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Multivariate Methods: Identify Inhomogeneity in Phytoplankton

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Abstract

Numerous worldwide policies, including European laws like the Water Framework Directive and the Marine Strategy Framework Directive, have long examined phytoplankton as a crucial environmental quality indicator. These regulations call for extensive monitoring networks that use indicators that represent various phytoplankton properties, such as composition, to measure water quality. Additionally, phytoplankton monitoring systems are necessary in bivalve mollusk growing sites worldwide in order to manage potential toxicity. The succession of species, which in turn is impacted by environmental changes, is a necessary component of phytoplankton assemblages. The examination of phytoplankton communities, however, is also accompanied by a number of sources of variance. The standard procedure for identifying and counting phytoplankton in the European Union is the microscope-based method using the Utermöhl technique. This strategy calls for highly specialized taxonomists, yet most studies exhibit bias since different taxonomists have different levels of knowledge.

Keywords: Water; Environmental; Phytoplankton; Taxonomists; Knowledge

Introduction

Diatom indices are an exception, according to some studies, where the mistake brought on by taxonomist variance has no impact when a harmonised approach is used. Plankton samples that have been preserved may potentially provide estimates of cell volume and artefacts related to species abundance. Traditional fixatives, such Lugol's iodine and glutaraldehyde, have been shown to cause phytoplankton cells to shrink, bulge, or even rupture, which can skew estimations of biomass and abundance. It is crucial to evaluate the variability provided by each source of uncertainty in order to build more precise phytoplankton counting techniques and be able to interpret their results. Such studies are rare, as far as we are aware. Some of the material that was already published concentrated on particular topics, such as the necessity for a harmonized methodology, or more precisely on a particular taxonomic group, or on the impact of taxonomic resolution. The purpose of the current study is to explore the identification of inhomogeneities in phytoplankton time series and determine whether or not environmental factors are the only possible causes of these variations. The goal of this work is not to compare methodologies among laboratories, but rather to demonstrate the While examining long-term trends or patterns in phytoplankton composition and abundance, the value of a prior data analysis. Although phytoplankton time-series may contain significant ecological data, they may also be impacted by methodological issues. A thorough examination of the potential interference in phytoplankton inter-annual variability, as indicated by taxonomist experience and fixative type, is therefore addressed. We employ a lengthy time series that includes coastal and offshore regions and accounts for the entire nano and microplankton ecosystem. This study uses information from the Basque Water Agency's Littoral Water Quality Monitoring and Control Network, which was utilised to execute the Water Framework Directive in the Northeast Atlantic Eco region. 16 sites along the Basque coast and three offshore stations in the southeast of the Bay of Biscay make up the dataset. The study area has a temperate and oceanic environment with mild winters and warm summers. Euhaline and unprotected water bodies line the coast. The hydrographic conditions are described in depth. Except for two offshore stations that had datasets of seven years, the time series under analysis was gathered over a period of 13 years. Only the spring and summer data were analysed, despite phytoplankton samples being collected regularly since 2007. since those were the seasons that the entire time series sampled [1].

Temperature, salinity, Secchi depth, suspended particles, ammonium, nitrate, phosphate, and silicate were the environmental variables considered in the analysis. In the field, the Secchi disc depth was measured as an estimator of the water transparency, the temperature and salinity of surface waters were recorded using a conductivity, temperature and depth multi-parametric probe (CTD), and surface water samples were taken for subsequent laboratory analyses. After the water was filtered via Whatman GF/C filters, the concentration of suspended particles was determined. Using a continuous-flow autoanalyzer, inorganic nutrients (ammonium, nitrate, silica, and phosphate) were assessed using the colorimetric techniques described in. Whenever the levels of nutrients fell below the value utilised for statistical analysis was equivalent to one half of the quantification limit (1.6 mol L1 for ammonium, nitrate, or silicate; 0.16 mol L1 for phosphate). Surface water was promptly preserved for phytoplankton and kept in 125 mL borosilicate bottles under dark, cool (4°C) conditions until analysis. Up until 2011, glutaraldehyde (0.1 percent v/v) and acidic Lugol's solution (0.4 percent v/v) were utilised for preservation. Under a Nikon diaphot TMD inverted microscope, taxonomic identification and cell counting were carried out on subsamples of 50 mL (sometimes, particle density was too high and 10 mL samples were used instead) using the Utermöhl method. 100 xs or 400 xs, depending on the size of the organism Magnification was employed, and the detection threshold for micro planktonic organisms using microscope counts was 20 cells L1 [2].

