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Using multitable techniques for assessing phytoplankton structure and succession in the Reservoir Marne (Seine catchment area, France)

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Abstract Micro-organisms, especially phytoplankton species, may be considered as potential indicators of local and more global changes in aquatic ecosystems and may thus constitute an excellent biomarker of water quality. Multitable analyses, such as partial triadic analysis and multiple coinertia analysis, are a well suited statistical tool to get a clear representation of the spatial and temporal organization of the assemblages of these different species and hence assess for the existence of changes in water quality. Handling of the few missing data was done using the NIPALS algorithm.

1 Material and methods

1.1 *Biological background and aims of the study*

Micro-organisms, especially phytoplankton species, may be considered as potential indicators of local and more global changes in aquatic ecosystems and may thus constitute an excellent biomarker of water quality. Assessing biological, chemical

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and physical influence on phytoplankton regulation is a key process to understand population structure and dynamics, population diversity and succession, and to propose, if necessary and when possible, a human-hand control before any excessive algal proliferation could occur. Such issues are of main concern to help scientists and water managers to make it possible for large-body reservoirs, lakes and ponds, to reach the “good ecological state” recommended by the Water Framework Directive (WFD) by 2015. One aim of our project was to identify both the spatial and temporal phytoplankton structure and dynamics in the Reservoir Marne (located in the Seine catchment area), referred to as one of the largest reservoirs in occidental Europe. In 2006, i.e. the first year of the project, the reservoir has been sampled once a month in March and April and then, once every two weeks between May and September. To assess for spatial heterogeneity, six stations and various depths for each station have been investigated. Stations K and J correspond to two nautical basins, station G receives water from two ‘feeding’ channels, stations I and H are close to the restitution channels and finally station N is more or less in the middle of the reservoir. This sampling strategy was chosen in order to obtain the best picture of the structure of the microbial organisms considering also human feasibility in terms of sampling and analysis.

1.2 Selection of species

Among the 282 phytoplankton species originally identified in the Reservoir Marne, 113 species were selected to be included in the multitable analysis, see Table 1 in [3] for details. The criterion for selection was that the relative abundance and biovolume of the species would be greater than a fixed value set to 0.01 %. It is a commonly used pattern of selection in phytoplankton community ecology studies.

1.3 Statistical methods

Since it was shown that the reservoir is not uniform as revealed by the phytoplankton abundance and structure which vary significantly from one sampling station to another and that a clear seasonal dynamics had been observed for the different microbial communities with main differences on a vertical scale, multitable analyses, such as partial triadic analysis, [7], and multiple coinertia analysis, [4], were a well suited statistical tool to get a clear representation of the spatial and temporal organization of the assemblages of the different species. Unfortunately, we experimented some failures in analyzing physical and chemical properties of several samples of water. As a result we had to deal with missing values and used the NIPALS algorithm, [8], as a way to try to solve our problem. Analyses were performed using the `pcaMethods`, [1], and `ade4`, [5] and [6], packages for the R software, [2].

2 Results

Investigations began with the spatial homogeneity of the Reservoir Marne through time. A rather good interstructure was revealed by the partial triadic analysis: on one hand, the arrows, Figure 1 left, head towards the same direction and on the other hand the \cos^2 are above average values for each of the table which is tantamount to a good representation of each of the tables on the compromise, Figure 1 right. This interstructure enables us to look at the compromise, a common temporal structure derived from each sampling station table, Figure 2 left and right, and check for its reproducibility among the 6 sampling stations (G, H, I, J, K and N), Figure 1 in [3]. The links highlighted by the interstructure between stations are sensible from a biological point of view if one looks at the different features of the stations such as maximum depth, distance from the shore, stream velocity and so on, depicted in 1.1. As one can spot on the compromise showing the temporal evolution of the phytoplankton community, left of 2, the phytoplankton community structure does not change between winter and spring. Then, after some time spent growing, the community structure undergo some changes between late spring and summer. The projection of variables, i.e. phytoplankton species, enables us not only to spot associations between species themselves but also to highlight which ones of the species are specific to some season of the year.

