is in general low along the river gradient. However, there are some peaks at sites 7-8-9, and one at point 23, which represents the change in species composition between polluted sites 23 and 24.

# =====

# The matrices of directional indices can be further analysed by ordination

library(ape) # The pcoa.R function used below is found in the {ape} package

# **Turnover** – The change in species composition between two sites along a gradient.

doubs.gaining.t.J = directional.response(fish, method= "gaining.turnover", relativize="J")

mat1 <- as.dist(doubs.gaining.t.J\$mat.out)

pcoa.out1 = pcoa(mat1) # PCoA of mat1

# ----

doubs.losing.t.J = directional.response(fish, method= "losing.turnover", relativize="J")

mat2 <- as.dist(doubs.losing.t.J\$mat.out)

pcoa.out2 = pcoa(mat2) # PCoA of mat2

# ----

doubs.neutral.t.J = directional.response(fish, method= "neutral.turnover", relativize="J")

mat3 <- as.dist(doubs.neutral.t.J\$mat.out)

pcoa.out3 = pcoa(mat3) # PCoA of mat3

# ----

par(mfrow=c(2,2))

biplot(pcoa.out1, type="n", main=c("PCoA ordination of Doubs data", "gaining turnover, Jaccard"))

lines(pcoa.out1\$vectors[,1:2], type="l", col="red")

points(pcoa.out1\$vectors[,1:2], type="p", pch=21, bg="white")

abline(h=0, v=0, col="grey")

biplot(pcoa.out2, type="n", main=c("PCoA ordination of Doubs data", "losing turnover, Jaccard"))

lines(pcoa.out2\$vectors[,1:2], type="l", col="red")

points(pcoa.out2\$vectors[,1:2], type="p", pch=21, bg="white")

abline(h=0, v=0, col="grey")

biplot(pcoa.out3, type="n", main=c("PCoA ordination of Doubs data", "neutral turnover, Jaccard"))

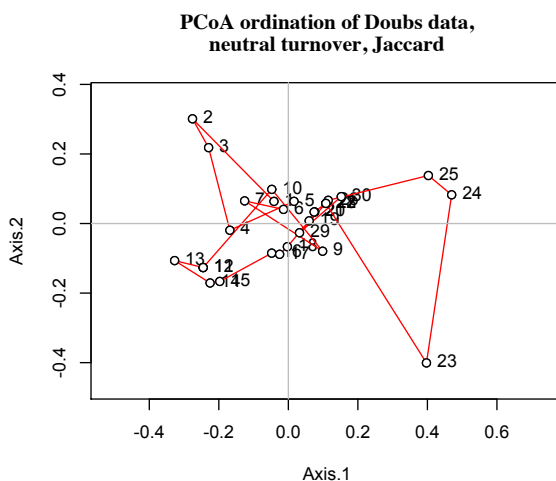
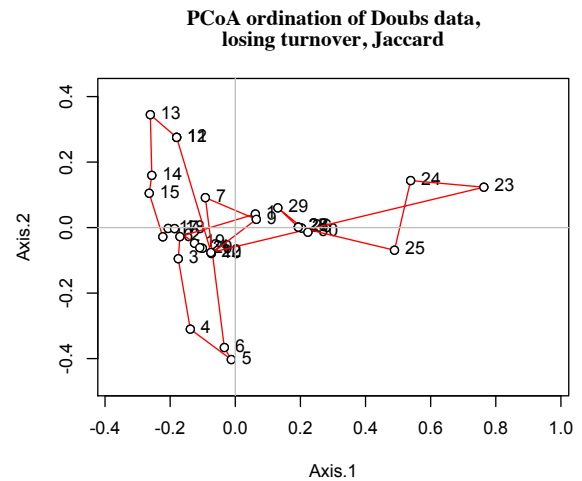
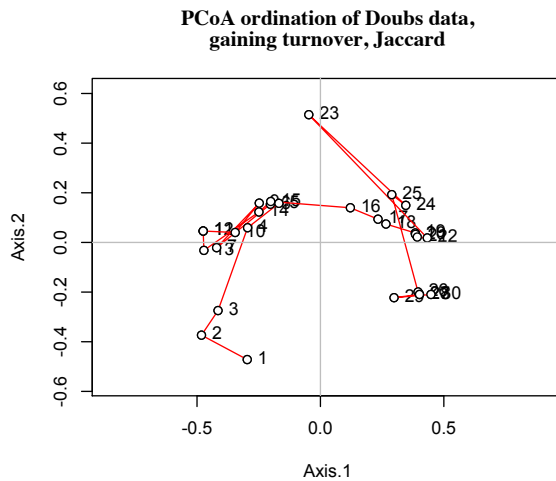
lines(pcoa.out3\$vectors[,1:2], type="l", col="red")

