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A DEVONIAN/CARBONIFEROUS CONODONT DATABASE — DOCUMENTATION AND USER'S MANUAL

by

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Introduction

This report describes a database program for recording, analyzing, and reporting Devonian and Carboniferous conodont samples. The authors' intention is to provide a program that not only can be used by colleagues working with Devonian and Carboniferous conodonts, but also can be easily expanded by colleagues working on conodonts of older or younger age. It also can serve, with some modification, as a basis for paleontological databases for other taxonomic groups.

This report consists of two parts. Part A is a document describing the program and serving as a user's manual. Part B presents the actual database program on disk in machine-readable form. Part B requires certain computer hardware and software to function. Readers not possessing appropriate hardware and software can use the descriptions in part A as a template for design of a similar database with their own resources. For practice in using the database, the program in part B includes updated records pertaining to 27 samples, all of them previously published in Lane, Sandberg, and Ziegler (1980); Sandberg and Dreesen (1984); Sandberg and Ziegler (1973); Sandberg, Ziegler, and Bultynck (1989); Sandberg and others (1988); or Ziegler and Sandberg (1990). These samples are from 14 localities and 19 conodont zones.

A preliminary version of the conodont database was demonstrated and discussed at a Pander Society workshop and symposium (Charpentier and Sandberg, 1990). The authors thank Anita Harris and Craig Wandrey for their reviews and suggestions.

In this document, names of files are presented in italics, for example *Samples*, while names of fields are presented in boldface, for example **Trivial name**. These conventions are not used, however, where the word is part of the name of a menu option, for example Add Localities.

System/software requirements

Use of the database program presented in part B of this report requires specific computer hardware and software. The program was originally designed for a Macintosh SE computer and will run on that model or any more advanced Macintosh computer, such as a member of the Macintosh II family. A hard disk and at least 1MB of RAM are required. System software should be at least 6.0.3, but the program is compatible with System 7. The screen layouts were designed to fit a small, SE-sized monitor, but will also fit larger monitors.

The database program was built using 4th Dimension software created by Acius, Inc. **A copy of 4th Dimension is necessary to run this program.** The runtime version 4th Dimension will perform most of the functions but will not allow creation of new species lists nor modification of the structure or routines. A full copy of 4th Dimension, including the design and user environments, is therefore highly recommended. Version 2.2.1, or a higher version, of 4th Dimension should be used.

Use of the conodont database software in this report requires some familiarity with 4th Dimension. Users unfamiliar with 4th Dimension should complete at least the Quickstart tutorials that come with the 4th Dimension software. The major 4th Dimension features with which users should be familiar are: entering the database, choosing records by highlighting, basic data entry skills, using choice lists, searching by layout or by the search editor, using the sort editor, and using the quick report editor. If modification of the software is desired, the more advanced tutorials would be helpful.

Installing the database

The two 3.5-in. DS floppy disks of U.S. Geological Survey Open-File Report 92-273B contain six files:

D/C - the main structure file for the database (353K in size)
D/C.data - a selection of data pertaining to 27 conodont samples, used as examples (556K in size)
CAI by state - a standardized report format
CAI report - a standardized report format
Taxon tabulation - a standardized report format
Read Me - a copy of this section

In order to install and use the database, first copy all the files (except **Read Me**) to the area where 4th Dimension resides on your computer. Then double-click the icon for file **D/C**.

To create another database with the same structure as **D/C**, follow this procedure:

1. Install the files from the disks into the area where 4th Dimension resides on your computer, if you have not done so already.
2. Duplicate the file **D/C** and rename the duplicate appropriately.
3. Double-click on the icon for the renamed duplicate file.
4. Click the button "New Data File" on the window that appears.
5. Click the "Save" button on the next window.
6. The new database opens at the runtime window and is ready for use.

Database structure

The structure of this program was created specifically to duplicate the paper forms used by Sandberg for the approximately 3500 samples he has analyzed since 1966. The latest version of this form is shown in figure 1. The main input layout for samples, for example, closely resembles Sandberg's paper form. Biofacies analyses built into the program were those most commonly run by Sandberg on his samples. These analyses and their methodology were first reported by Sandberg (1976), and later elaborated on by Sandberg and Ziegler (1979), Sandberg and Dreesen (1984), Sandberg and Gutschick (1984), Sandberg and others (1988), and Ziegler and Sandberg (1990).

The database structure is shown in figure 2, with relations between files indicated by arrows. Most of the data reside in three files: *Localities*, *Samples*, and *Species*. Each locality may have multiple related samples in a one-to-many relationship. The field **Locality name** in file *Localities* and the field **Locality** in file *Samples* are the relating fields. Each sample may have multiple related species in a one-to-many relationship. The field **Sample number** in file *Samples* and the field **Sample number** in file *Species* are the relating fields.

Three other files are used by some of the routines, and not for storage of data. The file *Zones* is used by the procedure that creates range charts. Three images used by that procedure are stored in the file named *Pictures*. The file *Lists* is used in the procedure that prints the contents of a list.

Fields

File: *Localities*

Locality Id: (Integer; Indexed, Unique) a unique integer assigned by the program to each locality record for identification purposes; not currently used by any procedure or displayed on any layout

Locality name: (Alpha 30; Indexed) name of the locality; used to relate the *Localities* file with the *Samples* file

Continent: (Alpha 13) name of the continent where the locality is situated

Region: (Alpha 30) name of the region in which the locality is situated

Country: (Alpha 20) name of the country in which the locality is situated

State: (Alpha 20) name of the state or province in which the locality is situated

County: (Alpha 20) name of the county in which the locality is situated

Map name: (Alpha 30) name of the map (in U.S., usually a 7.5-minute topographic quadrangle) that shows the locality

Latitude: (Real) latitude of the locality in decimal degrees; positive for northern hemisphere, negative for southern hemisphere

Longitude: (Real) longitude of the locality in decimal degrees; positive for eastern hemisphere, negative for southern hemisphere

District: (Alpha 30) name of the district in which the locality is situated, a district is hierarchically intermediate between a region and a locality

Average CAI: (Real) the average Color Alteration Index (CAI) value for samples from the locality

File: *Samples*

Sample Id: (Integer; Indexed) a unique integer assigned by the program to each sample record for identification purposes; not currently used by any procedure or displayed on any layout

Sample number: (Alpha 15; Mandatory, Indexed, Unique) the primary identifier of each sample; used to relate the *Samples* file with the *Species* file

Year collected: (Integer) the year in which the sample was collected

Total wt: (Real) the total weight of the sample

Lith samp wt: (Real) the weight of a lithologic sample (included in **Total wt**)

Thin x samp wt: (Real) the weight of a sample taken for thin-section preparation (included in **Total wt**)

Lithologic desc: (Text) a description of the sample lithology

Percent carb: (Real) the percent of the lithologic constituents that are carbonates

Ca Mg ratio: (Real) the molal ratio of calcium to magnesium in the sample

Thin sections: (Integer) the number of thin sections prepared from this sample

Strat position: (Text) the stratigraphic position of the sample, giving formation and/or member name and distance above or below a reference horizon

Locality: (Alpha 30; Indexed) name of the locality; used to relate the *Localities* file to the *Samples* file

Location: (Text) an extended description of the sample location including map reference; for U.S. samples usually includes land-grid location and county

Start wt 1: (Real) the starting weight in grams of the sample before the first acid treatment

Wt undiss 1: (Real) the weight in grams of the undissolved sample after the first acid treatment

Acid 1: (Alpha 20) the type of acid used in the first treatment

Amt acid 1: (Real) the amount of acid in milliliters used for the first acid treatment

Heat 1: (Boolean) whether heat was used during the first acid treatment

Started 1: (Date) the starting date of the first acid treatment

Finished 1: (Date) the finishing date of the first acid treatment

Start wt 2: (Real) the starting weight in grams of the sample before the second acid treatment

Wt undiss 2: (Real) the weight in grams of the undissolved sample after the second acid treatment

Acid 2: (Alpha 20) the type of acid used in the second treatment

Amt acid 2: (Real) the amount of acid in milliliters used for the second acid treatment

Heat 2: (Boolean) whether heat was used during the second acid treatment

Started 2: (Date) the starting date of the second acid treatment

Finished 2: (Date) the finishing date of the second acid treatment

Start wt 3: (Real) the starting weight in grams of the sample before the third acid treatment

Wt undiss 3: (Real) the weight in grams of the undissolved sample after the third acid treatment

Acid 3: (Alpha 20) the type of acid used in the third treatment

Amt acid 3: (Real) the amount of acid in milliliters used for the third acid treatment

Heat 3: (Boolean) whether heat was used during the third acid treatment

Started 3: (Date) the starting date of the third acid treatment

Finished 3: (Date) the finishing date of the third acid treatment

Undis samp lith: (Text) a description of the undissolved sample lithology

sf 125 180: (Boolean) whether the sample was sieved into a 125 to 180 mm size fraction

sf 180 250: (Boolean) whether the sample was sieved into a 180 to 250 mm size fraction

sf 250 425: (Boolean) whether the sample was sieved into a 250 to 425 mm size fraction

sf 425 850: (Boolean) whether the sample was sieved into a 425 to 850 mm size fraction

sf 850 2mm: (Boolean) whether the sample was sieved into a 850 mm to 2 mm size fraction

other sf: (Text) the other size fractions used in sieving

Bromoform: (Boolean) whether bromoform was used in the sample preparation

Meth iodide: (Boolean) whether methylene iodide was used in the sample preparation

Mag separator: (Boolean) whether the magnetic separator was used in the sample preparation

MEI BF mix: (Boolean) whether a combination of methylene iodide and bromoform was used in the sample preparation

CAI: (Real) the conodont color-alteration index, a measure of thermal maturity based on color of the conodont elements

Productivity: (Alpha 17) a qualitative measure of the number of conodonts per kilogram of rock dissolved: sterile, sparse (1-19), productive (20-199), or highly productive (200 or more)

No slides: (Integer) the number of microfossil slides on which conodont elements are mounted

Conodont zone: (Alpha 65) the age of the sample, expressed in words

Old age limit: (Integer) a code signifying the maximum age limit of the sample; assigned by procedure "Encode age"

Young age limit: (Integer) a code signifying the minimum age limit of the sample; assigned by procedure "Encode age"

Biofacies: (Alpha 35) the biofacies interpretation of the sample

Best size fract: (Alpha 20) the size fraction(s) with the most abundant conodonts

Heavy: (Text) a description of the heavy fraction of the acid residue

Light: (Text) a description of the light fraction of the acid residue

Foraminifera: (Boolean) whether the residue contains foraminifers

Radiolarians: (Boolean) whether the residue contains radiolarians

Sponge spicules: (Boolean) whether the residue contains sponge spicules

Framboids: (Boolean) whether the residue contains pyrite framboids

Glauconitized: (Boolean) whether some microfossils are glauconitized

Chloritized: (Boolean) whether some microfossils are chloritized

Phosphatized: (Boolean) whether some microfossils are phosphatized

Conodont pearls: (Boolean) whether the residue contains conodont pearls

Peloids: (Boolean) whether the residue contains peloids

Ooids: (Boolean) whether the residue contains ooids

Nanicella: (Boolean) whether the residue contains the calcareous foraminifer Nanicella

Ichthyoliths: (Boolean) whether the residue contains ichthyoliths

Barite: (Boolean) whether the residue contains barite

Ostracodes: (Boolean) whether the residue contains ostracodes

Hvf discard: (Boolean) whether the heavy fraction of the residue was discarded

Hvf stored: (Alpha 30) which portions (if any) of the heavy fraction of the residue were retained

Hvf stored in: (Alpha 40) the type of storage containers used for the retained heavy fraction of the residue (if any)

Lf discard: (Boolean) whether the light fraction of the residue was discarded

Lf stored: (Alpha 30) which portions (if any) of the light fraction of the residue were retained

Lf stored in: (Alpha 40) the type of storage containers used for the retained light fraction of the residue (if any)

Unacid wt: (Real) the weight of the sample left unacidized

Unacid stored: (Alpha 20) the container in which the unacidized sample is stored

Unacid remarks: (Text) originally remarks concerning disposition of the unacidized portion of the sample; now used for a description of specimens other than counted conodonts — for example, conodont scraps, ichthyoliths, or other microfossils — also mounted on slides

Comments: (Text) a general comment field; shows by whom and when the fauna was re-identified and by whom and when the sample was input to the database as well as other information and comments that do not have a specific field

Flags: (Text) particularly relevant comments that are deemed worthy of highlighting

Strat order: (Real) a numeric value showing the distance in meters above or below a reference horizon for the locality

Zone precision: (Boolean) whether the sample age has been clearly determined to a specific conodont zone

Silicified: (Boolean) whether the sample contains silicified fossils

File: *Species*

Sample number: (Alpha 15; Indexed) the primary identifier of each sample; used to relate the *Samples* file with the *Species* file

Genus: (Alpha 20; Indexed) the generic name of the specimens

Trivial name: (Alpha 25; Indexed) the trivial name of the specimens

Detail: (Alpha 25; Indexed) the subspecific or morphotype name of the specimens

Count: (Integer) the number of specimens

Slide: (Integer; Indexed) the number of the microfossil slide on which the specimens are mounted

Boxes: (Alpha 30) the numbered box(es) on the microfossil slide in which the specimens are mounted

Box: (Boolean) whether the specimens are stored in a container other than on a slide

Average: (Boolean) whether the counts were determined by an average sampling procedure rather than by strictly counting

Reworked: (Boolean) whether the specimens are reworked

Comments: (Text) general comments pertaining to the specimens

Element: (Alpha 3; Indexed) the type of conodont element

Questionable: (Boolean) whether the identification to a particular taxon is questionable

Avg size fract: (Alpha 15; Choices) the size fraction of residue for those specimen counts determined by an average sampling procedure

File: *Zones*

Zone name: (Alpha 30) the name of the zone

Top code: (Integer; Indexed) the integer code for the top (youngest age) of the zone

Bottom code: (Integer; Indexed) the integer code for the bottom (oldest age) of the zone

Num samp 1: (Alpha 4) the number of samples in the zone that include the first taxon

Line 1: (Picture) the picture (solid bar, dashed bar, or blank) used to show the range of the first taxon

Num samp 2: (Alpha 4) the number of samples in the zone that include the second taxon

Line 2: (Picture) the picture (solid bar, dashed bar, or blank) used to show the range of the second taxon

Num samp 3: (Alpha 4) the number of samples in the zone that include the third taxon

Line 3: (Picture) the picture (solid bar, dashed bar, or blank) used to show the range of the third taxon

Num samp 4: (Alpha 4) the number of samples in the zone that include the fourth taxon

Line 4: (Picture) the picture (solid bar, dashed bar, or blank) used to show the range of the fourth taxon

File: *Pictures*

Pic name: (Alpha 20) the name of the stored image

Image: (Picture) the stored image itself

File: *Lists*

Items: (Alpha 30) the item taken from a stored list

Runtime menu options

The main menu bar in the runtime environment contains eight columns (fig. 3). The options provided in this environment include all those needed in normal operation. Other options are available by using the "Quit to user" option to move to the user environment, and from there possibly to the design environment. The database design intentionally requires unusual procedures to be performed outside of the runtime environment so that passwords can provide some measure of security against accidental or unauthorized major changes (such as a change in database structure) by casual users.

This section presents the runtime menu options and an explanation of their uses.

Menu column: File   Option: Information

This option calls up a window which presents basic information about the database, including the version number.

Menu column: File   Option: Quit to user

This option transfers the screen to the user environment. From there the user can move either to the design environment or back to the runtime environment.

Menu column: File   Option: Quit to finder

This option closes the database. Closing can also be done by typing command-Q.

Menu column: Edit

All the normal Macintosh edit options, such as cut and paste, are available in this column. (**Tip:** Normal F [function] keys on an extended keyboard do not work as a substitute.)

Menu column: View   Option: Localities

This option displays the locality data. If a selection exists and is less than the entire *Localities* file, then the user is offered the option to view just the selection. Initially, the data are presented in a one-line format (fig. 4), but double-clicking on any record will display the full-record format (fig. 5).

Menu column: View   Option: Samples

This option displays the sample data. If a selection exists and is less than the entire *Samples* file, then the user is offered the option to view just the selection. Initially the data are presented in a one-line format (fig. 6), but double-clicking on any record will display the full-record format (fig. 7).

Menu column: View   Option: Species

This option displays the species data. If a selection exists and is less than the entire *Species* file, then the user is offered the option to view just the selection. Initially the data are presented in a one-line format (fig. 8), but double-clicking on any record will display the full-record format (fig. 9).

Menu column: View   Option: Lists

This option displays the contents of any list. An option to send the list to a printer is also provided. The list names are given in table 1. (**Tip:** Normal F [function] keys on an extended keyboard do not work as a substitute.)

Menu column: View   Option: Sort localities

This option performs a sort of the current *Localities* selection. The 4th Dimension sort editor is opened.

Menu column: View   Option: Sort samples

This option performs a sort of the current *Samples* selection. The 4th Dimension sort editor is opened.

Menu column: View   Option: Sort species

This option performs a sort of the current *Species* selection. The 4th Dimension sort editor is opened.

Menu column: Add   Option: Localities

This option allows entry of new records to the *Localities* file. The default input format (fig. 10) is used. New records will continue to be added until the user chooses "Cancel".

Menu column: Add   Option: Samples

This option allows entry of new records to the *Samples* file. The six-page default input format (figs. 11-16) is used.

To enter *Species* file records with the full-page *Species* input layout, double-click within the included layout on page 4 of the *Samples* input layout (fig. 14). Choose "Enter" after completing each *Species* record. To return to the *Sample* input layout, choose "Cancel" while at a blank *Species* input layout.

After entry, the program compares the total number of elements entered in the *Sample* record with the sum of those given in the *Species* records, and gives a warning message if they differ. The option to perform all four analyses on the sample is also given. New records will continue to be added until the user chooses "Cancel".

Menu column: Add Option: Species

This option allows entry of new records to the *Species* file. The default input format (fig. 17) is used. New records will continue to be added until the user chooses "Cancel". Note that species records are usually added along with the rest of the data pertaining to a sample as part of the Add Samples option.