In order to investigate time homogeneity of the Reservoir Marne, a multiple coinertia analysis was performed – at first a partial triadic analysis was used but no satisfying interstructure was revealed, thus preventing us from using this kind of analysis–. Due to paper length restrictions, only the results of the partial triadic analysis for samples collected at a depth of 3 meters can be analyzed here. Some additional material is available in an appendix published on the Internet, [3].

The commonly used classification of phytoplankton species does not appear to be relevant to characterize either the season or the features of the stations. The results of our analysis provides an alternative solution by showing relevant associations.

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Interstructure

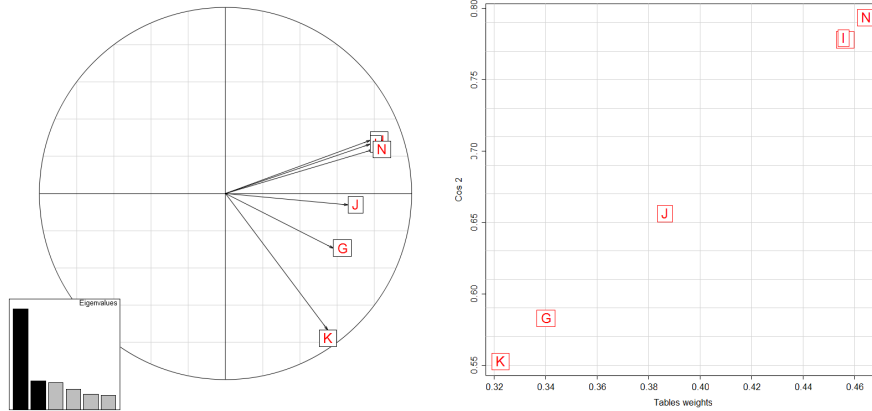


Fig. 1 Left: Temporal Interstructure derived from each sampling station table and their closeness according to the Axis 1 and Axis 2 computed from the partial triadic analysis. Right: \cos^2 and Table Weights.

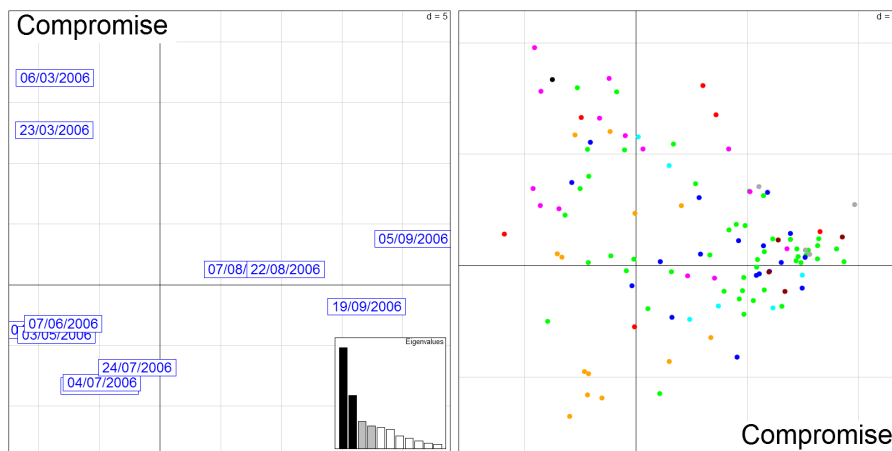


Fig. 2 Axis 1 and Axis 2 of the compromise for the partial triadic analysis. Left: Compromise with the temporal evolution of the phytoplankton community. Right: Phytoplankton Species colored by family and projected on the compromise of the partial triadic analysis.

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Appendix for tables and graphics

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Abstract Appendix for material (table and graphics) that could not be included in the article due to length restrictions.