points(pcoa.out3\$vectors[,1:2], type="p", pch=21, bg="white")

abline(h=0, v=0, col="grey")

# ----

### Ordination plots: see next page.



# Interpretation of the ordination plots with the original site labels of Verneaux. Site #8 was removed from the data matrix before the analysis. In the ordination plots, the sites are labelled #1 to 7, then #9 to 30. The three polluted sites are {23,24,25}.

In the analyses until now, we had examined only the relationship between adjacent sites. The ordination plots show **the overall relationship of the sites** based on different turnover concepts.

- Gaining turnover – The main suite of successive gains between adjacent sites goes from site #1 to 30. A cluster of sites #4 to 15 appears in the graph and another cluster with sites #26 to 30. Regarding gaining turnover, the ordination plot shows a gradual change in the community ("arch-effect") with the note that site 23 (the first polluted site) is an outlier.
- Losing turnover – The sites that stand out of the central cluster are #3-9, #12-15 and #23-25. These sites have lost species compared to the previous sites along the course of the river. The ordination plot shows that the most remarkable changes in the community compared to the upstream sites can be found at sites 23, 24 and 25 (large positive values on graph abscissa).
- Neutral turnover – The sites that stand out of the central cluster are #1-4 and #23-25, which have low richness.

# =====

## Part 2 – Distribution of the fish species associations

### # Prepare the data files

```
library(vegan)
# Chord transformation of the community data, before clustering or ordination
fish.chord = decostand(fish, "norm")      # data.frame "fish" was obtained on p. 1
# Transformation to presence-absence data (pa)
fish.pa = ifelse(fish>0, 1, 0)
```

# **Constrained clustering of the Doubs River fish data** using function `constr.hclust.R` of `adespatial`. — Site 8, where no fish had been caught, was **excluded** from this analysis. These **groups of sites** are used and shown at the bottom of the graphs on pp. 10 and 11 of this Supplement.

```
Doubs.clust <- constr.hclust(dist(fish.chord), method="ward.D2", chron=TRUE,
  coords=as.matrix(doubs$xy[-8,]))
```

```
plot(Doubs.clust, k=6, las=1, xlab="Eastings (km)", ylab="Northings (km)", cex=3,
  lwd=3)
```

```
cutree(Doubs.clust, k=4)      # Division of the sites into 4 groups
 1  2  3  4  5  6  7  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 1  1  1  1  1  1  1  1  1  1  1  1  1  2  2  2  2  2  3  3  3  3  3  3  4  4  4  4  4
```

```
cutree(Doubs.clust, k=5)
 1  2  3  4  5  6  7  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 1  1  1  1  1  1  1  1  1  1  1  1  1  2  2  2  2  2  3  3  3  4  4  4  5  5  5  5  5
```

```
cutree(Doubs.clust, k=6)
 1  2  3  4  5  6  7  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 1  2  2  2  2  2  2  2  2  2  2  2  2  3  3  3  3  3  4  4  4  5  5  5  6  6  6  6  6
```

# The innovation of the k=6 solution is the separation of site #1. That site only contains the brown trout, species *Satr* in the data file (*Salmo trutta fario*).

