# CMFRI *Winter School on* Impact of Climate Change on Indian Marine Fisheries

Lecture Notes

Part 2

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# THE PRIMER SOFTWARE AND ITS APPLICATION IN MARINE BIODIVERSITY STUDIES

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#### Introduction



Convention on Biological Diversity (CBD) was signed at the UNCED "Earth Summit" in Rio de Janeiro in June 1992, came into force in 1993, and has been ratified by more than 150 countries. Diversity is a fundamental concept of community ecology, having a long history in both theoretical and applied studies (May, 1988). Detectable changes in the abundance or species composition of mesozooplankton may reflect fundamental changes in the ocean environment affecting phytoplankton (Clark, 1992). In turn, because zooplankton are eaten by larger animals, some of which are of commercial importance, changes in zooplankton communities can provide early indications of imminent changes in the food conditions for fish, birds and mammals. Because many zooplankton are relatively short-lived and are capable of high growth rates, they respond quickly to environmental perturbations that influence diversity, such as point-source pollution and predation pressure.

Biodiversity includes diversity within species (genetic diversity), between species (organismal diversity) and between communities (ecological diversity) as defined by Harper and Hawksworth (1994). At the organismal level, the most widely used biodiversity measures are those based on the number of species present, perhaps adjusted for the number of individuals sampled, e.g. Margalef's Species richness index (d), or indices that describe the evenness of the distribution of the numbers of individuals among species, e.g. Pielou's evenness (J), or that combines both richness and evenness properties, e.g. Shannon's H' (Magurran 1991). These indices may be of value as comparative biodiversity measures in situation where sampling methods, sample size and habitat types are carefully controlled (Warwick and Clarke 1995).

In the last decade a variety of different biodiversity measures have been devised to measure the degree to which species are taxonomically related to each other such as "variations in taxonomic distinctness" and "average taxonomic distinctness" (Clarke and Warwick, 2001). AvTD is the measure of mean path length through the taxonomic tree connecting every pair of species in the list, while VarTD is simply the variance of these pairwise path lengths and reflects the unevenness of the taxonomic tree (Clarke and Warwick, 2001). These two indices are not dependent on sampling methods, sample size and habitat types and are widely used for broad scale geographical comparisons of biodiversity, environmental impact assessment and evaluation of surrogates for biodiversity estimation (Clarke and Warwick, 2001).

#### **PRIMER Software**

The PRIMER (Plymouth Routines In Multivariate Ecological Research) software was developed by Dr. Bob Clarke and Dr. Ray Gorley of Plymouth Marine Laboratory, UK (Clarke and Warwick, 1994). This software can perform analysis of ecological data entered in spreadsheets. It can be used for calculating various univariate biodiversity measures such as Margalef's index, Shannon-Weiner index, Brillouin's index, Simpson diversity index etc. The latest version of the software (PRIMER 6) consists of a wide range of univariate, graphical and multivariate routines for analysing the species/samples abundance (or biomass) matrices that arise in biological monitoring of environmental impact and more fundamental studies in community ecology, together with associated physico-chemical data. The methods make few, if any, assumptions about the form of the data ('non-metric' ordination and permutation tests are fundamental to the approach) and concentrate on approaches that are straightforward to understand and explain. The basic routines of the package cover: hierarchical clustering into sample (or species) groups (CLUSTER); ordination by non-metric multidimensional scaling (MDS) and principal components (PCA) to summarise patterns in species composition and environmental variables; permutation-based hypothesis testing (ANOSIM), an analogue of univariate ANOVA which tests for differences between groups of (multivariate) samples from different times, locations, experimental treatments etc; identifying the species primarily providing the discrimination between two observed sample clusters (SIMPER); the linking of multivariate biotic patterns to suites of environmental variables (BEST); comparative (Mantel-type) tests on similarity matrices (RELATE); standard diversity indices; dominance plots; species abundance distributions; aggregation of arrays to allow data analysis at higher taxonomic levels, etc.

A further unique feature of PRIMER 6 is the ability to calculate biodiversity indices based on the taxonomic distinctness or relatedness of the species making up a quantitative sample or species list, indices whose statistical properties are robust to variations in sampling effort. These routines allow formal hypothesis tests for change in biodiversity structure at a location (as measured by average and variation in taxonomic 'breadth' of the species list), from that 'expected' from a larger, regional species pool. It provides a possible way of comparing biodiversity patterns over wide space and time scales, when sampling effort is not controlled (Clarke and Warwick, 2001).

#### Application

The PRIMER software is widely used for various ecological studies. This methodology is cited in more than 1,000 academic research papers published in nearly 185 peer-reviewed journals. It can be used for multivariate, univariate and graphical analysis of "species by samples" array of abundance, biomass, area cover etc. It can be used for fundamental studies linking assemblages to environmental structure, field/ laboratory community experiments, dietary compositional studies etc. It is also used for wide scale regulatory and commercial use in assessing environmental impacts of oil exploration, industrial and agricultural discharges, mining, trawling, aquaculture etc. This software is very useful for calculating different biodiversity indices from large number of survey data covering different habitats.

#### Reference

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Fig. 1. Brochure of the PRIMER software showing its key features.