EPA-600/3-86-019

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# A COMPUTERIZED SYSTEM FOR THE EVALUATION OF AQUATIC HABITATS BASED ON ENVIRONMENTAL REQUIREMENTS AND POLLUTION TOLERANCE ASSOCIATIONS OF RESIDENT ORGANISMS

(DRAFT FINAL PROJECT REPORT)

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ABSTRACT

The Environmental Requirements and Pollution Tolerance (ERAPT) information retrieval and analysis system can be used interactively to predict and evaluate aquatic habitats and organism assemblages. ERAPT computerized data bases contain 57,345 biological, physical, chemical, and distributional characteristics drawn from 887 sources for 1,691 species of North American diatoms, blue-green algae, the insect orders Ephemeroptera (mayflies) and Plecoptera (stoneflies), the dipteran family Chironomidae (midges), and the fishes of U.S. E.P.A. Region V (North Central U.S.).

The system can predict environmental conditions from resident organisms, develop lists of species likely to occur under specified environmental conditions, identify organisms useful as indicators of environmental change, and interpret the environmental causes of changes in species composition. It can also be used to screen organism identifications by identifying tolerance incompatabilities and environmental associations.

The system was tested by comparing its prediction of environmental conditions based on the dominant fish community with environmental characteristics obtained from aquatic habitat surveys for 64 sites on three river systems in Ohio. An overall successful prediction rate of 95% was achieved. Where disagreements between predicted and reported environmental characterizations occurred, they almost always were among very similar tolerance ranges or habitat types.

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ACKNOWLEDGEMENTS

We are indebted to many individuals for their help and support during this project. The staff of the Corvallis Environmental Research Laboratory and Northrop Environmental Services provided many ideas and suggestions for the development of ERAPT system programs and data files, and assisted in the development and definition of the set of retrieval parameters and codes used by the system. We are particularly thankful for the assistance of Jack Gakstatter, Ronald Garton, Jim Giattina, Bob Hughes, Phil Larsen, and Bill Sanville. Paul Short and Martin B. Berg assisted in the accumulation and computer entry of Region V fish environmental data and in the testing of system programs. Data for system validation were supplied by the State of Ohio Environmental Protection Agency with the assistance of Daniel R. Dudley and Chris Yoder. Cornelius I. Weber of the Environmental Monitoring and Support Laboratory, Cincinnati, Ohio, deserves special thanks for his encouragement and support of this project. He and Donald J. Klemm also provided prepublication copies of environmental requirements and pollution tolerance characterizations for diatoms, blue-green algae, chironomids, Ephemeroptera, and Plecoptera which were incorporated into ERAPT data bases. The compilers of these data summaries, William M. Beck, Jr., Michael D. Hubbard and William L. Peters, Rex L. Lowe, Rebecca F. Surdick and Arden R. Gaufin, and Sam L. VanLandingham, deserve particular credit for accumulating this critical information. Finally, we are indebted to the over 500 biologists whose research results have been incorporated into the data bases used by the ERAPT system. It is only through their dedicated efforts that this information is available to the biological community.

# SECTION I

# INTRODUCTION

The Environmental Requirements and Pollution Tolerance (ERAPT) information retrieval and analysis system permits computerized prediction and evaluation of habitat characteristics and organism assemblages. ERAPT System data bases contain 57,660 parameter values representing environmental characterizations of 402 genera and 1,689 species of aquatic organisms in the diatoms, blue-green algae, the insect orders Ephemeroptera and Plecoptera, the dipteran family Chironomidae, and the fish species of U.S. Environmental Protection Agency (E.P.A.) Region V (North Central U.S.). The environmental characterizations used by the ERAPT system have been derived from 887 data sources, primarily from the published literature (Table 1). This represents a mean of 34.1 environmental parameters for each species, with 5.6 data sources per species and 4.2 species per genus. Information for the environmental characterization of diatoms, blue-green algae, chironomids, Ephemeroptera and Plecoptera are adapted from the E.P.A. publications: EPA-670/4-74-005, EPA-600/3-82-073, EPA-600/4-77-024, EPA-600/4-78-061, and EPA-600/4-78-062 developed by the E.P.A. Environmental Monitoring and Support Laboratory, Cincinnati, Ohio. Characterization of Region V fishes was done as part of this project.

## Background

Aquatic organisms long have been recognized as potentially useful indicators of habitat conditions and water quality. This is due to their ability to reflect conditions through time, to demonstrate the effects of disturbances after the environment has returned to apparently normal physical and chemical conditions, to integrate the effects of many different environmental factors and their interactions simultaneously, and to provide a living context for considerations of environmental quality. According to Sladecek (1973), the study and use of organisms as indicators of water quality began in Europe in 1848 with investigations on environmental relationships of Trichoptera by F. A. Kolenati. While much of the early investigation of aquatic indicator organisms concentrated on microorganisms, many other aquatic organisms possess attributes which make them well suited as indicators of environmental conditions. The basic requirements for indicator organisms are that they must be sensitive to environmental changes and have life spans and generation lengths which are appropriate for use in environmental assessment, long enough to reflect intermittent or occasional disturbances and short enough so that sensitive life stages may be subjected to adverse environmental conditions.

## ERAPT DATA BASE TOTALS

| | BLGR | CHIR | DIAT | EPHE | FISH | PLEC | Total |
|---|---|---|---|---|---|---|---|
| Authors | 420 | 34 | 48 | 200 | 56 | 125 | 887 |
| Records | 221 | 306 | 342 | 459 | 446 | 450 | 2,224 |
| Genera | 50 | 74 | 50 | 60 | 82 | 86 | 402 |
| Species | 161 | 232 | 295 | 399 | 243 | 364 | 1,691 |
| Citations | 2,289 | 529 | 2,726 | 1,207 | 971 | 1,767 | 9,489 |
| Entries | 4,364 | 8,156 | 5,510 | 6,806 | 24,824 | 7,685 | 57,345 |

Table 1. Summary totals for information in the ERAPT data bases.

The association between certain aquatic organisms and aquatic conditions has been known for a long time. The insect syrphid fly genus Eristalis has been associated with conditions of profound organic enrichment since ancient Greece (Clausen 1954). Anglers have associated aquatic insects with habitats of game fish for hundreds of years (Schwiebert 1973). Environmental classification schemes using chironomids and other aquatic insects, such as those reviewed by Brinkhurst (1974), have been available for at least 50 years. Discussions of the use of invertebrates as indicators of river and stream pollution are provided by Gaufin and Tarzwell (1952), Hynes (1958), and Goodnight (1973).

Given this association and the knowledge that aquatic organisms have been a fundamental component of aquatic habitat surveys, it is surprising that organisms play a relatively minor role in aquatic assessment. One reason may be the difficulties often encountered in comparing and summarizing information obtained by different researchers. This may be due to differences in organism identifications made by inexperienced personnel, or to inconsistent methods of data collection, analysis, or presentation. A second factor may be the many diverse outlets for publication of these data. They often appear only in progress and summary reports, receive little dissemination, and are frequently omitted from standard abstracting and indexing publications. Another factor is the great difficulty in developing quality control procedures for organism identifications. This has resulted in great variation in the quality and reliability of published associations between organisms and specific environmental conditions.

Investigators who compile data on aquatic organisms from more than one source have often found variation in pollution tolerance and environmental requirements information at both the genus and species levels. For example, in reviewing tolerances to decomposable organic wastes published in the E.P.A. Biological Field and Laboratory Methods manual (Weber 1973), Resh and Unzicker (1975) noted that 61 of the 89 genera known from more than one species had differing tolerance information for the different species. While justifiably concluding that generic identification was wholly inadequate for water quality evaluation, they left unanswered the question of how useful available data are at the species level.

Environmental data and reports vary widely in quality and reliability. Standardized methods for data acquisition and analysis and quality control procedures are reasonably well established for most biological, chemical, and physical environmental data. However, the association of specific organisms with these parameters rests on the reliability of species identifications performed by investigators of varying backgrounds, experience, and expertise. At present, the primary quality assurance mechanism for organism identifications is the competence and dedication of individual researchers. While independent verification of voucher specimens by taxonomic experts is possible, this

is a procedure which, even on a small scale, is time consuming and costly and, on a large scale, would significantly exceed our present resource of taxonomic experts (Irwin et al. 1973, Barr 1974, Edwards and Grotta 1975).

Publications providing summary information on the environmental relationships and tolerances of aquatic organisms are extremely useful in identifying potential indicator organisms and in establishing tolerance levels of organisms to specific environmental factors. However, unless the reference publication survey is extremely exhaustive or very selective, it may be difficult to establish useful trends among the vast amounts of often contradictory information reviewed.

Some publications providing useful summary information on the environmental requirements and pollution tolerances of aquatic organisms are: Proceedings of the Third Seminar on Biological Problems in Water Pollution (Tarzwell 1965) which includes discussions of environmental requirements of freshwater algae, protozoa, crustacea, annelids, insects, and fish; a manual on biological field and laboratory methods (Weber 1973) published by the E.P.A. which includes summaries of the tolerances of freshwater invertebrates to decomposable organic wastes; the appendix of Sladecek's (1973) water quality system monograph which includes many tables of tolerances of aquatic species to a variety of environmental conditions; a book on the pollution ecology of freshwater invertebrates (Hart and Fuller 1974) which includes information on environmental requirements for a number of invertebrate groups; general treatments of biological methods for water quality assessment (e.g., Cairns and Dickson 1973; James and Evison 1979) and a series of U.S. E.P.A. Environmental Monitoring and Support Laboratory (Cincinnati) water quality profiles for diatoms (Lowe 1974), Chironomidae (Beck 1977), Ephemeroptera (Hubbard and Peters 1978), Plecoptera (Surdick and Gaufin 1978), Trichoptera (Harris and Lawrence 1978), and blue-green algae (VanLandingham 1982). The U.S. Department of the Interior Fish and Wildlife Service also has been actively developing habitat suitability index models for fish and wildlife species (Schamberger et al. 1982).

While these reports have helped to make environmental information on aquatic organisms more accessible to biologists, much of the potential of this accumulated information still remains unexploited. This may be due to the taxonomic organization and fixed tabular format of these publications which limit the ways in which their data can be used. For example, most of these publications are organized by taxa rather than by environmental factors. This makes them difficult to use to predict the presence of organisms in a specific environment. Also, it is often difficult to determine which environmental requirements are consistent within a genus or higher taxonomic level and which environmental inconsistencies at the specific level could be due to errors in data collection or identification.

A computerized storage, retrieval and evaluation system for these data has been developed to enhance their usefulness by allowing queries based on taxonomic association, environmental parameters, or a combination of these factors. Since the environmental information for diverse taxonomic groups can be standardized, it is possible to answer questions concerning biological communities and their environments. In addition to being able to ask a variety of questions about requirements of organisms and environmental conditions, a major application of this system is the development of lists of taxa associated with specific environmental conditions which can serve as reference communities for environmental scientists. This system also can be used as a device for scrutinizing environmental data by comparing the known tolerances of organisms reported in monitoring and impact studies with the physical and chemical characteristics of the habitats from which they were collected. Discrepancies encountered in these comparisons are flagged as potential errors in data collection or specimen identification. Another quality control device possible with these data is comparison of the known ecological parameters associated with combinations of taxa reported to be collected together at individual sites. Inconsistencies in the environmental requirements of these taxa also can be flagged as potential errors in identification.

## System Operation

The ERAPT system consists of an integrated set of computer programs for the storage, retrieval, and manipulation of environmental requirements and pollution tolerance information on aquatic organisms. It has been developed for use on an IBM 370/3033 computer system at the University of Notre Dame. Data are stored and manipulated as hierarchically related environmental requirements and pollution tolerance categories representing tolerance ranges to specific pollutants or environmental conditions, geographic locations, general or specific habitat characteristics, and periods of appearance, emergence, or greatest abundance. At present the system uses 21 heading categories (Biological - stage, abundance, optimal growth period, reproductive season, reproductive behavior, feeding behavior; Chemical - hardness, salinity, nutrients, degradable organics, pH, oxygen; Physical - temperature, turbidity, current, general habitat, specific habitat, bottom type; Geographic - ecosystem regions, political geography) divided into 303 specific parameters. These categories and parameters were adapted from a set developed by the Aquatic Biology Section, Environmental Monitoring and Support Laboratory of the U.S. E.P.A. (Cincinnati, Ohio) for use with macroinvertebrates and diatoms (Lowe 1974, Beck 1977), and were expanded for fish and other aquatic organisms as part of this project in collaboration with the staff of the E.P.A. Corvallis Environmental Research Laboratory.

Data for ERAPT are encoded on tabular forms which may be produced by the system. These forms contain boxes which correspond to specific parameters such as stage, feeding behavior, or tolerance to environ-

mental conditions for an individual species from a single reference source. Data are coded on the forms by marking those environmental categories applicable to a particular species and environmental site or study. The ERAPT system reads the tabular forms as digitized X-Y coordinate values corresponding to each mark on a form. The computer then determines the relative location of each mark with respect to the form and stores this information with a list of environmental codes which identify the various parameters. Location tolerance values are stored by the program and used to eliminate ambiguous mark positions.

The digitized data are then standardized for the ERAPT system. Since data entry forms may contain any subset of the environmental categories included in the data base, the category codes stored with the digitized data are used to create a translation table which transforms the data to correspond with the full environmental category table used by the ERAPT system. During this process both direct and hierarchical correspondences between categories are established. For example, one set of data entry forms may contain the environmental category Mesosaprobic, whereas another may divide this category into alpha and beta ranges. During this step these parameters are hierarchically associated so that a parameter shown at a lower level of the environmental category hierarchy is included at all upper levels. There is no limit to the number of levels in a hierarchy and no requirement that the number of levels be consistent among parameters. For example, the heading salinity is divided into 11 categories with the categories Mesohalobous and Oligohalobous further subdivided into 2 and 3 parameters, respectively. This structure permits the ERAPT system to store, manipulate and use environmental information differing in precision without sacrificing the most reliable data.

During the standardization process the data are packed into computer memory locations as 1-bit word subsegments. This allows data to be stored very efficiently in computer memory. It also permits simultaneous multi-factor comparisons of environmental conditions by the computer. This greatly reduces processing time and costs, increasing the amount of information which can be processed and simplifying analysis and retrieval of the data.

The next procedure is the creation of a searchable data base. At this point the various components of the system are linked. The taxonomic categories are hierarchically connected in a manner similar to that described previously for environmental headings and parameters. This enables queries at any level of the taxonomic hierarchy. The linking operation involves the association and storage of memory addresses for the taxonomic names, environmental headings and parameters plus their definitions, author citations and references, environmental data, and a series of 2 to 8-character abbreviations which are used in the query and information retrieval process. The lowest taxonomic level directly accessible by the system is subspecies. However, data from individual sources are available to the system as an external file.

The data normally used by the system consist of two summaries of the information contained in the various reference sources for each taxon. They are stored as strings of binary digits which correspond to bit by bit iterative logical sums (OR) and products (AND) of parameter fields for each non-zero heading category for each taxon. Logical sums include all environmental parameters given by any source for each taxon in the system. For example, if one investigator reported that a species occurs in streams and another reported that the same species occurs in both lakes and streams, the logical sum for the general habitat heading category for that species would include both lakes and streams. The logical product summary includes only those parameters indicated by all sources containing environmental requirements or pollution tolerance information within each heading category for a taxon. Therefore, each product summary consists of those environmental parameters which are consistently associated with a taxon in the system. For the general habitat example given above, the product summary would show only lakes, since it was the only parameter indicated by all sources of information for the taxon. A summary of inconsistencies among investigators reporting information about any heading category for a taxon may be obtained by calculating the logical difference (exclusive OR) between the sum and product summaries. In this case parameters are only included in the summary if there is inconsistent information for that taxon within the data base. In the general habitat example, streams would be considered an inconsistent parameter since one source used the parameter and the other did not. For taxonomic categories above species, similar data summaries are maintained based on logical sums of the information for all lower taxonomic levels. The system also maintains the number of data sources which were summarized for each taxon and environmental heading category.

Information retrieval and analysis is accomplished using an interactive program. The program uses a simple command format for queries of the data base. These may be used to predict groups of organisms having a select set of environmental characteristics. Species may be evaluated for consistency of associated environmental information, providing lists of potential indicators. Groups of organisms may also be defined using abbreviated taxonomic names for characterization and evaluation. Species or groups of species may be compared to determine the similarities and differences in their environmental requirements. Information may be selected by taxonomic level, number of sources, or groups of environmental parameters.

Definitions of environmental retrieval codes are available during program operation. A complete help facility is also included to provide on line documentation on program commands and capabilities. A history of the searches performed during the session may be obtained. Program output can be formatted for different page widths and may include organism common names. Individual search statements or complete terminal sessions may be saved and later recalled for use with data bases containing information on other groups of organisms. The program can retain an almost unlimited number of saved searches and can provide

directories and lists of these upon request. The program will permit customization for a variety of printing and nonprinting computer terminals and can be directed to pause between output pages. Input may come from sources other than a terminal to permit other programs to interface directly with the system. Output may also be redirected to files or to a high-speed lineprinter.

## Future Development

Use of environmental indicator organsims on a regional basis appears to be particularly promising. Assessment systems based on a sound knowledge of a local fauna, such as that developed for Wisconsin by Hilsenhoff (1977), would seem to have a great probability for success. Development of local or regional environmental data bases is within the capabilities of the ERAPT system. This will be greatly facilitated by development of microprocessor-based versions of the retrieval and analysis programs. Microprocessor implementation of the ERAPT system on computers such as the I.B.M. PC and the Apple Macintosh is feasible and a prototype microcomputer version of the retrieval and analysis program is currently being developed.

One of the most interesting capabilities of the ERAPT system is its potential for screening environmental data. The ability to automatically detect apparent inconsistencies among the environmental tolerances of different organisms said to be collected together at a given site can be used both to flag errors in data collection and organism identifications and to evaluate the reliability of environmental data bases. For example, it would be possible to require that taxonomic experts confirm the identifications of organisms found to have inconsistent environmental information. This would provide a cost effective means of evaluating the quality of biological information. Where new environmental associations of organisms are found, the data bases can be modified, thereby eliminating future error flags for the taxa involved. It is even possible to use environmental characteristics as characters in taxonomic keys for organism identification. This is most applicable to computer based identification systems which permit users to skip missing or uncertain key characters such as the AUTOKEY taxonomic identification system for aquatic organisms (Hellenthal 1978).

Because the ERAPT system can accept output from other computer programs, it can be interfaced with ongoing environmental data collection projects to automatically summarize and evaluate information and to scan for probable changes in environmental conditions. Interfacing programs can convert numerical environmental data and codes unique to local or regional data collection projects so that they can be used with the ERAPT system. Output from the ERAPT system also can be used by other programs for environmental decision making and evaluation. Sources of environmental information within the data bases also can be evaluated. For example, it is possible to identify investigators who

have provided environmental information which frequently contradicts that supplied by other workers for the same organisms.

Because the ERAPT programs are independent of the kinds of data and organisms which they can process, the system has many applications to other areas of biological and environmental research. Alternate sets of biological categories or environmental parameters can be developed easily for terrestrial or marine environments or for microbial organisms or higher vertebrate groups. The system also has direct application to behavioral, physiological, and genetic organism information. Because of the structure and internal organization of the data used by the system, there is no limit to the amount of information which can be accumulated or queried for each kind of organism contained within a data base. System capacities are related only to the number of kinds of organisms and data catagories which can be accessed and evaluated as a group, and are easily modified within programs. There is also no limit to the number of groups which can be developed and programs permit transfer of search statements between organism groups if they have compatable data.

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## SECTION II

## TECHNICAL SYSTEM DESCRIPTION

### ERAPT Data Organization

The ERAPT system performs its search and analysis operations on data bases derived from three types of data files. The CODES file type defines the environmental retrieval codes used in compatible data bases and establishes their order and hierarchical relationships. The RAW DATA file type establishes the environmental retrieval and reference codes and taxonomic names for a single group of organisms and contains the environmental characteristics of the organisms derived from individual references. A RAW DATA file need not use all of the categories contained in a specific CODES file and may contain additional categories applicable to alternative CODES files. A single data base, therefore, may be used in conjunction with different CODES files to produce different searchable data bases. The third required file type defines the SOURCES of environmental information contained in a RAW DATA file. The CODES and SOURCES files may contain upper and lower case characters and are in a format which is compatible with the University of Waterloo text-formatting program, SCRIPT. The RAW DATA file is not formatted for direct text-processing and must contain only upper-case characters.