# =====

### Identify the species associations by concordance analysis, Legendre (2005)<sup>1</sup>

# Identify the fish species associations by Ward agglomerative clustering

```
cor.sp = cor(fish.chord)
sp.D = as.dist(1-cor.sp)
sp.clust.ward = hclust(sp.D, "ward.D2")
plot(sp.clust.ward, hang=-1)
```

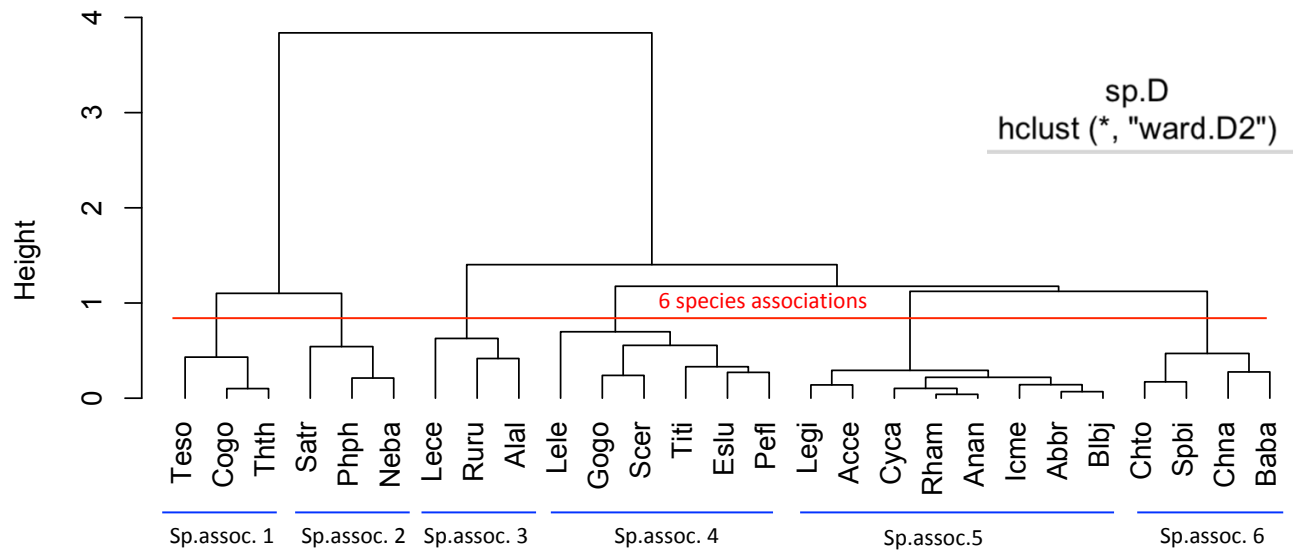
# The 6 **species clusters** could be delineated on the dendrogram by:

```
plot(sp.clust.ward, h=-1 )
rect.hclust(sp.clust.ward , k=6)
```

---

<sup>1</sup> Legendre, P. 2005. Species associations: the Kendall coefficient of concordance revisited. *Journal of Agricultural, Biological, and Environmental Statistics* 10: 226-245.

## Cluster Dendrogram



```
assoc.2 = cutree(sp.clust.ward, k=2)
assoc.3 = cutree(sp.clust.ward, k=3)
assoc.4 = cutree(sp.clust.ward, k=4)
assoc.5 = cutree(sp.clust.ward, k=5)
assoc.6 = cutree(sp.clust.ward, k=6)
```

