# BIOS a database for marine biological data

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**Abstract.** BIOS is a computerised database system for holding species distribution data. Emphasis has been placed on the flexibility in which stored information can be accessed. Multiple retrieval pathways permit simple enquiries to be answered or complicated interrogation sequences for statistical treatment of data. The structural organisation of the database is explained and details of its contents are listed. Examples of applications in the fields of zoogeography and ecology are given together with illustrations.

## Introduction

The Biology Group at the Institute of Oceanographic Sciences (IOS) has been engaged in sampling the North Atlantic for many years. During the past decade mid-water animals have been routinely caught with devices such as the Rectangular mid-water Trawl (RMT) system which employs acoustically operated opening and closing nets (Baker *et al.* 1973). The gear, which is monitored on board ship, is fished at prescribed depth horizons and has been worked from the surface to below 4500 metres. Earlier versions which comprised a pair of nets of 1 and 8 metres square have largely been superseded by a multiple system of 3 pairs (Roe and Shale, 1979). This recent development has increased the sampling rate and minimised the time between stations, reducing expensive ship time.

Benthic samples are currently collected with otter trawls (Merrett and Marshall, in press) and sledges (Aldred *et al.*1976), the latter types, like the RMT systems are monitored from the ship. Frequently camera and flash equipment are used to photograph the undisturbed substrate ahead of the advancing net mouth.

Physical oceanographic parameters important for understanding the structure and behaviour of the water masses have been measured with lowered hydrographic instruments such as CTD (Conductivity, Temperature and Depth) profilers. Sampling strategy is now often determined after a CTD dip has revealed the temperature and salinity structure of the water column.

This paper is intended to serve as an introduction to the Biology Group's computerised database system developed in response to the need to deal effectively with large and varied volumes of data that have accumulated as a result of IOS sampling activities. The system is an attempt to assimilate and integrate these forms of data so that interrogation sequences can be directed at a coherent body of stored information. The database thus fulfils two roles, firstly it acts as an archive or repository for data that are the by-products of research cruises, secondly, and perhaps of greater importance it functions as a powerful tool for data

analysis enabling information to be processed in ways which might prove impractical by conventional means.

## IDS (Integrated Data Store)

In late 1977 IOS installed a Honeywell 66/20 computer to handle part of its computational requirements. IDS which is one of the manufacturer's proprietary database packages is supported on this machine and has been used to create the BIOS database. Like other systems of its type IDS is based around the business oriented COBOL language developed in the early 1960s, which predates the more recent CODASYL (Conference on Data Systems Languages) database systems although it has a great many features in common.

In order to permit users to write their programs in FORTRAN (a more scientifically amenable language) IOS and Honeywell jointly developed an interface which although designed specifically for the Marine Information Advisory Service (MIAS) it has been made available to interested parties such as the Biology Group.

In essence, IDS permits the database designer to construct a computer file on which different types of data can be logically interrelated. The subject of database construction in general does not come within the scope of this paper but it is, however, desirable that the reader should appreciate some of the features of the IDS system so as to understand the nature of the BIOS design, to this end some of the techniques and alas, terminology will be introduced in later sections.

## Formats and Structure of IOS Biological Data

In 1972 an IOS Internal Report was produced entitled "An IOS Format for Species Distribution Data", which recommended in the absence of any internationally agreed standards, a number of formats which would enable data to be prepared on punch cards. In this form the data would be suitable for computer input facilitating zoogeographic statistical analysis. The recommendations made in this report were implemented and the preparation of the punched cards began. Prior to the installation of IOS' new computer, the cards were processed in a conventional manner using existing computer facilities.

The installation of the 66/20 computer with its IDS system led to the development of the BIOS database; no amendments were required to the existing card formats and since its inception in early 1978 tens of thousands of data cards have had their contents stored on the database.