### CODES file

The CODES file defines the retrieval codes used by all ERAPT system programs and establishes their hierarchical relationships (Figure 1). Each entry must begin on a new line and must contain four components: (1) a descriptive term or phrase; (2) a formal definition; (3) a hierarchical position value and retrieval code; and (4) a list of data bases which use the entry. A ' - ' sequence is used to separate the descriptive word or phrase from its associated definition. If the definition begins on a separate line, the ' - ' sequence must terminate the line containing the descriptive phrase. There is no limit to the length of the descriptive definition which may contain as many lines of text as necessary. On a new line immediately following the definition is the hierarchical position and retrieval code for the entry. This line must begin with a left bracket, '[' (EBCDIC hexadecimal value AD), and terminate with a right bracket, ']' (EBCDIC hexadecimal value BD). The hierarchical position is represented by a three digit integer number starting immediately after the left bracket. The hierarchical position number is followed by a 1 to 6-character upper-case alphanumeric retrieval code. The highest level categories are numbered '010' and must have 2-character retrieval codes. This 2-character code will appear as a prefix to all other codes for this category. All divisions of a major category must have a level value greater than ten, with

Figure 1. Codes file example.

```
.CC 7;.US ;.CE ;PHYSICAL CHARACTERISTICS OF HABITAT
.BR ;.US ;General Habitat -
General type of habitat.
[010GH]
(FISH, CHIR 10, DIAT 6, EPHE 8, PLEC 8, BLGR 6)
Marine - Characteristic of oceans and seas.
[020MARINE]
(FISH, CHIR 43, DIAT 33)
Neritic - Occurring typically above continental shelf
(close to shore).
[030MANERI]
(FISH, BLGR 47)
Oceanic - Occurring typically over deeper regions of oceans.
[030MAOCEA]
(FISH, BLGR 48)
Estuary - Characteristic of estuaries and brackish water habitats.
[020ESTUAR]
(FISH, CHIR 44, DIAT 34, BLGR 45)
Lentic Systems - Characteristic of lakes or ponds.
[020LENTIC]
(FISH, BLGR 39)
Lake - Characteristic of large inland bodies of standing water.
[030LELAKE]
(FISH, CHIR 45, DIAT 35, EPHE 33, PLEC 33)
Pond - Characteristic of small bodies of lentic water
with macrophytes covering most of bottom.
[030LEPOND]
(FISH, CHIR 46, DIAT 36, EPHE 34, PLEC 34)
Temporary Water - Characteristic of temporary lentic habitats.
[030LETEMP]
(FISH)
Littoral - Shallow margin of lake or pond associated with aquatic
vegetation.
[030LELITT]
(FISH, BLGR 46)
Limnetic - Free open water in lakes and ponds.
[030LELIMN]
(FISH)
Profundal - Bottom sediment of lakes below littoral zone, consisting
of exposed fine sediment free of vegetation.
[030LEPROF]
(FISH)
Benthic - Occurring on bottom of lentic habitats.
[030LEBENT]
(FISH, BLGR 38)
```

larger level values used to designate greater subdivisions of the retrieval code hierarchy. The last line of each record is used to indicate which RAW DATA files use the retrieval code. RAW DATA files are designated by upper case, 4-character codes. The program STRIP uses these codes to produce data entry sheets. This record must start with a left parenthesis, '(', followed by the codes for the data base names in which the retrieval code will be used and must end with a right parenthesis, ')'. Data base codes optionally may be followed by an integer number, indicating the order they are to be placed on the coding sheet. Multiple data base codes are separated by commas.

RAW DATA file

The RAW DATA file contains lists of retrieval codes, authors, taxonomic and common names, and environmental data for a related group of organisms (Figure 2). It consists of four sections: (1) the data base name code and revision date; (2) the list of retrieval codes; (3) a list of data source codes; and (4) taxonomic and common names plus environmental data arranged by source. The first line of the data base must contain the four character data base name in columns one to four and optionally a date of the form 'MM/DD/YY' beginning in column six.

The second line contains a three digit integer in columns one through three, indicating the number of category codes used in the data base. The following lines contain the ordered category codes, left justified, in eight 9-character columns.

The line following the category codes should contain a three digit integer, in columns one through three, indicating the number of source codes in the data base. The source codes should begin on the next line, left justified, in eight 9-character columns. If the number of source codes is zero, this line should be blank. The first three characters of the source code normally are author initials, or some other unique abbreviation of author initials or names. These characters are followed by the last two digits of the year the article was published. The sixth character is used to form unique codes if the first five characters match existing sources, using the next available letter of the alphabet. If the reference source differentiated environmental requirements by life stage, the seventh character position may contain an 'A', 'J', 'L' or 'S' to indicate that associated data pertain to adult, juvenile, larva or smolt life stages, respectively. Otherwise, the field is left blank. The eighth character position is currently not used and should be left blank.

The taxonomic list follows the list of author codes. Each taxonomic entry must appear on a separate line. The first twenty characters are for the scientific name. Columns 21-23 indicate the taxonomic level of the name (Table 1). If this number is negative the next line will begin the data section specific to this entry rather than another taxon. Columns 24-51 are for the common name, when appropriate. The names must be nested hierarchically, with each genus and species used only once.

Figure 2. RAW DATA file example.

```
FISH  2/07/85
278
STEGGS    STLARVA   STJUVENI STSMOLT   STADULT   ABABUNDA ABCOMMON ABUNCOMM
ABRARE    . . .     PGALB    PGBC      PGMAN     PGNWT    PGSAS    PGYUK
7
BEC83     LEE80     SPW79    E&U74     TMB81     TMB81 A  TMB81 J
OSTEICHTHYES          55BONEY FISHES
ACIPENSERIFORMES      45
ACIPENSERIDAE         35STURGEONS
ACIPENSER             25
FULVESCENS           -15LAKE STURGEON
4      BEC83     SPW79     E&U74     TMB81
103  1 30  5  9 19 34 85 99100117118126128207212217219221224225228238
237243244245246269271273275277  2 12  5  9 19 33 34 85 91 97124134128
230  3 11 19 20  5 23 34 85 97126127128233  4 42  5 19 20 34 97 85113
115117124128144205207209212217219221223224225228230231232233234235237
243244245250251250246269271273275277
SCAPHIRHYNCHUS        25
ALBUS                -15PALLID STURGEON
2      SPW79     E&U74
15  1  7  5  9 20 33 34100230  2  4  5229230233
PLATORYNCHUS         -15SHOVELNOSE STURGEON
4      BEC83     SPW79     E&U74     TMB81
 93  1 37  5 19 34 99115113100125128117151217219221224225226228230232
231233234235237238239240241243244245246249250251253  2  4  5 19 34230
  3  6 19  8  5 85 97233  4 38  5  8 34 99100113115125130144148217218
219221223224226228230231232233234235237238239240241243244245246249250
251253
POLYODONTIDAE         35PADDLEFISHES
POLYODON              25
SPATHULA             -15PADDLEFISH
4      BEC83     SPW79     E&U74     TMB81
 92  1 34  5  9 19 24 34 35 38 39 97212217219224226228230231232233234
235237237238240241243244245246249250251269  2 11  5 19 35 24100125127
126 85110230  3  7 19 35 24  5 85 97233  4 32  5  9 98 99100 97127126
217218219221222224225228230231233234235237238240241243244245246249250
251
```

| | | | |
|---|---|---|---|
| 75 | Kingdom | 39 | Infraorder |
| 70 | Subkingdom | 36 | Superfamily |
| 66 | Superphylum | 35 | Family |
| 65 | Phylum | 30 | Subfamily |
| 60 | Subphylum | 28 | Tribe |
| 56 | Superclass | 28 | Subtribe |
| 55 | Class | 26 | Supergenus |
| 50 | Subclass | 25 | Genus |
| 49 | Infraclass | 20 | Subgenus |
| 48 | Cohort | 16 | Superspecies |
| 46 | Superorder | 15 | Species |
| 45 | Order | 10 | Subspecies |
| 40 | Suborder | 5 | Race or Variety |

Table 1. Codes for levels in taxonomic hierarchy.

The data section, if present, has two parts: (1) the list of references specific to the entry, and (2) the data specific to each reference. Both of these sections begin with a three digit integer indicating the number of entries in each section, therefore, the data section may span as many lines as is necessary to contain the information. The section containing the author list is written in 9-character columns with the first position position replaced by the number of authors. The data line is written as twenty-four, 3-character columns. The first integer indicates the number of integers remaining in the section, the second indicates the source of the data to follow. The next value represents the number of environmental codes obtained from the source followed by additional integers corresponding to the positions of environmental parameters used in the table at the beginning of the file. The source number, number of codes, and parameter list fields are repeated for each source of information for the taxon.

SOURCES file

The SOURCES file is a list of author citations and their associated reference codes (Figure 3). The citations are separated from each other by a blank line. Each entry has five parts, terminated with a period: (1) the list of authors; (2) the year; (3) the title; (4) the source of the information; and (5) the source code and a list of codes for the data bases in which it is used. Each of these parts should begin on separate lines. The source and data base codes must be in upper-case letters and begin with ' REF: '. This is followed by the author code and a list of codes for the data bases in which the source is used, separated by spaces.

## ERAPT System Programs

The ERAPT system includes ten programs and four data files which interact with one another as illustrated in Figure 4. Data may be added to a data base interactively with the program EPAEDIT or by merging new data contained in files with the program DMERGE. If a small amount of data is to be added to a data base, then EPAEDIT would be preferred. If a large amount of data is to be entered or data from another data base are to be merged with existing data files then DMERGE may be used to automatically update RAW DATA files. DMERGE will add environmental data to any taxonomic entry in the data base, inserting new author codes into the data base as necessary.

Data may be entered into a computer by many means, including optical character readers, optical scanners, manual digitizers, and electronic drafting tablets. The basic concept of these systems is similar. A data form, which may be generated by the computer, is filled out by hand. Entries on the form are read as coordinates and translated into numbers which represent environmental codes. These data are then converted into a format acceptable as input by the program DMERGE.

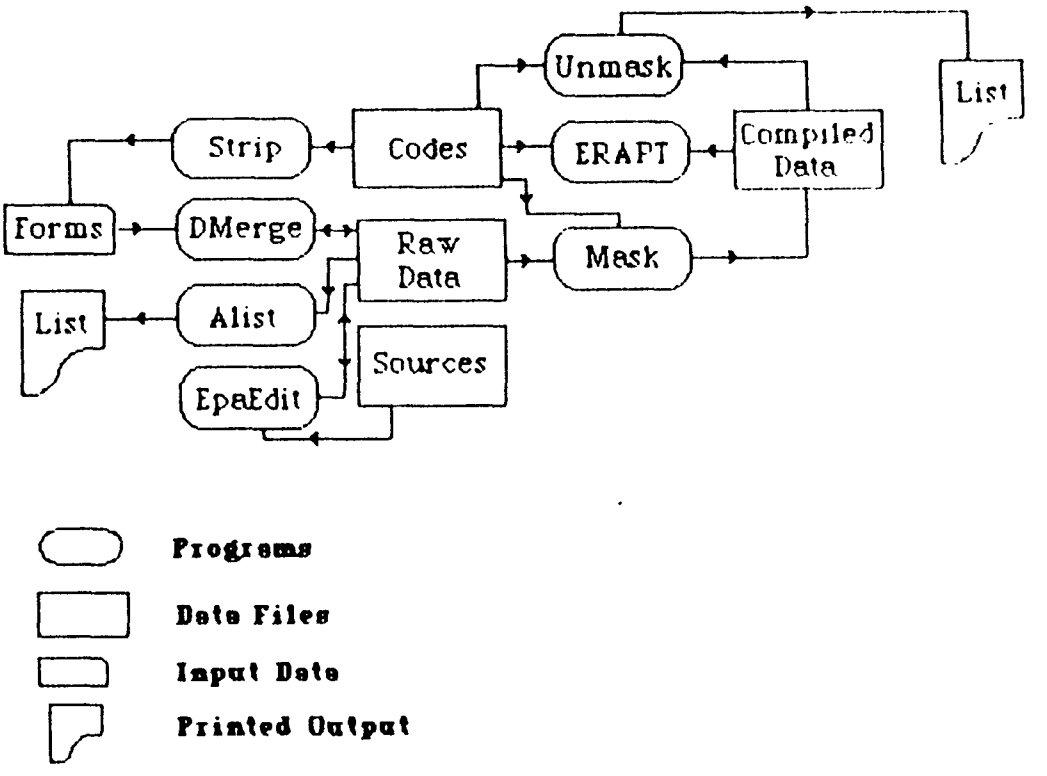
Figure 3. SOURCES data file example.

Aggus, Larry R. and William M. Bivin.
1982.
Habitat Suitability Index Models: Regression Models Based on Harvest of Coolwater Fishes in Reservoirs.
Fish and Wildlife Service. U.S. Department of the Interior.
FWS/OBS-82/10.25.
REF: A&B82 FISH

Bain, Mark B. and Jane L. Bain.
1982.
Habitat Suitability Index Models: Coastal Stocks of Striped Bass.
Fish and Wildlife Service. U.S. Department of the Interior.
FWS/OBS-82/10.1.
REF: B&B82 FISH

Becker, George C.
1983.
Fishes of Wisconsin.
The Universiy of Wisconsin Press.
REF: BEC83 FISH

Figure 4. ERAPT System organization.



The program STRIP uses the CODES file to produce a text file which is then processed by SCRIPT to produce data entry forms. Data entered on these forms are digitized using an optical character reader, manual digitizer, or an electronic drafting tablet. Although not totally automated, these three methods enable rapid and accurate data entry. If a large amount of data is to be entered an optical scanner should be considered. Forms for this type of entry are often used in automated test scoring, where the data are represented as ovals, usually darkened with a pencil. The advantages of this method are total automation and speed since the whole form is read in a single pass. However, developing and producing these forms in small quantities is expensive.

One method of data collection uses SCRIPT generated coding forms in conjunction with a microcomputer. The coding sheet is defined to the microcomputer, using the program INITPNTS, which makes a translation table for the coding sheet.

After the translation table is produced, the program XPAD is used to store data from the coding sheets as files on the microcomputer. Taxonomic name and author information are entered from the keyboard and the coordinate positions for environmental characteristics are digitized. These data then are transferred to a main frame computer in a format suitable for processing by the program DMERGE.

DMERGE is used on the main frame computer to combine new and existing data files. This final updated RAW DATA file should be compiled and evaluated for errors using the program MASK before either of the original data files is deleted. The program ALIST may be used to list the updated RAW DATA file. The program UNMASK may also be used to list the contents of the COMPILED DATA file. The program RUNOFF may be used to list program or data files. Once the RAW DATA file has been compiled and verified it can be used by the ERAPT retrieval and analysis program as a data base.

STRIP

The program STRIP is used to generate coding forms for use in data collection. The CODES data file is scanned by the program for the information to be used in making the form. This information is written to a file. This file and a file containing the initial formatting commands are processed by the text-formatting program SCRIPT. The result is the form in Figure 5.

INITPNTS

The program INITPNTS is used to enter environmental parameter codes positions from a master coding sheet into the microcomputer. It prompts for all necessary information, including the name of the output file when all of the points have been entered. The corresponding environmental parameter codes then are stored in a separate file in the same order. The program will accommodate 400 codes and their coordinates.

**Figure 5.** Coding form for environmental data.

CODING FORM FOR ENVIRONMENTAL

REV: 840528

STREAM: _____ _____ DATE: _____ BY: _____

LOCATION: _____ _____ REFERENCE: _____ _____

**Stage**

[] Eggs
[] Larvae
[] Juvenile
[] Smolt
[] Adult

**Abundance**

[] Abundant
[] Common
[] Uncommon
[] Rare

**Pollution Tolerance**

[] Saprophilic
[] Facultative
[] Saproxenous
[] Saprophobic

**Optimal Growth Period**

[] Winter
[] Spring
[] Summer
[] Autumn

**Reproductive Season**

[] Winter
[] Spring
[] Summer
[] Autumn

**Reproductive Behavior**

[] Complex
[] Simple
[] Lithophil
[] Phytophil
[] Peliphil
[] Xylophil
[] Pelagophil
[] Speleophil
[] Internal
[] Polyphil

**Feeding behavior**

[] Predator
[] Piscivore
[] Invertivore
[] Planktivore
[] Herbivore
[] Grazer
[] Browser
[] Omnivore
[] Scavenger
[] Detritivore
[] Parasite

**Hardness**

[] Non-calcareous and Acid
[] Slightly Calcareous
[] Moderately Calcareous
[] Highly Calcareous

**Salinity**

[] Poly- or Euhalobous
[] Polyhalobous
[] Euhalobous
[] Mesohalobous
[] Alpha Mesohalobous
[] Beta Mesohalobous
[] Oligohalobous
[] Halophilous
[] Halins Indifferent
[] Halophobous
[] Euryhalinous

**Nutrients**

[] Hypereutrophic
[] Eutrophic
[] Mesotrophic
[] Oligotrophic
[] Ultraoligotrophic
[] Dystrophic
[] Eurytrophic

**Degradable Organics**

[] Polysaprobic
[] Mesosaprobic
[] Alpha Mesosaprobic
[] Beta Mesosaprobic
[] Oligosaprobic

**pH**

[] Acidobiontic
[] Acidophilous
[] Neutral
[] Alkaliphilous
[] Alkalibiontic
[] pH Indifferent

**Oxygen**

[] Euoxyphilous
[] Mesoxyphilous
[] Oligoxyphilous
[] Anoxyphilous

**General Habitat**

[] Marine
[] Neritic
[] Oceanic
[] Estuary
[] Lentic Systems
[] Lake
[] Pond
[] Temporary Water
[] Littoral
[] Limnetic
[] Profundal
[] Benthic
[] Lotic Systems
[] Stream
[] Small Stream
[] Medium Stream
[] Large Stream
[] River
[] Small River
[] Medium River
[] Large River
[] Intermittent Flow
[] Interrupted Flow
[] Canopy Cover
[] Open
[] Spring
[] Cool spring
[] Hot Spring
[] Wetland
[] Bog
[] Swamp
[] Marsh

**Bottom Type**

[] Silt
[] Sand
[] Gravel or Pebble
[] Gravel
[] Pebble
[] Cobble or Rubble
[] Boulder
[] Bedrock or Claypan
[] Vegetation
[] Muck
[] Detritus

**Specific Habitat**

[] Nektonic
[] Riffle or rapid
[] Run
[] Pool
[] Off channel
[] Benthic
[] Pelagic
[] Nearshore
[] Other Specific Habitats

**Temperature**

[] Euthermal
[] Mesothermal
[] Low Mesothermal
[] Medium Mesothermal
[] High Mesothermal
[] Oligothermal
[] Low Oligothermal
[] Medium Oligothermal
[] High Oligothermal
[] Stenothermal
[] Metathermal
[] Eurythermal

**Turbidity**

[] Eulichtophilous
[] Mesolichtophilous
[] Oligolichtophilous

It only needs to be used once for the creation of a translation table for each type of coding sheet.

XPADIN

The XPADIN program allows entry of data into the ERAPT system using a graphics tablet digitizer. The program prompts for the name of a translation table file generated by INITPNTS. Then the name of the output file is requested. After the translation table is loaded, the program prompts for entry of the coding form boundaries. A coding sheet is placed on the digitizer in the template and the first and last positions on column one are marked with the stylus of the graphics tablet. Environmental characteristics are entered into the microcomputer by drawing horizontal lines next to the parameters on the form. If the mark entered is acceptable it will be displayed on the screen. Ambiguous marks result in visual and audible error messages and must be re-entered.

The scientific name is entered by marking the name spot on the template. The scientific name and reference are entered via the keyboard and control is returned to the graphics tablet digitizer. When entry of coding form data is completed, the "page finished" spot on the graphics tablet is marked. The form may be in two or three parts. If so, the additional parts may be entered by marking the "page" spot on the graphics tablet. Incorrect codes may be changed by marking the "delete" spot on the template, and then entering the position of the new code. Once generated, files containing new environmental information are transferred to the main frame computer for input to the program DMERGE.

DMERGE

The program DMERGE merges a new data set (Figure 6) into an existing data base, creating a new combined data base. Neither of the input data files are changed.

The program reads original RAW DATA files from unit 10, reads additional data from unit 12, and writes the merged file to unit 11. Units 1 and 2 are used as scratch space if the merger cannot be performed in a single pass. Units 5 and 6 are allocated to the keyboard for input and output.

During execution of the DMERGE program, the message "TERM NOT FOUND" may appear, followed by a taxonomic name which appeared in the new data file but was not present in the original RAW DATA file. The options are ADD, CHANGE, or SAVE. SAVE ends the program without the addition of the new taxonomic name or its associated data. ADD will insert a new species and its associated data into the merged RAW DATA file. CHANGE is used to modify a taxonomic name contained in the data file to be merged with original RAW DATA file.

Figure 6. DMERGE input data file example.

```
ESOX                025
NIGER               -15
001   BEC83
010   1   8   5   9 10 24 28 29 50 55
ESOX                025
AMERICANUS          -15
001   BEC83
012   1 11   5   7   9 21 24 25 30 42 48 55107
```

The program can merge environmental data of up to 200 genera or higher taxonomic levels and up to 800 species. An array is dimensioned at 10,000 integers to serve as workspace for the program. If this space is exceeded the current file is written to a scratch file and processing is performed in passes. Therefore, there is no limit to the amount of environmental data that can be merged into a data base. When all of the data to be merged is processed, a printed message indicates that the final processing pass is being made. When this step is complete the output file is a new RAW DATA file; ready for verification and compilation using the MASK program.

