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Application of an Objective Method for Detecting Changes in Fish Communities: Samar Sea, Philippines

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Abstract

Changes in ecological communities are often measured by the use of diversity or similarity indices. Although many indices are available, their statistical properties are usually unknown and significance cannot be assigned to the value of a similarity index or to the difference between two values of a diversity index.

FAUNSIM is a nonparametric method for determining the statistical significance of differences between two species assemblages for which no replicate samples are available. It makes use of Monte Carlo simulation and knowledge of the pool of species that may be found in the general region of interest. It generates an approximate probability distribution for the number of species expected to be common to the two assemblages of interest.

This method was applied to trawl survey data from Samar Sea, the Philippines. Using FAUNSIM, significant differences in the assemblages of demersal fish were found in both time and space. Deep and shallow stations were occupied by distinct assemblages. Assemblages at some stations changed significantly from 1979 to 1980. Visual inspection of changes in assemblages and standard diversity indices were not as effective as FAUNSIM in assessing the significance of observed changes in ecological communities.

Introduction

The fishery resources of many tropical marine environments are heavily exploited. The Samar Sea (located in the center of the Philippines) is an example of such an area (Fig. 1). The fish of this region were exploited by both "commercial" (> three gross tons) and "municipal" (<= three tons) vessels until 1977, when a ban on commercial fishing was gradually enforced by the government. By 1980 commercial vessels entered the region only on rare occasions (McManus 1985).

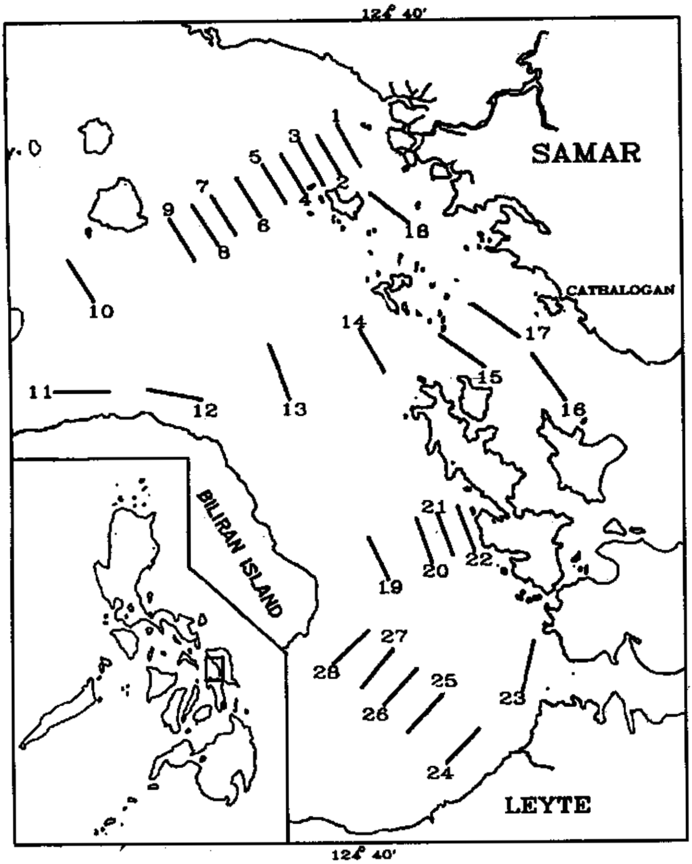

Fig. 1. Map showing the location of the Samar Sea and the sampling stations within. From Silvestre (1986).

During a 15-month period within 1979 and 1980, eleven cruises were made by a research vessel from the College of Fisheries, University of the Philippines, which sampled demersal fish at 28 stations in the Samar Sea (Fig. 1) (Silvestre 1986). The methods are described in detail by Armada et al. (1983). The results of these surveys were used in the analysis described herein.

A basic ecological question concerning areas where fishing may be a major influence, is whether the composition of fish species changes over time or space or both. To address this problem, one must be able to describe and compare different communities. Typically the state of a community has been described by use of diversity indices (Pielou 1977). Many of these indices are available (e.g., Sheldon 1969; Peet 1975; Washington 1984). However, each measures a different aspect of a community and their statistical properties are usually unknown. Thus, differences between values of a given index cannot usually be assigned statistical significance.