Menu column: Modify Option: Localities

This option allows the user to modify previously added records in the *Localities* file. The user chooses records to be modified from either a listing of the current selection or of the entire file. The choice of which records to modify is made by highlighting records on the displayed list. After clicking the "Done" button (or pressing the "Enter" key) the chosen records are presented one-by-one in input format (fig. 10) for modification. Records may be deleted by clicking the "Delete" button while in input format.

Menu column: Modify Option: Samples

This option allows the user to modify previously added records in the *Samples* file. The user chooses records to be modified from either a listing of the current selection or of the entire file. The choice of which records to modify is made by highlighting records on the displayed list. After clicking the "Done" button (or pressing the "Enter" key) the chosen records are presented one-by-one in input format (figs. 11-16) for modification. Records may be deleted by clicking the "Delete" button while in input format.

To modify *Species* file records with the full-page *Species* input layout, double-click on the particular *Species* record on page 4 of the *Samples* input layout (fig. 14). To enter additional *Species* file records with the full-page *Species* input layout, double-click below the current *Species* records on page 4 of the *Samples* input layout. Choose "Enter" after completing each *Species* record. To return to the *Sample* input layout, choose "Cancel" while at a *Species* input layout.

After entry, the program compares the total number of elements entered in the *Sample* record with the sum of those given in the *Species* records, and gives a warning message if they differ. The option to perform all four analyses on the sample is also given.

The Modify Samples option can also be chosen by typing command-M.

Menu column: Modify Option: Species

This option allows the user to modify previously added records in the *Species* file. The user chooses records to be modified from either a listing of the current selection or of the entire file. The choice of which records to modify is made by highlighting records on the displayed list. After clicking the "Done" button (or pressing the "Enter" key) the chosen records are presented one-by-one in input format (fig. 17) for modification. Records may be deleted by clicking the "Delete" button while in input format.

Menu column: Search Option: Localities

This option allows the user to search for records in the *Localities* file, using either the input layout or the 4th Dimension search editor. The corresponding records in the *Samples* and *Species* files are also found and made into the current selections for those files.

Menu column: Search Option: Samples

This option allows the user to search for records in the *Samples* file, using the 4th Dimension search editor. The corresponding records in the *Localities* and *Species* files are also found and made into the current selections for those files.

Menu column: Search Option: Species

This option allows the user to search for records in the *Species* file, using either the input layout or the 4th Dimension search editor. The corresponding records in the *Localities* and *Samples* files are also found and made into the current selections for those files.

Menu column: Search Option: By age range

This option allows the user to search for records in the *Samples* file, using a special search editor. The user inputs either one or two zone names, which are chosen from lists. If two zone names are given, the samples with ages within that inclusive range are selected. Samples from a single zone can be found by giving that zone name twice. A check box is provided in order to force a search within the current *Sample* selection. The corresponding records in the *Localities* and *Species* files are also found and made into the current selections for those files.

Menu column: Print Option: Localities

This option allows the user to print either the current selection or the entire *Localities* file using a default format (fig. 18).

Menu column: Print Option: Samples

This option allows the user to print either the current selection or the entire *Samples* file using a default format (fig. 19).

Menu column: Print Option: Species

This option prints the current selection from the *Species* file using a default format (fig. 20).

Menu column: Print Option: Report localities

This option opens the 4th Dimension quick report editor. The user then may design a quick report based on either the current selection or the entire *Localities* file. Two standard report formats are also offered (figs. 21 and 22).

Menu column: Print Option: Report samples

This option opens the 4th Dimension quick report editor. The user then may design a quick report based on either the current selection or the entire *Samples* file.

Menu column: Print Option: Report species

This option opens the 4th Dimension quick report editor. The user then may design a quick report based on the current selection from the *Species* file. A standard report format is also offered (fig. 23).

Menu column: Print Option: Sample report

This option prepares and prints a special report meant specifically as a notification of the paleontological analysis done on a particular sample. Data from all three main files are used (fig. 24). Comments are solicited from the user and printed as part of the report.

Menu column: Analyze Option: Totals

This option calculates basic counts of conodont elements from the current selection. Totals are given for the number of elements on each slide, the number stored in separate boxes, the number calculated from the average sampling process, and the grand total (fig. 25). Although normally used for a single sample, partial or multiple samples can be similarly analyzed by forming an appropriate selection with the search procedures.

Menu column: Analyze Option: Averaged data

This option analyzes that part of the data in the current selection pertaining to counts made by a conodont averaging procedure. The method of averaging conodont-rich residues too large to be completely picked involves counting taxa in random squares in a specifically drawn 1-cm grid on a cardboard tray. This technique, conceived by Sandberg and refined by Jamie L. Butler, U.S.G.S., has been found to give results repeatable to within 2%. Results are displayed in columns by genus and in rows by size fraction with appropriate column and row totals (fig. 26). If the selection does not include any averaged data, the user is notified and calculations are not continued. Although normally used for a single sample, partial or multiple samples can be similarly analyzed by forming an appropriate selection with the search procedures.

Menu column: Analyze Option: Biofacies

This option performs a biofacies analysis on Pa and I elements of the current selection. Belodellid elements are included when they are a significant proportion of the fauna (*Belodella* greater than 5% and *Polygnathus* plus *Belodella* greater than 80%), but the belodellid element counts are divided by five to give a more appropriate proportion of individuals. The proportions of each genus in the fauna, as well as the raw counts, are displayed (fig. 27). By pressing buttons the user can display the data as a bar chart (fig. 28) or as a pie chart (fig. 29). Although normally used for a single sample, partial or multiple samples can be similarly analyzed by forming an appropriate selection with the search procedures.

The Analyze Biofacies option can also be chosen by typing command-B.

Menu column: Analyze Option: Non Pa

This option summarizes counts of those elements not included in the biofacies analysis (fig. 30). These are sorted into the categories shown in table 2. As these categories were set up primarily for analysis of Late Devonian faunas, faunas of other ages will give less detailed results. Although normally used for a single sample, partial or multiple samples can be similarly analyzed by forming an appropriate selection with the search procedures.

Menu column: Analyze Option: All four analyses

This option consecutively performs all four of the previously described analyses: Totals, Averaged data, Biofacies, and Non Pa.

This option can also be chosen by typing command-F.

Menu column: Analyze   Option: Range chart

This option constructs a range chart for as many as four taxa. The user is first given a choice of constructing the chart based on the current selection or on the entire file. The former allows the user to construct charts for specific conditions, for example, only for North American occurrences. The user is then given the choice of using only samples with well-defined dates or of also using less-well-dated samples. The user is queried as to the taxonomic level and then may enter the taxonomic name through the keyboard or from choice lists. This process is repeated as many as four times, until the user indicates that there are no more taxa to be added.

The resulting chart (fig. 31) is scrollable. Solid bars indicate that a sample including that taxon has been identified for a particular zone. Dashed bars indicate that no samples with the taxon have been found for the particular zone, but that older and younger zones have yielded samples with the taxon. The numbers adjacent to the bars indicate the number of samples with the taxon for that zone. Clicking on a zone name and then clicking on the "Samples in Zone" button will display the sample numbers for those samples containing one or more of the taxa in the chart (fig. 32). Another button allows the option of sending the range chart to a printer. (**Tip:** If the user mistakenly clicks in the main window while the list of sample numbers is displayed, the list of sample numbers will be hidden under the main window. Because the system will not allow continuation until the list window is closed, press the "Enter" key.)

The Analyze Range chart option can also be chosen by typing command-R.

Menu column: Analyze   Option: Taxon range

This option calculates the range of a given taxon, either based on the entire database or on the current selection. The user may choose to use only samples with well-defined dates or to also use less well dated samples. The user is queried as to the taxonomic level and then may enter the taxonomic name through the keyboard or from choice lists. The resulting range is presented on the screen (fig. 33).

Menu column: Analyze   Option: Most common taxa

This option uses the current selection of the *Species* file, presenting the taxa in order of decreasing occurrence, as well as calculating the percentage of each taxon. The percents are calculated relative to only those samples that include the particular taxon, thus the sum of the percents in the list may be greater than 100. The user chooses the taxonomic level for the list. Only Pa and I elements are used in the calculations; all other element types are ignored. The results are presented in a scrollable list (fig. 34).

Menu column: Analyze Option: Most common associates
This option finds the taxa that are associated in the same samples as an identified taxon, either from the database as a whole or from the current selection. It presents the taxa in order of decreasing occurrence and calculates the percentage of each taxon. The percents are calculated relative to only those samples that include the particular taxon, thus the sum of the percents in the list may be greater than 100. Only Pa and I elements are used in the calculations, all other element types are ignored. The results are presented in a scrollable list (fig. 35).

User tips

Locality names and sample numbers are used to relate the three main files. It is highly recommended that these be stabilized before entering them into the database. Changing a sample number, for example, requires changing both the sample record and the associated species records. This can be accomplished, but with some difficulty. The problem occurs in that once the sample record is changed, the species records cannot be retrieved by sample number, but must be found by some other method of search.

Locality records must be entered before any of their related sample records. This allows the locality names to be entered into a choice list used in the *Samples* file input. Names must be chosen from this choice list when entering sample records so that the relation between the files will be assured.

Note that much use is made of choice lists and default values, especially for *Species* file input. The choice lists and defaults for a specific field can change because of input to other fields. Thus the choice list for **Trivial name** is determined by what generic name was entered for **Genus**. Similarly, Pa is the default **Element** value but entry of "Icriodus" for **Genus** resets the default **Element** value to "I".

Modification of database for non-Devonian/Carboniferous applications

Users wishing to tailor this database to their own applications will mainly need to change the lists to reflect their taxa and zones. The records in the *Zones* file and the global procedure "Encode age" will also need to reflect the zones for the particular application.

For a non-Devonian/Carboniferous conodont application or for a non-conodont application, the taxonomic lists will need to be changed. The "Genera list" should contain items appropriate to the application. All species and subspecies lists should be replaced by appropriate taxonomic lists. The zonal and biofacies lists also should be changed to more appropriate ones. As new lists cannot be created from the runtime environment, all revisions should be made from the design environment.

The zones are related to a numeric coding scheme listed in both the global procedure "Encode age" and in the *Zones* file records. Both of these must be changed to implement any different zonal framework. Note that these codes are also used in *Sample* layout "Paper file" in the script for field **Biofacies** on page 3.

The analytical procedures "Totals", "Averaged data", "Biofacies", and "Non Pa" are meant to be specific to the current application and may not be appropriate to the user's application without some reprogramming.

Further Information

Updated versions of this software are anticipated. Features likely to be added to later versions include additional layouts to conform to larger or color monitors and easier creation and modification of taxonomic lists. User comments are welcome and should be addressed to:

Ronald R. Charpentier
U.S. Geological Survey
MS 940 Box 25046
Denver Federal Center
Denver, CO 80225-0046

Users can be placed on a mailing list for information concerning future updates by contacting the senior author at the above address.

Further information concerning the techniques of biofacies analysis or of averaging large conodont samples by a random box count method should be addressed to Charles A. Sandberg at the same address.

References Cited

Charpentier, R.R., and Sandberg, C.A., 1990, Biofacies analysis of Late Devonian conodonts using a computer database: Geological Society of America Abstracts with Programs, v. 22, no. 1, p. 4.

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Sandberg, C. A., and Ziegler, W., 1973, Refinement of standard Upper Devonian conodont zonation based on sections in Nevada and West Germany: Geologica et Palaeontologica, v. 7, p. 97–122, 5 pls.

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Sandberg, C.A., Ziegler, W., and Bultynck, P., 1989, New standard conodont zones and early *Ancyrodella* phylogeny across Middle-Upper Devonian boundary: Courier Forschungsinstitut Senckenberg, v. 110, p. 195–230, 5 pls., 4 figs.

Sandberg, C.A., Ziegler, W., Dreesen, R., and Butler, J.L., 1988, Late Frasnian mass extinction; conodont event stratigraphy, global changes, and possible causes, *in* Ziegler, W., ed., 1st International Senckenberg Conference and 5th European Conodont Symposium (ECOS V), Contribution 1: Courier Forschungsinstitut Senckenberg, v. 102, p. 263–307, 2 pls., 15 figs., 6 tables.

Ziegler, W., and Sandberg, C.A., 1990, The Late Devonian standard conodont zonation: Courier Forschungsinstitut Senckenberg, v. 121, 115 p., 17 pls., 11 figs., 7 tables.

Table 1
List Names

Taxonomic names

Genera list — the choice list for generic names

Palmatolepis sp — an example of the naming convention for lists of trivial or specific names for a particular genus, that is the generic name plus " sp"

Palmatolepis gigas ssp — an example of the naming convention for lists of subspecific/morphotype names for a particular species, that is the generic name, a space, the trivial name, plus " ssp"

Element names

Elements — the normal choice list for element names

Icriodontid elements — the choice list for elements of such genera as *Icriodus*

Biofacies names

U Devonian biofacies — the choice list used for biofacies names with Devonian samples

Carb biofacies — the choice list used for biofacies names with Carboniferous samples

Zone names

Zones — a choice list giving the names of the other stage-level lists

Pennsylvanian zones — a choice list giving the names of Pennsylvanian zones, and some combinations of them

Chesterian zones — a choice list giving the names of Chesterian zones, and some combinations of them

Meramecian zones — a choice list giving the names of Meramecian zones, and some combinations of them

Osagean zones — a choice list giving the names of Osagean zones, and some combinations of them

Kinderhookian zones — a choice list giving the names of standard Kinderhookian zones, and some combinations of them

Famennian zones — a choice list giving the names of standard Famennian zones, and some combinations of them

Frasnian zones — a choice list giving the names of standard Frasnian zones, and some combinations of them

Givetian zones — a choice list giving the names of Givetian zones, and some combinations of them

Eifelian zones — a choice list giving the names of Eifelian zones, and some combinations of them

Early Devonian zones — a choice list giving the names of Early Devonian zones, and some combinations of them

All zones — a choice list giving the names of all the cited zones, and some combinations of them

Miscellaneous

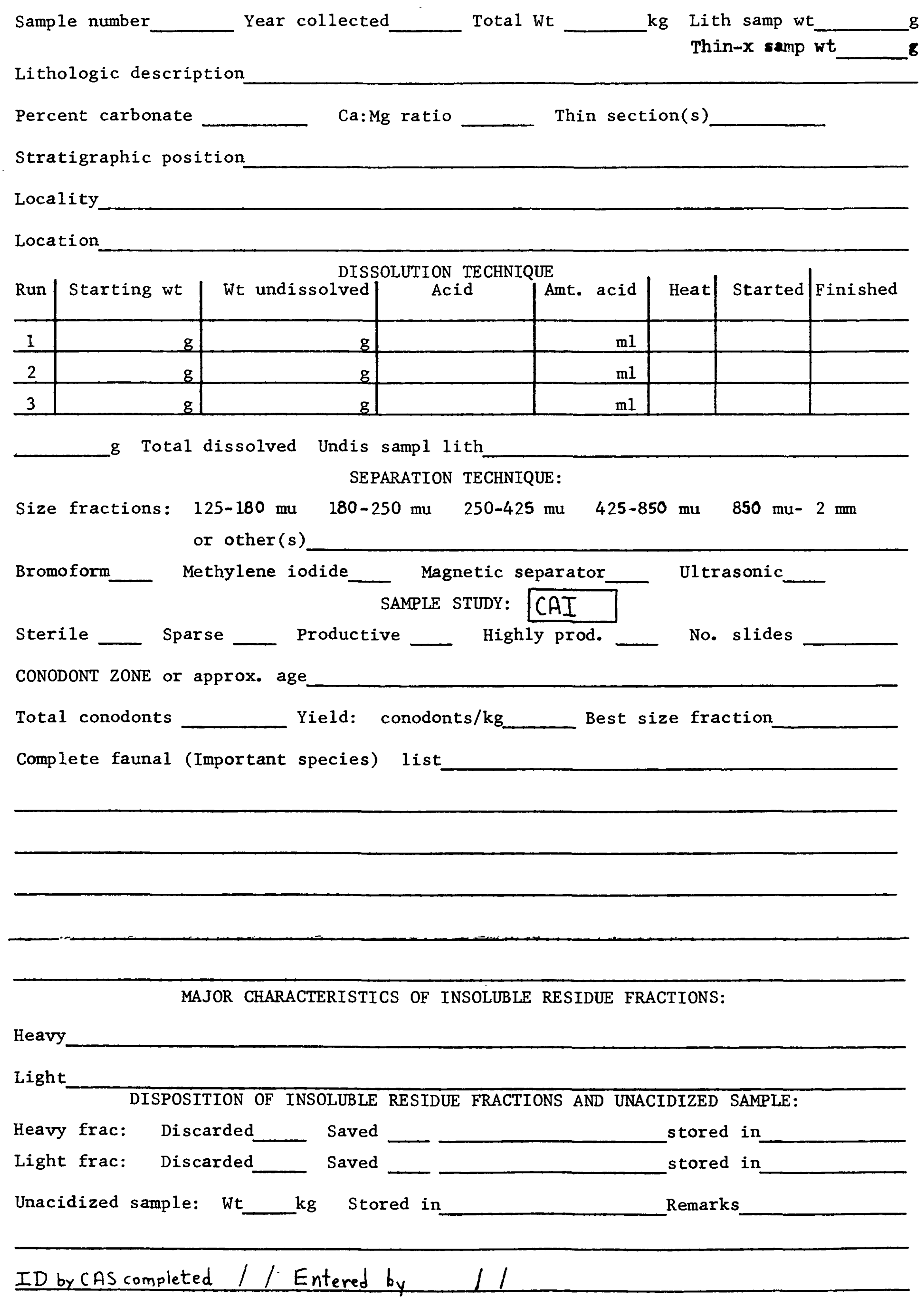
acids — a choice list showing the possible acids used for sample preparation

Locality list — a choice list of all the locality names from the *Localities* file, used in *Samples* file input to assure consistency in naming

Size ranges of HVF — a choice list of size ranges of the heavy fraction, used in *Species* file input

Table 2
Categories for Analysis "Non-Pa"

Palmatolepis Pb
Ancyrodella Pb
Ancyrognathus Pb
Mesotaxis Pb
Apatognathus Pb
Other Pb
Palmatolepis apparatus
Ancyrodella apparatus
Ancyrognathus apparatus
Mesotaxis apparatus
Polygnathus apparatus
Pandorinellina apparatus
Belodella
Panderodus/Neopanderodus
simple cones
Other ramiforms
reworked
Unidentified conodonts