EPAEDIT

The program EPAEDIT is an interactive editor for a RAW DATA file. The program has several functions: (1) add, delete, or replace data for a source or sources; (2) display information by author, species or code; and (3) search for information by species, common name or source code. The program reads the RAW DATA file as unit 10 and the SOURCES files unit 12. These files are not modified by the program. The revised RAW DATA file it is written to unit 1. Units 5 and 6 are allocated to the terminal for input and output.

MASK

The program MASK is used to standardize and compress a RAW DATA file into a COMPILED DATA file. This permits searches across different data bases as well as the taxonomic comparison and evaluation capabilities of the retrieval and analysis program. As part of the compilation process, information for each taxon from all sources is stored as two data summaries (Figure 7). The OR summary contains the information reported by any data source. The AND summary holds the information agreed upon by all sources. The program uses units 5 and 6 for terminal input and output. The CODES file is read from unit 10. The RAW DATA file to be compiled is read as unit 12. Unit 11 is used for output if the program results are written to a data file rather than to the line printer.

The MASK program produces only a list of summary statistics at the terminal unless errors are detected in the RAW DATA file. Error messages produced by the MASK program begin with three asterisks and may be preceded by system messages. Most are caused by read errors in the input file. Therefore, a copy of the RAW DATA file may be helpful in determining the specific problem which caused the error.

ALIST

The program ALIST will produce a readable text file from a RAW DATA file (Figure 8). The RAW DATA file is read from unit 10 and the text file is written to unit 9. Unit 6 is used to write diagnostic and error messages. The output file can be formatted and printed using RUNOFF.

Figure 7. COMPILED data file.

Truncated to fit the page:

```
FILENAME: FISH CREATED:  2/08/85 FROM INPUT FILE:  2/07/85
OSTEICHTHYES          55BONEY FISHES
ACIPENSERIFORMES      45
ACIPENSERIDAE         35STURGEONS
ACIPENSER             25
FULVESCENS           -15LAKE STURGEON
40402000004010400000000000004020401010000004000000
04401900E000000000000306160001D80DC00006008015 6A5DCFFE3F300045D40000
04401100A000000000000302100000100840000600800000000000000000000000000
SCAPHIRHYNCHUS        25
ALBUS                -15PALLID STURGEON
20201000001000100000000000001000000000000002000000
04400800E000000000000002120000000000000000000000000640000000000000000
04400800E000000000000002120000000000000000000000000600000000000000000
PLATORYNCHUS         -15SHOVELNOSE STURGEON
40402000003000300000000000003020200010200004000000
04801000A000000000000302160001D00A500000008900027DEFFFFF740000000000
04801000A000000000000002100001C00A000000008000000004000000000000000
POLYODONTIDAE         35PADDLEFISHES
POLYODON              25
SPATHULA             -15PADDLEFISH
40402000003030300000000000004000200000000004000000
04401080BB000000000000302 1E00A0000B8000000000002A7EEFFEFF700044000000
04401080900000000000000021000000009800000000000000004000000000000000
```

Figure 8. ALIST output file

```
CHORDATA              Phylum       CHORDATES

CYCLOSTOMATA          Class        HAGFISHES AND LAMPREYS

PETROMYZONTIFORMES    Order

PETROMYZONTIDAE       Family       LAMPREYS

ICHTYOMYZON           Genus

BDELLIUM              Species      OHIO LAMPREY
   Author: SPW79
      ST:LARVA  ST:ADULT  RB:COMPLE RB:LITHOP FB:PRPLAN FB:PARASI
      GH:RIMEDI GH:RILARG BT:GRAVEL SH:NERIFF SH:NEOFFC PG:IL
   Author: TMB81
      ST:ADULT  PT:SAPHOB GH:STSMAL GH:RIMEDI GH:RILARG CU:LIMNOB
      CU:LIMNOP PG:PA     PG:WV     PG:AL     PG:KY     PG:TN
      PG:IL     PG:IN     PG:OH
   Author: LEE80
      ST:JUVENI ST:ADULT  GP:SUMMER FB:PARASI GH:STREAM GH:RISMAL
      GH:RIMEDI GH:RILARG ER:2110   ER:2210   ER:2510   PG:PA
      PG:VA     PG:WV     PG:AL     PG:KY     PG:SC     PG:TN
      PG:IL     PG:IN     PG:OH

CASTANEUS             Species      CHESTNUT LAMPREY
   Author: BEC83
      ST:LARVA  ST:ADULT  RB:PHYTOP RB:XYLOPH FB:PRPLAN FB:PARASI
      GH:LELAKE GH:STLARG BT:SILT   BT:SAND   BT:GRAVEL BT:COBBLE
      BT:VEGETA SH:NERIFF CU:INDIFF CU:RHEOPH PG:AL     PG:KY
      PG:MS     PG:NC     PG:TN     PG:IL     PG:MI     PG:MN
      PG:WI     PG:AR     PG:LA     PG:OK     PG:TX     PG:IA
      PG:KS     PG:MO     PG:ND     PG:MAN
   Author: SPW79
      ST:ADULT  FB:PARASI GH:RIMEDI GH:RILARG PG:IL
   Author: E&U74
      ST:ADULT  AB:UNCOMM FB:PARASI GH:STREAM GH:RISMAL PG:MN
   Author: LEE80
      FB:PARASI GH:LELAKE GH:RIVER  ER:2110   ER:2210   ER:2310
      ER:2320   ER:2510   ER:2530   PG:AL     PG:GA     PG:KY
      PG:MS     PG:NC     PG:TN     PG:IL     PG:IN     PG:MI
      PG:MN     PG:WI     PG:AR     PG:LA     PG:TX     PG:IA
      PG:KS     PG:MO     PG:ND     PG:ONT    PG:MAN
```

RUNOFF

The program RUNOFF is designed to format files for printing on the line printer. The program reads the file to be formatted from unit 10 and writes the formatted file to unit 9, which is then sent to the printer using the IBM utility program IEBGENER. Units 5 and 6 are used for terminal input and output. The form type, form length, line spacing, line numbering, print train, device and number of copies all may be controlled using RUNOFF. RUNOFF is limited to printing fixed length files of 80 columns.

UNMASK

The program UNMASK will produce a readable text file or printed copy of a compiled data base (Figure 9). Units 5 and 6 are used for terminal input and output. Unit 9 is used for line printer output. The CODES file is read from unit 10 and a COMPILED DATA file is read from unit 12. Unit 11 is used for output if results are written to a data file rather than to the line printer.

ERAPT

ERAPT is an interactive environmental information retrieval and analysis program which uses information in any COMPILED DATA file. The program is independent of the data base or codes file used. The program reads the CODES file from unit 10. A COMPILED DATA file is read from unit 12. Units 5 and 6 are used for terminal input and output and unit 9 is used for any output to the line printer. Unit 14 is used to access HELP information on program commands, and NEWS notices. Unit 15 is used for the storage and retrieval of saved searches. Unit 16 is used as a temporary output file to store control information for the lineprinter if an offline printout is requested.

Notices and command syntax descriptions are contained in a HELP file so that thsi information may be changed without modifying the program. The format of this file is shown in Figure 10. Lines beginning with an '@' symbol are command definitions. The next 12 characters are the command word followed by a three digit integer number. The first digit indicates the number of lines in the syntax section, and the last two digits the number of lines in the explanation. Several terms may have the same definition if they follow one another on separate lines. When counting lines, those beginning with an '@' symbol are ignored. If a section is to be omitted a blank line should be in the file as in syntax line for the command HISTORY. The NEWS section begins with '#BEGIN NEWS' and terminates with '#END NEWS'. All of the intervening lines are printed as the NEWS message.

The data used by the ERAPT program are stored in memory in a bit mapped binary form to pack the information as efficiently as possible. The data structure and linkages are illustrated in Figure 11. For each taxonimoc entry in a data base the system maintains, the scientific

Figure 9. UNMASK output file example.

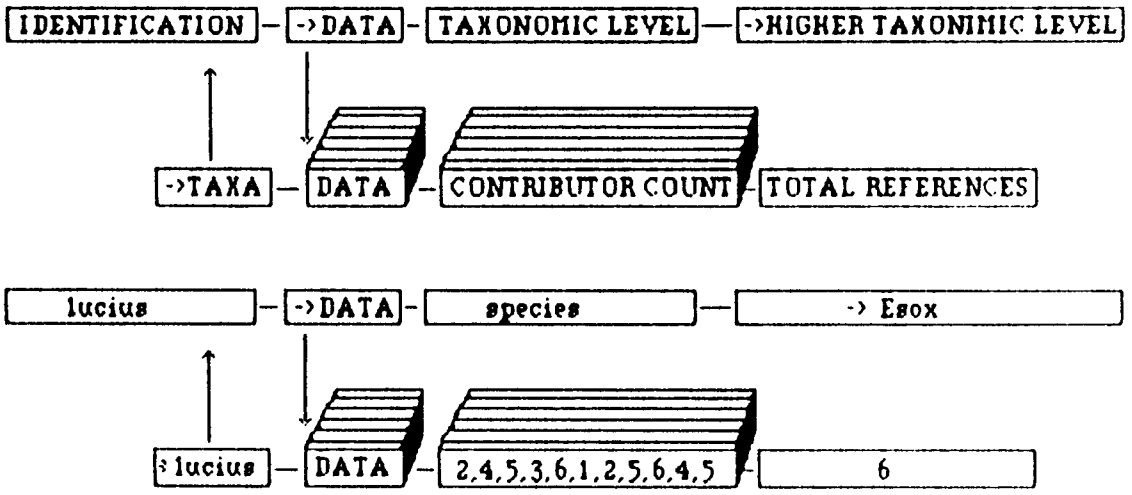
```
NOTURUS                <GENUS>
ELEUTHERUS             <SPECIES> MOUNTAIN MADTOM                    RC = 03
       ST 2 AB 1 PT 0 GP 0 RS 0 RB 0 FB 0 HA 0 SA 0 NU 0 OR 0 PH 0
       OX 0 GH 3 BT 3 SH 2 TE 0 TU 2 CU 2 ER 1 PG 3
   OR  ST:ADULT  AB:COMMON AB:UNCOMM GH:LOTIC  GH:STREAM GH:STLARG
       GH:RIVER  GH:RISMAL GH:RIMEDI GH:RILARG BT:SAND   BT:GRAPEB
       BT:GRAVEL BT:COBBLE BT:BOULDE BT:VEGETA SH:NEKTON SH:NERIFF
       TU:EULICH TU:MESOLI TU:OLIGOL CU:RHEOPH CU:RHEOBI ER:2000
       ER:2200   ER:2210   PG:REG03  PG:PA     PG:VA     PG:WV
       PG:REG04  PG:AL     PG:GA     PG:KY     PG:NC     PG:TN
       PG:REG05  PG:IL     PG:IN     PG:OH     PG:REG06  PG:AR
       PG:OK     PG:REG07  PG:MO
   AND ST:ADULT  AB:COMMON AB:UNCOMM GH:LOTIC  BT:GRAPEB BT:GRAVEL
       SH:NEKTON SH:NERIFF ER:2000   ER:2200   ER:2210   PG:REG05
       PG:IL
EXILIS                 <SPECIES> SLENDER MADTOM                     RC = 04
       ST 4 AB 2 PT 0 GP 0 RS 1 RB 0 FB 1 HA 0 SA 0 NU 0 OR 0 PH 0
       OX 0 GH 4 BT 3 SH 4 TE 0 TU 2 CU 3 ER 1 PG 3
   OR  ST:ADULT  AB:COMMON AB:UNCOMM RS:SPRING FB:PREDAT FB:PRINVE
       FB:HERBIV FB:HEGRAZ FB:DETRIT GH:LOTIC  GH:STREAM GH:STSMAL
       GH:STMEDI GH:STLARG BT:SAND   BT:GRAPEB BT:GRAVEL BT:COBBLE
       BT:BOULDE SH:NEKTON SH:NERIFF SH:NERUN  SH:NEPOOL SH:NEOFFC
       TU:EULICH CU:RHEOPH CU:RHEOBI ER:2000   ER:2200   ER:2210
       ER:2500   ER:2510   PG:REG04  PG:AL     PG:KY     PG:MS
       PG:TN     PG:REG05  PG:IL     PG:IN     PG:MN     PG:WI
       PG:REG06  PG:AR     PG:OK     PG:REG07  PG:IA     PG:KS
       PG:MO
   AND ST:ADULT  RS:SPRING FB:PREDAT FB:PRINVE FB:HERBIV FB:HEGRAZ
       FB:DETRIT GH:LOTIC  GH:STREAM BT:GRAPEB BT:GRAVEL SH:NEKTON
       TU:EULICH ER:2000   ER:2200   ER:2210   ER:2500   ER:2510
       PG:REG05  PG:IL
```

Figure 10. HELP file example.

```
@INPUT        105
@OUTPUT       105
TERMINAL/LINEPRINTER/UNIT ##
Redirects input or output to the terminal, lineprinter
or the unit specified by UNIT ##.  The use of the unit
is not advised.  If the Unit was not pre-allocated to
the program the program will err, this error cannot
be trapped so the program may quit running.
@HISTORY      101

Lists your search results in reverse chronological order.
@ECHO         101
ON/OFF
Turns on or off the echoing of search results.
#BEGIN NEWS
Updates for Version 8.0
The ability to work directly with binary data has been added
     to the system.  The command MASK produces binary masks
     as its result, not searches.  These masks may then be
     used as the argument to a logical operator, like AND,
     to produce a search or to combine two masks,
     See HELP MASK for more details.
#END NEWS
```

Figure 11. ERAPT program data structure and linkages.



name, taxonomic level, a pointer to the next higher taxonomic level, and a pointer to a data record if data are present. The data record includes information on the number of sources used in accumulating information for each environmental category and the total number of data sources used, a pointer back to the taxonomic record, and an array of binary environmental data. The pointers allow either taxonomic names or environmental data to be searched.

The results of these searches are placed on a stack for later reference. Twenty search results may be kept on the stack at a time and they may contain either lists of pointers to taxonomic entries or bit mapped data representing environmental category information.

This allows search results to be either lists of species or environmental characteristisc of a habitat, and permits these two distinctly different kinds of results to be compared or evaluated in subsequent queries. For example, it is possible to define a list of species to the system and request a list of their shared environmental requirements. This environmental description may then be compared to those developed for specific habitats or projected from alternative species assembladges.

## SECTION III

## ERAPT EXAMPLES

The following section provides a series of brief examples to illustrate some of the features and uses of the ERAPT system. The user would have entered the information on any line which begins with one of the system prompts: '>', or 'MORE-/E>'. All other lines contain output from the system. Scientific names entered on command lines have been abbreviated to the fewest characters required by the system. All of these examples are exact representations of ERAPT system input and output.

The examples are divided into three parts: 1) the question to be answered, 2) the list of ERAPT system commands and responses, and 3) a running commentary on the right side of the page explaining the commands used and search results.

## Predicting Environmental Change by Faunal Change

The fauna of a small stream has changed since a previous survey by the addition of one new species and the loss of two previously existing species. What might this indicate?

```
>QUALIFY PH BT
```

Consider only the information pH, and bottom type.

```
>DEFINE ES-AM ET-MIC/END
  ESOX AMERICANUS
  ETHEOSTOMA MICROPERCA
  SEARCH:  1 RECORDS:   2
```

Enter the two lost species.

```
>COMPARE 1
        PH 2 BT 2
    ALL PH:ALKALP BT:SAND   BT:GRAPEB BT:GRAVEL BT:VEGETA BT:DETRIT
  SEARCH:  2 MASK.
```

Determine common requirements of the older species.

```
>COMPARE NOTR-CHAL
  NOTROPIS CHALYBAEUS
        PH 1 BT 1
    ALL PH:ACIDOB PH:ACIDOP BT:SAND   BT:VEGETA
  SEARCH:  3 MASK.
```

Determine characteristics of the new species.

```
>2 NOT 3
  SEARCH:  4 MASK.
>PRINT
```

Determine the characteristics of the older species which are not shared by the new and print the list of differences.

---

```
   0  RECORDS.
  2 NOT 3
  SEARCH FROM OR SUMMARY
     SUM PH:ALKALP BT:GRAPEB BT:GRAVEL BT:DETRIT
>HELP/DEFINE PH BT
```

List definitions for all pH and bottom type codes.

| | |
|---|---|
| PH: | pH - Negative logarithm of hydrogen ion activity. |
| PH:ACIDOB | Acidobiontic - pH < 5.5. |
| PH:ACIDOP | Acidophilous - pH 5.6-6.5. |
| PH:NEUTRA | Neutral - ph 6.6 - 7.5. |
| PH:ALKALP | Alkaliphilous - pH 7.6-8.5. |
| PH:ALKALB | Alkalibiontic - pH > 8.5. |
| PH:INDIFF | pH Indifferent - Not pH dependent, found in both acid, neutral, and alkaline waters. |
| BT: | Bottom Type - Bottom requirements for satisfactory growth or reproduction. |
| BT:SILT | Silt - Particle size 0.0039-0.0625 mm. |
| BT:SAND | Sand - Particle size 0.0625-2.0 mm. |
| BT:GRAPEB | Gravel or Pebble - Particle size 2.0-64.0 mm. |
| BT:GRAVEL | Gravel - Particle size 2.0-16 mm. |
| BT:PEBBLE | Pebble - Particle size 16.0-64.0 mm. |
| BT:COBBLE | Cobble or Rubble - Particle size 64.0-256.0 mm. |
| BT:BOULDE | Boulder - Particle size > 256.0 mm. |
| BT:BEDROC | Bedrock or Claypan - Solid rock or clay bottom. |
| BT:VEGETA | Vegetation - Bottom covered with aquatic vegetation. |
| BT:MUCK | Muck - Bottom primarily composed of FPOM. |
| BT:DETRIT | Detritus - Bottom primarily composed of CPOM. |

## Subdividing Faunas by Environmental Conditions

Samples were obtained from a river which consisted of a series of deep pools connected by more shallow, riffle sections. Which species came from which areas of the river?

```
>DEFINE CAMP-ANOM HIODON-ALOS HYBOP-AES NOTROP-ATH NOTR-DORS HYB-X-P
 CAMPOSTOMA          ANOMALUM
 HIODON              ALOSOIDES
 HYBOPSIS            AESTIVALIS
 NOTROPIS            ATHERINOIDES
 NOTROPIS            DORSALIS
 HYBOPSIS            X-PUNCTATA
MORE-/E>CAMP-OLIGO ETHE-MAC DORO-PETE/END
 CAMPOSTOMA          OLIGOLEPIS
 ETHESTOMA           MACULATUM
 DOROSOMA            PETENENSE
 SEARCH:  1 RECORDS:   9
>1 AND SHNEPOOL
 SEARCH:  2 RECORDS:   6

>PRINT/COMMON
```

Define the list of species found in the river.

Which species are from pools?

List the species which occur in pools, including common names.

```
 6  RECORDS.
 1 AND SHNEPOOL
 SEARCH FROM OR SUMMARY

      DOROSOMA PETENENSE                THREADFIN SHAD
      HIODON ALOSOIDES                  GOLDEYE
      CAMPOSTOMA ANOMALUM               CENTRAL STONEROLLER
      CAMPOSTOMA OLIGOLEPIS             LARGESCALE STONEROLLER
      NOTROPIS ATHERINOIDES             EMERALD SHINER
      NOTROPIS DORSALIS                 BIGMOUTH SHINER
>1 AND SHNERIFF
 SEARCH:  3 RECORDS:   7
>PRINT/COMMON
```

Which species are from riffles?

List species which are found in riffles including common names.

```
 7  RECORDS.
 1 AND SHNERIFF
 SEARCH FROM OR SUMMARY

      DOROSOMA PETENENSE                THREADFIN SHAD
      HIODON ALOSOIDES                  GOLDEYE
      CAMPOSTOMA ANOMALUM               CENTRAL STONEROLLER
      CAMPOSTOMA OLIGOLEPIS             LARGESCALE STONEROLLER
      HYBOPSIS AESTAVALIS               SPECKLED CHUB
      HYBOPSIS X-PUNCTATA               GRAVEL CHUB
      ETHESTOMA MACULATUM               SPOTTED DARTER
```

## Evaluating Introduced Species

What species might be good choices to stock in the following habitat?

```
>NOT CURHEOPH
 SEARCH:  1 RECORDS: 253
>1 AND GHLEPOND BTVEGETA BTSAND BTGRAVEL FBPRPISC PGIL
 SEARCH:  2 RECORDS:  16
```

Exclude those which need current.