assoc.6

Cogo	Satr	Phph	Neba	Thth	Teso	Chna	Chto	Lele	Lece	Baba	Spbi	Gogo	Eslu	Pefl	Rham
1	2	2	2	1	1	3	3	4	5	3	3	4	4	4	6
Legi	Scer	Cyca	Titi	Abbr	Icme	Acce	Ruru	Blbj	Alal	Anan					
6	4	6	4	6	6	6	5	6	5	6					

```
# Concordance analysis of the species divided into 6 associations, found in vector assoc.6
# The analysis involves running the data into kendall.global.R (not shown) and kendall.post.R
```

```
( ken.post.2 = kendall.post(fish.chord, group=assoc.2) ) # Species Lece not significant
( ken.post.3 = kendall.post(fish.chord, group=assoc.3) ) # All species are significant
( ken.post.4 = kendall.post(fish.chord, group=assoc.4) )
( ken.post.5 = kendall.post(fish.chord, group=assoc.5) )
( ken.post.6 = kendall.post(fish.chord, group=assoc.6) ) # <= Most useful: 6 associations
```



# In the sequel, the ID of species groups 3, 5 and 6, was changed to follow the order in the dendrogram

```
$A_posteriori_tests_Group[[1]]
      Cogo      Thth      Teso
Spearman.mean 0.7904762 0.7547619 0.6642857
W.per.species 0.8603175 0.8365079 0.7761905
Prob          0.0010000 0.0010000 0.0010000
Corrected prob 0.0270000 0.0270000 0.0270000
```

```
$A_posteriori_tests_Group[[2]]
      Satr      Phph      Neba
Spearman.mean 0.6232998 0.7627365 0.6736598
W.per.species 0.7488665 0.8418243 0.7824398
Prob          0.0010000 0.0010000 0.0010000
Corrected prob 0.0270000 0.0270000 0.0270000
```

```
$A_posteriori_tests_Group[[3]] # The ID number of this association was changed
      Lece      Ruru      Alal
Spearman.mean 0.4410229 0.5656653 0.5501964
W.per.species 0.6273486 0.7104436 0.7001309
Prob          0.0030000 0.0010000 0.0010000
Corrected prob 0.0270000 0.0270000 0.0270000
```

```
$A_posteriori_tests_Group[[4]]
      Lele      Gogo      Eslu      Pefl      Scer      Titi
Spearman.mean 0.4701523 0.6737871 0.6523269 0.6267827 0.6407418 0.6363025
W.per.species 0.5584603 0.7281559 0.7102724 0.6889856 0.7006182 0.6969188
Prob          0.0020000 0.0010000 0.0010000 0.0010000 0.0010000 0.0010000
Corrected prob 0.0270000 0.0270000 0.0270000 0.0270000 0.0270000 0.0270000
```

```
$A_posteriori_tests_Group[[5]] # The ID number of this association was changed
      Rham      Legi      Cyca      Abbr      Icme      Acce
Spearman.mean 0.8616407 0.8576262 0.8549885 0.8647574 0.8219403 0.7980347
W.per.species 0.8789356 0.8754229 0.8731149 0.8816628 0.8441978 0.8232804
Prob          0.0010000 0.0010000 0.0010000 0.0010000 0.0010000 0.0010000
Corrected prob 0.0270000 0.0270000 0.0270000 0.0270000 0.0270000 0.0270000

      Blbj      Anan
Spearman.mean 0.8684929 0.8862498
W.per.species 0.8849313 0.9004686
Prob          0.0010000 0.0010000
Corrected prob 0.0270000 0.0270000
```

```
$A_posteriori_tests_Group[[6]] # The ID number of this association was changed
      Chna      Chto      Baba      Spbi
Spearman.mean 0.7383770 0.8097515 0.8083121 0.8406500
W.per.species 0.8037828 0.8573137 0.8562340 0.8804875
Prob          0.0010000 0.0010000 0.0010000 0.0010000
Corrected prob 0.0270000 0.0270000 0.0270000 0.0270000
```