Sample number______ Year collected______ Total Wt ______kg Lith samp wt______g

Thin-x samp wt______g

Lithologic description______

Percent carbonate ______ Ca:Mg ratio ______ Thin section(s)______

Stratigraphic position______

Locality______

Location______

DISSOLUTION TECHNIQUE

Run	Starting wt	Wt undissolved	Acid	Amt. acid	Heat	Started	Finished
1	g	g		ml			
2	g	g		ml			
3	g	g		ml			

______g Total dissolved Undis sampl lith______

SEPARATION TECHNIQUE:

Size fractions: 125-180 mu 180-250 mu 250-425 mu 425-850 mu 850 mu- 2 mm

or other(s)______

Bromoform____ Methylene iodide____ Magnetic separator____ Ultrasonic____

SAMPLE STUDY: CAI

Sterile ____ Sparse ____ Productive ____ Highly prod. ____ No. slides ______

CONODONT ZONE or approx. age______

Total conodonts ______ Yield: conodonts/kg______ Best size fraction______

Complete faunal (Important species) list______

MAJOR CHARACTERISTICS OF INSOLUBLE RESIDUE FRACTIONS:

Heavy______

Light______

DISPOSITION OF INSOLUBLE RESIDUE FRACTIONS AND UNACIDIZED SAMPLE:

Heavy frac: Discarded____ Saved ____ ______stored in______

Light frac: Discarded____ Saved ____ ______stored in______

Unacidized sample: Wt____kg Stored in______Remarks______

ID by CAS completed / / Entered by / /

FIGURE 1. — Example of paper form used for recording sample data

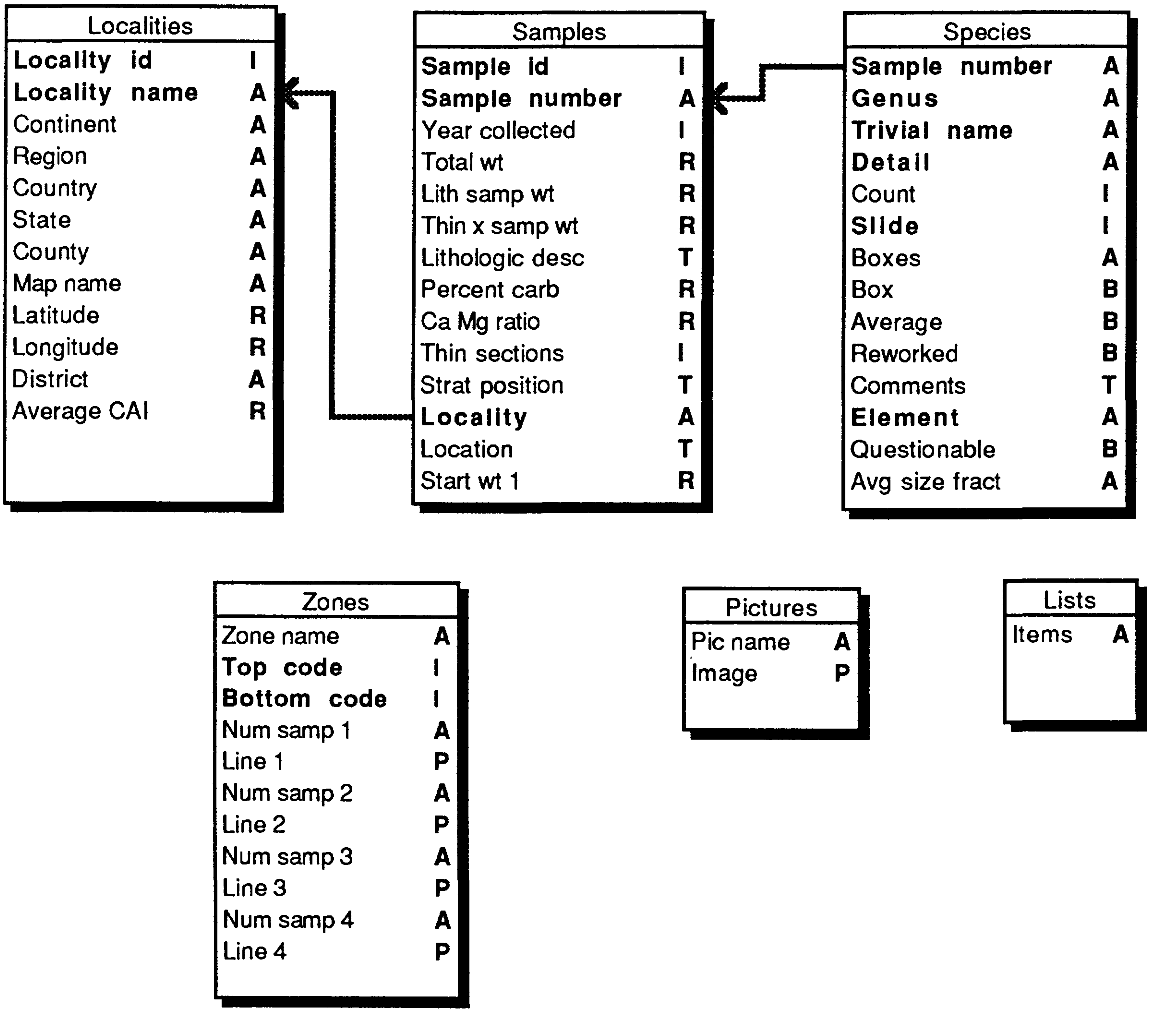


FIGURE 2. — Structure of the database showing files, their relations, and fields (Note that the file *Samples* also includes 69 other fields.)

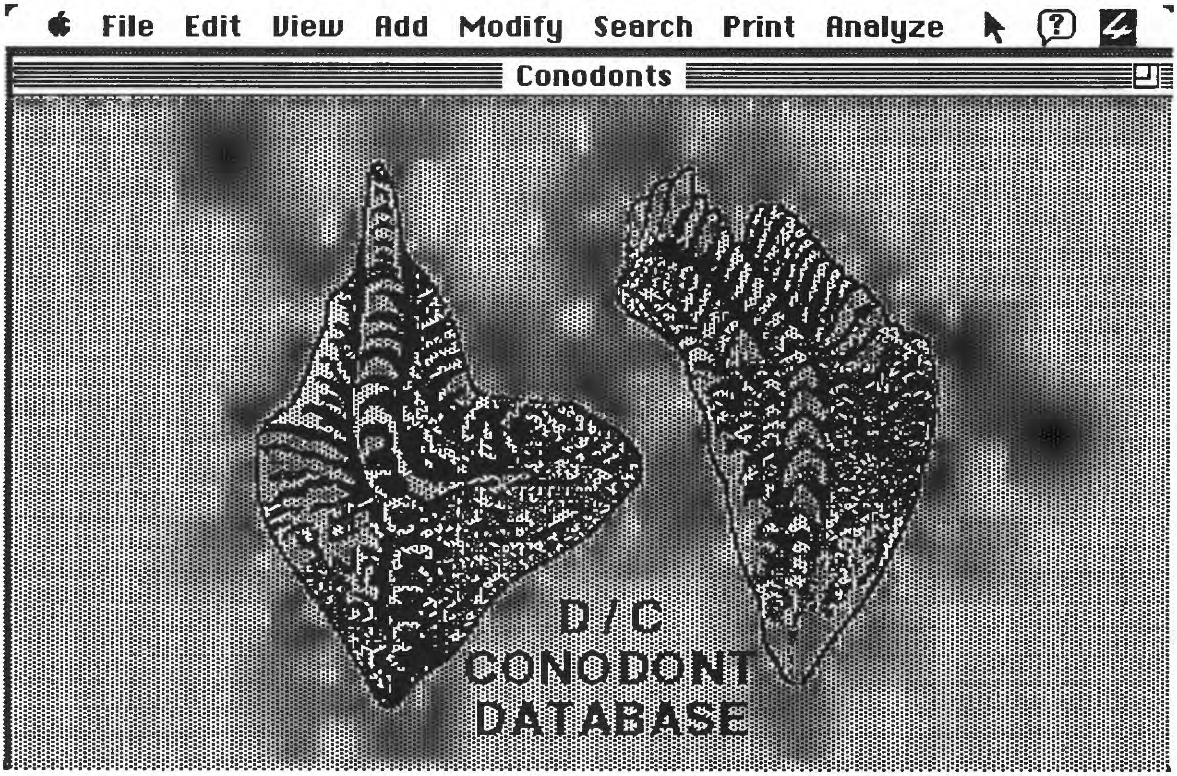
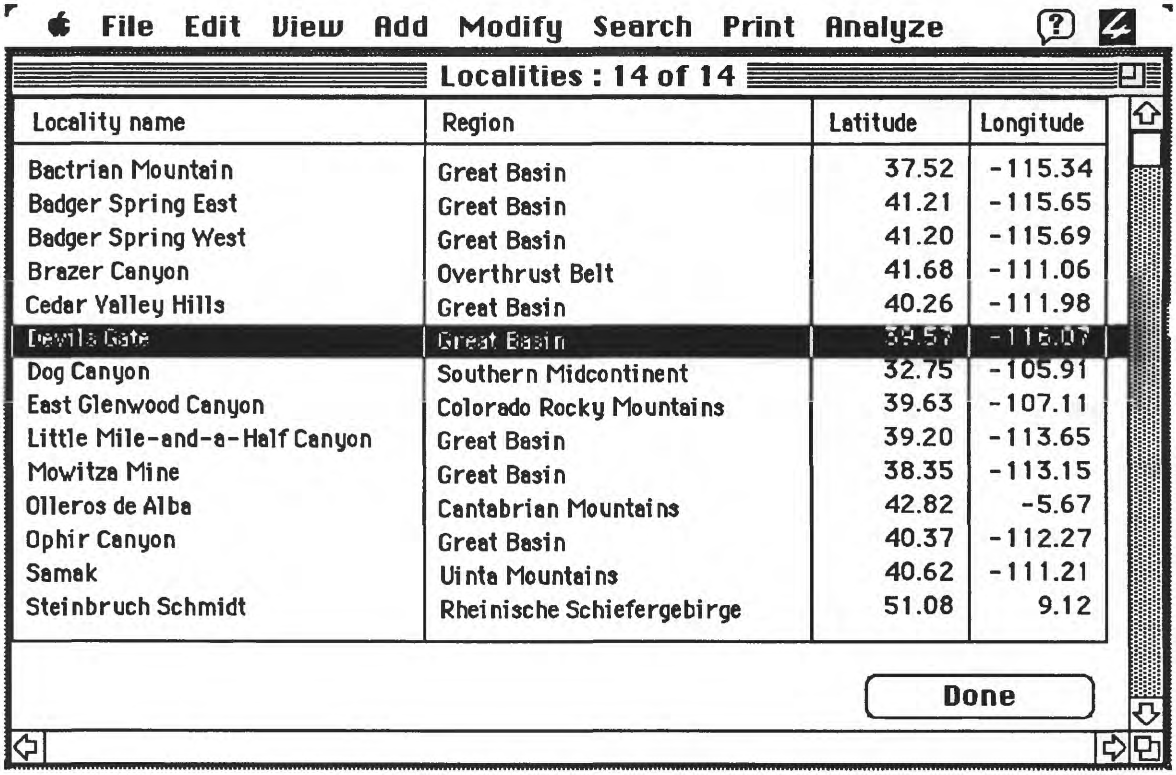


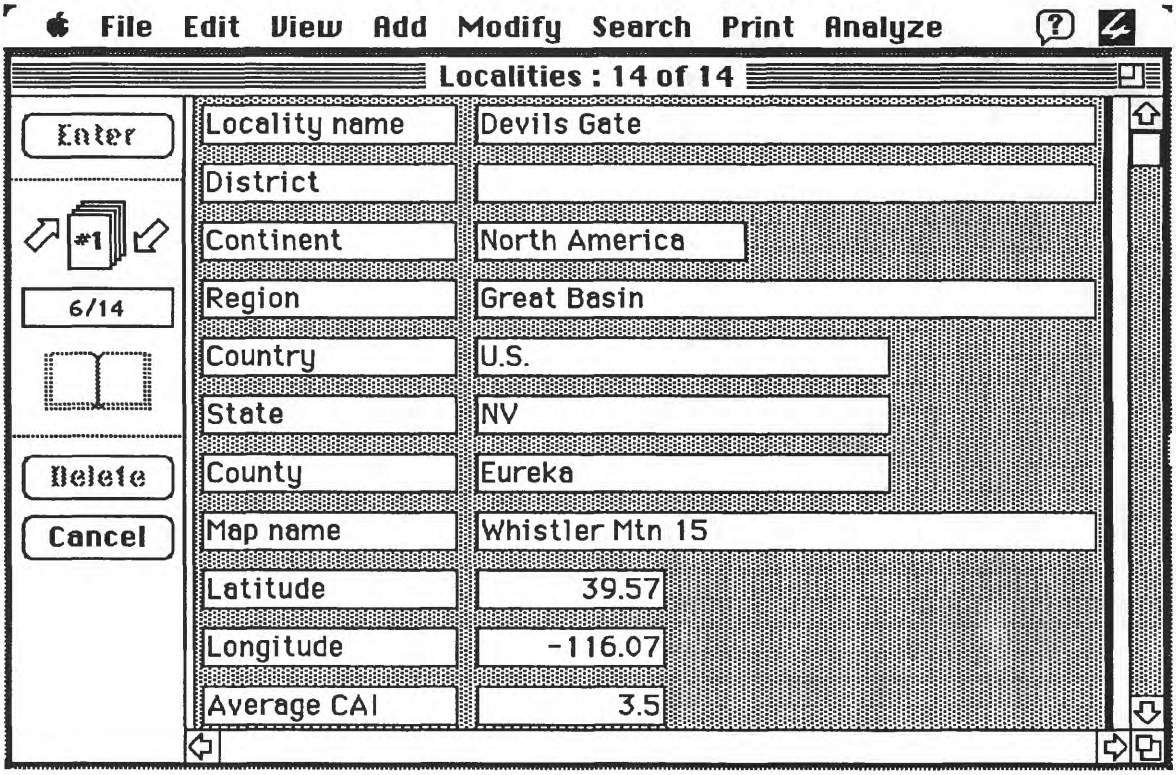
FIGURE 3. — Main screen for the database showing eight main menu columns



Localities : 14 of 14

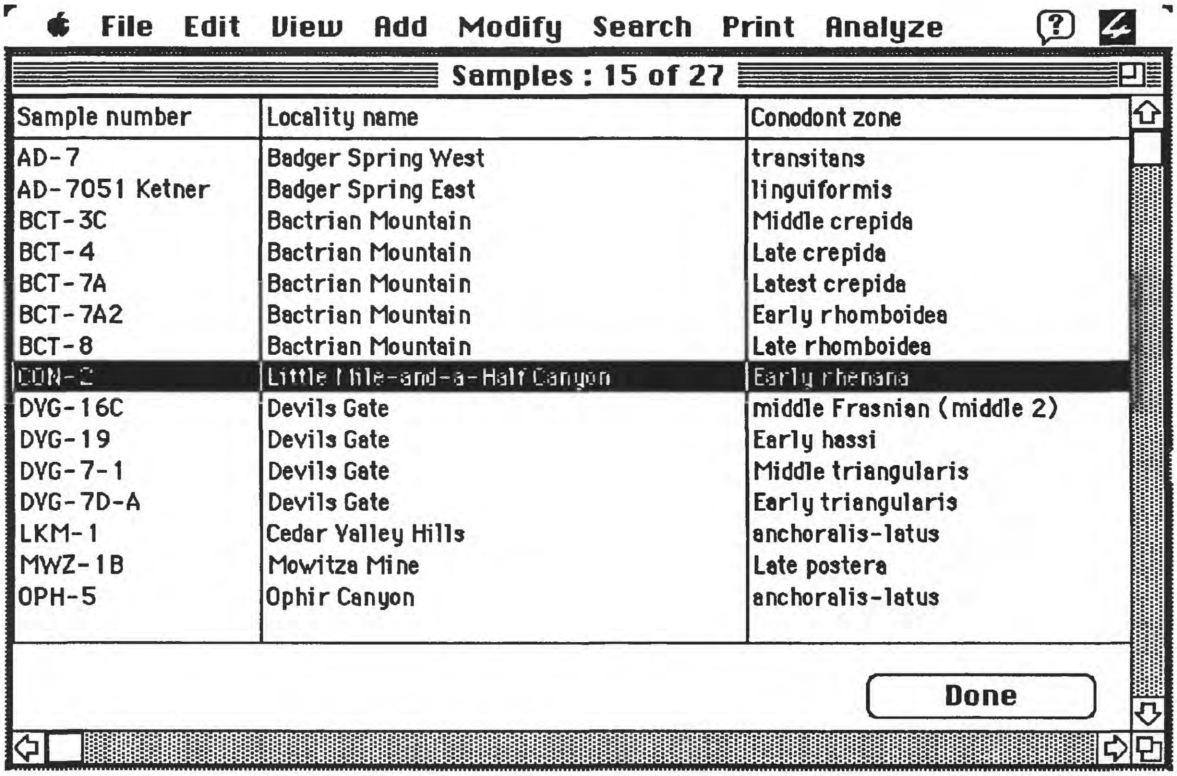
Locality name	Region	Latitude	Longitude
Bactrian Mountain	Great Basin	37.52	-115.34
Badger Spring East	Great Basin	41.21	-115.65
Badger Spring West	Great Basin	41.20	-115.69
Brazer Canyon	Overthrust Belt	41.68	-111.06
Cedar Valley Hills	Great Basin	40.26	-111.98
Devils Gate	Great Basin	39.57	-116.07
Dog Canyon	Southern Midcontinent	32.75	-105.91
East Glenwood Canyon	Colorado Rocky Mountains	39.63	-107.11
Little Mile-and-a-Half Canyon	Great Basin	39.20	-113.65
Mowitza Mine	Great Basin	38.35	-113.15
Olleros de Alba	Cantabrian Mountains	42.82	-5.67
Ophir Canyon	Great Basin	40.37	-112.27
Samak	Uinta Mountains	40.62	-111.21
Steinbruch Schmidt	Rheinische Schiefergebirge	51.08	9.12

FIGURE 4. — Multiple record format used by View Localities.