The pond to be stocked is in Illinois. The large pond has a vegetated sand and gravel bottom. The pond has an abundance of small forage fish but few piscivorous game fish.

```
>PRINT/COMMON
```

List the species of game fish which have these requirements and include common names.

```
16  RECORDS.
1 AND GHLEPOND BTVEGETA BTSAND BTGRAVEL FBPRPISC PGIL
SEARCH FROM OR SUMMARY

      SALMO TRUTTA                        BROWN TROUT
      SALVELINUS FONTINALIS               BROOK TROUT
      ESOX AMERICANUS
      ESOX AMERICANUS VERMICULATUS        GRASS PICKEREL
      SEMOTILUS ATROMACULATUS             CREEK CHUB
      ICTALURUS NEBULOSUS                 BROWN BULLHEAD
      ICTALURUS PUNCTATUS                 CHANNEL CATFISH
      CULAEA INCONSTANS                   BROOK STICKLEBACK
      LEPOMIS CYANELLUS                   GREEN SUNFISH
      LEPOMIS GULOSUS                     WARMOUTH
      LEPOMIS MACROCHIRUS                 BLUEGILL
      MICROPTERUS DOLOMIEUI               SMALLMOUTH BASS
      MICROPTERUS SALMOIDES               LARGEMOUTH BASS
      POMOXIS ANNULARIS                   WHITE CRAPPIE
      POMOXIS NIGROMACULATUS              BLACK CRAPPIE
      PERCA FLAVESCENS                    YELLOW PERCH
```

## Predicting Faunal Change by Environmental Change

If a forested area is to be cleared for farming, what will happen to the existing fauna of the stream if this causes siltation?

```
>DEFINE SALMO-GAI SALMO-TRUT SALV-FONT CLINO-FUND NOCOM-MICR NOTRO-ARD
 SALMO              GAIRDNERI
 SALMO              TRUTTA
 SALVELINUS         FONTINALIS
 CLINOSTOMUS        FUNDULOIDES
 NOCOMIS            MICROPOGON
 NOTROPIS           ARDENS
MORE-/E>AMBLO-RUP ETHE-BLEN ETHE-CAMU ETHE-FLAB PERC-EV/END
 AMBLOPLITES        RUPESTRIS
 ETHEOSTOMA         BLENNIOIDES
 ETHEOSTOMA         CAMURUM
 ETHEOSTOMA         FLABELLARE
 PERCINA            EVIDES
 SEARCH:  1 RECORDS:  11
>COMPARE 1/ALL
        ST11 AB 6 GP 1 RS10 RB 9 FB10 HA 1 SA 3 NU 1 PH 2 OX 2 GH11
        BT11 SH10 TE 7 TU11 CU11 ER11 PG11
    AND ST:ADULT  GP:SUMMER FB:PREDAT HA:SLIGHT SA:EURYHA NU:OLOGOT
        PH:ACIDOP PH:NEUTRA PH:ALKALP PH:INDIFF OX:EUOXYP OX:MESOXY
        GH:LOTIC  GH:STREAM SH:NEKTON ER:2000   ER:2200   ER:2210
        PG:REG03  PG:VA     PG:REG04  PG:KY     PG:NC     PG:TN
        PG:REG05  PG:OH
 SEARCH:  2 MASK.
>HELP/DEFINE HASLIGHT SAEURYHA OX
HA:          Hardness - Hardness of water measured as mg/l CaCO3.
HA:SLIGHT    Slightly Calcareous - Total hardness 20-100 mg/l CaCO3.
SA:          Salinity - Dissolved salt concentration for habitat.
SA:EURYHA    Euryhalinous - Occurs under broad range of salt
             concentrations. (CHIR 15, DIAT 19, BLGR 30)
OX:          Oxygen - Dissolved oxygen requirements for reproduction and
             growth.
OX:EUOXYP    Euoxyphilous - High oxygen concentration, O2 > 7.5 mg/l.
             (saturated)
OX:MESOXY    Mesoxyphilous - Moderate oxygen concentrations, O2 5.0-7.5 mg/l.
OX:OLIGOX    Oligoxyphilous - Low oxygen concentrations, O2 2.5-5.0 mg/l.
OX:ANOXYP    Anoxyphilous - Facultative anaerobic, O2 < 2.5 mg/l.
>1 AND BTSILT
 SEARCH:  3 RECORDS:   2
>PRINT
```

Enter the present fauna.

List the environmental factors common to all of the species.

List the definitions for HASLIGHT, SAEURYHA and all codes for dissolved oxygen.

Which of the current fauna can tolerate silt?

Print the silt tolerant species.

---

```
 2  RECORDS.
 1 AND BTSILT
 SEARCH FROM OR SUMMARY

AMBLOPLITES RUPESTRIS                ETHEOSTOMA FLABELLARE
```

## Finding Environmental Differences Among Species

Two closely related species rarely occur together. What environmental factors distinguish between them?

```
>QUALIFY DELETE ST PG RS AB ER
 DELETING...
```

Prevents information on stage political geography, reproductive season, abundance or ecoregion from being considered.

```
>COMPARE LEPOM-GIBB LEPOM-MEGAL/DIFFERENCE
  LEPOMIS GIBBOSUS
  LEPOMIS MEGALOTIS
        RB 2 FB 2 GH 2 BT 2 SH 2 TE 1 TU 2 CU 1
    DIF FB:HERBIV FB:HEGRAZ FB:HEBROW FB:OMNIVO GH:LELITT GH:RIMEDI
        BT:GRAPEB BT:GRAVEL BT:DETRIT SH:NEOFFC
```

Compare the two species for differences

The factors which differ between the species.

```
  LEPOMIS GIBBOSUS
    NOT BT:GRAPEB BT:GRAVEL SH:NEOFFC
```

Factors not characteristic of *Lepomis gibbosus*.

```
  LEPOMIS MEGALOTIS
    NOT FB:HERBIV FB:HEGRAZ FB:HEBROW FB:OMNIVO GH:LELITT GH:RIMEDI
        BT:DETRIT TE:MESOTH TE:MEHIGH CU:LIMNOB
```

Factors not characteristic of *Lepomis megalotis*.

## Identifying Indicator Organisms

A construction project along a river may cause it to become silted. Which species might be good indicators of changing turbidity for monitoring the river?

```
>DEFINE NOT-STRA NOT-FLAV CAT-CAT HIO-TER LEP-OSS HYP-NIG MICRO-PUNC
  NOTROPIS STRAMINEUS
  NOTURUS FLAVUS
  CATOSTOMUS CATOSTOMUS
  HIODON TERGISUS
  LEPISOSTEUS OSSEUS
  HYPENTELIUM NIGRICANS
  MICROPTERUS PUNCTULATUS
MORE-/END > MOXO-CAR MOX-DUQ PERC-MACRO ETHE-ZON COTT-BAIR/END
  MOXOSTOMA CARINATUM
  MOXOSTOMA DUQUESNEI
  PERCINA MACROCEPHALA
  ETHEOSTOMA ZONALE
  COTTUS BAIRDI
  SEARCH:  1 RECORDS:  12
>1 AND TUEULICH
  SEARCH:  2 RECORDS:  12
>2 NOT BTSILT
  SEARCH:  3 RECORDS:   8
>3 EVAL BT TU
  SEARCH:  4 RECORDS:   3
 CATOSTOMUS CATOSTOMUS                    RC:   6
        BT:GRAPEB BT:GRAVEL TU:EULICH
 MICROPTERUS PUNCTULATUS                  RC:   3
        BT:GRAPEB BT:GRAVEL TU:EULICH
 PERCINA MACROCEPHALA                     RC:   2
        BT:GRAPEB BT:GRAVEL BT:BOULDE TU:EULICH
>PRINT/COMMON
```

Enter a list of species.

Make sure that they are all found in clear water.

Remove those that would tollerate silt.

Find potential indicators for turbidity and bottom type.

List of species and requirements.

List the species and their common names.

---

```
  3  RECORDS.
 3 EVAL BT TU
 SEARCH FROM OR SUMMARY

      CATOSTOMUS CATOSTOMUS                LONGNOSE SUCKER
      MICROPTERUS PUNCTULATUS              SPOTTED BASS
      PERCINA MACROCEPHALA                 LONGHEAD DARTER
```

## Identifying Species by Environmental Conditions

Some specimens collected as part of an environmental monitoring study can be identified only to genus. Given a general knowledge of the habitat characteristics and geographic location, what species are likely?

```
>AND PGCH BTSAND BTGRAVEL GHLELAKE SHNENEAR TEMESOTH
 SEARCH: 1 RECORDS: 23
>1 FIND NOTROPIS/COMMON
NOTROPIS CORNUTUS          COMMON SHINER      RC: 6
NOTROPIS DORSALIS          BIGMOUTH SHINER    RC: 6
NOTROPIS HUDSONIUS         SPOTTAIL SHINER    RC: 5
```

Enter what is known about the habitat.

Of the 36 possible species of Notropis only these three are found in the habitat previously described.

## Interpreting Environmental Causes of Faunal Change

A species has reappeared in a habitat where it has not been collected for many years. What might the return of this species indicate?

```
>QUALIFY BT SH TE TU CU
```

Consider only physical information: bottom type, specific habitat, temperature, turbidity, and current.

```
>FIND NOTR-AT/SUM/COMMON
NOTROPIS ATHERINOIDES              EMERALD SHINER              RC: 5
      BT 2 SH 3 TE 1 TU 4 CU 2
   SUM BT:SAND   BT:GRAPEB BT:GRAVEL BT:MUCK   SH:NEKTON SH:NERUN
      SH:NEPOOL SH:NEOFFC SH:NEPELA TE:MESOTH TE:MEMEDI TU:EULICH
      TU:MESOLI TU:POLYLI CU:LIMNOP
```

List all of the information on the Emerald shiner.

A comparison between these factors and the current data should show any changes.

## Relocating Endangered Species

A rare species is found only in a small section of one river system. Due to changing environmental conditions this species may be lost if it cannot be relocated. Do other species have similar environmental requirements? What environmental characteristics must a potential relocation site have?

```
>QUALIFY BT SH PG
```

Only consider information on bottom type, specific habitat, and political geography.

```
>COMPARE NOTUR-T
 NOTURUS            TRAUTMANI
       BT 1 SH 1 PG 1
    AND BT:SILT   BT:SAND   BT:GRAPEB BT:GRAVEL BT:PEBBLE BT:BOULDE
       BT:VEGETA SH:NEKTON SH:NERIFF SHNERUN   PG:REG05  PG:OH
 SEARCH:  1 MASK.
>AND 1
 SEARCH:  2 RECORDS:   2
>PRINT/COMMON
```

Find the characteristics of Noturus trautmani and find all species which have identical requirements.

Print the 2 species found with their common names.

```
 2  RECORDS.
 AND 1
 SEARCH FROM OR SUMMARY

      RHINICHTHYS CATARACTAE                LONGNOSE DACE
      NOTURUS TRAUTMANI                     SCIOTO MADTOM
```

```
>QUALIFY RESET
  QUALIFICATION SET TO ALL.
```

Reset for all information.

```
>COMPARE 2
       ST 2 AB 1 RS 1 RB 1 FB 1 GH 1 BT 2 SH 2 TE 1 TU 1 CU 2 ER 2
       PG 2
    AND ST:ADULT  AB:RARE   RS:SPRING RS:SUMMER RS:AUTUMN RB:COMPLE
       RB:SIMPLE RB:LITHOP FB:PREDAT FB:PRINVE FB:PRPLAN GH:LENTIC
       GH:LELAKE GH:LOTIC  GH:STREAM GH:STSMAL GH:STMEDI GH:STLARG
       GH:RIVER  GH:RISMAL BT:SILT   BT:SAND   BT:GRAPEB BT:GRAVEL
       BT:PEBBLE BT:BOULDE BT:VEGETA SH:NEKTON SH:NERIFF SH:NERUN
       TE:MESOTH TE:MELOW  TE:MEMEDI TU:EULICH TU:MESOLI TU:OLIGOL
       TU:POLYLI CU:RHEOBI ER:2000   ER:2200   ER:2210   PG:REG05
       PG:OH
 SEARCH:  3 MASK.
```

Compare the species found to be identical to the Scioto madtom to determine what requirements they share.

## Predicting Unrelated Faunal Assemblages

Given the environmental characteristics of a stream habitat, predict the fish and mayfly communities likely to be present.

```
ERAPT FISH
   E.R.A.P.T. DATA BASE INFORMATION RETRIEVAL PROJECT.
> SAVE SITE#1                                          Save the following lines as
  BEGIN SEARCH SITE#1                                  search SITE#1
> AND GHSTREAM PHALKALP TEMESOTH TUEULICH PGREGO5      Enter the habitat description.
  SEARCH:  1 RECORDS:  13
> END                                                  Stop saving SITE#1.
  SEARCH ENDED
> PRINT                                                Print the species.
 ------------------------------------------------------
  13  RECORDS.
  AND GHSTREAM PHALKALP TEMESOTH TUEULICH PGREGO5
  SEARCH FROM OR SUMMARY
 SALMO GAIRDNERI                    SALVELINUS FONTINALIS
 ESOX AMERICANUS                    ESOX AMERICANUS VERMICULATUS
 ESOX LUCIUS                        NOTROPIS CORNUTUS
 SEMOTILUS ATROMACULATUS            LEPOMIS MACHROCHIRUS
 MICROPTERUS DOLOMIEUI              MICROPTERUS SALMOIDES
 POMOXIS NIGROMACULATUS             ETHEOSTOMA MICROPERCA
 PERCA FLAVESCENS
> END
A SEARCH WAS SAVED TO A TEMPORARY DATA FILE.  TO SAVE THIS FILE   A new library must be created
ENTER A FILE NAME (1-8 CHARACTERS) OR ENTER A <RETURN> AND THE    to keep the search that was
THE DATA SET WILL BE DELETED. > SAVELIB                           saved.
ERAPT EPHE SA(SAVELIB)                                            Enter the Mayfly data base
   E.R.A.P.T. DATA BASE INFORMATION RETRIEVAL PROJECT.            using the SaveFile SAVELIB.
> EXEC SITE#1                                                     Recall the save statements.
 *CLEAR
  DATA STACK CLEARED - READY FOR SEARCH 1.
 *AND GHSTREAM PHALKALP TEMESOTH TUEULICH PGREGO5
  SEARCH:  1 RECORDS:   9
 *END SITE#1
  SEARCH ENDED
> PRINT                                                           List the species that have
 ------------------------------------------------------           the same requirements as the
   9  RECORDS.                                                    fish species.
  AND GHSTREAM PHALKALP TEMESOTH TUEULICH PGREGO5
  SEARCH FROM OR SUMMARY
 ARTHROPLEA BIPUNCTATA              BAETISCA BAJKOVI
 CLOEON RUBROPICTUM                 EPEORUS VITREUS
 EPHERON ALBUM                      HEXAGENIA ATROCAUDATA
 HEZAGENIA MUNDA                    PARALEPTOPHLEBIA MOLLIS
 SIPHLONURUS QUEBECENSIS
> END
```

## Using One Faunal Assemblage to Predict Another

A group of fish species is known to occur together at a site under investigation. What stonefly species are predicted to occur in this habitat based on the environmental characteristics associated with the fish?

```
ERAPT FISH SAVEFILE(SAVELIB)

   E.R.A.P.T. DATA BASE INFORMATION RETRIEVAL PROJECT.
> QUALIFY PH GH TE TU


> COMPARE ESOX-AM MICRO-SAL ETHEO-MIC/KEEP/END
  ESOX                AMERICANUS
  MICROPTERUS         SALMOIDES
  ETHEOSTOMA          MICROPERCA
 KEEPING FISH001
         PH 3 GH 3 TE 3 TU 3
     AND PH:ALKALP GH:LENTIC GH:LELAKE GH:LEPOND GH:LELITT GH:LOTIC
         GH:STREAM TE:MESOTH TU:EULICH
  SEARCH:  1 MASK.
>END
ERAPT PLEC SAVE(SAVELIB)
   E.R.A.P.T. DATA BASE INFORMATION RETRIEVAL PROJECT.
> CATALOG
  CATALOG OF LIBRARY FILE:
  SITE#1              <SAVE>
  FISH001             <KEEP>
    2 FILES IN LIBRARY.
> GET FISH001
MORE-/END >
MORE-/END >
  SEARCH:  1 MASK.
  SEARCH ENDED
> AND 1
  SEARCH:  2 RECORDS:   1
> PRINT
```

Access the retrieval program and request the use of a SaveFile library called

Only consider information on pH, general habitat, temperature, and turbidity.

Compare the fish species found in the lake for their similarities and KEEP the result.

The similarities are stored in a search called FISH001.

List the files contained in the SaveFile library.

Get the result of the comparison of the fish species.

One species has the same requirements as the fish

Print this stonefly.

---

```
   1  RECORDS.
  MASK/C PHALKALP GHLENTIC GHLELAKE GHLELITT GHLOTIC  GHSTREAM TEMESOTH
  SEARCH FROM OR SUMMARY

 PARAGNETINA MEDIA
> END
```

## Evaluating Temporal Environmental Change

To evaluate environmental change in a river over time, an initial list of species is to be saved for comparison with any subsequent changes in the faunal composition of the habitat.

```
ERAPT FISH
   E.R.A.P.T. DATA BASE INFORMATION RETRIEVAL PROJECT.
> SAVE SITE#2
  BEGIN SEARCH SITE#2
```

Specify that all of the command lines which follow are to be saved as a search called SITE#2 until the END command is entered.

```
> DEFINE ESO-L HYBO-AM NOTR-DO NOTR-SPI CAT-COMM NOTE-CR
  ESOX              LUCIUS
  HYBOPSIS          AMBLOPS
  NOTROPIS          DORSALIS
  NOTROPIS          SPILOPTERUS
  CATOSTOMUS        COMMERSONI
  NOTEMIGONUS       CRYSOLEUCAS
MORE-/END > ICTA-NEB LEP-MEG LEP-MIC MICR-SAL PERC-FL
  ICTALURUS         NEBULOSUS
  LEPOMIS           MEGALOTIS
  LEPOMIS           MICROLOPHUS
  MICROPTERUS       SALMOIDES
  PERCA             FLAVESCENS
MORE-/END > ETHE-GRA ETHE-SPEC PERC-MAC/END
  ETHEOSTOMA        GRACILE
  ETHEOSTOMA        SPECTABILE
  PERCINA           MACROCEPHALA
  SEARCH:  1 RECORDS:  14
```

Enter the names of the species found at Site #2.

Include /END operand to terminate the definition of species.

```
> END SITE#2
  SEARCH ENDED
```

Stop saving lines into the file SITE#2.

```
> COMPARE 1
        ST14 AB 8 PT 2 RS11 RB11 FB14 HA 1 SA 5 PH 5 OX 4 GH14 BT14
        SH14 TE 8 TU14 CU 8 ER14 PG14
    AND ST:ADULT  PT:FACULT FB:PREDAT FB:PRINVE HA:MODERA GH:LOTIC
        GH:STREAM SH:NEKTON SH:NEPOOL TE:MESOTH ER:2000   ER:2200
        ER:2210   PG:REG05
  SEARCH:  2 MASK.
> END
```

Compare the defined species and list their similarities.

## SECTION IV

## VALIDATION

### Methods

Survey data for verification of the ERAPT system were obtained from the State of Ohio Environmental Protection Agency for 64 sites from 20 rivers, streams, and tributaries in the Cross Creek and Yellow Creek, Blanchard River, and Tuscarawas River systems in southeastern and northwestern Ohio. For each site a list of fish species and abundances and descriptive information on the habitat was provided. This included the dissolved oxygen, temperature, pH, turbidity, bottom type, and general and specific habitat characteristics of most sites, with current, degradable organics, and pollution information provided for a few of the sites.

The five numerically dominant species at each site were entered into the ERAPT system and used to predict local environmental conditions. These species accounted for at least one half of the total fishes collected and, therefore, were taken to be representative of the environmental conditions present within the habitat sampled. The ERAPT system's Compare function was used to identify the environmental characteristics common to each fish community. This information was used for comparison with the environmental description of each habitat.

Habitat characterization information for each collecting site was transformed into ERAPT environmental parameter codes directly from field survey forms. These data then were compared with the environmental descriptions predicted by the system from the associated dominant fish community for each category of environmental characteristic. The compared data were considered to be in agreement if they shared common environmental parameters. For example, a general habitat predicted by the fish assemblage as lake or large river was considered to be in agreement with a habitat characterized as either large river or lake. Likewise, a community predicted bottom type of gravel was considered to be in agreement with a habitat characterized as gravel, sand, and silt.