Unidentified forms 10 m was the term given to a collection of small nanophytoplankton cells that could not be classified into any taxonomic category. The identification and counting of phytoplankton was done

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by three different taxonomists working in the same lab. Samples from the years 2003, 2008, 2009, and from 2012 to 2015 were handled by Taxonomist #1. Taxonomist #3 identified and counted samples from 2004, while Taxonomist #2 worked with samples from 2005, 2006, 2007, 2010, and 2011. Within the analysis year, there were no staff changes. From the start of the time series, the experience of the taxonomists grew, reaching more specialised taxonomic levels. The levels of species or genus were attained in the majority of the identifications, especially those made by Taxonomist #3. To ensure that environmental data met the assumptions of normalcy and homoscedasticity, they were transformed and normalized. Separate studies were run for the spring and summer. To look for significant variations between years, each individual variable was put through a one-way Analysis of Variance (ANOVA) and a multiple range test (95 percent least significant difference, LSD). Additionally, nonmetric Multi Dimensional Scaling (MDS) ordination and cluster analyses based on Euclidean distance matrices were carried out to explore the variability of all environmental variables together. To check for significant differences at each cluster dendrogram node, Similarity Profile Analysis (SIMPROF) at alpha = 0.05 was included. The average values of each variable for each season and year were used in the MDS analysis, eliminating the data from the first 18 of the 19 sample locations. Since only samples from 2009 onward were used. Permutational multivariate analysis of variance was also performed to test for significant differences between years for the study of the 19 sampling locations. A 9999-permutation PERMANOVA was performed with "year" as a fixed factor. Pair-wise comparisons between the 13 different years were made using a second PERMANOVA with the same conditions. ANOVA was performed using Stat graphics Centurion XVI, cluster analyses were performed using PRIMER 6 statistical software (Primer-E Ltd., UK), and PERMANOV was performed using MDS and Studio. The list of phytoplankton species was standardized in accordance with Algae Base before being subjected to mathematical analysis [3].

To lessen the amount of noise in the data, rare taxa defined here as those occurring in less than 1% of the samples were eliminated from the analysis. Out of the 336 taxa, 129 were not included in the analysis. Data on phytoplankton abundance (cell L1) were converted using log (x + 1). The spring and summer were given separate analyses. Using zero-adjusted Bray-Curtis matrices, MDS and cluster analyses were carried out in the same manner as they were for the environmental data. These matrices were used to investigate how community assemblages vary from year to year. For ecological community study, MDS is a potent ordination technique that permits a significant presence of zero values and does not require. Analysis was done using the I 19 sample sites and (ii) average cell density values for each season and year, same like with the environmental data. Analysis was carried out at the virtual sampling unit level based on the densities of I the lowest taxonomic level that was available and (ii) the major taxonomic groups (autotrophic coccoids, chlorophytes, *Mesodinium spp*., cryptophytes, diatoms, dinoflagellates, euglenophytes, haptophytes, ochrophytes, and unidentified forms). Additionally, a PERMANOVA (9999 permutations) was run to look for any changes that might be connected to the fixed factor "fixative." The two fixatives were used to divide the dataset into two subgroups. The first subset, which included information for the three taxonomists and related to glutaraldehyde, was subjected to a second PERMANOVA with "taxonomist" as a fixed factor. As a post-hoc test for pairwise comparisons between the three different taxonomists, an additional PERMANOVA was used. Because it only had data for one taxonomist, the second subset, where the acidic Lugol's solution was utilised, could not be subjected to a second PERMANOVA. Long-term phytoplankton time series research should take into account the evidence of the uncertainty resulting from laboratory issues (i.e., changes in fixatives, experience, or changes in the taxonomist). We recommend that community studies be done at higher taxonomic levels whenever possible because the interference brought on by changes in the taxonomists was less at the level of large taxonomic groups. Further research should be done regarding the detection of anomalies in phytoplankton time series, along with thorough methods, tight standards, and ongoing learning [4].

Discussion

A principal issue of natural science is to characterize the anthropogenic impacts on oceanic communities in a quantitative way, giving location of disturbances at an early organize. Whereas biomass is used as a conventional model, a few species frequently demonstrate very tall and exceptionally variable plenitudes. Such cell abundance inconstancy appears appropriate for giving early warning data. The cell-abundance conveyances can serve to get experiences into unsettling influence examination and irritation diagnostics. The takeoff from the lognormal distribution was proposed as giving files of pollution. The assemblage-perturbation record, based on artful species, was delivered from a small number of species.

The well-documented steady design of Lake Kinneret annual progression was kept up amid numerous years (1969-1992), went with with the 1993-1994 anthropogenic impacts and consequent irritated a long time. The long term record of the Kinneret can be utilized to approve speculations considering the phytoplankton composition response on increased anthropogenic push. A few parts of phytoplankton (phyla) situated at particular locales of ordered conveyances can be particularly delicate beneath unsettling influences and, therefore, profitable for diagnostics. In this modern work, we endeavored to choose and compare the species distribution designs of the foremost curiously parts of a lake phytoplankton array, as seen from long-term monitoring. The general point of the ponder was a seek for demonstratively important quantitative changes in particular taxonomic structure designs based on species wealth of Lake Kinneret (Israel) phytoplankton [5].

Conclusion

As part of the schedule observing program, phytoplankton samples were collected fortnightly employing a 5-L bathometer at a fixed pelagic station at the most profound portion of the lake, from discrete profundities all through the water column. Microscopic counting of Lugol-preserved tests was delivered using inverted magnifying instrument. All phytoplankton species with individual cells more noteworthy than 2 μm in breadth were identified and checked concurring to species, and for the more abundant species with variable cell size also concurring to estimate categories. Since our person taxon isn't entirely a species but in a few cases too a estimate category inside a species, we refer to each as an Operational Ordered Unit (OTU). From the littler cell extend, as it were the moderately common colonyforming cyanobacteria were included. Test handling was described in detail [6].

Conflict of Interest

The authors declare no conflict of interest.

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