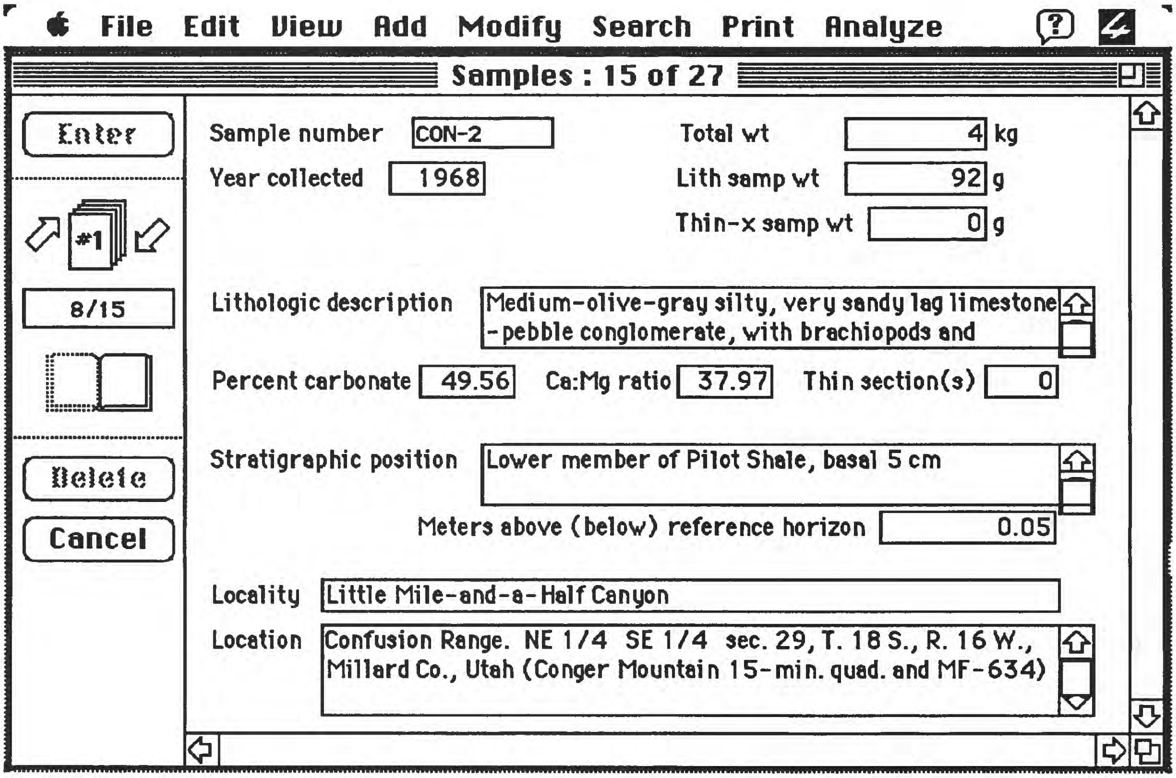
Locality name	Devils Gate
District	
Continent	North America
Region	Great Basin
Country	U.S.
State	NV
County	Eureka
Map name	Whistler Mtn 15
Latitude	39.57
Longitude	-116.07
Average CAI	3.5

FIGURE 5. — Single record format used by View Localities



Sample number	Locality name	Conodont zone
AD-7	Badger Spring West	transitans
AD-7051 Ketner	Badger Spring East	linguiformis
BCT-3C	Bactrian Mountain	Middle crepida
BCT-4	Bactrian Mountain	Late crepida
BCT-7A	Bactrian Mountain	Latest crepida
BCT-7A2	Bactrian Mountain	Early rhomboidea
BCT-8	Bactrian Mountain	Late rhomboidea
CON-2	Little Mile-and-a-Half Canyon	Early rhenana
DVG-16C	Devils Gate	middle Frasnian (middle 2)
DVG-19	Devils Gate	Early hassi
DVG-7-1	Devils Gate	Middle triangularis
DVG-7D-A	Devils Gate	Early triangularis
LKM-1	Cedar Valley Hills	anchoralis-latus
MWZ-1B	Mowitza Mine	Late postera
OPH-5	Ophir Canyon	anchoralis-latus

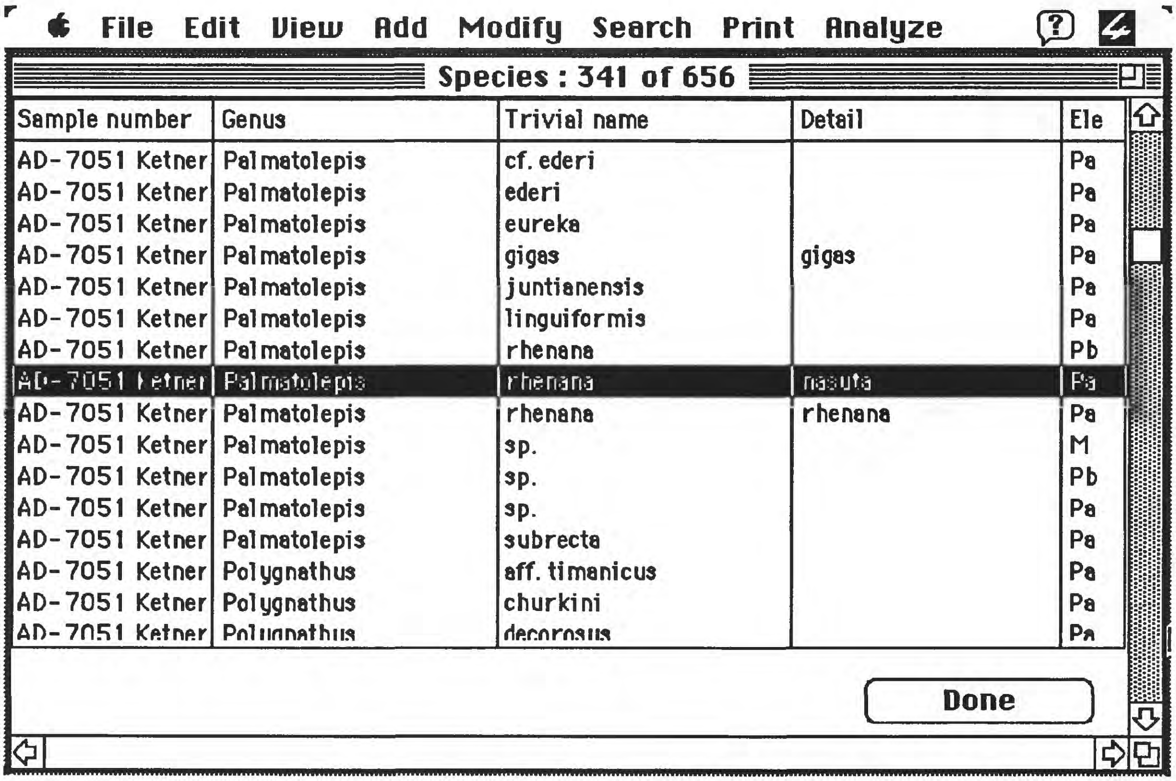
FIGURE 6. — Multiple record format used by View Samples



Samples : 15 of 27

Sample number CON-2
Year collected 1968
Total wt 4 kg
Lith samp wt 92 g
Thin-x samp wt 0 g
Lithologic description Medium-olive-gray silty, very sandy lag limestone -pebble conglomerate, with brachiopods and
Percent carbonate 49.56
Ca:Mg ratio 37.97
Thin section(s) 0
Stratigraphic position Lower member of Pilot Shale, basal 5 cm
Meters above (below) reference horizon 0.05
Locality Little Mile-and-a-Half Canyon
Location Confusion Range. NE 1/4 SE 1/4 sec. 29, T. 18 S., R. 16 W., Millard Co., Utah (Conger Mountain 15-min. quad. and MF-634)

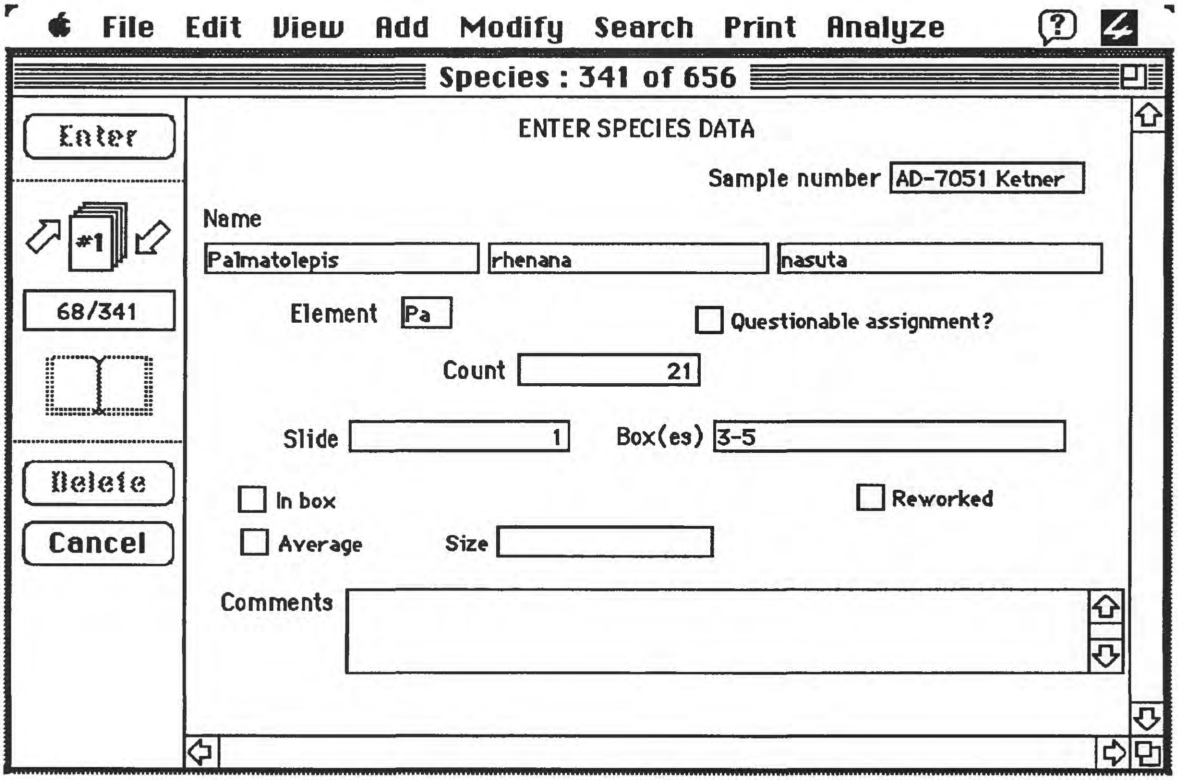
FIGURE 7. — Single record format used by View Samples



Species : 341 of 656

Sample number	Genus	Trivial name	Detail	Ele
AD-7051 Ketner	Palmatolepis	cf. ederi		Pa
AD-7051 Ketner	Palmatolepis	ederi		Pa
AD-7051 Ketner	Palmatolepis	eureka		Pa
AD-7051 Ketner	Palmatolepis	gigas	gigas	Pa
AD-7051 Ketner	Palmatolepis	juntianensis		Pa
AD-7051 Ketner	Palmatolepis	linguiformis		Pa
AD-7051 Ketner	Palmatolepis	rhenana		Pb
AD-7051 Ketner	Palmatolepis	rhenana	nasuta	Pa
AD-7051 Ketner	Palmatolepis	rhenana	rhenana	Pa
AD-7051 Ketner	Palmatolepis	sp.		M
AD-7051 Ketner	Palmatolepis	sp.		Pb
AD-7051 Ketner	Palmatolepis	sp.		Pa
AD-7051 Ketner	Palmatolepis	subrecta		Pa
AD-7051 Ketner	Polygnathus	aff. timanicus		Pa
AD-7051 Ketner	Polygnathus	churkini		Pa
AD-7051 Ketner	Polygnathus	decorosus		Pa

FIGURE 8. — Multiple record format used by View Species



ENTER SPECIES DATA

Sample number AD-7051 Ketner

Name

Palmatolepis rhenana nasuta

Element Pa

☐ Questionable assignment?

Count 21

Slide 1

Box(es) 3-5

☐ In box

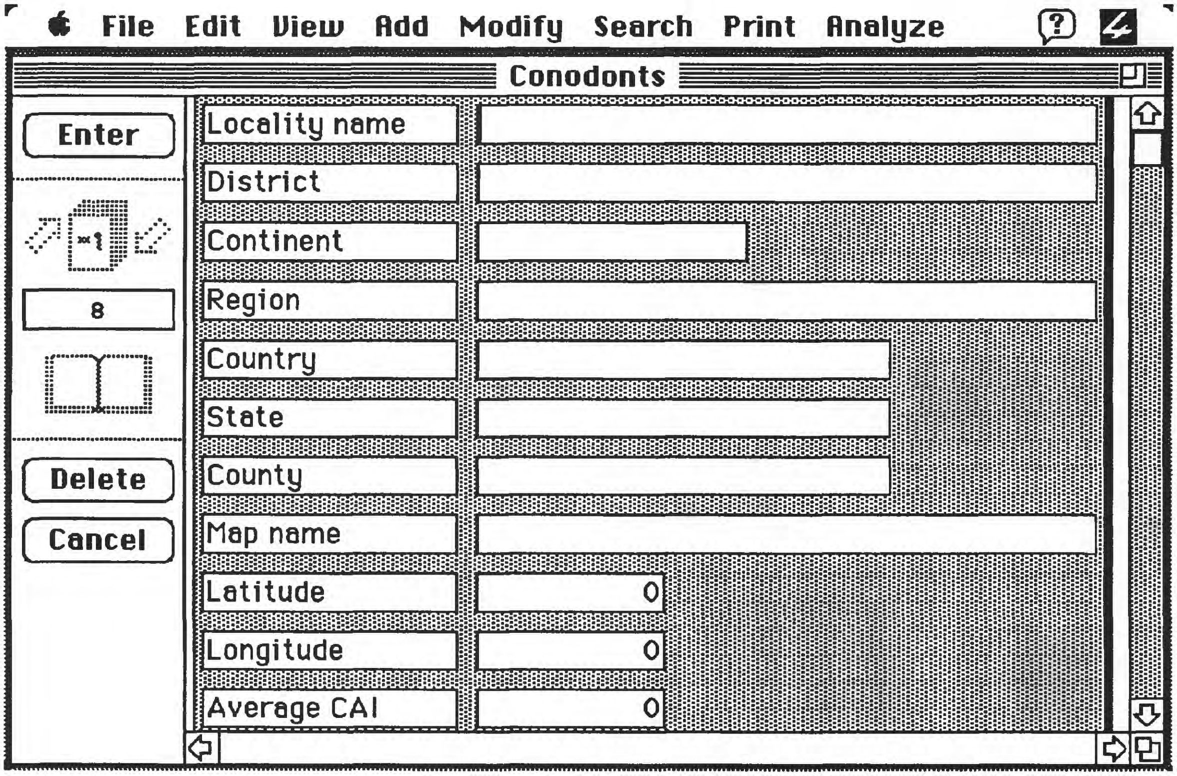
☐ Reworked

☐ Average

Size

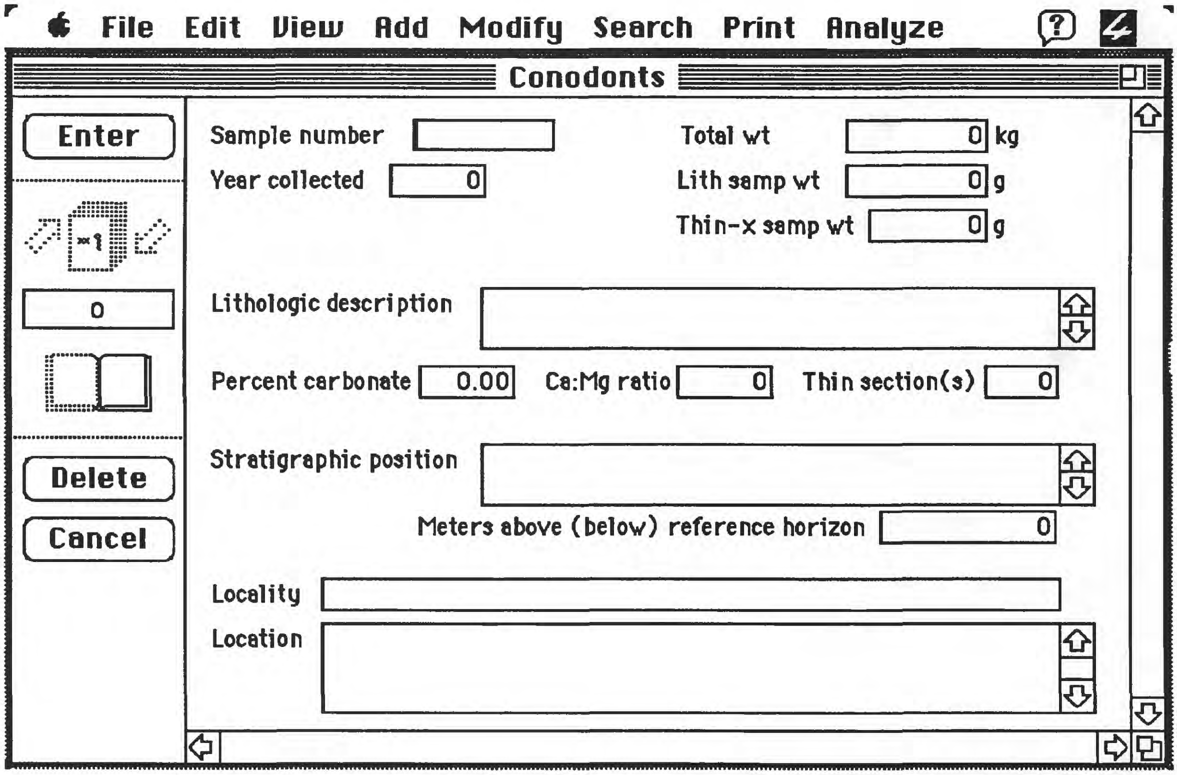
Comments

FIGURE 9. — Single record format used by View Species



Locality name	
District	
Continent	
Region	
Country	
State	
County	
Map name	
Latitude	0
Longitude	0
Average CAI	0