### Results and Discussion

In comparing 300 environmental characteristics obtained from field survey forms to those predicted by the ERAPT system from the dominant fish community, 285 showed agreement for an overall successful prediction rate of 95% (Tables 1-2). The successful prediction rates for the Cross Creek and Yellow Creek, Blanchard River, and Tuscarawas River systems were 95%, 97%, and 93%, respectively. There was 100% agreement between predicted and observed characterizations for temperature, current, and degradable organics in all three river systems. Those

## System Verification Results

| System | Cross Creek and Yellow Creek | | |

| River Systems | Cross & Yellow | | Tuscarawas | | Blanchard | | Total | |
|---|---|---|---|---|---|---|---|---|
| | No. of Sites | Agreement | No. of Sites | Agreement | No. of Sites | Agreement | No. of Sites | Agreement |
| $DO_2$ mg/l | 13 | 100% | 5 | 100% | 6 | 83% | 24 | 96% |
| Temperature | 18 | 100% | 6 | 100% | 7 | 100% | 31 | 100% |
| pH | 16 | 81% | 4 | 100% | 5 | 100% | 22 | 88% |
| Current | 2 | 100% | 3 | 100% | - | - | 5 | 100% |
| Turbidity | 22 | 82% | 2 | 100% | 8 | 100% | 32 | 88% |
| General Habitat | 34 | 100% | 11 | 91% | 17 | 100% | 62 | 98% |
| Bottom type | 33 | 97% | 10 | 80% | 16 | 100% | 59 | 95% |
| Organics | - | - | 3 | 100% | - | - | 3 | 100% |
| Specific Habitat | 31 | 97% | 10 | 90% | 16 | 94% | 57 | 95% |
| Pollution | - | - | 2 | 100% | - | - | 2 | 100% |

Table 2. Results of ERAPT system validation study.

environmental parameters not in complete agreement between observed and predicted characterizations were: general habitat (98%), dissolved oxygen (96%), specific habitat and bottom type (95%), and pH and turbidity (88%).

Turbidity and pH showed the lowest agreement between the predicted and observed values because of discrepancies in the characterization of sites in the Cross Creek and Yellow Creek system. The only other differences between reported and predicted results for this river system were for site 1 of Yellow Creek, which the ERAPT system predicted to be a large stream with a sand and gravel bottom, but which was reported to be a small river with a silt bottom.

Discrepancies in the results of turbidity comparisons may be due to the seasonal nature of turbidity in rivers. Conditions of high turbidity may have their greatest impact on specific life stages, and fishes may be insensitive to relatively turbid conditions during some portions of the year. The main disagreement in turbidity occurred over a three mile stretch of Cross Creek where three adjacent sampling sites were characterized as being more turbid than that predicted by the dominant fish community. This also could have been the result of recent environmental change which had not yet been expressed in the fish population through a sensitive life stage.

Reported and predicted values for pH differed at three sites in the Cross Creek and Yellow Creek system. In each case the reported pH was lower than that predicted by the dominant fish community. At two of the sites the fish assemblage predicted pH values of greater than 8.5, whereas field data indicated pH ranges of 8.1 to 8.5 and 7.3 to 7.8. At the third site the fish community predicted pH values in excess of 5.5, but the field data indicated a pH range of 2.8 to 4.0. These results also suggest changing environmental conditions which are not reflected yet in the fish community.

Four discrepancies between observed and predicted habitat characterizations were found from separate sites in the Tuscarawas River system. The specific habitat of one site was described as a run, whereas the ERAPT system predicted a pool habitat from dominant fish community. Another site was reported to have a depth of 0.45 m which fell just outside of the predicted range of 0.5 to 2.0 m. The other two sites were reported to have silt and clay bottoms instead of the predicted bottom type of sand.

Sites in the Blanchard River system showed only two disagreements between reported and predicted environmental characterizations. At one site in which the dissolved oxygen concentration was reported to be 2.1 to 5.0 ppm, the ERAPT system predicted levels of greater than 5.0 ppm. At another site the system predicted a water depth of 1.0 to 2.0 m, as opposed to the reported depth of 0.85 m.

While there were some disagreements between predicted and reported environmental characterizations, they almost always were among very similar tolerance ranges or habitat types. In addition, only one site which discrepancies between the observed and predicted characterizations of more than one kind of environmental parameter. This was site number 1 of Yellow Creek where there were minor disagreements in both specific habitat and bottom type. Overall, ERAPT system predictions of habitat characteristics from the dominant fish assemblages closely approximated the information obtained from field surveys at all of the sites evaluated.

## SECTION V

## ERAPT PROGRAM

The ERAPT program offers a broad range of retrieval and analysis capabilities for use in environmental assessment. These include the ability to characterize environmental conditions from resident organisms, to identify organism assemblages from environmental conditions, to predict changes in the biological community resulting from environmental change, and to identify environmental change for change in the species composition of a habitat.

### Abbreviations and Syntax

The scientific names may be abbreviated by the fewest letters to make them unique. *Esox lucius* may be abbreviated ES-L. If a combination is not unique the first matching entry will be used in DEFINE or COMPARE or all matching entries will be listed in the case of the FIND command.

The commands may be abbreviated with the fewest letters to make them unique. FIND may be abbreviated F but CLEAR must be CL. As a rule, the first two characters of all commands are sufficient.

All parameters which begin with a slash, /, are position independent and completely optional. Only the first character after the slash is required and it is the only character that is checked, therefore /DEFINE, /DEFINITION, /DEF, and /D are all synonymous.

The 2-8 character environmental retrieval codes may not be abbreviated. Code lists and definitions may be obtained through the help command.

Throughout this section several conventions are used in the command syntax.

Braces {}. Mutually exclusive parameters are enclosed in braces, {}.

Brackets []. Optional parameters are enclosed in brackets, [].

Slashes /. All options are preceded by a slash, /. The option is ended with a blank space or another option.

Numeral Signs #. All numeric parameters are represented using number sign, #, with each symbol representing a digit. A parameter with a range from 0 to 99 would be shown as ## whereas a range of 0 to 9 would be a #.

Characters XX. The symbol XX is used for two character category codes like PG, political geography. In the case of the QUALIFY command any 2 to 8 character code may be used.

Arrows <>. The symbols <> are used to represent keys on the terminal. <RETURN> is the enter or return key.

Examples:

OUTPUT {TERMINAL LINEPRINTER UNIT ## FILE ##}

One of these parameters <u>must</u> follow the command OUTPUT but <u>only one</u> may be used.

PRINT [##] [/OFFLINE] [/COMMON]

All parameters are optional and may be used separately. The first is expected to be a 1 or 2 digit number, the others are the parameters /OFFLINE and /COMMON.

QUALIFY {[ON]
[OFF]
[RESET]
[ADD XX ... XX:XXXXXX]
[DELETE XX ... XX:XXXXXX]
[XX ... XX:XXXXXX]}

There are 6 valid parameters. Only one of the 6 may be used on a command line at any time. Three are single word parameters: ON, OFF, and RESET; 2 have parameters of their own which must be present: ADD XX ... XX and DELETE XX ... XX; and the sixth parameter is just a list of 2 to 8 character category codes. A valid example would be QUALIFY DELETE PG BT:GRAVEL BT:SAND.

## Program Command List

The following is a list of the ERAPT information retrieval system commands and syntax. This information can be obtained from the ERAPT program by typing HELP followed by any command.

HELP The help command lists all the commands which can be used in the ERAPT program:

Example:

```
HELP
HELP IS AVAILABLE ON THE FOLLOWING COMMANDS:
  |          &          ~          ?
  AND        CATALOG    CLEAR      COMPARE
  DEFINE     DIFFERENCE ECHO       END
  EVALUATE   EXECUTE    FIND       GET
  HELP       HISTORY    INPUT      LINEPRINTER
  LEVEL      MASK       NEWS       NOT
  OR         OUTPUT     PRINT      QUALIFY
  RESET      SAVE       SOURCES    TERMINAL
  TIME       USE        WAIT       WIDTH
  XOR
ENTER HELP 'COMMAND'.
```

## Program Command Descriptions

The following pages are similar to the output obtained by typing 'HELP CommandName'.

**AND:** AND REQUIRED: AN SYNONYMS: &

PURPOSE:

AND searches the data base for all organisms which have the environmental parameter(s) specified or will combine two searches to produce a list of organisms or characteristics common to both lists.

SYNTAX:

[##] AND {[##] [XX:XXXXXX]} {[/CONTINUE] [/END]}

EXPLANATION:

/CONTINUE allows multiple lines to be entered.
/END ends the continuation.

EXAMPLE:

AND PG:IN PG:HI
The result will be those organisms in the data base which are found in both Indiana and Hawaii.

3 AND PG:IN PG:OH BT:SAND
The result will be those organisms in search 3 which also occur in IN and OH and prefer a bottom type of sand.

4 AND 5
The result will contain those organisms which were in both search 4 and search 5.

RELATED COMMANDS: OR, NOT, XOR, DIFFERENCE, &, |, ~

**CATALOG:** CATALOG REQUIRED: CA

PURPOSE:

Lists the names of the search files in the savefile library. See the ERAPT command for more information on the savefile. CATALOG lists two types of files: those generated from the SAVE command and those by the /KEEP option on COMPARE. The types are displayed to the right of the name as either <SAVE> or <KEEP>. If /SAVE is specified only the SAVE files will be listed. If /KEEP then only the KEEP files are listed. If a file name, FileName, is included its contents will be listed.

SYNTAX:
CATALOG [/SAVE][/KEEP][FileName]

NOTE: The CATALOG may not be used in a saved search and a warning message will be displayed if it is entered.

EXAMPLE:

```
>CATALOG
  CATALOG OF LIBRARY FILE:
  FISH001              <KEEP>
  OHIOEPA              <SAVE>
  OHIOEPA2             <SAVE>
  FISH002              <KEEP>
    4 FILE(S) IN LIBRARY.
```

The file types are listed in the right column.

RELATED COMMANDS: SAVE, EXECUTE, GET, COMPARE/KEEP

**CLEAR:** CLEAR REQUIRED: CL

PURPOSE:
This clears search memory. The next search will be 1. This is needed before a SAVE command. The results of all searches cannot total more than 1000 and the highest allowable search number is 20. If either of these limits is reached you will not be allowed to continue searching until the CLEAR command is issued.

SYNTAX:
CLEAR

**COMPARE:** COMPARE REQUIRED: CO

PURPOSE:
Compares 1 or more species or search results and returns the categories found in any species, /SUM; the categories found to be common to all species, /ALL; or categories which differ between the species, /DIF. /KEEP may be used to store the result of a comparison.

SYNTAX:
COMPARE {[GNS-[SPP] ... GNS-[SPP]] [[##] ... ##]} [/KEEP] [/ALL] [/DIF] [/SUM] {[/CONTINUE] [/END]}

EXPLANATION:

/CONTINUE allows multiple line input, /END terminates multiple line input. /SUM prints the sum, /ALL the product, /DIF the difference (default is to print the logical product, /ALL). A search will be saved having the same characteristics for each type of comparison specified except /DIF which does not result in a search. If the search is being saved, the record written to the library will be MASK/C followed by the category codes. If a single species is entered the search will contain those organisms which have the same environmental parameters as that species (if SAVE/LITERAL is used the species entered will be saved, not the result). /KEEP will save the results of a comparison in a separate file in the library. This option is not allowed in conjunction with SAVE and if used it will cause an error message.

EXAMPLES:

COMP ESOX-AMERICANUS ESOX-M/A/D

This will compare Esox americanus to the first species of Esox which begins with an 'M'. The similarities, /A, and the differences, /D, between the two species will be listed and a search will result containing all similar characteristis.

COMP ESOX-AMERICANUS/A

This will list the categories which all references for Esox americanus reported and save these categories as a search.

COMPARE ESOX-AMERICANUS/C
ESOX-MASQ
ESOX-NI/A/D/E

This will compare the 3 species listed and list their similarities, /A, and differences, /D. A search will be result containing characteristics common to all 3 species.

COMPARE 1 2

This will compare the species in search 1 and search 2. Their similarities will be listed and saved as a search statement.

COMPARE 1 ESOX-L

This compares the organisms in search 1 with Esox lucius. Their similarities will be listed.

RELATED COMMANDS: GET, DEFINE, FIND, CATALOG

**DEFINE:** DEFINE REQUIRED: DE

PURPOSE:

Allows a list of species to be entered into the computer. The result is a search which contains the species which were entered.

SYNTAX:

DEFINE Genus-species ... Genus-species {[/CONTINUE] [/END]}

EXPLANATION:

The list needs to be entered followed by /END. The /CONTINUE option is the default, input is continued on multiple lines until the /END is encountered.

RELATED COMMANDS: COMPARE

**DIFFERENCE:** DIFFERENCE REQUIRED: DI SYNONYMS: XOR

PURPOSE:

Compares two search results and returns a list containing the species or categories which were in one list or the other but not in both lists.

SYNTAX:

## DIFFERENCE ##

NOTE:

If the first list is omitted the default would be to use the entire data base, identical to NOT ##

RELATED COMMANDS: AND, OR, NOT, XOR, &, |, ~

**ECHO:** ECHO REQUIRED: EC

PURPOSE:

Causes statements read from a saved file to be displayed at the terminal.

SYNTAX:

ECHO {ON OFF}

EXPLANATION:

Turns on or off the printing of search statements read from a library file. Default condition is ON.

**END:** END REQUIRED: EN

PURPOSE:

Exits the program or ends a current SAVE.

SYNTAX:
END

NOTE:
If 2 SAVE commands are issued without an intervening END, an END command for the first SAVE will be issued automatically by the program before the second SAVE is begun. Nesting or recursion of SAVE is not allowed.

RELATED COMMANDS: SAVE

**EVALUATE:** EVALUATE REQUIRED: EV

PURPOSE:
EVALUATE is designed to find groups of organisms which could potentially be used as indicators of environmental conditions.

SYNTAX:
[XX] EVALUATE XX [##] [XX XX XX ##] {[/FULL][/SHORT]}

EXPLANATION:
XX is any two-character category code.
## is the minimum number of sources (default=1).
/FULL = Full listing (default), /SHORT = Short list.
A full listing will include all of the entries and the categories which were found to be consistent. A short listing will include only the taxa.

EXAMPLE:
EVALUATE BT CU 2 SH GH 3
This will find all organisms which have a minimum of 2 sources for information on bottom type and current and a minimum of 3 sources for information on specific habitat and general habitat. All organisms listed will have complete agreement of all of the references in these areas.

**EXECUTE:** EXECUTE REQUIRED: EX

PURPOSE:
Executes the search from the savefile.

SYNTAX:
EXECUTE SearchName

EXPLANATION:

You will be prompted for the 'SearchName' if it is omitted. If you wish to end the command at this point just type a carriage return <RETURN>.

NOTE:

You are not permitted to execute a saved search while saving a search. This eliminates the possibility that a search might call itself and become an infinite loop.

RELATED COMMANDS: GET, SAVE, CATALOG

**FIND:** FIND REQUIRED: F

PURPOSE:

Used to locate information on a taxon or group of related taxa. Common names may be listed with scientific names. Summaries of information about the taxa may also be listed.

SYNTAX:

```
## FIND [TAXON:][T1][-T2] {[/FULL] [/ALL] [/SUM]}
                [/COMMON]
```

EXPLANATION:

TAXON: ORDER,FAMILY,GENUS OR SPECIES (DEFAULT=GENUS)

T1 = The taxonomic name at the level specified by TAXON:

-T2 = The next lower taxonomic name. The dash must be included.

/FULL = Full listing (/ALL/SUM),

/ALL = All entries common to the references for the organism,

/SUM = All entries from any reference for the organism.

/COMMON will list the common names as well as the scientific names.

If the summaries agree, only the SUM summary is printed.

Use underscore for blanks, if necessary.

EXAMPLES:

FIND FAMILY:ESOCIDAE-ESOX/F

All information for the family Esocidae genus Esox will be listed.

FIND G:ESOX-LUCIUS/C

The reference count and the common name will be listed for the species Esox lucius.

F ESO-/C

The scientific and common names and reference count will be printed for all genera and species within the genera which have the first three letters 'ESO'.

RELATED COMMANDS: COMPARE

**GET:** GET REQUIRED: G

PURPOSE:

To recall the result of a COMPARE/KEEP from the library file.

SYNTAX:

GET Name

EXPLANATION:

You will be prompted for the 'name' if it is omitted. If you wish to end the command type carriage return, <RETURN>, rather than a name. A comparison which has been saved in this manner does not contain the CLEAR command and therefore does not reset the search stack.

NOTE:

You are not allowed to GET a file while you are saving a search.

RELATED COMMANDS: EXECUTE, CATALOG, COMPARE/KEEP

**HELP:** HELP REQUIRED: HE SYNONYMS: ?

PURPOSE:

Prints information for the COMMAND, category or code listed.

SYNTAX:

HELP [[COMMAND][/SYNTAX]] [/DEFINE[XX:XXXXXX]]

EXPLANATION:

If the option, /SYNTAX, is used, only the command syntax is listed. /DEFINE will list the categories used in the ERAPT system. If a category or code is listed, the /D option must be used. Help on categories will list all information on the category and all codes in the category. Help for a code will list the category and the one code. Multiple codes and categories may be entered but may not exceed one 80-character line.

EXAMPLES:

HELP

This will list all the commands.

HELP DEFINE

This will list all of the information on the DEFINE command.

HELP BT GHLOTIC PH/DEFINE

This will list all of the categories for bottom type, BT, and for pH, and provide definitions for the codes and it will list the definition for general habitat lotic, GHLOTIC.

**HISTORY:** HISTORY REQUIRED: HI

PURPOSE:

Lists all searches and the number of records found from your current search back through the first search.

SYNTAX:
HISTORY

**INPUT:** INPUT REQUIRED: IN

PURPOSE:

Redirects input from the terminal, lineprinter, or the unit number specified by UNIT ##.

SYNTAX:
INPUT {TERMINAL UNIT ## FILE ##}

NOTE:

The use of the unit number option is not advised. If the unit was not pre-allocated to the program, the program will err when a write or read is made to or from the unit. This error can not be trapped, so the program will stop abnormally.

RELATED COMMANDS: OUTPUT

**LEVEL:** LEVEL REQUIRED: LE

PURPOSE:

Returns the taxonomic level which is the highest taxon to be searched for or sets the highest acceptable taxon to return from logical operations: AND, OR, NOT, XOR. The default is species.

SYNTAX:
LEVEL [Taxon]

EXPLANATION:

Taxon is the taxonomic level to which you wish your searches restricted. It may be species, genus, family, or order.

EXAMPLES:

LEVEL

This will return the current setting for the taxa to be searched.

LEVEL GENUS

This will set the level to find only genera and all taxonomic levels lower than genus, i.e. species and subspecies, when the logical operators are used.

**LINEPRINTER:** LINEPRINTER REQUIRED: LI

PURPOSE:

Sets the width of the LINEPRINTER.

SYNTAX:

LINEPRINTER [WIDTH {WIDE NARROW}]

EXPLANATION:

If WIDTH is omitted the next time WIDTH is called it will affect the LINEPRINTER. If WIDTH is included, you must include either WIDE, 132 columns, or NARROW, 72 columns.

RELATED COMMANDS: TERMINAL, WIDTH

**MASK:** MASK REQUIRED: M

PURPOSE:

Defines a search containing a set of category codes to be used in logical operations with other searches.

SYNTAX:

MASK [XX:XXXXXX] {[/CONTINUE} [/END]}

EXPLAINATION:

Use /CONTINUE if more than one line is needed define the desired characters. You will be prompted for more input until /END is entered.

**NEWS:** NEWS REQUIRED: NE

PURPOSE:
Lists the notices and differences in this revision.

SYNTAX:
NEWS

EXAMPLE:
```
NEWS
CHANGES SINCE V6.03
The TIME command will now print the CPU time left in
     the logon session if the ON or OFF parameters
     are omitted.
     .
     .
     .
CHANGES SINCE V6.02
The help command has been changed, now enter HELP
     to get a list of the commands (many of which
     have been changed for the better). HELP
     followed by a command will list its syntax and
     give an explanation of its function.
     .
     .
     .
```

**NOT:** NOT REQUIRED: NOT SYNONYMS: ~

PURPOSE:
Finds all organisms which do not have the category or categories listed. If used on two search numbers then the species or categories in the first, not in the second, are returned.

SYNTAX: [##] NOT {[##] [XX:XXXXXX]} {[/CONTINUE] [/END]}

EXPLANATION:
/CONTINUE may be used to enter more than one line of parameters. You will be prompted for more lines until you enter /END on a line.

EXAMPLE:
```
NOT PG:IN
        All organisms not found in Indiana
3 NOT 4
        The result is all entries in search three
        which are not in search four.
```

RELATED COMMANDS: AND, OR, XOR, DIFFERENCE, &, |, ~

**OR:** OR REQUIRED: OR SYNONYMS: |

PURPOSE:
Lists all organisms which have any of the categories listed or combines two searches.

SYNTAX:
[##] OR {[##] [XX:XXXXXX]} {[/CONTINUE] [/END]}

EXPLANATION:
/CONTINUE may be used to enter more than one line of parameters. You will be prompted for more lines until you enter /END on a line.

EXAMPLE:
OR PG:IN BT:SAND
The result is any organism which is either found in Indiana or over a bottom type of sand.
3 OR 4
The result will be those entries in either search three or four.
3 OR PG:IN
The result will be all entries in search three and all entries found in IN.