IOS biological data is divided into several levels which constitute a hierarchy and it is this which forms the core or major axis of the database. Table I describes the main levels of data each of which is represented by its own card format. The data conforming to the hierarchy described in Table I is pyramidal in structure. For a given cruise only a single level 1 (CRUISE) format card is required. Each cruise will have a number of stations associated with it, each of which is represented with a level 2 (STATION) format card. Several samples taken with different devices may occur during a single station each having its own level 3 (SAMPLE) format card. Level 4 (SERIAL) formats, which refer to devices with numerous subsamples are rarely required but devices such as nets that catch or

Table I. Summary of the data hierarchy

| Level | Contents |
|-------|----------|
| 1 | Information about the organisation of a cruise e.g. ship code, cruise number and dates. |
| 2 | Information about an individual station e.g. its number, positions, times and date. |
| 3 | Details about a sample taken during a station such as device code, beginning and end positions and times. |
| 4 | Parameters associated with a subsample (this format is only required when using a serial sampler such as a Longhurst net or pump). |
| 5 | Details concerning a single species occurring within a sample. This format is varied, depending upon the type of animal or plant, but includes a species code, the total number of species caught, no. of adults, males, females and juvenile stages, biomass etc. |

trap animals invariably give rise to a number of level 5 (CATCH) format cards. This level being at the foot of the pyramid is by far the most numerous type of data format. Figure 1 is a graphical representation of a segment of the data structure; note how the data formats are interrelated. Level 4 has been omitted as it is rather infrequent.

*IDS and the BIOS database*

IDS stores information in "records", which are a collection of individual data fields that can be conveniently grouped together. Each of the punched card formats has an equivalent "record type", for example levels 1 and 5 have record types CRUISE and CATCH respectively. Figure 1 represents a 'natural' data hierarchy, the data base designer describes the relationships between its record types to IDS which can then model the structure. Related records are organised into "chains", for example all the STATION records associated with a CRUISE are linked together consecutively. The CRUISE record is known as the head or
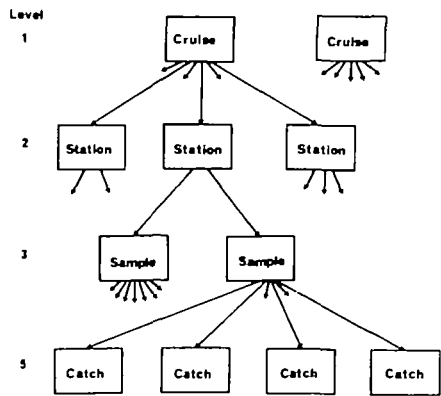


**Fig. 1.** Graphical representation of a segment of data illustrating the hierarchical relationship between record formats.

"master" of this chain whilst each STATION is a "detail". The records that form the details of the chain are not physically joined together, instead each will contain the file address of the next member in the chain (these forward addresses are called "pointers"). The CRUISE record that is a master of a chain of STATION records contains a pointer to the first details (a STATION record), the last STATION record contains a pointer back to the master, so the chain can be regarded as a closed loop.

A record that is a detail of one particular chain may be a master of another, thus SAMPLE records that are subordinate to STATION records in the data hierarchy are details of a chain headed by a STATION record. Similarly CATCH records are details of chains connected to their relevant SAMPLE records.

Figure 2 is a diagram which illustrates how IDS would treat the records shown in Figure 1. Pointers between records in a chain are represented by interconnecting lines. Note that at the top of the hierarchy a record type called CRUISE-MASTER has been inserted so as to include all CRUISE records themselves within a chain, this single record which is known as a Primary record also has an important system function.

*Data Retrieval Techniques*

IDS employs two practical methods of data retrieval; one accesses records directly, the other indirectly. The majority of the record types in the BIOS database can be accessed by both methods. Records that can be accessed (retrieved) directly contain one or more data-fields through which each is rendered unique. Each cruise record for example has a field containing a unique cruise number which may be used as a "key". IDS uses this cruise-number field to calculate the address of a specific record by means of a "randomising" algorithm. It is for this reason that record types that can be retrieved by this means are called calculated
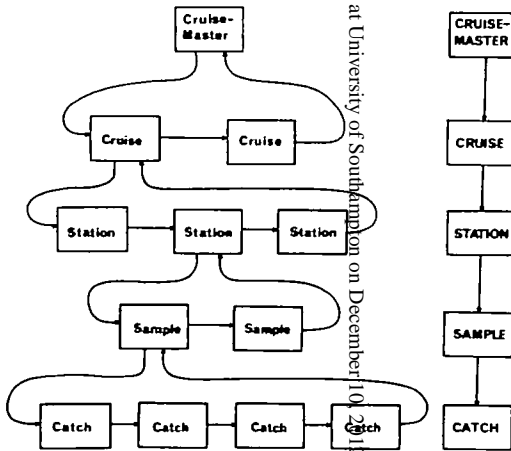


**Fig. 2.** Records are joined in 'chains', this diagram illustrates how IDS organises the records shown in figure 1. To the right hand side is a shorthand notational representation of the record relationships which is more convenient when describing an IDS structure. Chain formations are implicit.