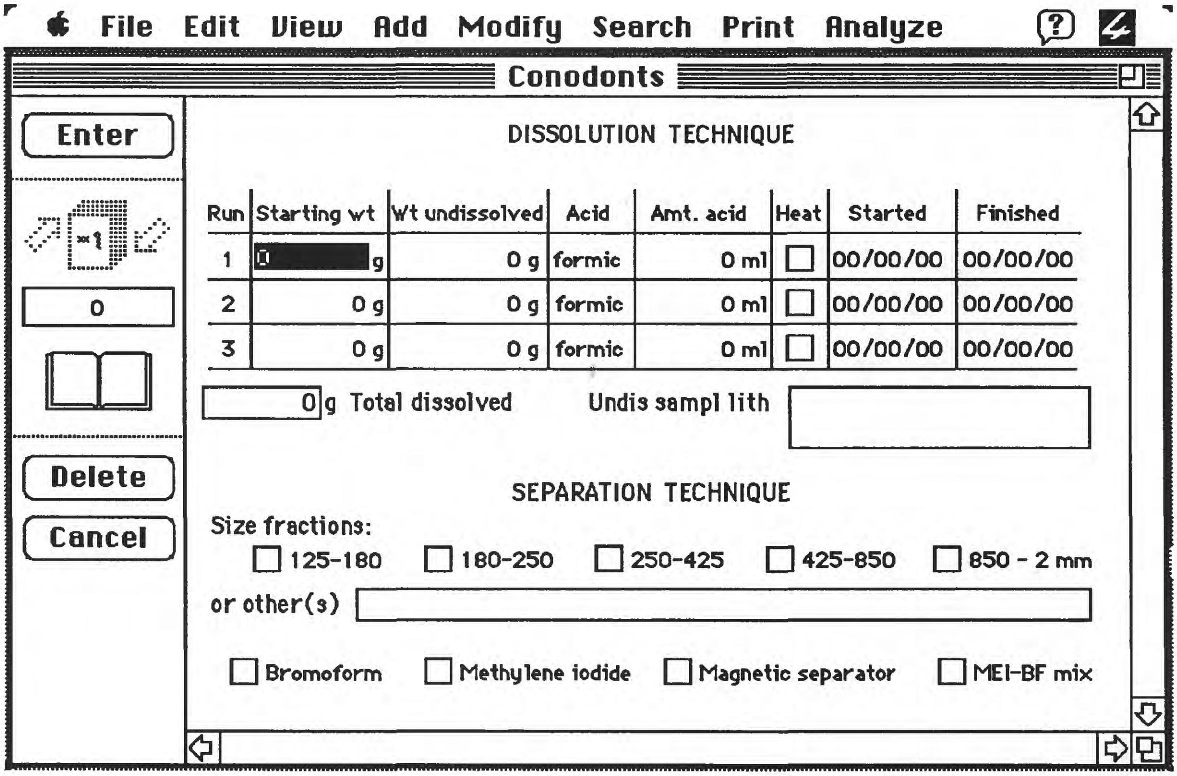
FIGURE 10. — Input format for *Localities*



Sample number
Year collected 0
Total wt 0 kg
Lith samp wt 0 g
Thin-x samp wt 0 g
Lithologic description
Percent carbonate 0.00
Ca:Mg ratio 0
Thin section(s) 0
Stratigraphic position
Meters above (below) reference horizon 0
Locality
Location

0

FIGURE 11. — Input format for *Samples*, page 1



DISSOLUTION TECHNIQUE

Run	Starting wt	Wt undissolved	Acid	Amt. acid	Heat	Started	Finished
1	0 g	0 g	formic	0 ml	☐	00/00/00	00/00/00
2	0 g	0 g	formic	0 ml	☐	00/00/00	00/00/00
3	0 g	0 g	formic	0 ml	☐	00/00/00	00/00/00

0 g Total dissolved

Undis sampl lith

SEPARATION TECHNIQUE

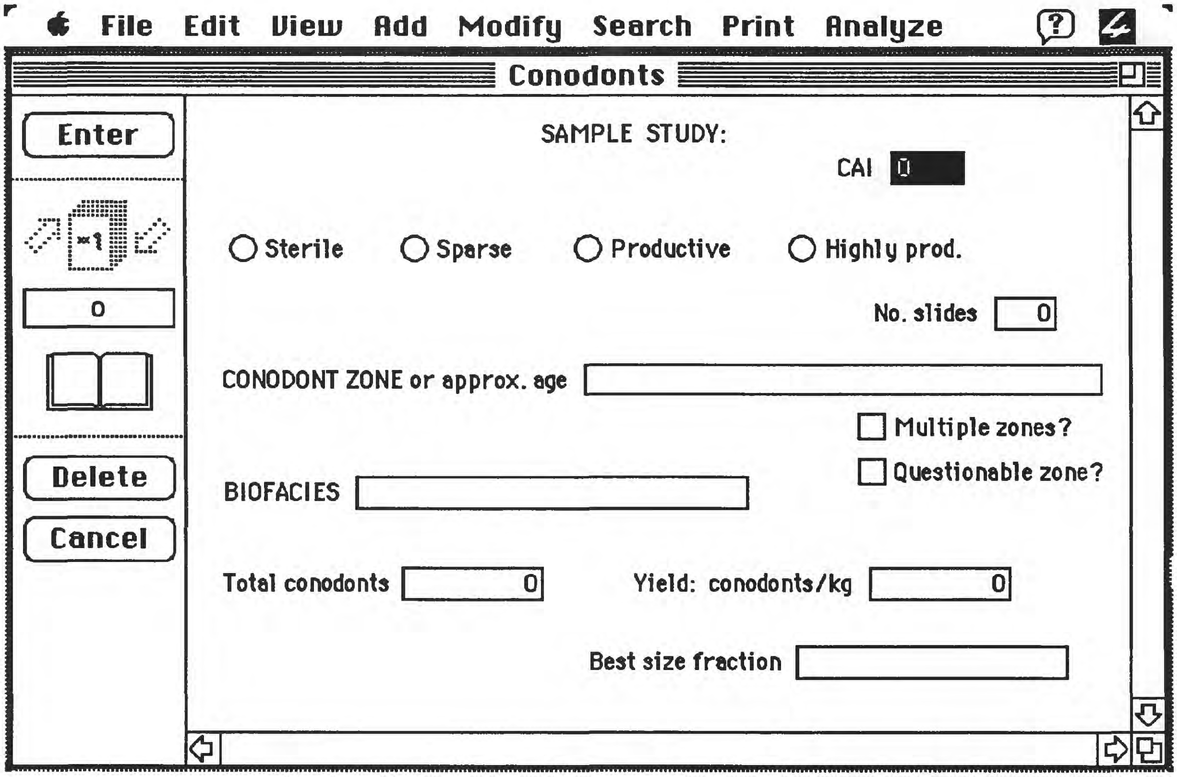
Size fractions:

☐ 125-180 ☐ 180-250 ☐ 250-425 ☐ 425-850 ☐ 850 - 2 mm

or other(s)

☐ Bromoform ☐ Methylene iodide ☐ Magnetic separator ☐ MEI-BF mix

FIGURE 12. — Input format for *Samples*, page 2



SAMPLE STUDY:

CAI 0

○ Sterile ○ Sparse ○ Productive ○ Highly prod.

No. slides 0

CONODONT ZONE or approx. age

☐ Multiple zones?

☐ Questionable zone?

BIOFACIES

Total conodonts 0

Yield: conodonts/kg 0

Best size fraction

FIGURE 13. — Input format for *Samples*, page 3

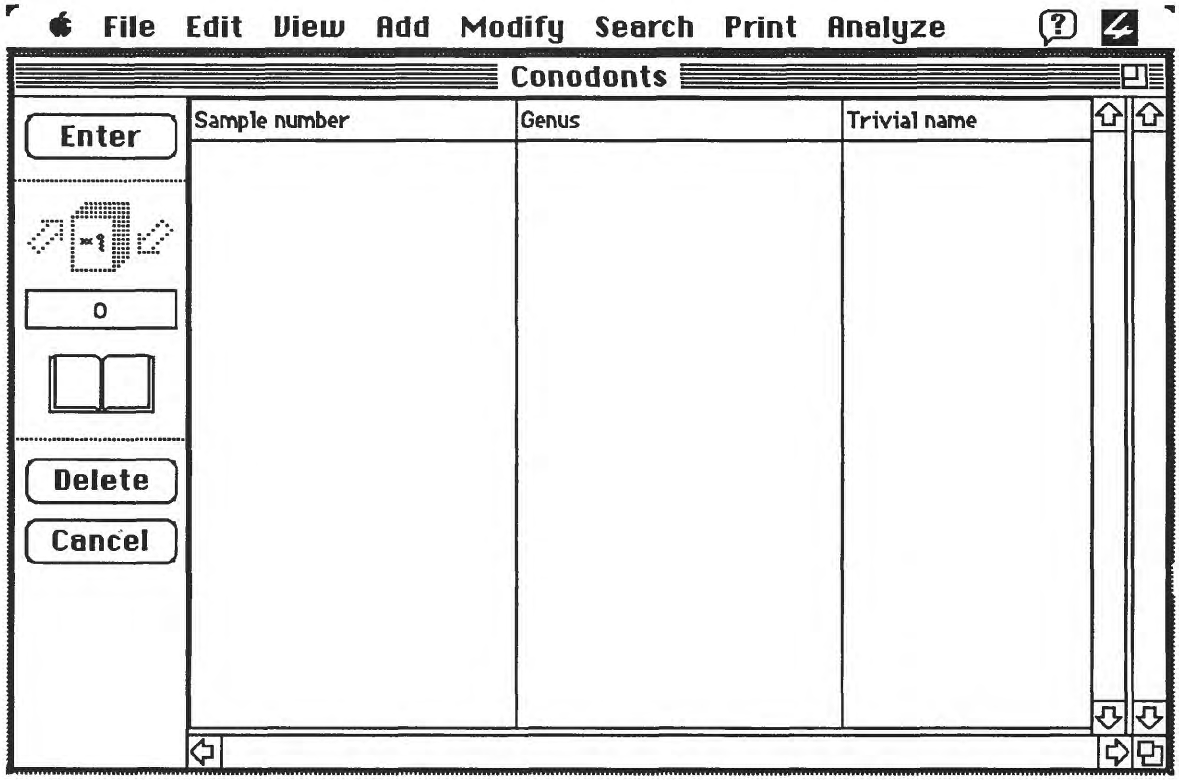
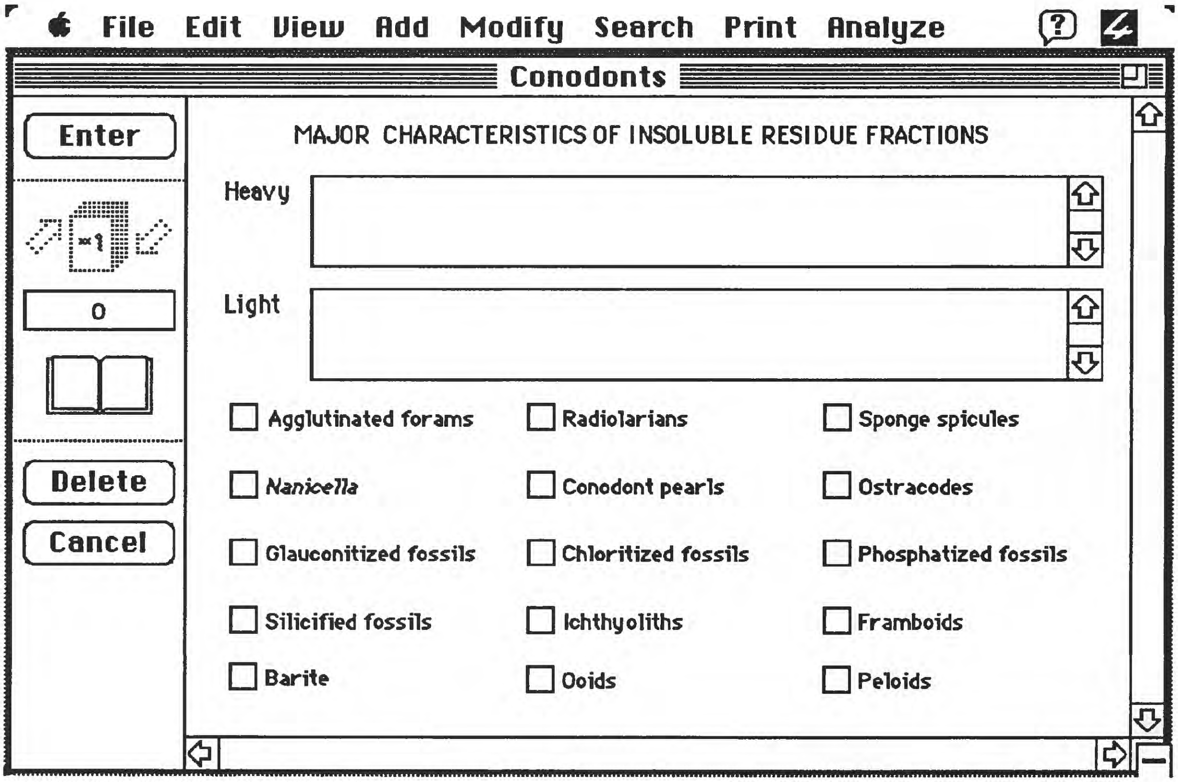


FIGURE 14. — Input format for *Samples*, page 4



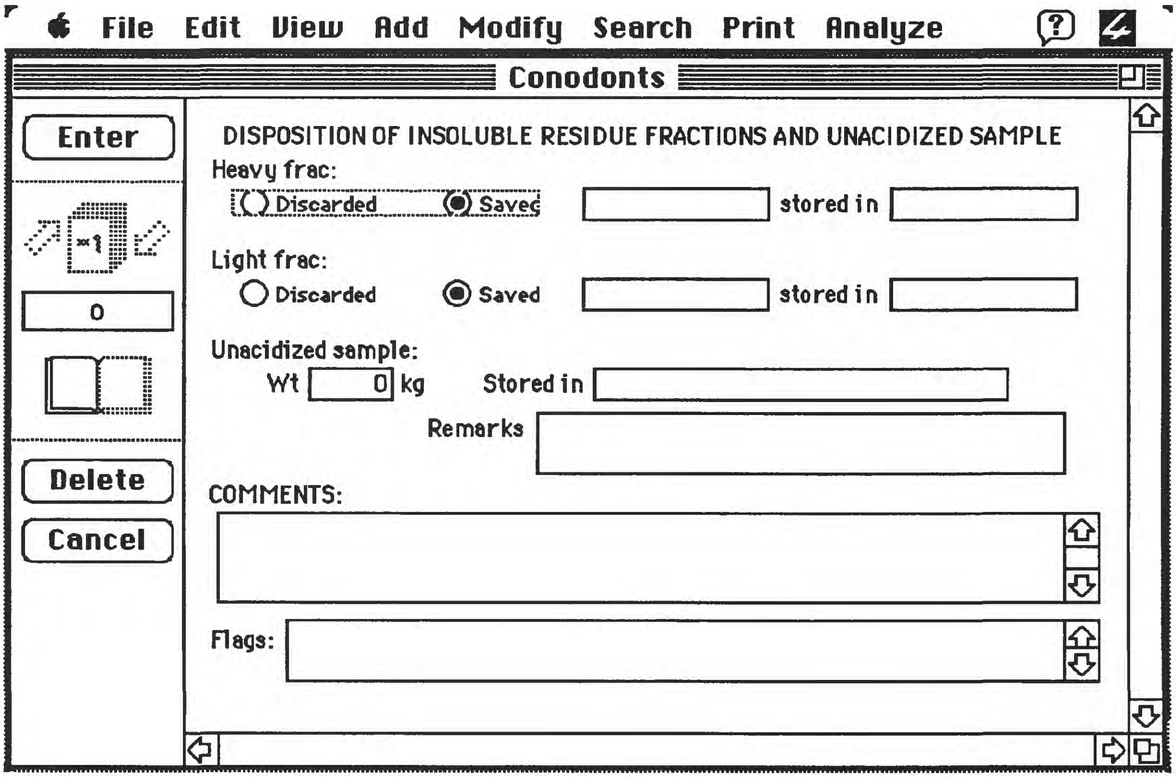
MAJOR CHARACTERISTICS OF INSOLUBLE RESIDUE FRACTIONS

Heavy

Light

- ☐ Agglutinated forams
- ☐ *Nanicella*
- ☐ Glauconitized fossils
- ☐ Silicified fossils
- ☐ Barite
- ☐ Radiolarians
- ☐ Conodont pearls
- ☐ Chloritized fossils
- ☐ Ichthyoliths
- ☐ Ooids
- ☐ Sponge spicules
- ☐ Ostracodes
- ☐ Phosphatized fossils
- ☐ Framboids
- ☐ Peloids

FIGURE 15. — Input format for *Samples*, page 5



DISPOSITION OF INSOLUBLE RESIDUE FRACTIONS AND UNACIDIZED SAMPLE

Heavy frac:
○ Discarded ● Saved stored in

Light frac:
○ Discarded ● Saved stored in

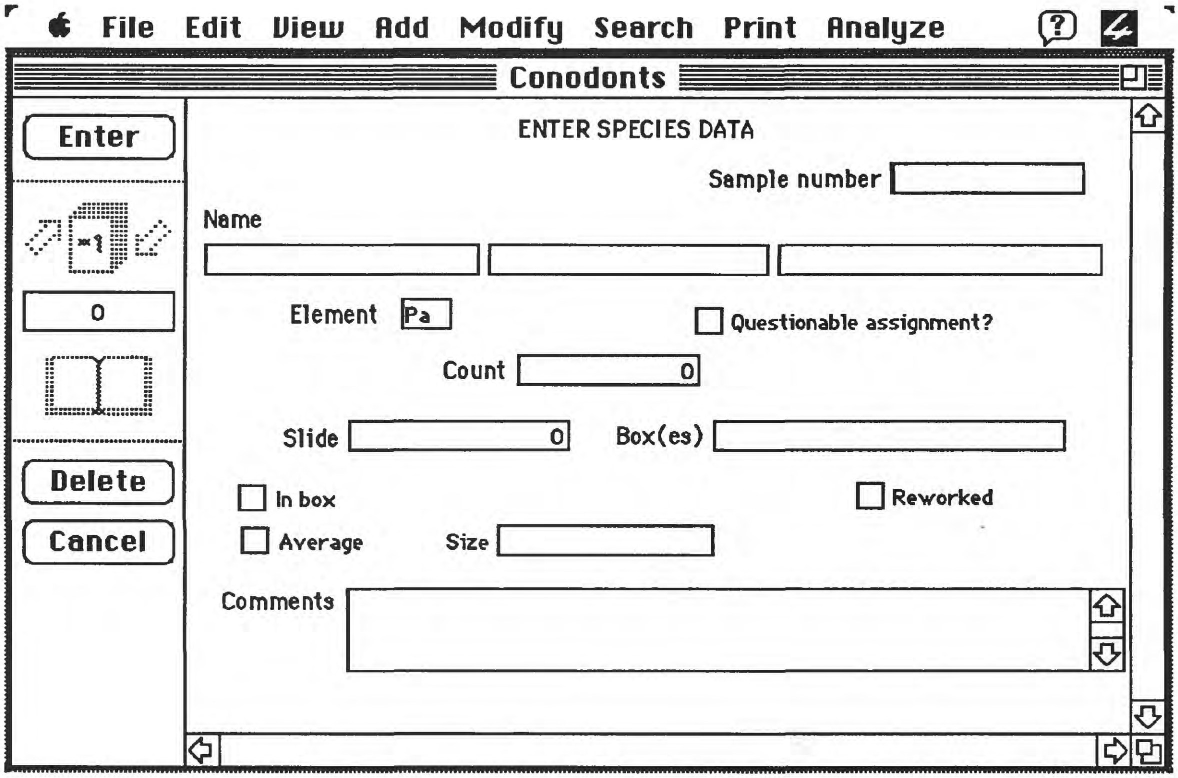
Unacidized sample:
Wt 0 kg Stored in

Remarks

COMMENTS:

Flags:

FIGURE 16. — Input format for *Samples*, page 6



ENTER SPECIES DATA

Sample number

Name

Element Pa

☐ Questionable assignment?