RELATED COMMANDS: AND, NOT, XOR, DIFFERENCE, &, |, ~

**OUTPUT:** OUTPUT REQUIRED: OU

PURPOSE:
Redirects output to the terminal, lineprinter, or the unit number specified by UNIT ##.

SYNTAX:
OUTPUT {TERMINAL LINEPRINTER UNIT ## FILE ##}

EXPLANATION:
The use of the unit number option is not advised. If the unit was not pre-allocated to the program, the program will err when a write or read is made to or from the unit.

The first time information is sent to the line printer you will be prompted to enter your name and mailing address so that the printout that you generate can be sent to you. When you end the search session you will be prompted for confirmation before your printout is sent to the lineprinter.

EXAMPLE:

OUTPUT LINEPRINTER

All search results will go to the line printer until OUTPUT TERMINAL is used.

RELATED COMMANDS: INPUT

**PRINT:** PRINT REQUIRED: P

PURPOSE:

Prints search ## to the output device.

SYNTAX:

PRINT [##] [/COMMON] [/OFFLINE]

EXPLANATION:

Defaults to the last search. Prints to the device you have set for output, normally your terminal. /COMMON lists the common names and the scientific names in the printout.

Print is sent to the lineprinter if /OFFLINE is specified.

EXAMPLE:

PRINT/C

Prints the last search with the common names.

PRINT 3

Prints search 3 at the terminal, or if output is redirected to the lineprinter, the search will be printed on the lineprinter.

PRINT 2 /OFFLINE

Prints search 2 to the lineprinter.

**QUALIFY:** QUALIFY REQUIRED: Q

PURPOSE:

It is used to suppress the printing of categories in a listing produced by the FIND or COMPARE commands.

SYNTAX:

```
QUALIFY {[ON]
         [OFF]
         [XX ... XX:XXXXXX]
         [ADD XX ... XX:XXXXXX]
         [DELETE XX ... XX:XXXXXX]
         [RESET]}
```

EXPLANATION:

XX is any category code (two to eight characters). ON causes the last qualification list to be used when output is produced by FIND or COMPARE. OFF causes all categories to be printed. Qualify (Q) followed by no options toggles ON and OFF and prints the status as it changes. RESET sets the qualify list to all categories (default condition). Q XX YY would set the list to print only the codes specified by XX and YY. Q ADD ZZ would now add the category ZZ to the list that would be printed. Q DEL XX takes XX out of the list so now only YY and ZZ would be printed.

EXAMPLES:

QUALIFY DELETE PG
Now when a full list is printed the regions, states, and provinces will not be printed.

QUALIFY ADD PGREG05 PGIN PGOH PGWI PGMN PGMI PGWI
Now if Region 5 or the states in Region 5 are present they will be printed.

**RESET**

RESET REQUIRED: RE

PURPOSE:

Resets the parameters for the commands USE, INPUT, OUTPUT to their default values: USE AND, INPUT TERMINAL, OUTPUT TERMINAL.

SYNTAX:
RESET

**SAVE:**

SAVE REQUIRED: SA

PURPOSE:

Used to save a series of commands into a library for later use.

SYNTAX:
SAVE FileName [/LITERAL]

EXPLANATION:

Saves a search named 'FileName' in the savefile. /LITERAL saves statements as they are typed. The major difference between this and the SAVE without the option is that, in the former case the results of COMPARE statements are saved, whereas with this option the COMPARE statement with the list of species is saved. All SAVEs are ended by END.

NOTES:

Not all statements are saved. The statements saved are those which affect searches: AND, OR, NOT, CONSISTENCY, COMPARE, END, INPUT, OUTPUT, and FIND. If /LITERAL is included all statements are saved as they are typed, except EXECUTE and CATALOG.

When a SAVE is started if the memory was not cleared by the CLEAR statement, a warning will be printed and the memory will be cleared.

If a duplicate FileName is found in the library you will be prompted to rename this SAVE.

If a search is being saved and you save a new one, the old search will be ended.

RELATED COMMANDS: CATALOG, EXECUTE, GET, COMPARE/KEEP

**SOURCES:** SOURCES REQUIRED: SO

PURPOSE:

Sets the minimum number of sources to be considered in all searches after this command is issued (default is 1).

SYNTAX:

SOURCES ##

EXAMPLE

SOURCES 5

Only organisms which have 5 sources will be considered when searching the data base.

**TERMINAL:** TERMINAL REQUIRED: TE

PURPOSE:

Sets the width of the TERMINAL.

SYNTAX:

TERMINAL [WIDTH {WIDE NARROW}]

EXPLANATION:

If WIDTH is omitted the next time WIDTH is called it will affect the TERMINAL. If WIDTH is included, you must include either WIDE, 132 columns, or NARROW, 72 columns.

RELATED COMMANDS: LINEPRINTER

**TIME:** TIME REQUIRED: TI

PURPOSE:

TIME prints the time you have left in the time sharing session. Or it can be used to determine how much time a statement takes to execute.

SYNTAX

TIME {[ON] [OFF]}

EXPLANATION:

TIME ON displays the CPU time of searches as they execute. TIME OFF (default) turns off this feature. This is the default. TIME prints the CPU time remaining for the logon session in seconds.

**USE:** USE REQUIRED: US

PURPOSE:

Selects the data summary to be searched. Searches from the AND summary consider information common to all sources for each organism. Searches from the OR summary use all available information on each organism.

SYNTAX:

USE {AND OR}

EXPLANATION:

All searches and comparisons made after this will use the summary which was chosen. The OR summary is the default. Use of the AND summary may substantially reduce the amount of information available during searches.

EXAMPLE:

USE AND

After this, when a search is performed, the information examined will be the information upon which all authors agreed for each species.

**WAIT:** WAIT REQUIRED: WA

PURPOSE:
WAIT changes the number of lines displayed on your terminal, to prevent information from scrolling off the top of a Video Display Terminal.

SYNTAX:
WAIT {[##] [ON] [OFF]}

EXPLANATION:
Causes the terminal to wait after ## lines for the user to enter a <C><RETURN> to terminate a listing or a <RETURN> to continue listing. The default is 20 lines. WAIT OFF lists without stopping, WAIT ON restores last wait value used.

**WIDTH:** WIDTH REQUIRED: WI

PURPOSE:
To change the number of columns which are displayed on your terminal or printer at the lineprinter.

SYNTAX:
WIDTH {WIDE NARROW}

EXPLANATION:
A WIDTH must be specified: use WIDE, 132 columns, or NARROW, 72 columns. The device affected is the last device changed (default is terminal). See TERMINAL or LINEPRINTER.

RELATED COMMANDS: TERMINAL, LINEPRINTER

**XOR:** XOR REQUIRED: X SYNONYMS: DIFFERENCE

PURPOSE:
Compares two search results and returns a list containing the species or categories which were in one list or the other but not in both lists.

SYNTAX:
## XOR ##

NOTE:
If the first list is omitted the default would be to use the entire data base, identical to NOT ##

RELATED COMMANDS: AND, OR, NOT, DIFFERENCE, &, |, ~

?: ? REQUIRED: ? SYNONYMS: HELP

PURPOSE:
An alternative form of help.

SYNTAX:
Refer to HELP

&: & REQUIRED: & SYNONYMS: AND

PURPOSE:
An alternative form of AND.

SYNTAX:
Refer to AND

RELATED COMMANDS: AND, OR, NOT, XOR, DIFFERENCE, |, ~

|: | REQUIRED: | SYNONYMS: OR

PURPOSE:
An alternative form of OR.

SYNTAX:
Refer to OR

RELATED COMMANDS: AND, OR, NOT, XOR, DIFFERENCE, &, ~

~: ~ REQUIRED: ~ SYNONYMS: NOT

PURPOSE:
An alternative form of NOT.

SYNTAX:
Refer to NOT

RELATED COMMANDS: AND, OR, NOT, XOR, DIFFERENCE, &, |,

## Program Messages

SEARCH LIST DOES NOT EXIST, RE-ENTER-

This message was caused by typing a search number which has not yet been done. Re-enter the number of the desired search. The remainder of the command has not been discarded and will be processed when a valid number is entered.

COMMAND CANNOT BE USED IN PRESENT CONTEXT.

A command was typed which was not used in a way understandable by the programs command interpreter.

MORE/E->

If you have included the /CONTINUE option on a command you will be prompted with this message to enter more lines or to enter /END to execute the command that you have entered. If you use the COMPARE command and forget to enter any species, you will be prompted with this message automatically.

ERROR - LIST DOES NOT EXIST.

The search number specified on the right side of an AND, OR, or NOT did not exist. The line was discarded and must be re-entered.

SEARCH HAS NO CODES FOR THIS DATA BASE.

All of the codes which were entered are not in the data base and the search will result in zero entries. This is a warning, and may appear if searches are run between data bases using the result of the COMPARE command.

STACK OVERFLOW - CAN'T CONTINUE, CLEAR STACK.

This is caused when the results of your searches exceed 1,000 entries or if you attempt to run more than 20 searches. To correct this situation type CLEAR.

ERROR IN OPTION - ASSUMING SHORT LISTING

An option other than /FULL was entered. The search will proceed as if no option was entered.

ERROR - INVALID OPTION IGNORED.

An option was entered on the FIND command which could not be interpreted. The option was discarded and execution will continue.

NOTHING TO FIND? - RE-ENTER LINE.

FIND was entered without a taxonomic name. The command has stopped and it must be re-entered correctly.

CAN'T FIND 'GENUS-SPECIES'.

The entry you tried to find does not exist in the data base. The name, in apostrophes, was the name which was searched for.

NO NEWS AVAILABLE.

There is no news section in the help file. If the HELP command does not work, there is a problem which should be reported to us.

ENTER USE PARAMETER-

The USE command was entered without the AND or the OR parameter. One of the two must be entered. If a bad parameter was entered this message will prompt you to enter a valid parameter. A <RETURN> cancels this command.

BAD SYNTAX OR TERM.

An unidentified term was entered after the USE command.

NOT A VALID USE PARAMETER.

A command was entered after USE but it was not AND or OR.

ENTER TERMINAL/FILE ## -

INPUT was entered without specifying TERMINAL or UNIT ##.

ERROR - 'xxxxxxx' NOT A DEVICE.

The name entered after INPUT or OUTPUT was not a device: TERMINAL, LINEPRINTER, or a UNIT ##.

CAN'T READ FROM LINEPRINTER.

LINEPRINTER is an output device only.

ENTER TERMINAL/LINEPRINTER/FILE ## -

OUTPUT was entered without specifying TERMINAL, LINEPRINTER, or a valid UNIT ##.

ERROR - SOURCES MUST BE FOLLOWED BY NUMBER.

The SOURCES command was entered without specifying the number of sources to be consided. The command is discarded and the sources are unaffected.

NOT A VALID WAIT OPTION.

The WAIT command was entered with an incorrect option. The valid options are ON, OFF or a number. The line is discarded.

ENTER WIDTH(WIDE/NARROW)-

WIDTH was entered without either WIDE (132 columns) or NARROW (72 columns). One of these terms must be entered.

UNRECOGNIZED WIDTH OPTION.

An option was entered after the WIDTH command which is invalid. The only valid options are WIDE or NARROW.

ERROR - PRINT OPTION IGNORED.

An option other than /OFFLINE or /COMMON was entered on the PRINT command and was discarded. The command will execute.

ENTER FILE NAME, OR <RETURN> TO CANCEL-

SAVE was entered without a search name. A name must be entered. If a <RETURN> is entered then the command is canceled.

NOTICE - SAVE ENDED LAST SEARCH.

If you were saving a search and have typed save again, the current search will be ended and a new search will be started.

LIBRARY MEMBER FileName EXISTS - RENAME MEMBER.

The name you want to use is already in use, the search will need a new name. You will be prompted to provide a new name.

WARNING - STACK LEVEL IS NOT 1, IT WILL
BE RESET, <RETURN> TO CONTINUE, <C> TO CANCEL->

The search memory must be at 1 to begin saving searches. If you do not type a <C> the memory will be cleared and the search will be started.

WRITE ERROR IN LIBRARY FILE.

This error should not occur. You will need to contact us if it does.

ERROR - SEARCH MAY NOT BE EXECUTED DURING SAVE.

This warning is printed if you attempt to execute a saved search while saving a search. This prevents you from executing the search that you are saving.

ENTER FILE NAME-

You are being prompted for the name of the saved search you wish to execute. If you enter an incorrect name or a blank line the library of searches will be cataloged for you.

CAN'T FIND FileName IN LIBRARY.

The name of the search you wish to execute does not exist. A catalog of the library will be printed for you.

ERROR - CATALOG MAY NOT BE EXECUTED DURING SAVE.

Just a warning message to prevent a CATALOG during a search. The CATALOG would cause the file to be damaged if it were performed during a SAVE, so it is not allowed.

NO FILES IN LIBRARY.

The library file contains no saved searches.

ERROR - CAN'T FIND SPECIES, RE-ENTER LINE:
ERROR AT:XXXXXXXX

The COMPARE or DEFINE command has not been able to interpret your input line. The error is listed in the line after the colon. The line that has been printed out has been discarded and you will now be prompted for more information with the prompt MORE/E->.

CAN'T FIND Genus-Species.

The COMPARE or DEFINE command could not locate the species listed and was discarded. The remainder of the line will be processed, and you will be prompted for more input, giving you an opportunity to correct the error.

ENTER YOUR NAME AND MAILING ADDRESS(3 LINES FOR ADDRESS)
NAME>
ADR1>
ADR2>
ADR3>

The first time offline output is specified you will be prompted

for the information listed above. It is necessary so that your printout can be sent to you. The computer will use the first 30 characters of each line.

ENTER <RETURN> TO CONTINUE, <C> TO CANCEL.

The number of lines specified in the WAIT command has been listed on your screen. This gives you the opportunity to inspect the output printed thus far or to cancel a listing if desired.

ERROR - CATEGORY 'XX' IS INVALID.

The category entered is not correct and the term will be discarded.

ERROR - CODE 'XX:XXXXXX' IS NOT VALID.

The code is not valid and the term will be discarded.

ERROR - '/X' IS NOT A VALID OPTION.

The option which you have selected is not valid and it will be discarded.

ERROR - COMMAND 'XXXXXXXXXXXX' IS AMBIGUOUS.

The command that has been entered does not contain enough letters to determine which of several commands it might be. The line will be discarded.

ERROR - 'XXXXXXXXXXXX' IS NOT A COMMAND.

The line entered is not recognized as a command and it is discarded.

ERROR - OPTION 'XXXXXX' IS AMBIGUOUS.

The option on the QUALIFY command contains too few characters to evaluate. The line is discarded.

ERROR - 'XXXXXX' IS NOT AN OPTION.

The option specified is not valid and will be discarded.

BAD TAXON, ASSUMING GENUS.

The taxonomic level you specified is not supported in the FIND or LEVEL command.

ERROR - THIS COMMAND MAY ONLY BE USED ON TWO SEARCH STATEMENTS.

The XOR or DIFFERENCE must only be used with search statements and category codes are not allowed.

NOTHING TO PRINT - SEARCH DOES NOT EXIST.

Print was used on a search number that did not exist.

**Error mesages from run time errors beyond the control of the user.**

If any of the following messages appear we need to be informed so that they may be corrected.

FATAL ERROR - DATA SPACE EXCEEDED.

WARNING - DATA FILE IS TOO LARGE.

This error will appear only if the data file was too large to load completely. Some of the data will not be searchable.

ERROR - EOF ENCOUNTERED IN CODES.

ERROR - GETCID FUNCTION HAS READ PAST EOF

# SECTION VI

## EPAEDIT PROGRAM

The EPAEDIT program is an interactive editor for ERAPT RAW DATA files. It can be used to add, delete, or replace environmental data, sources, and taxonomic entries and search for and display environmental information by scientific or common name or data source.

### Abbreviations and Syntax

All commands and parameters may be abbreviated as single characters and each argument of a command must be separated by a blank space. If a blank must be included in a compound argument, then an underscore character is used to represent the blank space. Since all operands may be abbreviated as single characters, their order is critical. In general, the command and its first argument must be included. The user will be prompted for any remaining information that is necessary.

Throughout this manual several conventions are used in the command syntax.

Braces {}. Mutually exclusive arguments are enclosed in braces, {}.

Brackets [ ]. Optional arguments are enclosed in brackets, [ ].

Numeral Signs #. All numeric arguments are represented using a number sign, #, with each symbol representing a digit. An argument with a range from 0 to 99 would be shown as ## whereas a range of 0 to 9 would be #.

Arrows <>. The symbols <> are used to represent keys on the terminal. <RETURN> is the enter or return key.

Apostrophes ´´. All variable information is shown enclosed in apostrophes. Apostrophes should not be used when this information is entered.

### Program Commands

The editor uses the following commands: Add, Bottom, Citation, Delete, End, Find, Help, List, New, Replace, Show, Top. The command description and examples are listed alphabetically. All entered lines must be ended by pressing <RETURN>.

## Program Command Descriptions

Add: Add is used to incorporate additional information from a previously defined data source into a taxon. You will be prompted to enter environmental codes. To quit entering codes enter a blank line by typing <RETURN>.

Add {Author ['Source-code']}
{Codes ['Source-code']}

Author: Key word to indicate that a new source is to be added. The 'Source-code' must exist in the data base and may not exist in the record which is being modified.

Codes: Key word to indicate that data is to be added to a source which exists both in the data base and in the record.

'Source-code' is a 1 to 8 character code indicating the reference source which is stored in the SOURCES file.

The command will prompt for the category codes to add with the message 'Code: '. Category codes may be entered on the line followed by a <RETURN>. Prompting will continue until a blank line is entered.

Bottom: Bottom is used to go to the end of the data file.

Citation: Citation is used to list the source for the keyword entered after the command. If no keyword is entered then the last keyword is used.

Citation 'Source-code'

'Source-code' is a 1 to 8-character code indicating the reference which is to be retrieved from the SOURCES data file. The code does not have to match any code in the file exactly. If the letter L is entered then the citation returned will begin with the letter L. If Citation is entered again without any 'Source-code' then the next citation beginning with an L will be displayed.

Delete: Delete is used to delete a taxonomic entry or source and its associated data, or a data value from the data base.

```
Delete {Taxa}
       {Author} ['Source-code']}
       {Code}   ['Source-code' ['Category-code']]}
```

Taxa: Indicates that the entire record and all information associated with it will be deleted. The entry is not deleted immediately, but is marked for deletion by changing its level to 100. When the data editing is finished the new file will not contain this record. If a record was accidently marked for deletion the record may be restored by replacing its level information with the proper taxonomic level.

Author: Indicates that a source is to be removed as well as all of its data. If the 'Source-code' is not entered you will be prompted for it. If all sources are to be deleted it is easier to replace the taxonomic level with a positive value. This will have the same effect as deleting all of the sources.

'Source-code' is a 1 to 8-character code indicating the reference which is stored in the SOURCES file.

Code: Indicates that a 'Category-code' within one 'Source-code' is to be removed. If either of these two arguments is omitted you will be prompted for it.

'Category-code' is a 1 to 8-character code indicating the environmental category.

End: End is used to terminate an editing session. The data with the editing changes may be saved or discarded. If no changes are made then the data will not be saved.

```
End  {Save}
     {Quit}
```

Save: Used to indicate that a new copy of the data base is to be written out to a file specified by the OUTFILE() argument on the editing command. The default file name is R.DEPAEDIT.SAVE. This file may not be re-edited until it is renamed and stored in the Partitioned dataset.

Quit: Used to indicate that no new data set will be written out, thereby discarding all changes that have been made.

Find: Find is used to locate a species by its common or scientific name or to locate a source. All searches begin with the present position in the data base. If Find is entered without any arguments then the last Find is repeated until the bottom of the data base is reached.

Find {Taxa 'Taxonomic-name'}
{Name 'Scientific-name'}
{Author 'Source-code'}

Taxa: Indicates that the next parameter will be a taxonomic name, and the first occurence of that name should be located. The 'Taxonomic-name' is searched by assuming that the characters entered are the first characters in the name, i.e. if the characters ES are entered then Esox will be found, but evides will not be found.

Name: Indicates that the next parameter will be a common name or a portion of a common name, and that the next name containing this sequence will be located. The sequence of characters may occur anywhere in the name.

Author: Indicates that the next parameter will be a source code, and the first occurence of that code will be located.

Help: Help is used to obtain information on the use of commands.

Help ['Command-name']

List: List is used to list a range of lines in the data base.

List # Line indicated.
# # Lines within the range of #-# in the order indicated.
* # Lines forward beginning with the current position.
+# Lines forward beginning with the current position same as * #.
-# Lines backward from the current position.

New: New is used to add a new reference to the source table. No sources may be added until their codes are inserted in the source table. The source data base still needs to be updated with the reference information.

New ['Source-code']

'Source-code' is a 1 to 8-character code indicating the reference which is stored in the SOURCES file.