Table 1 Phytoplankton family counts and color correspondence

Phytoplankton Family	Total Species	Selected Species ^a	Color
Cryptomonads	7	6	red
Cyanobacteria	33	18	blue
Desmidiates	26	4	darkred
Diatoms	46	14	magenta
Dinoflagellates	15	6	cyan
Euglenoids	16	4	darkgrey
Golden Algae	22	13	orange
Green Algae	111	47	green
Yellow-green Algae	6	1	black

^a Selection of species was carried out following the rules detailed in subsection 1.1 of the article.

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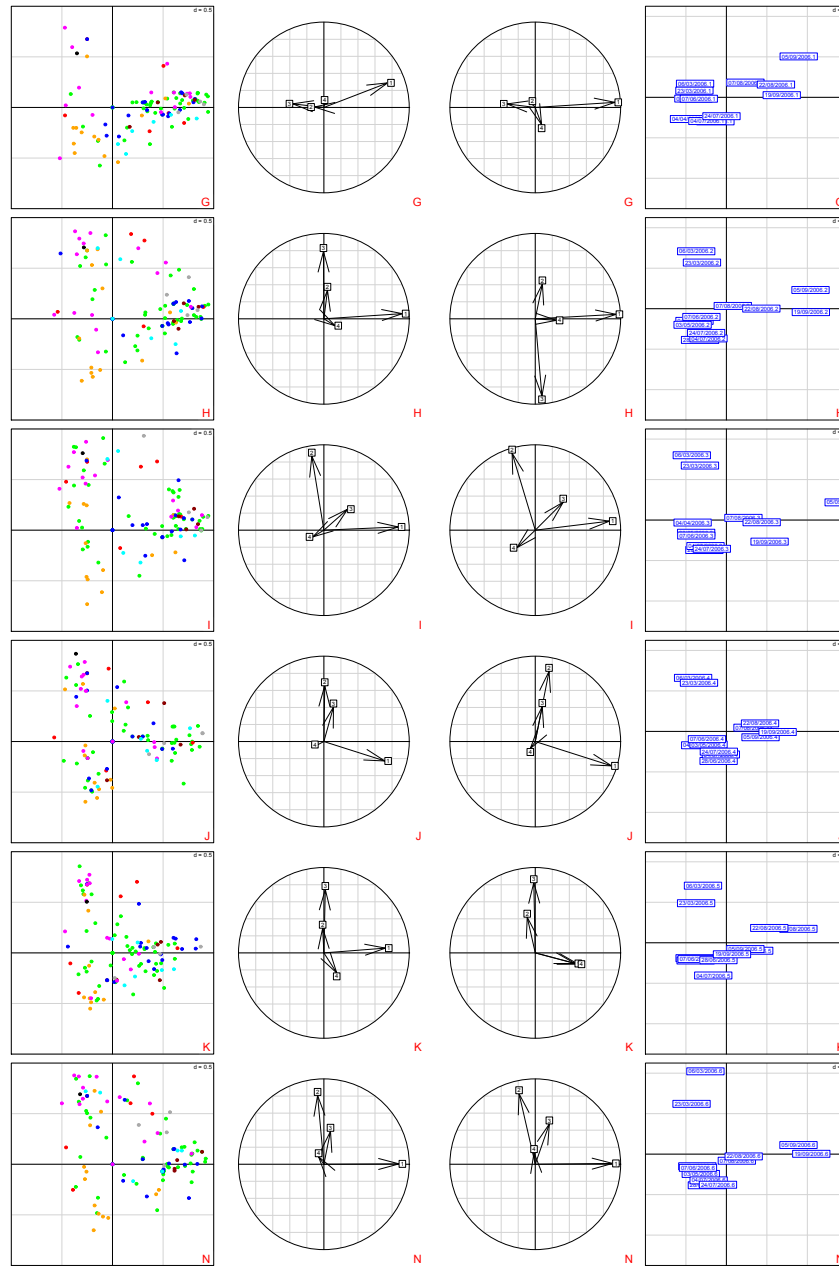


Fig. 1 Axis 1 and Axis 2. Reproducibility of the comprise for each of the six stations.