Count 0

Slide 0

Box(es)

☐ In box

☐ Reworked

☐ Average

Size

Comments

FIGURE 17. — Input format for *Species*

Locality name	Region	Latitude	Longitude
Bactrian Mountain	Great Basin	37.52	-115.34
Badger Spring East	Great Basin	41.21	-115.65
Badger Spring West	Great Basin	41.20	-115.69
Brazer Canyon	Overthrust Belt	41.68	-111.06
Cedar Valley Hills	Great Basin	40.26	-111.98
Devils Gate	Great Basin	39.57	-116.07
Dog Canyon	Southern Midcontinent	32.75	-105.91
East Glenwood Canyon	Colorado Rocky Mountains	39.63	-107.11
Little Mile-and-a-Half Canyon	Great Basin	39.20	-113.65
Mowitza Mine	Great Basin	38.35	-113.15
Olleros de Alba	Cantabrian Mountains	42.82	-5.67
Ophir Canyon	Great Basin	40.37	-112.27
Samak	Uinta Mountains	40.62	-111.21
Steinbruch Schmidt	Rheinische Schiefergebirge	51.08	9.12

FIGURE 18. — Output format used by Print Localities

Sample number	Locality name	Conodont zone
83-GER-4	Steinbruch Schmidt	Late rhenana
83-SP-1	Olleros de Alba	anchoralis-latus
83-SP-2	Olleros de Alba	mehli-Lower texanus
83-SP-3	Olleros de Alba	bilineatus-Upper Cavusgnathus
85-GER-78	Steinbruch Schmidt	Early triangularis
AD-7	Badger Spring West	transitans
AD-7051 Ketner	Badger Spring East	linguiformis
BCT-3C	Bactrian Mountain	Middle crepida
BCT-4	Bactrian Mountain	Late crepida
BCT-7A	Bactrian Mountain	Latest crepida
BCT-7A2	Bactrian Mountain	Early rhomboidea
BCT-8	Bactrian Mountain	Late rhomboidea
BZ-3	Brazer Canyon	anchoralis-latus
CON-2	Little Mile-and-a-Half Canyon	Early rhenana
DOG-4	Dog Canyon	anchoralis-latus
DVG-16C	Devils Gate	middle Frasnian (middle 2)
DVG-19	Devils Gate	Early hassi
DVG-7-1	Devils Gate	Middle triangularis
DVG-7D-A	Devils Gate	Early triangularis
EGL-10	East Glenwood Canyon	Late postera
KAM-5	Samak	Upper typicus
KAM-6	Samak	Upper typicus?
KAM-7	Samak	anchoralis-latus
KAM-8	Samak	anchoralis-latus
LKM-1	Cedar Valley Hills	anchoralis-latus
MWZ-1B	Mowitza Mine	Late postera
OPH-5	Ophir Canyon	anchoralis-latus

FIGURE 19. — Output format used by Print Samples

Sample number	Genus	Trivial name	Detail	Ele
83-SP-1	Bispathodus	utahensis		Pb
83-SP-1	Bispathodus	utahensis		Pa
83-SP-1	Doliognathus	latus	MORPHOTYPE 3	Pa
83-SP-1	Doliognathus	latus	MORPHOTYPE 3	Pa
83-SP-1	Doliognathus	latus	MORPHOTYPE 3	Pa
83-SP-1	Doliognathus	latus	MORPHOTYPE 3	Pa
83-SP-1	Doliognathus	latus	MORPHOTYPE 3	Pa
83-SP-1	Gnathodus	cuneiformis		Pa
83-SP-1	Gnathodus	pseudosemiglaber		Pa
83-SP-1	Gnathodus	pseudosemiglaber		Pa
83-SP-1	Gnathodus	pseudosemiglaber		Pa
83-SP-1	Gnathodus	pseudosemiglaber		Pa
83-SP-1	Gnathodus	punctatus		Pa
83-SP-1	indeterminate			M
83-SP-1	indeterminate			Sa
83-SP-1	indeterminate			Sc
83-SP-1	indeterminate			Pb
83-SP-1	indeterminate			Sb
83-SP-1	misc. ramiforms			S
83-SP-1	misc. ramiforms			S
83-SP-1	misc. ramiforms			S
83-SP-1	Polygnathus	bischoffi		Pa
83-SP-1	Polygnathus	communis	communis	Pa
83-SP-1	Protognathodus	cordiformis		Pa
83-SP-1	Pseudopolygnathus	oxypageus	MORPHOTYPE 1	Pa
83-SP-1	Pseudopolygnathus	pinnatus	MORPHOTYPE 2	Pa
83-SP-1	Pseudopolygnathus	pinnatus	MORPHOTYPE 2	Pa
83-SP-1	Pseudopolygnathus	pinnatus	MORPHOTYPE 2	Pa
83-SP-1	Pseudopolygnathus	pinnatus	MORPHOTYPE 2	Pa
83-SP-1	Pseudopolygnathus	pinnatus	MORPHOTYPE 2	Pa
83-SP-1	Siphonodella	obsoleta		Pa

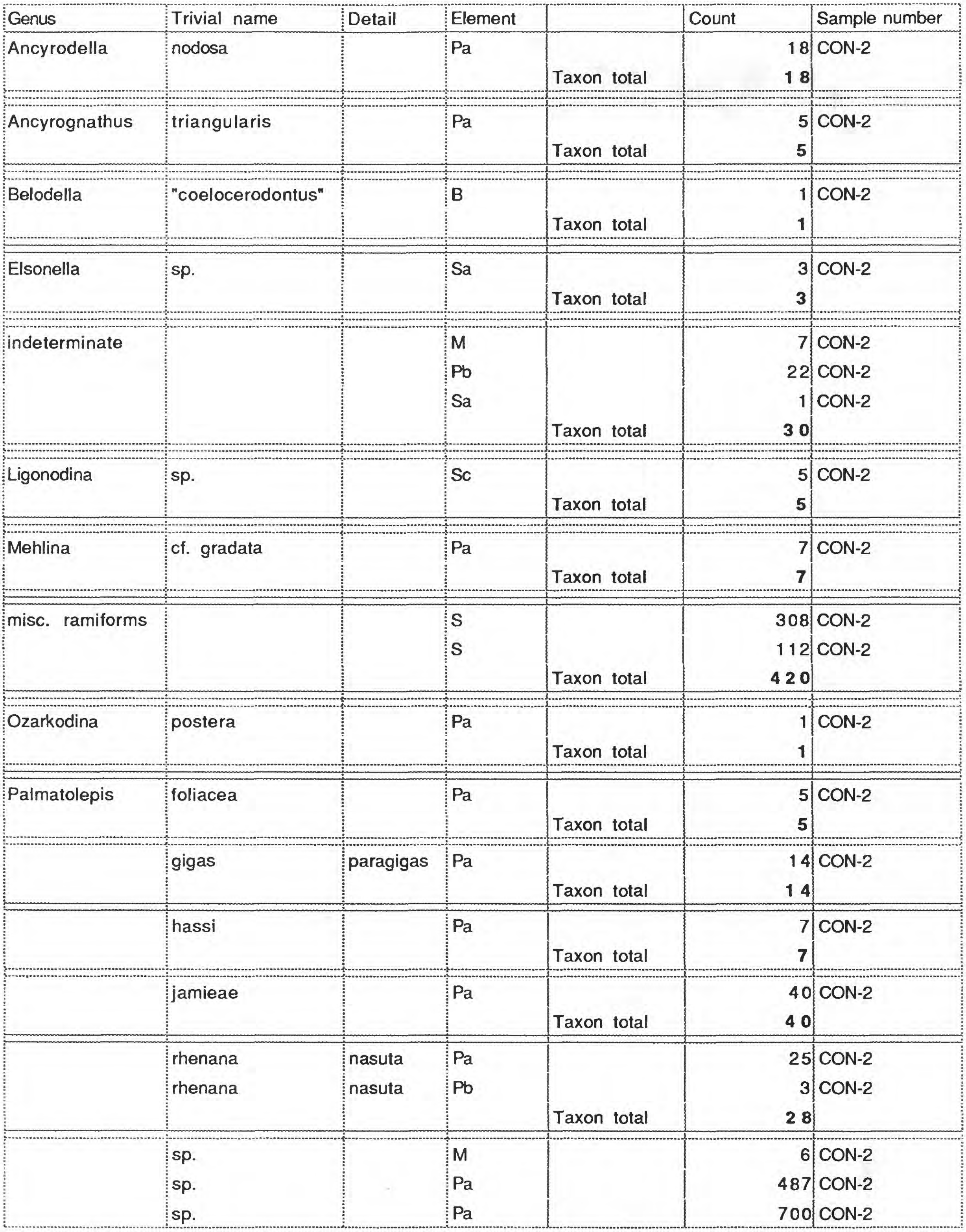
FIGURE 20. — Output format used by Print Species

State	County	Latitude	Longitude	Locality name	Average CAI
		42.82	-5.67	Olleros de Alba	2
CO	Eagle-Garfield line	39.63	-107.11	East Glenwood Canyon	3
Hessen		51.08	9.12	Steinbruch Schmidt	3
NM	Otero	32.75	-105.91	Dog Canyon	3
NV	Elko	41.20	-115.69	Badger Spring West	2.5
NV	Elko	41.21	-115.65	Badger Spring East	2
NV	Eureka	39.57	-116.07	Devils Gate	3.5
NV	Lincoln	37.52	-115.34	Bactrian Mountain	2
UT	Beaver	38.35	-113.15	Mowitza Mine	5
UT	Millard	39.20	-113.65	Little Mile-and-a-Half Canyon	2.5
UT	Rich	41.68	-111.06	Brazer Canyon	2
UT	Summit	40.62	-111.21	Samak	2
UT	Tooele	40.37	-112.27	Ophir Canyon	5
UT	Utah	40.26	-111.98	Cedar Valley Hills	4

FIGURE 21. — Output of *Localities* data in the format "CAI by state" used by Print Report Localities

Latitude	Longitude	State	County	Locality name	Average CAI
32.75	-105.91	NM	Otero	Dog Canyon	3
37.52	-115.34	NV	Lincoln	Bactrian Mountain	2
38.35	-113.15	UT	Beaver	Mowitza Mine	5
39.20	-113.65	UT	Millard	Little Mile-and-a-Half Canyon	2.5
39.57	-116.07	NV	Eureka	Devils Gate	3.5
39.63	-107.11	CO	Eagle-Garfield line	East Glenwood Canyon	3
40.26	-111.98	UT	Utah	Cedar Valley Hills	4
40.37	-112.27	UT	Tooele	Ophir Canyon	5
40.62	-111.21	UT	Summit	Samak	2
41.20	-115.69	NV	Elko	Badger Spring West	2.5
41.21	-115.65	NV	Elko	Badger Spring East	2
41.68	-111.06	UT	Rich	Brazer Canyon	2
42.82	-5.67			Olleros de Alba	2
51.08	9.12	Hessen		Steinbruch Schmidt	3

FIGURE 22. — Output of *Localities* data in the format “CAI report” used by Print Report Localities



Genus	Trivial name	Detail	Element		Count	Sample number
Ancyrodella	nodosa		Pa		18	CON-2
				Taxon total	**18**	
Ancyrognathus	triangularis		Pa		5	CON-2
				Taxon total	**5**	
Belodella	"coelocerodontus"		B		1	CON-2
				Taxon total	**1**	
Elsonella	sp.		Sa		3	CON-2
				Taxon total	**3**	
indeterminate			M		7	CON-2
			Pb		22	CON-2
			Sa		1	CON-2
				Taxon total	**30**	
Ligonodina	sp.		Sc		5	CON-2
				Taxon total	**5**	
Mehlina	cf. gradata		Pa		7	CON-2
				Taxon total	**7**	
misc. ramiforms			S		308	CON-2
			S		112	CON-2
				Taxon total	**420**	
Ozarkodina	postera		Pa		1	CON-2
				Taxon total	**1**	
Palmatolepis	foliacea		Pa		5	CON-2
				Taxon total	**5**	
	gigas	paragigas	Pa		14	CON-2
				Taxon total	**14**	
	hassi		Pa		7	CON-2
				Taxon total	**7**	
	jamieae		Pa		40	CON-2
				Taxon total	**40**	
	rhenana	nasuta	Pa		25	CON-2
	rhenana	nasuta	Pb		3	CON-2
				Taxon total	**28**	
	sp.		M		6	CON-2
	sp.		Pa		487	CON-2
	sp.		Pa		700	CON-2

FIGURE 23. — Output of *Species* data in the format "Taxon tabulation" used by Print Report Species

Genus	Trivial name	Detail	Element		Count	Sample number
Palmatolepis	sp.		Pa		1190	CON-2
	sp.		Pa		280	CON-2
	sp.		Pb		41	CON-2
	sp.		Sa		3	CON-2
	sp.		Sb		3	CON-2
	sp.		Sc		5	CON-2
				Taxon total	**2715**	
Polygnathus	aff. timanicus		Pa		2	CON-2
				Taxon total	**2**	
	morgani		Pa		11	CON-2
				Taxon total	**11**	
	pacificus		Pa		9	CON-2
				Taxon total	**9**	
	sp.		M		8	CON-2
	sp.		Pa		6	CON-2
	sp.		Pa		70	CON-2
	sp.		Pa		21	CON-2
	sp.		Pb		5	CON-2
	sp.		Sa		3	CON-2
	sp.		Sb		2	CON-2
	sp.		Sc		8	CON-2
	sp.		Sd		1	CON-2
				Taxon total	**124**	
	webbi		Pa		19	CON-2
				Taxon total	**19**	
				Grand total	**3464**	

FIGURE 23. — (continued)

CONODONT SAMPLE REPORT

SAMPLE NUMBER: CON-2

LOCALITY: Little Mile-and-a-Half Canyon

LOCATION: Confusion Range. NE 1/4 SE 1/4 sec. 29, T. 18 S., R. 16 W., Millard Co., Utah (Conger Mountain 15-min. quad. and MF-634)

LAT, LONG: 39.20° N, 113.65° W

LITHOLOGIC DESCRIPTION: Medium-olive-gray silty, very sandy lag limestone -pebble conglomerate, with brachiopods and dacryoconarids (Tentaculites)

STRATIGRAPHIC POSITION: Lower member of Pilot Shale, basal 5 cm

FAUNAL LIST (SLIDE ONLY):

TAXON	ELEMENT	COUNT
Ancyrodella nodosa	Pa	18
Ancyrognathus triangularis	Pa	5
Mehlina cf. gradata	Pa	7
Ozarkodina postera	Pa	1
Palmatolepis foliacea	Pa	5
Palmatolepis gigas paragigas	Pa	14
Palmatolepis hassi	Pa	7
Palmatolepis jamieae	Pa	40
Palmatolepis rhenana nasuta	Pa	25
Polygnathus aff. timanicus	Pa	2
Polygnathus morgani	Pa	11
Polygnathus pacificus	Pa	9
Polygnathus sp.	Pa	6
Polygnathus webbi	Pa	19
Belodella "coelocerodontus"	B	1
Elsonella sp.	Sa	3
indeterminate	M	7

FIGURE 24. — Output format used by Print Sample Report

indeterminate	Pb	22
indeterminate	Sa	1
Ligonodina sp.	Sc	5
Palmatolepis rhenana nasuta	Pb	3
Palmatolepis sp.	M	6
Palmatolepis sp.	Pb	41
Palmatolepis sp.	Sa	3
Palmatolepis sp.	Sb	3
Palmatolepis sp.	Sc	5
Polygnathus sp.	M	8
Polygnathus sp.	Pb	5
Polygnathus sp.	Sa	3
Polygnathus sp.	Sb	2
Polygnathus sp.	Sc	8
Polygnathus sp.	Sd	1