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records (abbreviated to calc) and the key data-fields known as calc-fields. A CRUISE record may be retrieved by specifying its cruise number which acts as a calc-field, IDS calculates the record address and its contents become available for examination.

Each STATION record can be retrieved via its station number. The numbering system is that used by the *"Discovery" Collections, numbers which run consecutively are further qualified by a series number but for simplicity the BIOS database amalgamates station and series numbers into a seven digit code. At the time of writing the current highest station number was 10160.

SAMPLE records are also of the calc type but unlike CRUISE and STATION records they use two calc-fields, the first one is the station number of their master STATION record, the other is a two digit device code. Although there is often more than one sample taken during a station a particular device is not used more than once, thus the station number and the device code yield a unique combination.

The other method of retrieval is indirect, a record with the desired characteristics is found by a process called "chain-walking". The master of a chain containing the record(s) in question is first retrieved probably via its calc field, then each record contains a pointer to the next one in the chain thus providing a method of access. Stepping along the chain the contents of each record are available for examination, this continues until the required record(s) has been encountered. In the event of all the records having been examined and the desired record(s) absent, the chain returns to the master and an alternative decision step has to be made.

As catch records do not possess calc-fields with which they can be retrieved directly, they are known as secondary records and must be retrieved by the method just described. Suppose data are required to be examined for a particular species within a known haul, it is first necessary to retrieve the SAMPLE record by supplying values for the station number and device codes calc fields. The retrieval is made with a FORTRAN subroutine call and then its attached chain of CATCH records may be 'walked' with repeated calls to another subroutine. Each CATCH record contains a 9 digit species code which may be tested against the one required; if this is not found, the chain is "exhausted" and control returned to the master SAMPLE record.

Whereas secondary records must be retrieved via chain walking, calc records may be retrieved by either method; the one chosen will depend upon the function. Listing of stations from a cruise is likely to employ chain walking but the detailed examination of a single STATION would normally use the 'CALC' method.

*Further Features of the BIOS database*

The concept of IDS and some of the basic features of the BIOS database system have now been discussed and the reader may now perhaps appreciate the structuring and some of the mechanisms of data retrieval. What advantage does this system have over more conventional techniques? If the database structure were

*started in 1925 for the purpose of whaling research.

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merely confined to that which has been described the answer to the question would be "very little". Retrieval of CATCH data would be restricted to a route via STATION and or SAMPLE records. Accepting that a computer would be used at some stage, the system, at best, would only be marginally more efficient than processing the data in a serial manner from media such as disk files or magnetic tapes.

In fact the BIOS database does not restrict retrievals to the afore-mentioned pathway. Peripheral to the central core of data records illustrated in figures 1 and 2 are a number of record types constructed to categorise attributes of both SAMPLE and CATCH records. This is made possible as IDS permits records to be masters and details to more than one type of chain. Figure 3 is a schematic diagram of the whole database structure using the notation introduced in figure 2. A description of the contents of each record type may be found in Table II.

As a consequence of the additional record organisation made evident in the full structural diagram, there are a number of pathways through which access to data has been optimised. The following is a list of primary retrieval routes other than the one already described.