Similarity indices are more appropriate for comparing two communities. A similarity index is a single number which indicates the amount of sameness or difference between two communities on some scale. However, the statistical properties of standard similarity indices (e.g., Simpson's or Jaccard's) are even less well known than those of diversity indices.

A nonparametric method, implemented as a computer program (FAUNSIM) employing Monte Carlo simulation, has been developed to make statistical comparisons between communities. It is based on work published by Henderson and Heron (1977) and Raup and Crick (1979). This method allows one to state and test a null hypothesis about community similarity. We used this method to examine changes in the species assemblage of demersal fish in the Samar Sea between and within years.

Methods

FAUNSIM involves a comparison between the observed number of species common to two assemblages and the probability distribution of the number expected to be common to the assemblages. A discussion of the theoretical development can be found in Raup and Crick (1979). The source code for the program that we wrote (in Quick BASIC version 4.0, Microsoft 1987) can be found in Saila et al. (in press) and is available upon request.

As initial conditions, one must know the number of species in each of the two communities of interest and the number of species shared by them. An estimate of the pool of species, which reflects the relative abundance of all species found within the region of interest, must also be available.

Monte Carlo simulations are used to generate the empirical probability distribution. For each pair of observed species assemblages, a pair of assemblages is constructed by randomly sampling species from the pool of species. The analysis proceeds by randomly selecting individuals from the species pool and recording their species identification, replacing the individual after each draw. If an individual is drawn from the pool whose species identification is already recorded in the theoretical community being generated, it is returned to the pool and another individual is drawn at random. This continues until the number of species in the generated community is equal to the number of species in the first natural community (A). Once that is complete, the process is repeated to generate a second community which has the same number of species as the second natural community (B). At this point the two generated communities are compared and the number of species that they share in common is recorded. This value provides one point of an approximate probability distribution describing the number of species expected to be common to the two assemblages.

This entire process is repeated many times (100 times in this study), and the number of species shared by each random assemblage is recorded for each repetition. The resulting frequency distribution is an estimate of the probability distribution of the expected number of species in common. The null hypothesis being tested is: the species are randomly 'sprinkled' in space (or time) and thus all subcommunities will be the same, given natural variability (Raup and Crick 1979). The probability that the two observed assemblages are dissimilar is determined by comparing the number of species common to those two assemblages with that of the distribution of expected commonalty. Rejection of the null hypothesis was at the 95% level or greater in this study. An index of similarity can be computed as 1 - (the probability that the expected number of shared species will be greater than the observed number of shared species).

FAUNSIM was used to compare the demersal fish communities at a number of stations within the Samar Sea in both time and space. Comparisons in space were made for both March 1979 (cruise 96) and March 1980 (cruise 107). The species pool consisted of the sum of the abundances (measured by biomass) of all the species sampled at all 28 stations of a given cruise. The species pool for temporal comparisons consisted of the mean abundance (by weight) of all the species sampled at the 28 stations for the two cruises of interest.

Community analyses using clustering methods (McManus 1985) have shown a difference between the communities of deep and shallow stations in the Samar Sea. The division between these communities fell at approximately the 30 m isobath (Fig. 1). The same division was used here to define the deep and shallow communities. These communities were compared in March 1979 and March 1980. Each community was also examined for differences over time by comparing them from 1979 to 1980 (March). The same spatial and temporal comparisons were made of the communities at stations 2 and 18. These two stations were chosen for their proximity and completeness of data.

Results and Discussion

Analysis of the shallow and deep communities by FAUNSIM showed there was a significant difference between these communities both in space and time (Table 1) (Fig. 2). Comparison of stations 2 and

Table 1. Results of faunal comparisons in the Samar Sea.

Communities compared	Year	Probability $K_{obs} < K_{exp}$	Similarity[1] index
Shallow and deep	1979	1.0	0.0
Shallow and deep	1980	1.0	0.0
Shallow	1979 and 1980	1.0	0.0
Deep	1979 and 1980	1.0	0.0
2 and 18	1979	0.2	0.69
2 and 18	1980	0.84	0.11
2	1979 and 1980	0.99	0.005
18	1979 and 1980	0.72	0.195

[1] Based on FAUNSIM.