# What were the dominant species in the three polluted sites #22, 23, 24?

```
apply(fish.chord[22:24,], 2, sum)
```

# The dominant species in the three polluted sites were: {10, 24, 26} = {Lece, Ruru, Alal}

# Vector *assoc* (list of species associations) will be used to draw plots shown in the next two pages

```
assoc = list(ass1=c(1,5,6), ass2=c(2,3,4), ass3=c(10,24,26), ass4=c(9,13,14,15,18,20),
ass5=c(16,17,19,21,22,23,25,27), ass6=c(7,8,11,12))
```

# Compute the matrix of **occurrences** (sites x 6 species associations)

# The sum.abund.R function is printed on p. 14

```
res.pa = sum.abund(fish.pa, assoc)
```

# Matrix printed on p. 12

```
dim(res.pa)
```

# 29 6

# Plot the sum of **occurrences** of 6 species associations across the sites

# Colour vector – Choice of colours. See: colors() and tests of colours on p. 14

```
line.col6 <- c("black","blue","darkgreen","turquoise","red1","maroon4")
```

```
plot(res.pa, type="n", main=c("Sum of occurrences", "in six species associations across sites"),
      xlim=c(1,29), ylim=c(0,8), xaxt="n", xlab="Doubs River sites", ylab="Sum of occurrences" )
axis(side=1, at=1:29, labels=1:29, cex.axis=0.7, las=1)
```

```
for(k in 1:6) {
```

```
  lines(res.pa[,k], type="l", col=line.col6[k])
```

```
  points(res.pa[,k], type="p", pch=21, col=line.col6[k], bg=line.col6[k], cex=0.5)
```

```
}
```

```
for(k in 1:6) {
```

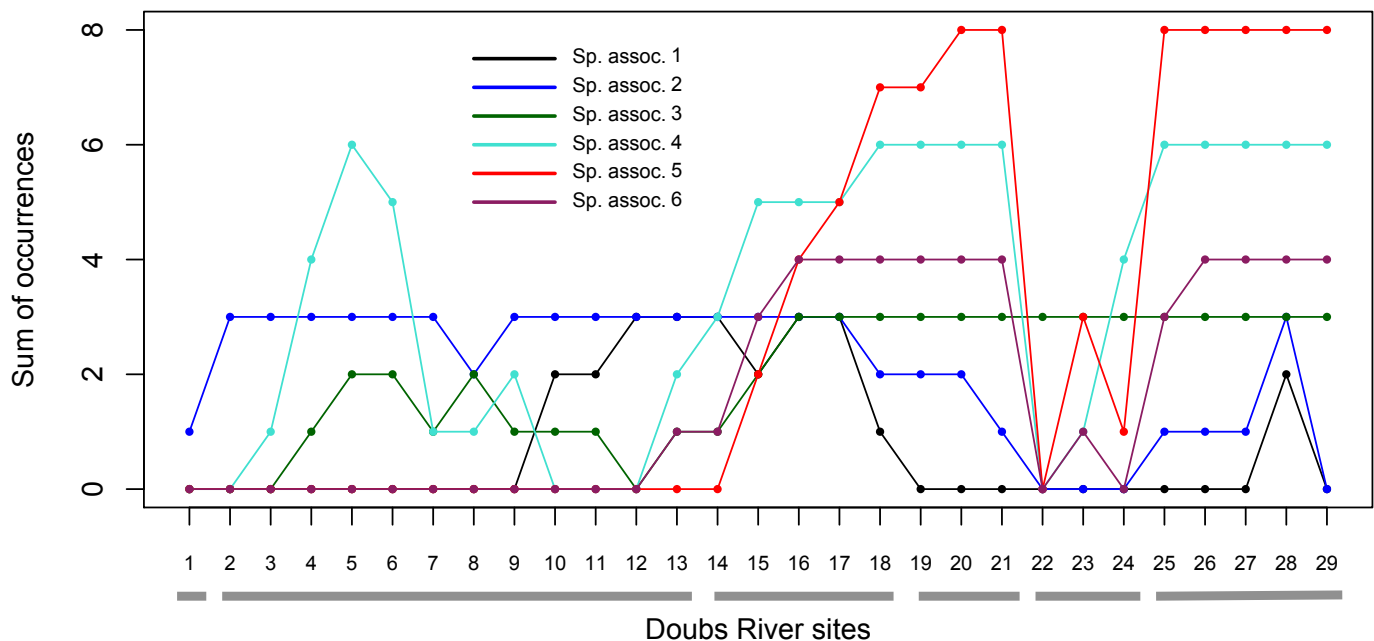
```
  lines(c(8, 10), rep(8,2)-k/2, type="l", col=line.col6[k], lwd=2)
```

```
  text(10, (8-k/2), labels=c("Sp. assoc."), pos=4, cex=0.7)
```

```
  text(13.0, (8.06-k/2), k, cex=0.7)
```

```
}
```