**Table II.**  Biological Database Record Structure

| Card Cols. | Description of Data-Fields |
|---|---|
| **Record type CRUISE Card format 101 (Level 1)** | |
| 1-2 | Country code |
| 3-4 | Institution code |
| 5-6 | Ship code |
| 7-9 | Cruise number |
| 22-27 | Start of cruise ddmmyy |
| 28-33 | End of cruise      " |
| 34-43 | International program or expedition |
| 44-46 | Number of stations during cruise |
| - | Comment ref. number |
| **Record type STATION Card format 201 (Level 2)** | |
| 7-9 | Cruise number |
| 10-16 | Station number |
| 22-31 | Station start time |
| 32-41 | Station stop time |
| 42-54 | Station start position |
| 55-67 | Station stop position |
| 68 | Light code |
| 69-72 | Mean sounding depth |
| 73 | No. of sampling devices |
| 74-76 | Ship's speed in 10ths of Knot |
| - | Comment ref. no. |

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| Card cols. | Description of Data-fields |
|---|---|

**Record type SAMPLE Card format 301 (Level 3)**

| | |
|---|---|
| 10-16 | Station number |
| 17-18 | Sampling device code |
| 22-27 | Time of net opening |
| 28-33 | Time of net closing |
| 34-46 | Position of net opening |
| 47-59 | Position of net closing |
| 60-65 | Sample size |
| 66-67 | Size option |
| 68-71 | Minimum depth of tow |
| 72-75 | Maximum depth of tow |
| - | Comment ref. no. |

**Record type ENVPARAM Card format 302**

| | |
|---|---|
| 22-23 | Parameter code 1 |
| 24-29 | Mean value of parameter 1 |
| 30-35 | Minimum value of parameter 1 |
| 36-41 | Maximum value of parameter 1 |
| 42-43 | Parameter code 2 |
| 44-49 | Mean value of parameter 2 |
| 50-55 | Minimum value of parameter 2 |
| 56-61 | Maximum value of parameter 2 |
| - | Comment ref. no. |

**Record type NET-INFO Card format 303**

| | |
|---|---|
| 10-16 | Station number |
| 17-18 | Sampling device |
| 21-56 | Gear information |
| 57-76 | CTD and TSD file ref |
| - | Comment ref. no. |

**Record type SERIAL Card format 401 (Level 4)**

| | |
|---|---|
| 19-21 | Number of subsample |
| 22-26 | Time of subsample |
| 27-31 | Position in M from start |
| 32-44 | Optional position |
| - | Comment ref. no. |

**Record type SENVPARA Card format 402**

| | |
|---|---|
| 22-23 | Parameter code 1 |
| 24-29 | Mean value of parameter 1 |
| 30-35 | Minimum value of parameter 1 |
| 36-41 | Maximum value of parameter 1 |
| 42-43 | Parameter code 2 |
| 44-49 | Mean value of parameter 2 |

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| Card cols. | Description of Data-fields |
|---|---|
| 50-55 | Minimum value of parameter 2 |
| 56-61 | Maximum value of parameter 2 |
| - | Comment ref. no. |

## Record type GENCATCH Card format 501 (Level 5)

| | |
|---|---|
| 10-16 | Station number |
| 17-18 | Net code |
| 22-30 | Species code |
| 31-35 | Total no. of animals caught |
| 36-40 | Total no. of adults caught |
| 41-45 | Number of males caught |
| 46-50 | Number of juveniles stage 1 caught |
| 51-55 | "        "        "        "     2   " |
| 56-60 | "        "        "        "     3   " |
| 61-65 | "        "        "        "     4   " |
| 66-68 | Multiplication factor |
| 69-74 | Biomass of subsample |
| 75-76 | Biomass code |
| - | Serial sampler flag |

## Record type LONGPUMP Card format 506 (Level 5)

| | |
|---|---|
| 10-16 | Station number |
| 17-18 | Net code |
| 19-21 | Depth interval in metres |
| 22-30 | Species code |
| 31-32 | Block number |
| 33-36 | No. of animals in subsample 1 |
| 37-40 | "    "    "    "    "    2 |
| 41-44 | "    "    "    "    "    3 |
| 45-48 | "    "    "    "    "    4 |
| 49-52 | "    "    "    "    "    5 |
| 53-56 | "    "    "    "    "    6 |
| 57-60 | "    "    "    "    "    7 |
| 61-64 | "    "    "    "    "    8 |
| 65-68 | "    "    "    "    "    9 |
| 69-72 | "    "    "    "    "   10 |
| 73-76 | Horiz. distance between subsamps M. |
| - | Comment ref. no. |