ZONE OR AGE: Early rhenana

BIOFACIES: II palmatolepid-polygnathid

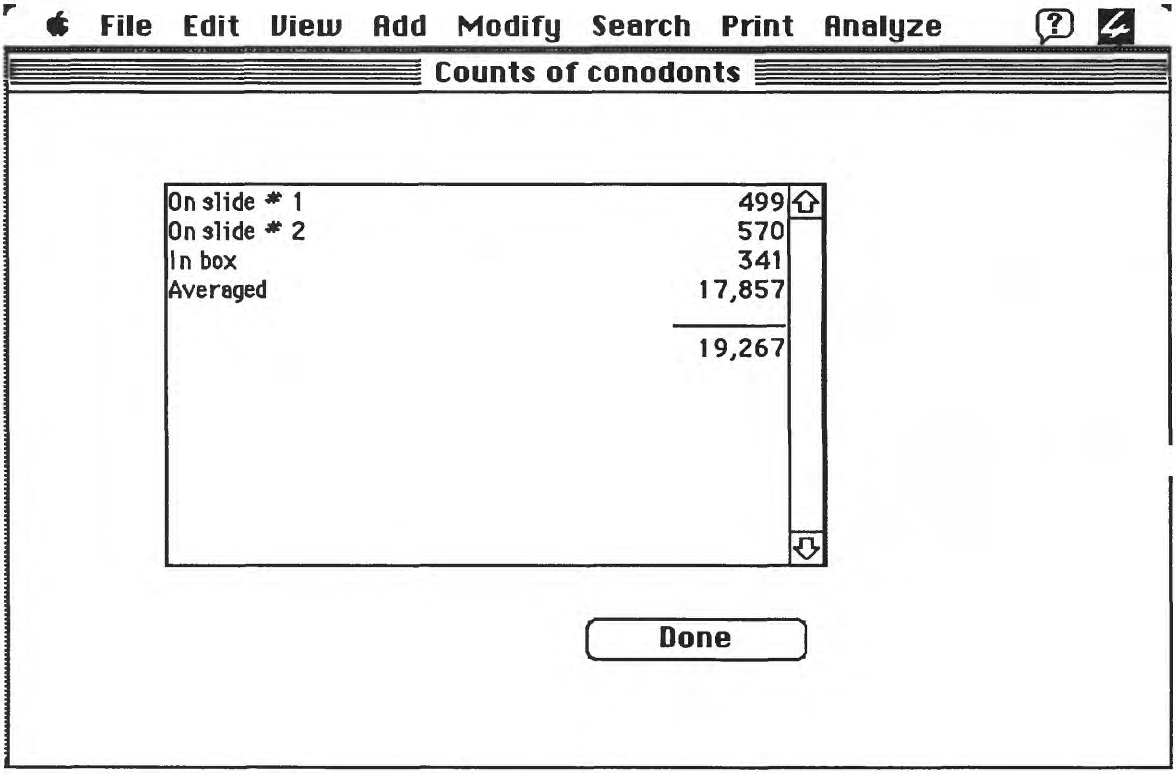
CAI VALUE: 2

REMARKS: This is meant to be an example of the remarks that can be entered when this report is generated.

Taxonomic names are constantly undergoing revision. This report should not be quoted or paraphrased in publication without my final recheck.

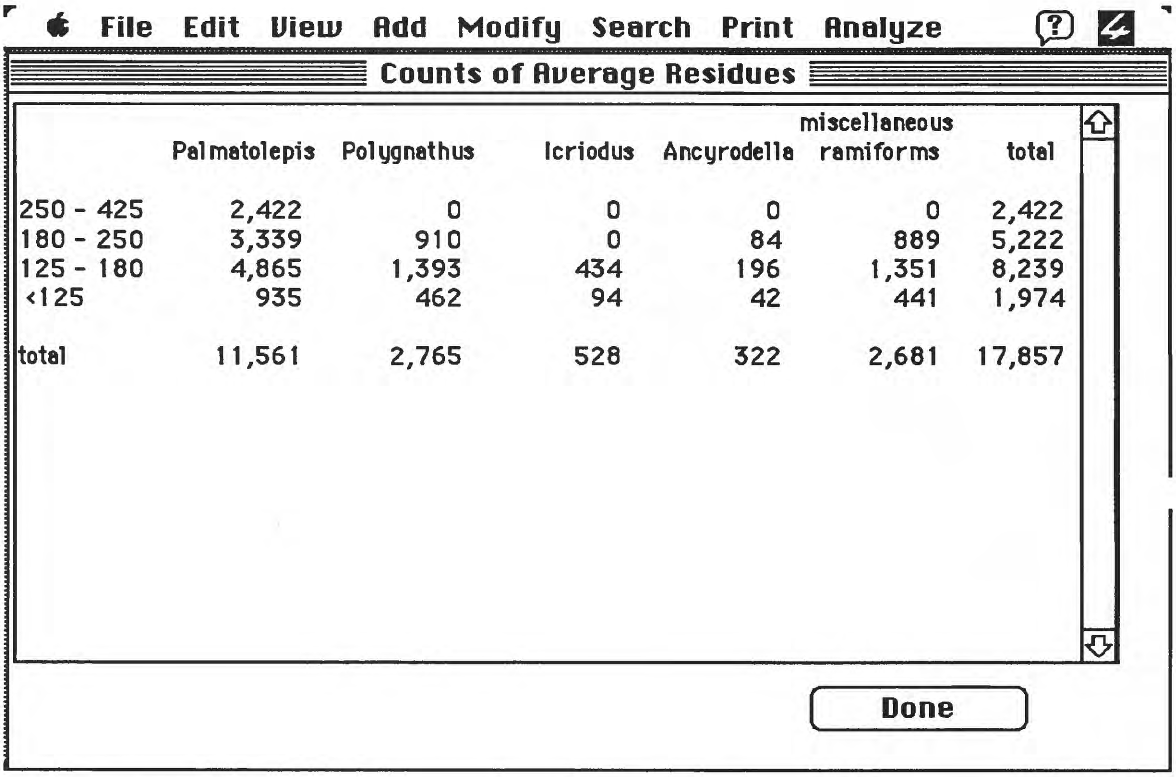
SIGNATURE______________________________ DATE______________

FIGURE 24. — (continued)



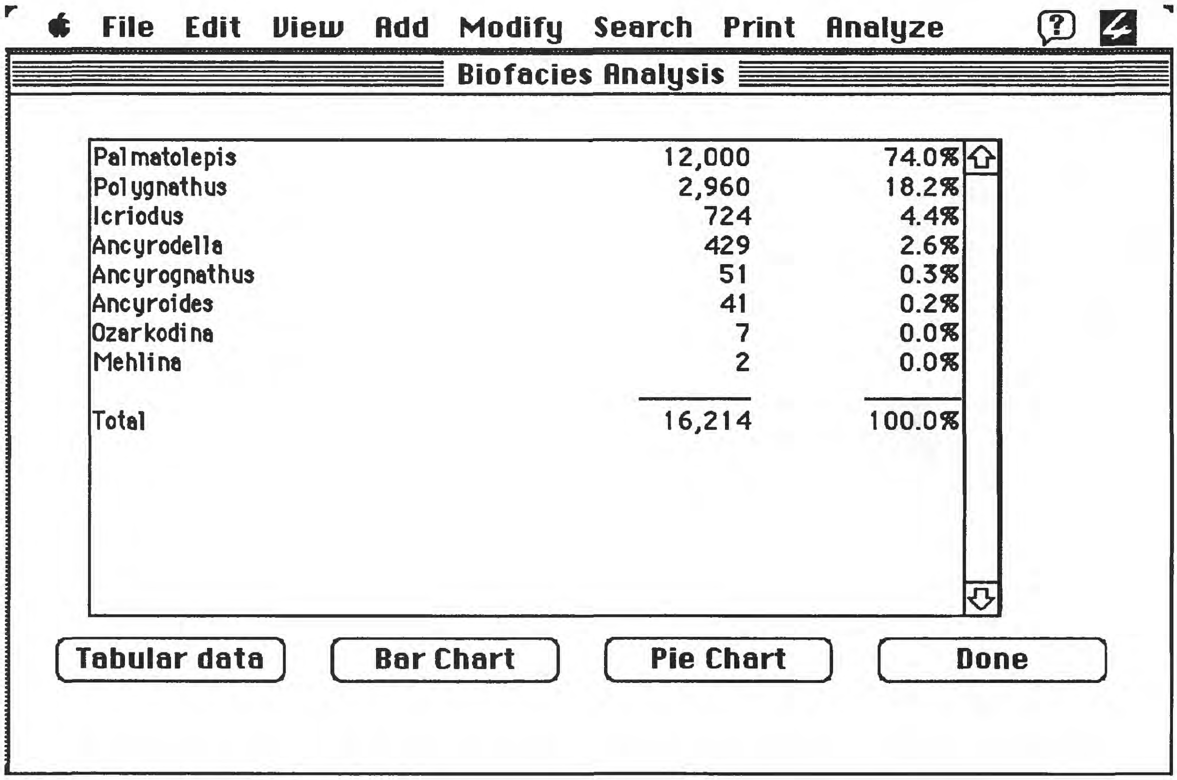
```
On slide # 1                499
On slide # 2                570
In box                      341
Averaged                 17,857
                         ------
                         19,267
```

FIGURE 25. — Output format used by Analyze Totals



	Palmatolepis	Polygnathus	Icriodus	Ancyrodella	miscellaneous ramiforms	total
250 - 425	2,422	0	0	0	0	2,422
180 - 250	3,339	910	0	84	889	5,222
125 - 180	4,865	1,393	434	196	1,351	8,239
<125	935	462	94	42	441	1,974
total	11,561	2,765	528	322	2,681	17,857

FIGURE 26. — Output format used by Analyze Averaged data



```
Palmatolepis              12,000      74.0%
Polygnathus                2,960      18.2%
Icriodus                     724       4.4%
Ancyrodella                  429       2.6%
Ancyrognathus                 51       0.3%
Ancyroides                    41       0.2%
Ozarkodina                     7       0.0%
Mehlina                        2       0.0%
                          ______     ______
Total                     16,214     100.0%
```

FIGURE 27. — Tabular data output format used by Analyze Biofacies

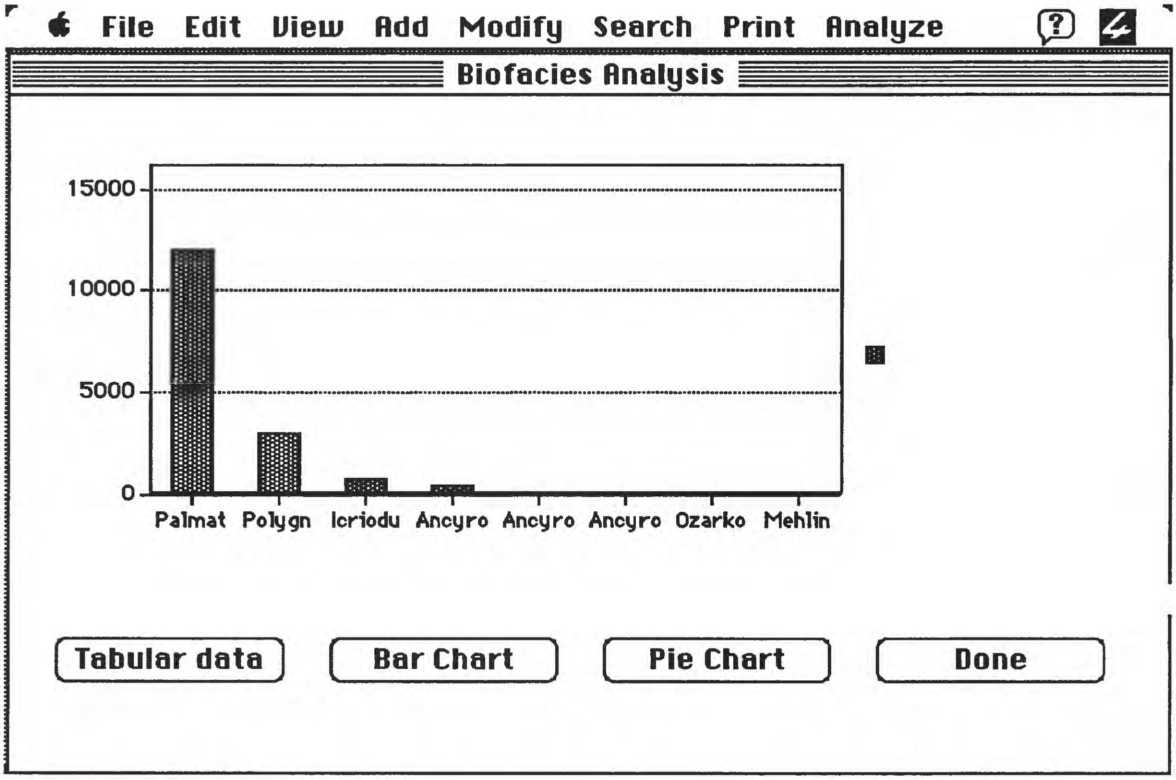


FIGURE 28. — Bar chart output format used by Analyze Biofacies

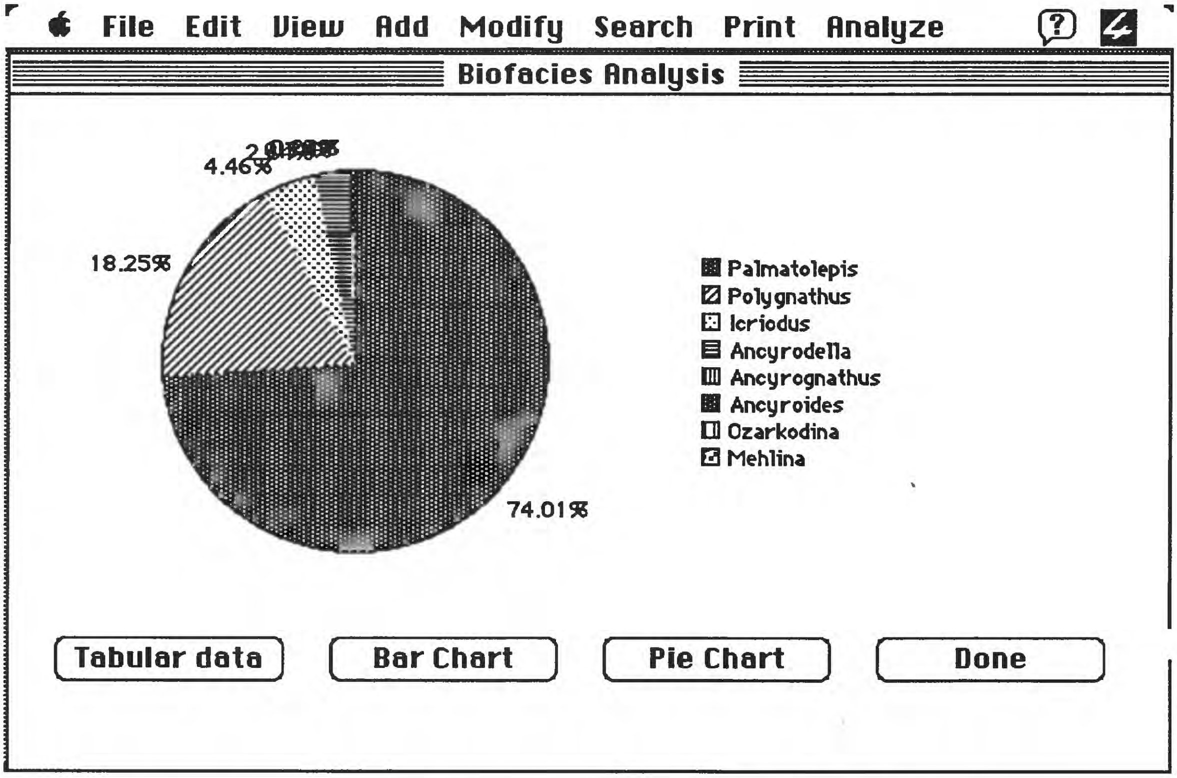
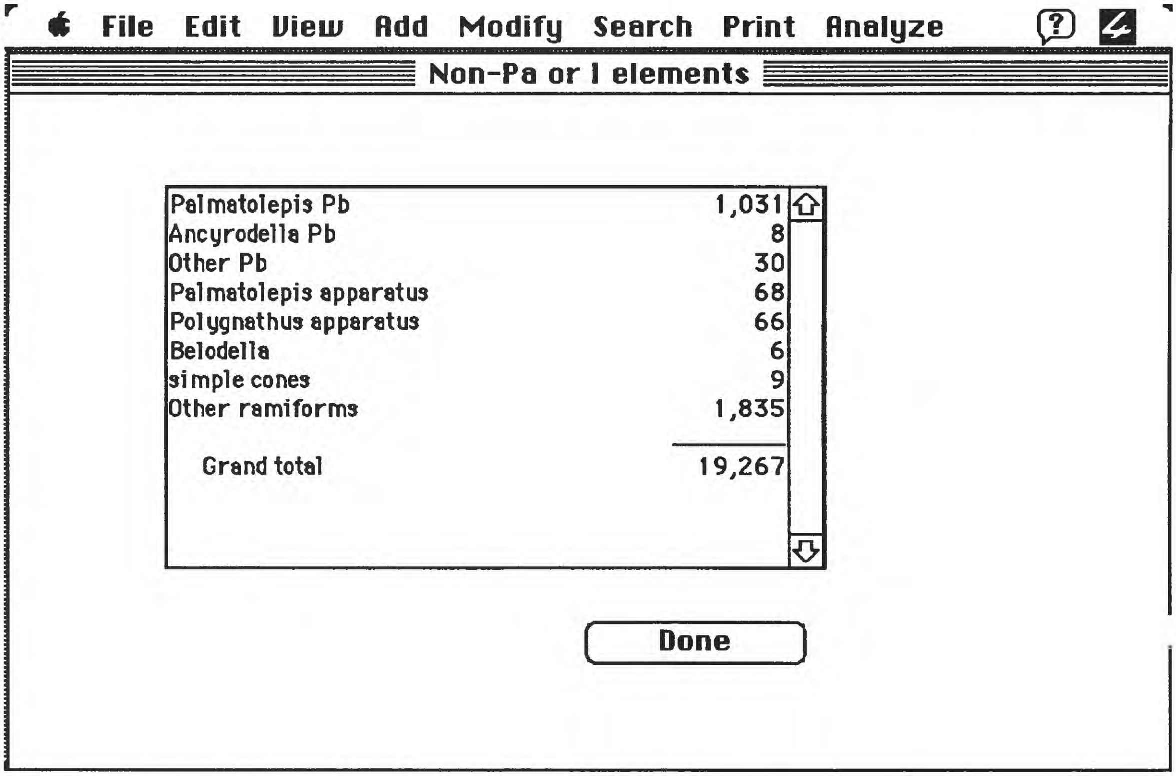