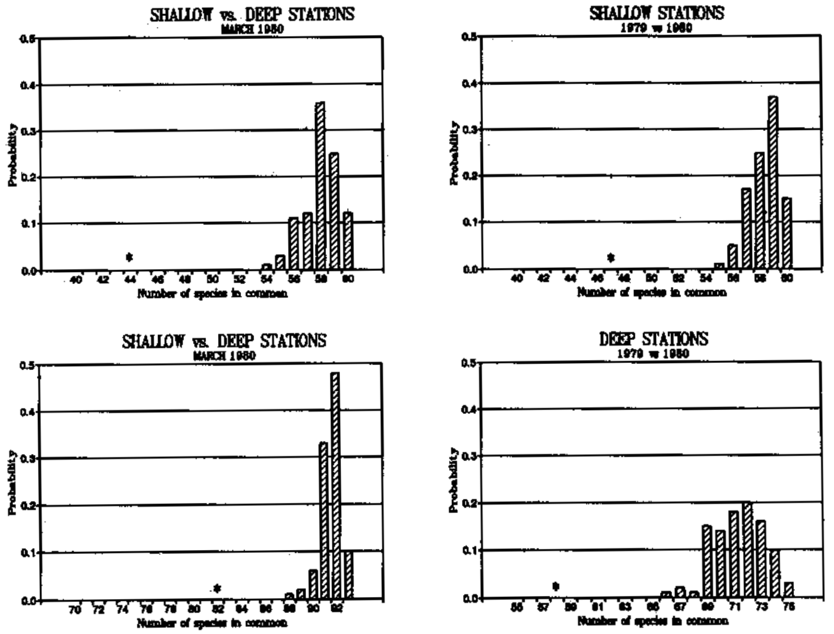

Fig. 2. Results of FAUNSIM analysis comparing the communities at shallow and deep stations. The vertical bars represent the probability that the associated number of species will be common to the two assemblages being compared. The asterisk identifies the number of species observed to be common to the two assemblages being compared.

18 showed that the communities there were not significantly different in March of 1979 or 1980 (Fig. 3). Temporally, station 18 did not change from 1979 to 1980, while station 2 did show a significant change (Table 1). The community structures are shown in Figs. 4 and 5. The number of species observed to be common to the shallow and deep communities was far less than would be expected from a random distribution. Thus, the shallow and deep stations were significantly different, supporting McManus' (1985) conclusions. Also, over time each of these communities shared fewer species than would be expected. This demonstrates a significant change from March 1979 to March 1980. Some differences can be seen visually in the communities (Fig. 4), but an objective method like FAUNSIM is necessary to determine the statistical significance of those differences.

Since stations 2 and 18 were located close together in similar habitat (McManus 1985), it is not surprising that they were not