## Record type DATATYPE Card format 550

| | |
|---|---|
| 1-3 | Data type format number |
| 5-22 | Description of data format |
| - | Comment ref. no. |

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Card cols.    Description of Data-fields

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Record type GENDATA Card format 560

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| 10-16 | Station number |
| 17-18 | Sampler code |
| 22-30 | Species name |
| 31-76 | Data |
| 78-80 | Data format code |
| - | Comment ref. no. |

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Record type GEAR Card format 220

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| 1-2 | Gear code |
| 4-12 | Gear name |

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Record type DEPTH Card format 230

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| 1-4 | Top of depth zone |

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Record type TENDEGSQ Card format 801

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| 1-4 | Corrected 10 degree Canadian square |

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Record type ONEDEGSQ Card format 802

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| - | 10 deg + 1 deg square component |

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Record type GROUP Card format 601

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| 1-3 | Group code GGG |
| 5-22 | Group name |

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Record type GENUS No card format

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| - | Genus code GGGggg |

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Record type SPECIES Card format 701

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| 1-9 | Species code GGGgggsss |
| 11-46 | Species name |

---

Record type LINKER No card format

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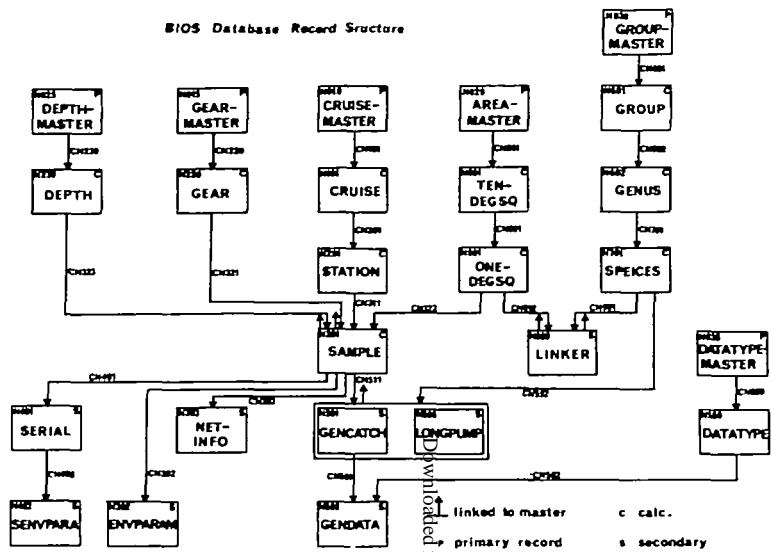| - | No fields, connects species to 1 deg. sqs. |

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Fig. 3. Overall database structural diagram. Record types indicated as being 'linked to master' contain pointers not only to adjacent records in their chains but also ones directly to their masters, speeding up certain retrievals. Record types which are shown as being recipient of more than one connecting line are members of more than one type of chain. Similarly record types that disseminate more than one connecting line are masters of more than one type of chain.

## i) *By Taxonomy*

Each CATCH record is a detail of a chain that links together records of the same species. The master of each of these chains is a SPECIES record which has as a calc-field the same 9 digit species code as the CATCH records in the chain. Retrieval of a SPECIES record therefore facilitates access to all data pertinent to that species.

The 9 digit species code is, in reality, a composite of 3 sets of 3, comprising codes for Group, Genus and Species. Whereas genus and species adhere to the Linnean system of classification the term "group" is used only as a loose taxon (e.g. Amphipoda, Ostracoda, Pisces and Reptilia). The Decapod species *Sergestes atlanticus,* for example, is represented in the database by the code 010036011

| Decapoda | Sergestes | atlanticus |
| --- | --- | --- |
| 010 | 036 | 011 |

From these sub codes has been erected a taxonomic hierarchy of records: GROUP, GENUS and SPECIES. These are included in the database structure and, being calc records, they permit data to be retrieved via any of the three levels. Access to CATCH records via species enables retrieval of the SAMPLE records which are their masters in another chain type. This is possible as retrievals may proceed upwards through a hierarchy as well as downwards. Co-ordination

between SPECIES and SAMPLE (or beyond) is useful as it is the latter record type which contains the spatial and temporal information about CATCH data. Questions such as "What are the recorded latitudinal limits of species x?" and "Is there any correlation between species x and y?" can easily be transformed into computer programmes which can access the database.