Replace: Replace is used to change any parameter in the data base. The code or source to be replaced must be unique within a record.

```
Replace {Taxa [´Taxonomic-name´]}
        {Name [´Common-name´]}
        {Level [´level-number´]}
        {Author [´Old-Source-code´ [´New-Source-code´]]}
        {Code  [´Source-code´ [´Old-code´ [´New-code´]]]}
```

Taxa: Allows for a taxonomic name to be changed without affecting its data.

Name: Allows replacement of the common name.

Level: Allows the level of an entry to be changed. The levels are represented by their numeric codes. Frequently used levels are: Genus, 25; Species, 15; Subspecies, 10. The level of an entry may be changed to remove it from the deletion list. If a taxon was marked for deletion it will have a level of 100. If all of the information for a taxon is to be deleted, the sign of the level must be changed to positive.

Code: Allows the replacement of single category codes.

Show: Show is used to display information for a taxonomic level.

```
Show {Authors}
     {Codes}
     {Author ´Source-code´}
     {Code ´Category-code´}
```

Authors: List all sources for a species. If the optional argument ´Source-code´ is included then only the data for that source is shown.

Codes: Display all sources and their associated codes. If the optional argument ´Category-code´ is included, then all sources who reported that code will be displayed.

Top: Top is used to go to the beginning of the data file.

## SECTION VII

## SYSTEM ACCESS AND IMPLEMENTATION

### Hardware and Software Requirements

The ERAPT Retrieval and Analysis System was developed for an IBM 370/3033 computer system at the University of Notre Dame. This system uses the MVS (multiple virtual storage) operating system, with extended TSO (time sharing option). The minimum region size requirement for running interactive ERAPT system programs is 512K. All main frame programs in the ERAPT system are written in the FORTRAN 77 Language and have been compiled using the IBM VSFORTRAN compiler. In the interest of program portability, IBM extensions to the ANSI FORTRAN 77 Language have been avoided.

Programs for entry of environmental data for the ERAPT system were developed for the Radio Shack TRS-80 Color Computer running under the Extended BASIC Operating System Version 1.0 with 32K of RAM. A Radio Shack TRS-80 X-PAD digitizing table, interfaced with the Color Computer was used to input environmental data from standard forms. All microcomputer programs were written in the TRS-80 Extended Disk BASIC language.

### Accessing University of Notre Dame Computer System

The ERAPT retrieval and analysis system can be accessed on the Univerity of Notre Dame computer system from ASCI computer terminals over telephone lines at 300 or 1200 baud. The Notre Dame computer may also be accessed through the Telenet telecommunications network. The computer is generally available from 8:00 AM until 2:00 AM, Monday through Friday, 8:00 AM to midnight Saturday, and after 4:00 PM on Sunday, Eastern Standard Time. For information on how to establish a Notre Dame Computer account or technical assistance on the ERAPT system contact R. A. Hellenthal (Phone 219-239-7255).

To logon to the Notre Dame Computer dial 219-283-2411 and wait for the computer to answer with a carrier signal. When accessing the system at 300 baud an "@" symbol will usually appear at the terminal when a connection to the computer has been established. No connect symbol will appear when the system is accessed at 1,200 baud. After a connection with the computer has been established, wait about 5 seconds and then press the zero key. After a few seconds, the message, "ENTER LOGON-" should appear at the terminal. Respond to this by typing:

```
LOGON tsoid ID(0212)
```

followed by pressing the RETURN key. "Tsoid" represents a valid account number for the University of Notre Dame computer. As part of the logon operation you should receive a message indicating that you have been attached to the Biology Command Library. The ERAPT may now be entered following any "READY" system response.

## Running the ERAPT Retrieval and Analysis Program

The ERAPT command is used to initiate the ERAPT retrieval and analysis program. Only the basic options required for program execution are described below. More detailed information on the operation and syntax of this command are provided in the section on ERAPT System Commands. In the following command descriptions, parameters not displayed in apostrophes must be entered as they appear, text displayed in apostrophes is replaced by an appropriate name or operand, and information displayed in brackets is optional. Neither brackets nor apostrophes may be entered as part of the command.

Syntax:

ERAPT 'database' [Savefile('name')]

'database' - the ERAPT data base to be used in search and evaluation operations. The following databases are currently available:

- FISH - Fishes of E.P.A. Region 5
- BLGR - Blue-green algae
- CHIR - Chironomidae (midges)
- DIAT - Diatoms
- EPHE - Ephemeroptera (mayflies)
- PLEC - Plecoptera (stoneflies)

[Savefile('name')] - an optional parameter which specifies the 'name' of a file to be used for the storage and retrieval of saved searches. If the SAVEFILE operand is omitted and a search is saved you will be prompted to enter a name for this file. The file name must begin with a letter, may not be more than 8 characters long, and may not contain punctuation marks or special symbols.

Example:

ERAPT FISH SAVEFILE(SEARCH)

The ERAPT program will be run and the fish data base will be accessed. The library SEARCH will be used to store and execute search expressions.

ERAPT FISH

The ERAPT program will be run and the fish data base will be searched but no search library will be attached.

## ERAPT System Commands

The following commands are used to execute the ERAPT system programs on an IBM 370/3033 computer system running the Time Sharing Option (TSO). These TSO commands provide a variety of run time options for the ERAPT programs and provide an interface between the user and resources available to the computer. The main operations which the TSO command lists perform are the allocation of files necessary to run the programs; the loading and execution of the ERAPT programs; the writing and submission of background jobs, in OS/VS2 MVS Job Control Language (JCL), to perform various tasks such as printing files on the line printers; and the response to errors during the process of interpreting the commands.

### ERAPT

The ERAPT command runs ERAPT program, controls the allocation of the data base files, and submits any offline output as a batch job using the IBM system utility program IEBGENER.

Syntax: ERAPT Database Savefile('Filename') Lines(#) Copies(#) Update
Myprog Mydata Mycodes Prefix('Tsoid') Ppn('Tsoid') Clist

Required: Database

Defaults: Lines(2) Copies(1)

Arguments:

Database: Four character name for the file to be searched. The file is expected to be a member of the partitioned data set ERAPT.SRCH(Database) on either the user's account or the default library account specified by Prefix().

Savefile('Filename'): Indicates the name of the file to attach into which information is saved. The file is created on the user's account with a 'SRCH' suffix.

Lines(#): Maximum number of lines that the line printer will print. The number indicates thousands. The default value of 2 therefore will allow 2000 lines to be printed on the line printer.

Copies(#): The number of copies of offline output that will be produced.

Update: Uses the latest version of the system which may or may not be the same as the current version in the library account specified by Prefix(). This version is stored in the account Ppn().

Myprog: Specifies that the account needed to find the program is the user's.

Mydata: Specifies that the data file SRCH.DATA(database) resides on the user's account and is to be used rather than the data in the library account.

Mycodes: Specifies that the file ERAPT.DATA(RECODE) is to be found on the user's account rather than in the library.

Prefix(): Specifies the default library prefix.

Ppn(): Specifies the default development account where the program resides if Update is specified.

Clist: Will turn on CONLIST, SYMLIST, MESSAGE, and LIST to aid in debugging the command file.

RUNOFF

The RUNOFF command runs the program RUNOFF and then uses the system utility program IEBGENER to produce a copy of the data set on the line printer. Special output forms and marginal line numbers may be requested.

Syntax: RUNOFF File Form() Prefix() Fcb() Lines() Linect() Spinwriter Tn Copies() Clist

Required: File

Defaults: Form(STD) Prefix(UserID) Copies(1) Fcb() Lines(3) Linect(0)

Arguments:

File: Fully qualified file name including extension. Prefix is specified using the Prefix option if it is other than the logon account.

Form(): Specifies the form to be used for the printout.

Fcb(): Specifies form spacing. VPPP V=lines/inch PPP=lines/page.

Prefix(): Specifies the default prefix.

Lines(): Maximum number of lines to print in thousands.

Linect(): Number of lines before a form feed is sent to the printer. This should be left at zero since RUNOFF issues form feed characters as needed.

Copies(): The number of copies of offline output that will be produced.

Spinwriter: Specifies that the output is to be routed back to the user's terminal.

Tn: Specifies the use of the TN (upper-lower case) print train for the printer.

Clist: Will turn on CONLIST, SYMLIST, MESSAGE, and LIST to aid in debugging the command file.

## EPAEDIT

The EPAEDIT command allows the EPAEDIT program to be run through TSO and controls the file allocations.

Syntax: EPAEDIT File Outfile('Filename') Prefix('Tsoid') Clist

Required: File

Defaults: Outfile(R.DEPAEDIT.SAVE)

Arguments:

File: Four character name for the file to be searched. The program allocates two files based on this name. The first file is the actual data base ERAPT.DATA(FileFORM) and the second is ERAPT.DATA(FileAUTH) containing the reference information. Both of these files reside on the prefix specified by Prefix().

Outfile(): Specifies the file which will be written if End Save is used to terminate the program. The command will not allow an existing data file to be re-written.

Prefix(): Specifies the default library prefix.

Clist: Will turn on CONLIST, SYMLIST, MESSAGE, and LIST to aid in debugging the command file.

SECTION VIII

ENVIRONMENTAL RETRIEVAL CODES

**BIOLOGICAL CHARACTERISTICS**

**Stage** - Stage or stages to which source of data refers. [010ST] (FISH, CHIR 1)

Eggs - Source data refers to egg stage. [020EGGS] (FISH, CHIR 1)

Larvae - Source data refers to larval stage or young of year fishes. [020LARVA] (FISH, CHIR 2)

Juvenile - Source data refers to juvenile stage. [020JUVENI] (FISH)

Smolt - Source data refers to smolt stage. [020SMOLT] (FISH)

Pupa - Source data refers to pupal stage. [020PUPA] (CHIR 3)

Adult - Source data refers to adult stage. [020ADULT] (FISH, CHIR 4)

**Abundance** - Typical abundance of adults. [010AB] (FISH)

Abundant - Expected in most habitats within its range and often the dominant species; expected in all collections. [020ABUNDA] (FISH)

Common - Expected in many habitats of its range but present in moderate numbers; usually collected. [020COMMON] (FISH)

Uncommon - Only occasionally present in habitats within its geographic range or present in small numbers; often not collected. [020UNCOMM] (FISH)

Rare - Occurs only in small number of habitats within its geographic range, but sometimes may be abundant in those habitats. [020RARE] (FISH)

**Pollution Tolerance** - Tolerance to decomposable organics. [010PT] (FISH, CHIR 5, DIAT 4, EPHE 3, PLEC 3, BLGR 2)

Saprophilic - Usually in organically polluted waters but also in clean waters. [020SAPHIL] (FISH, CHIR 20, DIAT 25, EPHE 11, PLEC 11, BLGR 12)

Facultative - Wide tolerance to organic pollution. [020FACULT] (FISH, CHIR 21, EPHE 12, PLEC 12)

Saproxenous - Usually in clean waters but also in organically polluted [020SAXENO] (FISH, CHIR 22, DIAT 26, EPHE 13, PLEC 13, BLGR 13)

Saprophobic - In water that has not been exposed to organic pollutants. [020SAPHOB] (FISH, CHIR 23, DIAT 27, EPHE 14, PLEC 14, BLGR 14)

**Optimal Growth Period** - Season of optimal growth. [010GP] (FISH, DIAT 8, BLGR 8)

Winter - Optimal growth in winter. [020WINTER] (FISH, DIAT 51, BLGR 60)

Spring - Optimal growth in spring. [020SPRING] (FISH, DIAT 52, BLGR 61)
Summer - Optimal growth in summer. [020SUMMER] (FISH, DIAT 53, BLGR 62)
Autumn - Optimal growth in autumn. [020AUTUMN] (FISH, DIAT 54, BLGR 63)

**Reproductive Season** - Period of reproduction or sexual maturity. [010RS] (FISH, CHIR 12, EPHE 10, PLEC 10)
Winter - Reproduction or sexual maturity in winter. [020WINTER] (FISH, CHIR 61, EPHE 45, PLEC 45)
Spring - Reproduction or sexual maturity in spring. [020SPRING] (FISH, CHIR 62, EPHE 46, PLEC 46)
Summer - Reproduction or sexual maturity in summer. [020SUMMER] (FISH, CHIR 63, EPHE 47, PLEC 47)
Autumn - Reproduction or sexual maturity in autumn. [020AUTUMN] (FISH, CHIR 64, EPHE 48, PLEC 48)

**Reproductive Behavior** - [010RB] (FISH)
Complex - Prepare nest or tend eggs. [020COMPLE] (FISH)
Simple - No nest preparation or tending of eggs. [020SIMPLE] (FISH)
Lithophil - Rocks or gravel preferred. [020LITHOP] (FISH)
Phytophil - Plants preferred. [020PHYTOP] (FISH)
Peliphil - Sand, silt, or mud preferred. [020PELIPH] (FISH)
Xylophil - Wood or debris preferred. [020XYLOPH] (FISH)
Pelagophil - Eggs released in open water. [020PELAGO] (FISH)
Speleophil - Holes, cavities, or burrows preferred. [020SPELEO] (FISH)
Internal - Internal fertilization. [020INTERN] (FISH)
Polyphil - No preferred substrate. [020POLYPH] (FISH)

**Feeding Behavior** - [010FB] (FISH, CHIR 13, EPHE 11,PLEC 11)
Predator - Feeds primarily on animals. [020PREDAT] (FISH, CHIR 65, EPHE 49, PLEC 49)
Piscivore - Feeds primarily on fish. [030PRPISC] (FISH)
Invertivore - Feeds primarily on macroinvertebrates. [030PRINVE] (FISH)
Planktivore - Feeds primarily on microinvertebrates. [030PRPLAN] (FISH)
Herbivore - Feeds primarily on plants. [020HERBIV] (FISH, CHIR 66, EPHE 50, PLEC 50)
Grazer - Feeds primarily on aufwuchs. [030HEGRAZ] (FISH)
Browser - Feeds primarily on macrophytes. [030HEBROW] (FISH)
Omnivore - Regularly feeds on both plants and animals. [020OMNIVO] (FISH, CHIR 67, EPHE 51, PLEC 51)
Scavenger - Regularly feeds on non-living animal matter. [020SCAVEN] (FISH, CHIR 68, EPHE 52, PLEC 52)
Detritivore - Typically feeds on nonliving plant material. [020DETRIT] (FISH)
Shredder - Feeds on coarse particulate organic matter. [030SHREDD]
Collector - Feeds on fine particulate organic matter. [030COLLEC]

Parasite - Feeds on host organisms for food, sometimes resulting in the death of the host. [020PARASI] (FISH)

**CHEMICAL CHARACTERISTICS OF HABITAT**

**Hardness** - Hardness of water measured as mg/1 $CaCO_3$. [010HA] (FISH)

Non-calcareous and Acid - Total hardness < 20 mg/1 $CaCO_3$. [020NONCAL] (FISH)

Slightly Calcareous - Total hardness 20-100 mg/1 $CaCO_3$. [020SLIGHT] (FISH)

Moderately Calcareous - Total hardness 100-200 mg/1 $CaCO_3$. [020MODERA] (FISH)

Highly Calcareous - Total hardness > 200 mg/1 $CaCO_3$. [020HIGHLY] (FISH)

**Salinity** - Dissolved salt concentration for habitat. [010SA] (FISH, CHIR 3, DIAT 3, BLGR 4)

Poly- or Euhalobous - Marine forms, salt concentration > 30,000 mg/1. [020POLEUH] (FISH, BLGR 22)

Polyhalobous - Salt concentration > 40,000 mg/1. [030POPOLY] (FISH, CHIR 11, DIAT 10)

Euhalobous - Marine forms, salt concentration 30,000-40,000 mg/1. [030POEUHA] (FISH, CHIR 12, DIAT 11)

Mesohalobous - Brackish-water forms, salt concentration 500-30,000 mg/1. [020MESOHA] (FISH, CHIR 13, DIAT 12, BLGR 23)

Alpha Mesohalobous - Alpha range, salt concentration 10,000-30,000 mg/1. [030MEALPH] (FISH, DIAT 13, BLGR 24)

Beta Mesohalobous - Beta range, salt concentration 500-10,000 mg/1. [030MEBETA] (FISH, DIAT 14, BLGR 25)

Oligohalobous - Freshwater forms, salt concentrations < 500 mg/1. [020OLIGOH] (FISH, CHIR 14, DIAT 15, BLGR 26)

Halophilous - Stimulated by small amounts of salt, range 150-500 mg/1. [030OLPHIL] (FISH, DIAT 16, BLGR 27)

Haline Indifferent - Tolerates small amounts of salt, range 50-150 mg/1. [030OLINDI] (FISH, DIAT 17, BLGR 28)

Halophobous - Does not tolerate small amounts of salt, < 50 mg/1. [030OLPHOB] (FISH, DIAT 18, BLGR 29)

Euryhalinous - Occurs under broad range of salt concentrations. [020EURYHA] (FISH, CHIR 15, DIAT 19, BLGR 30)

**Nutrients** - Characteristic nutrient concentrations. [010NU] (FISH, CHIR 4, DIAT 2, EPHE 2, PLEC 2, BLGR 3)

Hypereutrophic - Characteristic of extreme eutrophic conditions: total P > 100 ug/1, inorganic N > 1500 ug/1, organic N > 1200 ug/1. [020HYPERE] (FISH, BLGR 16)

Eutrophic - High nutrient concentrations: total P 30-100 ug/1, inorganic N 500-1500 ug/1, organic N 700-1200 ug/1. [020EUTROP] (FISH, CHIR 16, DIAT 6, EPHE 7, PLEC 7, BLGR 17)

Mesotrophic - Moderate nutrient concentrations: total P 10-30 ug/l, inorganic N 300-650 ug/l, organic N 400-700 ug/l. [020MESOTR] (FISH, CHIR 17, DIAT 7, EPHE 8, PLEC 8, BLGR 18)

Oligotrophic - Low nutrient concentrations: total P 5-10 ug/l, inorganic N 200-400 ug/l, organic N 200-400 ug/l. [020OLIGOT] (FISH, CHIR 188, DIAT 8, EPHE 9, PLEC 9, BLGR 19)

Ultraoligotrophic - Extremely low nutrient concentrations: total P < 5 ug/l, inorganic N < 200 ug/l, organic N < 200 ug/l. [020ULTRAO] (FISH)

Dystrophic - Rich in humic materials. [020DYSTRO] (FISH, CHIR 19, DIAT 9, EPHE 10, PLEC 10, BLGR 20)

Eurytrophic - Indifferent to inorganic nutrient content. [020EURYTR] (FISH, BLGR 21)

**Degradable Organics** - Typical association with degradable dissolved organics. [010OR] (FISH, DIAT 4, BLGR 2)

Polysaprobic - Zone of degradation and putrefaction, $O_2$ < 1 mg/l. [020POLYSA] (FISH, DIAT 20, BLGR 7)

Mesosaprobic - Zone where oxidation of organic load is proceeding, [020MESOSA] (FISH) $O_2$ 1-3 mg/l. (DIAT 21, BLGR 8)

Alpha Mesosaprobic - Alpha range of pollution, nitrogen as amino acids. [030MEALPH] (FISH, DIAT 22, BLGR 9)

Beta Mesosaprobic - Beta range of pollution, nitrogen as ammonia compounds. [030MEBETA] (FISH, DIAT 23, BLGR 10)

Oligosaprobic - Oxidation of biodegradables complete, high inorganics, $O_2$ > 3 mg/l. [020OLIGOS] (FISH, DIAT 24, BLGR 11)

**pH** - Negative logarithm of hydrogen ion activity. [010PH] (FISH, CHIR 2, DIAT 1, EPHE 1, PLEC 1, BLGR 1)

Acidobiontic - pH < 5.5. [020ACIDOB] (FISH, CHIR 5, DIAT 1, EPHE 1, PLEC 1, BLGR 1)

Acidophilous - pH 5.6-6.5. [020ACIDOP] (FISH, CHIR 6, DIAT 2, EPHE 2, PLEC 2, BLGR 2)

Neutral - ph 6.6 - 7.5. [020NEUTRA] (FISH, CHIR 7, DIAT 3, EPHE 3, PLEC 3)

Alkaliphilous - pH 7.6-8.5. [020ALKALP] (FISH, CHIR 8, DIAT 4, EPHE 4, PLEC 4, BLGR 4)

Alkalibiontic - pH > 8.5. [020ALKALB] (FISH, CHIR 9, DIAT 5, EPHE 5, PLEC 5, BLGR 5)

pH Indifferent - Not pH dependent, found in acid, neutral, and alkaline waters. [020INDIFF] (FISH, CHIR 10, BLGR 3, EPHE 6, PLEC 6)

**Oxygen** - Dissolved oxygen requirements for reproduction and growth. [010OX] (FISH, CHIR 6, EPHE 4, PLEC 4)

Euoxyphilous - High oxygen concentration, $O_2$ > 7.5 mg/l. (saturated) [020EUOXYP] (FISH, CHIR 24, EPHE 15, PLEC 15)