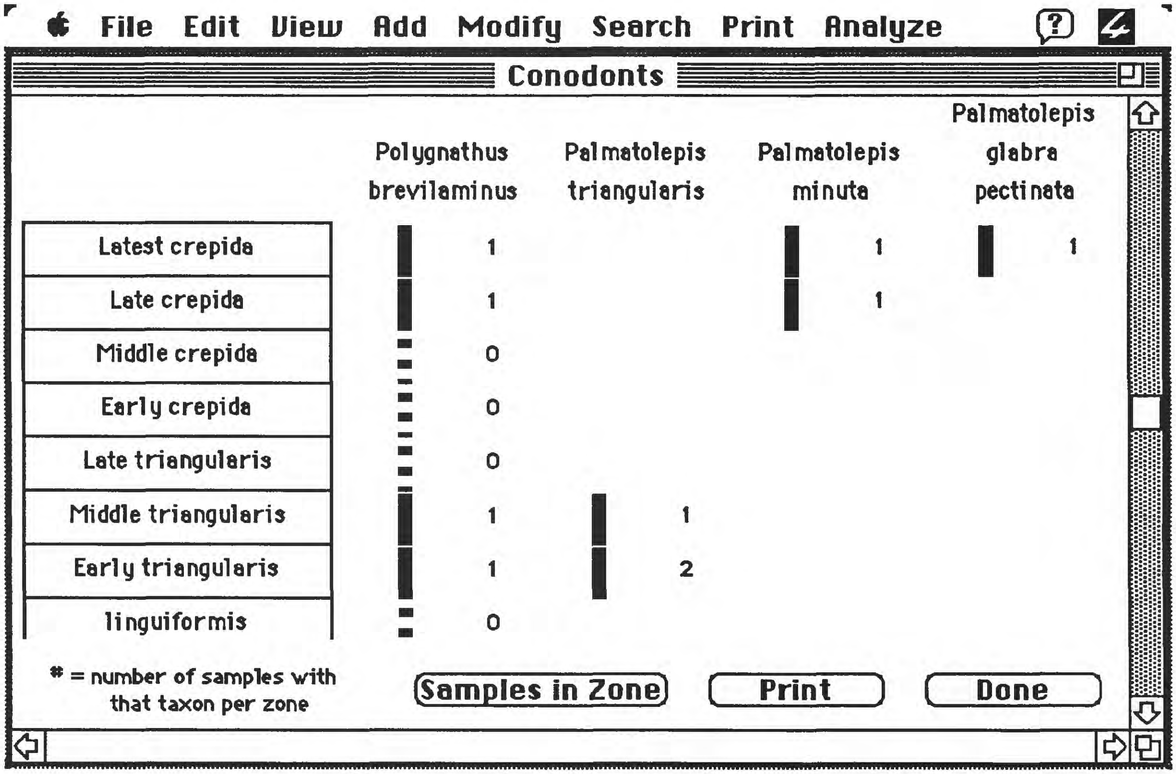
FIGURE 29. — Pie chart output format used by Analyze Biofacies



Non-Pa or I elements

```
Palmatolepis Pb                      1,031
Ancyrodella Pb                           8
Other Pb                                30
Palmatolepis apparatus                  68
Polygnathus apparatus                   66
Belodella                                6
simple cones                             9
Other ramiforms                      1,835
                                   -------
   Grand total                      19,267
```

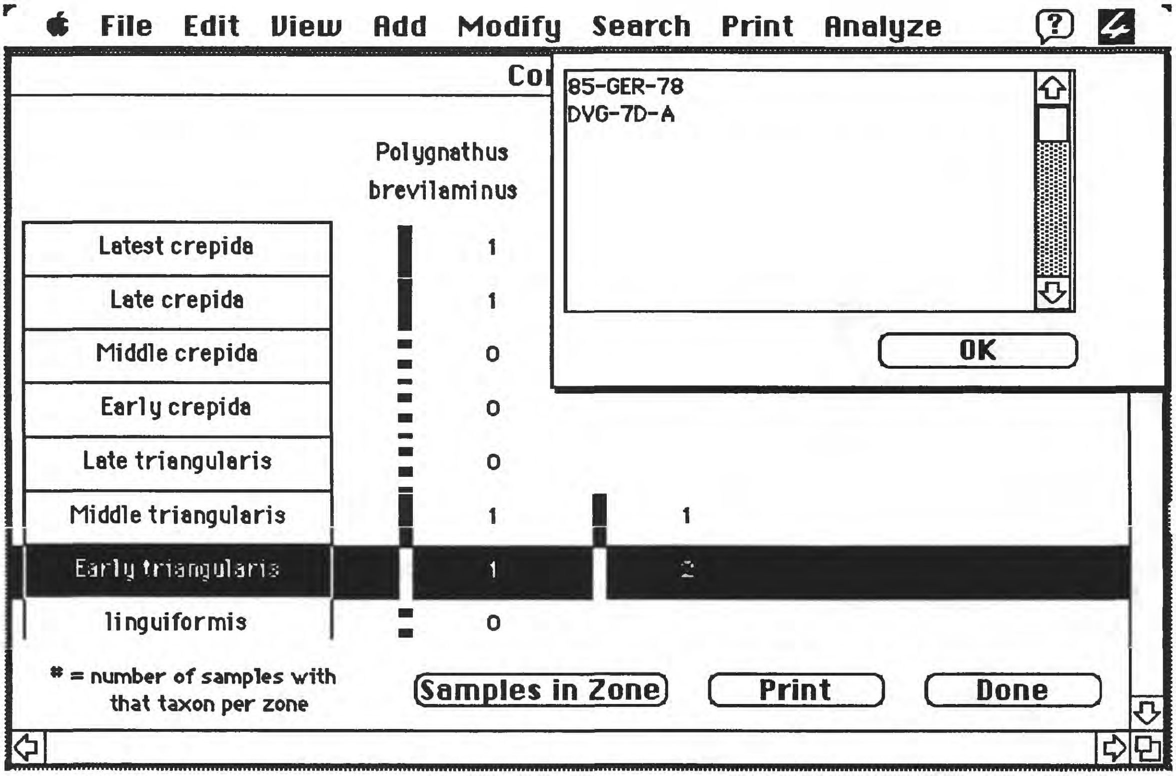
FIGURE 30. — Output format used by Analyze Non Pa



	Polygnathus brevilaminus	Palmatolepis triangularis	Palmatolepis minuta	Palmatolepis glabra pectinata
Latest crepida	1		1	1
Late crepida	1		1	
Middle crepida	0			
Early crepida	0			
Late triangularis	0			
Middle triangularis	1	1		
Early triangularis	1	2		
linguiformis	0			

= number of samples with that taxon per zone

FIGURE 31. — Output format used by Analyze Range Chart

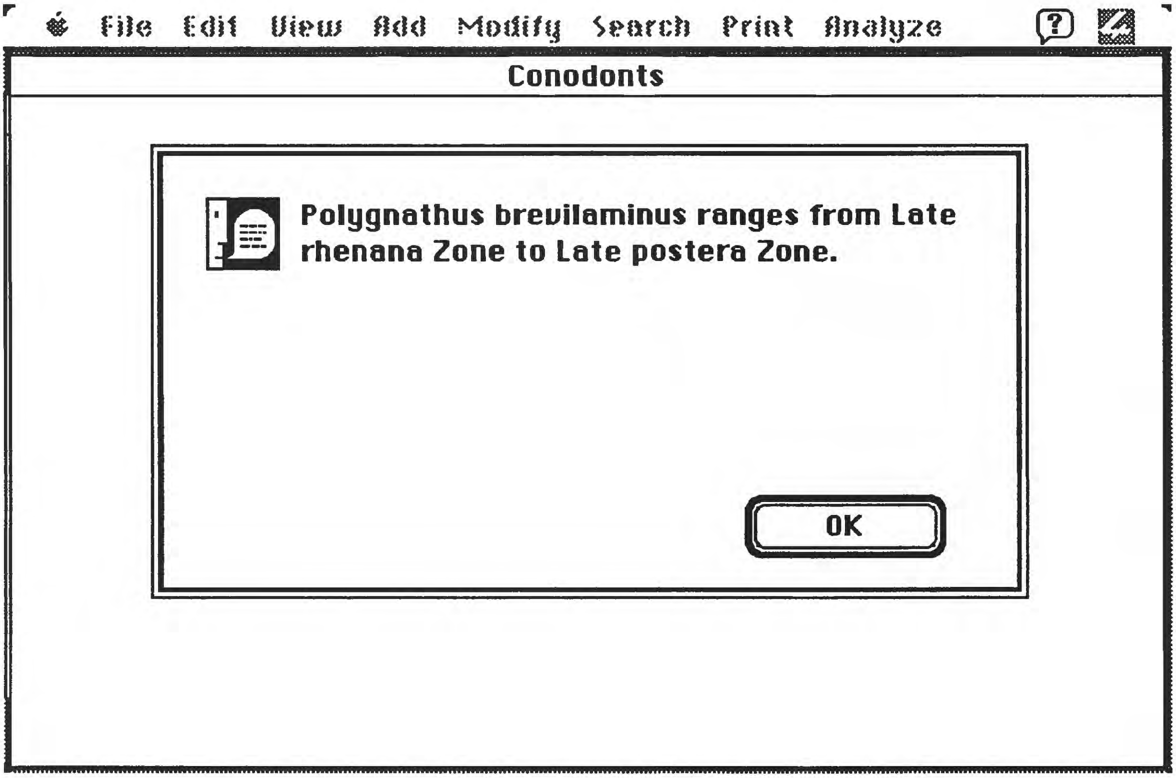


85-GER-78
DVG-7D-A

	Polygnathus brevilaminus	
Latest crepida	1	
Late crepida	1	
Middle crepida	0	
Early crepida	0	
Late triangularis	0	
Middle triangularis	1	1
Early triangularis	1	2
linguiformis	0	

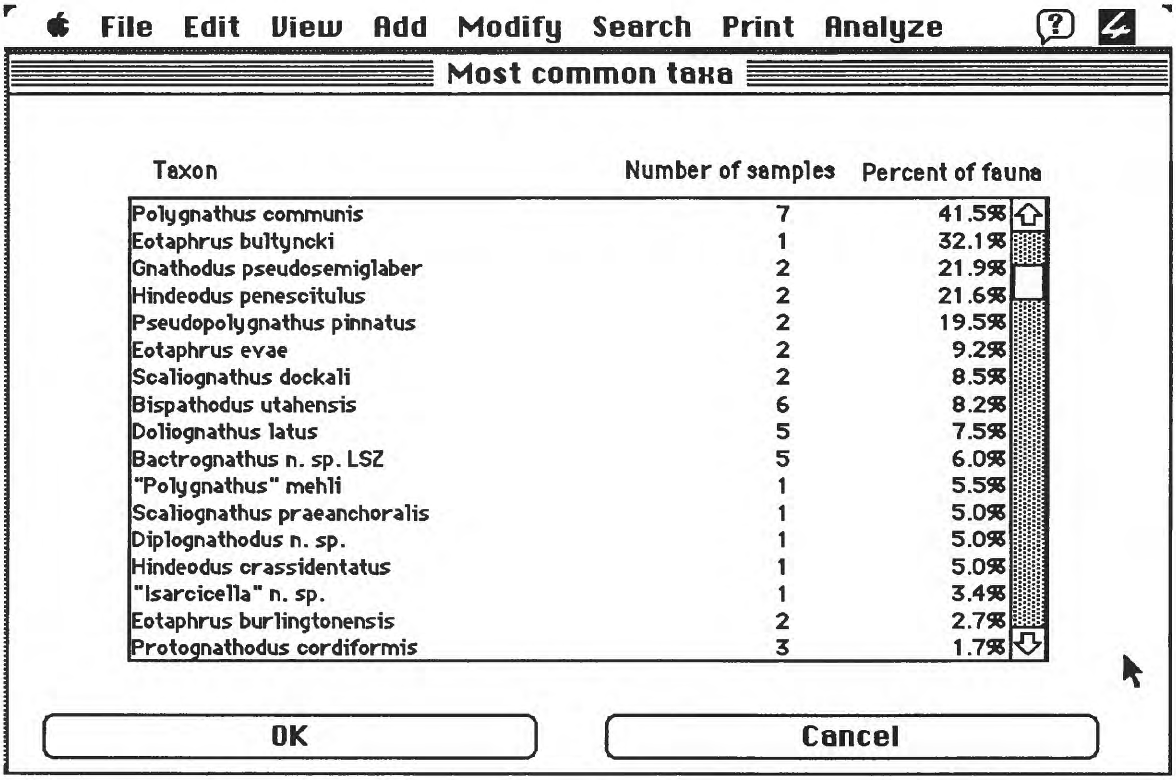
= number of samples with that taxon per zone

FIGURE 32. — Listing of samples in zone using Analyze Range Chart



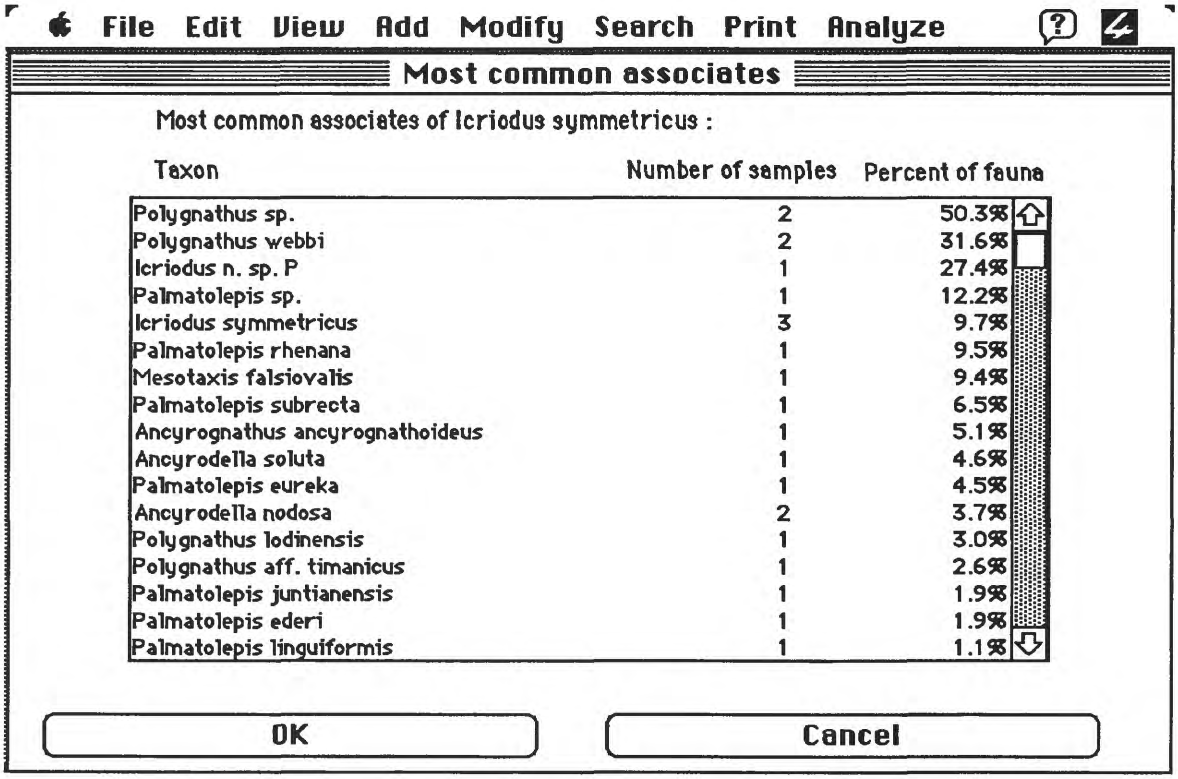
Polygnathus brevilaminus ranges from Late rhenana Zone to Late postera Zone.

FIGURE 33. — Output format used by Analyze Taxon Range



Taxon	Number of samples	Percent of fauna
Polygnathus communis	7	41.5%
Eotaphrus bultyncki	1	32.1%
Gnathodus pseudosemiglaber	2	21.9%
Hindeodus penescitulus	2	21.6%
Pseudopolygnathus pinnatus	2	19.5%
Eotaphrus evae	2	9.2%
Scaliognathus dockali	2	8.5%
Bispathodus utahensis	6	8.2%
Doliognathus latus	5	7.5%
Bactrognathus n. sp. LSZ	5	6.0%
"Polygnathus" mehli	1	5.5%
Scaliognathus praeanchoralis	1	5.0%
Diplognathodus n. sp.	1	5.0%
Hindeodus crassidentatus	1	5.0%
"Isarcicella" n. sp.	1	3.4%
Eotaphrus burlingtonensis	2	2.7%
Protognathodus cordiformis	3	1.7%

FIGURE 34. — Output format used by Analyze Most common taxa



Most common associates of Icriodus symmetricus :

Taxon	Number of samples	Percent of fauna
Polygnathus sp.	2	50.3%
Polygnathus webbi	2	31.6%
Icriodus n. sp. P	1	27.4%
Palmatolepis sp.	1	12.2%
Icriodus symmetricus	3	9.7%
Palmatolepis rhenana	1	9.5%
Mesotaxis falsiovalis	1	9.4%
Palmatolepis subrecta	1	6.5%
Ancyrognathus ancyrognathoideus	1	5.1%
Ancyrodella soluta	1	4.6%
Palmatolepis eureka	1	4.5%
Ancyrodella nodosa	2	3.7%
Polygnathus lodinensis	1	3.0%
Polygnathus aff. timanicus	1	2.6%
Palmatolepis juntianensis	1	1.9%
Palmatolepis ederi	1	1.9%
Palmatolepis linguiformis	1	1.1%

FIGURE 35. — Output format used by Analyze Most common associates