## ii) *By Gear type*

Each sample record refers to a haul or cast taken with a single sampling device which is represented by a two digit code. A GEAR record contains the name of a device and its code and SAMPLE records with this same device are arranged in a chain with the GEAR record as master. By classifying samples by their device, GEAR records make some kinds of data retrieval more efficient, for example, questions such as "List all samples from RMT 1s that occurred between the months of October and January" or 'Plot out all CTD stations occurring in latitudes higher than 65°N".

## iii) *By Depth*

Depth zones through which nets are fished or instruments lowered are defined by their minimum and maximum depth values (in metres). DEPTH records contain single depth values representing the minimum depth and connect in chains SAMPLE records of similar minimum depth. To list out all hauls taken between 1000 and 1200 metres the 1000m DEPTH record must be retrieved and then, by chain walking, the maximum depth of each haul can be tested for proximity to the prescribed lower depth. If a haul falls within specified tolerances it can be printed out. This method of classifying the depth attributes of hauls can cut out much processing by reducing the number of SAMPLE records to be examined.

## iv) *By Geography*

Each SAMPLE record has its geographical co-ordinates linked into a grid system of one and ten degree corrected Canadian Squares. Data occurring in a given square(s) can be accessed by retrieval of that square record and by examining the chain of SAMPLE records to which it is master.

Linkage between SPECIES and 1 DEGREE SQ. records is effected by the inclusion of "linker" (LINKER) records. These permit direct analysis of species within squares or, inversely, squares in which species have occurred. This device is useful for a preliminary examination of zoogeographic distribution.

## *Subsidiary Records*

SAMPLE-INFO records have been provided to accomodate comments about the performance of SAMPLE records, examples could include "Net torn due to large catch" or "Large angle on hydrographic wire due to high current". In addition these records can contain file references for physical oceanographic data such as CTD information. It is hoped that this will provide a mechanism for tying in other types of information with the biological data stored on the database.

GENCATCH records have no fixed format and may be used to store further information about species catches held in CATCH records. This might include

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size/frequency distributions or meristic characteristics of individual animals. DATATYPE records provide a convenient way of accessing this subsidiary data without looking at specific CATCH records.

*Retrieval Efficiency*

It is desirable when retrieving data from the database to keep the amount of chain-walking required to a minimum. A chain will grow in length as new data is stored and searching for particular record(s) will naturally take longer with subsequent increase in consumed computer time. Consider the following retrieval requests:

i)"Retrieve and display the SAMPLE record (station and net details) for the deepest recorded occurrence of *Paracalanus parvus*". First the SPECIES record must be retrieved directly via its calc key, then each member record of the subordinate CATCH chain accessed by chain-walking. The SAMPLE master of each CATCH record in the chain is then examined to test the depth fields for the deepest haul. If there are 1000 entries for the species, 1000 SAMPLE records would be tested before the relevant information could be displayed.

ii)"Retrieve and display the SAMPLE records for *P. parvus* occurring between the hours of 0700 and 1900". The same retrieval pathway will be required as for i) but perhaps half of the 1000 entries would be displayed.

Both examples will consume roughly the same amount of computer time but one might suggest that the structure is more applicable to request ii).

The structural design of the database reflects to a large degree the major applications of the system. Retrievals like example i) can be undertaken with ease although their execution is less efficient than if the database structure had been optimised toward them. As many record types as possible have been made of the calc type, this ensures that unforseen applications are more likely to take advantage of the direct retrieval method.

Very often there are alternative pathways leading to the same data so care is required when writing programs for complex retrievals that the required information is gained via the most direct route.

*Applications*

The database and its associated software offer wide scope for a number of biological studies. Several research projects have already benefited from the system and a library of useful programs is gradually being added to. There are a number of actual and potential applications some of which are listed below.

