miles in five weeks involving movement to Ocean Drive, South Carolina. Two white shrimp were recaptured off St. Augustine, Florida establishing migration records of 345 miles.

The pink and brown shrimp populations included in this study appear to be more endemic to North Carolina, whereas the major white shrimp population from the Cape Fear River area apparently contributes to the shrimp fishery off South Carolina, Georgia, and Florida.

Rough bottom terrain along most of the North Carolina coast restricts shrimping activities to relatively shallow waters. Perhaps additional catches of brown and pink shrimp can be made if suitable offshore towing areas are located and new types of gear developed.

Weekly length-frequency distribution curves were obtained by combining daily measurements of all marked shrimp. The modes of the length-frequency distribution curves for all three species were at, or increased to, "levels of equilibrium" in the mark-release areas that were apparently caused by migration of larger individuals from the area, immigration of smaller ones from upstream reaches, and growth within the mark-release area.

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THE DEVELOPMENT OF A TAXONOMIC CODE AND DESIGN OF A SYSTEM FOR THE ANALYSIS OF BIOLOGICAL DATA[1]

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ABSTRACT

The voluminous amounts of biological information collected for the Mississippi Estuarine Inventory required the development of a system for the automatic processing of this data.

The prime requirement of such a system was preparing a taxonomic code that could be easily updated and efficiently handled by EDP equipment. A modified version of the phylogenetic taxonomic structure was used to reduce the extent of the code and make optimum use of computer time. By the use of several search algorithms, computer memory requirements were substantially reduced.

The utilization of the coded input to present an output with scientific names rather than code eliminated the undesirable need for double reference. The necessity for the biologist to be involved directly with the processing is eliminated, thus freeing him to devote his talents to the comprehensive interpretation of the results.

INTRODUCTION

The ability of sophisticated electronic computers to reduce once time-consuming, laborious operations to a fraction of the time has resulted in an exponential increase in technical information. Recent improvements in sampling gear and recording methods have further added to this expanding volume of knowledge.

The handling of voluminous amounts of data, raw or processed, is nothing new to the field of biology and is certainly one of the characteristics of the science. Electronic computers are playing a major role in the solution to the problem of storage and retrieval of biological information. There are, however, some unique problems in the application of EDP equipment for the handling and analysis of biological data.

Dr. Luis Rene Rivas (1964) proposed a taxonomic code that would aid in the handling of biological data on an international basis. This code is very broad in scope encompassing all taxonomic levels except Kingdom and sub-species. The code developed at the Gulf Coast Research Laboratory was independently designed for flexibility and optimized for minimum time in handling by both personnel and computer.

DISCUSSION

In systematizing biological information for computer utilization, numerous parameters, sampling methods, sampling schemes, standards, methods of analysis and the possibility of several objectives must be considered. Maximum flexibility within the limitations of the EDP equipment being utilized is a primary objective of such a system.

The amount of biological information collected for the Mississippi Estuarine Inventory required the development of a system for the automatic processing of these data. Cross reference between physical parameters, maintained separately, and biological data was accomplished with the use of gear type, sample and station number. The difficulty arose in maintaining the identity of the species without requiring additional effort on the part of technical personnel or increasing costly computer time through elaborate and intricate programming. The prime requirement in solving this problem was preparation of a taxonomic code that could be easily updated and efficiently handled by EDP equipment.

Past efforts at taxonomic codes were either inadequate for our purposes, proposed or incomplete. The FAO code (1965) at present, is limited in its ability to handle genus and species. The taxonomic code, developed at our Laboratory and put into use in February, 1966, is structured on the binomial system of nomenclature.

An eleven-digit code was established representing five categories of taxonomic level. The first two digits indicate phyletic level groups except for the Arthropoda and Chordata. Classes of these two groups are indicated by the first two digits. The second pair of digits indicates the next lower taxon, the following three digits indicate family with the remaining two pair representing genus and species.

A list of species, encountered during the project, with their corresponding taxonomic codes serves as an internally stored reference table. The programmed computer, after accepting the numeric taxonomic code identifying the biological data, by an algorithmic search attempts to match this taxonomic code with the internally stored tables of codes. If the codes match, the corresponding species name from the table is used in the output list. If there is not a matching code in the table, caused by either an incomplete internal table or a specimen that is not completely identified, the code of the data is simply reproduced on the output list. If it proves helpful, it could easily be arranged to print the last identifiable level of the specimen. The output list consists therefore of

the name of the species or taxonomic code in addition to the results of the analysis performed on the data.

Using an off or on-line sort to arrange the taxonomic codes in numerical order, automatically places the specimens in a semi-phylogenetic order.

The implementation of this code in the handling of the various data has eliminated many time-consuming steps in progressing from raw data to the final comprehensive interpretation of the processed results. Future applications of such codes will be valuable in storage and retrieval of literature relating to the respective coded specimen.

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AN ANALYSIS OF THE GROWTH OF PACIFIC HERRING (CLUPEA PALLASII), LAKE STURGEON (ACIPENSER FULVESCENS) AND WHITE STURGEON (ACIPENSER TRANSMONTANOUS)

BY THE PARKER-LARKIN AND VON BERTALANFFY METHODS[1]

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ABSTRACT

The growth of the Pacific herring (*Clupea pallasii*), lake sturgeon (*Acipenser fulvescens*) and white sturgeon (*Acipenser transmontanous*) is analyzed by the application of Parker-Larkin and Von Bertalanffy equations. The physiological significance of the parameters of the two equations is discussed.

ACKNOWLEDGMENTS

INTRODUCTION

Of the parameters in the dynamics of fish populations, the measure of the rate of growth is of primary importance since growth is a basic determinant of productivity. In Fishery Science the growth equation of Von Bertalanffy is most commonly used (Beverton and Holt, 1957). The equation assumes asymptotic growth, and the difference between size and an "ultimate attainable size" determines growth rate. A linear

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[1] Based on a thesis submitted to the University of British Columbia in partial fulfillment of the requirements for the degree of Master of Science.