### Sum of occurrences in six species associations across sites



# The gray lines at the bottom of the graph represent **the 6 site groups** obtained by spatially-constrained clustering, on p. 7 of this document. They may prove useful for the interpretation of the directional beta diversity indices.

# Species association 3 (dark green) dominates the three polluted sites, #22–24.  
 # Compute the matrix of **abundances** (sites x 6 species associations)

# The sum.abun.R function printed on p. 14

res.abun = sum.abund(fish.chord, assoc)

# Matrix printed on p. 13

dim(res.abun)

# 29 6

# Plot the sum of **abundances** of 6 species associations across the sites

# Colour vector

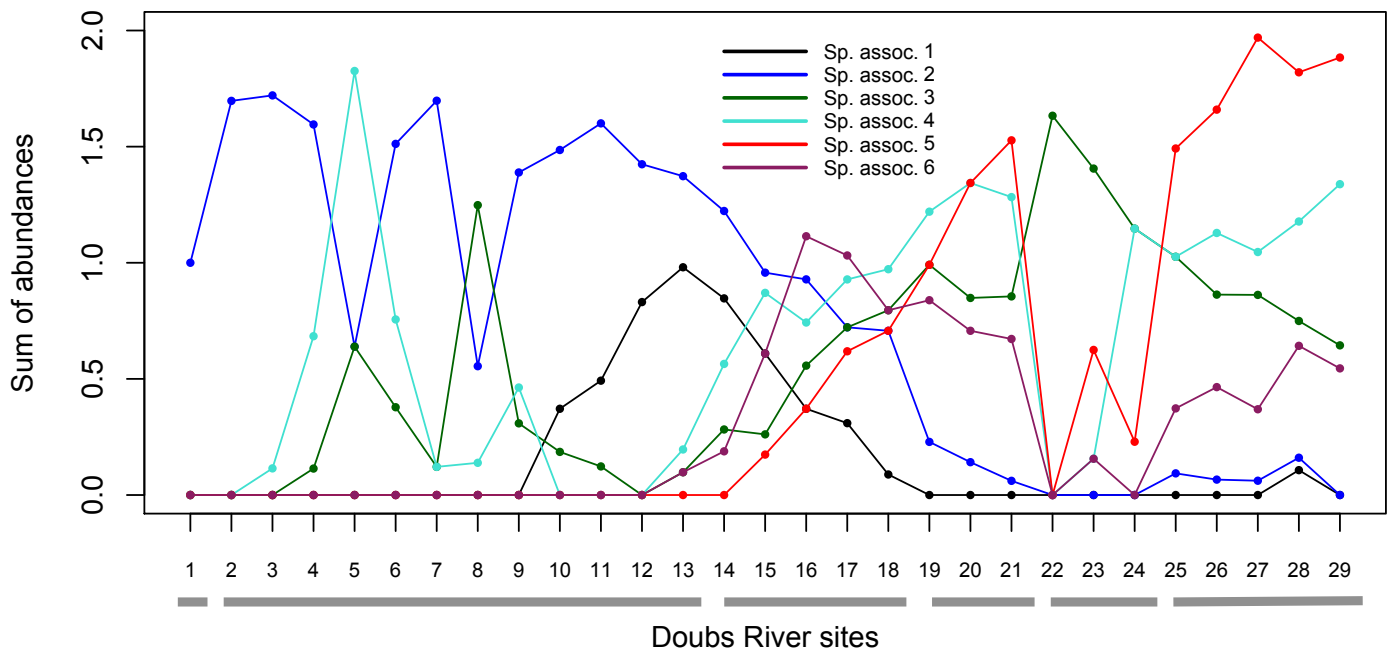
# Choice of colours: see: colours()