*Zoogeographical Studies*

The original requirement for a data retrieval system stemmed from the need to use a computer for the statistical treatment of zoogeographical data necessitating the use of large matrices. The present system was developed with this premise very much in mind. The data base configuration with its several methods for spatial organisation of data facilitates equally data analysis in the horizontal and vertical planes. Figure 4 is an example of graphical output derived from the program suite VERDI (VERtical DIstribution), which illustrates the vertical distribu-

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tion of species and showing the effect of diurnal migrations. Figure 5 is a plot of the geographical positions of stations which were used in the construction of figure 4.

Much work remains to be done on the co-ordination of physical oceanographic data with the biological data in the database; when complete the ability to automatically cross correlate the two types should prove very useful for studying the influence of hydrography upon animal distributions.

*Ecological Studies*

The dynamic nature of the marine environment poses quite severe problems for many types of ecological studies. The BIOS system whilst not simplifying these problems can to some extent alleviate difficulties in data processing, as the 'fixing' of data in time and space reduces the complexity of retrieval programs. Once written a program can be run repeatedly with varying parameters. Thus one written for community analysis can be used for a variety of animal types in different areas.

The taxonomic organisation of data which provides instant access to specified groups of organisms permits rapid analysis of species interactions simplifying the process of correlation between different species.

Repeated sampling in certain areas not only gives insight into the effectiveness of sampling techniques but also some measure of heterogeneity. Where seasonal coverage is relatively complete aspects of succession can be examined in great detail. Where the latitudinal range of sampling is great, large scale factors such as diversity gradients can be determined, the calculations being completed many times faster than by more conventional techniques.

*Running Programs*

The majority of users of the system are not "computer orientated" and would normally be dependent on someone who was to access and manipulate their data. To alleviate the problem a command program has been written to enable users with minimal computer expertise to run programs from a library. Generally the type of program that can be run via this method must have relatively simple input parameters. The user supplies the name of the program he wants to run together with his input data and the command program will initiate a computer run.

Figure 6 is an example of a sequence facilitating a ranked list of species within a specified sample. The input parameters required are the haul number, net code and the code of the group required to be listed. (See figure 7 for portion of output). User responses are underscored, comments are in brackets.

Where input parameters required to run a program are complex the use of "forms" on visual display units have proved useful, the VERDI program is a case in point. A simple command causes a form to be displayed on a V.D.U. screen. The user then fills in the input parameters asked for from the keyboard when complete the data on the screen is entered into the computer and is assembled into the required order and the required program run.
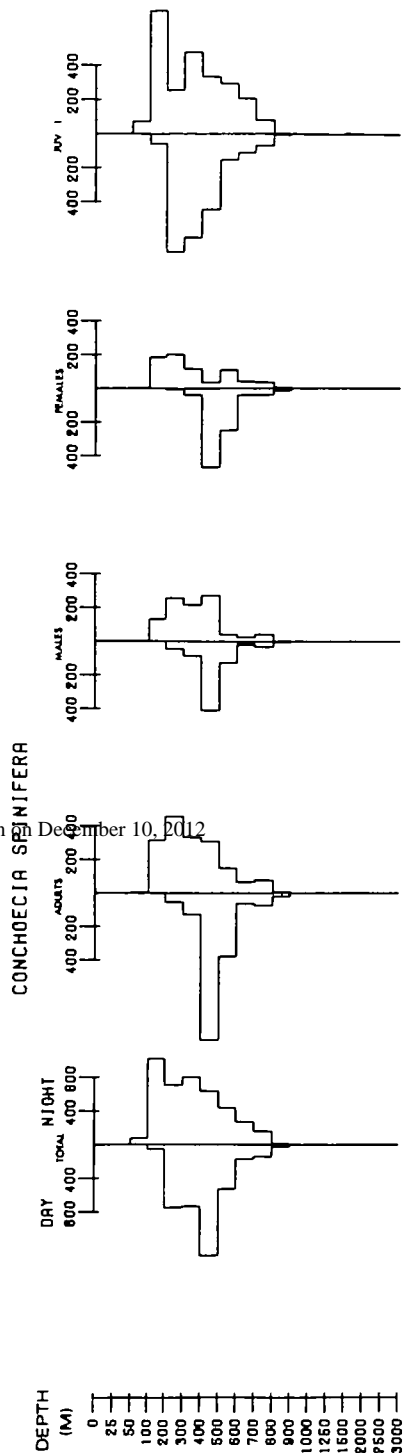
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Fig. 4. Histograms produced by the program suite VERDI illustrating the vertical distribution of a species of ostracod.