Mesoxyphilous - Moderate oxygen concentrations, $O_2$ 5.0-7.5 mg/l. [020MESOXY] (FISH, CHIR 25, EPHE 16, PLEC 16)

Oligoxyphilous - Low oxygen concentrations, $O_2$ 2.5-5.0 mg/l. [020OLIGOX] (FISH, CHIR 26, EPHE 17, PLEC 17)

Anoxyphilous - Facultative anaerobic, $O_2$ < 2.5 mg/l. [020ANOXYP] (FISH, CHIR 27)

**PHYSICAL CHARACTERISTICS OF HABITAT**

**General Habitat** - General type of habitat. [010GH] (FISH, CHIR 10, DIAT 6, EPHE 8, PLEC 8, BLGR 6)

Marine - Characteristic of oceans and seas. [020MARINE] (FISH, CHIR 43, DIAT 33)

Neritic - Occurring typically above continental shelf (close to shore). [030MANERI] (FISH, BLGR 47)

Oceanic - Occurring typically over deeper regions of oceans. [030MAOCEA] (FISH, BLGR 48)

Estuary - Characteristic of estuaries and brackish water habitats. [020ESTUAR] (FISH, CHIR 44, DIAT 34, BLGR 45)

Lentic Systems - Characteristic of lakes or ponds. [020LENTIC] (FISH, BLGR 39)

Lake - Characteristic of large inland bodies of standing water. [030LELAKE] (FISH, CHIR 45, DIAT 35, EPHE 33, PLEC 33)

Pond - Characteristic of small bodies of lentic water with macrophytes covering most of bottom. [030LEPOND] (FISH, CHIR 46, DIAT 36, EPHE 34, PLEC 34)

Temporary Water - Characteristic of temporary lentic habitats. [030LETEMP] (FISH)

Littoral - Shallow margin of lake or pond associated with aquatic vegetation. [030LELITT] (FISH, BLGR 46)

Limnetic - Free open water in lakes and ponds. [030LELIMN] (FISH)

Profundal - Bottom sediment of lakes below littoral zone, consisting of exposed fine sediment free of vegetation. [030LEPROF] (FISH)

Benthic - Occurring on bottom of lentic habitats. [030LEBENT] (FISH, BLGR 38)

Lotic Systems - Characteristic of lotic systems. [020LOTIC] (FISH, BLGR 43)

Stream - Characteristic of small flowing waters: width < 20.0 m, maximum depth < 2.0 m, low flow < 100 CFS. [030STREAM] (FISH, CHIR 48, DIAT 38, EPHE 36, PLEC 35)

Small Stream - width 0-2.7m, maximum depth 0-0.5m, low flow < 1 CFS. [040STSMAL] (FISH)

Medium Stream - width 2.7-7.5 m, maximum depth 0.5-1.0 m, low flow 1-10 CFS. [040STMEDI] (FISH)

Large Stream - width 7.5-20.0 m, maximum depth 1.0-2.0 m, low flow 10-100 CFS. [040STLARG] (FISH)

River - Characteristic of larger flowing waters: width > 20.0 m, maximum depth > 2.0 m, low flow > 100 CFS. [030RIVER] (FISH, CHIR 47, EPHE 35, PLEC 36)

Small River - width 20.0-54.0 m, maximum depth 2.0-4.0 m, low flow 100-1000 CFS. [040RISMAL] (FISH)

Medium River - width 54.0-148.0 m, maximum depth 4.0-8.0 m, low flow 1000-10,000 CFS. [040RIMEDI] (FISH)

Large River - width > 148.0 M, maximum depth > 8.0 m, low flow > 10,000 CFS. [040RILARG] (FISH)

Intermittent Flow - Flowing only part of year. [030INTERM] (FISH)

Interrupted Flow - Flow passes underground at some point or points. [030INTERU] (FISH)

Canopy Cover - Characteristic of stream with canopy covering. [030CANOPY] (FISH)

Open - Characteristic of stream without canopy covering. [030OPEN] (FISH)

Spring - Characteristic of springs and seepages. [020SPRING] (FISH, CHIR 49)

Cool spring - Occurring in cool springs and seepages. [030SPCOOL] (FISH, BLGR 41)

Hot Spring - Occurring in hot springs. [030SPHOT] (FISH, BLGR 42)

Sulphurous Spring - Occurring in sulphurous springs. [030SPSULF]

Aerophilous - Characteristic of non-submerged habitats. [020AEROPH] (DIAT 39, BLGR 44)

Wetland - Characteristic of bogs, swamps or marshes. [020WETLAN] (FISH, BLGR 40)

Bog - Occurring in areas characterized by bog vegetation (e.g., **Sphagnum**) [030WEBOG] (FISH)

Swamp - Occurring in standing or slowly flowing water among woody macrovegetation. [030WESWAM] (FISH)

Marsh - Occurring in standing or slowly flowing water among herbaceous macrovegetation. [030WEMARS] (FISH)

Eurytopic or Euryecious - Occurring in wide variety of habitats or environments. [020EURYTO] (BLGR 49)

Other General Habitats - Characteristic of other or unspecified aquatic habitats. [020OTHER] (CHIR 50, DIAT 40, EPHE 37, PLEC 37, BLGR 50)

**Bottom Type** - Bottom requirements for satisfactory growth or reproduction. [010BT] (FISH)

Silt - Particle size 0.0039-0.0625 mm. [020SILT] (FISH)

Sand - Particle size 0.0625-2.0 mm. [020SAND] (FISH)

Gravel or Pebble - Particle size 2.0-64.0 mm. [020GRAPEB] (FISH)

Gravel - Particle size 2.0-16 mm. [030GRAVEL] (FISH)

Pebble - Particle size 16.0-64.0 mm. [030PEBBLE] (FISH)

Cobble or Rubble - Particle size 64.0-256.0 mm. [020COBBLE] (FISH)

Boulder - Particle size > 256.0 mm. [020BOULDE] (FISH)

Bedrock or Claypan - Solid rock or clay bottom. [020BEDROC] (FISH) (FISH)

Muck - Bottom primarily composed of FPOM. [020MUCK] (FISH)

Detritus - Bottom primarily composed of CPOM. [020DETRIT] (FISH)

Specific Habitat - Specific type of habitat. [010SH] (FISH, CHIR 11, DIAT 7, EPHE 9, PLEC 9, BLGR 7)

Planktonic - Suspended in water. [020PLANKT] (BLGR 51)

Euplanktonic - Normally suspended, distribution current dependent. [030PLEUPL] (DIAT 41, BLGR 52)

Tychoplanktonic - Normally periphytic, but often suspended. [030PLTYCH] (DIAT 42, BLGR 53)

Nektonic - Free swimming. [020NEKTON] (FISH)

Riffle or rapid - characteristic of relatively shallow, white, turbulent or broken water. [030NERIFF] (FISH)

Run - characteristic of relatively deep, fast-moving water. [030NERUN] (FISH)

Pool - characteristic of relatively deep, slow-moving or ponded waters. [030NEPOOL] (FISH)

Off channel - characteristic of sloughs, backwaters, oxbows, tempory ponds, or temporary channels. [030NEOFFC] (FISH)

Benthic - characteristically found on or near the bottom of a river or a stream. [030NEBENT] (FISH)

Pelagic - characteristically found in the water column as opposed to in or on the substrate. [030NEPELA] (FISH)

Nearshore - characteristically close to the shore or on shallow bars of medium to large rivers. [030NENEAR] (FISH)

Periphytic - Occurring on substrate or submerged objects (Aufwuchs). [020PERIPH] (DIAT 43, BLGR 54)

Epibenthic - Occurring on, but not penetrating substrate. [030EPIBEN] (CHIR 51, EPHE 38, PLEC 38)

Embenthic - Occurring in substrate (penetrating). [030EMBENT] (CHIR 52, EPHE 39, PLEC 39)

Epipelic - Occurring on or in mud and silt. [030EPIPEL] (CHIR 53, DIAT 44, EPHE 40, PLEC 40, BLGR 55)

Episabulic - Occurring on or in sand. [030EPISAB] (CHIR 54, EPHE 41, PLEC 41)

Epilithic - Occurring on or under rocks. [030EPILIT] (CHIR 55, DIAT 45, EPHE 42, PLEC 42, BLGR 56)

Endolithic - Growing into rocks. [030ENDOLI]

Epixylous - Occurring on or burrowing into wood. [030EPIXYL] (CHIR 56, DIAT 46, EPHE 43, PLEC 43)

Epizooic - Occurring on or within animals. [030EPIZOO] (CHIR 57, DIAT 47)

Epiphytic - Occurring on or within plants. [030EPIPHI] (CHIR 58, DIAT 48, EPHE 44, PLEC 44, BLGR 57)

Attached - Normally sessile. [030ATTACH] (CHIR 59, DIAT 49)

Unattached - Normally free living and capable of locomotion. [030UNATTA] (CHIR 60, DIAT 50)

Other Specific Habitats - Occurring in other or unspecified specific habitats. [020OTHER] (FISH, BLGR 58)

Retreat Builder - Builds retreat. [020RETREA]

Case Maker - Builds case. [020CASEMA]

Free Living - Does not build case or retreat. [020FREELI]

**Temperature** - Temperature requirements for satisfactory growth, development, or reproduction. [010TE] (FISH, CHIR 7, DIAT 9, EPHE 5, PLEC 5, BLGR 9)

Euthermal - Warm-water forms, temperature usually > 30 C. [020EUTHER] (FISH, CHIR 28, DIAT 55, EPHE 18, PLEC 18, BLGR 64)

Mesothermal - Temperate-water forms, temperature usually 15-30 C. [020MESOTH] (FISH, CHIR 29, DIAT 56, EPHE 19, PLEC 19, BLGR 65)

Low Mesothermal - temperature usually 15-20 C. [030MELOW] (FISH)

Medium Mesothermal - temperature usually 20-25 C. [030MEMEDI] (FISH)

High Mesothermal - temperatures usually 25-30 C. [030MEHIGH] (FISH)

Oligothermal - Cold-water forms, temperature usually 0-15 C. [020OLIGOT] (FISH, CHIR 30, DIAT 57, EPHE 20, PLEC 20, BLGR 66)

Low Oligothermal - temperature usually 0-5 C. [030OLLOW] (FISH)

Medium Oligothermal - temperature usually 5-10 C. [030OLMEDI] (FISH)

High Oligothermal - temperature usually 10-15 C. [030OLHIGH] (FISH)

Stenothermal - Temperature range < 5 C. [020STENOT] (FISH, CHIR 31, DIAT 58, EPHE 21, PLEC 21, BLGR 67)

Metathermal - Temperature range 5-15 C. [020METATH] (FISH, CHIR 32, DIAT 59, EPHE 22, PLEC 22, BLGR 68)

Eurythermal - Temperature range > 15 C. [020EURYTH] (FISH, CHIR 33, DIAT 60, EPHE 23, PLEC 23, BLGR 69)

**Turbidity** - Characteristic turbidity of habitat. [010TU] (FISH, CHIR 4, EPHE 6, PLEC 6)

Eulichtophilous - Characteristic of low turbidity, clear water, < 100 JTU. [020EULICH] (FISH, CHIR 34, EPHE 24, PLEC 24)

Mesolichtophilous - Water generally clear, but occasionally clouded, 100-300 JTU. [020MESOLI] (FISH, CHIR 35, EPHE 25, PLEC 25)

Oligolichtophilous - Characteristic of high turbidity, murky water, > 300 JTU. [020OLIGOL] (FISH, CHIR 37, EPHE 27, PLEC 27)

Polylichtophilous - Occurring at wide range of turbidity. [020POLYLI] (FISH, CHIR 36, EPHE 26, PLEC 26)

**Current** - Current characteristics of habitat. [010CU] (FISH, CHIR 9, DIAT 5, EPHE 7, PLEC 7, BLGR 5)

Limnobiontic - Characteristic of standing waters only. [020LIMNOB] (FISH, CHIR 38, DIAT 28, EPHE 28, PLEC 28, BLGR 32)

Limnophilous - Usually in standing water, but may be in running water. [020LIMNOP] (FISH, CHIR 39, DIAT 29, EPHE 29, PLEC 29, BLGR 33)

Current Indifferent - Common in both standing and flowing waters. [020INDIFF] (FISH, CHIR 40, DIAT 30, EPHE 30, PLEC 30, BLGR 34)

Rheophilous - Usually in running water, but may be in standing water. [020RHEOPH] (FISH, CHIR 41, DIAT 31, EPHE 31, PLEC 31, BLGR 35)

Rheobiontic - Characteristic of running water only. [020RHEOBI] (FISH, CHIR 42, DIAT 32, EPHE 32, PLEC 32, BLGR 36)

## GEOGRAPHIC DISTRIBUTION

**Ecosystem Regions** - Bailey ecoregions. [010ER] (FISH)

- Polar Domain - 1000. [0201000] (FISH)
  - Tundra Division - 1200. [0301200] (FISH)
    - Arctic Tundra Province - 1210. [0401210] (FISH)
    - Bering Tundra Province - 1220. [0401220] (FISH)
    - Brooks Range Province - M1210. [040M1220] (FISH)
  - Subarctic Division - 1300. [0301300] (FISH)
    - Yukon Parkland Province - 1310. [0401310] (FISH)
    - Yukon Forest Province - 1320. [0401320] (FISH)
    - Alaska Range Province - M1310. [040M1310] (FISH)
- Humid Temperate Domain - 2000. [0202000] (FISH)
  - Warm Continental Division - 2100. [0302100] (FISH)
    - Laurentian Mixed Forest Province - 2110. [0402110] (FISH)
    - Columbia Forest Province - M2110. [040M2110] (FISH)
  - Hot Continental Division - 2200. [0302200] (FISH)
    - Eastern Deciduous Forest Province - 2210. [0402210] (FISH)
  - Subtropical Division - 2300. [0302300] (FISH)
    - Outer Coastal Plain Forest Province - 2310. [0402310] (FISH)
    - Southern Mixed Forest Province - 2320. [0402320] (FISH)
  - Marine Division - 2400. [0302400] (FISH)
    - Willamette Puget Forest Province - 2410. [0402410] (FISH)
    - Pacific Forest Province - M2410. [040M2410] (FISH)
  - Prairie Division - 2500. [0302500] (FISH)
    - Prairie Parkland Province - 2510. [0402510] (FISH)
    - Prairie Brushland Province - 2520. [0402520] (FISH)
    - Tall-grass Prairie Province - 2530. [0402530] (FISH)
  - Mediterranean Division - 2600. [0302600] (FISH)
    - California Grassland Province - 2610. [0402610] (FISH)
    - Sierran Forest Province - M2610. [040M2610] (FISH)
    - California Chaparral Province - M2620. [0402620] (FISH)
- Dry Domain - 3000. [0203000] (FISH)

Steppe Division - 3100. [0303100] (FISH)
Great Plains Short-grass Prairie Province - 3110. [0403110] (FISH)
Palouse Grassland Province - 3120. [0403120] (FISH)
Intermountain Sagebrush Province - 3130. [0403130] (FISH)
Mexican Highlands Shrub Steppe Province - 3140. [0403140] (FISH)
Rocky Mountain Forest Province - M3110. [040M3110] (FISH)
Upper Gila Mountains Forest Province - M3120. [040M3120] (FISH)
Colorado Plateau Province - P3130. [040M3130] (FISH)
Wyoming Basin Province - A3140. [040M3140] (FISH)
Desert Division - 3200. [0303200] (FISH)
Chihuahuan Desert Province - 3210. [0403210] (FISH)
American Desert Province (Mojave-Colorado-Sonoran) - 3220. [0403220] (FISH)
Humid Tropical Domain - 4000. [0204000] (FISH)
Tropical Savanna Division - 4100. [0304100] (FISH)
Everglades Province - 4110. [0404110] (FISH)
Rainforest Division - 4200. [0304200] (FISH)
Hawaiian Islands Province - M4210. [040M4210] (FISH)
Cultural Ecosystems - Initiated and maintained by man - 9000. [0209000] (FISH)
Croplands - Perennial production - 9100. [0309100] (FISH)
Urban or Industrial - Areas dominated by construction, roads and buildings - 9200. [0309200] (FISH)
**Political Geography** - Geographic distribution using US EPA regions, states, and provinces. [010PG] (FISH, CHIR 14, EPHE 12, PLEC 12)
Region 1 (NE-N) - Northeastern US states. [020REG01] (FISH, CHIR 69, EPHE 53, PLEC 53)
CT - Connecticut. [030CT] (FISH)
ME - Maine. [030ME] (FISH)
MA - Massachusetts. [030MA] (FISH)
NH - New Hampshire. [030NH] (FISH)
RI - Rhode Island. [030RI] (FISH)
VT - Vermont. [030VT] (FISH)
Region 2 (NE-C + PR) - Northeastern US states and other. [020REG02] (FISH, CHIR 70, EPHE 54, PLEC 54)
NJ - New Jersey. [030NJ] (FISH)
NY - New York. [030NY] (FISH)
PR - Puerto Rico. [030PR] (FISH)
Region 3 (NE-S) - Middle Atlantic US states. [020REG03] (FISH, CHIR 71, EPHE 55, PLEC 55)
DE - Delaware. [030DE] (FISH)
MD - Maryland. [030MD] (FISH)
PA - Pennsylvania. [030PA] (FISH)
VA - Virginia. [030VA] (FISH)
WV - West Virginia. [030WV] (FISH)

Region 4 (SE) - Southeastern US states. [020REG04] (FISH, CHIR 72, EPHE 56, PLEC 56)

AL - Alabama. [030AL] (FISH)
FL - Florida. [030FL] (FISH)
GA - Georgia. [030GA] (FISH)
KY - Kentucky. [030KY] (FISH)
MS - Mississippi. [030MS] (FISH)
NC - North Carolina. [030NC] (FISH)
SC - South Carolina. [030SC] (FISH)
TN - Tennessee. [030TN] (FISH)

Region 5 (W Great Lakes) - Western Great Lakes US states. [020REG05] (FISH, CHIR 73, EPHE 57, PLEC 57)

IL - Illinois. [030IL] (FISH)
IN - Indiana. [030IN] (FISH)
MI - Michigan. [030MI] (FISH)
MN - Minnesota. [030MN] (FISH)
OH - Ohio. [030OH] (FISH)
WI - Wisconsin. [030WI] (FISH)

Region 6 (SC) - South Central US states. [020REG06] (FISH, CHIR 74, EPHE 58, PLEC 58)

AR - Arkansas. [030AR] (FISH)
LA - Louisiana. [030LA] (FISH)
NM - New Mexico. [030NM] (FISH)
OK - Oklahoma. [030OK] (FISH)
TX - Texas. [030TX] (FISH)

Region 7 (C) - Central US states. [020REG07] (FISH, CHIR 75, EPHE 59, PLEC 59)

IA - Iowa. [030IA] (FISH)
KS - Kansas. [030KS] (FISH)
MO - Missouri. [030MO] (FISH)
NE - Nebraska. [030NE] (FISH)

Region 8 (Rocky Mt.) - Rocky Mountain US states. [020REG08] (FISH, CHIR 76, EPHE 60, PLEC 60)

CO - Colorado. [030CO] (FISH)
MT - Montana. [030MT] (FISH)
ND - North Dakota. [030ND] (FISH)
SD - South Dakota. [030SD] (FISH)
UT - Utah. [030UT] (FISH)
WY - Wyoming. [030WY] (FISH)

Region 9 (SW + Hi, Gu) - Southwestern US states and other. [020REG09] (FISH, CHIR 77, EPHE 61, PLEC 61)

AZ - Arizona. [030AZ] (FISH)
CA - California. [030CA] (FISH)
GU - Guam. [030GU] (FISH)
HI - Hawaii. [030HI] (FISH)
NV - Nevada. [030NV] (FISH)

Region 10 (NW + Ak) - Northwestern US states. [020REG10] (FISH, CHIR 78, EPHE 62, PLEC 62)

AK - Alaska. [030AK] (FISH)
ID - Idaho. [030ID] (FISH)
OR - Oregon. [030OR] (FISH)
WA - Washington. [030WA] (FISH)

Region 11 - Eastern Canadian provinces. [020REG11] (FISH, EPHE 63, PLEC 63)

NB - New Brunswick. [030NB] (FISH)
NF - Newfoundland. [030NF] (FISH)
NS - Nova Scotia. [030NS] (FISH)
ONT - Ontario. [030ONT] (FISH)
PEI - Prince Edward Island. [030PIE] (FISH)
QUE - Quebec. [030QUE] (FISH)

Region 12 - Western Canadian provinces and territories. [020REG12] (FISH, EPHE 64, PLEC 64)

ALB - Alberta. [030ALB] (FISH)
BC - British Columbia. [030BC] (FISH)
MAN - Manitoba. [030MAN] (FISH)
NWT - Northwest Territories. [030NWT] (FISH)
SAS - Saskatchewan. [030SAS] (FISH)
YUK - Yukon Territory. [030YUK] (FISH)

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