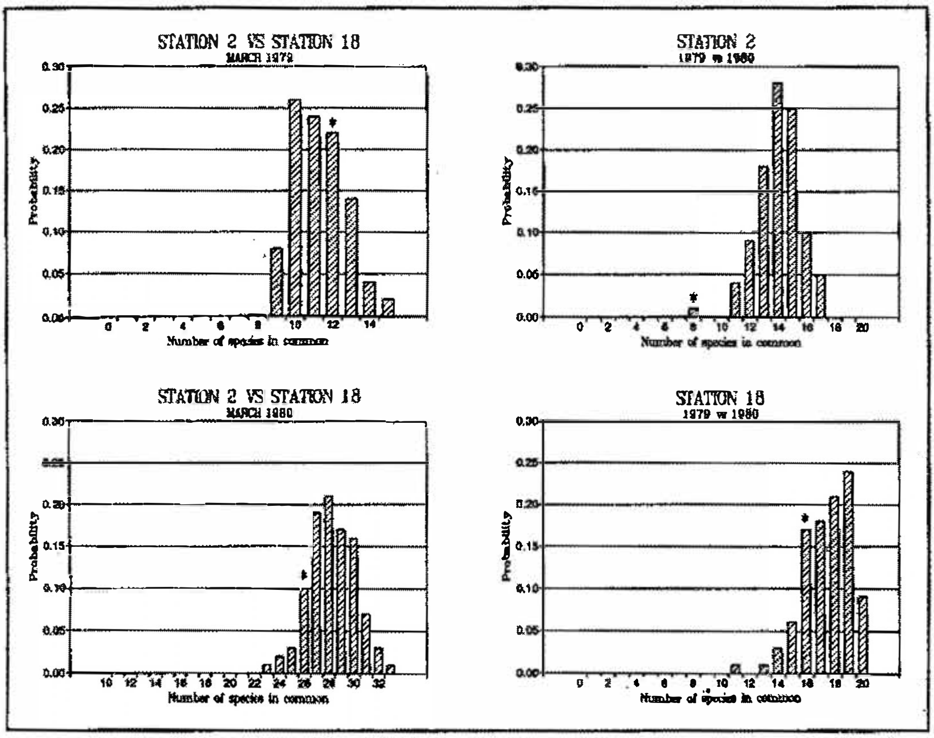

Fig. 3. Results of FAUNSIM analysis comparing the communities at stations 2 and 18. The vertical bars represent the probability that the associated number of species will be common to the two assemblages being compared. The asterisk identifies the number of species observed to be common to the two assemblages being compared.

significantly different within any one survey. While changes did occur in the communities at both of these stations from 1979 to 1980 (March), those at station 18 were not significant ($p = 0.28$, Table 1). Some of the differences between communities appeared to be significant upon visual inspection, but were not when critically tested by the FAUNSIM method (Fig. 4).

Comparison of faunal similarities with some standard diversity indices (Shannon and Weaver 1949; Pielou 1977) justifies the use of the FAUNSIM method (Table 2). There were a number of cases where large changes in the diversity indices were not significant (e.g., station 18, 1979-80) and where more moderate changes in these indices were significant (e.g., station 2, 1979-80). The Shannon-Wiener index (H') is composed of two components, richness and evenness. Changes in both of these components may counteract each other, resulting in little or no change in the diversity index when in fact a significant change has occurred in the community.

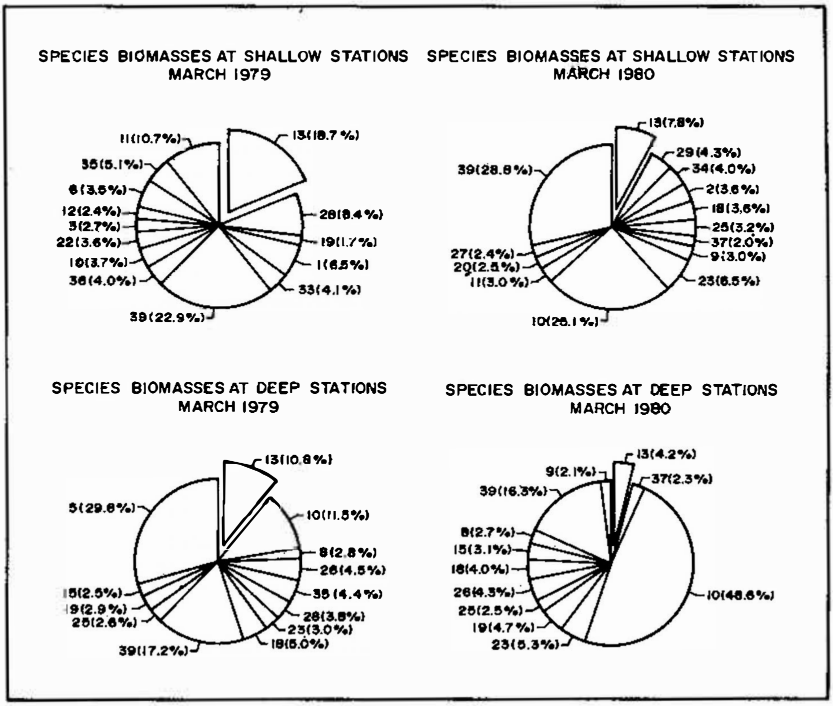

Fig. 4. Species compositions of the assemblages at the shallow and deep stations. The slice representing the contribution of squid (*Loligo* spp.) to the community abundance matrix has been offset in each case to emphasize the variability that may be displayed by a single species group.

Table 2. Conventional measures of diversity in the Samar Sea.