line.col6 <- c("black","blue","darkgreen","turquoise","red1","maroon4")

plot(res.abun, type="n", main=c("Sum of abundances", "in six species associations across sites"),  
 xlim=c(1,29), ylim=c(0,2), xaxt="n", xlab="Doubs River sites", ylab= "Sum of abundances" )  
 axis(side=1, at=1:29, labels=1:29, cex.axis=0.7, las=1)

```
for(k in 1:6) {
  lines(res.abun[,k], type="l", col=line.col6[k])
  points(res.abun[,k], type="p", pch=21, col=line.col6[k], bg=line.col6[k], cex=0.5)
}
for(k in 1:6) {
  lines(c(14, 16), rep(2.01,2.01)-k/10, type="l", col=line.col6[k], lwd=2)
  text(16, (2-k/10), labels=c("Sp. assoc."), pos=4, cex=0.7)
  text(19.0, (2.015-k/10), k, cex=0.7)
}
```

**Sum of abundances  
in six species associations across sites**



# Note – Species association 2 (blue) {Satr, Phph, Neba} dominates in the river upper course, sites #1–18; sp. association 3 (dark green) {Lece, Ruru, Alal} dominates in polluted sites sites #22–24.

# Matrix "res.pa" computed above, summing the number of **occurrences** of the 6 species associations at the 29 sites of Doubs River

```
res.pa
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    0    1    0    0    0    0
[2,]    0    3    0    0    0    0
[3,]    0    3    0    1    0    0
[4,]    0    3    1    4    0    0
[5,]    0    3    2    6    0    0
[6,]    0    3    2    5    0    0
[7,]    0    3    1    1    0    0
[8,]    0    2    2    1    0    0
[9,]    0    3    1    2    0    0
[10,]   2    3    1    0    0    0
[11,]   2    3    1    0    0    0
[12,]   3    3    0    0    0    0
[13,]   3    3    1    2    0    1
[14,]   3    3    1    3    0    1
[15,]   2    3    2    5    2    3
[16,]   3    3    3    5    4    4
[17,]   3    3    3    5    5    4
[18,]   1    2    3    6    7    4
[19,]   0    2    3    6    7    4
[20,]   0    2    3    6    8    4
[21,]   0    1    3    6    8    4
[22,]   0    0    3    0    0    0
[23,]   0    0    3    1    3    1
[24,]   0    0    3    4    1    0
[25,]   0    1    3    6    8    3
[26,]   0    1    3    6    8    4
[27,]   0    1    3    6    8    4
[28,]   2    3    3    6    8    4
[29,]   0    0    3    6    8    4
```

# =====

# Matrix "res.abun" computed above, summing the chord-transformed **abundances** of the 6 species associations at the 29 sites of Doubs River