STATIONS CONTAINING CONCOECIA SPINIFERA
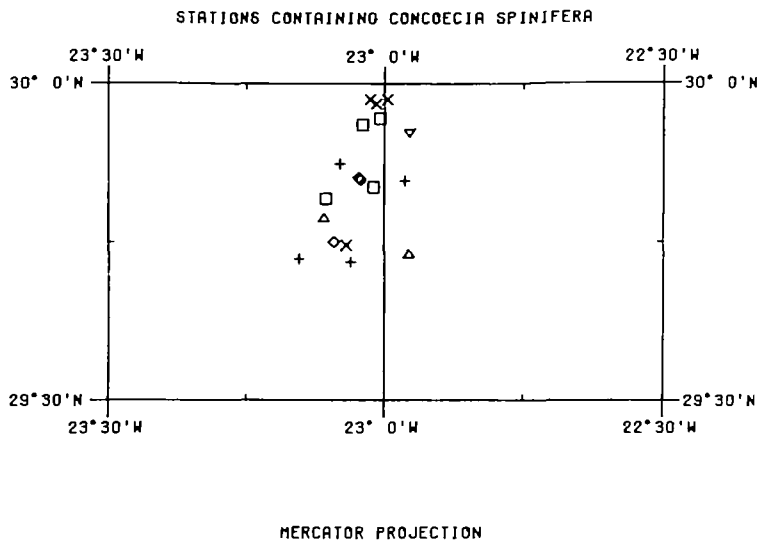


MERCATOR PROJECTION

**Fig. 5.** Plot of station positions used to construct the vertical distribution of animals in figure 4. The symbols represent depth zones.

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*CRUN RUNPROGS
**BIOS COMMAND RUN PROGRAM**
SURNAME? DOMANSKI
PROJECT? BIO
PROGRAM? DOMIN

**INPUT DATA**
LINE1?
826200,1,999 (species from all groups to be listed from an RMT 1)
LINE2?
826200,8,999
LINE3?
826300,1,022 (ostracods only to be listed from an RMT 1)
LINE4?
826300,8,010

**JOB INITIATED**
SNUMB 1926T
*
```

**Fig. 6.** Example of running a retrieval program via the command program.

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DECAPODS STATION 826300 NET 15 RMB GROUP CODE 10 13 SPECIES IN TOTAL NO. INDIVS = 20.0

| RANK | SP. NUMBER | SPECIES NAME | COUNT | FREQUENCY |
|------|-----------|--------------|-------|-----------|
| 1 | 10036000 | SERGESTES SP. | 7.21 | 0.360 |
| 2 | 10002001 | SYSTELLASPIS DEBILIS | 3.46 | 0.173 |
| 3 | 10033007 | GENNADAS TINAYREI | 2.45 | 0.122 |
| 4 | 10001001 | ACANTHEPHYRA PURPUREA | 2.02 | 0.101 |
| 5 | 10036011 | SERGESTES ATLANTICUS | 1.30 | 0.065 |
| 6 | 10033001 | GENNADAS VALENS | 0.87 | 0.043 |
| 7 | 10033000 | GENNADAS SP. | 0.72 | 0.036 |
| 8 | 10034000 | SERGIA SP. | 0.58 | 0.029 |
| 8 | 10036005 | SERGESTES SARGASSI | 0.58 | 0.029 |
| 10 | 10036002 | SERGESTES HENSENI | 0.43 | 0.022 |
| 11 | 10003001 | OPLOPHORUS SPINOSUS | 0.14 | 0.007 |
| 11 | 10036009 | SERGESTES PECTINATUS | 0.14 | 0.007 |
| 11 | 10017000 | ERYONEICUS SP. | 0.14 | 0.007 |
| | | | ------- | ----- |
| | | | 20.0 | 1.000 |

INDEX OF DOMINANCE = 0.1939

Fig. 7. Portion of output derived from the program run in figure 6. Numbers of animals have been expressed as numbers per $10,000m^3$ of water filtered.

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