Station	Cruise	Richness	H'	(H'/ln(S*)) Evenness
2	96	18	1.53	0.335
2	107	38	2.54	0.556
18	96	21	1.87	0.410
18	107	46	3.13	0.686
4	96	7	1.12	0.245
4	107	43	2.94	0.644
5	96	19	1.68	0.368
5	107	38	2.77	0.607
Shallow	96	39	3.12	0.683
Shallow	107	107	3.23	0.708
Deep	96	80	2.77	0.607
Deep	107	94	2.39	0.524

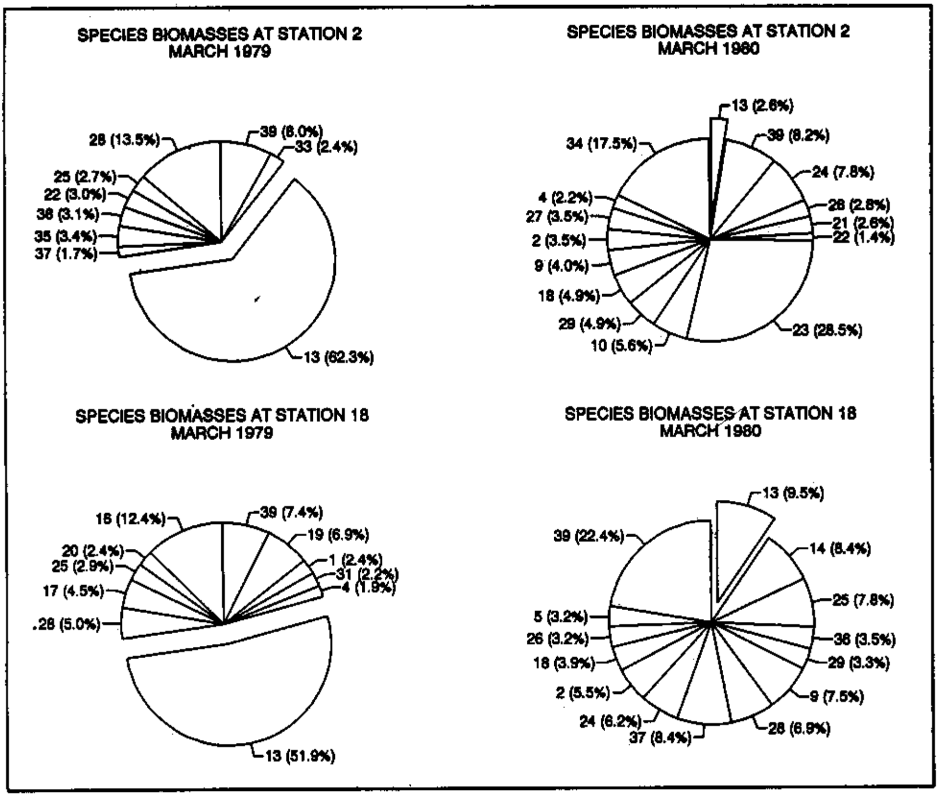

Fig. 5. Species compositions of the assemblages at stations 2 and 18. The slice representing the contribution of squid (*Loligo* spp.) to the community abundance matrix has been offset in each case to emphasize the variability that may be displayed by a single species group.

It is obvious from this discussion that FAUNSIM is effective at identifying statistically significant differences in species assemblages, but it tells us nothing about the mechanisms causing those differences. Looking more closely at the community structures in the Samar Sea, it becomes clear that not only richness and evenness, but also dominance ranking of the species, is important. For example, in March 1979 the shallow stations were dominated by squid (*Loligo* spp.), while the deep stations were dominated by *Decapterus macrosoma* and squid accounted for only 10.8% of the community (Fig. 4). However, the differences in diversity were relatively small (Table 2). Similar comparisons can be made for the other communities.

One can conceive of the situation where there are two communities with exactly the same richness and evenness, but whose species are ranked differently by dominance. Standard diversity indices would indicate that they were identical, while FAUNSIM would be able to distinguish significant differences between them.

Conclusions

The Samar Sea contains a diverse community of demersal fish. Recent surveys have shown changes in that community which may be related to changes in the fishing pressure exerted on that system. The significance of these changes must be established before an effective search for the mechanism(s) behind those changes can be mounted.

FAUNSIM is a method for objectively assigning statistical significance to the differences between natural communities. In the case of the Samar Sea it has discriminated between shallow and deep communities, as has been previously shown for the same region, and showed nonsignificant differences between closely located shallow communities. It has also detected significant shifts in some of these communities over time. This method can reveal community changes and their significance, but does not tell us anything about the mechanisms which have caused those changes. It is considered a useful first step in evaluating the effects of various types of perturbations on assemblages of organisms.

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