res.abun

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]
[1,]	0.00000000	1.00000000	0.00000000	0.00000000	0.00000000	0.00000000
[2,]	0.00000000	1.69705627	0.00000000	0.00000000	0.00000000	0.00000000
[3,]	0.00000000	1.72061800	0.00000000	0.1147079	0.00000000	0.00000000
[4,]	0.00000000	1.59544807	0.11396058	0.6837635	0.00000000	0.00000000
[5,]	0.00000000	0.63900965	0.63900965	1.8257419	0.00000000	0.00000000
[6,]	0.00000000	1.51185789	0.37796447	0.7559289	0.00000000	0.00000000
[7,]	0.00000000	1.69774938	0.12126781	0.1212678	0.00000000	0.00000000
[8,]	0.00000000	0.55470020	1.24807544	0.1386750	0.00000000	0.00000000
[9,]	0.00000000	1.38873015	0.30860670	0.4629100	0.00000000	0.00000000
[10,]	0.37139068	1.48556271	0.18569534	0.00000000	0.00000000	0.00000000
[11,]	0.49236596	1.60018938	0.12309149	0.00000000	0.00000000	0.00000000
[12,]	0.83074716	1.42413799	0.00000000	0.00000000	0.00000000	0.00000000
[13,]	0.98058068	1.37281295	0.09805807	0.1961161	0.00000000	0.09805807
[14,]	0.84664878	1.22293713	0.28221626	0.5644325	0.00000000	0.18814417
[15,]	0.60927180	0.95742711	0.26111648	0.8703883	0.1740777	0.60927180
[16,]	0.37139068	0.92847669	0.55708601	0.7427814	0.3713907	1.11417203
[17,]	0.30942637	0.72199487	0.72199487	0.9282791	0.6188527	1.03142125
[18,]	0.08838835	0.70710678	0.79549513	0.9722718	0.7071068	0.79549513
[19,]	0.00000000	0.22874786	0.99124071	1.2199886	0.9912407	0.83874214
[20,]	0.00000000	0.14142136	0.84852814	1.3435029	1.3435029	0.70710678
[21,]	0.00000000	0.06108472	0.85518611	1.2827792	1.5271181	0.67193194
[22,]	0.00000000	0.00000000	1.63299316	0.00000000	0.00000000	0.00000000
[23,]	0.00000000	0.00000000	1.40556386	0.1561738	0.6246950	0.15617376
[24,]	0.00000000	0.00000000	1.14707867	1.1470787	0.2294157	0.00000000
[25,]	0.00000000	0.09325048	1.02575529	1.0257553	1.4920077	0.37300192
[26,]	0.00000000	0.06637233	0.86284031	1.1283296	1.6593083	0.46460632
[27,]	0.00000000	0.06154575	0.86164044	1.0462777	1.9694639	0.36927447
[28,]	0.10705755	0.16058632	0.74940282	1.1776330	1.8199783	0.64234527
[29,]	0.00000000	0.00000000	0.64438608	1.3383403	1.8835901	0.54524976

# =====

## # An R function and a script used in the analyses presented in part 2 of this document

```

sum.abund <- function(Y, assoc)
# From p/a data: in each site, sum the occurrences of the species belonging to each group.
# From abundances: in each site, sum the abundances of the species belonging to each group
{
  out <- matrix(0, nrow(Y), length(assoc))
  for(k in 1:length(assoc)) {
    out[,k] <- apply(Y[,assoc[[k]]], 1, sum)
  }
  out
}

# =====

# Visual test of some colours to produce the graphs on pp. 10 and 11
# Available colours in R: type colours() or colors()

# Plot a graph with selected colours

line.col = c("black","grey60","blue","darkgreen","darkolivegreen","turquoise",
             "red1","coral2","gold1","magenta1","maroon4","olivedrab1")

plot(0:10, type="n", xlim=c(0,10), ylim=c(0,8), main=c("Test des couleurs de lignes"))
axis(side=1, at=1:29, labels=1:29, cex.axis=1, las=1)
for(k in 1:6) {
  lines(c(1,3), rep(1,2)+k, type="l", col=line.col[k], lwd=2)
}
for(k in 7:12) {
  lines(c(5,6), rep(1,2)+k-6, type="l", col=line.col[k], lwd=2)
}

# Colours selected for the graphs "Sum of occurrences" and "Sum of abundances"

line.col6 = c("black","blue","darkgreen","turquoise","red1","maroon4")

# =====

```